**Table S1. TBX2 ChIP- seq peaks.**

Shown are ChIP-seq peaks with a peak score threshold of 7 sorted by chromosomal position.

| Chromosome | Start | End | Name | Score | Strand | ThickStart | ThickEnd | ItemRGB | BlockCount | BlockSizes | BlockStarts | Feature | Start | End | Strand | gene_id | gene_name | p_id | transcript_id | tss_id |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr1 | 3979659 | 3979750 | MACS2_peak_1 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 21 | chr1 | unknown | gene | 3670551 | 3671348 | - | Xkr4 | Xkr4 | P15391 | NM_001011874 | TSS27105 |
| chr1 | 3979659 | 3979750 | MACS2_peak_1 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 21 | chr1 | unknown | gene | 4290845 | 4409187 | - | Rp1 | Rp1 | P17361 | NM_001195662 | TSS6138 |
| chr1 | 6274962 | 6275126 | MACS2_peak_2 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 36 | chr1 | unknown | gene | 6214661 | 6274275 | + | Rb1cc1 | Rb1cc1 | P16634 | NM_009826 | TSS4676 |
| chr1 | 6274962 | 6275126 | MACS2_peak_2 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 36 | chr1 | unknown | gene | 6359330 | 6394731 | + | Fam150a | Fam150a | P19323 | NM_001195732 | TSS1385 |
| chr1 | 6982150 | 6982276 | MACS2_peak_3 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 84 | chr1 | unknown | gene | 6487230 | 6858600 | + | St18 | St18 | P26336 | NM_001244692 | TSS14333 |
| chr1 | 6982150 | 6982276 | MACS2_peak_3 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 84 | chr1 | unknown | gene | 7088919 | 7169882 | + | Pcmtd1 | Pcmtd1 | P18329 | NM_183028 | TSS24769 |
| chr1 | 7814320 | 7814411 | MACS2_peak_4 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 70 | chr1 | unknown | gene | 7088919 | 7169882 | + | Pcmtd1 | Pcmtd1 | P18329 | NM_183028 | TSS24769 |
| chr1 | 7814320 | 7814411 | MACS2_peak_4 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 70 | chr1 | unknown | gene | 8359738 | 9299877 | - | Sntg1 | Sntg1 | P6945 | NM_001290390 | TSS11207 |
| chr1 | 9264099 | 9264207 | MACS2_peak_5 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 66 | chr1 | unknown | gene | 7088919 | 7169882 | + | Pcmtd1 | Pcmtd1 | P18329 | NM_183028 | TSS24769 |
| chr1 | 9264099 | 9264207 | MACS2_peak_5 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 66 | chr1 | unknown | gene | 9545407 | 9546621 | + | Rrs1 | Rrs1 | P15667 | NM_021511 | TSS9778 |
| chr1 | 10500855 | 10500989 | MACS2_peak_6 | 12 | + | 4.14966 | 5.12722 | 1.204 | 26 | chr1 | unknown | gene | 10137506 | 10232494 | - | Arfgef1 | Arfgef1 | P12121 | NM_001102430 | TSS25088 |
| chr1 | 10500855 | 10500989 | MACS2_peak_6 | 12 | + | 4.14966 | 5.12722 | 1.204 | 26 | chr1 | unknown | gene | 10708386 | 10865874 | - | Mir467e | Mir467e |  | NR_030645 | TSS1321 |
| chr1 | 10701195 | 10701286 | MACS2_peak_7 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 80 | chr1 | unknown | gene | 10137506 | 10232494 | - | Arfgef1 | Arfgef1 | P12121 | NM_001102430 | TSS25088 |
| chr1 | 10701195 | 10701286 | MACS2_peak_7 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 80 | chr1 | unknown | gene | 10708386 | 10865874 | - | Mir467e | Mir467e |  | NR_030645 | TSS1321 |
| chr1 | 10873654 | 10873745 | MACS2_peak_8 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 62 | chr1 | unknown | gene | 10708386 | 10865874 | - | Mir467e | Mir467e |  | NR_030645 | TSS1321 |
| chr1 | 10873654 | 10873745 | MACS2_peak_8 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 62 | chr1 | unknown | gene | 10993464 | 11297753 | + | Prex2 | Prex2 | P4722 | NM_029525 | TSS2393 |
| chr1 | 11637463 | 11637554 | MACS2_peak_9 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 25 | chr1 | unknown | gene | 10993464 | 11297753 | + | Prex2 | Prex2 | P4722 | NM_029525 | TSS2393 |
| chr1 | 11637463 | 11637554 | MACS2_peak_9 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 25 | chr1 | unknown | gene | 12425985 | 12426106 | + | Mir6341 | Mir6341 |  | NR_105759 | TSS7381 |
| chr1 | 12010522 | 12010630 | MACS2_peak_10 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 36 | chr1 | unknown | gene | 11414104 | 11974966 | + | A830018L16Rik | A830018L16Rik | P1699 | NM_001160369 | TSS20700 |
| chr1 | 12010522 | 12010630 | MACS2_peak_10 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 36 | chr1 | unknown | gene | 12425985 | 12426106 | + | Mir6341 | Mir6341 |  | NR_105759 | TSS7381 |
| chr1 | 12301021 | 12301112 | MACS2_peak_11 | 12 | + | 4.14966 | 5.12722 | 1.204 | 7 | chr1 | unknown | gene | 11414104 | 11974966 | + | A830018L16Rik | A830018L16Rik | P1699 | NM_001160369 | TSS20700 |
| chr1 | 12301021 | 12301112 | MACS2_peak_11 | 12 | + | 4.14966 | 5.12722 | 1.204 | 7 | chr1 | unknown | gene | 12425985 | 12426106 | + | Mir6341 | Mir6341 |  | NR_105759 | TSS7381 |
| chr1 | 12303269 | 12303386 | MACS2_peak_12 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 42 | chr1 | unknown | gene | 11414104 | 11974966 | + | A830018L16Rik | A830018L16Rik | P1699 | NM_001160369 | TSS20700 |
| chr1 | 12303269 | 12303386 | MACS2_peak_12 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 42 | chr1 | unknown | gene | 12425985 | 12426106 | + | Mir6341 | Mir6341 |  | NR_105759 | TSS7381 |
| chr1 | 12801854 | 12801953 | MACS2_peak_13 | 35 | + | 5.98489 | 8.51731 | 3.53253 | 44 | chr1 | unknown | gene | 12667562 | 12673090 | + | Gm17644 | Gm17644 |  | NR_045297 | TSS23459 |
| chr1 | 12801854 | 12801953 | MACS2_peak_13 | 35 | + | 5.98489 | 8.51731 | 3.53253 | 44 | chr1 | unknown | gene | 12866549 | 12990495 | - | Slco5a1 | Slco5a1 | P3874 | NM_172841 | TSS12448 |
| chr1 | 13180769 | 13180860 | MACS2_peak_14 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 43 | chr1 | unknown | gene | 13113427 | 13127163 | - | Prdm14 | Prdm14 | P25940 | NM_001081209 | TSS561 |
| chr1 | 13180769 | 13180860 | MACS2_peak_14 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 43 | chr1 | unknown | gene | 13564692 | 13589722 | - | Tram1 | Tram1 | P3457 | NM_028173 | TSS8599 |
| chr1 | 13746984 | 13747098 | MACS2_peak_15 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 49 | chr1 | unknown | gene | 13668770 | 13701383 | + | Xkr9 | Xkr9 | P14456 | NM_001011873 | TSS22448 |
| chr1 | 13746984 | 13747098 | MACS2_peak_15 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 49 | chr1 | unknown | gene | 13785684 | 13786929 | - | Gm5523 | Gm5523 |  | NR_004447 | TSS22046 |
| chr1 | 14062637 | 14062728 | MACS2_peak_16 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 44 | chr1 | unknown | gene | 13785684 | 13786929 | - | Gm5523 | Gm5523 |  | NR_004447 | TSS22046 |
| chr1 | 14062637 | 14062728 | MACS2_peak_16 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 44 | chr1 | unknown | gene | 14168957 | 14310199 | - | Eya1 | Eya1 | P2118 | NM_001252192 | TSS13463 |
| chr1 | 14066097 | 14066188 | MACS2_peak_17 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 17 | chr1 | unknown | gene | 13785684 | 13786929 | - | Gm5523 | Gm5523 |  | NR_004447 | TSS22046 |
| chr1 | 14066097 | 14066188 | MACS2_peak_17 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 17 | chr1 | unknown | gene | 14168957 | 14310199 | - | Eya1 | Eya1 | P2118 | NM_001252192 | TSS13463 |
| chr1 | 14127969 | 14128060 | MACS2_peak_18 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 54 | chr1 | unknown | gene | 13785684 | 13786929 | - | Gm5523 | Gm5523 |  | NR_004447 | TSS22046 |
| chr1 | 14127969 | 14128060 | MACS2_peak_18 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 54 | chr1 | unknown | gene | 14168957 | 14310199 | - | Eya1 | Eya1 | P2118 | NM_001252192 | TSS13463 |
| chr1 | 14463265 | 14463356 | MACS2_peak_19 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 37 | chr1 | unknown | gene | 14168957 | 14310199 | - | Eya1 | Eya1 | P2118 | NM_001252192 | TSS13463 |
| chr1 | 14463265 | 14463356 | MACS2_peak_19 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 37 | chr1 | unknown | gene | 14753345 | 14755748 | - | Msc | Msc | P2949 | NM_010827 | TSS18863 |
| chr1 | 15630552 | 15630672 | MACS2_peak_20 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 74 | chr1 | unknown | gene | 14872647 | 14918835 | - | Trpa1 | Trpa1 | P3256 | NM_177781 | TSS13378 |
| chr1 | 15630552 | 15630672 | MACS2_peak_20 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 74 | chr1 | unknown | gene | 15805645 | 15843082 | + | Terf1 | Terf1 | P3266 | NM_009352 | TSS6861 |
| chr1 | 15805295 | 15805386 | MACS2_peak_21 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 37 | chr1 | unknown | gene | 15312451 | 15711629 | + | Kcnb2 | Kcnb2 | P6376 | NM_001098528 | TSS26068 |
| chr1 | 15805295 | 15805386 | MACS2_peak_21 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 37 | chr1 | unknown | gene | 15805645 | 15843082 | + | Terf1 | Terf1 | P3266 | NM_009352 | TSS6861 |
| chr1 | 16308213 | 16308360 | MACS2_peak_22 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 77 | chr1 | unknown | gene | 16105881 | 16131417 | + | Rdh10 | Rdh10 | P9642 | NM_133832 | TSS118 |
| chr1 | 16308213 | 16308360 | MACS2_peak_22 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 77 | chr1 | unknown | gene | 16540787 | 16619338 | - | Ube2w | Ube2w | P3981 | NM_001271016 | TSS4923 |
| chr1 | 17077068 | 17077159 | MACS2_peak_23 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 23 | chr1 | unknown | gene | 16688455 | 16709537 | + | Ly96 | Ly96 | P23854 | NM_001159711 | TSS18488 |
| chr1 | 17077068 | 17077159 | MACS2_peak_23 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 23 | chr1 | unknown | gene | 17145372 | 17161509 | + | Gdap1 | Gdap1 | P21457 | NM_010267 | TSS17987 |
| chr1 | 17154751 | 17154842 | MACS2_peak_24 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 27 | chr1 | unknown | gene | 16994939 | 17097604 | - | Jph1 | Jph1 | P8024 | NM_020604 | TSS1235 |
| chr1 | 17154751 | 17154842 | MACS2_peak_24 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 27 | chr1 | unknown | gene | 17601900 | 17624970 | + | Pi15 | Pi15 | P26779 | NM_053191 | TSS7080 |
| chr1 | 17565428 | 17565547 | MACS2_peak_25 | 30 | + | 5.71265 | 7.93979 | 3.00019 | 42 | chr1 | unknown | gene | 17145372 | 17161509 | + | Gdap1 | Gdap1 | P21457 | NM_010267 | TSS17987 |
| chr1 | 17565428 | 17565547 | MACS2_peak_25 | 30 | + | 5.71265 | 7.93979 | 3.00019 | 42 | chr1 | unknown | gene | 17601900 | 17624970 | + | Pi15 | Pi15 | P26779 | NM_053191 | TSS7080 |
| chr1 | 21318955 | 21319046 | MACS2_peak_26 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 70 | chr1 | unknown | gene | 21285245 | 21298312 | - | Gm4956 | Gm4956 |  | NR_002858 | TSS22476 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr1 | 21318955 | 21319046 | MACS2_peak_26 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 70 | chr1 | unknown | gene | 21349676 | 21351093 | + | Khdc1a | Khdc1a | P6204 | NM_183322 | TSS23880 |
| chr1 | 21807425 | 21807575 | MACS2_peak_27 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 79 | chr1 | unknown | gene | 21383555 | 21384899 | + | Khdc1b | Khdc1b | P19992 | NM_001113187 | TSS18035 |
| chr1 | 21807425 | 21807575 | MACS2_peak_27 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 79 | chr1 | unknown | gene | 22288421 | 22805724 | - | Rims1 | Rims1 | P20713 | NM_183018 | TSS19892 |
| chr1 | 21916006 | 21916097 | MACS2_peak_28 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 23 | chr1 | unknown | gene | 21383555 | 21384899 | + | Khdc1b | Khdc1b | P19992 | NM_001113187 | TSS18035 |
| chr1 | 21916006 | 21916097 | MACS2_peak_28 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 23 | chr1 | unknown | gene | 22288421 | 22805724 | - | Rims1 | Rims1 | P20713 | NM_183018 | TSS19892 |
| chr1 | 22021035 | 22021133 | MACS2_peak_29 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 11 | chr1 | unknown | gene | 21398402 | 21961581 | - | Kcnq5 | Kcnq5 | P22432 | NM_001160139 | TSS2430 |
| chr1 | 22021035 | 22021133 | MACS2_peak_29 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 11 | chr1 | unknown | gene | 22288421 | 22805724 | - | Rims1 | Rims1 | P20713 | NM_183018 | TSS19892 |
| chr1 | 22706558 | 22706693 | MACS2_peak_30 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 61 | chr1 | unknown | gene | 21398402 | 21961581 | - | Kcnq5 | Kcnq5 | P22432 | NM_001160139 | TSS2430 |
| chr1 | 22706558 | 22706693 | MACS2_peak_30 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 61 | chr1 | unknown | gene | 23100473 | 23102231 | - | 4933415F23Rik | 4933415F23Rik | P19747 | NM_025746 | TSS19213 |
| chr1 | 23247313 | 23247415 | MACS2_peak_31 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 22 | chr1 | unknown | gene | 23100473 | 23102231 | - | 4933415F23Rik | 4933415F23Rik | P19747 | NM_025746 | TSS19213 |
| chr1 | 23247313 | 23247415 | MACS2_peak_31 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 22 | chr1 | unknown | gene | 23272268 | 23272339 | + | Mir30a | Mir30a | | NR_029533 | TSS12212 |
| chr1 | 24611597 | 24611959 | MACS2_peak_32 | 22 | + | 2.99129 | 6.95652 | 2.23828 | 26 | chr1 | unknown | gene | 24257682 | 24587437 | - | Col19a1 | Col19a1 | P8637 | NM_007733 | TSS8880 |
| chr1 | 24611597 | 24611959 | MACS2_peak_32 | 22 | + | 2.99129 | 6.95652 | 2.23828 | 26 | chr1 | unknown | gene | 24678543 | 24762736 | + | Lmbrd1 | Lmbrd1 | P2330 | NM_026719 | TSS4245 |
| chr1 | 24613071 | 24613623 | MACS2_peak_33 | 65 | + | 3.88544 | 11.76038 | 6.59546 | 44 | chr1 | unknown | gene | 24257682 | 24587437 | - | Col19a1 | Col19a1 | P8637 | NM_007733 | TSS8880 |
| chr1 | 24613071 | 24613623 | MACS2_peak_33 | 65 | + | 3.88544 | 11.76038 | 6.59546 | 44 | chr1 | unknown | gene | 24678543 | 24762736 | + | Lmbrd1 | Lmbrd1 | P2330 | NM_026719 | TSS4245 |
| chr1 | 24614751 | 24614993 | MACS2_peak_34 | 72 | + | 3.99241 | 12.40248 | 7.21821 | 84 | chr1 | unknown | gene | 24257682 | 24587437 | - | Col19a1 | Col19a1 | P8637 | NM_007733 | TSS8880 |
| chr1 | 24614751 | 24614993 | MACS2_peak_34 | 72 | + | 3.99241 | 12.40248 | 7.21821 | 84 | chr1 | unknown | gene | 24678543 | 24762736 | + | Lmbrd1 | Lmbrd1 | P2330 | NM_026719 | TSS4245 |
| chr1 | 24615683 | 24615779 | MACS2_peak_35 | 31 | + | 3.21287 | 8.06804 | 3.12116 | 38 | chr1 | unknown | gene | 24257682 | 24587437 | - | Col19a1 | Col19a1 | P8637 | NM_007733 | TSS8880 |
| chr1 | 24615683 | 24615779 | MACS2_peak_35 | 31 | + | 3.21287 | 8.06804 | 3.12116 | 38 | chr1 | unknown | gene | 24678543 | 24762736 | + | Lmbrd1 | Lmbrd1 | P2330 | NM_026719 | TSS4245 |
| chr1 | 24622029 | 24622120 | MACS2_peak_36 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 61 | chr1 | unknown | gene | 24257682 | 24587437 | - | Col19a1 | Col19a1 | P8637 | NM_007733 | TSS8880 |
| chr1 | 24622029 | 24622120 | MACS2_peak_36 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 61 | chr1 | unknown | gene | 24678543 | 24762736 | + | Lmbrd1 | Lmbrd1 | P2330 | NM_026719 | TSS4245 |
| chr1 | 25370565 | 25370656 | MACS2_peak_37 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 48 | chr1 | unknown | gene | 25276403 | 25276946 | - | Gm20172 | Gm20172 | P461 | NM_001204913 | TSS27614 |
| chr1 | 25370565 | 25370656 | MACS2_peak_37 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 48 | chr1 | unknown | gene | 26681800 | 26687426 | - | 4931408C20Rik | 4931408C20Rik | P18189 | NM_001033764 | TSS12422 |
| chr1 | 25705412 | 25705503 | MACS2_peak_38 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 4 | chr1 | unknown | gene | 25276403 | 25276946 | - | Gm20172 | Gm20172 | P461 | NM_001204913 | TSS27614 |
| chr1 | 25705412 | 25705503 | MACS2_peak_38 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 4 | chr1 | unknown | gene | 26681800 | 26687426 | - | 4931408C20Rik | 4931408C20Rik | P18189 | NM_001033764 | TSS12422 |
| chr1 | 26687077 | 26687435 | MACS2_peak_39 | 53 | + | 6.64792 | 10.4357 | 5.32658 | 276 | chr1 | unknown | gene | 25067475 | 25829707 | - | Adgrb3 | Adgrb3 | P3687 | NM_175642 | TSS20402 |
| chr1 | 26687077 | 26687435 | MACS2_peak_39 | 53 | + | 6.64792 | 10.4357 | 5.32658 | 276 | chr1 | unknown | gene | 28776121 | 28780198 | - | Gm597 | Gm597 | P4916 | NM_001013750 | TSS24877 |
| chr1 | 26894496 | 26894587 | MACS2_peak_40 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 15 | chr1 | unknown | gene | 26681800 | 26687426 | - | 4931408C20Rik | 4931408C20Rik | P18189 | NM_001033764 | TSS12422 |
| chr1 | 26894496 | 26894587 | MACS2_peak_40 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 15 | chr1 | unknown | gene | 28776121 | 28780198 | - | Gm597 | Gm597 | P4916 | NM_001013750 | TSS24877 |
| chr1 | 27661490 | 27661617 | MACS2_peak_41 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 8 | chr1 | unknown | gene | 26681800 | 26687426 | - | 4931408C20Rik | 4931408C20Rik | P18189 | NM_001033764 | TSS12422 |
| chr1 | 27661490 | 27661617 | MACS2_peak_41 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 8 | chr1 | unknown | gene | 28776121 | 28780198 | - | Gm597 | Gm597 | P4916 | NM_001013750 | TSS24877 |
| chr1 | 28115586 | 28115677 | MACS2_peak_42 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 85 | chr1 | unknown | gene | 26681800 | 26687426 | - | 4931408C20Rik | 4931408C20Rik | P18189 | NM_001033764 | TSS12422 |
| chr1 | 28115586 | 28115677 | MACS2_peak_42 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 85 | chr1 | unknown | gene | 28776121 | 28780198 | - | Gm597 | Gm597 | P4916 | NM_001013750 | TSS24877 |
| chr1 | 28633780 | 28633894 | MACS2_peak_43 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 56 | chr1 | unknown | gene | 26681800 | 26687426 | - | 4931408C20Rik | 4931408C20Rik | P18189 | NM_001033764 | TSS12422 |
| chr1 | 28633780 | 28633894 | MACS2_peak_43 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 56 | chr1 | unknown | gene | 28776121 | 28780198 | - | Gm597 | Gm597 | P4916 | NM_001013750 | TSS24877 |
| chr1 | 28662960 | 28663051 | MACS2_peak_44 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 9 | chr1 | unknown | gene | 26681800 | 26687426 | - | 4931408C20Rik | 4931408C20Rik | P18189 | NM_001033764 | TSS12422 |
| chr1 | 28662960 | 28663051 | MACS2_peak_44 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 9 | chr1 | unknown | gene | 28776121 | 28780198 | - | Gm597 | Gm597 | P4916 | NM_001013750 | TSS24877 |
| chr1 | 31513640 | 31513731 | MACS2_peak_45 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 81 | chr1 | unknown | gene | 31264846 | 31268061 | + | Gm4850 | Gm4850 | | NR_015347 | TSS5538 |
| chr1 | 31513640 | 31513731 | MACS2_peak_45 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 81 | chr1 | unknown | gene | 32172805 | 32657541 | + | Khdrbs2 | Khdrbs2 | P24307 | NM_133235 | TSS18753 |
| chr1 | 32153692 | 32153783 | MACS2_peak_46 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 27 | chr1 | unknown | gene | 31264846 | 31268061 | + | Gm4850 | Gm4850 | | NR_015347 | TSS5538 |
| chr1 | 32153692 | 32153783 | MACS2_peak_46 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 27 | chr1 | unknown | gene | 32172805 | 32657541 | + | Khdrbs2 | Khdrbs2 | P24307 | NM_133235 | TSS18753 |
| chr1 | 32552486 | 32552577 | MACS2_peak_47 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 80 | chr1 | unknown | gene | 32543545 | 32546827 | - | Gm5415 | Gm5415 | P1922 | NM_001164286 | TSS6791 |
| chr1 | 32552486 | 32552577 | MACS2_peak_47 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 80 | chr1 | unknown | gene | 33453807 | 33669794 | - | Prim2 | Prim2 | P16482 | NM_008922 | TSS17647 |
| chr1 | 35291028 | 35291150 | MACS2_peak_48 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 32 | chr1 | unknown | gene | 34849958 | 34877047 | + | Plekhb2 | Plekhb2 | P360 | NM_175421 | TSS27531 |
| chr1 | 35291028 | 35291150 | MACS2_peak_48 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 32 | chr1 | unknown | gene | 36068399 | 36104221 | + | Hs6st1 | Hs6st1 | P18861 | NM_015818 | TSS19783 |
| chr1 | 37871204 | 37871295 | MACS2_peak_49 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 24 | chr1 | unknown | gene | 37754571 | 37865298 | - | Tsga10 | Tsga10 | P12251 | NM_207228 | TSS16720 |
| chr1 | 37871204 | 37871295 | MACS2_peak_49 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 24 | chr1 | unknown | gene | 37872205 | 37875986 | + | Lipt1 | Lipt1 | P1582 | NM_001037918 | TSS7072 |
| chr1 | 40085342 | 40085433 | MACS2_peak_50 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 55 | chr1 | unknown | gene | 39900912 | 40024712 | + | Map4k4 | Map4k4 | P25008 | NM_008696 | TSS22746 |
| chr1 | 40085342 | 40085433 | MACS2_peak_50 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 55 | chr1 | unknown | gene | 40225079 | 40313393 | + | Il1r1 | Il1r1 | P4011 | NM_008362 | TSS10812 |
| chr1 | 40592241 | 40592332 | MACS2_peak_51 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 26 | chr1 | unknown | gene | 40515361 | 40549088 | + | Il18rap | Il18rap | P3293 | NM_010553 | TSS2560 |
| chr1 | 40592241 | 40592332 | MACS2_peak_51 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 26 | chr1 | unknown | gene | 40681711 | 40767999 | + | Slc9a2 | Slc9a2 | P19005 | NM_001033289 | TSS18075 |
| chr1 | 41314019 | 41314110 | MACS2_peak_52 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 23 | chr1 | unknown | gene | 41167559 | 41181252 | - | 4930448I06Rik | 4930448I06Rik | | NR_040475 | TSS20451 |
| chr1 | 41314019 | 41314110 | MACS2_peak_52 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 23 | chr1 | unknown | gene | 42648199 | 42694825 | - | Pantr1 | Pantr1 | | NR_027826 | TSS19386 |
| chr1 | 45760623 | 45760767 | MACS2_peak_53 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 54 | chr1 | unknown | gene | 45374330 | 45502914 | - | Col5a2 | Col5a2 | P5846 | NM_007737 | TSS22449 |
| chr1 | 45760623 | 45760767 | MACS2_peak_53 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 54 | chr1 | unknown | gene | 45795500 | 45823515 | + | Wdr75 | Wdr75 | P24619 | NM_028599 | TSS3235 |
| chr1 | 47473248 | 47473339 | MACS2_peak_54 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 42 | chr1 | unknown | gene | 47467020 | 47467125 | - | Mir6350 | Mir6350 | | NR_105768 | TSS354 |
| chr1 | 47473248 | 47473339 | MACS2_peak_54 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 42 | chr1 | unknown | gene | 50927522 | 51185481 | + | Tmeff2 | Tmeff2 | P18130 | NM_019790 | TSS19054 |
| chr1 | 47663873 | 47664045 | MACS2_peak_55 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 154 | chr1 | unknown | gene | 47467020 | 47467125 | - | Mir6350 | Mir6350 | | NR_105768 | TSS354 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr1 | 47663873 | 47664045 | MACS2_peak_55 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 154 | chr1 | unknown | gene | 50927522 | 51185481 | + | Tmeff2 | Tmeff2 | P18130 | NM_019790 | TSS19054 |
| chr1 | 50358375 | 50358466 | MACS2_peak_56 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 51 | chr1 | unknown | gene | 47467020 | 47467125 | - | Mir6350 | Mir6350 | | NR_105768 | TSS354 |
| chr1 | 50358375 | 50358466 | MACS2_peak_56 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 51 | chr1 | unknown | gene | 50927522 | 51185481 | + | Tmeff2 | Tmeff2 | P18130 | NM_019790 | TSS19054 |
| chr1 | 50474683 | 50474774 | MACS2_peak_57 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 54 | chr1 | unknown | gene | 47467020 | 47467125 | - | Mir6350 | Mir6350 | | NR_105768 | TSS354 |
| chr1 | 50474683 | 50474774 | MACS2_peak_57 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 54 | chr1 | unknown | gene | 50927522 | 51185481 | + | Tmeff2 | Tmeff2 | P18130 | NM_019790 | TSS19054 |
| chr1 | 50808867 | 50808970 | MACS2_peak_58 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 90 | chr1 | unknown | gene | 47467020 | 47467125 | - | Mir6350 | Mir6350 | | NR_105768 | TSS354 |
| chr1 | 50808867 | 50808970 | MACS2_peak_58 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 90 | chr1 | unknown | gene | 50927522 | 51185481 | + | Tmeff2 | Tmeff2 | P18130 | NM_019790 | TSS19054 |
| chr1 | 50979877 | 50979968 | MACS2_peak_59 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 73 | chr1 | unknown | gene | 47467020 | 47467125 | - | Mir6350 | Mir6350 | | NR_105768 | TSS354 |
| chr1 | 50979877 | 50979968 | MACS2_peak_59 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 73 | chr1 | unknown | gene | 51218385 | 51333779 | - | 9330175M20Rik | 9330175M20Rik | | NR_045151 | TSS22935 |
| chr1 | 51074232 | 51074395 | MACS2_peak_60 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 43 | chr1 | unknown | gene | 47467020 | 47467125 | - | Mir6350 | Mir6350 | | NR_105768 | TSS354 |
| chr1 | 51074232 | 51074395 | MACS2_peak_60 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 43 | chr1 | unknown | gene | 51218385 | 51333779 | - | 9330175M20Rik | 9330175M20Rik | | NR_045151 | TSS22935 |
| chr1 | 51241810 | 51241901 | MACS2_peak_61 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 39 | chr1 | unknown | gene | 50927522 | 51185481 | + | Tmeff2 | Tmeff2 | P18130 | NM_019790 | TSS19054 |
| chr1 | 51241810 | 51241901 | MACS2_peak_61 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 39 | chr1 | unknown | gene | 51289125 | 51301422 | + | Sdpr | Sdpr | P18810 | NM_138741 | TSS19159 |
| chr1 | 51823362 | 51823453 | MACS2_peak_62 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 25 | chr1 | unknown | gene | 51469487 | 51477915 | - | Nabp1 | Nabp1 | P2124 | NM_028696 | TSS13786 |
| chr1 | 51823362 | 51823453 | MACS2_peak_62 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 25 | chr1 | unknown | gene | 51987147 | 52106936 | + | Stat4 | Stat4 | P5657 | NM_001308266 | TSS26966 |
| chr1 | 52217655 | 52217746 | MACS2_peak_63 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 58 | chr1 | unknown | gene | 52119437 | 52159297 | + | Stat1 | Stat1 | P16907 | NM_001205314 | TSS14591 |
| chr1 | 52217655 | 52217746 | MACS2_peak_63 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 58 | chr1 | unknown | gene | 52455848 | 52500448 | - | Nab1 | Nab1 | P5933 | NM_008667 | TSS9319 |
| chr1 | 53076258 | 53076349 | MACS2_peak_64 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 43 | chr1 | unknown | gene | 53061662 | 53066631 | + | Mstn | Mstn | P3455 | NM_010834 | TSS6101 |
| chr1 | 53076258 | 53076349 | MACS2_peak_64 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 43 | chr1 | unknown | gene | 53158576 | 53187601 | - | 1700019A02Rik | 1700019A02Rik | P547 | NM_027070 | TSS18156 |
| chr1 | 53397677 | 53397768 | MACS2_peak_65 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 32 | chr1 | unknown | gene | 53344616 | 53352752 | - | Asnsd1 | Asnsd1 | P22138 | NM_133728 | TSS21309 |
| chr1 | 53397677 | 53397768 | MACS2_peak_65 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 32 | chr1 | unknown | gene | 53755511 | 53785215 | - | Stk17b | Stk17b | P22428 | NM_133810 | TSS10019 |
| chr1 | 54410553 | 54410647 | MACS2_peak_66 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 61 | chr1 | unknown | gene | 54250682 | 54368399 | + | Ccdc150 | Ccdc150 | P19714 | NM_030025 | TSS16702 |
| chr1 | 54410553 | 54410647 | MACS2_peak_66 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 61 | chr1 | unknown | gene | 54472999 | 54557580 | - | Pgap1 | Pgap1 | P25336 | NM_001163314 | TSS2104 |
| chr1 | 54667851 | 54667942 | MACS2_peak_67 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 10 | chr1 | unknown | gene | 54472999 | 54557580 | - | Pgap1 | Pgap1 | P25336 | NM_001163314 | TSS2104 |
| chr1 | 54667851 | 54667942 | MACS2_peak_67 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 10 | chr1 | unknown | gene | 54985169 | 55027366 | - | Sf3b1 | Sf3b1 | P7710 | NM_031179 | TSS7759 |
| chr1 | 55555192 | 55555358 | MACS2_peak_68 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 130 | chr1 | unknown | gene | 55300068 | 55363319 | - | Boll | Boll | P23975 | NM_001113367 | TSS12848 |
| chr1 | 55555192 | 55555358 | MACS2_peak_68 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 130 | chr1 | unknown | gene | 55931240 | 55972098 | + | 9130227L01Rik | 9130227L01Rik | | NR_045837 | TSS24325 |
| chr1 | 55817252 | 55817455 | MACS2_peak_69 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 69 | chr1 | unknown | gene | 55405945 | 55751463 | + | Plcl1 | Plcl1 | P26055 | NM_001114663 | TSS12870 |
| chr1 | 55817252 | 55817455 | MACS2_peak_69 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 69 | chr1 | unknown | gene | 55931240 | 55972098 | + | 9130227L01Rik | 9130227L01Rik | | NR_045837 | TSS24325 |
| chr1 | 56278743 | 56278834 | MACS2_peak_70 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 30 | chr1 | unknown | gene | 56018977 | 56020203 | + | 1700003I22Rik | 1700003I22Rik | | NR_126076 | TSS14567 |
| chr1 | 56278743 | 56278834 | MACS2_peak_70 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 30 | chr1 | unknown | gene | 56636050 | 56637376 | - | Hsfy2 | Hsfy2 | P1792 | NM_027661 | TSS17014 |
| chr1 | 56808607 | 56808698 | MACS2_peak_71 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 20 | chr1 | unknown | gene | 56636050 | 56637376 | - | Hsfy2 | Hsfy2 | P1792 | NM_027661 | TSS17014 |
| chr1 | 56808607 | 56808698 | MACS2_peak_71 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 20 | chr1 | unknown | gene | 56971468 | 56975196 | + | 9130024F11Rik | 9130024F11Rik | | NR_024326 | TSS19516 |
| chr1 | 56967484 | 56967575 | MACS2_peak_72 | 22 | + | 5.17464 | 6.9181 | 2.20183 | 24 | chr1 | unknown | gene | 56636050 | 56637376 | - | Hsfy2 | Hsfy2 | P1792 | NM_027661 | TSS17014 |
| chr1 | 56967484 | 56967575 | MACS2_peak_72 | 22 | + | 5.17464 | 6.9181 | 2.20183 | 24 | chr1 | unknown | gene | 56971468 | 56975196 | + | 9130024F11Rik | 9130024F11Rik | | NR_024326 | TSS19516 |
| chr1 | 57010463 | 57010564 | MACS2_peak_73 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 87 | chr1 | unknown | gene | 56971468 | 56975196 | + | 9130024F11Rik | 9130024F11Rik | | NR_024326 | TSS19516 |
| chr1 | 57010463 | 57010564 | MACS2_peak_73 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 87 | chr1 | unknown | gene | 57200644 | 57214996 | - | BC055402 | BC055402 | | NR_037990 | TSS3995 |
| chr1 | 57085374 | 57085465 | MACS2_peak_74 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 70 | chr1 | unknown | gene | 56971468 | 56975196 | + | 9130024F11Rik | 9130024F11Rik | | NR_024326 | TSS19516 |
| chr1 | 57085374 | 57085465 | MACS2_peak_74 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 70 | chr1 | unknown | gene | 57200644 | 57214996 | - | BC055402 | BC055402 | | NR_037990 | TSS3995 |
| chr1 | 57213270 | 57213361 | MACS2_peak_75 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 90 | chr1 | unknown | gene | 56971468 | 56975196 | + | 9130024F11Rik | 9130024F11Rik | | NR_024326 | TSS19516 |
| chr1 | 57213270 | 57213361 | MACS2_peak_75 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 90 | chr1 | unknown | gene | 57359221 | 57377544 | - | 4930558J18Rik | 4930558J18Rik | | NR_037999 | TSS7526 |
| chr1 | 57482617 | 57482708 | MACS2_peak_76 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 15 | chr1 | unknown | gene | 57406547 | 57415734 | + | 9430016H08Rik | 9430016H08Rik | P17356 | NM_001081181 | TSS5960 |
| chr1 | 57482617 | 57482708 | MACS2_peak_76 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 15 | chr1 | unknown | gene | 57774860 | 57946463 | + | Spats2l | Spats2l | P14803 | NM_144882 | TSS11107 |
| chr1 | 57688537 | 57688628 | MACS2_peak_77 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 9 | chr1 | unknown | gene | 57406547 | 57415734 | + | 9430016H08Rik | 9430016H08Rik | P17356 | NM_001081181 | TSS5960 |
| chr1 | 57688537 | 57688628 | MACS2_peak_77 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 9 | chr1 | unknown | gene | 57774860 | 57946463 | + | Spats2l | Spats2l | P14803 | NM_144882 | TSS11107 |
| chr1 | 57776224 | 57776315 | MACS2_peak_78 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 25 | chr1 | unknown | gene | 57406547 | 57415734 | + | 9430016H08Rik | 9430016H08Rik | P17356 | NM_001081181 | TSS5960 |
| chr1 | 57776224 | 57776315 | MACS2_peak_78 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 25 | chr1 | unknown | gene | 57955100 | 57970084 | - | Kctd18 | Kctd18 | | NR_027630 | TSS6655 |
| chr1 | 57874800 | 57874893 | MACS2_peak_79 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 82 | chr1 | unknown | gene | 57406547 | 57415734 | + | 9430016H08Rik | 9430016H08Rik | P17356 | NM_001081181 | TSS5960 |
| chr1 | 57874800 | 57874893 | MACS2_peak_79 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 82 | chr1 | unknown | gene | 57955100 | 57970084 | - | Kctd18 | Kctd18 | | NR_027630 | TSS6655 |
| chr1 | 57889377 | 57889528 | MACS2_peak_80 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 21 | chr1 | unknown | gene | 57406547 | 57415734 | + | 9430016H08Rik | 9430016H08Rik | P17356 | NM_001081181 | TSS5960 |
| chr1 | 57889377 | 57889528 | MACS2_peak_80 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 21 | chr1 | unknown | gene | 57955100 | 57970084 | - | Kctd18 | Kctd18 | | NR_027630 | TSS6655 |
| chr1 | 58391277 | 58391375 | MACS2_peak_81 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 65 | chr1 | unknown | gene | 58278325 | 58379264 | + | Aox2 | Aox2 | P16570 | NM_001008419 | TSS24063 |
| chr1 | 58391277 | 58391375 | MACS2_peak_81 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 65 | chr1 | unknown | gene | 58393135 | 58405066 | + | Bzw1 | Bzw1 | P21623 | NM_025824 | TSS9465 |
| chr1 | 59006683 | 59006774 | MACS2_peak_82 | 12 | + | 4.14966 | 5.12722 | 1.204 | 39 | chr1 | unknown | gene | 58973570 | 58994436 | + | Stradb | Stradb | P16143 | NM_172656 | TSS4496 |
| chr1 | 59006683 | 59006774 | MACS2_peak_82 | 12 | + | 4.14966 | 5.12722 | 1.204 | 39 | chr1 | unknown | gene | 59050505 | 59094860 | - | Als2cr11 | Als2cr11 | P17221 | NM_175200 | TSS1196 |
| chr1 | 59049093 | 59049184 | MACS2_peak_83 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 50 | chr1 | unknown | gene | 58973570 | 58994436 | + | Stradb | Stradb | P16143 | NM_172656 | TSS4496 |
| chr1 | 59049093 | 59049184 | MACS2_peak_83 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 50 | chr1 | unknown | gene | 59050505 | 59094860 | - | Als2cr11 | Als2cr11 | P17221 | NM_175200 | TSS1196 |
| chr1 | 59265885 | 59265976 | MACS2_peak_84 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 38 | chr1 | unknown | gene | 59162755 | 59237231 | - | Als2 | Als2 | P24628 | NM_001159948 | TSS21403 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr1 | 59265885 | 59265976 | MACS2_peak_84 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 38 | chr1 | unknown | gene | 59482146 | 59484678 | + | Fzd7 | Fzd7 | P8783 | NM_008057 | TSS24759 |
| chr1 | 59514835 | 59514926 | MACS2_peak_85 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 24 | chr1 | unknown | gene | 59482146 | 59484678 | + | Fzd7 | Fzd7 | P8783 | NM_008057 | TSS24759 |
| chr1 | 59514835 | 59514926 | MACS2_peak_85 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 24 | chr1 | unknown | gene | 59516263 | 59634262 | + | Gm973 | Gm973 | P6650 | NM_001013771 | TSS18155 |
| chr1 | 61666238 | 61666342 | MACS2_peak_86 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 43 | chr1 | unknown | gene | 61378431 | 61395904 | + | 9530026F06Rik | 9530026F06Rik | | NR_040483 | TSS2436 |
| chr1 | 61666238 | 61666342 | MACS2_peak_86 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 43 | chr1 | unknown | gene | 62703316 | 62815637 | + | Nrp2 | Nrp2 | P7296 | NM_001077405 | TSS11893 |
| chr1 | 61696948 | 61697039 | MACS2_peak_87 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 47 | chr1 | unknown | gene | 61378431 | 61395904 | + | 9530026F06Rik | 9530026F06Rik | | NR_040483 | TSS2436 |
| chr1 | 61696948 | 61697039 | MACS2_peak_87 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 47 | chr1 | unknown | gene | 62703316 | 62815637 | + | Nrp2 | Nrp2 | P7296 | NM_001077405 | TSS11893 |
| chr1 | 61919510 | 61919624 | MACS2_peak_88 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 26 | chr1 | unknown | gene | 61378431 | 61395904 | + | 9530026F06Rik | 9530026F06Rik | | NR_040483 | TSS2436 |
| chr1 | 61919510 | 61919624 | MACS2_peak_88 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 26 | chr1 | unknown | gene | 62703316 | 62815637 | + | Nrp2 | Nrp2 | P7296 | NM_001077405 | TSS11893 |
| chr1 | 62154826 | 62154917 | MACS2_peak_89 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 9 | chr1 | unknown | gene | 61378431 | 61395904 | + | 9530026F06Rik | 9530026F06Rik | | NR_040483 | TSS2436 |
| chr1 | 62154826 | 62154917 | MACS2_peak_89 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 9 | chr1 | unknown | gene | 62703316 | 62815637 | + | Nrp2 | Nrp2 | P7296 | NM_001077405 | TSS11893 |
| chr1 | 62161583 | 62161734 | MACS2_peak_90 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 61 | chr1 | unknown | gene | 61378431 | 61395904 | + | 9530026F06Rik | 9530026F06Rik | | NR_040483 | TSS2436 |
| chr1 | 62161583 | 62161734 | MACS2_peak_90 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 61 | chr1 | unknown | gene | 62703316 | 62815637 | + | Nrp2 | Nrp2 | P7296 | NM_001077405 | TSS11893 |
| chr1 | 64648674 | 64648765 | MACS2_peak_91 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 21 | chr1 | unknown | gene | 64606479 | 64616419 | - | Mettl21a | Mettl21a | P15623 | NM_025964 | TSS10336 |
| chr1 | 64648674 | 64648765 | MACS2_peak_91 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 21 | chr1 | unknown | gene | 64679868 | 64690659 | - | 2810408I11Rik | 2810408I11Rik | | NR_038009 | TSS26073 |
| chr1 | 65714283 | 65714374 | MACS2_peak_92 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 86 | chr1 | unknown | gene | 65311256 | 65388810 | + | Pth2r | Pth2r | P2094 | NM_139270 | TSS6706 |
| chr1 | 65714283 | 65714374 | MACS2_peak_92 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 86 | chr1 | unknown | gene | 65926521 | 65928243 | + | Crygf | Crygf | P24592 | NM_027010 | TSS4966 |
| chr1 | 66078532 | 66078679 | MACS2_peak_93 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 57 | chr1 | unknown | gene | 65926521 | 65928243 | + | Crygf | Crygf | P24592 | NM_027010 | TSS4966 |
| chr1 | 66078532 | 66078679 | MACS2_peak_93 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 57 | chr1 | unknown | gene | 66175328 | 66439007 | + | Map2 | Map2 | P7105 | NM_008632 | TSS22923 |
| chr1 | 66095657 | 66095748 | MACS2_peak_94 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 56 | chr1 | unknown | gene | 65926521 | 65928243 | + | Crygf | Crygf | P24592 | NM_027010 | TSS4966 |
| chr1 | 66095657 | 66095748 | MACS2_peak_94 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 56 | chr1 | unknown | gene | 66175328 | 66439007 | + | Map2 | Map2 | P7105 | NM_008632 | TSS22923 |
| chr1 | 66446964 | 66447055 | MACS2_peak_95 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 37 | chr1 | unknown | gene | 66175328 | 66439007 | + | Map2 | Map2 | P7105 | NM_008632 | TSS22923 |
| chr1 | 66446964 | 66447055 | MACS2_peak_95 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 37 | chr1 | unknown | gene | 66468446 | 66695596 | + | Unc80 | Unc80 | P24532 | NM_175510 | TSS19577 |
| chr1 | 70078506 | 70078597 | MACS2_peak_96 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 85 | chr1 | unknown | gene | 69531209 | 69685960 | - | Ikzf2 | Ikzf2 | P3423 | NM_011770 | TSS9768 |
| chr1 | 70078506 | 70078597 | MACS2_peak_96 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 85 | chr1 | unknown | gene | 70725714 | 70882215 | + | Vwc2l | Vwc2l | P7545 | NM_177164 | TSS4896 |
| chr1 | 70151163 | 70151254 | MACS2_peak_97 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 36 | chr1 | unknown | gene | 69531209 | 69685960 | - | Ikzf2 | Ikzf2 | P3423 | NM_011770 | TSS9768 |
| chr1 | 70151163 | 70151254 | MACS2_peak_97 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 36 | chr1 | unknown | gene | 70725714 | 70882215 | + | Vwc2l | Vwc2l | P7545 | NM_177164 | TSS4896 |
| chr1 | 70853319 | 70853410 | MACS2_peak_98 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 1 | chr1 | unknown | gene | 69826969 | 70724942 | + | Spag16 | Spag16 | P19688 | NM_029160 | TSS15925 |
| chr1 | 70853319 | 70853410 | MACS2_peak_98 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 1 | chr1 | unknown | gene | 71027534 | 71102807 | - | Bard1 | Bard1 | P16217 | NM_007525 | TSS19934 |
| chr1 | 71384503 | 71384594 | MACS2_peak_99 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 72 | chr1 | unknown | gene | 71027534 | 71102807 | - | Bard1 | Bard1 | P16217 | NM_007525 | TSS19934 |
| chr1 | 71384503 | 71384594 | MACS2_peak_99 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 72 | chr1 | unknown | gene | 71557155 | 71578671 | + | Atic | Atic | P16783 | NM_026195 | TSS6927 |
| chr1 | 71562269 | 71562360 | MACS2_peak_100 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 85 | chr1 | unknown | gene | 71243089 | 71414582 | - | Abca12 | Abca12 | P19120 | NM_175210 | TSS1227 |
| chr1 | 71562269 | 71562360 | MACS2_peak_100 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 85 | chr1 | unknown | gene | 71585472 | 71652982 | - | Fn1 | Fn1 | P1597 | NM_010233 | TSS16491 |
| chr1 | 73206726 | 73206817 | MACS2_peak_101 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 84 | chr1 | unknown | gene | 73016035 | 73025508 | + | 1700027A15Rik | 1700027A15Rik | | NR_038001 | TSS25701 |
| chr1 | 73206726 | 73206817 | MACS2_peak_101 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 84 | chr1 | unknown | gene | 73391384 | 73407569 | - | Pinc | Pinc | | NR_003202 | TSS6514 |
| chr1 | 74044018 | 74044161 | MACS2_peak_102 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 61 | chr1 | unknown | gene | 73618380 | 73864466 | - | 6030407O03Rik | 6030407O03Rik | | NR_045311 | TSS24272 |
| chr1 | 74044018 | 74044161 | MACS2_peak_102 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 61 | chr1 | unknown | gene | 74125540 | 74147746 | + | Rufy4 | Rufy4 | P18591 | NM_001170641 | TSS9499 |
| chr1 | 75602316 | 75602407 | MACS2_peak_103 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 24 | chr1 | unknown | gene | 75546265 | 75558890 | + | Slc4a3 | Slc4a3 | P14086 | NM_009208 | TSS18313 |
| chr1 | 75602316 | 75602407 | MACS2_peak_103 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 24 | chr1 | unknown | gene | 76489132 | 76502028 | + | Gm17751 | Gm17751 | | NR_038012 | TSS2722 |
| chr1 | 75834820 | 75834911 | MACS2_peak_104 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 25 | chr1 | unknown | gene | 75546265 | 75558890 | + | Slc4a3 | Slc4a3 | P14086 | NM_009208 | TSS18313 |
| chr1 | 75834820 | 75834911 | MACS2_peak_104 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 25 | chr1 | unknown | gene | 76489132 | 76502028 | + | Gm17751 | Gm17751 | | NR_038012 | TSS2722 |
| chr1 | 76033967 | 76034085 | MACS2_peak_105 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 43 | chr1 | unknown | gene | 75546265 | 75558890 | + | Slc4a3 | Slc4a3 | P14086 | NM_009208 | TSS18313 |
| chr1 | 76033967 | 76034085 | MACS2_peak_105 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 43 | chr1 | unknown | gene | 76489132 | 76502028 | + | Gm17751 | Gm17751 | | NR_038012 | TSS2722 |
| chr1 | 76944411 | 76944502 | MACS2_peak_106 | 12 | + | 4.14966 | 5.12722 | 1.204 | 14 | chr1 | unknown | gene | 76509559 | 76509643 | + | Mir6343 | Mir6343 | | NR_105761 | TSS11403 |
| chr1 | 76944411 | 76944502 | MACS2_peak_106 | 12 | + | 4.14966 | 5.12722 | 1.204 | 14 | chr1 | unknown | gene | 77367184 | 77515031 | - | Epha4 | Epha4 | P18452 | NM_007936 | TSS26264 |
| chr1 | 77658369 | 77658460 | MACS2_peak_107 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 37 | chr1 | unknown | gene | 77367184 | 77515031 | - | Epha4 | Epha4 | P18452 | NM_007936 | TSS26264 |
| chr1 | 77658369 | 77658460 | MACS2_peak_107 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 37 | chr1 | unknown | gene | 78101266 | 78196749 | - | Pax3 | Pax3 | P9871 | NM_001159520 | TSS5586 |
| chr1 | 77687755 | 77687846 | MACS2_peak_108 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 12 | chr1 | unknown | gene | 77367184 | 77515031 | - | Epha4 | Epha4 | P18452 | NM_007936 | TSS26264 |
| chr1 | 77687755 | 77687846 | MACS2_peak_108 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 12 | chr1 | unknown | gene | 78101266 | 78196749 | - | Pax3 | Pax3 | P9871 | NM_001159520 | TSS5586 |
| chr1 | 77879388 | 77879479 | MACS2_peak_109 | 12 | + | 4.14966 | 5.12722 | 1.204 | 17 | chr1 | unknown | gene | 77367184 | 77515031 | - | Epha4 | Epha4 | P18452 | NM_007936 | TSS26264 |
| chr1 | 77879388 | 77879479 | MACS2_peak_109 | 12 | + | 4.14966 | 5.12722 | 1.204 | 17 | chr1 | unknown | gene | 78101266 | 78196749 | - | Pax3 | Pax3 | P9871 | NM_001159520 | TSS5586 |
| chr1 | 77895892 | 77895983 | MACS2_peak_110 | 30 | + | 5.71265 | 7.93979 | 3.00019 | 78 | chr1 | unknown | gene | 77367184 | 77515031 | - | Epha4 | Epha4 | P18452 | NM_007936 | TSS26264 |
| chr1 | 77895892 | 77895983 | MACS2_peak_110 | 30 | + | 5.71265 | 7.93979 | 3.00019 | 78 | chr1 | unknown | gene | 78101266 | 78196749 | - | Pax3 | Pax3 | P9871 | NM_001159520 | TSS5586 |
| chr1 | 78118004 | 78118095 | MACS2_peak_111 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 9 | chr1 | unknown | gene | 77367184 | 77515031 | - | Epha4 | Epha4 | P18452 | NM_007936 | TSS26264 |
| chr1 | 78118004 | 78118095 | MACS2_peak_111 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 9 | chr1 | unknown | gene | 78310345 | 78417426 | + | Sgpp2 | Sgpp2 | P16400 | NM_001004173 | TSS10671 |
| chr1 | 78127055 | 78127146 | MACS2_peak_112 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 43 | chr1 | unknown | gene | 77367184 | 77515031 | - | Epha4 | Epha4 | P18452 | NM_007936 | TSS26264 |
| chr1 | 78127055 | 78127146 | MACS2_peak_112 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 43 | chr1 | unknown | gene | 78310345 | 78417426 | + | Sgpp2 | Sgpp2 | P16400 | NM_001004173 | TSS10671 |
| chr1 | 80009703 | 80009841 | MACS2_peak_113 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 81 | chr1 | unknown | gene | 79794320 | 79858665 | - | Serpine2 | Serpine2 | P23085 | NM_009255 | TSS23525 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr1 | 80009703 | 80009841 | MACS2_peak_113 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 81 | chr1 | unknown | gene | 80198698 | 80213664 | - | Fam124b | Fam124b | P8092 | NM_173425 | TSS4653 |
| chr1 | 80298235 | 80298326 | MACS2_peak_114 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 8 | chr1 | unknown | gene | 80198698 | 80213664 | - | Fam124b | Fam124b | P8092 | NM_173425 | TSS4653 |
| chr1 | 80298235 | 80298326 | MACS2_peak_114 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 8 | chr1 | unknown | gene | 80445931 | 80475660 | + | 1700016L21Rik | 1700016L21Rik | | NR_040460 | TSS1416 |
| chr1 | 80359666 | 80359787 | MACS2_peak_115 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 47 | chr1 | unknown | gene | 80266817 | 80340311 | - | Cul3 | Cul3 | P26666 | NM_016716 | TSS10329 |
| chr1 | 80359666 | 80359787 | MACS2_peak_115 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 47 | chr1 | unknown | gene | 80445931 | 80475660 | + | 1700016L21Rik | 1700016L21Rik | | NR_040460 | TSS1416 |
| chr1 | 80455507 | 80455598 | MACS2_peak_116 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 41 | chr1 | unknown | gene | 80266817 | 80340311 | - | Cul3 | Cul3 | P26666 | NM_016716 | TSS10329 |
| chr1 | 80455507 | 80455598 | MACS2_peak_116 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 41 | chr1 | unknown | gene | 80501067 | 80758448 | - | Dock10 | Dock10 | P3634 | NM_175291 | TSS22288 |
| chr1 | 80681691 | 80681782 | MACS2_peak_117 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 73 | chr1 | unknown | gene | 80445931 | 80475660 | + | 1700016L21Rik | 1700016L21Rik | | NR_040460 | TSS1416 |
| chr1 | 80681691 | 80681782 | MACS2_peak_117 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 73 | chr1 | unknown | gene | 81077316 | 81269552 | + | Nyap2 | Nyap2 | P5866 | NM_172849 | TSS1220 |
| chr1 | 81284522 | 81284613 | MACS2_peak_118 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 2 | chr1 | unknown | gene | 81077316 | 81269552 | + | Nyap2 | Nyap2 | P5866 | NM_172849 | TSS1220 |
| chr1 | 81284522 | 81284613 | MACS2_peak_118 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 2 | chr1 | unknown | gene | 82131915 | 82132019 | + | Mir6344 | Mir6344 | | NR_105762 | TSS5001 |
| chr1 | 81650738 | 81650829 | MACS2_peak_119 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 34 | chr1 | unknown | gene | 81077316 | 81269552 | + | Nyap2 | Nyap2 | P5866 | NM_172849 | TSS1220 |
| chr1 | 81650738 | 81650829 | MACS2_peak_119 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 34 | chr1 | unknown | gene | 82131915 | 82132019 | + | Mir6344 | Mir6344 | | NR_105762 | TSS5001 |
| chr1 | 81882344 | 81882435 | MACS2_peak_120 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 48 | chr1 | unknown | gene | 81077316 | 81269552 | + | Nyap2 | Nyap2 | P5866 | NM_172849 | TSS1220 |
| chr1 | 81882344 | 81882435 | MACS2_peak_120 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 48 | chr1 | unknown | gene | 82131915 | 82132019 | + | Mir6344 | Mir6344 | | NR_105762 | TSS5001 |
| chr1 | 82001360 | 82001451 | MACS2_peak_121 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 75 | chr1 | unknown | gene | 81077316 | 81269552 | + | Nyap2 | Nyap2 | P5866 | NM_172849 | TSS1220 |
| chr1 | 82001360 | 82001451 | MACS2_peak_121 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 75 | chr1 | unknown | gene | 82131915 | 82132019 | + | Mir6344 | Mir6344 | | NR_105762 | TSS5001 |
| chr1 | 82387998 | 82388134 | MACS2_peak_122 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 74 | chr1 | unknown | gene | 82233104 | 82290493 | - | Irs1 | Irs1 | P16792 | NM_010570 | TSS594 |
| chr1 | 82387998 | 82388134 | MACS2_peak_122 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 74 | chr1 | unknown | gene | 82450722 | 82586849 | - | Col4a4 | Col4a4 | P25821 | NM_007735 | TSS510 |
| chr1 | 83717930 | 83718021 | MACS2_peak_123 | 16 | + | 4.811 | 6.2687 | 1.67914 | 64 | chr1 | unknown | gene | 83255780 | 83408011 | - | Sphkap | Sphkap | P13498 | NM_172430 | TSS9737 |
| chr1 | 83717930 | 83718021 | MACS2_peak_123 | 16 | + | 4.811 | 6.2687 | 1.67914 | 64 | chr1 | unknown | gene | 84036292 | 84284370 | - | Pid1 | Pid1 | P7410 | NM_001003948 | TSS3847 |
| chr1 | 86354609 | 86354724 | MACS2_peak_124 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 82 | chr1 | unknown | gene | 86351980 | 86352127 | - | Gm24148 | Gm24148 | | NR_106184 | TSS13825 |
| chr1 | 86354609 | 86354724 | MACS2_peak_124 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 82 | chr1 | unknown | gene | 86356259 | 86356327 | - | Snord82 | Snord82 | | NR_002851 | TSS9422 |
| chr1 | 90279204 | 90279295 | MACS2_peak_125 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 13 | chr1 | unknown | gene | 90203979 | 90214909 | + | Ackr3 | Ackr3 | P6786 | NM_007722 | TSS19263 |
| chr1 | 90279204 | 90279295 | MACS2_peak_125 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 13 | chr1 | unknown | gene | 90603424 | 90612253 | + | Cops8 | Cops8 | P940 | NM_133805 | TSS13539 |
| chr1 | 94316411 | 94316520 | MACS2_peak_126 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 32 | chr1 | unknown | gene | 94038304 | 94052490 | - | Pdcd1 | Pdcd1 | P16929 | NM_008798 | TSS25178 |
| chr1 | 94316411 | 94316520 | MACS2_peak_126 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 32 | chr1 | unknown | gene | 94797441 | 94802472 | + | 4930440C22Rik | 4930440C22Rik | | NR_040473 | TSS14592 |
| chr1 | 94343256 | 94343347 | MACS2_peak_127 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 65 | chr1 | unknown | gene | 94038304 | 94052490 | - | Pdcd1 | Pdcd1 | P16929 | NM_008798 | TSS25178 |
| chr1 | 94343256 | 94343347 | MACS2_peak_127 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 65 | chr1 | unknown | gene | 94797441 | 94802472 | + | 4930440C22Rik | 4930440C22Rik | | NR_040473 | TSS14592 |
| chr1 | 94372701 | 94372792 | MACS2_peak_128 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 14 | chr1 | unknown | gene | 94038304 | 94052490 | - | Pdcd1 | Pdcd1 | P16929 | NM_008798 | TSS25178 |
| chr1 | 94372701 | 94372792 | MACS2_peak_128 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 14 | chr1 | unknown | gene | 94797441 | 94802472 | + | 4930440C22Rik | 4930440C22Rik | | NR_040473 | TSS14592 |
| chr1 | 94495475 | 94495566 | MACS2_peak_129 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 13 | chr1 | unknown | gene | 94038304 | 94052490 | - | Pdcd1 | Pdcd1 | P16929 | NM_008798 | TSS25178 |
| chr1 | 94495475 | 94495566 | MACS2_peak_129 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 13 | chr1 | unknown | gene | 94797441 | 94802472 | + | 4930440C22Rik | 4930440C22Rik | | NR_040473 | TSS14592 |
| chr1 | 94766034 | 94766125 | MACS2_peak_130 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 34 | chr1 | unknown | gene | 94038304 | 94052490 | - | Pdcd1 | Pdcd1 | P16929 | NM_008798 | TSS25178 |
| chr1 | 94766034 | 94766125 | MACS2_peak_130 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 34 | chr1 | unknown | gene | 94797441 | 94802472 | + | 4930440C22Rik | 4930440C22Rik | | NR_040473 | TSS14592 |
| chr1 | 95144708 | 95144799 | MACS2_peak_131 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 23 | chr1 | unknown | gene | 94797441 | 94802472 | + | 4930440C22Rik | 4930440C22Rik | | NR_040473 | TSS14592 |
| chr1 | 95144708 | 95144799 | MACS2_peak_131 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 23 | chr1 | unknown | gene | 95313627 | 95333939 | + | Fam174a | Fam174a | P10940 | NM_026321 | TSS13993 |
| chr1 | 95288715 | 95288806 | MACS2_peak_132 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 57 | chr1 | unknown | gene | 94797441 | 94802472 | + | 4930440C22Rik | 4930440C22Rik | | NR_040473 | TSS14592 |
| chr1 | 95288715 | 95288806 | MACS2_peak_132 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 57 | chr1 | unknown | gene | 95313627 | 95333939 | + | Fam174a | Fam174a | P10940 | NM_026321 | TSS13993 |
| chr1 | 95315771 | 95315893 | MACS2_peak_133 | 23 | + | 5.36409 | 7.26321 | 2.37531 | 52 | chr1 | unknown | gene | 94797441 | 94802472 | + | 4930440C22Rik | 4930440C22Rik | | NR_040473 | TSS14592 |
| chr1 | 95315771 | 95315893 | MACS2_peak_133 | 23 | + | 5.36409 | 7.26321 | 2.37531 | 52 | chr1 | unknown | gene | 95587681 | 95667261 | - | St8sia4 | St8sia4 | P21248 | NM_009183 | TSS25961 |
| chr1 | 95360933 | 95361024 | MACS2_peak_134 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 10 | chr1 | unknown | gene | 95313627 | 95333939 | + | Fam174a | Fam174a | P10940 | NM_026321 | TSS13993 |
| chr1 | 95360933 | 95361024 | MACS2_peak_134 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 10 | chr1 | unknown | gene | 95587681 | 95667261 | - | St8sia4 | St8sia4 | P21248 | NM_009183 | TSS25961 |
| chr1 | 95653213 | 95653304 | MACS2_peak_135 | 23 | + | 5.33156 | 7.20295 | 2.32792 | 47 | chr1 | unknown | gene | 95313627 | 95333939 | + | Fam174a | Fam174a | P10940 | NM_026321 | TSS13993 |
| chr1 | 95653213 | 95653304 | MACS2_peak_135 | 23 | + | 5.33156 | 7.20295 | 2.32792 | 47 | chr1 | unknown | gene | 95701183 | 95716518 | - | 4930598F16Rik | 4930598F16Rik | | NR_040479 | TSS19909 |
| chr1 | 96486215 | 96486313 | MACS2_peak_136 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 64 | chr1 | unknown | gene | 95990658 | 96021758 | - | 1700063A18Rik | 1700063A18Rik | | NR_040467 | TSS18229 |
| chr1 | 96486215 | 96486313 | MACS2_peak_136 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 64 | chr1 | unknown | gene | 96612056 | 96662573 | - | 4930533P14Rik | 4930533P14Rik | | NR_040478 | TSS10219 |
| chr1 | 97037996 | 97038087 | MACS2_peak_137 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 29 | chr1 | unknown | gene | 96906175 | 96997560 | - | Slco6b1 | Slco6b1 | | NR_120500 | TSS5022 |
| chr1 | 97037996 | 97038087 | MACS2_peak_137 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 29 | chr1 | unknown | gene | 97059448 | 97128174 | - | Slco6c1 | Slco6c1 | P13774 | NM_028942 | TSS10399 |
| chr1 | 99218089 | 99218212 | MACS2_peak_138 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 69 | chr1 | unknown | gene | 98421123 | 98509220 | + | Slco6d1 | Slco6d1 | P12437 | NM_001164233 | TSS13182 |
| chr1 | 99218089 | 99218212 | MACS2_peak_138 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 69 | chr1 | unknown | gene | 99772764 | 100484701 | + | Cntnap5b | Cntnap5b | P24210 | NM_172851 | TSS16827 |
| chr1 | 101765817 | 101765908 | MACS2_peak_139 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 23 | chr1 | unknown | gene | 101155767 | 101175202 | + | Gm20268 | Gm20268 | | NR_037989 | TSS4388 |
| chr1 | 101765817 | 101765908 | MACS2_peak_139 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 23 | chr1 | unknown | gene | 104768818 | 104994385 | + | Cdh20 | Cdh20 | P7984 | NM_011800 | TSS17519 |
| chr1 | 104591529 | 104591620 | MACS2_peak_140 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 22 | chr1 | unknown | gene | 101155767 | 101175202 | + | Gm20268 | Gm20268 | | NR_037989 | TSS4388 |
| chr1 | 104591529 | 104591620 | MACS2_peak_140 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 22 | chr1 | unknown | gene | 104768818 | 104994385 | + | Cdh20 | Cdh20 | P7984 | NM_011800 | TSS17519 |
| chr1 | 105756270 | 105756361 | MACS2_peak_141 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 63 | chr1 | unknown | gene | 105663860 | 105753623 | + | 2310035C23Rik | 2310035C23Rik | P25258 | NM_173187 | TSS11719 |
| chr1 | 105756270 | 105756361 | MACS2_peak_141 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 63 | chr1 | unknown | gene | 105780722 | 105844866 | + | Tnfrsf11a | Tnfrsf11a | P8127 | NM_009399 | TSS14409 |
| chr1 | 106538202 | 106538293 | MACS2_peak_142 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 51 | chr1 | unknown | gene | 106171868 | 106393340 | + | Phlpp1 | Phlpp1 | P14290 | NM_133821 | TSS1362 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr1 | 106538202 | 106538293 | MACS2_peak_142 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 51 | chr1 | unknown | gene | 106546495 | 106546631 | - | Mir3473f | Mir3473f | | NR_106164 | TSS17125 |
| chr1 | 107529631 | 107529722 | MACS2_peak_143 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 22 | chr1 | unknown | gene | 107511422 | 107524941 | + | Serpinb2 | Serpinb2 | P23352 | NM_001174170 | TSS2100 |
| chr1 | 107529631 | 107529722 | MACS2_peak_143 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 22 | chr1 | unknown | gene | 107590005 | 107607325 | + | Serpinb8 | Serpinb8 | P10312 | NM_011459 | TSS20186 |
| chr1 | 107670978 | 107671069 | MACS2_peak_144 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 67 | chr1 | unknown | gene | 107590005 | 107607325 | + | Serpinb8 | Serpinb8 | P10312 | NM_011459 | TSS20186 |
| chr1 | 107670978 | 107671069 | MACS2_peak_144 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 67 | chr1 | unknown | gene | 107917258 | 107950947 | + | D830032E09Rik | D830032E09Rik | | NR_102306 | TSS16210 |
| chr1 | 108792087 | 108792178 | MACS2_peak_145 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 35 | chr1 | unknown | gene | 107917258 | 107950947 | + | D830032E09Rik | D830032E09Rik | | NR_102306 | TSS16210 |
| chr1 | 108792087 | 108792178 | MACS2_peak_145 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 35 | chr1 | unknown | gene | 109983736 | 110138355 | + | Cdh7 | Cdh7 | P14333 | NM_172853 | TSS12817 |
| chr1 | 109580138 | 109580229 | MACS2_peak_146 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 32 | chr1 | unknown | gene | 107917258 | 107950947 | + | D830032E09Rik | D830032E09Rik | | NR_102306 | TSS16210 |
| chr1 | 109580138 | 109580229 | MACS2_peak_146 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 32 | chr1 | unknown | gene | 109983736 | 110138355 | + | Cdh7 | Cdh7 | P14333 | NM_172853 | TSS12817 |
| chr1 | 110045526 | 110045617 | MACS2_peak_147 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 6 | chr1 | unknown | gene | 107917258 | 107950947 | + | D830032E09Rik | D830032E09Rik | | NR_102306 | TSS16210 |
| chr1 | 110045526 | 110045617 | MACS2_peak_147 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 6 | chr1 | unknown | gene | 110889194 | 110977372 | - | Cdh19 | Cdh19 | P22218 | NM_001081386 | TSS21571 |
| chr1 | 110219329 | 110219420 | MACS2_peak_148 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 72 | chr1 | unknown | gene | 109983736 | 110138355 | + | Cdh7 | Cdh7 | P14333 | NM_172853 | TSS12817 |
| chr1 | 110219329 | 110219420 | MACS2_peak_148 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 72 | chr1 | unknown | gene | 110889194 | 110977372 | - | Cdh19 | Cdh19 | P22218 | NM_001081386 | TSS21571 |
| chr1 | 115017221 | 115017312 | MACS2_peak_149 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 6 | chr1 | unknown | gene | 111858701 | 111864918 | - | Dsel | Dsel | P21817 | NM_001081316 | TSS13841 |
| chr1 | 115017221 | 115017312 | MACS2_peak_149 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 6 | chr1 | unknown | gene | 115685136 | 116580674 | + | Cntnap5a | Cntnap5a | P26401 | NM_001077425 | TSS1319 |
| chr1 | 116248589 | 116248680 | MACS2_peak_150 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 69 | chr1 | unknown | gene | 111858701 | 111864918 | - | Dsel | Dsel | P21817 | NM_001081316 | TSS13841 |
| chr1 | 116248589 | 116248680 | MACS2_peak_150 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 69 | chr1 | unknown | gene | 118298517 | 118311066 | - | Tsn | Tsn | P10675 | NM_011650 | TSS16557 |
| chr1 | 116596771 | 116596862 | MACS2_peak_151 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 13 | chr1 | unknown | gene | 115685136 | 116580674 | + | Cntnap5a | Cntnap5a | P26401 | NM_001077425 | TSS1319 |
| chr1 | 116596771 | 116596862 | MACS2_peak_151 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 13 | chr1 | unknown | gene | 118298517 | 118311066 | - | Tsn | Tsn | P10675 | NM_011650 | TSS16557 |
| chr1 | 118137257 | 118137348 | MACS2_peak_152 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 57 | chr1 | unknown | gene | 115685136 | 116580674 | + | Cntnap5a | Cntnap5a | P26401 | NM_001077425 | TSS1319 |
| chr1 | 118137257 | 118137348 | MACS2_peak_152 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 57 | chr1 | unknown | gene | 118298517 | 118311066 | - | Tsn | Tsn | P10675 | NM_011650 | TSS16557 |
| chr1 | 119529583 | 119529674 | MACS2_peak_153 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 45 | chr1 | unknown | gene | 119526153 | 119527563 | + | Tmem185b | Tmem185b | P965 | NM_146103 | TSS21846 |
| chr1 | 119529583 | 119529674 | MACS2_peak_153 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 45 | chr1 | unknown | gene | 119545032 | 119649000 | - | Epb4.1l5 | Epb4.1l5 | P12536 | NM_145506 | TSS11231 |
| chr1 | 119570775 | 119570866 | MACS2_peak_154 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 21 | chr1 | unknown | gene | 119529479 | 119536165 | - | 3830432H09Rik | 3830432H09Rik | | NR_126486 | TSS5208 |
| chr1 | 119570775 | 119570866 | MACS2_peak_154 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 21 | chr1 | unknown | gene | 119658092 | 119837071 | - | Ptpn4 | Ptpn4 | P19629 | NM_019933 | TSS12349 |
| chr1 | 119656956 | 119657047 | MACS2_peak_155 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 49 | chr1 | unknown | gene | 119545032 | 119649000 | - | Epb4.1l5 | Epb4.1l5 | P12536 | NM_145506 | TSS11231 |
| chr1 | 119656956 | 119657047 | MACS2_peak_155 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 49 | chr1 | unknown | gene | 119658092 | 119837071 | - | Ptpn4 | Ptpn4 | P19629 | NM_019933 | TSS12349 |
| chr1 | 119959228 | 119959319 | MACS2_peak_156 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 63 | chr1 | unknown | gene | 119907898 | 119913168 | - | Tmem177 | Tmem177 | P18598 | NM_175106 | TSS23735 |
| chr1 | 119959228 | 119959319 | MACS2_peak_156 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 63 | chr1 | unknown | gene | 120006979 | 120063282 | + | Sctr | Sctr | P3876 | NM_001012322 | TSS9349 |
| chr1 | 124352147 | 124352244 | MACS2_peak_157 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 20 | chr1 | unknown | gene | 123332137 | 124045443 | - | Dpp10 | Dpp10 | P4176 | NM_199021 | TSS20171 |
| chr1 | 124352147 | 124352244 | MACS2_peak_157 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 20 | chr1 | unknown | gene | 125392904 | 125435727 | - | Actr3 | Actr3 | P12432 | NM_001205385 | TSS4721 |
| chr1 | 126859925 | 126860020 | MACS2_peak_158 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 7 | chr1 | unknown | gene | 125913635 | 126830632 | - | Nckap5 | Nckap5 | P12535 | NM_176957 | TSS13771 |
| chr1 | 126859925 | 126860020 | MACS2_peak_158 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 7 | chr1 | unknown | gene | 127204985 | 127482725 | + | Mgat5 | Mgat5 | P10640 | NM_145128 | TSS6206 |
| chr1 | 126914792 | 126914890 | MACS2_peak_159 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 21 | chr1 | unknown | gene | 125913635 | 126830632 | - | Nckap5 | Nckap5 | P12535 | NM_176957 | TSS13771 |
| chr1 | 126914792 | 126914890 | MACS2_peak_159 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 21 | chr1 | unknown | gene | 127204985 | 127482725 | + | Mgat5 | Mgat5 | P10640 | NM_145128 | TSS6206 |
| chr1 | 127452375 | 127452466 | MACS2_peak_160 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 63 | chr1 | unknown | gene | 125913635 | 126830632 | - | Nckap5 | Nckap5 | P12535 | NM_176957 | TSS13771 |
| chr1 | 127452375 | 127452466 | MACS2_peak_160 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 63 | chr1 | unknown | gene | 127490341 | 127677629 | - | Tmem163 | Tmem163 | P10797 | NM_028135 | TSS20591 |
| chr1 | 127752117 | 127752225 | MACS2_peak_161 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 54 | chr1 | unknown | gene | 127490341 | 127677629 | - | Tmem163 | Tmem163 | P10797 | NM_028135 | TSS20591 |
| chr1 | 127752117 | 127752225 | MACS2_peak_161 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 54 | chr1 | unknown | gene | 127753616 | 127774054 | - | 2900009J06Rik | 2900009J06Rik | | NR_045298 | TSS22048 |
| chr1 | 129502646 | 129502737 | MACS2_peak_162 | 8 | + | 3.95075 | 4.76 | 0.89171 | 8 | chr1 | unknown | gene | 128588198 | 128592209 | - | Cxcr4 | Cxcr4 | P12599 | NM_009911 | TSS8806 |
| chr1 | 129502646 | 129502737 | MACS2_peak_162 | 8 | + | 3.95075 | 4.76 | 0.89171 | 8 | chr1 | unknown | gene | 130388527 | 130422958 | - | Cd55b | Cd55b | P15518 | NM_007827 | TSS7485 |
| chr1 | 130832717 | 130832844 | MACS2_peak_163 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 47 | chr1 | unknown | gene | 130800901 | 130814653 | + | Fcamr | Fcamr | P24152 | NM_144960 | TSS19875 |
| chr1 | 130832717 | 130832844 | MACS2_peak_163 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 47 | chr1 | unknown | gene | 130865776 | 130880651 | + | Fcmr | Fcmr | P19735 | NM_026976 | TSS124 |
| chr1 | 131386245 | 131386346 | MACS2_peak_164 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 23 | chr1 | unknown | gene | 131254601 | 131279563 | - | Ikbke | Ikbke | P25173 | NM_019777 | TSS11806 |
| chr1 | 131386245 | 131386346 | MACS2_peak_164 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 23 | chr1 | unknown | gene | 131527988 | 131538929 | + | Fam72a | Fam72a | P15116 | NM_175382 | TSS5661 |
| chr1 | 131586266 | 131586357 | MACS2_peak_165 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 35 | chr1 | unknown | gene | 131527988 | 131538929 | + | Fam72a | Fam72a | P15116 | NM_175382 | TSS5661 |
| chr1 | 131586266 | 131586357 | MACS2_peak_165 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 35 | chr1 | unknown | gene | 131599113 | 131609745 | + | Avpr1b | Avpr1b | P5538 | NM_011924 | TSS2388 |
| chr1 | 132223109 | 132223200 | MACS2_peak_166 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 7 | chr1 | unknown | gene | 132198087 | 132198184 | + | Mir135b | Mir135b | | NR_029777 | TSS14046 |
| chr1 | 132223109 | 132223200 | MACS2_peak_166 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 7 | chr1 | unknown | gene | 132298625 | 132304792 | + | Klhdc8a | Klhdc8a | P14431 | NM_144810 | TSS13337 |
| chr1 | 133311526 | 133311678 | MACS2_peak_167 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 78 | chr1 | unknown | gene | 133246096 | 133303435 | + | Plekha6 | Plekha6 | P5014 | NM_182930 | TSS21079 |
| chr1 | 133311526 | 133311678 | MACS2_peak_167 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 78 | chr1 | unknown | gene | 133327211 | 133329645 | + | Kiss1 | Kiss1 | P7259 | NM_178260 | TSS23515 |
| chr1 | 133608878 | 133608985 | MACS2_peak_168 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 62 | chr1 | unknown | gene | 133382299 | 133424212 | - | Sox13 | Sox13 | P2665 | NM_011439 | TSS7570 |
| chr1 | 133608878 | 133608985 | MACS2_peak_168 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 62 | chr1 | unknown | gene | 133619870 | 133661399 | - | Zc3h11a | Zc3h11a | P19509 | NM_144530 | TSS7287 |
| chr1 | 135005993 | 135006084 | MACS2_peak_169 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 29 | chr1 | unknown | gene | 134962564 | 134973946 | + | Ube2t | Ube2t | P26318 | NM_001278115 | TSS8494 |
| chr1 | 135005993 | 135006084 | MACS2_peak_169 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 29 | chr1 | unknown | gene | 135108497 | 135132575 | - | Ptprv | Ptprv | P5168 | NM_007955 | TSS342 |
| chr1 | 136293407 | 136293603 | MACS2_peak_170 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 35 | chr1 | unknown | gene | 136258913 | 136260873 | - | Gpr25 | Gpr25 | P22896 | NM_001101516 | TSS27190 |
| chr1 | 136293407 | 136293603 | MACS2_peak_170 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 35 | chr1 | unknown | gene | 136411915 | 136415519 | - | 9230116N13Rik | 9230116N13Rik | | NR_024328 | TSS10002 |
| chr1 | 137572457 | 137572561 | MACS2_peak_171 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 59 | chr1 | unknown | gene | 136843583 | 136960290 | - | Nr5a2 | Nr5a2 | P6974 | NM_030676 | TSS1442 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr1 | 137572457 | 137572561 | MACS2_peak_171 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 59 | chr1 | unknown | gene | 137966454 | 137966541 | + | Mir181a-1 | Mir181a-1 | | NR_029795 | TSS14421 |
| chr1 | 137644477 | 137644568 | MACS2_peak_172 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 46 | chr1 | unknown | gene | 136843583 | 136960290 | - | Nr5a2 | Nr5a2 | P6974 | NM_030676 | TSS1442 |
| chr1 | 137644477 | 137644568 | MACS2_peak_172 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 46 | chr1 | unknown | gene | 137966454 | 137966541 | + | Mir181a-1 | Mir181a-1 | | NR_029795 | TSS14421 |
| chr1 | 137749087 | 137749178 | MACS2_peak_173 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 23 | chr1 | unknown | gene | 136843583 | 136960290 | - | Nr5a2 | Nr5a2 | P6974 | NM_030676 | TSS1442 |
| chr1 | 137749087 | 137749178 | MACS2_peak_173 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 23 | chr1 | unknown | gene | 137966454 | 137966541 | + | Mir181a-1 | Mir181a-1 | | NR_029795 | TSS14421 |
| chr1 | 137797922 | 137798065 | MACS2_peak_174 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 70 | chr1 | unknown | gene | 136843583 | 136960290 | - | Nr5a2 | Nr5a2 | P6974 | NM_030676 | TSS1442 |
| chr1 | 137797922 | 137798065 | MACS2_peak_174 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 70 | chr1 | unknown | gene | 137966454 | 137966541 | + | Mir181a-1 | Mir181a-1 | | NR_029795 | TSS14421 |
| chr1 | 140288921 | 140289037 | MACS2_peak_175 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 36 | chr1 | unknown | gene | 140085854 | 140183276 | - | Cfh | Cfh | P18392 | NM_009888 | TSS11640 |
| chr1 | 140288921 | 140289037 | MACS2_peak_175 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 36 | chr1 | unknown | gene | 140570175 | 140656402 | - | 4930590L20Rik | 4930590L20Rik | | NR_040604 | TSS1315 |
| chr1 | 140593057 | 140593148 | MACS2_peak_176 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 12 | chr1 | unknown | gene | 140085854 | 140183276 | - | Cfh | Cfh | P18392 | NM_009888 | TSS11640 |
| chr1 | 140593057 | 140593148 | MACS2_peak_176 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 12 | chr1 | unknown | gene | 143607498 | 143702624 | - | Cdc73 | Cdc73 | P25009 | NM_145991 | TSS367 |
| chr1 | 142366027 | 142366118 | MACS2_peak_177 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 80 | chr1 | unknown | gene | 140570175 | 140656402 | - | 4930590L20Rik | 4930590L20Rik | | NR_040604 | TSS1315 |
| chr1 | 142366027 | 142366118 | MACS2_peak_177 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 80 | chr1 | unknown | gene | 143607498 | 143702624 | - | Cdc73 | Cdc73 | P25009 | NM_145991 | TSS367 |
| chr1 | 142766429 | 142766555 | MACS2_peak_178 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 85 | chr1 | unknown | gene | 140570175 | 140656402 | - | 4930590L20Rik | 4930590L20Rik | | NR_040604 | TSS1315 |
| chr1 | 142766429 | 142766555 | MACS2_peak_178 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 85 | chr1 | unknown | gene | 143607498 | 143702624 | - | Cdc73 | Cdc73 | P25009 | NM_145991 | TSS367 |
| chr1 | 143065009 | 143065100 | MACS2_peak_179 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 12 | chr1 | unknown | gene | 140570175 | 140656402 | - | 4930590L20Rik | 4930590L20Rik | | NR_040604 | TSS1315 |
| chr1 | 143065009 | 143065100 | MACS2_peak_179 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 12 | chr1 | unknown | gene | 143607498 | 143702624 | - | Cdc73 | Cdc73 | P25009 | NM_145991 | TSS367 |
| chr1 | 143129933 | 143130024 | MACS2_peak_180 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 54 | chr1 | unknown | gene | 140570175 | 140656402 | - | 4930590L20Rik | 4930590L20Rik | | NR_040604 | TSS1315 |
| chr1 | 143129933 | 143130024 | MACS2_peak_180 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 54 | chr1 | unknown | gene | 143607498 | 143702624 | - | Cdc73 | Cdc73 | P25009 | NM_145991 | TSS367 |
| chr1 | 143751559 | 143751650 | MACS2_peak_181 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 14 | chr1 | unknown | gene | 143739348 | 143746639 | + | Glrx2 | Glrx2 | P16387 | NM_001038593 | TSS26203 |
| chr1 | 143751559 | 143751650 | MACS2_peak_181 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 14 | chr1 | unknown | gene | 143777277 | 143806728 | + | Uchl5 | Uchl5 | P23547 | NM_019562 | TSS5024 |
| chr1 | 144375128 | 144375219 | MACS2_peak_182 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 48 | chr1 | unknown | gene | 144244668 | 144249037 | - | Rgs1 | Rgs1 | P4727 | NM_015811 | TSS17638 |
| chr1 | 144375128 | 144375219 | MACS2_peak_182 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 48 | chr1 | unknown | gene | 144519689 | 144567667 | - | Rgs21 | Rgs21 | | NR_110891 | TSS7940 |
| chr1 | 145294272 | 145294427 | MACS2_peak_183 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 65 | chr1 | unknown | gene | 144752840 | 144775241 | - | Rgs18 | Rgs18 | P13362 | NM_022881 | TSS24872 |
| chr1 | 145294272 | 145294427 | MACS2_peak_183 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 65 | chr1 | unknown | gene | 146495665 | 146902117 | + | Brinp3 | Brinp3 | P24497 | NM_153539 | TSS18121 |
| chr1 | 145512188 | 145512279 | MACS2_peak_184 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 47 | chr1 | unknown | gene | 144752840 | 144775241 | - | Rgs18 | Rgs18 | P13362 | NM_022881 | TSS24872 |
| chr1 | 145512188 | 145512279 | MACS2_peak_184 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 47 | chr1 | unknown | gene | 146495665 | 146902117 | + | Brinp3 | Brinp3 | P24497 | NM_153539 | TSS18121 |
| chr1 | 145549917 | 145550008 | MACS2_peak_185 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 13 | chr1 | unknown | gene | 144752840 | 144775241 | - | Rgs18 | Rgs18 | P13362 | NM_022881 | TSS24872 |
| chr1 | 145549917 | 145550008 | MACS2_peak_185 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 13 | chr1 | unknown | gene | 146495665 | 146902117 | + | Brinp3 | Brinp3 | P24497 | NM_153539 | TSS18121 |
| chr1 | 145648913 | 145649004 | MACS2_peak_186 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 43 | chr1 | unknown | gene | 144752840 | 144775241 | - | Rgs18 | Rgs18 | P13362 | NM_022881 | TSS24872 |
| chr1 | 145648913 | 145649004 | MACS2_peak_186 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 43 | chr1 | unknown | gene | 146495665 | 146902117 | + | Brinp3 | Brinp3 | P24497 | NM_153539 | TSS18121 |
| chr1 | 146375429 | 146375520 | MACS2_peak_187 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 41 | chr1 | unknown | gene | 144752840 | 144775241 | - | Rgs18 | Rgs18 | P13362 | NM_022881 | TSS24872 |
| chr1 | 146375429 | 146375520 | MACS2_peak_187 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 41 | chr1 | unknown | gene | 146495665 | 146902117 | + | Brinp3 | Brinp3 | P24497 | NM_153539 | TSS18121 |
| chr1 | 146652606 | 146652697 | MACS2_peak_188 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 57 | chr1 | unknown | gene | 144752840 | 144775241 | - | Rgs18 | Rgs18 | P13362 | NM_022881 | TSS24872 |
| chr1 | 146652606 | 146652697 | MACS2_peak_188 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 57 | chr1 | unknown | gene | 149829618 | 149961290 | - | Pla2g4a | Pla2g4a | P21901 | NM_001305632 | TSS20550 |
| chr1 | 149874535 | 149874626 | MACS2_peak_189 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 4 | chr1 | unknown | gene | 146495665 | 146902117 | + | Brinp3 | Brinp3 | P24497 | NM_153539 | TSS18121 |
| chr1 | 149874535 | 149874626 | MACS2_peak_189 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 4 | chr1 | unknown | gene | 150024260 | 150052202 | - | Mir7652 | Mir7652 | | NR_106112 | TSS26386 |
| chr1 | 149941462 | 149941553 | MACS2_peak_190 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 15 | chr1 | unknown | gene | 146495665 | 146902117 | + | Brinp3 | Brinp3 | P24497 | NM_153539 | TSS18121 |
| chr1 | 149941462 | 149941553 | MACS2_peak_190 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 15 | chr1 | unknown | gene | 150024260 | 150052202 | - | Mir7652 | Mir7652 | | NR_106112 | TSS26386 |
| chr1 | 150706824 | 150706915 | MACS2_peak_191 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 65 | chr1 | unknown | gene | 150449411 | 150466165 | - | Prg4 | Prg4 | P25230 | NM_001110146 | TSS15689 |
| chr1 | 150706824 | 150706915 | MACS2_peak_191 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 65 | chr1 | unknown | gene | 151138033 | 151144095 | + | C730036E19Rik | C730036E19Rik | | NR_038011 | TSS13868 |
| chr1 | 150747276 | 150747372 | MACS2_peak_192 | 30 | + | 5.71265 | 7.93979 | 3.00019 | 50 | chr1 | unknown | gene | 150449411 | 150466165 | - | Prg4 | Prg4 | P25230 | NM_001110146 | TSS15689 |
| chr1 | 150747276 | 150747372 | MACS2_peak_192 | 30 | + | 5.71265 | 7.93979 | 3.00019 | 50 | chr1 | unknown | gene | 151138033 | 151144095 | + | C730036E19Rik | C730036E19Rik | | NR_038011 | TSS13868 |
| chr1 | 150762483 | 150762625 | MACS2_peak_193 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 70 | chr1 | unknown | gene | 150449411 | 150466165 | - | Prg4 | Prg4 | P25230 | NM_001110146 | TSS15689 |
| chr1 | 150762483 | 150762625 | MACS2_peak_193 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 70 | chr1 | unknown | gene | 151138033 | 151144095 | + | C730036E19Rik | C730036E19Rik | | NR_038011 | TSS13868 |
| chr1 | 150878950 | 150879041 | MACS2_peak_194 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 44 | chr1 | unknown | gene | 150449411 | 150466165 | - | Prg4 | Prg4 | P25230 | NM_001110146 | TSS15689 |
| chr1 | 150878950 | 150879041 | MACS2_peak_194 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 44 | chr1 | unknown | gene | 151138033 | 151144095 | + | C730036E19Rik | C730036E19Rik | | NR_038011 | TSS13868 |
| chr1 | 150997646 | 150997737 | MACS2_peak_195 | 16 | + | 4.811 | 6.2687 | 1.67914 | 23 | chr1 | unknown | gene | 150562501 | 150993051 | - | Hmcn1 | Hmcn1 | P23167 | NM_001024720 | TSS15253 |
| chr1 | 150997646 | 150997737 | MACS2_peak_195 | 16 | + | 4.811 | 6.2687 | 1.67914 | 23 | chr1 | unknown | gene | 151138033 | 151144095 | + | C730036E19Rik | C730036E19Rik | | NR_038011 | TSS13868 |
| chr1 | 151721763 | 151721854 | MACS2_peak_196 | 12 | + | 4.14966 | 5.12722 | 1.204 | 56 | chr1 | unknown | gene | 151571372 | 151718346 | + | Fam129a | Fam129a | P6644 | NM_022018 | TSS3181 |
| chr1 | 151721763 | 151721854 | MACS2_peak_196 | 12 | + | 4.14966 | 5.12722 | 1.204 | 56 | chr1 | unknown | gene | 151755373 | 151818713 | + | Edem3 | Edem3 | P5550 | NM_001039644 | TSS24729 |
| chr1 | 151820730 | 151820821 | MACS2_peak_197 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 12 | chr1 | unknown | gene | 151755373 | 151818713 | + | Edem3 | Edem3 | P5550 | NM_001039644 | TSS24729 |
| chr1 | 151820730 | 151820821 | MACS2_peak_197 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 12 | chr1 | unknown | gene | 151884523 | 152090320 | - | 1700025G04Rik | 1700025G04Rik | P6862 | NM_197990 | TSS16992 |
| chr1 | 152072463 | 152072570 | MACS2_peak_198 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 37 | chr1 | unknown | gene | 151755373 | 151818713 | + | Edem3 | Edem3 | P5550 | NM_001039644 | TSS24729 |
| chr1 | 152072463 | 152072570 | MACS2_peak_198 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 37 | chr1 | unknown | gene | 152370735 | 152386584 | - | Tsen15 | Tsen15 | P3566 | NM_025677 | TSS19976 |
| chr1 | 152497210 | 152497301 | MACS2_peak_199 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 56 | chr1 | unknown | gene | 152370735 | 152386584 | - | Tsen15 | Tsen15 | P3566 | NM_025677 | TSS19976 |
| chr1 | 152497210 | 152497301 | MACS2_peak_199 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 56 | chr1 | unknown | gene | 152517529 | 152625010 | - | Rgl1 | Rgl1 | P880 | NM_016846 | TSS13842 |
| chr1 | 152872347 | 152872483 | MACS2_peak_200 | 7 | + | 3.39397 | 3.87422 | 0.75855 | 52 | chr1 | unknown | gene | 152807889 | 152836114 | + | Ncf2 | Ncf2 | P12329 | NM_010877 | TSS26769 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr1 | 152872347 | 152872483 | MACS2_peak_200 | 7 | + | 3.39397 | 3.87422 | 0.75855 | 52 | chr1 | unknown | gene | 152955100 | 153115670 | + | Nmnat2 | Nmnat2 | P24649 | NM_175460 | TSS1577 |
| chr1 | 152903988 | 152904079 | MACS2_peak_201 | 24 | + | 5.43036 | 7.38735 | 2.49399 | 61 | chr1 | unknown | gene | 152836994 | 152902537 | - | Smg7 | Smg7 | P15488 | NM_001160257 | TSS17678 |
| chr1 | 152903988 | 152904079 | MACS2_peak_201 | 24 | + | 5.43036 | 7.38735 | 2.49399 | 61 | chr1 | unknown | gene | 152955100 | 153115670 | + | Nmnat2 | Nmnat2 | P24649 | NM_175460 | TSS1577 |
| chr1 | 154020546 | 154020637 | MACS2_peak_202 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 17 | chr1 | unknown | gene | 153899928 | 153908182 | + | Glul | Glul | P6555 | NM_008131 | TSS15079 |
| chr1 | 154020546 | 154020637 | MACS2_peak_202 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 17 | chr1 | unknown | gene | 154201186 | 154205674 | + | Zfp648 | Zfp648 | P18249 | NM_001204908 | TSS24205 |
| chr1 | 154670796 | 154670887 | MACS2_peak_203 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 74 | chr1 | unknown | gene | 154255688 | 154270416 | + | 4930532M18Rik | 4930532M18Rik | | NR_108050 | TSS25753 |
| chr1 | 154670796 | 154670887 | MACS2_peak_203 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 74 | chr1 | unknown | gene | 155096366 | 155099430 | - | Ier5 | Ier5 | P7507 | NM_010500 | TSS1605 |
| chr1 | 156012199 | 156012335 | MACS2_peak_204 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 74 | chr1 | unknown | gene | 155844963 | 155973255 | - | Cep350 | Cep350 | P1968 | NM_001039184 | TSS22153 |
| chr1 | 156012199 | 156012335 | MACS2_peak_204 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 74 | chr1 | unknown | gene | 156035663 | 156065458 | + | Tor1aip2 | Tor1aip2 | P6262 | NM_172843 | TSS3689 |
| chr1 | 158739876 | 158739967 | MACS2_peak_205 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 43 | chr1 | unknown | gene | 158362303 | 158688750 | + | Astn1 | Astn1 | P14959 | NM_007495 | TSS7124 |
| chr1 | 158739876 | 158739967 | MACS2_peak_205 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 43 | chr1 | unknown | gene | 159232325 | 159344838 | + | Rfwd2 | Rfwd2 | P2208 | NM_011931 | TSS2800 |
| chr1 | 158776428 | 158776519 | MACS2_peak_206 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 45 | chr1 | unknown | gene | 158362303 | 158688750 | + | Astn1 | Astn1 | P14959 | NM_007495 | TSS7124 |
| chr1 | 158776428 | 158776519 | MACS2_peak_206 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 45 | chr1 | unknown | gene | 159232325 | 159344838 | + | Rfwd2 | Rfwd2 | P2208 | NM_011931 | TSS2800 |
| chr1 | 160779922 | 160780013 | MACS2_peak_207 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 36 | chr1 | unknown | gene | 160576667 | 160577753 | - | Gpr52 | Gpr52 | P18086 | NM_001146330 | TSS5301 |
| chr1 | 160779922 | 160780013 | MACS2_peak_207 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 36 | chr1 | unknown | gene | 160906410 | 160967797 | + | Rc3h1 | Rc3h1 | P395 | NM_001024952 | TSS6968 |
| chr1 | 160941254 | 160941346 | MACS2_peak_208 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 14 | chr1 | unknown | gene | 160219173 | 160792938 | - | Rabgap1l | Rabgap1l | P1279 | NM_001038621 | TSS11216 |
| chr1 | 160941254 | 160941346 | MACS2_peak_208 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 14 | chr1 | unknown | gene | 160978605 | 161002463 | + | Serpinc1 | Serpinc1 | P24948 | NM_080844 | TSS280 |
| chr1 | 162595808 | 162595970 | MACS2_peak_209 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 83 | chr1 | unknown | gene | 162533671 | 162548256 | - | Mettl13 | Mettl13 | P23302 | NM_144877 | TSS1048 |
| chr1 | 162595808 | 162595970 | MACS2_peak_209 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 83 | chr1 | unknown | gene | 162639149 | 162649201 | + | Myoc | Myoc | P6065 | NM_010865 | TSS26817 |
| chr1 | 162671729 | 162671856 | MACS2_peak_210 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 46 | chr1 | unknown | gene | 162647242 | 162658115 | - | 7420461P10Rik | 7420461P10Rik | P6261 | NM_001177581 | TSS5154 |
| chr1 | 162671729 | 162671856 | MACS2_peak_210 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 46 | chr1 | unknown | gene | 162793882 | 162812549 | - | Fmo4 | Fmo4 | P12749 | NM_144878 | TSS21754 |
| chr1 | 162847911 | 162848002 | MACS2_peak_211 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 19 | chr1 | unknown | gene | 162793882 | 162812549 | - | Fmo4 | Fmo4 | P12749 | NM_144878 | TSS21754 |
| chr1 | 162847911 | 162848002 | MACS2_peak_211 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 19 | chr1 | unknown | gene | 162875046 | 162898712 | - | Fmo2 | Fmo2 | P7075 | NM_018881 | TSS26703 |
| chr1 | 163019234 | 163019325 | MACS2_peak_212 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 61 | chr1 | unknown | gene | 162953799 | 162984491 | - | Fmo3 | Fmo3 | P22791 | NM_008030 | TSS21749 |
| chr1 | 163019234 | 163019325 | MACS2_peak_212 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 61 | chr1 | unknown | gene | 163024301 | 163085670 | - | Mroh9 | Mroh9 | P2159 | NM_030071 | TSS13439 |
| chr1 | 163368907 | 163369006 | MACS2_peak_213 | 29 | + | 5.67577 | 7.86521 | 2.93324 | 53 | chr1 | unknown | gene | 163245118 | 163312635 | - | Prrx1 | Prrx1 | P19043 | NM_175686 | TSS23884 |
| chr1 | 163368907 | 163369006 | MACS2_peak_213 | 29 | + | 5.67577 | 7.86521 | 2.93324 | 53 | chr1 | unknown | gene | 163384908 | 163403583 | - | Gorab | Gorab | P18243 | NM_178883 | TSS2777 |
| chr1 | 163392786 | 163392877 | MACS2_peak_214 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 79 | chr1 | unknown | gene | 163245118 | 163312635 | - | Prrx1 | Prrx1 | P19043 | NM_175686 | TSS23884 |
| chr1 | 163392786 | 163392877 | MACS2_peak_214 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 79 | chr1 | unknown | gene | 163702992 | 163725055 | - | Mettl11b | Mettl11b | P12307 | NM_001143956 | TSS17533 |
| chr1 | 165571226 | 165571350 | MACS2_peak_215 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 46 | chr1 | unknown | gene | 165461207 | 165480939 | + | Mpc2 | Mpc2 | P4866 | NM_027430 | TSS8006 |
| chr1 | 165571226 | 165571350 | MACS2_peak_215 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 46 | chr1 | unknown | gene | 165592180 | 165634393 | - | Mpzl1 | Mpzl1 | P2434 | NM_001001880 | TSS21285 |
| chr1 | 165919394 | 165919485 | MACS2_peak_216 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 42 | chr1 | unknown | gene | 165788680 | 165869122 | + | Cd247 | Cd247 | | NR_103716 | TSS26715 |
| chr1 | 165919394 | 165919485 | MACS2_peak_216 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 42 | chr1 | unknown | gene | 166098147 | 166127898 | - | Dusp27 | Dusp27 | P19558 | NM_001033344 | TSS24887 |
| chr1 | 166050156 | 166050256 | MACS2_peak_217 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 56 | chr1 | unknown | gene | 165865153 | 166002622 | - | Pou2f1 | Pou2f1 | P20142 | NM_011137 | TSS9962 |
| chr1 | 166050156 | 166050256 | MACS2_peak_217 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 56 | chr1 | unknown | gene | 166098147 | 166127898 | - | Dusp27 | Dusp27 | P19558 | NM_001033344 | TSS24887 |
| chr1 | 166076139 | 166076249 | MACS2_peak_218 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 79 | chr1 | unknown | gene | 165865153 | 166002622 | - | Pou2f1 | Pou2f1 | P20142 | NM_011137 | TSS9962 |
| chr1 | 166076139 | 166076249 | MACS2_peak_218 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 79 | chr1 | unknown | gene | 166098147 | 166127898 | - | Dusp27 | Dusp27 | P19558 | NM_001033344 | TSS24887 |
| chr1 | 166531239 | 166531330 | MACS2_peak_219 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 56 | chr1 | unknown | gene | 166483612 | 166497520 | - | Gm4846 | Gm4846 | P19282 | NM_001164306 | TSS18540 |
| chr1 | 166531239 | 166531330 | MACS2_peak_219 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 56 | chr1 | unknown | gene | 166628970 | 166647693 | - | Gm4847 | Gm4847 | P12023 | NM_001164312 | TSS21623 |
| chr1 | 167280225 | 167280316 | MACS2_peak_220 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 48 | chr1 | unknown | gene | 167001416 | 167091302 | + | Fam78b | Fam78b | P13011 | NM_001160262 | TSS9117 |
| chr1 | 167280225 | 167280316 | MACS2_peak_220 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 48 | chr1 | unknown | gene | 167290124 | 167290225 | + | Mir6347 | Mir6347 | | NR_105765 | TSS17534 |
| chr1 | 168105269 | 168105360 | MACS2_peak_221 | 16 | + | 4.811 | 6.2687 | 1.67914 | 54 | chr1 | unknown | gene | 167689557 | 167846761 | + | Lmx1a | Lmx1a | P7080 | NM_033652 | TSS15609 |
| chr1 | 168105269 | 168105360 | MACS2_peak_221 | 16 | + | 4.811 | 6.2687 | 1.67914 | 54 | chr1 | unknown | gene | 168119363 | 168431504 | - | Pbx1 | Pbx1 | P6172 | NM_008783 | TSS10182 |
| chr1 | 168284476 | 168284581 | MACS2_peak_222 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 29 | chr1 | unknown | gene | 167689557 | 167846761 | + | Lmx1a | Lmx1a | P7080 | NM_033652 | TSS15609 |
| chr1 | 168284476 | 168284581 | MACS2_peak_222 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 29 | chr1 | unknown | gene | 168490642 | 168490762 | + | Mir6348 | Mir6348 | | NR_105766 | TSS15358 |
| chr1 | 168951560 | 168951651 | MACS2_peak_223 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 24 | chr1 | unknown | gene | 168490642 | 168490762 | + | Mir6348 | Mir6348 | | NR_105766 | TSS15358 |
| chr1 | 168951560 | 168951651 | MACS2_peak_223 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 24 | chr1 | unknown | gene | 169497933 | 169531464 | - | Nuf2 | Nuf2 | P7658 | NM_023284 | TSS23666 |
| chr1 | 169714619 | 169714710 | MACS2_peak_224 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 71 | chr1 | unknown | gene | 169655500 | 169692340 | + | Rgs5 | Rgs5 | P5708 | NM_009063 | TSS21766 |
| chr1 | 169714619 | 169714710 | MACS2_peak_224 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 71 | chr1 | unknown | gene | 169741476 | 169747523 | - | Rgs4 | Rgs4 | P1565 | NM_009062 | TSS12277 |
| chr1 | 169802107 | 169802198 | MACS2_peak_225 | 30 | + | 5.75374 | 8.01681 | 3.07172 | 56 | chr1 | unknown | gene | 169741476 | 169747523 | - | Rgs4 | Rgs4 | P1565 | NM_009062 | TSS12277 |
| chr1 | 169802107 | 169802198 | MACS2_peak_225 | 30 | + | 5.75374 | 8.01681 | 3.07172 | 56 | chr1 | unknown | gene | 169928938 | 169934200 | + | 1700084C01Rik | 1700084C01Rik | P14574 | NM_001033185 | TSS8816 |
| chr1 | 171111428 | 171111519 | MACS2_peak_226 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 23 | chr1 | unknown | gene | 171064590 | 171064652 | - | Mir6546 | Mir6546 | | NR_106103 | TSS12540 |
| chr1 | 171111428 | 171111519 | MACS2_peak_226 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 23 | chr1 | unknown | gene | 171121660 | 171126785 | + | Cfap126 | Cfap126 | P20253 | NM_001081275 | TSS16298 |
| chr1 | 171540447 | 171540676 | MACS2_peak_227 | 28 | + | 4.97951 | 7.75 | 2.8271 | 53 | chr1 | unknown | gene | 171518123 | 171535294 | - | Itln1 | Itln1 | P5936 | NM_010584 | TSS7732 |
| chr1 | 171540447 | 171540676 | MACS2_peak_227 | 28 | + | 4.97951 | 7.75 | 2.8271 | 53 | chr1 | unknown | gene | 171559192 | 171582884 | + | Cd244 | Cd244 | P23804 | NM_018729 | TSS22171 |
| chr1 | 171988046 | 171988151 | MACS2_peak_228 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 16 | chr1 | unknown | gene | 171917536 | 171942592 | + | Slamf6 | Slamf6 | P3753 | NM_030710 | TSS27228 |
| chr1 | 171988046 | 171988151 | MACS2_peak_228 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 16 | chr1 | unknown | gene | 172004370 | 172027268 | - | Vangl2 | Vangl2 | P1559 | NM_033509 | TSS19941 |
| chr1 | 172225412 | 172225503 | MACS2_peak_229 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 76 | chr1 | unknown | gene | 172209893 | 172219690 | - | Casq1 | Casq1 | P17487 | NM_009813 | TSS1800 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr1 | 172225412 | 172225503 | MACS2_peak_229 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 76 | chr1 | unknown | gene | 172271708 | 172297892 | - | Atp1a2 | Atp1a2 | P6757 | NM_178405 | TSS9491 |
| chr1 | 173429989 | 173430080 | MACS2_peak_230 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 68 | chr1 | unknown | gene | 173334253 | 173367494 | - | Cadm3 | Cadm3 | P2884 | NM_053199 | TSS14310 |
| chr1 | 173429989 | 173430080 | MACS2_peak_230 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 68 | chr1 | unknown | gene | 173521310 | 173535957 | - | BC094916 | BC094916 | P16962 | NM_001024721 | TSS9936 |
| chr1 | 173801923 | 173802014 | MACS2_peak_231 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 33 | chr1 | unknown | gene | 173747293 | 173766919 | - | Ifi204 | Ifi204 | P11187 | NM_008329 | TSS6783 |
| chr1 | 173801923 | 173802014 | MACS2_peak_231 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 33 | chr1 | unknown | gene | 173857219 | 173880187 | - | Mndal | Mndal | P12310 | NM_001170853 | TSS13009 |
| chr1 | 173807659 | 173807761 | MACS2_peak_232 | 46 | + | 6.64256 | 9.7473 | 4.67773 | 54 | chr1 | unknown | gene | 173747293 | 173766919 | - | Ifi204 | Ifi204 | P11187 | NM_008329 | TSS6783 |
| chr1 | 173807659 | 173807761 | MACS2_peak_232 | 46 | + | 6.64256 | 9.7473 | 4.67773 | 54 | chr1 | unknown | gene | 173857219 | 173880187 | - | Mndal | Mndal | P12310 | NM_001170853 | TSS13009 |
| chr1 | 174223040 | 174223178 | MACS2_peak_233 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 84 | chr1 | unknown | gene | 174158721 | 174159740 | + | Olfr420 | Olfr420 | P16411 | NM_146305 | TSS5974 |
| chr1 | 174223040 | 174223178 | MACS2_peak_233 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 84 | chr1 | unknown | gene | 174249888 | 174250925 | - | Olfr419 | Olfr419 | P16295 | NM_146715 | TSS21697 |
| chr1 | 174714229 | 174714388 | MACS2_peak_234 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 88 | chr1 | unknown | gene | 174448624 | 174449602 | + | Olfr220 | Olfr220 | P5205 | NM_207694 | TSS16174 |
| chr1 | 174714229 | 174714388 | MACS2_peak_234 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 88 | chr1 | unknown | gene | 174833784 | 174921819 | - | Grem2 | Grem2 | P24472 | NM_011825 | TSS10452 |
| chr1 | 174777888 | 174777979 | MACS2_peak_235 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 19 | chr1 | unknown | gene | 174448624 | 174449602 | + | Olfr220 | Olfr220 | P5205 | NM_207694 | TSS16174 |
| chr1 | 174777888 | 174777979 | MACS2_peak_235 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 19 | chr1 | unknown | gene | 174833784 | 174921819 | - | Grem2 | Grem2 | P24472 | NM_011825 | TSS10452 |
| chr1 | 174917966 | 174918057 | MACS2_peak_236 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 19 | chr1 | unknown | gene | 174501824 | 174821245 | + | Fmn2 | Fmn2 | P24180 | NM_019445 | TSS26960 |
| chr1 | 174917966 | 174918057 | MACS2_peak_236 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 19 | chr1 | unknown | gene | 175059075 | 175492545 | - | Rgs7 | Rgs7 | P24698 | NM_001199003 | TSS19209 |
| chr1 | 175583016 | 175583107 | MACS2_peak_237 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 36 | chr1 | unknown | gene | 175059075 | 175492545 | - | Rgs7 | Rgs7 | P24698 | NM_001199003 | TSS19209 |
| chr1 | 175583016 | 175583107 | MACS2_peak_237 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 36 | chr1 | unknown | gene | 175601377 | 175625573 | - | Fh1 | Fh1 | P5816 | NM_010209 | TSS873 |
| chr1 | 175698195 | 175698286 | MACS2_peak_238 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 29 | chr1 | unknown | gene | 175662420 | 175692536 | - | Opn3 | Opn3 | P625 | NM_010098 | TSS5277 |
| chr1 | 175698195 | 175698286 | MACS2_peak_238 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 29 | chr1 | unknown | gene | 175698592 | 175815366 | + | Wdr64 | Wdr64 | P13751 | NM_029453 | TSS26330 |
| chr1 | 176753572 | 176753663 | MACS2_peak_239 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 78 | chr1 | unknown | gene | 175962305 | 176274874 | - | Pld5 | Pld5 | P22543 | NM_001195816 | TSS23850 |
| chr1 | 176753572 | 176753663 | MACS2_peak_239 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 78 | chr1 | unknown | gene | 176772324 | 176772423 | - | Mir350 | Mir350 | | NR_029775 | TSS12203 |
| chr1 | 177113896 | 177114024 | MACS2_peak_240 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 51 | chr1 | unknown | gene | 176814659 | 177020144 | + | Sdccag8 | Sdccag8 | P24983 | NM_029756 | TSS2419 |
| chr1 | 177113896 | 177114024 | MACS2_peak_240 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 51 | chr1 | unknown | gene | 177444660 | 177448671 | + | Zbtb18 | Zbtb18 | P24895 | NM_001012330 | TSS18823 |
| chr1 | 177274526 | 177274617 | MACS2_peak_241 | 12 | + | 4.14966 | 5.12722 | 1.204 | 12 | chr1 | unknown | gene | 177022114 | 177248721 | - | Akt3 | Akt3 | P7587 | NM_011785 | TSS17851 |
| chr1 | 177274526 | 177274617 | MACS2_peak_241 | 12 | + | 4.14966 | 5.12722 | 1.204 | 12 | chr1 | unknown | gene | 177444660 | 177448671 | + | Zbtb18 | Zbtb18 | P24895 | NM_001012330 | TSS18823 |
| chr1 | 178826819 | 178826910 | MACS2_peak_242 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 76 | chr1 | unknown | gene | 178405880 | 178481428 | + | Efcab2 | Efcab2 | P9531 | NM_026626 | TSS5765 |
| chr1 | 178826819 | 178826910 | MACS2_peak_242 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 76 | chr1 | unknown | gene | 178955038 | 179517951 | - | Smyd3 | Smyd3 | P26568 | NM_027188 | TSS8506 |
| chr1 | 179149960 | 179150051 | MACS2_peak_243 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 32 | chr1 | unknown | gene | 178529124 | 178932228 | + | Kif26b | Kif26b | P10339 | NM_001161665 | TSS14010 |
| chr1 | 179149960 | 179150051 | MACS2_peak_243 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 32 | chr1 | unknown | gene | 179528055 | 179546131 | - | Tfb2m | Tfb2m | P26766 | NM_008249 | TSS11462 |
| chr1 | 179183283 | 179183374 | MACS2_peak_244 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 45 | chr1 | unknown | gene | 178529124 | 178932228 | + | Kif26b | Kif26b | P10339 | NM_001161665 | TSS14010 |
| chr1 | 179183283 | 179183374 | MACS2_peak_244 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 45 | chr1 | unknown | gene | 179528055 | 179546131 | - | Tfb2m | Tfb2m | P26766 | NM_008249 | TSS11462 |
| chr1 | 181743012 | 181743182 | MACS2_peak_245 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 123 | chr1 | unknown | gene | 181509632 | 181511385 | - | Ccdc121 | Ccdc121 | P1063 | NM_207280 | TSS19552 |
| chr1 | 181743012 | 181743182 | MACS2_peak_245 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 123 | chr1 | unknown | gene | 181815314 | 181842401 | - | Lbr | Lbr | P14318 | NM_133815 | TSS14953 |
| chr1 | 182570609 | 182570700 | MACS2_peak_246 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 4 | chr1 | unknown | gene | 182467258 | 182517354 | - | Capn2 | Capn2 | P21094 | NM_009794 | TSS8173 |
| chr1 | 182570609 | 182570700 | MACS2_peak_246 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 4 | chr1 | unknown | gene | 182747125 | 182749122 | - | Ccdc185 | Ccdc185 | P9678 | NM_001033547 | TSS10334 |
| chr1 | 182727363 | 182727515 | MACS2_peak_247 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 81 | chr1 | unknown | gene | 182565006 | 182632107 | + | Capn8 | Capn8 | P12650 | NM_001145806 | TSS8428 |
| chr1 | 182727363 | 182727515 | MACS2_peak_247 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 81 | chr1 | unknown | gene | 182747125 | 182749122 | - | Ccdc185 | Ccdc185 | P9678 | NM_001033547 | TSS10334 |
| chr1 | 183299145 | 183299536 | MACS2_peak_248 | 73 | + | 7.99733 | 12.48785 | 7.30009 | 77 | chr1 | unknown | gene | 183276341 | 183297008 | - | Brox | Brox | P7586 | NM_027861 | TSS8949 |
| chr1 | 183299145 | 183299536 | MACS2_peak_248 | 73 | + | 7.99733 | 12.48785 | 7.30009 | 77 | chr1 | unknown | gene | 183326235 | 183369529 | - | Mia3 | Mia3 | P2193 | NM_177389 | TSS22131 |
| chr1 | 183369931 | 183370022 | MACS2_peak_249 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 32 | chr1 | unknown | gene | 183326235 | 183369529 | - | Mia3 | Mia3 | P2193 | NM_177389 | TSS22131 |
| chr1 | 183369931 | 183370022 | MACS2_peak_249 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 32 | chr1 | unknown | gene | 183388884 | 183409353 | + | Taf1a | Taf1a | P25160 | NM_021466 | TSS17881 |
| chr1 | 184297140 | 184297231 | MACS2_peak_250 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 15 | chr1 | unknown | gene | 184034460 | 184074523 | + | Dusp10 | Dusp10 | P20955 | NM_022019 | TSS12384 |
| chr1 | 184297140 | 184297231 | MACS2_peak_250 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 15 | chr1 | unknown | gene | 184527840 | 184557691 | - | 1700112H15Rik | 1700112H15Rik | | NR_040472 | TSS13400 |
| chr1 | 184361905 | 184362018 | MACS2_peak_251 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 42 | chr1 | unknown | gene | 184034460 | 184074523 | + | Dusp10 | Dusp10 | P20955 | NM_022019 | TSS12384 |
| chr1 | 184361905 | 184362018 | MACS2_peak_251 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 42 | chr1 | unknown | gene | 184527840 | 184557691 | - | 1700112H15Rik | 1700112H15Rik | | NR_040472 | TSS13400 |
| chr1 | 185925401 | 185925492 | MACS2_peak_252 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 29 | chr1 | unknown | gene | 185497305 | 185498014 | + | 5033404E19Rik | 5033404E19Rik | | NR_033600 | TSS27475 |
| chr1 | 185925401 | 185925492 | MACS2_peak_252 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 29 | chr1 | unknown | gene | 186087731 | 186117250 | - | Lyplal1 | Lyplal1 | P7404 | NM_146106 | TSS11185 |
| chr1 | 186224611 | 186224702 | MACS2_peak_253 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 79 | chr1 | unknown | gene | 186087731 | 186117250 | - | Lyplal1 | Lyplal1 | P7404 | NM_146106 | TSS11185 |
| chr1 | 186224611 | 186224702 | MACS2_peak_253 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 79 | chr1 | unknown | gene | 186511837 | 186558681 | - | A730004F24Rik | A730004F24Rik | | NR_131158 | TSS6051 |
| chr1 | 186229559 | 186229650 | MACS2_peak_254 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 13 | chr1 | unknown | gene | 186087731 | 186117250 | - | Lyplal1 | Lyplal1 | P7404 | NM_146106 | TSS11185 |
| chr1 | 186229559 | 186229650 | MACS2_peak_254 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 13 | chr1 | unknown | gene | 186511837 | 186558681 | - | A730004F24Rik | A730004F24Rik | | NR_131158 | TSS6051 |
| chr1 | 186405386 | 186405573 | MACS2_peak_255 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 30 | chr1 | unknown | gene | 186087731 | 186117250 | - | Lyplal1 | Lyplal1 | P7404 | NM_146106 | TSS11185 |
| chr1 | 186405386 | 186405573 | MACS2_peak_255 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 30 | chr1 | unknown | gene | 186511837 | 186558681 | - | A730004F24Rik | A730004F24Rik | | NR_131158 | TSS6051 |
| chr1 | 189369859 | 189370002 | MACS2_peak_256 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 81 | chr1 | unknown | gene | 188971097 | 189007612 | - | Kctd3 | Kctd3 | P25000 | NM_172650 | TSS22471 |
| chr1 | 189369859 | 189370002 | MACS2_peak_256 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 81 | chr1 | unknown | gene | 189640613 | 189688086 | - | Cenpf | Cenpf | P25186 | NM_001081363 | TSS18867 |
| chr1 | 189600658 | 189600776 | MACS2_peak_257 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 65 | chr1 | unknown | gene | 189207929 | 189402273 | - | Kcnk2 | Kcnk2 | P21999 | NM_010607 | TSS19498 |
| chr1 | 189600658 | 189600776 | MACS2_peak_257 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 65 | chr1 | unknown | gene | 189640613 | 189688086 | - | Cenpf | Cenpf | P25186 | NM_001081363 | TSS18867 |
| chr1 | 189703139 | 189703230 | MACS2_peak_258 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 27 | chr1 | unknown | gene | 189640613 | 189688086 | - | Cenpf | Cenpf | P25186 | NM_001081363 | TSS18867 |

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr1 | 189703139 | 189703230 | MACS2_peak_258 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 27 | chr1 | unknown | gene | 189728267 | 189870055 | + | Ptpn14 | Ptpn14 | P18110 | NM_008976 | TSS22866 |
| chr1 | 190795641 | 190795773 | MACS2_peak_259 | 35 | + | 5.98489 | 8.51731 | 3.53253 | 70 | chr1 | unknown | gene | 190121776 | 190170680 | - | Prox1 | Prox1 | P2108 | NM_008937 | TSS11281 |
| chr1 | 190795641 | 190795773 | MACS2_peak_259 | 35 | + | 5.98489 | 8.51731 | 3.53253 | 70 | chr1 | unknown | gene | 190925107 | 190945091 | + | Angel2 | Angel2 | P8452 | NM_001199020 | TSS24393 |
| chr1 | 191555391 | 191555482 | MACS2_peak_260 | 25 | + | 5.46411 | 7.45132 | 2.55202 | 65 | chr1 | unknown | gene | 191351980 | 191396416 | - | Ppp2r5a | Ppp2r5a | P15345 | NM_144880 | TSS4417 |
| chr1 | 191555391 | 191555482 | MACS2_peak_260 | 25 | + | 5.46411 | 7.45132 | 2.55202 | 65 | chr1 | unknown | gene | 191575635 | 191621464 | + | Ints7 | Ints7 | P23551 | NM_001306204 | TSS16749 |
| chr1 | 191555610 | 191555701 | MACS2_peak_261 | 24 | + | 5.43036 | 7.38735 | 2.49399 | 34 | chr1 | unknown | gene | 191351980 | 191396416 | - | Ppp2r5a | Ppp2r5a | P15345 | NM_144880 | TSS4417 |
| chr1 | 191555610 | 191555701 | MACS2_peak_261 | 24 | + | 5.43036 | 7.38735 | 2.49399 | 34 | chr1 | unknown | gene | 191575635 | 191621464 | + | Ints7 | Ints7 | P23551 | NM_001306204 | TSS16749 |
| chr1 | 191726961 | 191727052 | MACS2_peak_262 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 69 | chr1 | unknown | gene | 191575635 | 191621464 | + | Ints7 | Ints7 | P23551 | NM_001306204 | TSS16749 |
| chr1 | 191726961 | 191727052 | MACS2_peak_262 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 69 | chr1 | unknown | gene | 191821472 | 191831357 | + | Nek2 | Nek2 | P11966 | NM_010892 | TSS13364 |
| chr1 | 192299296 | 192299387 | MACS2_peak_263 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 51 | chr1 | unknown | gene | 192136897 | 192151025 | + | Gm10516 | Gm10516 | | NR_033536 | TSS24591 |
| chr1 | 192299296 | 192299387 | MACS2_peak_263 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 51 | chr1 | unknown | gene | 192512827 | 192771219 | - | Hhat | Hhat | P24845 | NM_144881 | TSS19353 |
| chr1 | 193906002 | 193906104 | MACS2_peak_264 | 23 | + | 5.33156 | 7.20295 | 2.32792 | 59 | chr1 | unknown | gene | 193507462 | 193507530 | - | Mir205 | Mir205 | | NR_029592 | TSS24117 |
| chr1 | 193906002 | 193906104 | MACS2_peak_264 | 23 | + | 5.33156 | 7.20295 | 2.32792 | 59 | chr1 | unknown | gene | 194212186 | 194222759 | - | 4930503O07Rik | 4930503O07Rik | | NR_040477 | TSS4 |
| chr1 | 194018322 | 194018413 | MACS2_peak_265 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 63 | chr1 | unknown | gene | 193507462 | 193507530 | - | Mir205 | Mir205 | | NR_029592 | TSS24117 |
| chr1 | 194018322 | 194018413 | MACS2_peak_265 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 63 | chr1 | unknown | gene | 194212186 | 194222759 | - | 4930503O07Rik | 4930503O07Rik | | NR_040477 | TSS4 |
| chr10 | 4112788 | 4112879 | MACS2_peak_266 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 51 | chr10 | unknown | gene | 3740376 | 3964452 | + | Plekhg1 | Plekhg1 | P26697 | NM_001159942 | TSS26276 |
| chr10 | 4112788 | 4112879 | MACS2_peak_266 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 51 | chr10 | unknown | gene | 4266328 | 4359471 | + | Akap12 | Akap12 | P2226 | NM_031185 | TSS6588 |
| chr10 | 4572232 | 4572323 | MACS2_peak_267 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 33 | chr10 | unknown | gene | 4509871 | 4561111 | + | Ccdc170 | Ccdc170 | P3221 | NM_001195672 | TSS21780 |
| chr10 | 4572232 | 4572323 | MACS2_peak_267 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 33 | chr10 | unknown | gene | 4611988 | 5001423 | + | Esr1 | Esr1 | P7636 | NM_007956 | TSS20758 |
| chr10 | 4587933 | 4588024 | MACS2_peak_268 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 5 | chr10 | unknown | gene | 4509871 | 4561111 | + | Ccdc170 | Ccdc170 | P3221 | NM_001195672 | TSS21780 |
| chr10 | 4587933 | 4588024 | MACS2_peak_268 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 5 | chr10 | unknown | gene | 4611988 | 5001423 | + | Esr1 | Esr1 | P7636 | NM_007956 | TSS20758 |
| chr10 | 5512089 | 5512180 | MACS2_peak_269 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 5 | chr10 | unknown | gene | 4611988 | 5001423 | + | Esr1 | Esr1 | P7636 | NM_007956 | TSS20758 |
| chr10 | 5512089 | 5512180 | MACS2_peak_269 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 5 | chr10 | unknown | gene | 5593727 | 5604701 | + | Myct1 | Myct1 | P8691 | NM_026793 | TSS22764 |
| chr10 | 5622226 | 5622317 | MACS2_peak_270 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 35 | chr10 | unknown | gene | 5593727 | 5604701 | + | Myct1 | Myct1 | P8691 | NM_026793 | TSS22764 |
| chr10 | 5622226 | 5622317 | MACS2_peak_270 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 35 | chr10 | unknown | gene | 5639217 | 5647614 | + | Vip | Vip | P23362 | NM_011702 | TSS9656 |
| chr10 | 8509546 | 8509767 | MACS2_peak_271 | 25 | + | 5.46411 | 7.45132 | 2.55202 | 148 | chr10 | unknown | gene | 7905647 | 7956123 | - | Tab2 | Tab2 | P11354 | NM_138667 | TSS13792 |
| chr10 | 8509546 | 8509767 | MACS2_peak_271 | 25 | + | 5.46411 | 7.45132 | 2.55202 | 148 | chr10 | unknown | gene | 8722218 | 8885858 | - | Sash1 | Sash1 | P17628 | NM_175155 | TSS10761 |
| chr10 | 8997399 | 8997490 | MACS2_peak_272 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 60 | chr10 | unknown | gene | 8722218 | 8885858 | - | Sash1 | Sash1 | P17628 | NM_175155 | TSS10761 |
| chr10 | 8997399 | 8997490 | MACS2_peak_272 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 60 | chr10 | unknown | gene | 9627258 | 9674963 | - | Samd5 | Samd5 | P18361 | NM_177271 | TSS17088 |
| chr10 | 9008972 | 9009092 | MACS2_peak_273 | 25 | + | 5.46411 | 7.45132 | 2.55202 | 72 | chr10 | unknown | gene | 8722218 | 8885858 | - | Sash1 | Sash1 | P17628 | NM_175155 | TSS10761 |
| chr10 | 9008972 | 9009092 | MACS2_peak_273 | 25 | + | 5.46411 | 7.45132 | 2.55202 | 72 | chr10 | unknown | gene | 9627258 | 9674963 | - | Samd5 | Samd5 | P18361 | NM_177271 | TSS17088 |
| chr10 | 9987320 | 9987430 | MACS2_peak_274 | 49 | + | 6.77503 | 10.04021 | 4.94691 | 58 | chr10 | unknown | gene | 9755546 | 9900683 | - | Stxbp5 | Stxbp5 | P4872 | NM_001081344 | TSS5961 |
| chr10 | 9987320 | 9987430 | MACS2_peak_274 | 49 | + | 6.77503 | 10.04021 | 4.94691 | 58 | chr10 | unknown | gene | 10335702 | 10472314 | - | Adgb | Adgb | P12982 | NM_001127353 | TSS5517 |
| chr10 | 10205574 | 10205692 | MACS2_peak_275 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 74 | chr10 | unknown | gene | 9755546 | 9900683 | - | Stxbp5 | Stxbp5 | P4872 | NM_001081344 | TSS5961 |
| chr10 | 10205574 | 10205692 | MACS2_peak_275 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 74 | chr10 | unknown | gene | 10335702 | 10472314 | - | Adgb | Adgb | P12982 | NM_001127353 | TSS5517 |
| chr10 | 11527876 | 11527967 | MACS2_peak_276 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 78 | chr10 | unknown | gene | 11343444 | 11457417 | + | Epm2a | Epm2a | P7183 | NM_010146 | TSS26610 |
| chr10 | 11527876 | 11527967 | MACS2_peak_276 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 78 | chr10 | unknown | gene | 12382187 | 12861646 | - | Utrn | Utrn | P263 | NM_011682 | TSS243 |
| chr10 | 12502505 | 12502596 | MACS2_peak_277 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 68 | chr10 | unknown | gene | 11343444 | 11457417 | + | Epm2a | Epm2a | P7183 | NM_010146 | TSS26610 |
| chr10 | 12502505 | 12502596 | MACS2_peak_277 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 68 | chr10 | unknown | gene | 12916645 | 12923127 | - | B230208H11Rik | B230208H11Rik | | NR_038027 | TSS16494 |
| chr10 | 14202727 | 14202818 | MACS2_peak_278 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 28 | chr10 | unknown | gene | 13966378 | 14149736 | + | Hivep2 | Hivep2 | P5897 | NM_010437 | TSS6094 |
| chr10 | 14202727 | 14202818 | MACS2_peak_278 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 28 | chr10 | unknown | gene | 14402584 | 14544915 | - | Adgrg6 | Adgrg6 | P21635 | NM_001002268 | TSS22412 |
| chr10 | 16414504 | 16414595 | MACS2_peak_279 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 52 | chr10 | unknown | gene | 15791776 | 15807065 | + | C330004P14Rik | C330004P14Rik | | NR_131087 | TSS10568 |
| chr10 | 16414504 | 16414595 | MACS2_peak_279 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 52 | chr10 | unknown | gene | 16951093 | 17095782 | - | Gm20125 | Gm20125 | | NR_038020 | TSS7111 |
| chr10 | 17215063 | 17215154 | MACS2_peak_280 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 86 | chr10 | unknown | gene | 16951093 | 17095782 | - | Gm20125 | Gm20125 | | NR_038020 | TSS7111 |
| chr10 | 17215063 | 17215154 | MACS2_peak_280 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 86 | chr10 | unknown | gene | 17723227 | 17724755 | + | Cited2 | Cited2 | P1138 | NM_010828 | TSS1130 |
| chr10 | 17632124 | 17632215 | MACS2_peak_281 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 50 | chr10 | unknown | gene | 16951093 | 17095782 | - | Gm20125 | Gm20125 | | NR_038020 | TSS7111 |
| chr10 | 17632124 | 17632215 | MACS2_peak_281 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 50 | chr10 | unknown | gene | 17723227 | 17724755 | + | Cited2 | Cited2 | P1138 | NM_010828 | TSS1130 |
| chr10 | 18006035 | 18006126 | MACS2_peak_282 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 39 | chr10 | unknown | gene | 17900465 | 17947782 | - | Heca | Heca | P18127 | NM_001033432 | TSS5904 |
| chr10 | 18006035 | 18006126 | MACS2_peak_282 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 39 | chr10 | unknown | gene | 18011259 | 18023252 | - | Abracl | Abracl | P22850 | NM_028440 | TSS17211 |
| chr10 | 18075020 | 18075111 | MACS2_peak_283 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 18 | chr10 | unknown | gene | 18011259 | 18023252 | - | Abracl | Abracl | P22850 | NM_028440 | TSS17211 |
| chr10 | 18075020 | 18075111 | MACS2_peak_283 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 18 | chr10 | unknown | gene | 18129021 | 18210890 | - | Ect2l | Ect2l | P9429 | NM_001195036 | TSS10698 |
| chr10 | 18252311 | 18252402 | MACS2_peak_284 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 60 | chr10 | unknown | gene | 18213684 | 18234981 | - | Ccdc28a | Ccdc28a | P7891 | NM_144820 | TSS8127 |
| chr10 | 18252311 | 18252402 | MACS2_peak_284 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 60 | chr10 | unknown | gene | 18407674 | 18531973 | + | Nhsl1 | Nhsl1 | P24573 | NM_173390 | TSS12055 |
| chr10 | 19592478 | 19592574 | MACS2_peak_285 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 65 | chr10 | unknown | gene | 19356538 | 19357450 | + | Olig3 | Olig3 | P2172 | NM_053008 | TSS20748 |
| chr10 | 19592478 | 19592574 | MACS2_peak_285 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 65 | chr10 | unknown | gene | 19622027 | 19632918 | + | Il22ra2 | Il22ra2 | P16184 | NM_178258 | TSS2192 |
| chr10 | 20668665 | 20668756 | MACS2_peak_286 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 25 | chr10 | unknown | gene | 20347818 | 20360540 | + | Mtfr2 | Mtfr2 | P17552 | NM_027930 | TSS3086 |
| chr10 | 20668665 | 20668756 | MACS2_peak_286 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 25 | chr10 | unknown | gene | 20952546 | 21079086 | + | Ahi1 | Ahi1 | P17358 | NM_026203 | TSS7812 |
| chr10 | 20951042 | 20951133 | MACS2_peak_287 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 30 | chr10 | unknown | gene | 20398003 | 20724696 | - | Pde7b | Pde7b | P12111 | NM_013875 | TSS13205 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr10 | 20951042 | 20951133 | MACS2_peak_287 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 30 | chr10 | unknown | gene | 20952546 | 21079086 | + | Ahi1 | Ahi1 | P17358 | NM_026203 | TSS7812 |
| chr10 | 20965740 | 20965831 | MACS2_peak_288 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 58 | chr10 | unknown | gene | 20398003 | 20724696 | - | Pde7b | Pde7b | P12111 | NM_013875 | TSS13205 |
| chr10 | 20965740 | 20965831 | MACS2_peak_288 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 58 | chr10 | unknown | gene | 21124929 | 21160718 | - | Myb | Myb | P21019 | NM_001198914 | TSS1948 |
| chr10 | 21054784 | 21054875 | MACS2_peak_289 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 9 | chr10 | unknown | gene | 20398003 | 20724696 | - | Pde7b | Pde7b | P12111 | NM_013875 | TSS13205 |
| chr10 | 21054784 | 21054875 | MACS2_peak_289 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 9 | chr10 | unknown | gene | 21124929 | 21160718 | - | Myb | Myb | P21019 | NM_001198914 | TSS1948 |
| chr10 | 21110093 | 21110184 | MACS2_peak_290 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 77 | chr10 | unknown | gene | 20952546 | 21079086 | + | Ahi1 | Ahi1 | P17358 | NM_026203 | TSS7812 |
| chr10 | 21110093 | 21110184 | MACS2_peak_290 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 77 | chr10 | unknown | gene | 21124929 | 21160718 | - | Myb | Myb | P21019 | NM_001198914 | TSS1948 |
| chr10 | 23120408 | 23120500 | MACS2_peak_291 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 11 | chr10 | unknown | gene | 22817274 | 22819903 | - | Tcf21 | Tcf21 | P16403 | NM_011545 | TSS9220 |
| chr10 | 23120408 | 23120500 | MACS2_peak_291 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 11 | chr10 | unknown | gene | 23785182 | 23787209 | - | Rps12 | Rps12 | P13303 | NM_011295 | TSS25610 |
| chr10 | 23188116 | 23188207 | MACS2_peak_292 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 40 | chr10 | unknown | gene | 22817274 | 22819903 | - | Tcf21 | Tcf21 | P16403 | NM_011545 | TSS9220 |
| chr10 | 23188116 | 23188207 | MACS2_peak_292 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 40 | chr10 | unknown | gene | 23785182 | 23787209 | - | Rps12 | Rps12 | P13303 | NM_011295 | TSS25610 |
| chr10 | 23412435 | 23412526 | MACS2_peak_293 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 26 | chr10 | unknown | gene | 23104167 | 23349903 | - | Eya4 | Eya4 | P12298 | NM_010167 | TSS5587 |
| chr10 | 23412435 | 23412526 | MACS2_peak_293 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 26 | chr10 | unknown | gene | 23785182 | 23787209 | - | Rps12 | Rps12 | P13303 | NM_011295 | TSS25610 |
| chr10 | 23615820 | 23615911 | MACS2_peak_294 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 29 | chr10 | unknown | gene | 23104167 | 23349903 | - | Eya4 | Eya4 | P12298 | NM_010167 | TSS5587 |
| chr10 | 23615820 | 23615911 | MACS2_peak_294 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 29 | chr10 | unknown | gene | 23785182 | 23787209 | - | Rps12 | Rps12 | P13303 | NM_011295 | TSS25610 |
| chr10 | 24182141 | 24182285 | MACS2_peak_295 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 54 | chr10 | unknown | gene | 24108487 | 24109534 | - | Taar9 | Taar9 | P11459 | NM_001010831 | TSS10650 |
| chr10 | 24182141 | 24182285 | MACS2_peak_295 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 54 | chr10 | unknown | gene | 24223516 | 24301629 | + | Moxd1 | Moxd1 | P7176 | NM_021509 | TSS17882 |
| chr10 | 25017291 | 25017382 | MACS2_peak_296 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 24 | chr10 | unknown | gene | 24915206 | 24927368 | - | Arg1 | Arg1 | P12448 | NM_007482 | TSS25161 |
| chr10 | 25017291 | 25017382 | MACS2_peak_296 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 24 | chr10 | unknown | gene | 25169089 | 25299163 | - | Akap7 | Akap7 | P26603 | NM_018747 | TSS564 |
| chr10 | 25082706 | 25082797 | MACS2_peak_297 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 73 | chr10 | unknown | gene | 24915206 | 24927368 | - | Arg1 | Arg1 | P12448 | NM_007482 | TSS25161 |
| chr10 | 25082706 | 25082797 | MACS2_peak_297 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 73 | chr10 | unknown | gene | 25169089 | 25299163 | - | Akap7 | Akap7 | P26603 | NM_018747 | TSS564 |
| chr10 | 26156592 | 26156730 | MACS2_peak_298 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 61 | chr10 | unknown | gene | 26078254 | 26079447 | + | Gm9767 | Gm9767 | | NR_028030 | TSS2142 |
| chr10 | 26156592 | 26156730 | MACS2_peak_298 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 61 | chr10 | unknown | gene | 26229706 | 26271973 | + | Samd3 | Samd3 | P19121 | NM_001013766 | TSS3486 |
| chr10 | 26999145 | 26999236 | MACS2_peak_299 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 37 | chr10 | unknown | gene | 26772511 | 26917096 | + | Arhgap18 | Arhgap18 | P906 | NM_176837 | TSS13768 |
| chr10 | 26999145 | 26999236 | MACS2_peak_299 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 37 | chr10 | unknown | gene | 27389865 | 27397225 | + | 4930579H20Rik | 4930579H20Rik | | NR_131034 | TSS25633 |
| chr10 | 27696789 | 27696880 | MACS2_peak_300 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 35 | chr10 | unknown | gene | 26981284 | 27616796 | - | Lama2 | Lama2 | P24797 | NM_008481 | TSS23811 |
| chr10 | 27696789 | 27696880 | MACS2_peak_300 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 35 | chr10 | unknown | gene | 28074819 | 28595855 | + | Ptprk | Ptprk | P13568 | NM_008983 | TSS20090 |
| chr10 | 28134650 | 28134821 | MACS2_peak_301 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 89 | chr10 | unknown | gene | 26981284 | 27616796 | - | Lama2 | Lama2 | P24797 | NM_008481 | TSS23811 |
| chr10 | 28134650 | 28134821 | MACS2_peak_301 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 89 | chr10 | unknown | gene | 28668359 | 28880992 | + | Themis | Themis | P12605 | NM_001305663 | TSS13746 |
| chr10 | 29040061 | 29040152 | MACS2_peak_302 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 32 | chr10 | unknown | gene | 28972287 | 28986292 | - | 2310057J18Rik | 2310057J18Rik | P9686 | NM_026336 | TSS27606 |
| chr10 | 29040061 | 29040152 | MACS2_peak_302 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 32 | chr10 | unknown | gene | 29143995 | 29199055 | + | Soga3 | Soga3 | P22531 | NM_026138 | TSS7994 |
| chr10 | 33864660 | 33864775 | MACS2_peak_303 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 78 | chr10 | unknown | gene | 33766423 | 33782115 | - | Gm4794 | Gm4794 | P11037 | NM_001101452 | TSS9179 |
| chr10 | 33864660 | 33864775 | MACS2_peak_303 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 78 | chr10 | unknown | gene | 33905110 | 33914567 | + | Rsph4a | Rsph4a | P16671 | NM_001162957 | TSS1914 |
| chr10 | 36118334 | 36118425 | MACS2_peak_304 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 29 | chr10 | unknown | gene | 34483399 | 34608571 | + | Frk | Frk | P1634 | NM_010237 | TSS18767 |
| chr10 | 36118334 | 36118425 | MACS2_peak_304 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 29 | chr10 | unknown | gene | 36506806 | 36833511 | + | Hs3st5 | Hs3st5 | P2225 | NM_001253355 | TSS8717 |
| chr10 | 37289681 | 37289772 | MACS2_peak_305 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 65 | chr10 | unknown | gene | 37133242 | 37138535 | - | Marcks | Marcks | P25202 | NM_008538 | TSS10486 |
| chr10 | 37289681 | 37289772 | MACS2_peak_305 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 65 | chr10 | unknown | gene | 38175773 | 38181903 | + | 4930591E09Rik | 4930591E09Rik | | NR_131035 | TSS12516 |
| chr10 | 38105744 | 38105847 | MACS2_peak_306 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 25 | chr10 | unknown | gene | 37133242 | 37138535 | - | Marcks | Marcks | P25202 | NM_008538 | TSS10486 |
| chr10 | 38105744 | 38105847 | MACS2_peak_306 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 25 | chr10 | unknown | gene | 38175773 | 38181903 | + | 4930591E09Rik | 4930591E09Rik | | NR_131035 | TSS12516 |
| chr10 | 38506636 | 38506727 | MACS2_peak_307 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 62 | chr10 | unknown | gene | 38175773 | 38181903 | + | 4930591E09Rik | 4930591E09Rik | | NR_131035 | TSS12516 |
| chr10 | 38506636 | 38506727 | MACS2_peak_307 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 62 | chr10 | unknown | gene | 38820540 | 38821779 | - | Rfpl4b | Rfpl4b | P7451 | NM_001177783 | TSS3055 |
| chr10 | 38676304 | 38676395 | MACS2_peak_308 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 65 | chr10 | unknown | gene | 38175773 | 38181903 | + | 4930591E09Rik | 4930591E09Rik | | NR_131035 | TSS12516 |
| chr10 | 38676304 | 38676395 | MACS2_peak_308 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 65 | chr10 | unknown | gene | 38820540 | 38821779 | - | Rfpl4b | Rfpl4b | P7451 | NM_001177783 | TSS3055 |
| chr10 | 38863968 | 38864059 | MACS2_peak_309 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 29 | chr10 | unknown | gene | 38820540 | 38821779 | - | Rfpl4b | Rfpl4b | P7451 | NM_001177783 | TSS3055 |
| chr10 | 38863968 | 38864059 | MACS2_peak_309 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 29 | chr10 | unknown | gene | 38965514 | 39110033 | + | Lama4 | Lama4 | P4792 | NM_010681 | TSS12504 |
| chr10 | 40085257 | 40085427 | MACS2_peak_310 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 138 | chr10 | unknown | gene | 40001572 | 40024916 | - | AI317395 | AI317395 | P20185 | NM_144821 | TSS20895 |
| chr10 | 40085257 | 40085427 | MACS2_peak_310 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 138 | chr10 | unknown | gene | 40223245 | 40246975 | - | Rpf2 | Rpf2 | P22039 | NM_023323 | TSS16757 |
| chr10 | 41340990 | 41341081 | MACS2_peak_311 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 36 | chr10 | unknown | gene | 41188171 | 41303052 | - | Fig4 | Fig4 | P3744 | NM_133999 | TSS23405 |
| chr10 | 41340990 | 41341081 | MACS2_peak_311 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 36 | chr10 | unknown | gene | 41450357 | 41465042 | + | Zbtb24 | Zbtb24 | P11950 | NM_001277229 | TSS23063 |
| chr10 | 43022925 | 43023016 | MACS2_peak_312 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 14 | chr10 | unknown | gene | 42860511 | 42957744 | + | Scml4 | Scml4 | P19690 | NM_172938 | TSS7821 |
| chr10 | 43022925 | 43023016 | MACS2_peak_312 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 14 | chr10 | unknown | gene | 43174698 | 43176565 | + | 9030612E09Rik | 9030612E09Rik | | NR_102361 | TSS11641 |
| chr10 | 44098753 | 44099023 | MACS2_peak_313 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 244 | chr10 | unknown | gene | 43950306 | 44004068 | - | Aim1 | Aim1 | P3303 | NM_172393 | TSS5751 |
| chr10 | 44098753 | 44099023 | MACS2_peak_313 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 244 | chr10 | unknown | gene | 44170446 | 44219585 | + | Speer5-ps1 | Speer5-ps1 | | NR_001582 | TSS6216 |
| chr10 | 45103557 | 45103648 | MACS2_peak_314 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 27 | chr10 | unknown | gene | 44437173 | 44458508 | - | Prdm1 | Prdm1 | P19863 | NM_007548 | TSS21854 |
| chr10 | 45103557 | 45103648 | MACS2_peak_314 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 27 | chr10 | unknown | gene | 45289304 | 45317980 | + | Popdc3 | Popdc3 | P2006 | NM_024286 | TSS7783 |
| chr10 | 45424782 | 45424945 | MACS2_peak_315 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 45 | chr10 | unknown | gene | 45335761 | 45369309 | + | Bves | Bves | P3429 | NM_024285 | TSS25575 |
| chr10 | 45424782 | 45424945 | MACS2_peak_315 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 45 | chr10 | unknown | gene | 45577828 | 45711536 | + | Hace1 | Hace1 | P25759 | NM_172473 | TSS15374 |
| chr10 | 46286612 | 46286769 | MACS2_peak_316 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 73 | chr10 | unknown | gene | 46244748 | 46244770 | + | Snord14c | Snord14c | | NR_028276 | TSS23421 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr10 | 46286612 | 46286769 | MACS2_peak_316 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 73 | chr10 | unknown | gene | 49093680 | 49095843 | - | C130030K03Rik | C130030K03Rik | | NR_046212 | TSS9223 |
| chr10 | 46597163 | 46597254 | MACS2_peak_317 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 19 | chr10 | unknown | gene | 46244748 | 46244770 | + | Snord14c | Snord14c | | NR_028276 | TSS23421 |
| chr10 | 46597163 | 46597254 | MACS2_peak_317 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 19 | chr10 | unknown | gene | 49093680 | 49095843 | - | C130030K03Rik | C130030K03Rik | | NR_046212 | TSS9223 |
| chr10 | 46697512 | 46697603 | MACS2_peak_318 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 79 | chr10 | unknown | gene | 46244748 | 46244770 | + | Snord14c | Snord14c | | NR_028276 | TSS23421 |
| chr10 | 46697512 | 46697603 | MACS2_peak_318 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 79 | chr10 | unknown | gene | 49093680 | 49095843 | - | C130030K03Rik | C130030K03Rik | | NR_046212 | TSS9223 |
| chr10 | 47874066 | 47874157 | MACS2_peak_319 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 72 | chr10 | unknown | gene | 46244748 | 46244770 | + | Snord14c | Snord14c | | NR_028276 | TSS23421 |
| chr10 | 47874066 | 47874157 | MACS2_peak_319 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 72 | chr10 | unknown | gene | 49093680 | 49095843 | - | C130030K03Rik | C130030K03Rik | | NR_046212 | TSS9223 |
| chr10 | 51053421 | 51053512 | MACS2_peak_320 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 49 | chr10 | unknown | gene | 50895650 | 50984341 | + | Sim1 | Sim1 | P7016 | NM_011376 | TSS18861 |
| chr10 | 51053421 | 51053512 | MACS2_peak_320 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 49 | chr10 | unknown | gene | 51480611 | 51486329 | + | Lilr4b | Lilr4b | P19730 | NM_008147 | TSS3747 |
| chr10 | 53775494 | 53775614 | MACS2_peak_321 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 46 | chr10 | unknown | gene | 53633144 | 53750880 | - | Fam184a | Fam184a | P7433 | NM_001081428 | TSS5010 |
| chr10 | 53775494 | 53775614 | MACS2_peak_321 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 46 | chr10 | unknown | gene | 53906032 | 54075796 | - | Man1a | Man1a | P12423 | NM_008548 | TSS21271 |
| chr10 | 54065395 | 54065486 | MACS2_peak_322 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 2 | chr10 | unknown | gene | 53633144 | 53750880 | - | Fam184a | Fam184a | P7433 | NM_001081428 | TSS5010 |
| chr10 | 54065395 | 54065486 | MACS2_peak_322 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 2 | chr10 | unknown | gene | 54075921 | 54081081 | + | Gm16998 | Gm16998 | | NR_038016 | TSS22256 |
| chr10 | 54176542 | 54176647 | MACS2_peak_323 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 18 | chr10 | unknown | gene | 54075921 | 54081081 | + | Gm16998 | Gm16998 | | NR_038016 | TSS22256 |
| chr10 | 54176542 | 54176647 | MACS2_peak_323 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 18 | chr10 | unknown | gene | 56014293 | 56228632 | - | Tbc1d32 | Tbc1d32 | P24378 | NM_001033385 | TSS8730 |
| chr10 | 58389391 | 58389482 | MACS2_peak_324 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 82 | chr10 | unknown | gene | 58255525 | 58304164 | + | Gcc2 | Gcc2 | P22369 | NM_027375 | TSS11503 |
| chr10 | 58389391 | 58389482 | MACS2_peak_324 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 82 | chr10 | unknown | gene | 58446851 | 58493968 | + | Ranbp2 | Ranbp2 | P9562 | NM_011240 | TSS19305 |
| chr10 | 60005729 | 60005837 | MACS2_peak_325 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 64 | chr10 | unknown | gene | 59987908 | 60003112 | - | Anapc16 | Anapc16 | P9158 | NM_025514 | TSS1819 |
| chr10 | 60005729 | 60005837 | MACS2_peak_325 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 64 | chr10 | unknown | gene | 60106256 | 60131481 | + | Spock2 | Spock2 | P22842 | NM_052994 | TSS19957 |
| chr10 | 65177277 | 65177430 | MACS2_peak_326 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 43 | chr10 | unknown | gene | 63430097 | 65002833 | + | Ctnna3 | Ctnna3 | P16728 | NM_177612 | TSS10244 |
| chr10 | 65177277 | 65177430 | MACS2_peak_326 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 43 | chr10 | unknown | gene | 66120608 | 66124064 | - | 1700023F02Rik | 1700023F02Rik | | NR_038039 | TSS23937 |
| chr10 | 68192310 | 68192401 | MACS2_peak_327 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 58 | chr10 | unknown | gene | 67979597 | 68041917 | + | Rtkn2 | Rtkn2 | P10782 | NM_001081346 | TSS6615 |
| chr10 | 68192310 | 68192401 | MACS2_peak_327 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 58 | chr10 | unknown | gene | 68319064 | 68321142 | - | 4930545H06Rik | 4930545H06Rik | | NR_045357 | TSS27480 |
| chr10 | 68446267 | 68446542 | MACS2_peak_328 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 242 | chr10 | unknown | gene | 68319064 | 68321142 | - | 4930545H06Rik | 4930545H06Rik | | NR_045357 | TSS27480 |
| chr10 | 68446267 | 68446542 | MACS2_peak_328 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 242 | chr10 | unknown | gene | 68723745 | 68778857 | + | Tmem26 | Tmem26 | P3056 | NM_177794 | TSS27213 |
| chr10 | 68586806 | 68586909 | MACS2_peak_329 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 76 | chr10 | unknown | gene | 68430955 | 68541857 | - | 1700040L02Rik | 1700040L02Rik | P18165 | NM_028491 | TSS615 |
| chr10 | 68586806 | 68586909 | MACS2_peak_329 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 76 | chr10 | unknown | gene | 68723745 | 68778857 | + | Tmem26 | Tmem26 | P3056 | NM_177794 | TSS27213 |
| chr10 | 68856389 | 68856480 | MACS2_peak_330 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 2 | chr10 | unknown | gene | 68723745 | 68778857 | + | Tmem26 | Tmem26 | P3056 | NM_177794 | TSS27213 |
| chr10 | 68856389 | 68856480 | MACS2_peak_330 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 2 | chr10 | unknown | gene | 69208551 | 69289689 | + | Rhobtb1 | Rhobtb1 | P20606 | NM_001252636 | TSS24939 |
| chr10 | 69337634 | 69337725 | MACS2_peak_331 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 41 | chr10 | unknown | gene | 69208551 | 69289689 | + | Rhobtb1 | Rhobtb1 | P20606 | NM_001252636 | TSS24939 |
| chr10 | 69337634 | 69337725 | MACS2_peak_331 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 41 | chr10 | unknown | gene | 69533707 | 70027436 | + | Ank3 | Ank3 | P15190 | NM_170689 | TSS1379 |
| chr10 | 70080989 | 70081116 | MACS2_peak_332 | 35 | + | 6.07165 | 8.598 | 3.58294 | 66 | chr10 | unknown | gene | 69533707 | 70027436 | + | Ank3 | Ank3 | P15190 | NM_170689 | TSS1379 |
| chr10 | 70080989 | 70081116 | MACS2_peak_332 | 35 | + | 6.07165 | 8.598 | 3.58294 | 66 | chr10 | unknown | gene | 70097120 | 70189278 | + | Ccdc6 | Ccdc6 | P24362 | NM_001111121 | TSS12260 |
| chr10 | 70624352 | 70624572 | MACS2_peak_333 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 206 | chr10 | unknown | gene | 70557685 | 70599107 | - | Phyhipl | Phyhipl | P8392 | NM_001162846 | TSS20329 |
| chr10 | 70624352 | 70624572 | MACS2_peak_333 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 206 | chr10 | unknown | gene | 70925095 | 71159616 | - | Bicc1 | Bicc1 | P16060 | NM_031397 | TSS2292 |
| chr10 | 71370757 | 71370848 | MACS2_peak_334 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 23 | chr10 | unknown | gene | 71330493 | 71344754 | - | Cisd1 | Cisd1 | P15380 | NM_134007 | TSS423 |
| chr10 | 71370757 | 71370848 | MACS2_peak_334 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 23 | chr10 | unknown | gene | 71979884 | 71980690 | - | 1700049L16Rik | 1700049L16Rik | | NR_003644 | TSS13326 |
| chr10 | 71645441 | 71645532 | MACS2_peak_335 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 10 | chr10 | unknown | gene | 71347792 | 71381818 | + | Ipmk | Ipmk | P7179 | NM_027184 | TSS6045 |
| chr10 | 71645441 | 71645532 | MACS2_peak_335 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 10 | chr10 | unknown | gene | 71979884 | 71980690 | - | 1700049L16Rik | 1700049L16Rik | | NR_003644 | TSS13326 |
| chr10 | 75981367 | 75981458 | MACS2_peak_336 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 71 | chr10 | unknown | gene | 75948311 | 75949462 | + | Vpreb3 | Vpreb3 | P25580 | NM_009514 | TSS3928 |
| chr10 | 75981367 | 75981458 | MACS2_peak_336 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 71 | chr10 | unknown | gene | 76008925 | 76009017 | + | Mir6409 | Mir6409 | | NR_105836 | TSS489 |
| chr10 | 82861153 | 82861244 | MACS2_peak_337 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 52 | chr10 | unknown | gene | 82812122 | 82824242 | + | 1700028I16Rik | 1700028I16Rik | | NR_038042 | TSS13615 |
| chr10 | 82861153 | 82861244 | MACS2_peak_337 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 52 | chr10 | unknown | gene | 82866625 | 82867834 | + | Eid3 | Eid3 | P7651 | NM_025499 | TSS11485 |
| chr10 | 84335523 | 84335627 | MACS2_peak_338 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 50 | chr10 | unknown | gene | 83722864 | 83762762 | + | 1500009L16Rik | 1500009L16Rik | P12715 | NM_001145198 | TSS21227 |
| chr10 | 84335523 | 84335627 | MACS2_peak_338 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 50 | chr10 | unknown | gene | 84371318 | 84440357 | - | Nuak1 | Nuak1 | P3389 | NM_001004363 | TSS8202 |
| chr10 | 84641873 | 84641982 | MACS2_peak_339 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 37 | chr10 | unknown | gene | 84576946 | 84613726 | + | Tcp11l2 | Tcp11l2 | P24371 | NM_146008 | TSS15987 |
| chr10 | 84641873 | 84641982 | MACS2_peak_339 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 37 | chr10 | unknown | gene | 84756047 | 84905227 | + | Rfx4 | Rfx4 | P12206 | NM_001024918 | TSS18610 |
| chr10 | 85057418 | 85057509 | MACS2_peak_340 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 31 | chr10 | unknown | gene | 84917612 | 85015187 | + | Ric8b | Ric8b | P2077 | NM_001013441 | TSS24442 |
| chr10 | 85057418 | 85057509 | MACS2_peak_340 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 31 | chr10 | unknown | gene | 85097018 | 85102495 | - | Fhl4 | Fhl4 | P8349 | NM_010214 | TSS10530 |
| chr10 | 86684919 | 86685010 | MACS2_peak_341 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 65 | chr10 | unknown | gene | 86048745 | 86498896 | - | Syn3 | Syn3 | P4416 | NM_013722 | TSS2158 |
| chr10 | 86684919 | 86685010 | MACS2_peak_341 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 65 | chr10 | unknown | gene | 86685526 | 86689954 | + | 1810014B01Rik | 1810014B01Rik | | NR_015572 | TSS20839 |
| chr10 | 87709819 | 87709941 | MACS2_peak_342 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 70 | chr10 | unknown | gene | 87521794 | 87583578 | + | Pah | Pah | P2486 | NM_008777 | TSS15624 |
| chr10 | 87709819 | 87709941 | MACS2_peak_342 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 70 | chr10 | unknown | gene | 87859055 | 87930734 | + | Igf1 | Igf1 | P583 | NM_010512 | TSS25669 |
| chr10 | 87833733 | 87833824 | MACS2_peak_343 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 33 | chr10 | unknown | gene | 87521794 | 87583578 | + | Pah | Pah | P2486 | NM_008777 | TSS15624 |
| chr10 | 87833733 | 87833824 | MACS2_peak_343 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 33 | chr10 | unknown | gene | 87859055 | 87930734 | + | Igf1 | Igf1 | P583 | NM_010512 | TSS25669 |
| chr10 | 87971407 | 87971498 | MACS2_peak_344 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 16 | chr10 | unknown | gene | 87966670 | 87968017 | + | Tyms-ps | Tyms-ps | | NR_000040 | TSS27627 |
| chr10 | 87971407 | 87971498 | MACS2_peak_344 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 16 | chr10 | unknown | gene | 88091071 | 88092189 | + | Pmch | Pmch | P8022 | NM_029971 | TSS13999 |
| chr10 | 88125693 | 88125850 | MACS2_peak_345 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 27 | chr10 | unknown | gene | 88091071 | 88092189 | + | Pmch | Pmch | P8022 | NM_029971 | TSS13999 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr10 | 88125693 | 88125850 | MACS2_peak_345 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 27 | chr10 | unknown | gene | 88146991 | 88178247 | + | Nup37 | Nup37 | P8889 | NM_027191 | TSS17904 |
| chr10 | 89078639 | 89078730 | MACS2_peak_346 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 21 | chr10 | unknown | gene | 88885991 | 88926335 | + | Slc5a8 | Slc5a8 | P20263 | NM_145423 | TSS6680 |
| chr10 | 89078639 | 89078730 | MACS2_peak_346 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 21 | chr10 | unknown | gene | 89408822 | 89443967 | - | Gas2l3 | Gas2l3 | P8051 | NM_001284344 | TSS22928 |
| chr10 | 89117477 | 89117568 | MACS2_peak_347 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 42 | chr10 | unknown | gene | 88885991 | 88926335 | + | Slc5a8 | Slc5a8 | P20263 | NM_145423 | TSS6680 |
| chr10 | 89117477 | 89117568 | MACS2_peak_347 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 42 | chr10 | unknown | gene | 89408822 | 89443967 | - | Gas2l3 | Gas2l3 | P8051 | NM_001284344 | TSS22928 |
| chr10 | 89862391 | 89862482 | MACS2_peak_348 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 14 | chr10 | unknown | gene | 89744990 | 89818051 | + | Uhrf1bp1l | Uhrf1bp1l | P20796 | NM_029166 | TSS16170 |
| chr10 | 89862391 | 89862482 | MACS2_peak_348 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 14 | chr10 | unknown | gene | 89873508 | 90969914 | + | Anks1b | Anks1b | P18232 | NM_001128086 | TSS18277 |
| chr10 | 90847190 | 90847281 | MACS2_peak_349 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 57 | chr10 | unknown | gene | 89744990 | 89818051 | + | Uhrf1bp1l | Uhrf1bp1l | P20796 | NM_029166 | TSS16170 |
| chr10 | 90847190 | 90847281 | MACS2_peak_349 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 57 | chr10 | unknown | gene | 90989310 | 91082743 | - | Apaf1 | Apaf1 | P23944 | NM_001042558 | TSS18154 |
| chr10 | 93680636 | 93680735 | MACS2_peak_350 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 65 | chr10 | unknown | gene | 93665243 | 93665854 | - | Gm8580 | Gm8580 | | NR_027478 | TSS15508 |
| chr10 | 93680636 | 93680735 | MACS2_peak_350 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 65 | chr10 | unknown | gene | 93831554 | 93857928 | + | Usp44 | Usp44 | P9270 | NM_001206851 | TSS24105 |
| chr10 | 93689817 | 93690133 | MACS2_peak_351 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 183 | chr10 | unknown | gene | 93674217 | 93683322 | - | Gm15915 | Gm15915 | | NR_038017 | TSS12525 |
| chr10 | 93689817 | 93690133 | MACS2_peak_351 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 183 | chr10 | unknown | gene | 93831554 | 93857928 | + | Usp44 | Usp44 | P9270 | NM_001206851 | TSS24105 |
| chr10 | 94758516 | 94758615 | MACS2_peak_352 | 23 | + | 5.36409 | 7.26321 | 2.37531 | 35 | chr10 | unknown | gene | 94673492 | 94688613 | - | Cep83os | Cep83os | | NR_015524 | TSS9415 |
| chr10 | 94758516 | 94758615 | MACS2_peak_352 | 23 | + | 5.36409 | 7.26321 | 2.37531 | 35 | chr10 | unknown | gene | 94790865 | 94944578 | - | Plxnc1 | Plxnc1 | P15159 | NM_018797 | TSS6810 |
| chr10 | 95003790 | 95003937 | MACS2_peak_353 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 76 | chr10 | unknown | gene | 94790865 | 94944578 | - | Plxnc1 | Plxnc1 | P15159 | NM_018797 | TSS6810 |
| chr10 | 95003790 | 95003937 | MACS2_peak_353 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 76 | chr10 | unknown | gene | 95120581 | 95145825 | - | Gm29684 | Gm29684 | | NR_131146 | TSS20712 |
| chr10 | 95062645 | 95062736 | MACS2_peak_354 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 39 | chr10 | unknown | gene | 94790865 | 94944578 | - | Plxnc1 | Plxnc1 | P15159 | NM_018797 | TSS6810 |
| chr10 | 95062645 | 95062736 | MACS2_peak_354 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 39 | chr10 | unknown | gene | 95120581 | 95145825 | - | Gm29684 | Gm29684 | | NR_131146 | TSS20712 |
| chr10 | 95117729 | 95117820 | MACS2_peak_355 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 35 | chr10 | unknown | gene | 94790865 | 94944578 | - | Plxnc1 | Plxnc1 | P15159 | NM_018797 | TSS6810 |
| chr10 | 95117729 | 95117820 | MACS2_peak_355 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 35 | chr10 | unknown | gene | 95120581 | 95145825 | - | Gm29684 | Gm29684 | | NR_131146 | TSS20712 |
| chr10 | 96077623 | 96077819 | MACS2_peak_356 | 123 | + | 10.43987 | 17.68996 | 12.32544 | 55 | chr10 | unknown | gene | 95940662 | 96042204 | + | Eea1 | Eea1 | P19724 | NM_001001932 | TSS6980 |
| chr10 | 96077623 | 96077819 | MACS2_peak_356 | 123 | + | 10.43987 | 17.68996 | 12.32544 | 55 | chr10 | unknown | gene | 96226206 | 96248708 | + | 4930459C07Rik | 4930459C07Rik | | NR_110448 | TSS26097 |
| chr10 | 96262702 | 96262793 | MACS2_peak_357 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 45 | chr10 | unknown | gene | 96226206 | 96248708 | + | 4930459C07Rik | 4930459C07Rik | | NR_110448 | TSS26097 |
| chr10 | 96262702 | 96262793 | MACS2_peak_357 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 45 | chr10 | unknown | gene | 96617000 | 96618643 | + | Btg1 | Btg1 | P25603 | NM_007569 | TSS7862 |
| chr10 | 96358249 | 96358340 | MACS2_peak_358 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 2 | chr10 | unknown | gene | 96226206 | 96248708 | + | 4930459C07Rik | 4930459C07Rik | | NR_110448 | TSS26097 |
| chr10 | 96358249 | 96358340 | MACS2_peak_358 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 2 | chr10 | unknown | gene | 96617000 | 96618643 | + | Btg1 | Btg1 | P25603 | NM_007569 | TSS7862 |
| chr10 | 96719946 | 96720078 | MACS2_peak_359 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 48 | chr10 | unknown | gene | 96617000 | 96618643 | + | Btg1 | Btg1 | P25603 | NM_007569 | TSS7862 |
| chr10 | 96719946 | 96720078 | MACS2_peak_359 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 48 | chr10 | unknown | gene | 97035767 | 97061059 | + | 4930556N09Rik | 4930556N09Rik | | NR_045358 | TSS6249 |
| chr10 | 97094873 | 97094964 | MACS2_peak_360 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 27 | chr10 | unknown | gene | 97035767 | 97061059 | + | 4930556N09Rik | 4930556N09Rik | | NR_045358 | TSS6249 |
| chr10 | 97094873 | 97094964 | MACS2_peak_360 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 27 | chr10 | unknown | gene | 97423477 | 97423562 | + | Mir3966 | Mir3966 | | NR_039547 | TSS1360 |
| chr10 | 97179849 | 97179940 | MACS2_peak_361 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 42 | chr10 | unknown | gene | 97035767 | 97061059 | + | 4930556N09Rik | 4930556N09Rik | | NR_045358 | TSS6249 |
| chr10 | 97179849 | 97179940 | MACS2_peak_361 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 42 | chr10 | unknown | gene | 97423477 | 97423562 | + | Mir3966 | Mir3966 | | NR_039547 | TSS1360 |
| chr10 | 97424318 | 97424409 | MACS2_peak_362 | 32 | + | 5.8651 | 8.25694 | 3.2954 | 58 | chr10 | unknown | gene | 97423477 | 97423562 | + | Mir3966 | Mir3966 | | NR_039547 | TSS1360 |
| chr10 | 97424318 | 97424409 | MACS2_peak_362 | 32 | + | 5.8651 | 8.25694 | 3.2954 | 58 | chr10 | unknown | gene | 97479499 | 97517655 | + | Dcn | Dcn | P9016 | NM_001190451 | TSS18192 |
| chr10 | 97486333 | 97486482 | MACS2_peak_363 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 71 | chr10 | unknown | gene | 97423477 | 97423562 | + | Mir3966 | Mir3966 | | NR_039547 | TSS1360 |
| chr10 | 97486333 | 97486482 | MACS2_peak_363 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 71 | chr10 | unknown | gene | 97565500 | 97572051 | + | Lum | Lum | P10455 | NM_008524 | TSS18681 |
| chr10 | 98126275 | 98126366 | MACS2_peak_364 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 13 | chr10 | unknown | gene | 97681413 | 97967090 | - | Gm10754 | Gm10754 | | NR_033537 | TSS1353 |
| chr10 | 98126275 | 98126366 | MACS2_peak_364 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 13 | chr10 | unknown | gene | 98299926 | 98351867 | - | Gm8633 | Gm8633 | | NR_045179 | TSS26336 |
| chr10 | 98173917 | 98174008 | MACS2_peak_365 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 44 | chr10 | unknown | gene | 97681413 | 97967090 | - | Gm10754 | Gm10754 | | NR_033537 | TSS1353 |
| chr10 | 98173917 | 98174008 | MACS2_peak_365 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 44 | chr10 | unknown | gene | 98299926 | 98351867 | - | Gm8633 | Gm8633 | | NR_045179 | TSS26336 |
| chr10 | 98543463 | 98543604 | MACS2_peak_366 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 77 | chr10 | unknown | gene | 98299926 | 98351867 | - | Gm8633 | Gm8633 | | NR_045179 | TSS26336 |
| chr10 | 98543463 | 98543604 | MACS2_peak_366 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 77 | chr10 | unknown | gene | 98915151 | 99023119 | + | Atp2b1 | Atp2b1 | P22315 | NM_026482 | TSS25045 |
| chr10 | 99007508 | 99007616 | MACS2_peak_367 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 45 | chr10 | unknown | gene | 98299926 | 98351867 | - | Gm8633 | Gm8633 | | NR_045179 | TSS26336 |
| chr10 | 99007508 | 99007616 | MACS2_peak_367 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 45 | chr10 | unknown | gene | 99107170 | 99196730 | + | Poc1b | Poc1b | P22544 | NM_027740 | TSS4111 |
| chr10 | 99172503 | 99172594 | MACS2_peak_368 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 10 | chr10 | unknown | gene | 99108134 | 99110151 | + | Galnt4 | Galnt4 | P1354 | NM_015737 | TSS15890 |
| chr10 | 99172503 | 99172594 | MACS2_peak_368 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 10 | chr10 | unknown | gene | 99263230 | 99266299 | + | Dusp6 | Dusp6 | P5223 | NM_026268 | TSS388 |
| chr10 | 99949105 | 99949196 | MACS2_peak_369 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 36 | chr10 | unknown | gene | 99757704 | 99759201 | - | Csl | Csl | P2148 | NM_027945 | TSS3132 |
| chr10 | 99949105 | 99949196 | MACS2_peak_369 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 36 | chr10 | unknown | gene | 100015823 | 100100412 | + | Kitl | Kitl | P23606 | NM_013598 | TSS3961 |
| chr10 | 100300337 | 100300430 | MACS2_peak_370 | 31 | + | 5.82147 | 8.1379 | 3.18452 | 28 | chr10 | unknown | gene | 100015823 | 100100412 | + | Kitl | Kitl | P23606 | NM_013598 | TSS3961 |
| chr10 | 100300337 | 100300430 | MACS2_peak_370 | 31 | + | 5.82147 | 8.1379 | 3.18452 | 28 | chr10 | unknown | gene | 100335675 | 100382539 | + | Gm4312 | Gm4312 | P415 | NM_001166636 | TSS27673 |
| chr10 | 100326313 | 100326410 | MACS2_peak_371 | 40 | + | 6.17076 | 9.08297 | 4.03867 | 29 | chr10 | unknown | gene | 100015823 | 100100412 | + | Kitl | Kitl | P23606 | NM_013598 | TSS3961 |
| chr10 | 100326313 | 100326410 | MACS2_peak_371 | 40 | + | 6.17076 | 9.08297 | 4.03867 | 29 | chr10 | unknown | gene | 100335675 | 100382539 | + | Gm4312 | Gm4312 | P415 | NM_001166636 | TSS27673 |
| chr10 | 100883620 | 100883771 | MACS2_peak_372 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 74 | chr10 | unknown | gene | 100592385 | 100618101 | + | 1700017N19Rik | 1700017N19Rik | P26087 | NM_001081246 | TSS9409 |
| chr10 | 100883620 | 100883771 | MACS2_peak_372 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 74 | chr10 | unknown | gene | 101681486 | 102389363 | + | Mgat4c | Mgat4c | P12852 | NM_001205098 | TSS11133 |
| chr10 | 101555289 | 101555423 | MACS2_peak_373 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 51 | chr10 | unknown | gene | 100592385 | 100618101 | + | 1700017N19Rik | 1700017N19Rik | P26087 | NM_001081246 | TSS9409 |
| chr10 | 101555289 | 101555423 | MACS2_peak_373 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 51 | chr10 | unknown | gene | 101681486 | 102389363 | + | Mgat4c | Mgat4c | P12852 | NM_001205098 | TSS11133 |
| chr10 | 103207040 | 103207131 | MACS2_peak_374 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 38 | chr10 | unknown | gene | 103007846 | 103028606 | - | Alx1 | Alx1 | P18267 | NM_172553 | TSS14741 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr10 | 103207040 | 103207131 | MACS2_peak_374 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 38 | chr10 | unknown | gene | 103367807 | 103418394 | + | Slc6a15 | Slc6a15 | P9901 | NM_001252330 | TSS1668 |
| chr10 | 103221070 | 103221161 | MACS2_peak_375 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 23 | chr10 | unknown | gene | 103007846 | 103028606 | - | Alx1 | Alx1 | P18267 | NM_172553 | TSS14741 |
| chr10 | 103221070 | 103221161 | MACS2_peak_375 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 23 | chr10 | unknown | gene | 103367807 | 103418394 | + | Slc6a15 | Slc6a15 | P9901 | NM_001252330 | TSS1668 |
| chr10 | 103703212 | 103703303 | MACS2_peak_376 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 64 | chr10 | unknown | gene | 103367807 | 103418394 | + | Slc6a15 | Slc6a15 | P9901 | NM_001252330 | TSS1668 |
| chr10 | 103703212 | 103703303 | MACS2_peak_376 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 64 | chr10 | unknown | gene | 104142986 | 104196203 | + | Gm8764 | Gm8764 | P19612 | NM_001270900 | TSS9627 |
| chr10 | 103908128 | 103908267 | MACS2_peak_377 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 33 | chr10 | unknown | gene | 103367807 | 103418394 | + | Slc6a15 | Slc6a15 | P9901 | NM_001252330 | TSS1668 |
| chr10 | 103908128 | 103908267 | MACS2_peak_377 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 33 | chr10 | unknown | gene | 104142986 | 104196203 | + | Gm8764 | Gm8764 | P19612 | NM_001270900 | TSS9627 |
| chr10 | 104031966 | 104032072 | MACS2_peak_378 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 66 | chr10 | unknown | gene | 103367807 | 103418394 | + | Slc6a15 | Slc6a15 | P9901 | NM_001252330 | TSS1668 |
| chr10 | 104031966 | 104032072 | MACS2_peak_378 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 66 | chr10 | unknown | gene | 104142986 | 104196203 | + | Gm8764 | Gm8764 | P19612 | NM_001270900 | TSS9627 |
| chr10 | 104662475 | 104662566 | MACS2_peak_379 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 19 | chr10 | unknown | gene | 104287268 | 104287376 | + | Mir6411 | Mir6411 | | NR_105838 | TSS22870 |
| chr10 | 104662475 | 104662566 | MACS2_peak_379 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 19 | chr10 | unknown | gene | 105187663 | 105573749 | - | Tmtc2 | Tmtc2 | P23423 | NM_177368 | TSS10795 |
| chr10 | 104969044 | 104969135 | MACS2_peak_380 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 9 | chr10 | unknown | gene | 104287268 | 104287376 | + | Mir6411 | Mir6411 | | NR_105838 | TSS22870 |
| chr10 | 104969044 | 104969135 | MACS2_peak_380 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 9 | chr10 | unknown | gene | 105187663 | 105573749 | - | Tmtc2 | Tmtc2 | P23423 | NM_177368 | TSS10795 |
| chr10 | 104989740 | 104989831 | MACS2_peak_381 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 23 | chr10 | unknown | gene | 104287268 | 104287376 | + | Mir6411 | Mir6411 | | NR_105838 | TSS22870 |
| chr10 | 104989740 | 104989831 | MACS2_peak_381 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 23 | chr10 | unknown | gene | 105187663 | 105573749 | - | Tmtc2 | Tmtc2 | P23423 | NM_177368 | TSS10795 |
| chr10 | 105525999 | 105526095 | MACS2_peak_382 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 32 | chr10 | unknown | gene | 104287268 | 104287376 | + | Mir6411 | Mir6411 | | NR_105838 | TSS22870 |
| chr10 | 105525999 | 105526095 | MACS2_peak_382 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 32 | chr10 | unknown | gene | 105574550 | 105583870 | + | Gm15663 | Gm15663 | | NR_038032 | TSS4109 |
| chr10 | 105842249 | 105842340 | MACS2_peak_383 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 79 | chr10 | unknown | gene | 105763184 | 105841319 | - | Mettl25 | Mettl25 | P6481 | NM_207522 | TSS5179 |
| chr10 | 105842249 | 105842340 | MACS2_peak_383 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 79 | chr10 | unknown | gene | 106470309 | 106933468 | + | Ppfia2 | Ppfia2 | P6015 | NM_177373 | TSS6305 |
| chr10 | 106005339 | 106005430 | MACS2_peak_384 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 38 | chr10 | unknown | gene | 105841478 | 105847178 | + | Ccdc59 | Ccdc59 | P16200 | NM_025602 | TSS4130 |
| chr10 | 106005339 | 106005430 | MACS2_peak_384 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 38 | chr10 | unknown | gene | 106470309 | 106933468 | + | Ppfia2 | Ppfia2 | P6015 | NM_177373 | TSS6305 |
| chr10 | 106681795 | 106681886 | MACS2_peak_385 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 68 | chr10 | unknown | gene | 106555194 | 106602480 | - | 4930532I03Rik | 4930532I03Rik | | NR_131027 | TSS2769 |
| chr10 | 106681795 | 106681886 | MACS2_peak_385 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 68 | chr10 | unknown | gene | 106936163 | 107123583 | - | Acss3 | Acss3 | P11215 | NM_001142804 | TSS23941 |
| chr10 | 107769495 | 107769626 | MACS2_peak_386 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 90 | chr10 | unknown | gene | 107517359 | 107719872 | - | Ptprq | Ptprq | P11722 | NM_001081432 | TSS2708 |
| chr10 | 107769495 | 107769626 | MACS2_peak_386 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 90 | chr10 | unknown | gene | 107946644 | 107977832 | + | Gm29685 | Gm29685 | | NR_131147 | TSS19712 |
| chr10 | 109018714 | 109018882 | MACS2_peak_387 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 89 | chr10 | unknown | gene | 108497649 | 109010975 | - | Syt1 | Syt1 | P18537 | NM_009306 | TSS25916 |
| chr10 | 109018714 | 109018882 | MACS2_peak_387 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 89 | chr10 | unknown | gene | 109683438 | 110000219 | - | Nav3 | Nav3 | P2711 | NM_001081035 | TSS8082 |
| chr10 | 109341317 | 109341482 | MACS2_peak_388 | 12 | + | 4.14966 | 5.12722 | 1.204 | 84 | chr10 | unknown | gene | 108497649 | 109010975 | - | Syt1 | Syt1 | P18537 | NM_009306 | TSS25916 |
| chr10 | 109341317 | 109341482 | MACS2_peak_388 | 12 | + | 4.14966 | 5.12722 | 1.204 | 84 | chr10 | unknown | gene | 109683438 | 110000219 | - | Nav3 | Nav3 | P2711 | NM_001081035 | TSS8082 |
| chr10 | 109734050 | 109734146 | MACS2_peak_389 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 55 | chr10 | unknown | gene | 108497649 | 109010975 | - | Syt1 | Syt1 | P18537 | NM_009306 | TSS25916 |
| chr10 | 109734050 | 109734146 | MACS2_peak_389 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 55 | chr10 | unknown | gene | 110600649 | 110615961 | + | 9230102K24Rik | 9230102K24Rik | | NR_028438 | TSS3104 |
| chr10 | 110023058 | 110023149 | MACS2_peak_390 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 40 | chr10 | unknown | gene | 109683438 | 110000219 | - | Nav3 | Nav3 | P2711 | NM_001081035 | TSS8082 |
| chr10 | 110023058 | 110023149 | MACS2_peak_390 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 40 | chr10 | unknown | gene | 110600649 | 110615961 | + | 9230102K24Rik | 9230102K24Rik | | NR_028438 | TSS3104 |
| chr10 | 110281812 | 110281959 | MACS2_peak_391 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 8 | chr10 | unknown | gene | 109683438 | 110000219 | - | Nav3 | Nav3 | P2711 | NM_001081035 | TSS8082 |
| chr10 | 110281812 | 110281959 | MACS2_peak_391 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 8 | chr10 | unknown | gene | 110600649 | 110615961 | + | 9230102K24Rik | 9230102K24Rik | | NR_028438 | TSS3104 |
| chr10 | 110352060 | 110352151 | MACS2_peak_392 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 14 | chr10 | unknown | gene | 109683438 | 110000219 | - | Nav3 | Nav3 | P2711 | NM_001081035 | TSS8082 |
| chr10 | 110352060 | 110352151 | MACS2_peak_392 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 14 | chr10 | unknown | gene | 110600649 | 110615961 | + | 9230102K24Rik | 9230102K24Rik | | NR_028438 | TSS3104 |
| chr10 | 111831150 | 111831241 | MACS2_peak_393 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 72 | chr10 | unknown | gene | 111586718 | 111594273 | - | 4933440J02Rik | 4933440J02Rik | | NR_045344 | TSS22384 |
| chr10 | 111831150 | 111831241 | MACS2_peak_393 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 72 | chr10 | unknown | gene | 111854520 | 111874376 | - | Gm20758 | Gm20758 | | NR_046029 | TSS21752 |
| chr10 | 111847755 | 111847846 | MACS2_peak_394 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 56 | chr10 | unknown | gene | 111586718 | 111594273 | - | 4933440J02Rik | 4933440J02Rik | | NR_045344 | TSS22384 |
| chr10 | 111847755 | 111847846 | MACS2_peak_394 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 56 | chr10 | unknown | gene | 111854520 | 111874376 | - | Gm20758 | Gm20758 | | NR_046029 | TSS21752 |
| chr10 | 112756506 | 112756597 | MACS2_peak_395 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 14 | chr10 | unknown | gene | 112271122 | 112462092 | + | Kcnc2 | Kcnc2 | P7846 | NM_001025581 | TSS7312 |
| chr10 | 112756506 | 112756597 | MACS2_peak_395 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 14 | chr10 | unknown | gene | 112925427 | 112928722 | - | Atxn7l3b | Atxn7l3b | P7500 | NM_001033474 | TSS16346 |
| chr10 | 113167091 | 113167215 | MACS2_peak_396 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 76 | chr10 | unknown | gene | 112925427 | 112928722 | - | Atxn7l3b | Atxn7l3b | P7500 | NM_001033474 | TSS16346 |
| chr10 | 113167091 | 113167215 | MACS2_peak_396 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 76 | chr10 | unknown | gene | 113586577 | 113614774 | + | Mir669h | Mir669h | | NR_035418 | TSS11313 |
| chr10 | 113896116 | 113896207 | MACS2_peak_397 | 7 | + | 3.33222 | 3.76219 | 0.71769 | 18 | chr10 | unknown | gene | 113586577 | 113614774 | + | Mir669h | Mir669h | | NR_035418 | TSS11313 |
| chr10 | 113896116 | 113896207 | MACS2_peak_397 | 7 | + | 3.33222 | 3.76219 | 0.71769 | 18 | chr10 | unknown | gene | 114398820 | 114801300 | - | Trhde | Trhde | P17896 | NM_146241 | TSS23296 |
| chr10 | 114206131 | 114206240 | MACS2_peak_398 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 27 | chr10 | unknown | gene | 113586577 | 113614774 | + | Mir669h | Mir669h | | NR_035418 | TSS11313 |
| chr10 | 114206131 | 114206240 | MACS2_peak_398 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 27 | chr10 | unknown | gene | 114398820 | 114801300 | - | Trhde | Trhde | P17896 | NM_146241 | TSS23296 |
| chr10 | 114619783 | 114619874 | MACS2_peak_399 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 50 | chr10 | unknown | gene | 113586577 | 113614774 | + | Mir669h | Mir669h | | NR_035418 | TSS11313 |
| chr10 | 114619783 | 114619874 | MACS2_peak_399 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 50 | chr10 | unknown | gene | 115078640 | 115184889 | - | Tph2 | Tph2 | P282 | NM_173391 | TSS26303 |
| chr10 | 115060730 | 115060821 | MACS2_peak_400 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 38 | chr10 | unknown | gene | 114398820 | 114801300 | - | Trhde | Trhde | P17896 | NM_146241 | TSS23296 |
| chr10 | 115060730 | 115060821 | MACS2_peak_400 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 38 | chr10 | unknown | gene | 115078640 | 115184889 | - | Tph2 | Tph2 | P282 | NM_173391 | TSS26303 |
| chr10 | 115764223 | 115764324 | MACS2_peak_401 | 50 | + | 6.87285 | 10.15897 | 5.05896 | 74 | chr10 | unknown | gene | 115450313 | 115587493 | - | Lgr5 | Lgr5 | P25827 | NM_010195 | TSS2467 |
| chr10 | 115764223 | 115764324 | MACS2_peak_401 | 50 | + | 6.87285 | 10.15897 | 5.05896 | 74 | chr10 | unknown | gene | 115817283 | 115849396 | + | Tspan8 | Tspan8 | P22306 | NM_001168679 | TSS82 |
| chr10 | 115776629 | 115776720 | MACS2_peak_402 | 7 | + | 3.66524 | 4.26823 | 0.75855 | 38 | chr10 | unknown | gene | 115450313 | 115587493 | - | Lgr5 | Lgr5 | P25827 | NM_010195 | TSS2467 |
| chr10 | 115776629 | 115776720 | MACS2_peak_402 | 7 | + | 3.66524 | 4.26823 | 0.75855 | 38 | chr10 | unknown | gene | 115817283 | 115849396 | + | Tspan8 | Tspan8 | P22306 | NM_001168679 | TSS82 |
| chr10 | 115987375 | 115987466 | MACS2_peak_403 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 62 | chr10 | unknown | gene | 115817283 | 115849396 | + | Tspan8 | Tspan8 | P22306 | NM_001168679 | TSS82 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr10 | 115987375 | 115987466 | MACS2_peak_403 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 62 | chr10 | unknown | gene | 116018362 | 116273826 | + | Ptprr | Ptprr | P23661 | NM_011217 | TSS6919 |
| chr10 | 116679808 | 116679899 | MACS2_peak_404 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 41 | chr10 | unknown | gene | 116485160 | 116581457 | - | Cnot2 | Cnot2 | P8171 | NM_028082 | TSS13238 |
| chr10 | 116679808 | 116679899 | MACS2_peak_404 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 41 | chr10 | unknown | gene | 116723066 | 116729177 | - | 1700030O20Rik | 1700030O20Rik | | NR_045345 | TSS10046 |
| chr10 | 117513830 | 117513921 | MACS2_peak_405 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 26 | chr10 | unknown | gene | 117344667 | 117376898 | - | Cpsf6 | Cpsf6 | P21040 | NM_001013391 | TSS8697 |
| chr10 | 117513830 | 117513921 | MACS2_peak_405 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 26 | chr10 | unknown | gene | 117629499 | 117683520 | + | Cpm | Cpm | P7015 | NM_027468 | TSS2612 |
| chr10 | 118531178 | 118531274 | MACS2_peak_406 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 83 | chr10 | unknown | gene | 118441046 | 118445261 | + | Ifng | Ifng | P4694 | NM_008337 | TSS20224 |
| chr10 | 118531178 | 118531274 | MACS2_peak_406 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 83 | chr10 | unknown | gene | 118859348 | 118868769 | - | Dyrk2 | Dyrk2 | P25271 | NM_001014390 | TSS27522 |
| chr10 | 119322604 | 119322695 | MACS2_peak_407 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 43 | chr10 | unknown | gene | 119198811 | 119239708 | - | Cand1 | Cand1 | P19383 | NM_027994 | TSS10734 |
| chr10 | 119322604 | 119322695 | MACS2_peak_407 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 43 | chr10 | unknown | gene | 119413443 | 119426864 | + | 1700025F24Rik | 1700025F24Rik | | NR_040578 | TSS25710 |
| chr10 | 119792215 | 119792306 | MACS2_peak_408 | 29 | + | 5.67577 | 7.86521 | 2.93324 | 37 | chr10 | unknown | gene | 119746061 | 119761699 | - | Grip1os2 | Grip1os2 | | NR_045359 | TSS2034 |
| chr10 | 119792215 | 119792306 | MACS2_peak_408 | 29 | + | 5.67577 | 7.86521 | 2.93324 | 37 | chr10 | unknown | gene | 119825203 | 119852390 | - | Grip1os1 | Grip1os1 | | NR_131760 | TSS19131 |
| chr10 | 120849330 | 120849421 | MACS2_peak_409 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 68 | chr10 | unknown | gene | 120765731 | 120778886 | + | 4921513I03Rik | 4921513I03Rik | | NR_038003 | TSS24804 |
| chr10 | 120849330 | 120849421 | MACS2_peak_409 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 68 | chr10 | unknown | gene | 120857628 | 120863328 | + | Gm15910 | Gm15910 | | NR_038023 | TSS15801 |
| chr10 | 120984918 | 120985015 | MACS2_peak_410 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 72 | chr10 | unknown | gene | 120923410 | 120979326 | - | Lemd3 | Lemd3 | P16914 | NM_001081193 | TSS1407 |
| chr10 | 120984918 | 120985015 | MACS2_peak_410 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 72 | chr10 | unknown | gene | 121034003 | 121099879 | + | Wif1 | Wif1 | P10522 | NM_011915 | TSS19258 |
| chr10 | 122316027 | 122316118 | MACS2_peak_411 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 20 | chr10 | unknown | gene | 122119696 | 122130558 | + | Gm4489 | Gm4489 | | NR_027637 | TSS9414 |
| chr10 | 122316027 | 122316118 | MACS2_peak_411 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 20 | chr10 | unknown | gene | 122448498 | 122452360 | + | Avpr1a | Avpr1a | P23858 | NM_016847 | TSS24863 |
| chr10 | 122734376 | 122734467 | MACS2_peak_412 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 33 | chr10 | unknown | gene | 122679314 | 122679415 | + | Mir8104 | Mir8104 | | NR_106182 | TSS5652 |
| chr10 | 122734376 | 122734467 | MACS2_peak_412 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 33 | chr10 | unknown | gene | 122985639 | 122985724 | - | Mirlet7i | Mirlet7i | | NR_029527 | TSS1151 |
| chr10 | 123648930 | 123649021 | MACS2_peak_413 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 5 | chr10 | unknown | gene | 123105005 | 123196915 | - | Usp15 | Usp15 | P2013 | NM_001301628 | TSS9533 |
| chr10 | 123648930 | 123649021 | MACS2_peak_413 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 5 | chr10 | unknown | gene | 124469073 | 124524488 | + | 4930503E24Rik | 4930503E24Rik | | NR_028310 | TSS7390 |
| chr10 | 124545076 | 124545209 | MACS2_peak_414 | 61 | + | 7.43052 | 11.30786 | 6.16647 | 66 | chr10 | unknown | gene | 124469073 | 124524488 | + | 4930503E24Rik | 4930503E24Rik | | NR_028310 | TSS7390 |
| chr10 | 124545076 | 124545209 | MACS2_peak_414 | 61 | + | 7.43052 | 11.30786 | 6.16647 | 66 | chr10 | unknown | gene | 125227484 | 125328535 | - | Slc16a7 | Slc16a7 | P905 | NM_011391 | TSS26 |
| chr10 | 125269697 | 125269788 | MACS2_peak_415 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 66 | chr10 | unknown | gene | 124469073 | 124524488 | + | 4930503E24Rik | 4930503E24Rik | | NR_028310 | TSS7390 |
| chr10 | 125269697 | 125269788 | MACS2_peak_415 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 66 | chr10 | unknown | gene | 125966218 | 126014920 | + | Lrig3 | Lrig3 | P7711 | NM_177152 | TSS14007 |
| chr10 | 126615552 | 126615643 | MACS2_peak_416 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 72 | chr10 | unknown | gene | 125966218 | 126014920 | + | Lrig3 | Lrig3 | P7711 | NM_177152 | TSS14007 |
| chr10 | 126615552 | 126615643 | MACS2_peak_416 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 72 | chr10 | unknown | gene | 126710281 | 126710391 | - | Mir378d | Mir378d | | NR_105841 | TSS25398 |
| chr10 | 126927831 | 126927922 | MACS2_peak_417 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 17 | chr10 | unknown | gene | 126868427 | 126901288 | - | Xrcc6bp1 | Xrcc6bp1 | P2856 | NM_026858 | TSS14513 |
| chr10 | 126927831 | 126927922 | MACS2_peak_417 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 17 | chr10 | unknown | gene | 126978716 | 126996486 | + | Ctdsp2 | Ctdsp2 | P12829 | NM_001113470 | TSS24128 |
| chr10 | 128095431 | 128095522 | MACS2_peak_418 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 58 | chr10 | unknown | gene | 128083306 | 128090119 | + | Atp5b | Atp5b | P6789 | NM_016774 | TSS1523 |
| chr10 | 128095431 | 128095522 | MACS2_peak_418 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 58 | chr10 | unknown | gene | 128129469 | 128180297 | - | Rbms2 | Rbms2 | P21599 | NM_001039080 | TSS25016 |
| chr10 | 128782819 | 128782910 | MACS2_peak_419 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 34 | chr10 | unknown | gene | 128747878 | 128766090 | + | Wibg | Wibg | P11673 | NM_001253705 | TSS603 |
| chr10 | 128782819 | 128782910 | MACS2_peak_419 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 34 | chr10 | unknown | gene | 128790909 | 128799100 | + | Mmp19 | Mmp19 | P26614 | NM_001164197 | TSS12843 |
| chr10 | 129568365 | 129568456 | MACS2_peak_420 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 42 | chr10 | unknown | gene | 129540538 | 129541474 | + | Olfr792 | Olfr792 | P5769 | NM_001011849 | TSS12054 |
| chr10 | 129568365 | 129568456 | MACS2_peak_420 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 42 | chr10 | unknown | gene | 129570656 | 129571619 | + | Olfr794 | Olfr794 | P23236 | NM_146378 | TSS25881 |
| chr10 | 129959296 | 129959392 | MACS2_peak_421 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 52 | chr10 | unknown | gene | 129945103 | 129946060 | - | Olfr818 | Olfr818 | P5350 | NM_146777 | TSS25667 |
| chr10 | 129959296 | 129959392 | MACS2_peak_421 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 52 | chr10 | unknown | gene | 129965735 | 129966698 | - | Olfr819 | Olfr819 | P3896 | NM_001165944 | TSS23409 |
| chr11 | 3103925 | 3104038 | MACS2_peak_422 | 125 | + | 9.76161 | 17.92969 | 12.55378 | 67 | chr11 | unknown | gene | 3124020 | 3131944 | + | Pisd-ps1 | Pisd-ps1 | | NR_003517 | TSS10201 |
| chr11 | 3573426 | 3573539 | MACS2_peak_423 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 31 | chr11 | unknown | gene | 3517521 | 3539292 | - | Smtn | Smtn | P8149 | NM_001284428 | TSS3480 |
| chr11 | 3573426 | 3573539 | MACS2_peak_423 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 31 | chr11 | unknown | gene | 3639784 | 3648814 | - | Tug1 | Tug1 | | NR_110490 | TSS16719 |
| chr11 | 3884141 | 3884232 | MACS2_peak_424 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 6 | chr11 | unknown | gene | 3703730 | 3863867 | - | Osbp2 | Osbp2 | P15984 | NM_001302630 | TSS24620 |
| chr11 | 3884141 | 3884232 | MACS2_peak_424 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 6 | chr11 | unknown | gene | 3886087 | 3895087 | - | 4921536K21Rik | 4921536K21Rik | P15204 | NM_026150 | TSS27021 |
| chr11 | 4096769 | 4096883 | MACS2_peak_425 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 46 | chr11 | unknown | gene | 4091480 | 4095282 | - | Mtfp1 | Mtfp1 | P5886 | NM_026443 | TSS10088 |
| chr11 | 4096769 | 4096883 | MACS2_peak_425 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 46 | chr11 | unknown | gene | 4097039 | 4118678 | - | Sec14l2 | Sec14l2 | P11639 | NM_144520 | TSS12067 |
| chr11 | 5397609 | 5397700 | MACS2_peak_426 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 35 | chr11 | unknown | gene | 5191552 | 5261525 | - | Kremen1 | Kremen1 | P11182 | NM_032396 | TSS8003 |
| chr11 | 5397609 | 5397700 | MACS2_peak_426 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 35 | chr11 | unknown | gene | 5520640 | 5525242 | + | Xbp1 | Xbp1 | P15191 | NM_013842 | TSS27656 |
| chr11 | 5433412 | 5433503 | MACS2_peak_427 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 29 | chr11 | unknown | gene | 5191552 | 5261525 | - | Kremen1 | Kremen1 | P11182 | NM_032396 | TSS8003 |
| chr11 | 5433412 | 5433503 | MACS2_peak_427 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 29 | chr11 | unknown | gene | 5520640 | 5525242 | + | Xbp1 | Xbp1 | P15191 | NM_013842 | TSS27656 |
| chr11 | 7665845 | 7665983 | MACS2_peak_428 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 64 | chr11 | unknown | gene | 7206090 | 7213790 | - | Igfbp3 | Igfbp3 | P19133 | NM_008343 | TSS4035 |
| chr11 | 7665845 | 7665983 | MACS2_peak_428 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 64 | chr11 | unknown | gene | 8431651 | 8664535 | - | Tns3 | Tns3 | P6000 | NM_001083587 | TSS10318 |
| chr11 | 11339895 | 11339986 | MACS2_peak_429 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 34 | chr11 | unknown | gene | 11114015 | 11261520 | + | Vwc2 | Vwc2 | P1037 | NM_177033 | TSS23336 |
| chr11 | 11339895 | 11339986 | MACS2_peak_429 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 34 | chr11 | unknown | gene | 11489265 | 11515100 | + | 4930415F15Rik | 4930415F15Rik | P21205 | NM_028669 | TSS25490 |
| chr11 | 11479588 | 11479679 | MACS2_peak_430 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 51 | chr11 | unknown | gene | 11280039 | 11462364 | - | Zpbp | Zpbp | P11689 | NM_015785 | TSS8924 |
| chr11 | 11479588 | 11479679 | MACS2_peak_430 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 51 | chr11 | unknown | gene | 11489265 | 11515100 | + | 4930415F15Rik | 4930415F15Rik | P21205 | NM_028669 | TSS25490 |
| chr11 | 14039626 | 14039717 | MACS2_peak_431 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 50 | chr11 | unknown | gene | 12236675 | 12464722 | - | Cobl | Cobl | P12945 | NM_172496 | TSS13136 |
| chr11 | 14039626 | 14039717 | MACS2_peak_431 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 50 | chr11 | unknown | gene | 14072102 | 14179041 | - | 4930554G24Rik | 4930554G24Rik | | NR_131011 | TSS17979 |
| chr11 | 14355664 | 14355831 | MACS2_peak_432 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 133 | chr11 | unknown | gene | 14072102 | 14179041 | - | 4930554G24Rik | 4930554G24Rik | | NR_131011 | TSS17979 |
| chr11 | 14355664 | 14355831 | MACS2_peak_432 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 133 | chr11 | unknown | gene | 14560335 | 14599225 | - | 1700046C09Rik | 1700046C09Rik | | NR_045918 | TSS16657 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr11 | 16874516 | 16874643 | MACS2_peak_433 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 84 | chr11 | unknown | gene | 16501637 | 16508193 | - | Sec61g | Sec61g | P16389 | NM_001109972 | TSS25971 |
| chr11 | 16874516 | 16874643 | MACS2_peak_433 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 84 | chr11 | unknown | gene | 16934708 | 16951282 | - | Eldr | Eldr | | NR_110422 | TSS13084 |
| chr11 | 17037783 | 17037900 | MACS2_peak_434 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 39 | chr11 | unknown | gene | 16971205 | 17008598 | - | Plek | Plek | P19966 | NM_019549 | TSS25730 |
| chr11 | 17037783 | 17037900 | MACS2_peak_434 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 39 | chr11 | unknown | gene | 17051933 | 17078564 | + | Cnrip1 | Cnrip1 | P13065 | NM_029861 | TSS1207 |
| chr11 | 17609170 | 17609261 | MACS2_peak_435 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 36 | chr11 | unknown | gene | 17257617 | 17266695 | + | C1d | C1d | P1140 | NM_020558 | TSS25402 |
| chr11 | 17609170 | 17609261 | MACS2_peak_435 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 36 | chr11 | unknown | gene | 17938748 | 17953794 | - | Etaa1 | Etaa1 | P2117 | NM_026576 | TSS4406 |
| chr11 | 17856746 | 17856837 | MACS2_peak_436 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 27 | chr11 | unknown | gene | 17257617 | 17266695 | + | C1d | C1d | P1140 | NM_020558 | TSS25402 |
| chr11 | 17856746 | 17856837 | MACS2_peak_436 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 27 | chr11 | unknown | gene | 17938748 | 17953794 | - | Etaa1 | Etaa1 | P2117 | NM_026576 | TSS4406 |
| chr11 | 18344286 | 18344377 | MACS2_peak_437 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 22 | chr11 | unknown | gene | 18095985 | 18103385 | + | Gm12018 | Gm12018 | | NR_131129 | TSS7934 |
| chr11 | 18344286 | 18344377 | MACS2_peak_437 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 22 | chr11 | unknown | gene | 18880427 | 19018232 | - | Meis1 | Meis1 | P4473 | NM_001193271 | TSS16317 |
| chr11 | 18938718 | 18938812 | MACS2_peak_438 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 42 | chr11 | unknown | gene | 18095985 | 18103385 | + | Gm12018 | Gm12018 | | NR_131129 | TSS7934 |
| chr11 | 18938718 | 18938812 | MACS2_peak_438 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 42 | chr11 | unknown | gene | 19065274 | 19075740 | + | 4933406G16Rik | 4933406G16Rik | | NR_046037 | TSS17469 |
| chr11 | 19605403 | 19605494 | MACS2_peak_439 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 32 | chr11 | unknown | gene | 19065274 | 19075740 | + | 4933406G16Rik | 4933406G16Rik | | NR_046037 | TSS17469 |
| chr11 | 19605403 | 19605494 | MACS2_peak_439 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 32 | chr11 | unknown | gene | 19924441 | 20021447 | + | Spred2 | Spred2 | P24909 | NM_033523 | TSS19661 |
| chr11 | 19617129 | 19617264 | MACS2_peak_440 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 83 | chr11 | unknown | gene | 19065274 | 19075740 | + | 4933406G16Rik | 4933406G16Rik | | NR_046037 | TSS17469 |
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| chr11 | 19647067 | 19647186 | MACS2_peak_441 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 83 | chr11 | unknown | gene | 19065274 | 19075740 | + | 4933406G16Rik | 4933406G16Rik | | NR_046037 | TSS17469 |
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| chr11 | 20202670 | 20202761 | MACS2_peak_442 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 37 | chr11 | unknown | gene | 20062303 | 20112852 | - | Actr2 | Actr2 | P17749 | NM_146243 | TSS23818 |
| chr11 | 20202670 | 20202761 | MACS2_peak_442 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 37 | chr11 | unknown | gene | 20227036 | 20249424 | - | Cep68 | Cep68 | P19348 | NM_172260 | TSS11331 |
| chr11 | 21240521 | 21240612 | MACS2_peak_443 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 65 | chr11 | unknown | gene | 21091323 | 21148523 | + | Peli1 | Peli1 | P12238 | NM_023324 | TSS2971 |
| chr11 | 21240521 | 21240612 | MACS2_peak_443 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 65 | chr11 | unknown | gene | 21321125 | 21371267 | - | Ugp2 | Ugp2 | P2451 | NM_001290634 | TSS10392 |
| chr11 | 21404741 | 21404832 | MACS2_peak_444 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 27 | chr11 | unknown | gene | 21321125 | 21371267 | - | Ugp2 | Ugp2 | P2451 | NM_001290634 | TSS10392 |
| chr11 | 21404741 | 21404832 | MACS2_peak_444 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 27 | chr11 | unknown | gene | 21494729 | 21511180 | - | 4932414J04Rik | 4932414J04Rik | | NR_028259 | TSS15916 |
| chr11 | 21642069 | 21642204 | MACS2_peak_445 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 75 | chr11 | unknown | gene | 21556691 | 21571732 | - | Mdh1 | Mdh1 | P3577 | NM_008618 | TSS1466 |
| chr11 | 21642069 | 21642204 | MACS2_peak_445 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 75 | chr11 | unknown | gene | 21994763 | 22001651 | - | Otx1 | Otx1 | P4724 | NM_011023 | TSS22829 |
| chr11 | 23607876 | 23607967 | MACS2_peak_446 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 50 | chr11 | unknown | gene | 23558059 | 23558842 | - | Gm12060 | Gm12060 | | NR_004857 | TSS17257 |
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| chr11 | 24039832 | 24039923 | MACS2_peak_447 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 39 | chr11 | unknown | gene | 23862645 | 23895038 | - | Papolg | Papolg | P3813 | NM_172555 | TSS19670 |
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| chr11 | 24672925 | 24673089 | MACS2_peak_448 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 80 | chr11 | unknown | gene | 24481908 | 24569951 | + | 4933430M04Rik | 4933430M04Rik | | NR_045857 | TSS15111 |
| chr11 | 24672925 | 24673089 | MACS2_peak_448 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 80 | chr11 | unknown | gene | 24721005 | 24730722 | - | Gm10466 | Gm10466 | | NR_033491 | TSS15738 |
| chr11 | 25205048 | 25205188 | MACS2_peak_449 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 88 | chr11 | unknown | gene | 24721005 | 24730722 | - | Gm10466 | Gm10466 | | NR_033491 | TSS15738 |
| chr11 | 25205048 | 25205188 | MACS2_peak_449 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 88 | chr11 | unknown | gene | 25326106 | 25367137 | + | 4933427E13Rik | 4933427E13Rik | | NR_045853 | TSS17527 |
| chr11 | 25581267 | 25581358 | MACS2_peak_450 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 83 | chr11 | unknown | gene | 25326106 | 25367137 | + | 4933427E13Rik | 4933427E13Rik | | NR_045853 | TSS17527 |
| chr11 | 25581267 | 25581358 | MACS2_peak_450 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 83 | chr11 | unknown | gene | 25616845 | 26210576 | - | 5730522E02Rik | 5730522E02Rik | | NR_027973 | TSS4983 |
| chr11 | 26230790 | 26230885 | MACS2_peak_451 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 42 | chr11 | unknown | gene | 25616845 | 26210576 | - | 5730522E02Rik | 5730522E02Rik | | NR_027973 | TSS4983 |
| chr11 | 26230790 | 26230885 | MACS2_peak_451 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 42 | chr11 | unknown | gene | 26387083 | 26471360 | + | Fancl | Fancl | P26085 | NM_025923 | TSS12108 |
| chr11 | 26479761 | 26479886 | MACS2_peak_452 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 73 | chr11 | unknown | gene | 26387083 | 26471360 | + | Fancl | Fancl | P26085 | NM_025923 | TSS12108 |
| chr11 | 26479761 | 26479886 | MACS2_peak_452 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 73 | chr11 | unknown | gene | 26785107 | 26787859 | + | Gm12070 | Gm12070 | | NR_002890 | TSS11001 |
| chr11 | 27587059 | 27587167 | MACS2_peak_453 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 81 | chr11 | unknown | gene | 26785107 | 26787859 | + | Gm12070 | Gm12070 | | NR_002890 | TSS11001 |
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| chr11 | 28979680 | 28979771 | MACS2_peak_454 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 15 | chr11 | unknown | gene | 28853204 | 28926318 | + | Efemp1 | Efemp1 | P25053 | NM_146015 | TSS5707 |
| chr11 | 28979680 | 28979771 | MACS2_peak_454 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 15 | chr11 | unknown | gene | 29130750 | 29161483 | + | Pnpt1 | Pnpt1 | P10938 | NM_027869 | TSS6792 |
| chr11 | 29738195 | 29738286 | MACS2_peak_455 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 14 | chr11 | unknown | gene | 29547949 | 29578231 | + | Clhc1 | Clhc1 | P8905 | NM_001163521 | TSS3304 |
| chr11 | 29738195 | 29738286 | MACS2_peak_455 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 14 | chr11 | unknown | gene | 29743050 | 30026033 | - | Eml6 | Eml6 | P18093 | NM_146016 | TSS515 |
| chr11 | 30289191 | 30289282 | MACS2_peak_456 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 22 | chr11 | unknown | gene | 30099394 | 30219726 | - | Sptbn1 | Sptbn1 | P20386 | NM_175836 | TSS13554 |
| chr11 | 30289191 | 30289282 | MACS2_peak_456 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 22 | chr11 | unknown | gene | 30426005 | 30471764 | - | 4930505A04Rik | 4930505A04Rik | P25312 | NM_001100394 | TSS13054 |
| chr11 | 30515046 | 30515169 | MACS2_peak_457 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 35 | chr11 | unknown | gene | 30426005 | 30471764 | - | 4930505A04Rik | 4930505A04Rik | P25312 | NM_001100394 | TSS13054 |
| chr11 | 30515046 | 30515169 | MACS2_peak_457 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 35 | chr11 | unknown | gene | 30771774 | 30880361 | + | Psme4 | Psme4 | P6367 | NM_134013 | TSS20159 |
| chr11 | 30784160 | 30784266 | MACS2_peak_458 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 41 | chr11 | unknown | gene | 30505991 | 30649379 | - | Acyp2 | Acyp2 | P1826 | NM_029344 | TSS8157 |
| chr11 | 30784160 | 30784266 | MACS2_peak_458 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 41 | chr11 | unknown | gene | 30885357 | 30892719 | + | Gpr75 | Gpr75 | P11320 | NM_175490 | TSS3106 |
| chr11 | 34544302 | 34544591 | MACS2_peak_459 | 135 | + | 10.64081 | 18.97324 | 13.56551 | 217 | chr11 | unknown | gene | 34314821 | 34419905 | + | Fam196b | Fam196b | P23281 | NM_001025382 | TSS17684 |
| chr11 | 34544302 | 34544591 | MACS2_peak_459 | 135 | + | 10.64081 | 18.97324 | 13.56551 | 217 | chr11 | unknown | gene | 34809184 | 34833641 | - | Spdl1 | Spdl1 | P10591 | NM_027411 | TSS7818 |
| chr11 | 34544771 | 34544992 | MACS2_peak_460 | 123 | + | 10.15896 | 17.74636 | 12.38048 | 60 | chr11 | unknown | gene | 34314821 | 34419905 | + | Fam196b | Fam196b | P23281 | NM_001025382 | TSS17684 |
| chr11 | 34544771 | 34544992 | MACS2_peak_460 | 123 | + | 10.15896 | 17.74636 | 12.38048 | 60 | chr11 | unknown | gene | 34809184 | 34833641 | - | Spdl1 | Spdl1 | P10591 | NM_027411 | TSS7818 |
| chr11 | 34681681 | 34682199 | MACS2_peak_461 | 195 | + | 11.86077 | 25.11963 | 19.55364 | 202 | chr11 | unknown | gene | 34314821 | 34419905 | + | Fam196b | Fam196b | P23281 | NM_001025382 | TSS17684 |
| chr11 | 34681681 | 34682199 | MACS2_peak_461 | 195 | + | 11.86077 | 25.11963 | 19.55364 | 202 | chr11 | unknown | gene | 34809184 | 34833641 | - | Spdl1 | Spdl1 | P10591 | NM_027411 | TSS7818 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr11 | 34682968 | 34683104 | MACS2_peak_462 | 51 | + | 6.33398 | 10.2692 | 5.16579 | 62 | chr11 | unknown | gene | 34314821 | 34419905 | + | Fam196b | Fam196b | P23281 | NM_001025382 | TSS17684 |
| chr11 | 34682968 | 34683104 | MACS2_peak_462 | 51 | + | 6.33398 | 10.2692 | 5.16579 | 62 | chr11 | unknown | gene | 34809184 | 34833641 | - | Spdl1 | Spdl1 | P10591 | NM_027411 | TSS7818 |
| chr11 | 34737130 | 34737230 | MACS2_peak_463 | 49 | + | 6.77503 | 10.04021 | 4.94691 | 49 | chr11 | unknown | gene | 34314821 | 34419905 | + | Fam196b | Fam196b | P23281 | NM_001025382 | TSS17684 |
| chr11 | 34737130 | 34737230 | MACS2_peak_463 | 49 | + | 6.77503 | 10.04021 | 4.94691 | 49 | chr11 | unknown | gene | 34809184 | 34833641 | - | Spdl1 | Spdl1 | P10591 | NM_027411 | TSS7818 |
| chr11 | 34973840 | 34973940 | MACS2_peak_464 | 13 | + | 4.63699 | 5.94477 | 1.394 | 71 | chr11 | unknown | gene | 34809184 | 34833641 | - | Spdl1 | Spdl1 | P10591 | NM_027411 | TSS7818 |
| chr11 | 34973840 | 34973940 | MACS2_peak_464 | 13 | + | 4.63699 | 5.94477 | 1.394 | 71 | chr11 | unknown | gene | 35121455 | 35708142 | + | Slit3 | Slit3 | P5277 | NM_011412 | TSS22674 |
| chr11 | 35421875 | 35421966 | MACS2_peak_465 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 34 | chr11 | unknown | gene | 34809184 | 34833641 | - | Spdl1 | Spdl1 | P10591 | NM_027411 | TSS7818 |
| chr11 | 35421875 | 35421966 | MACS2_peak_465 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 34 | chr11 | unknown | gene | 35616815 | 35616925 | + | Mir218-2 | Mir218-2 | | NR_029799 | TSS295 |
| chr11 | 36326780 | 36326871 | MACS2_peak_466 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 55 | chr11 | unknown | gene | 35839177 | 35980089 | - | Wwc1 | Wwc1 | P14089 | NM_170779 | TSS2477 |
| chr11 | 36326780 | 36326871 | MACS2_peak_466 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 55 | chr11 | unknown | gene | 37658988 | 37673166 | + | Gm12128 | Gm12128 | | NR_131154 | TSS20214 |
| chr11 | 36729269 | 36729360 | MACS2_peak_467 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 8 | chr11 | unknown | gene | 35839177 | 35980089 | - | Wwc1 | Wwc1 | P14089 | NM_170779 | TSS2477 |
| chr11 | 36729269 | 36729360 | MACS2_peak_467 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 8 | chr11 | unknown | gene | 37658988 | 37673166 | + | Gm12128 | Gm12128 | | NR_131154 | TSS20214 |
| chr11 | 37108991 | 37109082 | MACS2_peak_468 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 25 | chr11 | unknown | gene | 36006655 | 36944166 | - | Tenm2 | Tenm2 | P7880 | NM_001290702 | TSS17592 |
| chr11 | 37108991 | 37109082 | MACS2_peak_468 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 25 | chr11 | unknown | gene | 37658988 | 37673166 | + | Gm12128 | Gm12128 | | NR_131154 | TSS20214 |
| chr11 | 37250718 | 37250809 | MACS2_peak_469 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 68 | chr11 | unknown | gene | 36006655 | 36944166 | - | Tenm2 | Tenm2 | P7880 | NM_001290702 | TSS17592 |
| chr11 | 37250718 | 37250809 | MACS2_peak_469 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 68 | chr11 | unknown | gene | 37658988 | 37673166 | + | Gm12128 | Gm12128 | | NR_131154 | TSS20214 |
| chr11 | 37618634 | 37618725 | MACS2_peak_470 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 41 | chr11 | unknown | gene | 36006655 | 36944166 | - | Tenm2 | Tenm2 | P7880 | NM_001290702 | TSS17592 |
| chr11 | 37618634 | 37618725 | MACS2_peak_470 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 41 | chr11 | unknown | gene | 37658988 | 37673166 | + | Gm12128 | Gm12128 | | NR_131154 | TSS20214 |
| chr11 | 38006737 | 38006828 | MACS2_peak_471 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 35 | chr11 | unknown | gene | 37658988 | 37673166 | + | Gm12128 | Gm12128 | | NR_131154 | TSS20214 |
| chr11 | 38006737 | 38006828 | MACS2_peak_471 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 35 | chr11 | unknown | gene | 38491547 | 38520045 | - | Gm12130 | Gm12130 | | NR_040295 | TSS26234 |
| chr11 | 38222643 | 38222734 | MACS2_peak_472 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 3 | chr11 | unknown | gene | 37658988 | 37673166 | + | Gm12128 | Gm12128 | | NR_131154 | TSS20214 |
| chr11 | 38222643 | 38222734 | MACS2_peak_472 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 3 | chr11 | unknown | gene | 38491547 | 38520045 | - | Gm12130 | Gm12130 | | NR_040295 | TSS26234 |
| chr11 | 38876464 | 38876555 | MACS2_peak_473 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 50 | chr11 | unknown | gene | 38491547 | 38520045 | - | Gm12130 | Gm12130 | | NR_040295 | TSS26234 |
| chr11 | 38876464 | 38876555 | MACS2_peak_473 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 50 | chr11 | unknown | gene | 39307702 | 39390225 | - | 4930553C11Rik | 4930553C11Rik | | NR_126439 | TSS14293 |
| chr11 | 44713562 | 44713686 | MACS2_peak_474 | 23 | + | 5.33156 | 7.20295 | 2.32792 | 67 | chr11 | unknown | gene | 44586316 | 44591229 | + | 4930597A21Rik | 4930597A21Rik | | NR_126460 | TSS11354 |
| chr11 | 44713562 | 44713686 | MACS2_peak_474 | 23 | + | 5.33156 | 7.20295 | 2.32792 | 67 | chr11 | unknown | gene | 45102865 | 45116928 | - | Gm12159 | Gm12159 | | NR_045100 | TSS19496 |
| chr11 | 44878126 | 44878286 | MACS2_peak_475 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 137 | chr11 | unknown | gene | 44586316 | 44591229 | + | 4930597A21Rik | 4930597A21Rik | | NR_126460 | TSS11354 |
| chr11 | 44878126 | 44878286 | MACS2_peak_475 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 137 | chr11 | unknown | gene | 45102865 | 45116928 | - | Gm12159 | Gm12159 | | NR_045100 | TSS19496 |
| chr11 | 45635981 | 45636072 | MACS2_peak_476 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 9 | chr11 | unknown | gene | 45102865 | 45116928 | - | Gm12159 | Gm12159 | | NR_045100 | TSS19496 |
| chr11 | 45635981 | 45636072 | MACS2_peak_476 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 9 | chr11 | unknown | gene | 45808082 | 45842878 | + | F630206G17Rik | F630206G17Rik | | NR_045876 | TSS24874 |
| chr11 | 46441611 | 46441718 | MACS2_peak_477 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 78 | chr11 | unknown | gene | 46436946 | 46441281 | + | Med7 | Med7 | P26785 | NM_001104557 | TSS7519 |
| chr11 | 46441611 | 46441718 | MACS2_peak_477 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 78 | chr11 | unknown | gene | 46454930 | 46479446 | + | Havcr2 | Havcr2 | P16940 | NM_134250 | TSS22239 |
| chr11 | 46822064 | 46822155 | MACS2_peak_478 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 75 | chr11 | unknown | gene | 46740222 | 46778613 | + | Havcr1 | Havcr1 | P24538 | NM_001166632 | TSS21675 |
| chr11 | 46822064 | 46822155 | MACS2_peak_478 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 75 | chr11 | unknown | gene | 46978782 | 47379302 | - | Sgcd | Sgcd | P9623 | NM_011891 | TSS172 |
| chr11 | 48303836 | 48303927 | MACS2_peak_479 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 20 | chr11 | unknown | gene | 47739591 | 48074583 | - | Mir6380 | Mir6380 | | NR_105801 | TSS12109 |
| chr11 | 48303836 | 48303927 | MACS2_peak_479 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 20 | chr11 | unknown | gene | 48800359 | 48806045 | + | Gnb2l1 | Gnb2l1 | P5990 | NM_008143 | TSS12234 |
| chr11 | 48434470 | 48434582 | MACS2_peak_480 | 32 | + | 5.8651 | 8.25694 | 3.2954 | 48 | chr11 | unknown | gene | 47739591 | 48074583 | - | Mir6380 | Mir6380 | | NR_105801 | TSS12109 |
| chr11 | 48434470 | 48434582 | MACS2_peak_480 | 32 | + | 5.8651 | 8.25694 | 3.2954 | 48 | chr11 | unknown | gene | 48800359 | 48806045 | + | Gnb2l1 | Gnb2l1 | P5990 | NM_008143 | TSS12234 |
| chr11 | 54140020 | 54140154 | MACS2_peak_481 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 63 | chr11 | unknown | gene | 54100923 | 54131260 | + | P4ha2 | P4ha2 | P25349 | NM_011031 | TSS421 |
| chr11 | 54140020 | 54140154 | MACS2_peak_481 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 63 | chr11 | unknown | gene | 54177771 | 54213288 | - | 4933405E24Rik | 4933405E24Rik | | NR_045506 | TSS6894 |
| chr11 | 54140548 | 54140642 | MACS2_peak_482 | 47 | + | 6.68747 | 9.84528 | 4.77037 | 40 | chr11 | unknown | gene | 54100923 | 54131260 | + | P4ha2 | P4ha2 | P25349 | NM_011031 | TSS421 |
| chr11 | 54140548 | 54140642 | MACS2_peak_482 | 47 | + | 6.68747 | 9.84528 | 4.77037 | 40 | chr11 | unknown | gene | 54177771 | 54213288 | - | 4933405E24Rik | 4933405E24Rik | | NR_045506 | TSS6894 |
| chr11 | 54463595 | 54463686 | MACS2_peak_483 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 12 | chr11 | unknown | gene | 54370651 | 54426679 | + | Meikin | Meikin | P16100 | NM_029105 | TSS9967 |
| chr11 | 54463595 | 54463686 | MACS2_peak_483 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 12 | chr11 | unknown | gene | 54522844 | 54696105 | + | Rapgef6 | Rapgef6 | P6094 | NM_001252494 | TSS10919 |
| chr11 | 57540993 | 57541084 | MACS2_peak_484 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 24 | chr11 | unknown | gene | 57518664 | 57530244 | + | Mfap3 | Mfap3 | P22763 | NM_180599 | TSS3642 |
| chr11 | 57540993 | 57541084 | MACS2_peak_484 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 24 | chr11 | unknown | gene | 57645441 | 57784728 | + | Galnt10 | Galnt10 | P454 | NM_134189 | TSS6745 |
| chr11 | 58954418 | 58954509 | MACS2_peak_485 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 25 | chr11 | unknown | gene | 58948910 | 58949320 | + | Hist3h2ba | Hist3h2ba | P22148 | NM_030082 | TSS11104 |
| chr11 | 58954418 | 58954509 | MACS2_peak_485 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 25 | chr11 | unknown | gene | 58954684 | 58955130 | + | Hist3h2a | Hist3h2a | P7852 | NM_178218 | TSS2621 |
| chr11 | 60540222 | 60540313 | MACS2_peak_486 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 67 | chr11 | unknown | gene | 60469338 | 60527425 | + | Myo15 | Myo15 | P13749 | NM_010862 | TSS6487 |
| chr11 | 60540222 | 60540313 | MACS2_peak_486 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 67 | chr11 | unknown | gene | 60699689 | 60713210 | + | Llgl1 | Llgl1 | P21438 | NM_008502 | TSS4945 |
| chr11 | 61495004 | 61495095 | MACS2_peak_487 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 70 | chr11 | unknown | gene | 61488811 | 61494266 | - | Mapk7 | Mapk7 | P15214 | NM_011841 | TSS10693 |
| chr11 | 61495004 | 61495095 | MACS2_peak_487 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 70 | chr11 | unknown | gene | 61505171 | 61512794 | + | B9d1 | B9d1 | P4181 | NM_013717 | TSS24649 |
| chr11 | 62109497 | 62109588 | MACS2_peak_488 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 19 | chr11 | unknown | gene | 61871306 | 61930076 | - | Akap10 | Akap10 | P95 | NM_019921 | TSS21320 |
| chr11 | 62109497 | 62109588 | MACS2_peak_488 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 19 | chr11 | unknown | gene | 62248983 | 62265725 | + | Adora2b | Adora2b | P8592 | NM_007413 | TSS20034 |
| chr11 | 65265421 | 65265512 | MACS2_peak_489 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 42 | chr11 | unknown | gene | 65002038 | 65162638 | - | Arhgap44 | Arhgap44 | P11892 | NM_175003 | TSS12273 |
| chr11 | 65265421 | 65265512 | MACS2_peak_489 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 42 | chr11 | unknown | gene | 65277653 | 65287833 | - | Gm12295 | Gm12295 | | NR_040280 | TSS13622 |
| chr11 | 65295686 | 65295777 | MACS2_peak_490 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 35 | chr11 | unknown | gene | 65277653 | 65287833 | - | Gm12295 | Gm12295 | | NR_040280 | TSS13622 |
| chr11 | 65295686 | 65295777 | MACS2_peak_490 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 35 | chr11 | unknown | gene | 65688243 | 65788244 | - | Map2k4 | Map2k4 | P6074 | NM_009157 | TSS18436 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr11 | 65627648 | 65627739 | MACS2_peak_491 | 25 | + | 5.46411 | 7.45132 | 2.55202 | 28 | chr11 | unknown | gene | 65277653 | 65287833 | - | Gm12295 | Gm12295 | | NR_040280 | TSS13622 |
| chr11 | 65627648 | 65627739 | MACS2_peak_491 | 25 | + | 5.46411 | 7.45132 | 2.55202 | 28 | chr11 | unknown | gene | 65688243 | 65788244 | - | Map2k4 | Map2k4 | P6074 | NM_009157 | TSS18436 |
| chr11 | 66437047 | 66437140 | MACS2_peak_492 | 49 | + | 6.77503 | 10.04021 | 4.94691 | 43 | chr11 | unknown | gene | 65831323 | 66168467 | - | Dnah9 | Dnah9 | P22660 | NM_001099633 | TSS20154 |
| chr11 | 66437047 | 66437140 | MACS2_peak_492 | 49 | + | 6.77503 | 10.04021 | 4.94691 | 43 | chr11 | unknown | gene | 66905631 | 66947086 | - | Gm12298 | Gm12298 | | NR_033539 | TSS12458 |
| chr11 | 68949695 | 68949786 | MACS2_peak_493 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 33 | chr11 | unknown | gene | 68921834 | 68926967 | - | Odf4 | Odf4 | P7332 | NM_145746 | TSS2934 |
| chr11 | 68949695 | 68949786 | MACS2_peak_493 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 33 | chr11 | unknown | gene | 68968130 | 68972123 | + | Slc25a35 | Slc25a35 | P18382 | NM_028048 | TSS24961 |
| chr11 | 69631625 | 69631716 | MACS2_peak_494 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 23 | chr11 | unknown | gene | 69622108 | 69623658 | + | Sat2 | Sat2 | P24565 | NM_026991 | TSS13983 |
| chr11 | 69631625 | 69631716 | MACS2_peak_494 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 23 | chr11 | unknown | gene | 69632970 | 69652699 | + | Fxr2 | Fxr2 | P16864 | NM_011814 | TSS6335 |
| chr11 | 70320394 | 70320485 | MACS2_peak_495 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 56 | chr11 | unknown | gene | 70241454 | 70255272 | - | Alox12 | Alox12 | P12376 | NM_007440 | TSS15038 |
| chr11 | 70320394 | 70320485 | MACS2_peak_495 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 56 | chr11 | unknown | gene | 70344146 | 70352005 | - | Alox15 | Alox15 | P3104 | NM_009660 | TSS6076 |
| chr11 | 70651586 | 70651677 | MACS2_peak_496 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 17 | chr11 | unknown | gene | 70647588 | 70651214 | + | Rnf167 | Rnf167 | P26643 | NM_027445 | TSS4762 |
| chr11 | 70651586 | 70651677 | MACS2_peak_496 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 17 | chr11 | unknown | gene | 70651846 | 70654480 | - | Pfn1 | Pfn1 | P17353 | NM_011072 | TSS5896 |
| chr11 | 71113378 | 71113469 | MACS2_peak_497 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 27 | chr11 | unknown | gene | 71031940 | 71033402 | - | 6330403K07Rik | 6330403K07Rik | P739 | NM_134022 | TSS19414 |
| chr11 | 71113378 | 71113469 | MACS2_peak_497 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 27 | chr11 | unknown | gene | 71153101 | 71230733 | - | Nlrp1b | Nlrp1b | P22085 | NM_001040696 | TSS27422 |
| chr11 | 75490496 | 75490609 | MACS2_peak_498 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 75 | chr11 | unknown | gene | 75468049 | 75470563 | + | Tlcd2 | Tlcd2 | P3208 | NM_027249 | TSS21662 |
| chr11 | 75490496 | 75490609 | MACS2_peak_498 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 75 | chr11 | unknown | gene | 75510093 | 75512843 | + | Rilp | Rilp | P5717 | NM_001029938 | TSS26931 |
| chr11 | 75736134 | 75736225 | MACS2_peak_499 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 79 | chr11 | unknown | gene | 75679258 | 75703503 | + | Crk | Crk | P11535 | NM_001277219 | TSS12345 |
| chr11 | 75736134 | 75736225 | MACS2_peak_499 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 79 | chr11 | unknown | gene | 75769089 | 75795893 | - | Doc2b | Doc2b | P3204 | NM_007873 | TSS9501 |
| chr11 | 76112571 | 76112668 | MACS2_peak_500 | 35 | + | 5.98489 | 8.51731 | 3.53253 | 34 | chr11 | unknown | gene | 76019194 | 76027637 | - | Fam101b | Fam101b | P22289 | NM_029658 | TSS27023 |
| chr11 | 76112571 | 76112668 | MACS2_peak_500 | 35 | + | 5.98489 | 8.51731 | 3.53253 | 34 | chr11 | unknown | gene | 76202055 | 76208179 | + | Fam57a | Fam57a | P15502 | NM_027773 | TSS25705 |
| chr11 | 76591891 | 76591993 | MACS2_peak_501 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 17 | chr11 | unknown | gene | 76416731 | 76577739 | - | Abr | Abr | P5968 | NM_001291186 | TSS14452 |
| chr11 | 76591891 | 76591993 | MACS2_peak_501 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 17 | chr11 | unknown | gene | 76672469 | 76673244 | + | Bhlha9 | Bhlha9 | P11846 | NM_177182 | TSS26605 |
| chr11 | 76911255 | 76911362 | MACS2_peak_502 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 57 | chr11 | unknown | gene | 76777207 | 76846966 | - | Cpd | Cpd | P10540 | NM_007754 | TSS16838 |
| chr11 | 76911255 | 76911362 | MACS2_peak_502 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 57 | chr11 | unknown | gene | 76945655 | 76986627 | + | Blmh | Blmh | P14664 | NM_178645 | TSS6542 |
| chr11 | 77159022 | 77159113 | MACS2_peak_503 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 18 | chr11 | unknown | gene | 77044291 | 77078398 | - | Ccdc55 | Ccdc55 | P15527 | NM_001012309 | TSS6600 |
| chr11 | 77159022 | 77159113 | MACS2_peak_503 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 18 | chr11 | unknown | gene | 77216424 | 77455480 | + | Ssh2 | Ssh2 | P6600 | NM_177710 | TSS9403 |
| chr11 | 77608612 | 77608703 | MACS2_peak_504 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 67 | chr11 | unknown | gene | 77529161 | 77607815 | - | Taok1 | Taok1 | P26075 | NM_144825 | TSS25459 |
| chr11 | 77608612 | 77608703 | MACS2_peak_504 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 67 | chr11 | unknown | gene | 77686138 | 77709735 | + | Nufip2 | Nufip2 | P22479 | NM_001024205 | TSS12846 |
| chr11 | 81303517 | 81303608 | MACS2_peak_505 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 33 | chr11 | unknown | gene | 80858388 | 80867704 | + | Spaca3 | Spaca3 | P13345 | NM_029367 | TSS8926 |
| chr11 | 81303517 | 81303608 | MACS2_peak_505 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 33 | chr11 | unknown | gene | 81572501 | 81573473 | - | 1700071K01Rik | 1700071K01Rik | P12550 | NM_001033765 | TSS15472 |
| chr11 | 82169921 | 82170012 | MACS2_peak_506 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 77 | chr11 | unknown | gene | 82115184 | 82116634 | + | Ccl8 | Ccl8 | P19974 | NM_021443 | TSS16885 |
| chr11 | 82169921 | 82170012 | MACS2_peak_506 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 77 | chr11 | unknown | gene | 82176665 | 82179744 | - | Ccl1 | Ccl1 | P2447 | NM_011329 | TSS21139 |
| chr11 | 83233878 | 83233986 | MACS2_peak_507 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 38 | chr11 | unknown | gene | 83223575 | 83226584 | + | AI662270 | AI662270 | | NR_015519 | TSS10449 |
| chr11 | 83233878 | 83233986 | MACS2_peak_507 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 38 | chr11 | unknown | gene | 83275111 | 83286726 | - | Slfn14 | Slfn14 | P13319 | NM_001166028 | TSS18236 |
| chr11 | 85026181 | 85026272 | MACS2_peak_508 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 49 | chr11 | unknown | gene | 84957753 | 84965805 | + | Car4 | Car4 | P18754 | NM_007607 | TSS8549 |
| chr11 | 85026181 | 85026272 | MACS2_peak_508 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 49 | chr11 | unknown | gene | 85171095 | 85180971 | + | 1700125H20Rik | 1700125H20Rik | P4527 | NM_028589 | TSS6879 |
| chr11 | 85508001 | 85508171 | MACS2_peak_509 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 88 | chr11 | unknown | gene | 85311253 | 85346193 | + | Ppm1d | Ppm1d | P13899 | NM_016910 | TSS4657 |
| chr11 | 85508001 | 85508171 | MACS2_peak_509 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 88 | chr11 | unknown | gene | 85702199 | 85719744 | - | Bcas3os1 | Bcas3os1 | | NR_045875 | TSS27328 |
| chr11 | 85713434 | 85713570 | MACS2_peak_510 | 23 | + | 5.26766 | 7.08584 | 2.32792 | 57 | chr11 | unknown | gene | 85311253 | 85346193 | + | Ppm1d | Ppm1d | P13899 | NM_016910 | TSS4657 |
| chr11 | 85713434 | 85713570 | MACS2_peak_510 | 23 | + | 5.26766 | 7.08584 | 2.32792 | 57 | chr11 | unknown | gene | 85760615 | 85760702 | - | Mir5110 | Mir5110 | | NR_039570 | TSS19761 |
| chr11 | 86051002 | 86051150 | MACS2_peak_511 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 68 | chr11 | unknown | gene | 86002657 | 86024350 | - | Gm20759 | Gm20759 | | NR_046030 | TSS9242 |
| chr11 | 86051002 | 86051150 | MACS2_peak_511 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 68 | chr11 | unknown | gene | 86058135 | 86201193 | - | Brip1 | Brip1 | P5557 | NM_178309 | TSS7302 |
| chr11 | 86176897 | 86176988 | MACS2_peak_512 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 14 | chr11 | unknown | gene | 86002657 | 86024350 | - | Gm20759 | Gm20759 | | NR_046030 | TSS9242 |
| chr11 | 86176897 | 86176988 | MACS2_peak_512 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 14 | chr11 | unknown | gene | 86201359 | 86304443 | + | Brip1os | Brip1os | | NR_130958 | TSS4851 |
| chr11 | 86260198 | 86260289 | MACS2_peak_513 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 9 | chr11 | unknown | gene | 86210682 | 86257568 | - | Ints2 | Ints2 | P469 | NM_027421 | TSS4649 |
| chr11 | 86260198 | 86260289 | MACS2_peak_513 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 9 | chr11 | unknown | gene | 86265714 | 86357525 | - | Med13 | Med13 | P14750 | NM_001080931 | TSS12452 |
| chr11 | 86278672 | 86278779 | MACS2_peak_514 | 23 | + | 5.36409 | 7.26321 | 2.37531 | 56 | chr11 | unknown | gene | 86210682 | 86257568 | - | Ints2 | Ints2 | P469 | NM_027421 | TSS4649 |
| chr11 | 86278672 | 86278779 | MACS2_peak_514 | 23 | + | 5.36409 | 7.26321 | 2.37531 | 56 | chr11 | unknown | gene | 86415843 | 86520291 | + | Mir467c | Mir467c | | NR_030571 | TSS1895 |
| chr11 | 88194832 | 88194923 | MACS2_peak_515 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 21 | chr11 | unknown | gene | 88099145 | 88194140 | + | Cuedc1 | Cuedc1 | P236 | NM_198013 | TSS16339 |
| chr11 | 88194832 | 88194923 | MACS2_peak_515 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 21 | chr11 | unknown | gene | 88294042 | 88294554 | + | 1700106J16Rik | 1700106J16Rik | P13130 | NM_028859 | TSS10802 |
| chr11 | 89188277 | 89188368 | MACS2_peak_516 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 22 | chr11 | unknown | gene | 89073840 | 89093064 | + | Gm525 | Gm525 | P11326 | NM_001033266 | TSS19115 |
| chr11 | 89188277 | 89188368 | MACS2_peak_516 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 22 | chr11 | unknown | gene | 89300637 | 89302020 | - | Nog | Nog | P14745 | NM_008711 | TSS23026 |
| chr11 | 90189989 | 90190091 | MACS2_peak_517 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 60 | chr11 | unknown | gene | 90030347 | 90035753 | + | Tmem100 | Tmem100 | P3243 | NM_026433 | TSS11539 |
| chr11 | 90189989 | 90190091 | MACS2_peak_517 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 60 | chr11 | unknown | gene | 90249475 | 90276863 | + | Mmd | Mmd | P14113 | NM_026178 | TSS10514 |
| chr11 | 93901887 | 93902022 | MACS2_peak_518 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 86 | chr11 | unknown | gene | 93859242 | 93885657 | - | Utp18 | Utp18 | P4859 | NM_001013375 | TSS16630 |
| chr11 | 93901887 | 93902022 | MACS2_peak_518 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 86 | chr11 | unknown | gene | 93949813 | 93956256 | - | Nme2 | Nme2 | P10585 | NM_001077529 | TSS11441 |
| chr11 | 94108913 | 94109004 | MACS2_peak_519 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 32 | chr11 | unknown | gene | 93958924 | 93968521 | - | Nme1 | Nme1 | P18141 | NM_008704 | TSS18760 |
| chr11 | 94108913 | 94109004 | MACS2_peak_519 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 32 | chr11 | unknown | gene | 94211453 | 94214728 | + | Tob1 | Tob1 | P12858 | NM_009427 | TSS655 |

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr11 | 96349127 | 96349218 | MACS2_peak_520 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 49 | chr11 | unknown | gene | 96323125 | 96346399 | + | Hoxb3 | Hoxb3 | P20125 | NM_001079869 | TSS24468 |
| chr11 | 96349127 | 96349218 | MACS2_peak_520 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 49 | chr11 | unknown | gene | 96351631 | 96353629 | + | Hoxb2 | Hoxb2 | P8415 | NM_134032 | TSS26860 |
| chr11 | 96555445 | 96555536 | MACS2_peak_521 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 30 | chr11 | unknown | gene | 96446898 | 96464547 | - | Gm11529 | Gm11529 | | NR_033524 | TSS8137 |
| chr11 | 96555445 | 96555536 | MACS2_peak_521 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 30 | chr11 | unknown | gene | 96767548 | 96777555 | - | Snx11 | Snx11 | P18271 | NM_028965 | TSS12730 |
| chr11 | 97218710 | 97218830 | MACS2_peak_522 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 37 | chr11 | unknown | gene | 97159709 | 97187585 | - | Kpnb1 | Kpnb1 | P21544 | NM_008379 | TSS21774 |
| chr11 | 97218710 | 97218830 | MACS2_peak_522 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 37 | chr11 | unknown | gene | 97315715 | 97328568 | + | Mrpl45 | Mrpl45 | P22600 | NM_025927 | TSS15516 |
| chr11 | 97777033 | 97777124 | MACS2_peak_523 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 39 | chr11 | unknown | gene | 97771480 | 97775858 | - | 1700001P01Rik | 1700001P01Rik | P17809 | NM_028156 | TSS26005 |
| chr11 | 97777033 | 97777124 | MACS2_peak_523 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 39 | chr11 | unknown | gene | 97777525 | 97782356 | - | Rpl23 | Rpl23 | P8180 | NM_022891 | TSS23274 |
| chr11 | 98246611 | 98246759 | MACS2_peak_524 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 10 | chr11 | unknown | gene | 98152154 | 98193083 | - | Med1 | Med1 | P11279 | NM_134027 | TSS18455 |
| chr11 | 98246611 | 98246759 | MACS2_peak_524 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 10 | chr11 | unknown | gene | 98262605 | 98262662 | + | Mir5119 | Mir5119 | | NR_039579 | TSS21184 |
| chr11 | 98947922 | 98948013 | MACS2_peak_525 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 39 | chr11 | unknown | gene | 98907888 | 98921205 | + | Cdc6 | Cdc6 | P12787 | NM_001025779 | TSS23299 |
| chr11 | 98947922 | 98948013 | MACS2_peak_525 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 39 | chr11 | unknown | gene | 98982179 | 98983016 | - | Gjd3 | Gjd3 | P11609 | NM_178596 | TSS25119 |
| chr11 | 99582476 | 99582567 | MACS2_peak_526 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 39 | chr11 | unknown | gene | 99579976 | 99580965 | - | Krtap1-5 | Krtap1-5 | P6578 | NM_027157 | TSS1875 |
| chr11 | 99582476 | 99582567 | MACS2_peak_526 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 39 | chr11 | unknown | gene | 99590460 | 99591319 | - | Krtap1-3 | Krtap1-3 | P11409 | NM_001085526 | TSS17518 |
| chr11 | 101791117 | 101791244 | MACS2_peak_527 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 44 | chr11 | unknown | gene | 101769741 | 101785310 | - | Etv4 | Etv4 | P10217 | NM_008815 | TSS20023 |
| chr11 | 101791117 | 101791244 | MACS2_peak_527 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 44 | chr11 | unknown | gene | 101877509 | 101894005 | - | Meox1 | Meox1 | P18923 | NM_010791 | TSS22487 |
| chr11 | 103845890 | 103845992 | MACS2_peak_528 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 45 | chr11 | unknown | gene | 103774174 | 103818021 | + | Wnt3 | Wnt3 | P22794 | NM_009521 | TSS20319 |
| chr11 | 103845890 | 103845992 | MACS2_peak_528 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 45 | chr11 | unknown | gene | 103966724 | 103983749 | + | Arf2 | Arf2 | P19836 | NM_001304574 | TSS25401 |
| chr11 | 104472952 | 104473043 | MACS2_peak_529 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 33 | chr11 | unknown | gene | 104333228 | 104442291 | - | Kansl1 | Kansl1 | P12638 | NM_001081045 | TSS22160 |
| chr11 | 104472952 | 104473043 | MACS2_peak_529 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 33 | chr11 | unknown | gene | 104502525 | 104550389 | - | Cdc27 | Cdc27 | P361 | NM_001285989 | TSS11486 |
| chr11 | 105798307 | 105798412 | MACS2_peak_530 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 26 | chr11 | unknown | gene | 105360797 | 105456735 | - | Mar-10 | Mar-10 | P576 | NM_172568 | TSS6976 |
| chr11 | 105798307 | 105798412 | MACS2_peak_530 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 26 | chr11 | unknown | gene | 105933703 | 105944147 | - | Cyb561 | Cyb561 | P18614 | NM_007805 | TSS13137 |
| chr11 | 105905902 | 105906071 | MACS2_peak_531 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 84 | chr11 | unknown | gene | 105360797 | 105456735 | - | Mar-10 | Mar-10 | P576 | NM_172568 | TSS6976 |
| chr11 | 105905902 | 105906071 | MACS2_peak_531 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 84 | chr11 | unknown | gene | 105933703 | 105944147 | - | Cyb561 | Cyb561 | P18614 | NM_007805 | TSS13137 |
| chr11 | 106999762 | 106999891 | MACS2_peak_532 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 83 | chr11 | unknown | gene | 106988628 | 106999525 | - | Kpna2 | Kpna2 | P17168 | NM_010655 | TSS14797 |
| chr11 | 106999762 | 106999891 | MACS2_peak_532 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 83 | chr11 | unknown | gene | 107028222 | 107029775 | + | 1810010H24Rik | 1810010H24Rik | P6440 | NM_001163473 | TSS3951 |
| chr11 | 107167535 | 107167644 | MACS2_peak_533 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 83 | chr11 | unknown | gene | 107157407 | 107166793 | + | Gm11715 | Gm11715 | P3103 | NM_001308498 | TSS8302 |
| chr11 | 107167535 | 107167644 | MACS2_peak_533 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 83 | chr11 | unknown | gene | 107207891 | 107469938 | - | Pitpnc1 | Pitpnc1 | P3112 | NM_145823 | TSS7850 |
| chr11 | 107199077 | 107199178 | MACS2_peak_534 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 18 | chr11 | unknown | gene | 107166660 | 107189257 | - | Nol11 | Nol11 | P174 | NM_001161329 | TSS9046 |
| chr11 | 107199077 | 107199178 | MACS2_peak_534 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 18 | chr11 | unknown | gene | 107207891 | 107469938 | - | Pitpnc1 | Pitpnc1 | P3112 | NM_145823 | TSS7850 |
| chr11 | 108489493 | 108489584 | MACS2_peak_535 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 21 | chr11 | unknown | gene | 108395296 | 108414295 | + | Apoh | Apoh | P4862 | NM_013475 | TSS25512 |
| chr11 | 108489493 | 108489584 | MACS2_peak_535 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 21 | chr11 | unknown | gene | 108920348 | 108949395 | + | Axin2 | Axin2 | P8406 | NM_015732 | TSS11754 |
| chr11 | 109757617 | 109757708 | MACS2_peak_536 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 33 | chr11 | unknown | gene | 109672925 | 109721715 | - | Fam20a | Fam20a | P3437 | NM_153782 | TSS16864 |
| chr11 | 109757617 | 109757708 | MACS2_peak_536 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 33 | chr11 | unknown | gene | 109788290 | 109827905 | - | 1700012B07Rik | 1700012B07Rik | P1244 | NM_001162428 | TSS24609 |
| chr11 | 110092174 | 110092265 | MACS2_peak_537 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 29 | chr11 | unknown | gene | 109933405 | 109995816 | - | Abca8b | Abca8b | P23240 | NM_013851 | TSS18749 |
| chr11 | 110092174 | 110092265 | MACS2_peak_537 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 29 | chr11 | unknown | gene | 110100821 | 110168153 | - | Abca9 | Abca9 | P15545 | NM_147220 | TSS20059 |
| chr11 | 110202873 | 110203005 | MACS2_peak_538 | 23 | + | 5.26766 | 7.08584 | 2.32792 | 63 | chr11 | unknown | gene | 110100821 | 110168153 | - | Abca9 | Abca9 | P15545 | NM_147220 | TSS20059 |
| chr11 | 110202873 | 110203005 | MACS2_peak_538 | 23 | + | 5.26766 | 7.08584 | 2.32792 | 63 | chr11 | unknown | gene | 110269368 | 110337716 | - | Abca5 | Abca5 | P14802 | NM_147219 | TSS17003 |
| chr11 | 112141042 | 112141133 | MACS2_peak_539 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 59 | chr11 | unknown | gene | 111066163 | 111073070 | + | Kcnj2 | Kcnj2 | P25813 | NM_008425 | TSS2651 |
| chr11 | 112141042 | 112141133 | MACS2_peak_539 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 59 | chr11 | unknown | gene | 112663926 | 112711356 | - | BC006965 | BC006965 | | NR_024085 | TSS25668 |
| chr11 | 112762908 | 112762999 | MACS2_peak_540 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 73 | chr11 | unknown | gene | 112663926 | 112711356 | - | BC006965 | BC006965 | | NR_024085 | TSS25668 |
| chr11 | 112762908 | 112762999 | MACS2_peak_540 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 73 | chr11 | unknown | gene | 112782209 | 112785510 | + | Sox9 | Sox9 | P25086 | NM_011448 | TSS18301 |
| chr11 | 114349288 | 114349379 | MACS2_peak_541 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 40 | chr11 | unknown | gene | 114198257 | 114199199 | + | 1700092K14Rik | 1700092K14Rik | | NR_045930 | TSS7999 |
| chr11 | 114349288 | 114349379 | MACS2_peak_541 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 40 | chr11 | unknown | gene | 114413404 | 114448860 | - | 4932435O22Rik | 4932435O22Rik | | NR_027643 | TSS22430 |
| chr11 | 114973460 | 114973575 | MACS2_peak_542 | 108 | + | 9.78615 | 16.21324 | 10.89553 | 64 | chr11 | unknown | gene | 114956277 | 114960417 | - | Cd300c | Cd300c | P1664 | NM_199225 | TSS20929 |
| chr11 | 114973460 | 114973575 | MACS2_peak_542 | 108 | + | 9.78615 | 16.21324 | 10.89553 | 64 | chr11 | unknown | gene | 114982445 | 114989810 | - | Cd300ld | Cd300ld | P23987 | NM_145437 | TSS2349 |
| chr11 | 118728531 | 118728622 | MACS2_peak_543 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 29 | chr11 | unknown | gene | 118476959 | 118487507 | + | Engase | Engase | P5677 | NM_172573 | TSS13998 |
| chr11 | 118728531 | 118728622 | MACS2_peak_543 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 29 | chr11 | unknown | gene | 118988187 | 118992841 | + | Enpp7 | Enpp7 | P4121 | NM_001030291 | TSS783 |
| chr11 | 119036740 | 119036831 | MACS2_peak_544 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 71 | chr11 | unknown | gene | 119023028 | 119029170 | + | Cbx2 | Cbx2 | P9770 | NM_007623 | TSS27002 |
| chr11 | 119036740 | 119036831 | MACS2_peak_544 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 71 | chr11 | unknown | gene | 119038435 | 119040850 | - | Cbx8 | Cbx8 | P16840 | NM_013926 | TSS25483 |
| chr12 | 3109855 | 3110102 | MACS2_peak_545 | 2470 | + | 54.64653 | 256.44046 | 247.00465 | 103 | chr12 | unknown | gene | 3235790 | 3250374 | + | Rab10os | Rab10os | | NR_015551 | TSS25810 |
| chr12 | 3622679 | 3622770 | MACS2_peak_546 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 24 | chr12 | unknown | gene | 3426856 | 3502372 | + | Asxl2 | Asxl2 | P24331 | NM_172421 | TSS24375 |
| chr12 | 3622679 | 3622770 | MACS2_peak_546 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 24 | chr12 | unknown | gene | 3806979 | 3907747 | + | Dnmt3a | Dnmt3a | P22795 | NM_007872 | TSS9570 |
| chr12 | 9642714 | 9642805 | MACS2_peak_547 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 67 | chr12 | unknown | gene | 9574441 | 9580625 | + | Osr1 | Osr1 | P14098 | NM_011859 | TSS21277 |
| chr12 | 9642714 | 9642805 | MACS2_peak_547 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 67 | chr12 | unknown | gene | 10369970 | 10390133 | + | Nt5c1b | Nt5c1b | P2640 | NM_027588 | TSS25478 |
| chr12 | 10392810 | 10392901 | MACS2_peak_548 | 12 | + | 4.14966 | 5.12722 | 1.204 | 7 | chr12 | unknown | gene | 10369970 | 10390133 | + | Nt5c1b | Nt5c1b | P2640 | NM_027588 | TSS25478 |
| chr12 | 10392810 | 10392901 | MACS2_peak_548 | 12 | + | 4.14966 | 5.12722 | 1.204 | 7 | chr12 | unknown | gene | 10446387 | 10531303 | + | Gm38407 | Gm38407 | | NR_110487 | TSS13708 |
| chr12 | 13106420 | 13106511 | MACS2_peak_549 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 66 | chr12 | unknown | gene | 12936092 | 12941836 | - | Mycn | Mycn | P23470 | NM_008709 | TSS3519 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr12 | 13106420 | 13106511 | MACS2_peak_549 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 66 | chr12 | unknown | gene | 13219306 | 13249119 | - | Ddx1 | Ddx1 | P3317 | NM_134040 | TSS8809 |
| chr12 | 20062266 | 20062357 | MACS2_peak_550 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 19 | chr12 | unknown | gene | 18514509 | 18534191 | + | 5730507C01Rik | 5730507C01Rik | P11332 | NM_001033157 | TSS807 |
| chr12 | 20062266 | 20062357 | MACS2_peak_550 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 19 | chr12 | unknown | gene | 20804391 | 20815779 | - | 1700030C10Rik | 1700030C10Rik |  | NR_015521 | TSS9551 |
| chr12 | 21372702 | 21372793 | MACS2_peak_551 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 36 | chr12 | unknown | gene | 21316391 | 21323471 | + | Iah1 | Iah1 | P7213 | NM_026347 | TSS25499 |
| chr12 | 21372702 | 21372793 | MACS2_peak_551 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 36 | chr12 | unknown | gene | 21390328 | 21417091 | - | Ywhaq | Ywhaq | P23727 | NM_011739 | TSS15533 |
| chr12 | 25845269 | 25845360 | MACS2_peak_552 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 11 | chr12 | unknown | gene | 25129173 | 25132274 | + | Gm17746 | Gm17746 |  | NR_045844 | TSS16313 |
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| chr12 | 30578565 | 30578770 | MACS2_peak_553 | 50 | + | 6.87285 | 10.15897 | 5.05896 | 152 | chr12 | unknown | gene | 30410558 | 30467358 | - | 2310016D03Rik | 2310016D03Rik |  | NR_045491 | TSS7497 |
| chr12 | 30578565 | 30578770 | MACS2_peak_553 | 50 | + | 6.87285 | 10.15897 | 5.05896 | 152 | chr12 | unknown | gene | 30584442 | 30588747 | + | Tmem18 | Tmem18 | P3943 | NM_172049 | TSS6779 |
| chr12 | 31380661 | 31380752 | MACS2_peak_554 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 27 | chr12 | unknown | gene | 31331561 | 31351339 | - | Dld | Dld | P947 | NM_007861 | TSS22680 |
| chr12 | 31380661 | 31380752 | MACS2_peak_554 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 27 | chr12 | unknown | gene | 31438218 | 31473495 | + | Slc26a3 | Slc26a3 | P16252 | NM_021353 | TSS6108 |
| chr12 | 31769191 | 31769282 | MACS2_peak_555 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 43 | chr12 | unknown | gene | 31706866 | 31713926 | - | Gpr22 | Gpr22 | P17283 | NM_175191 | TSS2954 |
| chr12 | 31769191 | 31769282 | MACS2_peak_555 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 43 | chr12 | unknown | gene | 31926454 | 31950210 | - | Hbp1 | Hbp1 | P6536 | NM_153198 | TSS12542 |
| chr12 | 33421723 | 33421818 | MACS2_peak_556 | 49 | + | 6.77503 | 10.04021 | 4.94691 | 46 | chr12 | unknown | gene | 33394853 | 33401229 | + | Efcab10 | Efcab10 | P12572 | NM_029152 | TSS25528 |
| chr12 | 33421723 | 33421818 | MACS2_peak_556 | 49 | + | 6.77503 | 10.04021 | 4.94691 | 46 | chr12 | unknown | gene | 33429623 | 33438080 | + | Twistnb | Twistnb | P26691 | NM_172253 | TSS24849 |
| chr12 | 33596814 | 33596905 | MACS2_peak_557 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 42 | chr12 | unknown | gene | 33429623 | 33438080 | + | Twistnb | Twistnb | P26691 | NM_172253 | TSS24849 |
| chr12 | 33596814 | 33596905 | MACS2_peak_557 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 42 | chr12 | unknown | gene | 33928424 | 33928996 | + | Ferd3l | Ferd3l | P12467 | NM_033522 | TSS993 |
| chr12 | 33959567 | 33959658 | MACS2_peak_558 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 37 | chr12 | unknown | gene | 33928424 | 33928996 | + | Ferd3l | Ferd3l | P12467 | NM_033522 | TSS993 |
| chr12 | 33959567 | 33959658 | MACS2_peak_558 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 37 | chr12 | unknown | gene | 34047581 | 34917095 | - | Hdac9 | Hdac9 | P24183 | NM_001271386 | TSS5698 |
| chr12 | 34095633 | 34095813 | MACS2_peak_559 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 149 | chr12 | unknown | gene | 33957670 | 33959831 | + | Twist1 | Twist1 | P20282 | NM_011658 | TSS3973 |
| chr12 | 34095633 | 34095813 | MACS2_peak_559 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 149 | chr12 | unknown | gene | 34984760 | 34985844 | + | Prps1l1 | Prps1l1 | P18257 | NM_029294 | TSS3224 |
| chr12 | 34805395 | 34805529 | MACS2_peak_560 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 62 | chr12 | unknown | gene | 33957670 | 33959831 | + | Twist1 | Twist1 | P20282 | NM_011658 | TSS3973 |
| chr12 | 34805395 | 34805529 | MACS2_peak_560 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 62 | chr12 | unknown | gene | 34984760 | 34985844 | + | Prps1l1 | Prps1l1 | P18257 | NM_029294 | TSS3224 |
| chr12 | 34905667 | 34905758 | MACS2_peak_561 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 17 | chr12 | unknown | gene | 33957670 | 33959831 | + | Twist1 | Twist1 | P20282 | NM_011658 | TSS3973 |
| chr12 | 34905667 | 34905758 | MACS2_peak_561 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 17 | chr12 | unknown | gene | 34984760 | 34985844 | + | Prps1l1 | Prps1l1 | P18257 | NM_029294 | TSS3224 |
| chr12 | 35621989 | 35622111 | MACS2_peak_562 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 57 | chr12 | unknown | gene | 35497978 | 35534623 | - | Ahr | Ahr | P15351 | NM_013464 | TSS8604 |
| chr12 | 35621989 | 35622111 | MACS2_peak_562 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 57 | chr12 | unknown | gene | 35672290 | 35695118 | - | 9130015A21Rik | 9130015A21Rik |  | NR_045050 | TSS21577 |
| chr12 | 35816271 | 35816362 | MACS2_peak_563 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 67 | chr12 | unknown | gene | 35672290 | 35695118 | - | 9130015A21Rik | 9130015A21Rik |  | NR_045050 | TSS21577 |
| chr12 | 35816271 | 35816362 | MACS2_peak_563 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 67 | chr12 | unknown | gene | 35925620 | 35949546 | + | Agr3 | Agr3 | P20982 | NM_207531 | TSS1856 |
| chr12 | 36092371 | 36092462 | MACS2_peak_564 | 32 | + | 5.82623 | 8.17465 | 3.21814 | 46 | chr12 | unknown | gene | 36090378 | 36091829 | + | Gm5434 | Gm5434 |  | NR_003649 | TSS20233 |
| chr12 | 36092371 | 36092462 | MACS2_peak_564 | 32 | + | 5.82623 | 8.17465 | 3.21814 | 46 | chr12 | unknown | gene | 36157123 | 36196401 | + | Ankmy2 | Ankmy2 | P5703 | NM_146033 | TSS7607 |
| chr12 | 36136125 | 36136220 | MACS2_peak_565 | 30 | + | 5.71265 | 7.93979 | 3.00019 | 24 | chr12 | unknown | gene | 36090378 | 36091829 | + | Gm5434 | Gm5434 |  | NR_003649 | TSS20233 |
| chr12 | 36136125 | 36136220 | MACS2_peak_565 | 30 | + | 5.71265 | 7.93979 | 3.00019 | 24 | chr12 | unknown | gene | 36157123 | 36196401 | + | Ankmy2 | Ankmy2 | P5703 | NM_146033 | TSS7607 |
| chr12 | 36497826 | 36497917 | MACS2_peak_566 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 26 | chr12 | unknown | gene | 36314168 | 36317447 | + | Sostdc1 | Sostdc1 | P8150 | NM_025312 | TSS20101 |
| chr12 | 36497826 | 36497917 | MACS2_peak_566 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 26 | chr12 | unknown | gene | 36816204 | 36816278 | + | Mir5099 | Mir5099 |  | NR_039558 | TSS17464 |
| chr12 | 36649883 | 36650000 | MACS2_peak_567 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 27 | chr12 | unknown | gene | 36314168 | 36317447 | + | Sostdc1 | Sostdc1 | P8150 | NM_025312 | TSS20101 |
| chr12 | 36649883 | 36650000 | MACS2_peak_567 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 27 | chr12 | unknown | gene | 36816204 | 36816278 | + | Mir5099 | Mir5099 |  | NR_039558 | TSS17464 |
| chr12 | 36828765 | 36828856 | MACS2_peak_568 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 20 | chr12 | unknown | gene | 36816204 | 36816278 | + | Mir5099 | Mir5099 |  | NR_039558 | TSS17464 |
| chr12 | 36828765 | 36828856 | MACS2_peak_568 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 20 | chr12 | unknown | gene | 37108545 | 37178377 | + | Meox2 | Meox2 | P8259 | NM_008584 | TSS24850 |
| chr12 | 36908031 | 36908122 | MACS2_peak_569 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 64 | chr12 | unknown | gene | 36816204 | 36816278 | + | Mir5099 | Mir5099 |  | NR_039558 | TSS17464 |
| chr12 | 36908031 | 36908122 | MACS2_peak_569 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 64 | chr12 | unknown | gene | 37108545 | 37178377 | + | Meox2 | Meox2 | P8259 | NM_008584 | TSS24850 |
| chr12 | 37077159 | 37077250 | MACS2_peak_570 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 29 | chr12 | unknown | gene | 36816204 | 36816278 | + | Mir5099 | Mir5099 |  | NR_039558 | TSS17464 |
| chr12 | 37077159 | 37077250 | MACS2_peak_570 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 29 | chr12 | unknown | gene | 37108545 | 37178377 | + | Meox2 | Meox2 | P8259 | NM_008584 | TSS24850 |
| chr12 | 37175446 | 37175537 | MACS2_peak_571 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 60 | chr12 | unknown | gene | 36816204 | 36816278 | + | Mir5099 | Mir5099 |  | NR_039558 | TSS17464 |
| chr12 | 37175446 | 37175537 | MACS2_peak_571 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 60 | chr12 | unknown | gene | 37241638 | 37581524 | + | Agmo | Agmo | P2186 | NM_178767 | TSS5270 |
| chr12 | 37284782 | 37284873 | MACS2_peak_572 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 20 | chr12 | unknown | gene | 37108545 | 37178377 | + | Meox2 | Meox2 | P8259 | NM_008584 | TSS24850 |
| chr12 | 37284782 | 37284873 | MACS2_peak_572 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 20 | chr12 | unknown | gene | 37880704 | 38630690 | + | Dgkb | Dgkb | P4775 | NM_178681 | TSS26619 |
| chr12 | 37427065 | 37427202 | MACS2_peak_573 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 84 | chr12 | unknown | gene | 37108545 | 37178377 | + | Meox2 | Meox2 | P8259 | NM_008584 | TSS24850 |
| chr12 | 37427065 | 37427202 | MACS2_peak_573 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 84 | chr12 | unknown | gene | 37880704 | 38630690 | + | Dgkb | Dgkb | P4775 | NM_178681 | TSS26619 |
| chr12 | 37471058 | 37471149 | MACS2_peak_574 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 13 | chr12 | unknown | gene | 37108545 | 37178377 | + | Meox2 | Meox2 | P8259 | NM_008584 | TSS24850 |
| chr12 | 37471058 | 37471149 | MACS2_peak_574 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 13 | chr12 | unknown | gene | 37880704 | 38630690 | + | Dgkb | Dgkb | P4775 | NM_178681 | TSS26619 |
| chr12 | 37630626 | 37630717 | MACS2_peak_575 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 20 | chr12 | unknown | gene | 37241638 | 37581524 | + | Agmo | Agmo | P2186 | NM_178767 | TSS5270 |
| chr12 | 37630626 | 37630717 | MACS2_peak_575 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 20 | chr12 | unknown | gene | 37880704 | 38630690 | + | Dgkb | Dgkb | P4775 | NM_178681 | TSS26619 |
| chr12 | 38586332 | 38586451 | MACS2_peak_576 | 25 | + | 5.46411 | 7.45132 | 2.55202 | 60 | chr12 | unknown | gene | 37241638 | 37581524 | + | Agmo | Agmo | P2186 | NM_178767 | TSS5270 |
| chr12 | 38586332 | 38586451 | MACS2_peak_576 | 25 | + | 5.46411 | 7.45132 | 2.55202 | 60 | chr12 | unknown | gene | 38780257 | 38865769 | + | Etv1 | Etv1 | P21487 | NM_007960 | TSS23580 |
| chr12 | 38591767 | 38591858 | MACS2_peak_577 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 20 | chr12 | unknown | gene | 37241638 | 37581524 | + | Agmo | Agmo | P2186 | NM_178767 | TSS5270 |
| chr12 | 38591767 | 38591858 | MACS2_peak_577 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 20 | chr12 | unknown | gene | 38780257 | 38865769 | + | Etv1 | Etv1 | P21487 | NM_007960 | TSS23580 |
| chr12 | 39310167 | 39310286 | MACS2_peak_578 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 32 | chr12 | unknown | gene | 38780257 | 38865769 | + | Etv1 | Etv1 | P21487 | NM_007960 | TSS23580 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr12 | 39310167 | 39310286 | MACS2_peak_578 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 32 | chr12 | unknown | gene | 40033290 | 40037987 | - | Arl4a | Arl4a | P13606 | NM_007487 | TSS7359 |
| chr12 | 39312867 | 39312958 | MACS2_peak_579 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 14 | chr12 | unknown | gene | 38780257 | 38865769 | + | Etv1 | Etv1 | P21487 | NM_007960 | TSS23580 |
| chr12 | 39312867 | 39312958 | MACS2_peak_579 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 14 | chr12 | unknown | gene | 40033290 | 40037987 | - | Arl4a | Arl4a | P13606 | NM_007487 | TSS7359 |
| chr12 | 40118067 | 40118158 | MACS2_peak_580 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 45 | chr12 | unknown | gene | 40033290 | 40037987 | - | Arl4a | Arl4a | P13606 | NM_007487 | TSS7359 |
| chr12 | 40118067 | 40118158 | MACS2_peak_580 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 45 | chr12 | unknown | gene | 40176385 | 40199315 | - | Lsmem1 | Lsmem1 | P15577 | NM_001033437 | TSS9652 |
| chr12 | 41486936 | 41487084 | MACS2_peak_581 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 64 | chr12 | unknown | gene | 41451667 | 41486057 | - | Lrrn3 | Lrrn3 | P25865 | NM_001271708 | TSS322 |
| chr12 | 41486936 | 41487084 | MACS2_peak_581 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 64 | chr12 | unknown | gene | 44205896 | 44210068 | - | Dnajb9 | Dnajb9 | P4801 | NM_013760 | TSS13066 |
| chr12 | 41670376 | 41670467 | MACS2_peak_582 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 73 | chr12 | unknown | gene | 41451667 | 41486057 | - | Lrrn3 | Lrrn3 | P25865 | NM_001271708 | TSS322 |
| chr12 | 41670376 | 41670467 | MACS2_peak_582 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 73 | chr12 | unknown | gene | 44205896 | 44210068 | - | Dnajb9 | Dnajb9 | P4801 | NM_013760 | TSS13066 |
| chr12 | 44837639 | 44837730 | MACS2_peak_583 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 32 | chr12 | unknown | gene | 44328884 | 44598587 | + | Nrcam | Nrcam | P6098 | NM_176930 | TSS15506 |
| chr12 | 44837639 | 44837730 | MACS2_peak_583 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 32 | chr12 | unknown | gene | 44852485 | 45074483 | - | Stxbp6 | Stxbp6 | P11424 | NM_144552 | TSS4114 |
| chr12 | 46164911 | 46165051 | MACS2_peak_584 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 83 | chr12 | unknown | gene | 44852485 | 45074483 | - | Stxbp6 | Stxbp6 | P11424 | NM_144552 | TSS4114 |
| chr12 | 46164911 | 46165051 | MACS2_peak_584 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 83 | chr12 | unknown | gene | 46694516 | 46818751 | - | Nova1 | Nova1 | P15328 | NM_021361 | TSS25802 |
| chr12 | 49386474 | 49386565 | MACS2_peak_585 | 26 | + | 5.53289 | 7.58332 | 2.67506 | 25 | chr12 | unknown | gene | 49382882 | 49385931 | + | Foxg1 | Foxg1 | P5777 | NM_001160112 | TSS11475 |
| chr12 | 49386474 | 49386565 | MACS2_peak_585 | 26 | + | 5.53289 | 7.58332 | 2.67506 | 25 | chr12 | unknown | gene | 49389651 | 49407346 | + | 3110039M20Rik | 3110039M20Rik | | NR_026733 | TSS26759 |
| chr12 | 50473775 | 50473866 | MACS2_peak_586 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 24 | chr12 | unknown | gene | 49476992 | 49480862 | - | 1810007C17Rik | 1810007C17Rik | | NR_045472 | TSS22759 |
| chr12 | 50473775 | 50473866 | MACS2_peak_586 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 24 | chr12 | unknown | gene | 51005155 | 51062543 | + | 1700008C04Rik | 1700008C04Rik | | NR_126468 | TSS1104 |
| chr12 | 52489840 | 52489963 | MACS2_peak_587 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 90 | chr12 | unknown | gene | 52097745 | 52310764 | + | Nubpl | Nubpl | P9693 | NM_029760 | TSS14195 |
| chr12 | 52489840 | 52489963 | MACS2_peak_587 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 90 | chr12 | unknown | gene | 52516076 | 52567338 | + | Arhgap5 | Arhgap5 | P22528 | NM_009706 | TSS20768 |
| chr12 | 53395646 | 53395737 | MACS2_peak_588 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 20 | chr12 | unknown | gene | 52699382 | 53151015 | + | Akap6 | Akap6 | P9547 | NM_198111 | TSS7860 |
| chr12 | 53395646 | 53395737 | MACS2_peak_588 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 20 | chr12 | unknown | gene | 54178980 | 54203561 | - | Egln3 | Egln3 | P17164 | NM_028133 | TSS2048 |
| chr12 | 53897472 | 53897563 | MACS2_peak_589 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 8 | chr12 | unknown | gene | 52699382 | 53151015 | + | Akap6 | Akap6 | P9547 | NM_198111 | TSS7860 |
| chr12 | 53897472 | 53897563 | MACS2_peak_589 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 8 | chr12 | unknown | gene | 54178980 | 54203561 | - | Egln3 | Egln3 | P17164 | NM_028133 | TSS2048 |
| chr12 | 53996825 | 53996916 | MACS2_peak_590 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 25 | chr12 | unknown | gene | 52699382 | 53151015 | + | Akap6 | Akap6 | P9547 | NM_198111 | TSS7860 |
| chr12 | 53996825 | 53996916 | MACS2_peak_590 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 25 | chr12 | unknown | gene | 54178980 | 54203561 | - | Egln3 | Egln3 | P17164 | NM_028133 | TSS2048 |
| chr12 | 54209944 | 54210042 | MACS2_peak_591 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 36 | chr12 | unknown | gene | 54178980 | 54203561 | - | Egln3 | Egln3 | P17164 | NM_028133 | TSS2048 |
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| chr12 | 54329092 | 54329183 | MACS2_peak_592 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 28 | chr12 | unknown | gene | 54233614 | 54242320 | + | 1700104L18Rik | 1700104L18Rik | | NR_108033 | TSS7747 |
| chr12 | 54329092 | 54329183 | MACS2_peak_592 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 28 | chr12 | unknown | gene | 54387732 | 54391318 | - | Gm7550 | Gm7550 | | NR_033689 | TSS11930 |
| chr12 | 54617465 | 54617556 | MACS2_peak_593 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 63 | chr12 | unknown | gene | 54387732 | 54391318 | - | Gm7550 | Gm7550 | | NR_033689 | TSS11930 |
| chr12 | 54617465 | 54617556 | MACS2_peak_593 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 63 | chr12 | unknown | gene | 54645373 | 54656483 | - | Sptssa | Sptssa | P14566 | NM_134054 | TSS9430 |
| chr12 | 55297848 | 55297939 | MACS2_peak_594 | 12 | + | 4.14966 | 5.12722 | 1.204 | 86 | chr12 | unknown | gene | 55155103 | 55262218 | + | Srp54b | Srp54b | P7559 | NM_001100109 | TSS24418 |
| chr12 | 55297848 | 55297939 | MACS2_peak_594 | 12 | + | 4.14966 | 5.12722 | 1.204 | 86 | chr12 | unknown | gene | 55302636 | 55382400 | + | 1110008L16Rik | 1110008L16Rik | P7366 | NM_025373 | TSS2523 |
| chr12 | 56698122 | 56698238 | MACS2_peak_595 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 83 | chr12 | unknown | gene | 56611396 | 56613059 | - | Nkx2-9 | Nkx2-9 | P8961 | NM_008701 | TSS18781 |
| chr12 | 56698122 | 56698238 | MACS2_peak_595 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 83 | chr12 | unknown | gene | 56712633 | 57196939 | - | Slc25a21 | Slc25a21 | P7201 | NM_001167976 | TSS6403 |
| chr12 | 58072986 | 58073077 | MACS2_peak_596 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 57 | chr12 | unknown | gene | 57661457 | 57662911 | - | BC042761 | BC042761 | | NR_131112 | TSS5728 |
| chr12 | 58072986 | 58073077 | MACS2_peak_596 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 57 | chr12 | unknown | gene | 58211803 | 58213768 | + | Sstr1 | Sstr1 | P7766 | NM_009216 | TSS6286 |
| chr12 | 59413185 | 59413276 | MACS2_peak_597 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 35 | chr12 | unknown | gene | 59200654 | 59219479 | - | Fbxo33 | Fbxo33 | P9365 | NM_001033156 | TSS414 |
| chr12 | 59413185 | 59413276 | MACS2_peak_597 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 35 | chr12 | unknown | gene | 61499659 | 61521820 | - | Gm20063 | Gm20063 | | NR_045049 | TSS8294 |
| chr12 | 62709728 | 62709819 | MACS2_peak_598 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 23 | chr12 | unknown | gene | 62687786 | 62688336 | + | Spanxn4 | Spanxn4 | | NR_131949 | TSS27667 |
| chr12 | 62709728 | 62709819 | MACS2_peak_598 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 23 | chr12 | unknown | gene | 64471332 | 64474690 | - | Fscb | Fscb | P14990 | NM_001163271 | TSS2386 |
| chr12 | 63145723 | 63145853 | MACS2_peak_599 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 70 | chr12 | unknown | gene | 62687786 | 62688336 | + | Spanxn4 | Spanxn4 | | NR_131949 | TSS27667 |
| chr12 | 63145723 | 63145853 | MACS2_peak_599 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 70 | chr12 | unknown | gene | 64471332 | 64474690 | - | Fscb | Fscb | P14990 | NM_001163271 | TSS2386 |
| chr12 | 63695249 | 63695342 | MACS2_peak_600 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 13 | chr12 | unknown | gene | 62687786 | 62688336 | + | Spanxn4 | Spanxn4 | | NR_131949 | TSS27667 |
| chr12 | 63695249 | 63695342 | MACS2_peak_600 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 13 | chr12 | unknown | gene | 64471332 | 64474690 | - | Fscb | Fscb | P14990 | NM_001163271 | TSS2386 |
| chr12 | 64016928 | 64017019 | MACS2_peak_601 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 82 | chr12 | unknown | gene | 62687786 | 62688336 | + | Spanxn4 | Spanxn4 | | NR_131949 | TSS27667 |
| chr12 | 64016928 | 64017019 | MACS2_peak_601 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 82 | chr12 | unknown | gene | 64471332 | 64474690 | - | Fscb | Fscb | P14990 | NM_001163271 | TSS2386 |
| chr12 | 65583649 | 65583772 | MACS2_peak_602 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 47 | chr12 | unknown | gene | 65225516 | 65228454 | + | Wdr20rt | Wdr20rt | P11758 | NM_027614 | TSS356 |
| chr12 | 65583649 | 65583772 | MACS2_peak_602 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 47 | chr12 | unknown | gene | 66283378 | 66284357 | - | Rpl10l | Rpl10l | P13968 | NM_001162933 | TSS1139 |
| chr12 | 66128294 | 66128385 | MACS2_peak_603 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 51 | chr12 | unknown | gene | 65225516 | 65228454 | + | Wdr20rt | Wdr20rt | P11758 | NM_027614 | TSS356 |
| chr12 | 66128294 | 66128385 | MACS2_peak_603 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 51 | chr12 | unknown | gene | 66283378 | 66284357 | - | Rpl10l | Rpl10l | P13968 | NM_001162933 | TSS1139 |
| chr12 | 67059316 | 67059666 | MACS2_peak_604 | 179 | + | 12.48143 | 23.47493 | 17.95214 | 146 | chr12 | unknown | gene | 66283378 | 66284357 | - | Rpl10l | Rpl10l | P13968 | NM_001162933 | TSS1139 |
| chr12 | 67059316 | 67059666 | MACS2_peak_604 | 179 | + | 12.48143 | 23.47493 | 17.95214 | 146 | chr12 | unknown | gene | 67656741 | 67669271 | - | Gm17821 | Gm17821 | | NR_033146 | TSS4809 |
| chr12 | 69654077 | 69654376 | MACS2_peak_605 | 128 | + | 10.4429 | 18.24423 | 12.86058 | 105 | chr12 | unknown | gene | 69577627 | 69582986 | - | Vcpkmt | Vcpkmt | P1520 | NM_001033236 | TSS18228 |
| chr12 | 69654077 | 69654376 | MACS2_peak_605 | 128 | + | 10.4429 | 18.24423 | 12.86058 | 105 | chr12 | unknown | gene | 69690435 | 69724796 | - | L2hgdh | L2hgdh | P11620 | NM_145443 | TSS692 |
| chr12 | 69671005 | 69671096 | MACS2_peak_606 | 12 | + | 4.14966 | 5.12722 | 1.204 | 52 | chr12 | unknown | gene | 69577627 | 69582986 | - | Vcpkmt | Vcpkmt | P1520 | NM_001033236 | TSS18228 |
| chr12 | 69671005 | 69671096 | MACS2_peak_606 | 12 | + | 4.14966 | 5.12722 | 1.204 | 52 | chr12 | unknown | gene | 69690435 | 69724796 | - | L2hgdh | L2hgdh | P11620 | NM_145443 | TSS692 |
| chr12 | 70077824 | 70077984 | MACS2_peak_607 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 36 | chr12 | unknown | gene | 69965012 | 69986767 | - | Sav1 | Sav1 | P20741 | NM_022028 | TSS1582 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr12 | 70077824 | 70077984 | MACS2_peak_607 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 36 | chr12 | unknown | gene | 70154170 | 70183206 | + | Abhd12b | Abhd12b | P12944 | NM_001195033 | TSS9216 |
| chr12 | 70167333 | 70167445 | MACS2_peak_608 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 34 | chr12 | unknown | gene | 70011434 | 70112035 | - | Nin | Nin | P5713 | NM_001081453 | TSS10497 |
| chr12 | 70167333 | 70167445 | MACS2_peak_608 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 34 | chr12 | unknown | gene | 70190814 | 70227583 | - | Pygl | Pygl | P6769 | NM_133198 | TSS24714 |
| chr12 | 70608130 | 70608221 | MACS2_peak_609 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 30 | chr12 | unknown | gene | 70453153 | 70466156 | + | Tmx1 | Tmx1 | P23977 | NM_028339 | TSS23325 |
| chr12 | 70608130 | 70608221 | MACS2_peak_609 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 30 | chr12 | unknown | gene | 70825513 | 70899668 | + | Frmd6 | Frmd6 | P1603 | NM_028127 | TSS14744 |
| chr12 | 71446457 | 71446623 | MACS2_peak_610 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 13 | chr12 | unknown | gene | 71309883 | 71318894 | + | Dact1 | Dact1 | P10784 | NM_001190466 | TSS7567 |
| chr12 | 71446457 | 71446623 | MACS2_peak_610 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 13 | chr12 | unknown | gene | 71540606 | 71556133 | + | 4930404H11Rik | 4930404H11Rik | | NR_045941 | TSS1392 |
| chr12 | 72004954 | 72005045 | MACS2_peak_611 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 37 | chr12 | unknown | gene | 71831067 | 71989888 | + | Daam1 | Daam1 | P10047 | NM_172464 | TSS6563 |
| chr12 | 72004954 | 72005045 | MACS2_peak_611 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 37 | chr12 | unknown | gene | 72069617 | 72070991 | - | Gpr135 | Gpr135 | P17780 | NM_181752 | TSS8423 |
| chr12 | 72912861 | 72912952 | MACS2_peak_612 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 62 | chr12 | unknown | gene | 72761210 | 72793741 | + | Ppm1a | Ppm1a | P1974 | NM_008910 | TSS16880 |
| chr12 | 72912861 | 72912952 | MACS2_peak_612 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 62 | chr12 | unknown | gene | 72939944 | 72941795 | + | Six6 | Six6 | P1032 | NM_011384 | TSS19782 |
| chr12 | 73271225 | 73271316 | MACS2_peak_613 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 67 | chr12 | unknown | gene | 73100258 | 73113184 | - | Six4 | Six4 | P19128 | NM_011382 | TSS4939 |
| chr12 | 73271225 | 73271316 | MACS2_peak_613 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 67 | chr12 | unknown | gene | 73280409 | 73286688 | - | Trmt5 | Trmt5 | P25166 | NM_029580 | TSS12924 |
| chr12 | 74803903 | 74804031 | MACS2_peak_614 | 84 | + | 8.41195 | 13.6962 | 8.46432 | 52 | chr12 | unknown | gene | 74297473 | 74299189 | + | Dbpht2 | Dbpht2 | P6935 | NM_198866 | TSS19545 |
| chr12 | 74803903 | 74804031 | MACS2_peak_614 | 84 | + | 8.41195 | 13.6962 | 8.46432 | 52 | chr12 | unknown | gene | 74897216 | 75176528 | - | Kcnh5 | Kcnh5 | P6906 | NM_172805 | TSS5683 |
| chr12 | 74804253 | 74804471 | MACS2_peak_615 | 72 | + | 7.85404 | 12.44522 | 7.25844 | 149 | chr12 | unknown | gene | 74297473 | 74299189 | + | Dbpht2 | Dbpht2 | P6935 | NM_198866 | TSS19545 |
| chr12 | 74804253 | 74804471 | MACS2_peak_615 | 72 | + | 7.85404 | 12.44522 | 7.25844 | 149 | chr12 | unknown | gene | 74897216 | 75176528 | - | Kcnh5 | Kcnh5 | P6906 | NM_172805 | TSS5683 |
| chr12 | 75429256 | 75429412 | MACS2_peak_616 | 88 | + | 8.79765 | 14.09289 | 8.84823 | 81 | chr12 | unknown | gene | 75411719 | 75416781 | - | Gphb5 | Gphb5 | P12173 | NM_175644 | TSS6232 |
| chr12 | 75429256 | 75429412 | MACS2_peak_616 | 88 | + | 8.79765 | 14.09289 | 8.84823 | 81 | chr12 | unknown | gene | 75450880 | 75596200 | - | Ppp2r5e | Ppp2r5e | P16734 | NM_012024 | TSS24081 |
| chr12 | 75441413 | 75441520 | MACS2_peak_617 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 33 | chr12 | unknown | gene | 75411719 | 75416781 | - | Gphb5 | Gphb5 | P12173 | NM_175644 | TSS6232 |
| chr12 | 75441413 | 75441520 | MACS2_peak_617 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 33 | chr12 | unknown | gene | 75450880 | 75596200 | - | Ppp2r5e | Ppp2r5e | P16734 | NM_012024 | TSS24081 |
| chr12 | 77196885 | 77196976 | MACS2_peak_618 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 37 | chr12 | unknown | gene | 76937268 | 76962025 | - | Max | Max | P3375 | NM_001146176 | TSS21210 |
| chr12 | 77196885 | 77196976 | MACS2_peak_618 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 37 | chr12 | unknown | gene | 77238103 | 77475316 | + | Fut8 | Fut8 | P11220 | NM_016893 | TSS16501 |
| chr12 | 77553852 | 77553943 | MACS2_peak_619 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 17 | chr12 | unknown | gene | 77238103 | 77475316 | + | Fut8 | Fut8 | P11220 | NM_016893 | TSS16501 |
| chr12 | 77553852 | 77553943 | MACS2_peak_619 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 17 | chr12 | unknown | gene | 78226654 | 78683911 | + | Gphn | Gphn | P11304 | NM_172952 | TSS7660 |
| chr12 | 77820682 | 77820773 | MACS2_peak_620 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 32 | chr12 | unknown | gene | 77238103 | 77475316 | + | Fut8 | Fut8 | P11220 | NM_016893 | TSS16501 |
| chr12 | 77820682 | 77820773 | MACS2_peak_620 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 32 | chr12 | unknown | gene | 78226654 | 78683911 | + | Gphn | Gphn | P11304 | NM_172952 | TSS7660 |
| chr12 | 78046102 | 78046193 | MACS2_peak_621 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 17 | chr12 | unknown | gene | 77238103 | 77475316 | + | Fut8 | Fut8 | P11220 | NM_016893 | TSS16501 |
| chr12 | 78046102 | 78046193 | MACS2_peak_621 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 17 | chr12 | unknown | gene | 78226654 | 78683911 | + | Gphn | Gphn | P11304 | NM_172952 | TSS7660 |
| chr12 | 78572238 | 78572329 | MACS2_peak_622 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 16 | chr12 | unknown | gene | 77238103 | 77475316 | + | Fut8 | Fut8 | P11220 | NM_016893 | TSS16501 |
| chr12 | 78572238 | 78572329 | MACS2_peak_622 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 16 | chr12 | unknown | gene | 78691534 | 78734389 | + | Fam71d | Fam71d | P4900 | NM_027597 | TSS26458 |
| chr12 | 79503139 | 79503272 | MACS2_peak_623 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 82 | chr12 | unknown | gene | 79232346 | 79296282 | - | Zfyve26 | Zfyve26 | P10838 | NM_001008550 | TSS1305 |
| chr12 | 79503139 | 79503272 | MACS2_peak_623 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 82 | chr12 | unknown | gene | 79917018 | 79936264 | - | 9430078K24Rik | 9430078K24Rik | | NR_131073 | TSS19542 |
| chr12 | 80051624 | 80051715 | MACS2_peak_624 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 30 | chr12 | unknown | gene | 79917018 | 79936264 | - | 9430078K24Rik | 9430078K24Rik | | NR_131073 | TSS19542 |
| chr12 | 80051624 | 80051715 | MACS2_peak_624 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 30 | chr12 | unknown | gene | 80107759 | 80112875 | - | Zfp36l1 | Zfp36l1 | P6806 | NM_007564 | TSS14320 |
| chr12 | 80654617 | 80654757 | MACS2_peak_625 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 68 | chr12 | unknown | gene | 80634022 | 80643766 | - | Erh | Erh | P20604 | NM_007951 | TSS2546 |
| chr12 | 80654617 | 80654757 | MACS2_peak_625 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 68 | chr12 | unknown | gene | 80686374 | 80692466 | - | Plekhd1os | Plekhd1os | | NR_037995 | TSS2248 |
| chr12 | 82895815 | 82895906 | MACS2_peak_626 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 3 | chr12 | unknown | gene | 82170015 | 82450044 | + | Sipa1l1 | Sipa1l1 | P19667 | NM_001167983 | TSS3793 |
| chr12 | 82895815 | 82895906 | MACS2_peak_626 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 3 | chr12 | unknown | gene | 82932519 | 82939155 | - | 1700085C21Rik | 1700085C21Rik | | NR_046045 | TSS1723 |
| chr12 | 83926433 | 83926540 | MACS2_peak_627 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 74 | chr12 | unknown | gene | 83794033 | 83921934 | - | Numb | Numb | P3296 | NM_001272056 | TSS16366 |
| chr12 | 83926433 | 83926540 | MACS2_peak_627 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 74 | chr12 | unknown | gene | 83950607 | 83952503 | + | 2410016O06Rik | 2410016O06Rik | P16869 | NM_023633 | TSS16960 |
| chr12 | 83942670 | 83942761 | MACS2_peak_628 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 59 | chr12 | unknown | gene | 83794033 | 83921934 | - | Numb | Numb | P3296 | NM_001272056 | TSS16366 |
| chr12 | 83942670 | 83942761 | MACS2_peak_628 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 59 | chr12 | unknown | gene | 83950607 | 83952503 | + | 2410016O06Rik | 2410016O06Rik | P16869 | NM_023633 | TSS16960 |
| chr12 | 84834473 | 84834693 | MACS2_peak_629 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 57 | chr12 | unknown | gene | 84773269 | 84774717 | + | Isca2 | Isca2 | P2360 | NM_028863 | TSS14820 |
| chr12 | 84834473 | 84834693 | MACS2_peak_629 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 57 | chr12 | unknown | gene | 84875801 | 84879755 | + | D030025P21Rik | D030025P21Rik | | NR_028577 | TSS20637 |
| chr12 | 86026952 | 86027043 | MACS2_peak_630 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 20 | chr12 | unknown | gene | 85815454 | 85824545 | - | 0610007P14Rik | 0610007P14Rik | P22293 | NM_021446 | TSS19007 |
| chr12 | 86026952 | 86027043 | MACS2_peak_630 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 20 | chr12 | unknown | gene | 86056742 | 86077932 | - | Tgfb3 | Tgfb3 | P23841 | NM_009368 | TSS18346 |
| chr12 | 88813562 | 88813653 | MACS2_peak_631 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 33 | chr12 | unknown | gene | 88360513 | 88461192 | + | Adck1 | Adck1 | P21348 | NM_001277297 | TSS15003 |
| chr12 | 88813562 | 88813653 | MACS2_peak_631 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 33 | chr12 | unknown | gene | 90724551 | 90738284 | - | Dio2 | Dio2 | P4379 | NM_010050 | TSS1713 |
| chr12 | 89070274 | 89070365 | MACS2_peak_632 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 35 | chr12 | unknown | gene | 88360513 | 88461192 | + | Adck1 | Adck1 | P21348 | NM_001277297 | TSS15003 |
| chr12 | 89070274 | 89070365 | MACS2_peak_632 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 35 | chr12 | unknown | gene | 90724551 | 90738284 | - | Dio2 | Dio2 | P4379 | NM_010050 | TSS1713 |
| chr12 | 90089006 | 90089097 | MACS2_peak_633 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 44 | chr12 | unknown | gene | 88360513 | 88461192 | + | Adck1 | Adck1 | P21348 | NM_001277297 | TSS15003 |
| chr12 | 90089006 | 90089097 | MACS2_peak_633 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 44 | chr12 | unknown | gene | 90724551 | 90738284 | - | Dio2 | Dio2 | P4379 | NM_010050 | TSS1713 |
| chr12 | 90930342 | 90930433 | MACS2_peak_634 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 60 | chr12 | unknown | gene | 90724551 | 90738284 | - | Dio2 | Dio2 | P4379 | NM_010050 | TSS1713 |
| chr12 | 90930342 | 90930433 | MACS2_peak_634 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 60 | chr12 | unknown | gene | 90998491 | 91384409 | - | Cep128 | Cep128 | P688 | NM_181815 | TSS4054 |
| chr12 | 92461505 | 92461611 | MACS2_peak_635 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 34 | chr12 | unknown | gene | 91806042 | 91849031 | - | Sel1l | Sel1l | P6563 | NM_001039089 | TSS761 |
| chr12 | 92461505 | 92461611 | MACS2_peak_635 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 34 | chr12 | unknown | gene | 93416456 | 93444823 | - | 4930559C10Rik | 4930559C10Rik | | NR_126436 | TSS5132 |
| chr12 | 92835027 | 92835162 | MACS2_peak_636 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 72 | chr12 | unknown | gene | 91806042 | 91849031 | - | Sel1l | Sel1l | P6563 | NM_001039089 | TSS761 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr12 | 92835027 | 92835162 | MACS2_peak_636 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 72 | chr12 | unknown | gene | 93416456 | 93444823 | - | 4930559C10Rik | 4930559C10Rik | | NR_126436 | TSS5132 |
| chr12 | 93576924 | 93577015 | MACS2_peak_637 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 55 | chr12 | unknown | gene | 93416456 | 93444823 | - | 4930559C10Rik | 4930559C10Rik | | NR_126436 | TSS5132 |
| chr12 | 93576924 | 93577015 | MACS2_peak_637 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 55 | chr12 | unknown | gene | 93927337 | 95139186 | + | Mir8099-2 | Mir8099-2 | | NR_106201_1 | TSS21198 |
| chr12 | 93880172 | 93880263 | MACS2_peak_638 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 26 | chr12 | unknown | gene | 93416456 | 93444823 | - | 4930559C10Rik | 4930559C10Rik | | NR_126436 | TSS5132 |
| chr12 | 93880172 | 93880263 | MACS2_peak_638 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 26 | chr12 | unknown | gene | 93927337 | 95139186 | + | Mir8099-2 | Mir8099-2 | | NR_106201_1 | TSS21198 |
| chr12 | 94416293 | 94416390 | MACS2_peak_639 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 58 | chr12 | unknown | gene | 93416456 | 93444823 | - | 4930559C10Rik | 4930559C10Rik | | NR_126436 | TSS5132 |
| chr12 | 94416293 | 94416390 | MACS2_peak_639 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 58 | chr12 | unknown | gene | 95692225 | 95780872 | + | Flrt2 | Flrt2 | P13526 | NM_201518 | TSS8410 |
| chr12 | 95434890 | 95434981 | MACS2_peak_640 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 18 | chr12 | unknown | gene | 93927337 | 95139186 | + | Mir8099-2 | Mir8099-2 | | NR_106201_1 | TSS21198 |
| chr12 | 95434890 | 95434981 | MACS2_peak_640 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 18 | chr12 | unknown | gene | 95692225 | 95780872 | + | Flrt2 | Flrt2 | P13526 | NM_201518 | TSS8410 |
| chr12 | 95525896 | 95525987 | MACS2_peak_641 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 13 | chr12 | unknown | gene | 93927337 | 95139186 | + | Mir8099-2 | Mir8099-2 | | NR_106201_1 | TSS21198 |
| chr12 | 95525896 | 95525987 | MACS2_peak_641 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 13 | chr12 | unknown | gene | 95692225 | 95780872 | + | Flrt2 | Flrt2 | P13526 | NM_201518 | TSS8410 |
| chr12 | 96163681 | 96163825 | MACS2_peak_642 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 71 | chr12 | unknown | gene | 96046620 | 96047222 | - | 1700019M22Rik | 1700019M22Rik | | NR_103800 | TSS20774 |
| chr12 | 96163681 | 96163825 | MACS2_peak_642 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 71 | chr12 | unknown | gene | 98202299 | 98259329 | - | Galc | Galc | P20390 | NM_008079 | TSS23224 |
| chr12 | 97061445 | 97061776 | MACS2_peak_643 | 354 | + | 17.59101 | 41.30196 | 35.43587 | 233 | chr12 | unknown | gene | 96046620 | 96047222 | - | 1700019M22Rik | 1700019M22Rik | | NR_103800 | TSS20774 |
| chr12 | 97061445 | 97061776 | MACS2_peak_643 | 354 | + | 17.59101 | 41.30196 | 35.43587 | 233 | chr12 | unknown | gene | 98202299 | 98259329 | - | Galc | Galc | P20390 | NM_008079 | TSS23224 |
| chr12 | 97749067 | 97749158 | MACS2_peak_644 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 71 | chr12 | unknown | gene | 96046620 | 96047222 | - | 1700019M22Rik | 1700019M22Rik | | NR_103800 | TSS20774 |
| chr12 | 97749067 | 97749158 | MACS2_peak_644 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 71 | chr12 | unknown | gene | 98202299 | 98259329 | - | Galc | Galc | P20390 | NM_008079 | TSS23224 |
| chr12 | 97796531 | 97796662 | MACS2_peak_645 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 58 | chr12 | unknown | gene | 96046620 | 96047222 | - | 1700019M22Rik | 1700019M22Rik | | NR_103800 | TSS20774 |
| chr12 | 97796531 | 97796662 | MACS2_peak_645 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 58 | chr12 | unknown | gene | 98202299 | 98259329 | - | Galc | Galc | P20390 | NM_008079 | TSS23224 |
| chr12 | 97872726 | 97872817 | MACS2_peak_646 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 9 | chr12 | unknown | gene | 96046620 | 96047222 | - | 1700019M22Rik | 1700019M22Rik | | NR_103800 | TSS20774 |
| chr12 | 97872726 | 97872817 | MACS2_peak_646 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 9 | chr12 | unknown | gene | 98202299 | 98259329 | - | Galc | Galc | P20390 | NM_008079 | TSS23224 |
| chr12 | 99060219 | 99060310 | MACS2_peak_647 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 50 | chr12 | unknown | gene | 98920573 | 98982574 | + | Ttc8 | Ttc8 | P6719 | NM_029553 | TSS878 |
| chr12 | 99060219 | 99060310 | MACS2_peak_647 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 50 | chr12 | unknown | gene | 99161276 | 99162808 | - | 4930474N09Rik | 4930474N09Rik | | NR_038130 | TSS12615 |
| chr12 | 100979562 | 100979653 | MACS2_peak_648 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 37 | chr12 | unknown | gene | 100876681 | 100908198 | - | Gpr68 | Gpr68 | P24730 | NM_001177674 | TSS16014 |
| chr12 | 100979562 | 100979653 | MACS2_peak_648 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 37 | chr12 | unknown | gene | 101021672 | 101021768 | - | Mir1190 | Mir1190 | | NR_035421 | TSS23952 |
| chr12 | 101999033 | 101999124 | MACS2_peak_649 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 72 | chr12 | unknown | gene | 101918900 | 101958157 | - | Atxn3 | Atxn3 | P11097 | NM_029705 | TSS3859 |
| chr12 | 101999033 | 101999124 | MACS2_peak_649 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 72 | chr12 | unknown | gene | 102129418 | 102266497 | + | Slc24a4 | Slc24a4 | P10679 | NM_172152 | TSS4818 |
| chr12 | 102417360 | 102417451 | MACS2_peak_650 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 66 | chr12 | unknown | gene | 102283073 | 102390144 | + | Rin3 | Rin3 | P2343 | NM_177620 | TSS7873 |
| chr12 | 102417360 | 102417451 | MACS2_peak_650 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 66 | chr12 | unknown | gene | 102469133 | 102497527 | + | Golga5 | Golga5 | P11481 | NM_001199004 | TSS7558 |
| chr12 | 102723249 | 102723340 | MACS2_peak_651 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 61 | chr12 | unknown | gene | 102568582 | 102704816 | - | Itpk1 | Itpk1 | P25567 | NM_172584 | TSS11622 |
| chr12 | 102723249 | 102723340 | MACS2_peak_651 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 61 | chr12 | unknown | gene | 102739829 | 102743661 | - | Moap1 | Moap1 | P15035 | NM_001142937 | TSS6840 |
| chr12 | 102955244 | 102955335 | MACS2_peak_652 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 81 | chr12 | unknown | gene | 102899305 | 102900337 | + | Cox8c | Cox8c | P21280 | NM_001039049 | TSS22388 |
| chr12 | 102955244 | 102955335 | MACS2_peak_652 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 81 | chr12 | unknown | gene | 103196907 | 103242146 | - | Prima1 | Prima1 | P6881 | NM_133364 | TSS4188 |
| chr12 | 104110435 | 104110526 | MACS2_peak_653 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 32 | chr12 | unknown | gene | 104101112 | 104105353 | + | Serpina5 | Serpina5 | P3122 | NM_172953 | TSS11759 |
| chr12 | 104110435 | 104110526 | MACS2_peak_653 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 32 | chr12 | unknown | gene | 104112723 | 104121518 | + | Serpina3a | Serpina3a | P1674 | NM_001167705 | TSS5198 |
| chr12 | 105271228 | 105271319 | MACS2_peak_654 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 26 | chr12 | unknown | gene | 105216754 | 105222652 | - | Tcl1 | Tcl1 | P1326 | NM_001309485 | TSS26191 |
| chr12 | 105271228 | 105271319 | MACS2_peak_654 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 26 | chr12 | unknown | gene | 105336593 | 105383930 | + | Tunar | Tunar | | NR_045047 | TSS26325 |
| chr12 | 105451298 | 105451389 | MACS2_peak_655 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 9 | chr12 | unknown | gene | 105394855 | 105403760 | - | Gm2721 | Gm2721 | | NR_045085 | TSS17799 |
| chr12 | 105451298 | 105451389 | MACS2_peak_655 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 9 | chr12 | unknown | gene | 105453855 | 105487829 | + | D430019H16Rik | D430019H16Rik | P9673 | NM_001252508 | TSS25327 |
| chr12 | 105959955 | 105960093 | MACS2_peak_656 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 80 | chr12 | unknown | gene | 105784701 | 105836860 | + | Papola | Papola | P24330 | NM_011112 | TSS1084 |
| chr12 | 105959955 | 105960093 | MACS2_peak_656 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 80 | chr12 | unknown | gene | 106010262 | 106075038 | + | Vrk1 | Vrk1 | P22533 | NM_001029843 | TSS19510 |
| chr12 | 106382546 | 106382637 | MACS2_peak_657 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 20 | chr12 | unknown | gene | 106010262 | 106075038 | + | Vrk1 | Vrk1 | P22533 | NM_001029843 | TSS19510 |
| chr12 | 106382546 | 106382637 | MACS2_peak_657 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 20 | chr12 | unknown | gene | 106442651 | 106447666 | - | 1700121N20Rik | 1700121N20Rik | | NR_036593 | TSS10597 |
| chr12 | 111041461 | 111041597 | MACS2_peak_658 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 71 | chr12 | unknown | gene | 110994397 | 111013872 | + | 6030440G07Rik | 6030440G07Rik | | NR_036598 | TSS14438 |
| chr12 | 111041461 | 111041597 | MACS2_peak_658 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 71 | chr12 | unknown | gene | 111159849 | 111184491 | - | 4930595D18Rik | 4930595D18Rik | | NR_130987 | TSS2172 |
| chr12 | 111539517 | 111539608 | MACS2_peak_659 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 59 | chr12 | unknown | gene | 111484608 | 111485770 | - | Gm266 | Gm266 | P10969 | NM_001033248 | TSS9619 |
| chr12 | 111539517 | 111539608 | MACS2_peak_659 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 59 | chr12 | unknown | gene | 111540945 | 111541066 | + | Snora28 | Snora28 | | NR_033168 | TSS27529 |
| chr12 | 113777808 | 113777899 | MACS2_peak_660 | 13 | + | 4.60921 | 5.8944 | 1.34955 | 25 | chr12 | unknown | gene | 113543907 | 113546273 | + | Adam6a | Adam6a | P14565 | NM_174885 | TSS12144 |
| chr12 | 113777808 | 113777899 | MACS2_peak_660 | 13 | + | 4.60921 | 5.8944 | 1.34955 | 25 | chr12 | unknown | gene | 114469406 | 114469466 | - | Mir7094-1 | Mir7094-1 | | NR_106062 | TSS12256 |
| chr12 | 114420685 | 114420787 | MACS2_peak_661 | 42 | + | 6.42673 | 9.29353 | 4.24338 | 53 | chr12 | unknown | gene | 113543907 | 113546273 | + | Adam6a | Adam6a | P14565 | NM_174885 | TSS12144 |
| chr12 | 114420685 | 114420787 | MACS2_peak_661 | 42 | + | 6.42673 | 9.29353 | 4.24338 | 53 | chr12 | unknown | gene | 114469406 | 114469466 | - | Mir7094-1 | Mir7094-1 | | NR_106062 | TSS12256 |
| chr12 | 114517823 | 114517951 | MACS2_peak_662 | 43 | + | 6.46877 | 9.37984 | 4.32457 | 61 | chr12 | unknown | gene | 114513634 | 114513694 | - | Mir7094-2 | Mir7094-2 | | NR_106063 | TSS5437 |
| chr12 | 114517823 | 114517951 | MACS2_peak_662 | 43 | + | 6.46877 | 9.37984 | 4.32457 | 61 | chr12 | unknown | gene | 115695719 | 115695794 | - | Mir6388 | Mir6388 | | NR_105810 | TSS8124 |
| chr12 | 115456833 | 115456924 | MACS2_peak_663 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 62 | chr12 | unknown | gene | 114513634 | 114513694 | - | Mir7094-2 | Mir7094-2 | | NR_106063 | TSS5437 |
| chr12 | 115456833 | 115456924 | MACS2_peak_663 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 62 | chr12 | unknown | gene | 115695719 | 115695794 | - | Mir6388 | Mir6388 | | NR_105810 | TSS8124 |
| chr12 | 115554934 | 115555025 | MACS2_peak_664 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 38 | chr12 | unknown | gene | 114513634 | 114513694 | - | Mir7094-2 | Mir7094-2 | | NR_106063 | TSS5437 |
| chr12 | 115554934 | 115555025 | MACS2_peak_664 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 38 | chr12 | unknown | gene | 115695719 | 115695794 | - | Mir6388 | Mir6388 | | NR_105810 | TSS8124 |
| chr12 | 115672076 | 115672242 | MACS2_peak_665 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 80 | chr12 | unknown | gene | 114513634 | 114513694 | - | Mir7094-2 | Mir7094-2 | | NR_106063 | TSS5437 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr12 | 115672076 | 115672242 | MACS2_peak_665 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 80 | chr12 | unknown | gene | 115695719 | 115695794 | - | Mir6388 | Mir6388 |  | NR_105810 | TSS8124 |
| chr12 | 115682946 | 115683097 | MACS2_peak_666 | 50 | + | 6.87285 | 10.15897 | 5.05896 | 65 | chr12 | unknown | gene | 114513634 | 114513694 | - | Mir7094-2 | Mir7094-2 |  | NR_106063 | TSS5437 |
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| chr12 | 115993979 | 115994108 | MACS2_peak_667 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 88 | chr12 | unknown | gene | 115695719 | 115695794 | - | Mir6388 | Mir6388 |  | NR_105810 | TSS8124 |
| chr12 | 115993979 | 115994108 | MACS2_peak_667 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 88 | chr12 | unknown | gene | 116047723 | 116060544 | + | Zfp386 | Zfp386 | P25919 | NM_001004066 | TSS6343 |
| chr12 | 115997733 | 115997824 | MACS2_peak_668 | 13 | + | 4.58175 | 5.84496 | 1.3392 | 44 | chr12 | unknown | gene | 115695719 | 115695794 | - | Mir6388 | Mir6388 |  | NR_105810 | TSS8124 |
| chr12 | 115997733 | 115997824 | MACS2_peak_668 | 13 | + | 4.58175 | 5.84496 | 1.3392 | 44 | chr12 | unknown | gene | 116047723 | 116060544 | + | Zfp386 | Zfp386 | P25919 | NM_001004066 | TSS6343 |
| chr12 | 118597162 | 118597316 | MACS2_peak_669 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 87 | chr12 | unknown | gene | 118518296 | 118530193 | - | D230030E09Rik | D230030E09Rik |  | NR_045947 | TSS17056 |
| chr12 | 118597162 | 118597316 | MACS2_peak_669 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 87 | chr12 | unknown | gene | 118846328 | 118849872 | + | Sp8 | Sp8 | P1638 | NM_177082 | TSS5348 |
| chr12 | 119009335 | 119009509 | MACS2_peak_670 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 40 | chr12 | unknown | gene | 118867823 | 118966421 | - | Abcb5 | Abcb5 | P12860 | NM_029961 | TSS7662 |
| chr12 | 119009335 | 119009509 | MACS2_peak_670 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 40 | chr12 | unknown | gene | 119162802 | 119237798 | - | Itgb8 | Itgb8 | P17351 | NM_177290 | TSS22426 |
| chr12 | 119054523 | 119054616 | MACS2_peak_671 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 71 | chr12 | unknown | gene | 118867823 | 118966421 | - | Abcb5 | Abcb5 | P12860 | NM_029961 | TSS7662 |
| chr12 | 119054523 | 119054616 | MACS2_peak_671 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 71 | chr12 | unknown | gene | 119162802 | 119237798 | - | Itgb8 | Itgb8 | P17351 | NM_177290 | TSS22426 |
| chr12 | 119084622 | 119084713 | MACS2_peak_672 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 6 | chr12 | unknown | gene | 118867823 | 118966421 | - | Abcb5 | Abcb5 | P12860 | NM_029961 | TSS7662 |
| chr12 | 119084622 | 119084713 | MACS2_peak_672 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 6 | chr12 | unknown | gene | 119162802 | 119237798 | - | Itgb8 | Itgb8 | P17351 | NM_177290 | TSS22426 |
| chr12 | 119540560 | 119540731 | MACS2_peak_673 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 90 | chr12 | unknown | gene | 119443409 | 119465672 | + | Macc1 | Macc1 | P4289 | NM_001163136 | TSS894 |
| chr12 | 119540560 | 119540731 | MACS2_peak_673 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 90 | chr12 | unknown | gene | 119945961 | 120018581 | + | Tmem196 | Tmem196 | P17637 | NM_001294154 | TSS9550 |
| chr12 | 119783000 | 119783091 | MACS2_peak_674 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 35 | chr12 | unknown | gene | 119443409 | 119465672 | + | Macc1 | Macc1 | P4289 | NM_001163136 | TSS894 |
| chr12 | 119783000 | 119783091 | MACS2_peak_674 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 35 | chr12 | unknown | gene | 119945961 | 120018581 | + | Tmem196 | Tmem196 | P17637 | NM_001294154 | TSS9550 |
| chr13 | 3373064 | 3373232 | MACS2_peak_675 | 165 | + | 12.14678 | 22.04049 | 16.55548 | 86 | chr13 | unknown | gene | 3149474 | 3189678 | + | Speer6-ps1 | Speer6-ps1 |  | NR_001581 | TSS23983 |
| chr13 | 3373064 | 3373232 | MACS2_peak_675 | 165 | + | 12.14678 | 22.04049 | 16.55548 | 86 | chr13 | unknown | gene | 3478302 | 3492398 | + | 2810429I04Rik | 2810429I04Rik |  | NR_015522 | TSS27272 |
| chr13 | 5465455 | 5465546 | MACS2_peak_676 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 64 | chr13 | unknown | gene | 4592489 | 4609123 | - | Akr1e1 | Akr1e1 | P16998 | NM_018859 | TSS17826 |
| chr13 | 5465455 | 5465546 | MACS2_peak_676 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 64 | chr13 | unknown | gene | 5855508 | 5858092 | - | 1700016G22Rik | 1700016G22Rik |  | NR_045891 | TSS24732 |
| chr13 | 5689541 | 5689716 | MACS2_peak_677 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 13 | chr13 | unknown | gene | 4592489 | 4609123 | - | Akr1e1 | Akr1e1 | P16998 | NM_018859 | TSS17826 |
| chr13 | 5689541 | 5689716 | MACS2_peak_677 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 13 | chr13 | unknown | gene | 5855508 | 5858092 | - | 1700016G22Rik | 1700016G22Rik |  | NR_045891 | TSS24732 |
| chr13 | 5995813 | 5995904 | MACS2_peak_678 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 54 | chr13 | unknown | gene | 5861488 | 5867283 | + | Klf6 | Klf6 | P20373 | NM_011803 | TSS11340 |
| chr13 | 5995813 | 5995904 | MACS2_peak_678 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 54 | chr13 | unknown | gene | 6548156 | 6579743 | + | Pitrm1 | Pitrm1 | P8329 | NM_145131 | TSS16861 |
| chr13 | 8885345 | 8885436 | MACS2_peak_679 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 28 | chr13 | unknown | gene | 8802965 | 8871736 | - | Wdr37 | Wdr37 | P15250 | NM_001039388 | TSS12199 |
| chr13 | 8885345 | 8885436 | MACS2_peak_679 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 28 | chr13 | unknown | gene | 8885605 | 8890635 | + | Idi1 | Idi1 | P6817 | NM_145360 | TSS10181 |
| chr13 | 9297681 | 9297783 | MACS2_peak_680 | 16 | + | 4.811 | 6.2687 | 1.67914 | 80 | chr13 | unknown | gene | 9093904 | 9170942 | + | Larp4b | Larp4b | P4844 | NM_172585 | TSS23768 |
| chr13 | 9297681 | 9297783 | MACS2_peak_680 | 16 | + | 4.811 | 6.2687 | 1.67914 | 80 | chr13 | unknown | gene | 9684835 | 9765314 | - | Zmynd11 | Zmynd11 | P22058 | NM_144516 | TSS11660 |
| chr13 | 10677870 | 10677980 | MACS2_peak_681 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 29 | chr13 | unknown | gene | 9876612 | 10360803 | - | Chrm3 | Chrm3 | P26583 | NM_033269 | TSS18597 |
| chr13 | 10677870 | 10677980 | MACS2_peak_681 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 29 | chr13 | unknown | gene | 11522051 | 11525682 | + | Zp4-ps | Zp4-ps |  | NR_027813 | TSS25830 |
| chr13 | 12213450 | 12213541 | MACS2_peak_682 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 12 | chr13 | unknown | gene | 12182716 | 12186488 | - | Gm10336 | Gm10336 |  | NR_045170 | TSS2132 |
| chr13 | 12213450 | 12213541 | MACS2_peak_682 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 12 | chr13 | unknown | gene | 12269426 | 12340500 | - | Actn2 | Actn2 | P6302 | NM_033268 | TSS16742 |
| chr13 | 13755271 | 13755397 | MACS2_peak_683 | 23 | + | 5.36409 | 7.26321 | 2.37531 | 62 | chr13 | unknown | gene | 13437601 | 13510067 | + | Nid1 | Nid1 | P9558 | NM_010917 | TSS25407 |
| chr13 | 13755271 | 13755397 | MACS2_peak_683 | 23 | + | 5.36409 | 7.26321 | 2.37531 | 62 | chr13 | unknown | gene | 13784058 | 13825375 | + | Gng4 | Gng4 | P20407 | NM_001302997 | TSS23877 |
| chr13 | 14075975 | 14076066 | MACS2_peak_684 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 16 | chr13 | unknown | gene | 14052444 | 14063401 | - | Ggps1 | Ggps1 | P25175 | NM_010282 | TSS8683 |
| chr13 | 14075975 | 14076066 | MACS2_peak_684 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 16 | chr13 | unknown | gene | 14226437 | 14523226 | - | Hecw1 | Hecw1 | P26274 | NM_001081348 | TSS8234 |
| chr13 | 14301993 | 14302084 | MACS2_peak_685 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 33 | chr13 | unknown | gene | 14063783 | 14197733 | + | Arid4b | Arid4b | P14151 | NM_198122 | TSS6347 |
| chr13 | 14301993 | 14302084 | MACS2_peak_685 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 33 | chr13 | unknown | gene | 14610300 | 14613018 | - | Mrpl32 | Mrpl32 | P10427 | NM_029271 | TSS24414 |
| chr13 | 14816639 | 14816808 | MACS2_peak_686 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 84 | chr13 | unknown | gene | 14630244 | 14637829 | + | AW209491 | AW209491 | P19827 | NM_001104646 | TSS23425 |
| chr13 | 14816639 | 14816808 | MACS2_peak_686 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 84 | chr13 | unknown | gene | 15463722 | 15726781 | + | Gli3 | Gli3 | P10595 | NM_008130 | TSS26243 |
| chr13 | 15130151 | 15130283 | MACS2_peak_687 | 19 | + | 4.99813 | 6.6079 | 1.96269 | 83 | chr13 | unknown | gene | 14630244 | 14637829 | + | AW209491 | AW209491 | P19827 | NM_001104646 | TSS23425 |
| chr13 | 15130151 | 15130283 | MACS2_peak_687 | 19 | + | 4.99813 | 6.6079 | 1.96269 | 83 | chr13 | unknown | gene | 15463722 | 15726781 | + | Gli3 | Gli3 | P10595 | NM_008130 | TSS26243 |
| chr13 | 15870013 | 15870104 | MACS2_peak_688 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 49 | chr13 | unknown | gene | 15807242 | 15827537 | + | A530046M15Rik | A530046M15Rik |  | NR_046131 | TSS7433 |
| chr13 | 15870013 | 15870104 | MACS2_peak_688 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 49 | chr13 | unknown | gene | 16014474 | 16027129 | + | Inhba | Inhba | P12007 | NM_008380 | TSS27100 |
| chr13 | 16282931 | 16283022 | MACS2_peak_689 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 43 | chr13 | unknown | gene | 16014474 | 16027129 | + | Inhba | Inhba | P12007 | NM_008380 | TSS27100 |
| chr13 | 16282931 | 16283022 | MACS2_peak_689 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 43 | chr13 | unknown | gene | 16857474 | 17694732 | - | Sugct | Sugct | P6857 | NM_138654 | TSS15575 |
| chr13 | 16477237 | 16477328 | MACS2_peak_690 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 58 | chr13 | unknown | gene | 16014474 | 16027129 | + | Inhba | Inhba | P12007 | NM_008380 | TSS27100 |
| chr13 | 16477237 | 16477328 | MACS2_peak_690 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 58 | chr13 | unknown | gene | 16857474 | 17694732 | - | Sugct | Sugct | P6857 | NM_138654 | TSS15575 |
| chr13 | 16519088 | 16519264 | MACS2_peak_691 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 21 | chr13 | unknown | gene | 16014474 | 16027129 | + | Inhba | Inhba | P12007 | NM_008380 | TSS27100 |
| chr13 | 16519088 | 16519264 | MACS2_peak_691 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 21 | chr13 | unknown | gene | 16857474 | 17694732 | - | Sugct | Sugct | P6857 | NM_138654 | TSS15575 |
| chr13 | 16939288 | 16939379 | MACS2_peak_692 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 69 | chr13 | unknown | gene | 16014474 | 16027129 | + | Inhba | Inhba | P12007 | NM_008380 | TSS27100 |
| chr13 | 16939288 | 16939379 | MACS2_peak_692 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 69 | chr13 | unknown | gene | 17695412 | 17697042 | + | Mplkip | Mplkip | P10394 | NM_025479 | TSS27381 |
| chr13 | 16989557 | 16989722 | MACS2_peak_693 | 43 | + | 6.46877 | 9.37984 | 4.32457 | 81 | chr13 | unknown | gene | 16014474 | 16027129 | + | Inhba | Inhba | P12007 | NM_008380 | TSS27100 |
| chr13 | 16989557 | 16989722 | MACS2_peak_693 | 43 | + | 6.46877 | 9.37984 | 4.32457 | 81 | chr13 | unknown | gene | 17695412 | 17697042 | + | Mplkip | Mplkip | P10394 | NM_025479 | TSS27381 |
| chr13 | 18269709 | 18269837 | MACS2_peak_694 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 42 | chr13 | unknown | gene | 18084946 | 18100202 | - | 4930448F12Rik | 4930448F12Rik |  | NR_046032 | TSS5265 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr13 | 18269709 | 18269837 | MACS2_peak_694 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 42 | chr13 | unknown | gene | 18717291 | 18866200 | + | Vps41 | Vps41 | P15013 | NM_172120 | TSS25964 |
| chr13 | 18595670 | 18595761 | MACS2_peak_695 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 28 | chr13 | unknown | gene | 18124959 | 18382039 | - | Pou6f2 | Pou6f2 | P10929 | NM_175006 | TSS108 |
| chr13 | 18595670 | 18595761 | MACS2_peak_695 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 28 | chr13 | unknown | gene | 18717291 | 18866200 | + | Vps41 | Vps41 | P15013 | NM_172120 | TSS25964 |
| chr13 | 19805314 | 19805405 | MACS2_peak_696 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 63 | chr13 | unknown | gene | 19727416 | 19732951 | - | A530099J19Rik | A530099J19Rik | P5947 | NM_175688 | TSS1492 |
| chr13 | 19805314 | 19805405 | MACS2_peak_696 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 63 | chr13 | unknown | gene | 20090506 | 20605299 | + | Elmo1 | Elmo1 | P9601 | NM_080288 | TSS23816 |
| chr13 | 20722443 | 20722534 | MACS2_peak_697 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 24 | chr13 | unknown | gene | 20090506 | 20605299 | + | Elmo1 | Elmo1 | P9601 | NM_080288 | TSS23816 |
| chr13 | 20722443 | 20722534 | MACS2_peak_697 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 24 | chr13 | unknown | gene | 20794112 | 21023337 | + | Aoah | Aoah | P8399 | NM_001281854 | TSS17055 |
| chr13 | 21423957 | 21424048 | MACS2_peak_698 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 21 | chr13 | unknown | gene | 21387003 | 21402755 | - | Zkscan3 | Zkscan3 | P19333 | NM_023685 | TSS24481 |
| chr13 | 21423957 | 21424048 | MACS2_peak_698 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 21 | chr13 | unknown | gene | 21442174 | 21453727 | - | Zscan26 | Zscan26 | P24390 | NM_001013786 | TSS6486 |
| chr13 | 23291552 | 23291692 | MACS2_peak_699 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 54 | chr13 | unknown | gene | 23278349 | 23282267 | + | 4933404K08Rik | 4933404K08Rik | | NR_046038 | TSS26461 |
| chr13 | 23291552 | 23291692 | MACS2_peak_699 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 54 | chr13 | unknown | gene | 23313524 | 23385799 | + | 4930586N03Rik | 4930586N03Rik | | NR_131052 | TSS7511 |
| chr13 | 26337648 | 26337739 | MACS2_peak_700 | 7 | + | 3.39397 | 3.87422 | 0.75855 | 20 | chr13 | unknown | gene | 26283158 | 26312406 | - | 1700092E19Rik | 1700092E19Rik | | NR_045933 | TSS13980 |
| chr13 | 26337648 | 26337739 | MACS2_peak_700 | 7 | + | 3.39397 | 3.87422 | 0.75855 | 20 | chr13 | unknown | gene | 26768171 | 26770088 | - | Hdgfl1 | Hdgfl1 | P10771 | NM_008232 | TSS21240 |
| chr13 | 28308001 | 28308115 | MACS2_peak_701 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 55 | chr13 | unknown | gene | 28142483 | 28151302 | + | Prl5a1 | Prl5a1 | P9611 | NM_023746 | TSS26906 |
| chr13 | 28308001 | 28308115 | MACS2_peak_701 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 55 | chr13 | unknown | gene | 28460033 | 28885422 | - | 2610307P16Rik | 2610307P16Rik | | NR_045053 | TSS7509 |
| chr13 | 28528530 | 28528621 | MACS2_peak_702 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 34 | chr13 | unknown | gene | 28142483 | 28151302 | + | Prl5a1 | Prl5a1 | P9611 | NM_023746 | TSS26906 |
| chr13 | 28528530 | 28528621 | MACS2_peak_702 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 34 | chr13 | unknown | gene | 28710780 | 28710873 | - | Mir6368 | Mir6368 | | NR_105787 | TSS2283 |
| chr13 | 28757640 | 28757731 | MACS2_peak_703 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 50 | chr13 | unknown | gene | 28710780 | 28710873 | - | Mir6368 | Mir6368 | | NR_105787 | TSS2283 |
| chr13 | 28757640 | 28757731 | MACS2_peak_703 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 50 | chr13 | unknown | gene | 28950729 | 28953021 | - | Sox4 | Sox4 | P10035 | NM_009238 | TSS16349 |
| chr13 | 29353933 | 29354110 | MACS2_peak_704 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 158 | chr13 | unknown | gene | 29014413 | 29040336 | + | A330102I10Rik | A330102I10Rik | | NR_045077 | TSS12198 |
| chr13 | 29353933 | 29354110 | MACS2_peak_704 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 158 | chr13 | unknown | gene | 29906574 | 29985668 | - | E2f3 | E2f3 | P23533 | NM_001289920 | TSS16402 |
| chr13 | 29856224 | 29856332 | MACS2_peak_705 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 56 | chr13 | unknown | gene | 29191745 | 29855673 | - | Cdkal1 | Cdkal1 | | NR_131896 | TSS18482 |
| chr13 | 29856224 | 29856332 | MACS2_peak_705 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 56 | chr13 | unknown | gene | 29906574 | 29985668 | - | E2f3 | E2f3 | P23533 | NM_001289920 | TSS16402 |
| chr13 | 30245719 | 30245821 | MACS2_peak_706 | 46 | + | 6.66445 | 9.76294 | 4.69236 | 44 | chr13 | unknown | gene | 30136489 | 30245469 | + | Mboat1 | Mboat1 | P4194 | NM_153546 | TSS7145 |
| chr13 | 30245719 | 30245821 | MACS2_peak_706 | 46 | + | 6.66445 | 9.76294 | 4.69236 | 44 | chr13 | unknown | gene | 30336355 | 30382033 | + | Agtr1a | Agtr1a | P7426 | NM_177322 | TSS806 |
| chr13 | 30888337 | 30888428 | MACS2_peak_707 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 44 | chr13 | unknown | gene | 30749257 | 30763667 | + | Irf4 | Irf4 | P20161 | NM_013674 | TSS20055 |
| chr13 | 30888337 | 30888428 | MACS2_peak_707 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 44 | chr13 | unknown | gene | 30946575 | 30947674 | - | Hus1b | Hus1b | P21215 | NM_153072 | TSS5614 |
| chr13 | 30973455 | 30973551 | MACS2_peak_708 | 27 | + | 5.56793 | 7.65146 | 2.73702 | 77 | chr13 | unknown | gene | 30946575 | 30947674 | - | Hus1b | Hus1b | P21215 | NM_153072 | TSS5614 |
| chr13 | 30973455 | 30973551 | MACS2_peak_708 | 27 | + | 5.56793 | 7.65146 | 2.73702 | 77 | chr13 | unknown | gene | 31213409 | 31241086 | - | 4930401O12Rik | 4930401O12Rik | | NR_045957 | TSS1366 |
| chr13 | 31809592 | 31809683 | MACS2_peak_709 | 23 | + | 5.29942 | 7.14384 | 2.32792 | 61 | chr13 | unknown | gene | 31806645 | 31808869 | + | Foxc1 | Foxc1 | P19168 | NM_008592 | TSS5431 |
| chr13 | 31809592 | 31809683 | MACS2_peak_709 | 23 | + | 5.29942 | 7.14384 | 2.32792 | 61 | chr13 | unknown | gene | 31819585 | 32338483 | - | Gmds | Gmds | P6965 | NM_146041 | TSS21232 |
| chr13 | 32877356 | 32877447 | MACS2_peak_710 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 30 | chr13 | unknown | gene | 32842091 | 32851185 | - | Serpinb1a | Serpinb1a | P24544 | NM_025429 | TSS4623 |
| chr13 | 32877356 | 32877447 | MACS2_peak_710 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 30 | chr13 | unknown | gene | 32881396 | 32898140 | - | Serpinb1c | Serpinb1c | P21813 | NM_173051 | TSS25581 |
| chr13 | 33585468 | 33585559 | MACS2_peak_711 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 77 | chr13 | unknown | gene | 33562485 | 33569317 | - | Gm6093 | Gm6093 | | NR_131140 | TSS13044 |
| chr13 | 33585468 | 33585559 | MACS2_peak_711 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 77 | chr13 | unknown | gene | 33661404 | 33671472 | + | Serpinb6d | Serpinb6d | P26070 | NM_001076790 | TSS25422 |
| chr13 | 34103306 | 34103407 | MACS2_peak_712 | 17 | + | 4.85997 | 6.37162 | 1.7717 | 29 | chr13 | unknown | gene | 34074279 | 34077929 | - | Tubb2a | Tubb2a | P6144 | NM_009450 | TSS13803 |
| chr13 | 34103306 | 34103407 | MACS2_peak_712 | 17 | + | 4.85997 | 6.37162 | 1.7717 | 29 | chr13 | unknown | gene | 34127007 | 34130233 | - | Tubb2b | Tubb2b | P14369 | NM_023716 | TSS18013 |
| chr13 | 35236091 | 35236182 | MACS2_peak_713 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 74 | chr13 | unknown | gene | 35210659 | 35212048 | - | 1700019C18Rik | 1700019C18Rik | | NR_126478 | TSS5580 |
| chr13 | 35236091 | 35236182 | MACS2_peak_713 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 74 | chr13 | unknown | gene | 35659861 | 35872670 | + | Cdyl | Cdyl | P1020 | NM_009881 | TSS9666 |
| chr13 | 35576655 | 35576746 | MACS2_peak_714 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 32 | chr13 | unknown | gene | 35210659 | 35212048 | - | 1700019C18Rik | 1700019C18Rik | | NR_126478 | TSS5580 |
| chr13 | 35576655 | 35576746 | MACS2_peak_714 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 32 | chr13 | unknown | gene | 35659861 | 35872670 | + | Cdyl | Cdyl | P1020 | NM_009881 | TSS9666 |
| chr13 | 37361401 | 37361492 | MACS2_peak_715 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 18 | chr13 | unknown | gene | 36867177 | 37050244 | - | F13a1 | F13a1 | P8048 | NM_028784 | TSS18128 |
| chr13 | 37361401 | 37361492 | MACS2_peak_715 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 18 | chr13 | unknown | gene | 37826037 | 37949115 | + | Rreb1 | Rreb1 | P12618 | NM_026830 | TSS3033 |
| chr13 | 37407085 | 37407176 | MACS2_peak_716 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 79 | chr13 | unknown | gene | 36867177 | 37050244 | - | F13a1 | F13a1 | P8048 | NM_028784 | TSS18128 |
| chr13 | 37407085 | 37407176 | MACS2_peak_716 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 79 | chr13 | unknown | gene | 37826037 | 37949115 | + | Rreb1 | Rreb1 | P12618 | NM_026830 | TSS3033 |
| chr13 | 37856119 | 37856283 | MACS2_peak_717 | 7 | + | 3.35255 | 3.79878 | 0.75025 | 76 | chr13 | unknown | gene | 37345344 | 37418622 | + | Ly86 | Ly86 | P16662 | NM_010745 | TSS1774 |
| chr13 | 37856119 | 37856283 | MACS2_peak_717 | 7 | + | 3.35255 | 3.79878 | 0.75025 | 76 | chr13 | unknown | gene | 37971400 | 37994083 | - | Ssr1 | Ssr1 | P14304 | NM_025965 | TSS9793 |
| chr13 | 38997886 | 38997977 | MACS2_peak_718 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 15 | chr13 | unknown | gene | 38960618 | 38966297 | + | 5033403F01Rik | 5033403F01Rik | | NR_131019 | TSS18721 |
| chr13 | 38997886 | 38997977 | MACS2_peak_718 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 15 | chr13 | unknown | gene | 40001881 | 40287983 | - | Ofcc1 | Ofcc1 | P24288 | NM_172143 | TSS19621 |
| chr13 | 39264563 | 39264654 | MACS2_peak_719 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 18 | chr13 | unknown | gene | 38960618 | 38966297 | + | 5033403F01Rik | 5033403F01Rik | | NR_131019 | TSS18721 |
| chr13 | 39264563 | 39264654 | MACS2_peak_719 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 18 | chr13 | unknown | gene | 40001881 | 40287983 | - | Ofcc1 | Ofcc1 | P24288 | NM_172143 | TSS19621 |
| chr13 | 40173631 | 40173784 | MACS2_peak_720 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 140 | chr13 | unknown | gene | 38960618 | 38966297 | + | 5033403F01Rik | 5033403F01Rik | | NR_131019 | TSS18721 |
| chr13 | 40173631 | 40173784 | MACS2_peak_720 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 140 | chr13 | unknown | gene | 40715302 | 40734920 | - | Tfap2a | Tfap2a | P16394 | NM_001301674 | TSS22049 |
| chr13 | 40372290 | 40372423 | MACS2_peak_721 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 68 | chr13 | unknown | gene | 40001881 | 40287983 | - | Ofcc1 | Ofcc1 | P24288 | NM_172143 | TSS19621 |
| chr13 | 40372290 | 40372423 | MACS2_peak_721 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 68 | chr13 | unknown | gene | 40715302 | 40734920 | - | Tfap2a | Tfap2a | P16394 | NM_001301674 | TSS22049 |
| chr13 | 42634483 | 42634574 | MACS2_peak_722 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 23 | chr13 | unknown | gene | 42301269 | 42306879 | + | Edn1 | Edn1 | P17631 | NM_010104 | TSS20853 |
| chr13 | 42634483 | 42634574 | MACS2_peak_722 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 23 | chr13 | unknown | gene | 42680798 | 43135189 | + | Phactr1 | Phactr1 | P15741 | NM_001302635 | TSS404 |
| chr13 | 42642286 | 42642377 | MACS2_peak_723 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 9 | chr13 | unknown | gene | 42301269 | 42306879 | + | Edn1 | Edn1 | P17631 | NM_010104 | TSS20853 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr13 | 42642286 | 42642377 | MACS2_peak_723 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 9 | chr13 | unknown | gene | 42680798 | 43135189 | + | Phactr1 | Phactr1 | P15741 | NM_001302635 | TSS404 |
| chr13 | 43336994 | 43337085 | MACS2_peak_724 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 23 | chr13 | unknown | gene | 43195518 | 43303497 | - | Gfod1 | Gfod1 | P14510 | NM_001033399 | TSS8967 |
| chr13 | 43336994 | 43337085 | MACS2_peak_724 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 23 | chr13 | unknown | gene | 43370715 | 43394812 | + | Sirt5 | Sirt5 | P12823 | NM_178848 | TSS19378 |
| chr13 | 43895673 | 43895764 | MACS2_peak_725 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 44 | chr13 | unknown | gene | 43785111 | 43801685 | + | Cd83 | Cd83 | P818 | NM_001289915 | TSS12679 |
| chr13 | 43895673 | 43895764 | MACS2_peak_725 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 44 | chr13 | unknown | gene | 44121166 | 44125179 | + | Gm5083 | Gm5083 | | NR_045285 | TSS20020 |
| chr13 | 43945450 | 43945541 | MACS2_peak_726 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 35 | chr13 | unknown | gene | 43785111 | 43801685 | + | Cd83 | Cd83 | P818 | NM_001289915 | TSS12679 |
| chr13 | 43945450 | 43945541 | MACS2_peak_726 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 35 | chr13 | unknown | gene | 44121166 | 44125179 | + | Gm5083 | Gm5083 | | NR_045285 | TSS20020 |
| chr13 | 44069677 | 44069768 | MACS2_peak_727 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 37 | chr13 | unknown | gene | 43785111 | 43801685 | + | Cd83 | Cd83 | P818 | NM_001289915 | TSS12679 |
| chr13 | 44069677 | 44069768 | MACS2_peak_727 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 37 | chr13 | unknown | gene | 44121166 | 44125179 | + | Gm5083 | Gm5083 | | NR_045285 | TSS20020 |
| chr13 | 45130753 | 45130844 | MACS2_peak_728 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 78 | chr13 | unknown | gene | 44922079 | 45001972 | - | Dtnbp1 | Dtnbp1 | P7384 | NM_025772 | TSS12478 |
| chr13 | 45130753 | 45130844 | MACS2_peak_728 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 78 | chr13 | unknown | gene | 45389741 | 45410510 | + | Mylip | Mylip | P8635 | NM_153789 | TSS27046 |
| chr13 | 45454650 | 45454756 | MACS2_peak_729 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 40 | chr13 | unknown | gene | 45389741 | 45410510 | + | Mylip | Mylip | P8635 | NM_153789 | TSS27046 |
| chr13 | 45454650 | 45454756 | MACS2_peak_729 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 40 | chr13 | unknown | gene | 45507443 | 45546053 | + | Gmpr | Gmpr | P21417 | NM_025508 | TSS21176 |
| chr13 | 46076250 | 46076341 | MACS2_peak_730 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 54 | chr13 | unknown | gene | 45549755 | 45964991 | - | Atxn1 | Atxn1 | P7427 | NM_001199305 | TSS3855 |
| chr13 | 46076250 | 46076341 | MACS2_peak_730 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 54 | chr13 | unknown | gene | 46273720 | 46299689 | + | Stmnd1 | Stmnd1 | P10272 | NM_001005422 | TSS15210 |
| chr13 | 47023333 | 47023424 | MACS2_peak_731 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 38 | chr13 | unknown | gene | 47012556 | 47014779 | - | Nhlrc1 | Nhlrc1 | P10158 | NM_175340 | TSS9958 |
| chr13 | 47023333 | 47023424 | MACS2_peak_731 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 38 | chr13 | unknown | gene | 47023542 | 47043217 | - | Tpmt | Tpmt | P13306 | NM_016785 | TSS22712 |
| chr13 | 47148540 | 47148631 | MACS2_peak_732 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 59 | chr13 | unknown | gene | 47084766 | 47106221 | - | Dek | Dek | P22674 | NM_025900 | TSS11922 |
| chr13 | 47148540 | 47148631 | MACS2_peak_732 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 59 | chr13 | unknown | gene | 47910434 | 47934301 | + | G630093K05Rik | G630093K05Rik | | NR_045156 | TSS17071 |
| chr13 | 47675443 | 47675534 | MACS2_peak_733 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 47 | chr13 | unknown | gene | 47122719 | 47244501 | + | Rnf144b | Rnf144b | P25760 | NM_146042 | TSS11177 |
| chr13 | 47675443 | 47675534 | MACS2_peak_733 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 47 | chr13 | unknown | gene | 47910434 | 47934301 | + | G630093K05Rik | G630093K05Rik | | NR_045156 | TSS17071 |
| chr13 | 48230505 | 48230616 | MACS2_peak_734 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 68 | chr13 | unknown | gene | 47960329 | 48018608 | - | 4931429P17Rik | 4931429P17Rik | | NR_038004 | TSS4844 |
| chr13 | 48230505 | 48230616 | MACS2_peak_734 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 68 | chr13 | unknown | gene | 48261426 | 48264036 | + | Id4 | Id4 | P16207 | NM_031166 | TSS18234 |
| chr13 | 48980601 | 48980692 | MACS2_peak_735 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 64 | chr13 | unknown | gene | 48968111 | 48969905 | + | Fam120aos | Fam120aos | | NR_015601 | TSS15087 |
| chr13 | 48980601 | 48980692 | MACS2_peak_735 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 64 | chr13 | unknown | gene | 49036301 | 49148328 | - | Wnk2 | Wnk2 | P7073 | NM_001290313 | TSS27338 |
| chr13 | 49016220 | 49016311 | MACS2_peak_736 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 33 | chr13 | unknown | gene | 48968111 | 48969905 | + | Fam120aos | Fam120aos | | NR_015601 | TSS15087 |
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| chr13 | 49608213 | 49608304 | MACS2_peak_737 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 28 | chr13 | unknown | gene | 49582746 | 49592387 | + | Omd | Omd | P17632 | NM_012050 | TSS7471 |
| chr13 | 49608213 | 49608304 | MACS2_peak_737 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 28 | chr13 | unknown | gene | 49653077 | 49678436 | + | Nol8 | Nol8 | P7435 | NM_001271397 | TSS1564 |
| chr13 | 49878444 | 49878576 | MACS2_peak_738 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 48 | chr13 | unknown | gene | 49682129 | 49733741 | + | Iars | Iars | P12694 | NM_172015 | TSS1978 |
| chr13 | 49878444 | 49878576 | MACS2_peak_738 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 48 | chr13 | unknown | gene | 50245180 | 50250264 | - | Gm906 | Gm906 | P9650 | NM_001033438 | TSS25625 |
| chr13 | 51159811 | 51159902 | MACS2_peak_739 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 25 | chr13 | unknown | gene | 51100879 | 51149161 | + | Spin1 | Spin1 | P9694 | NM_001283030 | TSS25400 |
| chr13 | 51159811 | 51159902 | MACS2_peak_739 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 25 | chr13 | unknown | gene | 51171024 | 51174793 | + | Nxnl2 | Nxnl2 | P2689 | NM_029173 | TSS12745 |
| chr13 | 53329773 | 53329864 | MACS2_peak_740 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 19 | chr13 | unknown | gene | 53109316 | 53285877 | - | Ror2 | Ror2 | P678 | NM_013846 | TSS21384 |
| chr13 | 53329773 | 53329864 | MACS2_peak_740 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 19 | chr13 | unknown | gene | 53332747 | 53377349 | - | Sptlc1 | Sptlc1 | P23984 | NM_009269 | TSS11461 |
| chr13 | 54016433 | 54016530 | MACS2_peak_741 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 22 | chr13 | unknown | gene | 53648584 | 53650081 | + | 4930555G21Rik | 4930555G21Rik | | NR_131010 | TSS15792 |
| chr13 | 54016433 | 54016530 | MACS2_peak_741 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 22 | chr13 | unknown | gene | 54051182 | 54055658 | - | Drd1 | Drd1 | P21464 | NM_010076 | TSS4376 |
| chr13 | 54101550 | 54101641 | MACS2_peak_742 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 5 | chr13 | unknown | gene | 54051182 | 54055658 | - | Drd1 | Drd1 | P21464 | NM_010076 | TSS4376 |
| chr13 | 54101550 | 54101641 | MACS2_peak_742 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 5 | chr13 | unknown | gene | 54192128 | 54221340 | + | Hrh2 | Hrh2 | P15952 | NM_001010973 | TSS4671 |
| chr13 | 56132772 | 56132895 | MACS2_peak_743 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 32 | chr13 | unknown | gene | 55825053 | 55830940 | - | Pitx1 | Pitx1 | P17106 | NM_011097 | TSS18523 |
| chr13 | 56132772 | 56132895 | MACS2_peak_743 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 32 | chr13 | unknown | gene | 56173702 | 56178885 | - | Tifab | Tifab | P21865 | NM_145976 | TSS2653 |
| chr13 | 60071707 | 60071798 | MACS2_peak_744 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 43 | chr13 | unknown | gene | 59771878 | 59823147 | - | Zcchc6 | Zcchc6 | P9358 | NM_153538 | TSS4183 |
| chr13 | 60071707 | 60071798 | MACS2_peak_744 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 43 | chr13 | unknown | gene | 60174404 | 60176941 | - | Gas1 | Gas1 | P13043 | NM_008086 | TSS20504 |
| chr13 | 60820410 | 60820501 | MACS2_peak_745 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 62 | chr13 | unknown | gene | 60798249 | 60802844 | - | Ctsll3 | Ctsll3 | P24025 | NM_027344 | TSS795 |
| chr13 | 60820410 | 60820501 | MACS2_peak_745 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 62 | chr13 | unknown | gene | 60842611 | 60864416 | - | 4930486L24Rik | 4930486L24Rik | P14564 | NM_178098 | TSS27454 |
| chr13 | 62930064 | 62930155 | MACS2_peak_746 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 16 | chr13 | unknown | gene | 62864752 | 62888043 | - | Fbp1 | Fbp1 | P24487 | NM_019395 | TSS9062 |
| chr13 | 62930064 | 62930155 | MACS2_peak_746 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 16 | chr13 | unknown | gene | 62964892 | 63326096 | + | 2010111I01Rik | 2010111I01Rik | P15381 | NM_001289924 | TSS27372 |
| chr13 | 65907754 | 65907845 | MACS2_peak_747 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 11 | chr13 | unknown | gene | 65278853 | 65297582 | + | Zfp369 | Zfp369 | P26421 | NM_178364 | TSS27591 |
| chr13 | 65907754 | 65907845 | MACS2_peak_747 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 11 | chr13 | unknown | gene | 66113452 | 66122836 | + | Gm10324 | Gm10324 | P26873 | NM_001177832 | TSS8687 |
| chr13 | 66430239 | 66430330 | MACS2_peak_748 | 13 | + | 4.3209 | 5.66955 | 1.3392 | 30 | chr13 | unknown | gene | 66113452 | 66122836 | + | Gm10324 | Gm10324 | P26873 | NM_001177832 | TSS8687 |
| chr13 | 66430239 | 66430330 | MACS2_peak_748 | 13 | + | 4.3209 | 5.66955 | 1.3392 | 30 | chr13 | unknown | gene | 66900620 | 66905311 | - | Uqcrb | Uqcrb | P1960 | NM_026219 | TSS27300 |
| chr13 | 66431666 | 66431757 | MACS2_peak_749 | 9 | + | 3.92657 | 4.876 | 0.99788 | 32 | chr13 | unknown | gene | 66113452 | 66122836 | + | Gm10324 | Gm10324 | P26873 | NM_001177832 | TSS8687 |
| chr13 | 66431666 | 66431757 | MACS2_peak_749 | 9 | + | 3.92657 | 4.876 | 0.99788 | 32 | chr13 | unknown | gene | 66900620 | 66905311 | - | Uqcrb | Uqcrb | P1960 | NM_026219 | TSS27300 |
| chr13 | 66793331 | 66793422 | MACS2_peak_750 | 13 | + | 4.32419 | 5.39568 | 1.3392 | 74 | chr13 | unknown | gene | 66418113 | 66441022 | - | 2410141K09Rik | 2410141K09Rik | P26557 | NM_183119 | TSS21442 |
| chr13 | 66793331 | 66793422 | MACS2_peak_750 | 13 | + | 4.32419 | 5.39568 | 1.3392 | 74 | chr13 | unknown | gene | 66900620 | 66905311 | - | Uqcrb | Uqcrb | P1960 | NM_026219 | TSS27300 |
| chr13 | 69321221 | 69321312 | MACS2_peak_751 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 37 | chr13 | unknown | gene | 68620042 | 68999295 | - | Adcy2 | Adcy2 | P8526 | NM_153534 | TSS2206 |
| chr13 | 69321221 | 69321312 | MACS2_peak_751 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 37 | chr13 | unknown | gene | 69497958 | 69533864 | - | Papd7 | Papd7 | P2852 | NM_001169131 | TSS15384 |
| chr13 | 70230475 | 70230566 | MACS2_peak_752 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 75 | chr13 | unknown | gene | 70021958 | 70119949 | + | Gm3772 | Gm3772 | | NR_131156 | TSS26785 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr13 | 70230475 | 70230566 | MACS2_peak_752 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 75 | chr13 | unknown | gene | 70232821 | 70248122 | + | 4930520P13Rik | 4930520P13Rik | | NR_036596 | TSS20029 |
| chr13 | 75967020 | 75967111 | MACS2_peak_753 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 13 | chr13 | unknown | gene | 75869536 | 75943532 | - | Rhobtb3 | Rhobtb3 | P12323 | NM_028493 | TSS23629 |
| chr13 | 75967020 | 75967111 | MACS2_peak_753 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 13 | chr13 | unknown | gene | 75967738 | 75998769 | + | Spata9 | Spata9 | P21925 | NM_029343 | TSS8660 |
| chr13 | 77438900 | 77439060 | MACS2_peak_754 | 1518 | + | 47.64086 | 158.93123 | 151.83784 | 83 | chr13 | unknown | gene | 77043087 | 77135468 | - | Ankrd32 | Ankrd32 | P25726 | NM_134071 | TSS16625 |
| chr13 | 77438900 | 77439060 | MACS2_peak_754 | 1518 | + | 47.64086 | 158.93123 | 151.83784 | 83 | chr13 | unknown | gene | 77708689 | 78163655 | + | Fam172a | Fam172a | P22954 | NM_001163420 | TSS8141 |
| chr13 | 79255714 | 79255805 | MACS2_peak_755 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 84 | chr13 | unknown | gene | 78198016 | 78236564 | + | A830082K12Rik | A830082K12Rik | | NR_045195 | TSS6925 |
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| chr13 | 79330199 | 79330329 | MACS2_peak_756 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 51 | chr13 | unknown | gene | 78198016 | 78236564 | + | A830082K12Rik | A830082K12Rik | | NR_045195 | TSS6925 |
| chr13 | 79330199 | 79330329 | MACS2_peak_756 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 51 | chr13 | unknown | gene | 80883421 | 80893426 | + | Arrdc3 | Arrdc3 | P12590 | NM_001042591 | TSS11785 |
| chr13 | 79959728 | 79959819 | MACS2_peak_757 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 20 | chr13 | unknown | gene | 78198016 | 78236564 | + | A830082K12Rik | A830082K12Rik | | NR_045195 | TSS6925 |
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| chr13 | 80006667 | 80006774 | MACS2_peak_758 | 23 | + | 5.29942 | 7.14384 | 2.32792 | 75 | chr13 | unknown | gene | 78198016 | 78236564 | + | A830082K12Rik | A830082K12Rik | | NR_045195 | TSS6925 |
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| chr13 | 80442925 | 80443065 | MACS2_peak_759 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 26 | chr13 | unknown | gene | 78198016 | 78236564 | + | A830082K12Rik | A830082K12Rik | | NR_045195 | TSS6925 |
| chr13 | 80442925 | 80443065 | MACS2_peak_759 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 26 | chr13 | unknown | gene | 80883421 | 80893426 | + | Arrdc3 | Arrdc3 | P12590 | NM_001042591 | TSS11785 |
| chr13 | 80708896 | 80708987 | MACS2_peak_760 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 11 | chr13 | unknown | gene | 78198016 | 78236564 | + | A830082K12Rik | A830082K12Rik | | NR_045195 | TSS6925 |
| chr13 | 80708896 | 80708987 | MACS2_peak_760 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 11 | chr13 | unknown | gene | 80883421 | 80893426 | + | Arrdc3 | Arrdc3 | P12590 | NM_001042591 | TSS11785 |
| chr13 | 80936132 | 80936265 | MACS2_peak_761 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 50 | chr13 | unknown | gene | 80883421 | 80893426 | + | Arrdc3 | Arrdc3 | P12590 | NM_001042591 | TSS11785 |
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| chr13 | 81865165 | 81865256 | MACS2_peak_762 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 5 | chr13 | unknown | gene | 81783291 | 81796697 | + | Cetn3 | Cetn3 | P14873 | NM_007684 | TSS13085 |
| chr13 | 81865165 | 81865256 | MACS2_peak_762 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 5 | chr13 | unknown | gene | 82698274 | 82698333 | - | Mir3961 | Mir3961 | | NR_039537 | TSS10934 |
| chr13 | 82159433 | 82159603 | MACS2_peak_763 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 53 | chr13 | unknown | gene | 81783291 | 81796697 | + | Cetn3 | Cetn3 | P14873 | NM_007684 | TSS13085 |
| chr13 | 82159433 | 82159603 | MACS2_peak_763 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 53 | chr13 | unknown | gene | 82698274 | 82698333 | - | Mir3961 | Mir3961 | | NR_039537 | TSS10934 |
| chr13 | 82984428 | 82984540 | MACS2_peak_764 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 25 | chr13 | unknown | gene | 82698274 | 82698333 | - | Mir3961 | Mir3961 | | NR_039537 | TSS10934 |
| chr13 | 82984428 | 82984540 | MACS2_peak_764 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 25 | chr13 | unknown | gene | 83504033 | 83662631 | + | Mef2c | Mef2c | P3397 | NM_025282 | TSS8009 |
| chr13 | 83300601 | 83300692 | MACS2_peak_765 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 52 | chr13 | unknown | gene | 82698274 | 82698333 | - | Mir3961 | Mir3961 | | NR_039537 | TSS10934 |
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| chr13 | 84768082 | 84768173 | MACS2_peak_766 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 48 | chr13 | unknown | gene | 84222295 | 84294880 | + | Tmem161b | Tmem161b | P15924 | NM_175187 | TSS14252 |
| chr13 | 84768082 | 84768173 | MACS2_peak_766 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 48 | chr13 | unknown | gene | 85189476 | 85212778 | + | Ccnh | Ccnh | P6648 | NM_023243 | TSS27579 |
| chr13 | 85127012 | 85127203 | MACS2_peak_767 | 160 | + | 11.87055 | 21.53959 | 16.06482 | 116 | chr13 | unknown | gene | 84222295 | 84294880 | + | Tmem161b | Tmem161b | P15924 | NM_175187 | TSS14252 |
| chr13 | 85127012 | 85127203 | MACS2_peak_767 | 160 | + | 11.87055 | 21.53959 | 16.06482 | 116 | chr13 | unknown | gene | 85189476 | 85212778 | + | Ccnh | Ccnh | P6648 | NM_023243 | TSS27579 |
| chr13 | 85127318 | 85127409 | MACS2_peak_768 | 39 | + | 6.21234 | 8.94875 | 3.91275 | 49 | chr13 | unknown | gene | 84222295 | 84294880 | + | Tmem161b | Tmem161b | P15924 | NM_175187 | TSS14252 |
| chr13 | 85127318 | 85127409 | MACS2_peak_768 | 39 | + | 6.21234 | 8.94875 | 3.91275 | 49 | chr13 | unknown | gene | 85189476 | 85212778 | + | Ccnh | Ccnh | P6648 | NM_023243 | TSS27579 |
| chr13 | 85568656 | 85568747 | MACS2_peak_769 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 44 | chr13 | unknown | gene | 85214698 | 85288907 | - | Rasa1 | Rasa1 | P14826 | NM_145452 | TSS22254 |
| chr13 | 85568656 | 85568747 | MACS2_peak_769 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 44 | chr13 | unknown | gene | 86044797 | 86046675 | - | Cox7c | Cox7c | P4052 | NM_007749 | TSS19697 |
| chr13 | 85593022 | 85593113 | MACS2_peak_770 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 14 | chr13 | unknown | gene | 85214698 | 85288907 | - | Rasa1 | Rasa1 | P14826 | NM_145452 | TSS22254 |
| chr13 | 85593022 | 85593113 | MACS2_peak_770 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 14 | chr13 | unknown | gene | 86044797 | 86046675 | - | Cox7c | Cox7c | P4052 | NM_007749 | TSS19697 |
| chr13 | 85735646 | 85735737 | MACS2_peak_771 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 41 | chr13 | unknown | gene | 85214698 | 85288907 | - | Rasa1 | Rasa1 | P14826 | NM_145452 | TSS22254 |
| chr13 | 85735646 | 85735737 | MACS2_peak_771 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 41 | chr13 | unknown | gene | 86044797 | 86046675 | - | Cox7c | Cox7c | P4052 | NM_007749 | TSS19697 |
| chr13 | 85835585 | 85835676 | MACS2_peak_772 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 13 | chr13 | unknown | gene | 85214698 | 85288907 | - | Rasa1 | Rasa1 | P14826 | NM_145452 | TSS22254 |
| chr13 | 85835585 | 85835676 | MACS2_peak_772 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 13 | chr13 | unknown | gene | 86044797 | 86046675 | - | Cox7c | Cox7c | P4052 | NM_007749 | TSS19697 |
| chr13 | 86077151 | 86077312 | MACS2_peak_773 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 128 | chr13 | unknown | gene | 86044797 | 86046675 | - | Cox7c | Cox7c | P4052 | NM_007749 | TSS19697 |
| chr13 | 86077151 | 86077312 | MACS2_peak_773 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 128 | chr13 | unknown | gene | 88821471 | 89319820 | + | Edil3 | Edil3 | P3424 | NM_010103 | TSS6316 |
| chr13 | 86081118 | 86081209 | MACS2_peak_774 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 11 | chr13 | unknown | gene | 86044797 | 86046675 | - | Cox7c | Cox7c | P4052 | NM_007749 | TSS19697 |
| chr13 | 86081118 | 86081209 | MACS2_peak_774 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 11 | chr13 | unknown | gene | 88821471 | 89319820 | + | Edil3 | Edil3 | P3424 | NM_010103 | TSS6316 |
| chr13 | 88398332 | 88398441 | MACS2_peak_775 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 50 | chr13 | unknown | gene | 86044797 | 86046675 | - | Cox7c | Cox7c | P4052 | NM_007749 | TSS19697 |
| chr13 | 88398332 | 88398441 | MACS2_peak_775 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 50 | chr13 | unknown | gene | 88821471 | 89319820 | + | Edil3 | Edil3 | P3424 | NM_010103 | TSS6316 |
| chr13 | 88633038 | 88633129 | MACS2_peak_776 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 41 | chr13 | unknown | gene | 86044797 | 86046675 | - | Cox7c | Cox7c | P4052 | NM_007749 | TSS19697 |
| chr13 | 88633038 | 88633129 | MACS2_peak_776 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 41 | chr13 | unknown | gene | 88821471 | 89319820 | + | Edil3 | Edil3 | P3424 | NM_010103 | TSS6316 |
| chr13 | 88960651 | 88960742 | MACS2_peak_777 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 51 | chr13 | unknown | gene | 86044797 | 86046675 | - | Cox7c | Cox7c | P4052 | NM_007749 | TSS19697 |
| chr13 | 88960651 | 88960742 | MACS2_peak_777 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 51 | chr13 | unknown | gene | 89540635 | 89608149 | + | Hapln1 | Hapln1 | P11690 | NM_013500 | TSS989 |
| chr13 | 89265540 | 89265631 | MACS2_peak_778 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 26 | chr13 | unknown | gene | 86044797 | 86046675 | - | Cox7c | Cox7c | P4052 | NM_007749 | TSS19697 |
| chr13 | 89265540 | 89265631 | MACS2_peak_778 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 26 | chr13 | unknown | gene | 89540635 | 89608149 | + | Hapln1 | Hapln1 | P11690 | NM_013500 | TSS989 |
| chr13 | 89384506 | 89384597 | MACS2_peak_779 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 54 | chr13 | unknown | gene | 88821471 | 89319820 | + | Edil3 | Edil3 | P3424 | NM_010103 | TSS6316 |
| chr13 | 89384506 | 89384597 | MACS2_peak_779 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 54 | chr13 | unknown | gene | 89540635 | 89608149 | + | Hapln1 | Hapln1 | P11690 | NM_013500 | TSS989 |
| chr13 | 89493086 | 89493177 | MACS2_peak_780 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 79 | chr13 | unknown | gene | 88821471 | 89319820 | + | Edil3 | Edil3 | P3424 | NM_010103 | TSS6316 |
| chr13 | 89493086 | 89493177 | MACS2_peak_780 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 79 | chr13 | unknown | gene | 89540635 | 89608149 | + | Hapln1 | Hapln1 | P11690 | NM_013500 | TSS989 |
| chr13 | 89649126 | 89649217 | MACS2_peak_781 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 52 | chr13 | unknown | gene | 89540635 | 89608149 | + | Hapln1 | Hapln1 | P11690 | NM_013500 | TSS989 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr13 | 89649126 | 89649217 | MACS2_peak_781 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 52 | chr13 | unknown | gene | 89655309 | 89742512 | - | Vcan | Vcan | P25945 | NM_001081249 | TSS15677 |
| chr13 | 89838602 | 89838693 | MACS2_peak_782 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 59 | chr13 | unknown | gene | 89655309 | 89742512 | - | Vcan | Vcan | P25945 | NM_001081249 | TSS15677 |
| chr13 | 89838602 | 89838693 | MACS2_peak_782 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 59 | chr13 | unknown | gene | 89848913 | 90089608 | - | Xrcc4 | Xrcc4 | P12100 | NM_028012 | TSS17946 |
| chr13 | 90169945 | 90170036 | MACS2_peak_783 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 33 | chr13 | unknown | gene | 90089666 | 90104445 | + | Tmem167 | Tmem167 | P20404 | NM_025335 | TSS20738 |
| chr13 | 90169945 | 90170036 | MACS2_peak_783 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 33 | chr13 | unknown | gene | 90883448 | 90905292 | - | Atp6ap1l | Atp6ap1l | P5895 | NM_001145879 | TSS25275 |
| chr13 | 90235102 | 90235193 | MACS2_peak_784 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 45 | chr13 | unknown | gene | 90089666 | 90104445 | + | Tmem167 | Tmem167 | P20404 | NM_025335 | TSS20738 |
| chr13 | 90235102 | 90235193 | MACS2_peak_784 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 45 | chr13 | unknown | gene | 90883448 | 90905292 | - | Atp6ap1l | Atp6ap1l | P5895 | NM_001145879 | TSS25275 |
| chr13 | 91101472 | 91101563 | MACS2_peak_785 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 50 | chr13 | unknown | gene | 90923121 | 90924683 | + | Rps23 | Rps23 | P17918 | NM_024175 | TSS10884 |
| chr13 | 91101472 | 91101563 | MACS2_peak_785 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 50 | chr13 | unknown | gene | 91368989 | 91388085 | - | A830009L08Rik | A830009L08Rik | | NR_045161 | TSS3129 |
| chr13 | 91482423 | 91482526 | MACS2_peak_786 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 70 | chr13 | unknown | gene | 91368989 | 91388085 | - | A830009L08Rik | A830009L08Rik | | NR_045161 | TSS3129 |
| chr13 | 91482423 | 91482526 | MACS2_peak_786 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 70 | chr13 | unknown | gene | 91701664 | 91741872 | - | 4833422C13Rik | 4833422C13Rik | | NR_015501 | TSS3802 |
| chr13 | 92232520 | 92232611 | MACS2_peak_787 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 35 | chr13 | unknown | gene | 91880406 | 91988042 | - | Rasgrf2 | Rasgrf2 | P3631 | NM_009027 | TSS10737 |
| chr13 | 92232520 | 92232611 | MACS2_peak_787 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 35 | chr13 | unknown | gene | 92354782 | 92384803 | + | Dhfr | Dhfr | P22786 | NM_010049 | TSS11345 |
| chr13 | 92580351 | 92580443 | MACS2_peak_788 | 30 | + | 5.71265 | 7.93979 | 3.00019 | 41 | chr13 | unknown | gene | 92574631 | 92575966 | - | Spz1 | Spz1 | P18883 | NM_030237 | TSS24851 |
| chr13 | 92580351 | 92580443 | MACS2_peak_788 | 30 | + | 5.71265 | 7.93979 | 3.00019 | 41 | chr13 | unknown | gene | 92611137 | 92708137 | + | Serinc5 | Serinc5 | P21883 | NM_172588 | TSS6759 |
| chr13 | 92780714 | 92780835 | MACS2_peak_789 | 12 | + | 4.14966 | 5.12722 | 1.204 | 69 | chr13 | unknown | gene | 92611137 | 92708137 | + | Serinc5 | Serinc5 | P21883 | NM_172588 | TSS6759 |
| chr13 | 92780714 | 92780835 | MACS2_peak_789 | 12 | + | 4.14966 | 5.12722 | 1.204 | 69 | chr13 | unknown | gene | 92844786 | 92852894 | + | Mtx3 | Mtx3 | P24336 | NM_001162945 | TSS10031 |
| chr13 | 93462682 | 93462828 | MACS2_peak_790 | 43 | + | 6.46831 | 9.40295 | 4.34724 | 70 | chr13 | unknown | gene | 93304494 | 93402229 | + | Homer1 | Homer1 | P26425 | NM_011982 | TSS44 |
| chr13 | 93462682 | 93462828 | MACS2_peak_790 | 43 | + | 6.46831 | 9.40295 | 4.34724 | 70 | chr13 | unknown | gene | 93616890 | 93637496 | - | Bhmt | Bhmt | P4131 | NM_016668 | TSS23917 |
| chr13 | 93897358 | 93897449 | MACS2_peak_791 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 38 | chr13 | unknown | gene | 93790776 | 93790837 | + | Mir5624 | Mir5624 | | NR_049198 | TSS25000 |
| chr13 | 93897358 | 93897449 | MACS2_peak_791 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 38 | chr13 | unknown | gene | 94057795 | 94192101 | + | Lhfpl2 | Lhfpl2 | P6006 | NM_172589 | TSS10806 |
| chr13 | 95636864 | 95636988 | MACS2_peak_792 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 86 | chr13 | unknown | gene | 95601788 | 95618374 | - | F2r | F2r | P6694 | NM_010169 | TSS7208 |
| chr13 | 95636864 | 95636988 | MACS2_peak_792 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 86 | chr13 | unknown | gene | 95696919 | 95701558 | + | F2rl2 | F2rl2 | P5790 | NM_010170 | TSS7034 |
| chr13 | 96690687 | 96690781 | MACS2_peak_793 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 22 | chr13 | unknown | gene | 96648961 | 96670936 | - | Hmgcr | Hmgcr | P17419 | NM_008255 | TSS23200 |
| chr13 | 96690687 | 96690781 | MACS2_peak_793 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 22 | chr13 | unknown | gene | 96924688 | 96947565 | + | Gcnt4 | Gcnt4 | P1841 | NM_001166065 | TSS6432 |
| chr13 | 97337472 | 97337563 | MACS2_peak_794 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 20 | chr13 | unknown | gene | 97241104 | 97253040 | + | Enc1 | Enc1 | P15723 | NM_007930 | TSS9615 |
| chr13 | 97337472 | 97337563 | MACS2_peak_794 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 20 | chr13 | unknown | gene | 97434969 | 97497664 | + | Lincenc1 | Lincenc1 | | NR_110432 | TSS8762 |
| chr13 | 97654100 | 97654191 | MACS2_peak_795 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 13 | chr13 | unknown | gene | 97559999 | 97583994 | + | Gm5086 | Gm5086 | | NR_046157 | TSS10357 |
| chr13 | 97654100 | 97654191 | MACS2_peak_795 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 13 | chr13 | unknown | gene | 97898594 | 98206165 | - | Arhgef28 | Arhgef28 | P1479 | NM_012026 | TSS10069 |
| chr13 | 98314575 | 98314666 | MACS2_peak_796 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 15 | chr13 | unknown | gene | 98263075 | 98273966 | + | Ankra2 | Ankra2 | P15463 | NM_001271391 | TSS12808 |
| chr13 | 98314575 | 98314666 | MACS2_peak_796 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 15 | chr13 | unknown | gene | 98354244 | 98355990 | + | Foxd1 | Foxd1 | P13025 | NM_008242 | TSS2582 |
| chr13 | 100489386 | 100489477 | MACS2_peak_797 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 50 | chr13 | unknown | gene | 100407769 | 100452864 | - | Naip1 | Naip1 | P7369 | NM_008670 | TSS23404 |
| chr13 | 100489386 | 100489477 | MACS2_peak_797 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 50 | chr13 | unknown | gene | 100497366 | 100552498 | - | Ocln | Ocln | P12256 | NM_008756 | TSS10025 |
| chr13 | 101817484 | 101817620 | MACS2_peak_798 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 64 | chr13 | unknown | gene | 101680760 | 101768217 | - | Pik3r1 | Pik3r1 | P20599 | NM_001024955 | TSS16094 |
| chr13 | 101817484 | 101817620 | MACS2_peak_798 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 64 | chr13 | unknown | gene | 102693557 | 102706433 | + | Cd180 | Cd180 | P19038 | NM_008533 | TSS3839 |
| chr13 | 101895611 | 101895702 | MACS2_peak_799 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 58 | chr13 | unknown | gene | 101680760 | 101768217 | - | Pik3r1 | Pik3r1 | P20599 | NM_001024955 | TSS16094 |
| chr13 | 101895611 | 101895702 | MACS2_peak_799 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 58 | chr13 | unknown | gene | 102693557 | 102706433 | + | Cd180 | Cd180 | P19038 | NM_008533 | TSS3839 |
| chr13 | 102312096 | 102312189 | MACS2_peak_800 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 8 | chr13 | unknown | gene | 101680760 | 101768217 | - | Pik3r1 | Pik3r1 | P20599 | NM_001024955 | TSS16094 |
| chr13 | 102312096 | 102312189 | MACS2_peak_800 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 8 | chr13 | unknown | gene | 102693557 | 102706433 | + | Cd180 | Cd180 | P19038 | NM_008533 | TSS3839 |
| chr13 | 102717743 | 102717834 | MACS2_peak_801 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 11 | chr13 | unknown | gene | 102693557 | 102706433 | + | Cd180 | Cd180 | P19038 | NM_008533 | TSS3839 |
| chr13 | 102717743 | 102717834 | MACS2_peak_801 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 11 | chr13 | unknown | gene | 102732488 | 103334192 | - | Mast4 | Mast4 | P629 | NM_175171 | TSS7742 |
| chr13 | 103581485 | 103581576 | MACS2_peak_802 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 1 | chr13 | unknown | gene | 102732488 | 103334192 | - | Mast4 | Mast4 | P629 | NM_175171 | TSS7742 |
| chr13 | 103581485 | 103581576 | MACS2_peak_802 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 1 | chr13 | unknown | gene | 103741614 | 103763953 | - | Srek1 | Srek1 | P20098 | NM_172592 | TSS26121 |
| chr13 | 103897219 | 103897310 | MACS2_peak_803 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 45 | chr13 | unknown | gene | 103741614 | 103763953 | - | Srek1 | Srek1 | P20098 | NM_172592 | TSS26121 |
| chr13 | 103897219 | 103897310 | MACS2_peak_803 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 45 | chr13 | unknown | gene | 104023438 | 104109456 | - | Nln | Nln | P19387 | NM_029447 | TSS20203 |
| chr13 | 103975626 | 103975717 | MACS2_peak_804 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 29 | chr13 | unknown | gene | 103818785 | 103920586 | - | Erbb2ip | Erbb2ip | P4122 | NM_001005868 | TSS11837 |
| chr13 | 103975626 | 103975717 | MACS2_peak_804 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 29 | chr13 | unknown | gene | 104023438 | 104109456 | - | Nln | Nln | P19387 | NM_029447 | TSS20203 |
| chr13 | 104231997 | 104232088 | MACS2_peak_805 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 27 | chr13 | unknown | gene | 104205121 | 104228801 | - | Ppwd1 | Ppwd1 | P7036 | NM_172807 | TSS11554 |
| chr13 | 104231997 | 104232088 | MACS2_peak_805 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 27 | chr13 | unknown | gene | 104287872 | 104493704 | + | Adamts6 | Adamts6 | P8714 | NM_001081020 | TSS13903 |
| chr13 | 104450905 | 104451037 | MACS2_peak_806 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 64 | chr13 | unknown | gene | 104228610 | 104249519 | + | Cenpk | Cenpk | P16050 | NM_181061 | TSS11392 |
| chr13 | 104450905 | 104451037 | MACS2_peak_806 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 64 | chr13 | unknown | gene | 104631326 | 104816728 | - | Cwc27 | Cwc27 | P26239 | NM_026072 | TSS15811 |
| chr13 | 104937285 | 104937404 | MACS2_peak_807 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 36 | chr13 | unknown | gene | 104845282 | 104863713 | - | Fam159b | Fam159b | P4141 | NM_029984 | TSS254 |
| chr13 | 104937285 | 104937404 | MACS2_peak_807 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 36 | chr13 | unknown | gene | 104947152 | 105054214 | - | Rgs7bp | Rgs7bp | P24971 | NM_029879 | TSS5489 |
| chr13 | 105767997 | 105768135 | MACS2_peak_808 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 36 | chr13 | unknown | gene | 105443692 | 105445519 | + | Htr1a | Htr1a | P14954 | NM_008308 | TSS18138 |
| chr13 | 105767997 | 105768135 | MACS2_peak_808 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 36 | chr13 | unknown | gene | 106794438 | 106936915 | - | Ipo11 | Ipo11 | P126 | NM_029665 | TSS11829 |
| chr13 | 106147637 | 106147728 | MACS2_peak_809 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 11 | chr13 | unknown | gene | 105443692 | 105445519 | + | Htr1a | Htr1a | P14954 | NM_008308 | TSS18138 |
| chr13 | 106147637 | 106147728 | MACS2_peak_809 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 11 | chr13 | unknown | gene | 106794438 | 106936915 | - | Ipo11 | Ipo11 | P126 | NM_029665 | TSS11829 |
| chr13 | 106447498 | 106447589 | MACS2_peak_810 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 44 | chr13 | unknown | gene | 105443692 | 105445519 | + | Htr1a | Htr1a | P14954 | NM_008308 | TSS18138 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr13 | 106447498 | 106447589 | MACS2_peak_810 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 44 | chr13 | unknown | gene | 106794438 | 106936915 | - | Ipo11 | Ipo11 | P126 | NM_029665 | TSS11829 |
| chr13 | 107774260 | 107774351 | MACS2_peak_811 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 8 | chr13 | unknown | gene | 107761060 | 107761087 | - | Mir325 | Mir325 | | NR_029759 | TSS200 |
| chr13 | 107774260 | 107774351 | MACS2_peak_811 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 8 | chr13 | unknown | gene | 108044473 | 108047686 | + | Smim15 | Smim15 | P1017 | NM_001048250 | TSS3130 |
| chr13 | 107818132 | 107818223 | MACS2_peak_812 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 54 | chr13 | unknown | gene | 107761060 | 107761087 | - | Mir325 | Mir325 | | NR_029759 | TSS200 |
| chr13 | 107818132 | 107818223 | MACS2_peak_812 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 54 | chr13 | unknown | gene | 108044473 | 108047686 | + | Smim15 | Smim15 | P1017 | NM_001048250 | TSS3130 |
| chr13 | 107886271 | 107886362 | MACS2_peak_813 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 13 | chr13 | unknown | gene | 107761060 | 107761087 | - | Mir325 | Mir325 | | NR_029759 | TSS200 |
| chr13 | 107886271 | 107886362 | MACS2_peak_813 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 13 | chr13 | unknown | gene | 108044473 | 108047686 | + | Smim15 | Smim15 | P1017 | NM_001048250 | TSS3130 |
| chr13 | 108153225 | 108153331 | MACS2_peak_814 | 32 | + | 5.82623 | 8.17465 | 3.21814 | 85 | chr13 | unknown | gene | 108044473 | 108047686 | + | Smim15 | Smim15 | P1017 | NM_001048250 | TSS3130 |
| chr13 | 108153225 | 108153331 | MACS2_peak_814 | 32 | + | 5.82623 | 8.17465 | 3.21814 | 85 | chr13 | unknown | gene | 108158737 | 108194124 | + | Ercc8 | Ercc8 | P26343 | NM_028042 | TSS3152 |
| chr13 | 109478157 | 109478284 | MACS2_peak_815 | 27 | + | 5.56793 | 7.65146 | 2.73702 | 48 | chr13 | unknown | gene | 109324743 | 109324823 | + | Mir582 | Mir582 | | NR_030644 | TSS2716 |
| chr13 | 109478157 | 109478284 | MACS2_peak_815 | 27 | + | 5.56793 | 7.65146 | 2.73702 | 48 | chr13 | unknown | gene | 109903808 | 109903888 | + | Mir1904 | Mir1904 | | NR_035442 | TSS11342 |
| chr13 | 111410976 | 111411082 | MACS2_peak_816 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 68 | chr13 | unknown | gene | 111255012 | 111256263 | + | Actbl2 | Actbl2 | P19557 | NM_175497 | TSS23641 |
| chr13 | 111410976 | 111411082 | MACS2_peak_816 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 68 | chr13 | unknown | gene | 111425679 | 111490041 | - | Gpbp1 | Gpbp1 | P521 | NM_028487 | TSS7582 |
| chr13 | 111488045 | 111488194 | MACS2_peak_817 | 13 | + | 4.44925 | 5.61072 | 1.3392 | 75 | chr13 | unknown | gene | 111255012 | 111256263 | + | Actbl2 | Actbl2 | P19557 | NM_175497 | TSS23641 |
| chr13 | 111488045 | 111488194 | MACS2_peak_817 | 13 | + | 4.44925 | 5.61072 | 1.3392 | 75 | chr13 | unknown | gene | 111686177 | 111715141 | + | Mier3 | Mier3 | P10342 | NM_172593 | TSS10949 |
| chr13 | 112237812 | 112237915 | MACS2_peak_818 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 90 | chr13 | unknown | gene | 111867935 | 111871937 | + | Gm15326 | Gm15326 | | NR_130345 | TSS7819 |
| chr13 | 112237812 | 112237915 | MACS2_peak_818 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 90 | chr13 | unknown | gene | 112288450 | 112383579 | + | Ankrd55 | Ankrd55 | P12202 | NM_029898 | TSS19983 |
| chr13 | 112578200 | 112578291 | MACS2_peak_819 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 40 | chr13 | unknown | gene | 112464069 | 112504445 | + | Il6st | Il6st | P8812 | NM_010560 | TSS1838 |
| chr13 | 112578200 | 112578291 | MACS2_peak_819 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 40 | chr13 | unknown | gene | 112598332 | 112652310 | - | Ddx4 | Ddx4 | P21688 | NM_001145885 | TSS1018 |
| chr13 | 112610497 | 112610588 | MACS2_peak_820 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 31 | chr13 | unknown | gene | 112522806 | 112580662 | - | Il31ra | Il31ra | P12226 | NM_139299 | TSS24518 |
| chr13 | 112610497 | 112610588 | MACS2_peak_820 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 31 | chr13 | unknown | gene | 112660765 | 112731664 | + | Slc38a9 | Slc38a9 | P14399 | NM_178746 | TSS17651 |
| chr13 | 113721218 | 113721309 | MACS2_peak_821 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 43 | chr13 | unknown | gene | 113662895 | 113663492 | - | Hspb3 | Hspb3 | P14426 | NM_019960 | TSS26446 |
| chr13 | 113721218 | 113721309 | MACS2_peak_821 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 43 | chr13 | unknown | gene | 113794507 | 114154856 | + | Arl15 | Arl15 | P16726 | NM_172595 | TSS5207 |
| chr13 | 114474826 | 114474917 | MACS2_peak_822 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 69 | chr13 | unknown | gene | 114452261 | 114458586 | - | Fst | Fst | P11317 | NM_008046 | TSS16616 |
| chr13 | 114474826 | 114474917 | MACS2_peak_822 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 69 | chr13 | unknown | gene | 114607227 | 114697822 | + | 4930544M13Rik | 4930544M13Rik | | NR_045976 | TSS7486 |
| chr13 | 114856360 | 114856510 | MACS2_peak_823 | 44 | + | 6.54536 | 9.54302 | 4.48275 | 87 | chr13 | unknown | gene | 114818236 | 114828357 | + | Mocs2 | Mocs2 | P12958 | NM_001113375 | TSS3511 |
| chr13 | 114856360 | 114856510 | MACS2_peak_823 | 44 | + | 6.54536 | 9.54302 | 4.48275 | 87 | chr13 | unknown | gene | 114958080 | 115101531 | - | Itga1 | Itga1 | P26896 | NM_001033228 | TSS4699 |
| chr13 | 115016775 | 115016866 | MACS2_peak_824 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 57 | chr13 | unknown | gene | 114835911 | 114931933 | - | Itga2 | Itga2 | P23036 | NM_008396 | TSS2514 |
| chr13 | 115016775 | 115016866 | MACS2_peak_824 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 57 | chr13 | unknown | gene | 115088354 | 115089919 | - | Pelo | Pelo | P20435 | NM_134058 | TSS25312 |
| chr13 | 115747437 | 115747528 | MACS2_peak_825 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 49 | chr13 | unknown | gene | 114958080 | 115101531 | - | Itga1 | Itga1 | P26896 | NM_001033228 | TSS4699 |
| chr13 | 115747437 | 115747528 | MACS2_peak_825 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 49 | chr13 | unknown | gene | 116298269 | 116309422 | - | Isl1 | Isl1 | P1769 | NM_021459 | TSS1618 |
| chr13 | 115923362 | 115923455 | MACS2_peak_826 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 75 | chr13 | unknown | gene | 114958080 | 115101531 | - | Itga1 | Itga1 | P26896 | NM_001033228 | TSS4699 |
| chr13 | 115923362 | 115923455 | MACS2_peak_826 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 75 | chr13 | unknown | gene | 116298269 | 116309422 | - | Isl1 | Isl1 | P1769 | NM_021459 | TSS1618 |
| chr13 | 116348282 | 116348422 | MACS2_peak_827 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 71 | chr13 | unknown | gene | 116298269 | 116309422 | - | Isl1 | Isl1 | P1769 | NM_021459 | TSS1618 |
| chr13 | 116348282 | 116348422 | MACS2_peak_827 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 71 | chr13 | unknown | gene | 116854823 | 117025470 | - | Parp8 | Parp8 | P23941 | NM_001081009 | TSS8883 |
| chr13 | 116479623 | 116479714 | MACS2_peak_828 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 38 | chr13 | unknown | gene | 116298269 | 116309422 | - | Isl1 | Isl1 | P1769 | NM_021459 | TSS1618 |
| chr13 | 116479623 | 116479714 | MACS2_peak_828 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 38 | chr13 | unknown | gene | 116854823 | 117025470 | - | Parp8 | Parp8 | P23941 | NM_001081009 | TSS8883 |
| chr13 | 117075963 | 117076054 | MACS2_peak_829 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 32 | chr13 | unknown | gene | 116854823 | 117025470 | - | Parp8 | Parp8 | P23941 | NM_001081009 | TSS8883 |
| chr13 | 117075963 | 117076054 | MACS2_peak_829 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 32 | chr13 | unknown | gene | 117130024 | 117135884 | + | Gm6416 | Gm6416 | | NR_046023 | TSS597 |
| chr13 | 117839007 | 117839098 | MACS2_peak_830 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 33 | chr13 | unknown | gene | 117706763 | 117720011 | - | 4933413L06Rik | 4933413L06Rik | | NR_045508 | TSS2666 |
| chr13 | 117839007 | 117839098 | MACS2_peak_830 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 33 | chr13 | unknown | gene | 118380109 | 118387234 | - | Mrps30 | Mrps30 | P4029 | NM_021556 | TSS1112 |
| chr13 | 118184749 | 118184883 | MACS2_peak_831 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 83 | chr13 | unknown | gene | 117602319 | 117976234 | + | Hcn1 | Hcn1 | P22950 | NM_010408 | TSS25012 |
| chr13 | 118184749 | 118184883 | MACS2_peak_831 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 83 | chr13 | unknown | gene | 118380109 | 118387234 | - | Mrps30 | Mrps30 | P4029 | NM_021556 | TSS1112 |
| chr13 | 118542216 | 118542307 | MACS2_peak_832 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 61 | chr13 | unknown | gene | 118380109 | 118387234 | - | Mrps30 | Mrps30 | P4029 | NM_021556 | TSS1112 |
| chr13 | 118542216 | 118542307 | MACS2_peak_832 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 61 | chr13 | unknown | gene | 118556167 | 118588629 | + | 1700003P14Rik | 1700003P14Rik | | NR_045982 | TSS17971 |
| chr13 | 118771424 | 118771515 | MACS2_peak_833 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 58 | chr13 | unknown | gene | 118603409 | 118658743 | - | Gm10732 | Gm10732 | | NR_131153 | TSS24984 |
| chr13 | 118771424 | 118771515 | MACS2_peak_833 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 58 | chr13 | unknown | gene | 119334316 | 119409257 | - | Nnt | Nnt | P24789 | NM_008710 | TSS23912 |
| chr13 | 119035382 | 119035473 | MACS2_peak_834 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 72 | chr13 | unknown | gene | 118714698 | 118789316 | + | Fgf10 | Fgf10 | P25011 | NM_008002 | TSS17430 |
| chr13 | 119035382 | 119035473 | MACS2_peak_834 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 72 | chr13 | unknown | gene | 119334316 | 119409257 | - | Nnt | Nnt | P24789 | NM_008710 | TSS23912 |
| chr13 | 119252026 | 119252238 | MACS2_peak_835 | 16 | + | 4.80683 | 6.28208 | 1.69221 | 183 | chr13 | unknown | gene | 118714698 | 118789316 | + | Fgf10 | Fgf10 | P25011 | NM_008002 | TSS17430 |
| chr13 | 119252026 | 119252238 | MACS2_peak_835 | 16 | + | 4.80683 | 6.28208 | 1.69221 | 183 | chr13 | unknown | gene | 119334316 | 119409257 | - | Nnt | Nnt | P24789 | NM_008710 | TSS23912 |
| chr14 | 6156193 | 6156284 | MACS2_peak_836 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 64 | chr14 | unknown | gene | 5438069 | 5807939 | - | Gm3383 | Gm3383 | P4803 | NM_001291093 | TSS9986 |
| chr14 | 6156193 | 6156284 | MACS2_peak_836 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 64 | chr14 | unknown | gene | 6259746 | 6287250 | - | LOC100861615 | LOC100861615 | P18107 | NM_001270812 | TSS21455 |
| chr14 | 8286653 | 8286744 | MACS2_peak_837 | 44 | + | 6.54536 | 9.54302 | 4.48275 | 54 | chr14 | unknown | gene | 8225510 | 8259019 | - | Acox2 | Acox2 | P10645 | NM_001161667 | TSS11867 |
| chr14 | 8286653 | 8286744 | MACS2_peak_837 | 44 | + | 6.54536 | 9.54302 | 4.48275 | 54 | chr14 | unknown | gene | 8296277 | 8309776 | - | Fam107a | Fam107a | P17332 | NM_183187 | TSS13782 |
| chr14 | 9201264 | 9201355 | MACS2_peak_838 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 9 | chr14 | unknown | gene | 8666389 | 8673378 | + | 4930455B14Rik | 4930455B14Rik | | NR_045968 | TSS25003 |
| chr14 | 9201264 | 9201355 | MACS2_peak_838 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 9 | chr14 | unknown | gene | 9550093 | 11162035 | - | Fhit | Fhit | P9585 | NM_010210 | TSS21192 |
| chr14 | 10982710 | 10982863 | MACS2_peak_839 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 21 | chr14 | unknown | gene | 10738552 | 10779001 | + | Fhitos | Fhitos | | NR_131139 | TSS10607 |

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr14 | 10982710 | 10982863 | MACS2_peak_839 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 21 | chr14 | unknown | gene | 11282476 | 11282561 | + | Mir5124b | Mir5124b | | NR_105811 | TSS2887 |
| chr14 | 11489042 | 11489139 | MACS2_peak_840 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 28 | chr14 | unknown | gene | 11282476 | 11282561 | + | Mir5124b | Mir5124b | | NR_105811 | TSS2887 |
| chr14 | 11489042 | 11489139 | MACS2_peak_840 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 28 | chr14 | unknown | gene | 11553552 | 12237873 | + | Ptprg | Ptprg | P17277 | NM_008981 | TSS19101 |
| chr14 | 11740496 | 11740587 | MACS2_peak_841 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 14 | chr14 | unknown | gene | 11282476 | 11282561 | + | Mir5124b | Mir5124b | | NR_105811 | TSS2887 |
| chr14 | 11740496 | 11740587 | MACS2_peak_841 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 14 | chr14 | unknown | gene | 12284202 | 12303231 | + | 3830406C13Rik | 3830406C13Rik | P25903 | NM_146051 | TSS13932 |
| chr14 | 12199367 | 12199500 | MACS2_peak_842 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 53 | chr14 | unknown | gene | 11282476 | 11282561 | + | Mir5124b | Mir5124b | | NR_105811 | TSS2887 |
| chr14 | 12199367 | 12199500 | MACS2_peak_842 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 53 | chr14 | unknown | gene | 12284202 | 12303231 | + | 3830406C13Rik | 3830406C13Rik | P25903 | NM_146051 | TSS13932 |
| chr14 | 13664613 | 13664704 | MACS2_peak_843 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 42 | chr14 | unknown | gene | 13284779 | 13613981 | + | Synpr | Synpr | P6338 | NM_028052 | TSS19863 |
| chr14 | 13664613 | 13664704 | MACS2_peak_843 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 42 | chr14 | unknown | gene | 13670875 | 13682372 | + | Sntn | Sntn | P9407 | NM_177624 | TSS24166 |
| chr14 | 13720454 | 13720545 | MACS2_peak_844 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 56 | chr14 | unknown | gene | 13670875 | 13682372 | + | Sntn | Sntn | P9407 | NM_177624 | TSS24166 |
| chr14 | 13720454 | 13720545 | MACS2_peak_844 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 56 | chr14 | unknown | gene | 13949011 | 13961203 | - | Thoc7 | Thoc7 | P8420 | NM_025435 | TSS15762 |
| chr14 | 14107255 | 14107346 | MACS2_peak_845 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 18 | chr14 | unknown | gene | 14012490 | 14103324 | + | Atxn7 | Atxn7 | P1014 | NM_139227 | TSS11460 |
| chr14 | 14107255 | 14107346 | MACS2_peak_845 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 18 | chr14 | unknown | gene | 14112184 | 14120883 | - | Psmd6 | Psmd6 | P7067 | NM_025550 | TSS17208 |
| chr14 | 15269747 | 15269838 | MACS2_peak_846 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 48 | chr14 | unknown | gene | 14820814 | 15006693 | + | Nek10 | Nek10 | P3062 | NM_001195229 | TSS7645 |
| chr14 | 15269747 | 15269838 | MACS2_peak_846 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 48 | chr14 | unknown | gene | 15357515 | 15438987 | - | Lrrc3b | Lrrc3b | P25307 | NM_146052 | TSS19398 |
| chr14 | 19415708 | 19415936 | MACS2_peak_847 | 498 | + | 7.54634 | 55.92111 | 49.84741 | 143 | chr14 | unknown | gene | 18573576 | 18893627 | - | Ube2e2 | Ube2e2 | P536 | NM_144839 | TSS20629 |
| chr14 | 19415708 | 19415936 | MACS2_peak_847 | 498 | + | 7.54634 | 55.92111 | 49.84741 | 143 | chr14 | unknown | gene | 19594137 | 19602518 | - | Gm5458 | Gm5458 | P15675 | NM_001024706 | TSS8666 |
| chr14 | 19416137 | 19416292 | MACS2_peak_848 | 319 | + | 6.00777 | 37.73015 | 31.91448 | 75 | chr14 | unknown | gene | 18573576 | 18893627 | - | Ube2e2 | Ube2e2 | P536 | NM_144839 | TSS20629 |
| chr14 | 19416137 | 19416292 | MACS2_peak_848 | 319 | + | 6.00777 | 37.73015 | 31.91448 | 75 | chr14 | unknown | gene | 19594137 | 19602518 | - | Gm5458 | Gm5458 | P15675 | NM_001024706 | TSS8666 |
| chr14 | 19416945 | 19417656 | MACS2_peak_849 | 402 | + | 6.74492 | 46.16045 | 40.22018 | 655 | chr14 | unknown | gene | 18573576 | 18893627 | - | Ube2e2 | Ube2e2 | P536 | NM_144839 | TSS20629 |
| chr14 | 19416945 | 19417656 | MACS2_peak_849 | 402 | + | 6.74492 | 46.16045 | 40.22018 | 655 | chr14 | unknown | gene | 19594137 | 19602518 | - | Gm5458 | Gm5458 | P15675 | NM_001024706 | TSS8666 |
| chr14 | 19417772 | 19417920 | MACS2_peak_850 | 629 | + | 8.57778 | 69.13506 | 62.91064 | 72 | chr14 | unknown | gene | 18573576 | 18893627 | - | Ube2e2 | Ube2e2 | P536 | NM_144839 | TSS20629 |
| chr14 | 19417772 | 19417920 | MACS2_peak_850 | 629 | + | 8.57778 | 69.13506 | 62.91064 | 72 | chr14 | unknown | gene | 19594137 | 19602518 | - | Gm5458 | Gm5458 | P15675 | NM_001024706 | TSS8666 |
| chr14 | 19418067 | 19418302 | MACS2_peak_851 | 177 | + | 4.62497 | 23.31333 | 17.79628 | 159 | chr14 | unknown | gene | 18573576 | 18893627 | - | Ube2e2 | Ube2e2 | P536 | NM_144839 | TSS20629 |
| chr14 | 19418067 | 19418302 | MACS2_peak_851 | 177 | + | 4.62497 | 23.31333 | 17.79628 | 159 | chr14 | unknown | gene | 19594137 | 19602518 | - | Gm5458 | Gm5458 | P15675 | NM_001024706 | TSS8666 |
| chr14 | 19418597 | 19418918 | MACS2_peak_852 | 756 | + | 9.5436 | 82.10292 | 75.65164 | 230 | chr14 | unknown | gene | 18573576 | 18893627 | - | Ube2e2 | Ube2e2 | P536 | NM_144839 | TSS20629 |
| chr14 | 19418597 | 19418918 | MACS2_peak_852 | 756 | + | 9.5436 | 82.10292 | 75.65164 | 230 | chr14 | unknown | gene | 19594137 | 19602518 | - | Gm5458 | Gm5458 | P15675 | NM_001024706 | TSS8666 |
| chr14 | 19419313 | 19419418 | MACS2_peak_853 | 206 | + | 4.9252 | 26.21395 | 20.62163 | 32 | chr14 | unknown | gene | 18573576 | 18893627 | - | Ube2e2 | Ube2e2 | P536 | NM_144839 | TSS20629 |
| chr14 | 19419313 | 19419418 | MACS2_peak_853 | 206 | + | 4.9252 | 26.21395 | 20.62163 | 32 | chr14 | unknown | gene | 19594137 | 19602518 | - | Gm5458 | Gm5458 | P15675 | NM_001024706 | TSS8666 |
| chr14 | 19609693 | 19609806 | MACS2_peak_854 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 49 | chr14 | unknown | gene | 19594137 | 19602518 | - | Gm5458 | Gm5458 | P15675 | NM_001024706 | TSS8666 |
| chr14 | 19609693 | 19609806 | MACS2_peak_854 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 49 | chr14 | unknown | gene | 19751256 | 19811196 | + | Nid2 | Nid2 | P14927 | NM_008695 | TSS25929 |
| chr14 | 20387851 | 20387942 | MACS2_peak_855 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 70 | chr14 | unknown | gene | 20348161 | 20382984 | + | Fam149b | Fam149b | P10204 | NM_172379 | TSS23827 |
| chr14 | 20387851 | 20387942 | MACS2_peak_855 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 70 | chr14 | unknown | gene | 20391230 | 20393493 | - | Mrps16 | Mrps16 | P1918 | NM_025440 | TSS25094 |
| chr14 | 20402636 | 20402736 | MACS2_peak_856 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 43 | chr14 | unknown | gene | 20391230 | 20393493 | - | Mrps16 | Mrps16 | P1918 | NM_025440 | TSS25094 |
| chr14 | 20402636 | 20402736 | MACS2_peak_856 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 43 | chr14 | unknown | gene | 20455260 | 20480133 | - | Anxa7 | Anxa7 | P5035 | NM_001110794 | TSS10680 |
| chr14 | 20573749 | 20573860 | MACS2_peak_857 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 90 | chr14 | unknown | gene | 20546292 | 20570680 | + | 1810062O18Rik | 1810062O18Rik | | NR_033571 | TSS4732 |
| chr14 | 20573749 | 20573860 | MACS2_peak_857 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 90 | chr14 | unknown | gene | 20649101 | 20656540 | - | Myoz1 | Myoz1 | P7989 | NM_021508 | TSS19919 |
| chr14 | 21229396 | 21229539 | MACS2_peak_858 | 12 | + | 4.14966 | 5.12722 | 1.204 | 7 | chr14 | unknown | gene | 21033741 | 21052442 | - | Ap3m1 | Ap3m1 | P9766 | NM_018829 | TSS17572 |
| chr14 | 21229396 | 21229539 | MACS2_peak_858 | 12 | + | 4.14966 | 5.12722 | 1.204 | 7 | chr14 | unknown | gene | 21499769 | 21670873 | + | Kat6b | Kat6b | P17156 | NM_001205241 | TSS3965 |
| chr14 | 21356439 | 21356555 | MACS2_peak_859 | 13 | + | 4.52781 | 5.74876 | 1.3392 | 88 | chr14 | unknown | gene | 21033741 | 21052442 | - | Ap3m1 | Ap3m1 | P9766 | NM_018829 | TSS17572 |
| chr14 | 21356439 | 21356555 | MACS2_peak_859 | 13 | + | 4.52781 | 5.74876 | 1.3392 | 88 | chr14 | unknown | gene | 21499769 | 21670873 | + | Kat6b | Kat6b | P17156 | NM_001205241 | TSS3965 |
| chr14 | 21608656 | 21608783 | MACS2_peak_860 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 44 | chr14 | unknown | gene | 21052573 | 21447938 | + | Adk | Adk | P5900 | NM_134079 | TSS25018 |
| chr14 | 21608656 | 21608783 | MACS2_peak_860 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 44 | chr14 | unknown | gene | 21676571 | 21714576 | - | Dupd1 | Dupd1 | P14091 | NM_001013826 | TSS11072 |
| chr14 | 21904455 | 21904546 | MACS2_peak_861 | 12 | + | 4.14966 | 5.12722 | 1.204 | 29 | chr14 | unknown | gene | 21845860 | 21848872 | - | Comtd1 | Comtd1 | P6489 | NM_026965 | TSS8443 |
| chr14 | 21904455 | 21904546 | MACS2_peak_861 | 12 | + | 4.14966 | 5.12722 | 1.204 | 29 | chr14 | unknown | gene | 21983961 | 21989601 | - | Zfp503 | Zfp503 | P17914 | NM_145459 | TSS19708 |
| chr14 | 22760600 | 22760723 | MACS2_peak_862 | 31 | + | 5.69703 | 8.07589 | 3.1286 | 43 | chr14 | unknown | gene | 22507173 | 22542798 | - | 4930405A10Rik | 4930405A10Rik | | NR_046307 | TSS24560 |
| chr14 | 22760600 | 22760723 | MACS2_peak_862 | 31 | + | 5.69703 | 8.07589 | 3.1286 | 43 | chr14 | unknown | gene | 23038194 | 23094571 | - | Gm10248 | Gm10248 | | NR_033550 | TSS6378 |
| chr14 | 23114606 | 23114698 | MACS2_peak_863 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 39 | chr14 | unknown | gene | 23038194 | 23094571 | - | Gm10248 | Gm10248 | | NR_033550 | TSS6378 |
| chr14 | 23114606 | 23114698 | MACS2_peak_863 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 39 | chr14 | unknown | gene | 23298693 | 24004125 | - | Kcnma1 | Kcnma1 | P15064 | NM_001253359 | TSS1266 |
| chr14 | 23131912 | 23132150 | MACS2_peak_864 | 13 | + | 4.55462 | 5.79642 | 1.3392 | 52 | chr14 | unknown | gene | 23038194 | 23094571 | - | Gm10248 | Gm10248 | | NR_033550 | TSS6378 |
| chr14 | 23131912 | 23132150 | MACS2_peak_864 | 13 | + | 4.55462 | 5.79642 | 1.3392 | 52 | chr14 | unknown | gene | 23298693 | 24004125 | - | Kcnma1 | Kcnma1 | P15064 | NM_001253359 | TSS1266 |
| chr14 | 23524196 | 23524300 | MACS2_peak_865 | 26 | + | 5.49828 | 7.51662 | 2.61219 | 74 | chr14 | unknown | gene | 23038194 | 23094571 | - | Gm10248 | Gm10248 | | NR_033550 | TSS6378 |
| chr14 | 23524196 | 23524300 | MACS2_peak_865 | 26 | + | 5.49828 | 7.51662 | 2.61219 | 74 | chr14 | unknown | gene | 24004990 | 24005837 | + | 4930519K11Rik | 4930519K11Rik | | NR_131107 | TSS14904 |
| chr14 | 25047996 | 25048087 | MACS2_peak_866 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 62 | chr14 | unknown | gene | 24490680 | 24495786 | + | Rps24 | Rps24 | P25231 | NM_011297 | TSS6485 |
| chr14 | 25047996 | 25048087 | MACS2_peak_866 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 62 | chr14 | unknown | gene | 25139794 | 25143241 | - | 4930572O13Rik | 4930572O13Rik | | NR_045718 | TSS7710 |
| chr14 | 25222343 | 25222434 | MACS2_peak_867 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 9 | chr14 | unknown | gene | 25139794 | 25143241 | - | 4930572O13Rik | 4930572O13Rik | | NR_045718 | TSS7710 |
| chr14 | 25222343 | 25222434 | MACS2_peak_867 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 9 | chr14 | unknown | gene | 25459184 | 25663047 | + | Zmiz1 | Zmiz1 | P23698 | NM_183208 | TSS19025 |
| chr14 | 26928229 | 26928320 | MACS2_peak_868 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 32 | chr14 | unknown | gene | 26894603 | 26915150 | + | Asb14 | Asb14 | P7836 | NM_080856 | TSS18328 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr14 | 26928229 | 26928320 | MACS2_peak_868 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 32 | chr14 | unknown | gene | 27000361 | 27002104 | + | Hesx1 | Hesx1 | P2942 | NM_010420 | TSS13116 |
| chr14 | 27918589 | 27918680 | MACS2_peak_869 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 9 | chr14 | unknown | gene | 27482404 | 27508432 | - | Ccdc66 | Ccdc66 | P5611 | NM_177111 | TSS10432 |
| chr14 | 27918589 | 27918680 | MACS2_peak_869 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 9 | chr14 | unknown | gene | 28505472 | 28522940 | + | Wnt5a | Wnt5a | P21393 | NM_009524 | TSS26922 |
| chr14 | 28928362 | 28928453 | MACS2_peak_870 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 54 | chr14 | unknown | gene | 28505472 | 28522940 | + | Wnt5a | Wnt5a | P21393 | NM_009524 | TSS26922 |
| chr14 | 28928362 | 28928453 | MACS2_peak_870 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 54 | chr14 | unknown | gene | 29018207 | 29027754 | + | Lrtm1 | Lrtm1 | P8996 | NM_176920 | TSS18187 |
| chr14 | 30055862 | 30055987 | MACS2_peak_871 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 81 | chr14 | unknown | gene | 30008999 | 30036890 | + | Chdh | Chdh | P7190 | NM_001136240 | TSS11125 |
| chr14 | 30055862 | 30055987 | MACS2_peak_871 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 81 | chr14 | unknown | gene | 30458035 | 30463282 | + | 4831407H17Rik | 4831407H17Rik | | NR_131095 | TSS10727 |
| chr14 | 30723088 | 30723179 | MACS2_peak_872 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 20 | chr14 | unknown | gene | 30654374 | 30690609 | + | Rft1 | Rft1 | P20893 | NM_177815 | TSS19578 |
| chr14 | 30723088 | 30723179 | MACS2_peak_872 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 20 | chr14 | unknown | gene | 30825593 | 30874476 | + | Tmem110 | Tmem110 | P10705 | NM_028839 | TSS15682 |
| chr14 | 32277350 | 32277441 | MACS2_peak_873 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 9 | chr14 | unknown | gene | 32180165 | 32201748 | - | Timm23 | Timm23 | P15882 | NM_016897 | TSS4810 |
| chr14 | 32277350 | 32277441 | MACS2_peak_873 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 9 | chr14 | unknown | gene | 32322018 | 32347629 | + | Ogdhl | Ogdhl | P14087 | NM_001081130 | TSS11329 |
| chr14 | 32950687 | 32950843 | MACS2_peak_874 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 77 | chr14 | unknown | gene | 32856755 | 32937862 | + | Vstm4 | Vstm4 | P12793 | NM_178791 | TSS8912 |
| chr14 | 32950687 | 32950843 | MACS2_peak_874 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 77 | chr14 | unknown | gene | 32959546 | 33185066 | - | Wdfy4 | Wdfy4 | P10087 | NM_001146022 | TSS13151 |
| chr14 | 33199481 | 33199648 | MACS2_peak_875 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 90 | chr14 | unknown | gene | 32959546 | 33185066 | - | Wdfy4 | Wdfy4 | P10087 | NM_001146022 | TSS13151 |
| chr14 | 33199481 | 33199648 | MACS2_peak_875 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 90 | chr14 | unknown | gene | 33216822 | 33369578 | + | Arhgap22 | Arhgap22 | P26871 | NM_153800 | TSS4897 |
| chr14 | 33826405 | 33826515 | MACS2_peak_876 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 58 | chr14 | unknown | gene | 33808071 | 33811283 | - | 4930503F20Rik | 4930503F20Rik | | NR_131113 | TSS18503 |
| chr14 | 33826405 | 33826515 | MACS2_peak_876 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 58 | chr14 | unknown | gene | 33923586 | 33934513 | + | Gdf10 | Gdf10 | P20366 | NM_145741 | TSS14967 |
| chr14 | 34540524 | 34540615 | MACS2_peak_877 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 18 | chr14 | unknown | gene | 34511620 | 34522735 | - | 9230112D13Rik | 9230112D13Rik | P2953 | NM_030062 | TSS27249 |
| chr14 | 34540524 | 34540615 | MACS2_peak_877 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 18 | chr14 | unknown | gene | 34590617 | 34599958 | - | Opn4 | Opn4 | P20740 | NM_001128599 | TSS26188 |
| chr14 | 38257210 | 38257301 | MACS2_peak_878 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 44 | chr14 | unknown | gene | 37120444 | 37135322 | - | Ghitm | Ghitm | P21455 | NM_078478 | TSS4885 |
| chr14 | 38257210 | 38257301 | MACS2_peak_878 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 44 | chr14 | unknown | gene | 38368950 | 39472800 | - | Nrg3 | Nrg3 | P5266 | NM_001190187 | TSS8322 |
| chr14 | 40899522 | 40899613 | MACS2_peak_879 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 19 | chr14 | unknown | gene | 40815867 | 40892965 | - | Sh2d4b | Sh2d4b | P8339 | NM_177816 | TSS22227 |
| chr14 | 40899522 | 40899613 | MACS2_peak_879 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 19 | chr14 | unknown | gene | 40906443 | 40966807 | - | Tspan14 | Tspan14 | P22268 | NM_145928 | TSS10406 |
| chr14 | 40959426 | 40959517 | MACS2_peak_880 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 36 | chr14 | unknown | gene | 40815867 | 40892965 | - | Sh2d4b | Sh2d4b | P8339 | NM_177816 | TSS22227 |
| chr14 | 40959426 | 40959517 | MACS2_peak_880 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 36 | chr14 | unknown | gene | 40993739 | 41013775 | - | Fam213a | Fam213a | P18355 | NM_027464 | TSS15970 |
| chr14 | 41009959 | 41010054 | MACS2_peak_881 | 41 | + | 6.38524 | 9.20923 | 4.16094 | 54 | chr14 | unknown | gene | 40906443 | 40966807 | - | Tspan14 | Tspan14 | P22268 | NM_145928 | TSS10406 |
| chr14 | 41009959 | 41010054 | MACS2_peak_881 | 41 | + | 6.38524 | 9.20923 | 4.16094 | 54 | chr14 | unknown | gene | 41049208 | 41069074 | - | Dydc2 | Dydc2 | P10721 | NM_027717 | TSS9924 |
| chr14 | 41718703 | 41718794 | MACS2_peak_882 | 24 | + | 5.43036 | 7.38735 | 2.49399 | 22 | chr14 | unknown | gene | 41172211 | 41185198 | - | Sftpd | Sftpd | P18211 | NM_009160 | TSS12482 |
| chr14 | 41718703 | 41718794 | MACS2_peak_882 | 24 | + | 5.43036 | 7.38735 | 2.49399 | 22 | chr14 | unknown | gene | 41767171 | 43015568 | - | Gm10377 | Gm10377 | P19126 | NM_001244671 | TSS23453 |
| chr14 | 42176188 | 42176320 | MACS2_peak_883 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 46 | chr14 | unknown | gene | 42089749 | 42095277 | - | 1700091H14Rik | 1700091H14Rik | | NR_073362 | TSS7166 |
| chr14 | 42176188 | 42176320 | MACS2_peak_883 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 46 | chr14 | unknown | gene | 42254658 | 42260048 | - | Gm17026 | Gm17026 | | NR_105055 | TSS27135 |
| chr14 | 45269727 | 45269818 | MACS2_peak_884 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 37 | chr14 | unknown | gene | 45134447 | 45219394 | - | Txndc16 | Txndc16 | P11884 | NM_172597 | TSS22921 |
| chr14 | 45269727 | 45269818 | MACS2_peak_884 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 37 | chr14 | unknown | gene | 45283086 | 45318490 | - | Ero1l | Ero1l | P1482 | NM_015774 | TSS15969 |
| chr14 | 45390129 | 45390220 | MACS2_peak_885 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 48 | chr14 | unknown | gene | 45376420 | 45388796 | - | Gnpnat1 | Gnpnat1 | P25785 | NM_019425 | TSS12001 |
| chr14 | 45390129 | 45390220 | MACS2_peak_885 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 48 | chr14 | unknown | gene | 45458791 | 45530065 | - | Fermt2 | Fermt2 | P15621 | NM_146054 | TSS6596 |
| chr14 | 45487490 | 45487581 | MACS2_peak_886 | 12 | + | 4.14966 | 5.12722 | 1.204 | 3 | chr14 | unknown | gene | 45376420 | 45388796 | - | Gnpnat1 | Gnpnat1 | P25785 | NM_019425 | TSS12001 |
| chr14 | 45487490 | 45487581 | MACS2_peak_886 | 12 | + | 4.14966 | 5.12722 | 1.204 | 3 | chr14 | unknown | gene | 45543709 | 45562876 | + | 4930527F14Rik | 4930527F14Rik | | NR_045809 | TSS14936 |
| chr14 | 45542981 | 45543072 | MACS2_peak_887 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 49 | chr14 | unknown | gene | 45458791 | 45530065 | - | Fermt2 | Fermt2 | P15621 | NM_146054 | TSS6596 |
| chr14 | 45542981 | 45543072 | MACS2_peak_887 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 49 | chr14 | unknown | gene | 45543709 | 45562876 | + | 4930527F14Rik | 4930527F14Rik | | NR_045809 | TSS14936 |
| chr14 | 46079083 | 46079174 | MACS2_peak_888 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 23 | chr14 | unknown | gene | 45657960 | 45658053 | - | Mir5131 | Mir5131 | | NR_039593 | TSS15012 |
| chr14 | 46079083 | 46079174 | MACS2_peak_888 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 23 | chr14 | unknown | gene | 46379523 | 46383606 | + | Gm15217 | Gm15217 | | NR_037981 | TSS24832 |
| chr14 | 46165065 | 46165156 | MACS2_peak_889 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 42 | chr14 | unknown | gene | 45657960 | 45658053 | - | Mir5131 | Mir5131 | | NR_039593 | TSS15012 |
| chr14 | 46165065 | 46165156 | MACS2_peak_889 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 42 | chr14 | unknown | gene | 46379523 | 46383606 | + | Gm15217 | Gm15217 | | NR_037981 | TSS24832 |
| chr14 | 46707744 | 46707835 | MACS2_peak_890 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 16 | chr14 | unknown | gene | 46645816 | 46673775 | - | D330046F09Rik | D330046F09Rik | | NR_131909 | TSS11649 |
| chr14 | 46707744 | 46707835 | MACS2_peak_890 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 16 | chr14 | unknown | gene | 46760540 | 46771487 | + | Cdkn3 | Cdkn3 | P6743 | NM_028222 | TSS15281 |
| chr14 | 46712034 | 46712125 | MACS2_peak_891 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 12 | chr14 | unknown | gene | 46645816 | 46673775 | - | D330046F09Rik | D330046F09Rik | | NR_131909 | TSS11649 |
| chr14 | 46712034 | 46712125 | MACS2_peak_891 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 12 | chr14 | unknown | gene | 46760540 | 46771487 | + | Cdkn3 | Cdkn3 | P6743 | NM_028222 | TSS15281 |
| chr14 | 46835143 | 46835276 | MACS2_peak_892 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 88 | chr14 | unknown | gene | 46808148 | 46822103 | - | Gmfb | Gmfb | P21211 | NM_022023 | TSS14390 |
| chr14 | 46835143 | 46835276 | MACS2_peak_892 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 88 | chr14 | unknown | gene | 46882964 | 47101459 | + | Samd4 | Samd4 | P10720 | NM_001037221 | TSS12127 |
| chr14 | 47712068 | 47712159 | MACS2_peak_893 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 40 | chr14 | unknown | gene | 47540892 | 47568406 | - | Atg14 | Atg14 | P8843 | NM_172599 | TSS4636 |
| chr14 | 47712068 | 47712159 | MACS2_peak_893 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 40 | chr14 | unknown | gene | 47898863 | 47944189 | + | 4930447J18Rik | 4930447J18Rik | | NR_045959 | TSS4050 |
| chr14 | 48265550 | 48265641 | MACS2_peak_894 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 8 | chr14 | unknown | gene | 48120868 | 48256582 | + | Peli2 | Peli2 | P5515 | NM_033602 | TSS22144 |
| chr14 | 48265550 | 48265641 | MACS2_peak_894 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 8 | chr14 | unknown | gene | 48446351 | 48512157 | + | Tmem260 | Tmem260 | P19074 | NM_172600 | TSS10739 |
| chr14 | 54375524 | 54375615 | MACS2_peak_895 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 15 | chr14 | unknown | gene | 54360840 | 54368451 | + | Oxa1l | Oxa1l | P10213 | NM_026936 | TSS20915 |
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| chr14 | 54575959 | 54576050 | MACS2_peak_896 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 39 | chr14 | unknown | gene | 54541784 | 54554361 | - | Haus4 | Haus4 | P13954 | NM_145462 | TSS20455 |
| chr14 | 54575959 | 54576050 | MACS2_peak_896 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 39 | chr14 | unknown | gene | 54583662 | 54605908 | - | 4931414P19Rik | 4931414P19Rik | P16635 | NM_028890 | TSS22442 |
| chr14 | 58611332 | 58611423 | MACS2_peak_897 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 6 | chr14 | unknown | gene | 58072685 | 58109578 | + | Fgf9 | Fgf9 | P11918 | NM_013518 | TSS5958 |

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr14 | 58611332 | 58611423 | MACS2_peak_897 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 6 | chr14 | unknown | gene | 59133039 | 59142847 | - | 1700129C05Rik | 1700129C05Rik | P5046 | NM_026461 | TSS26632 |
| chr14 | 59030078 | 59030169 | MACS2_peak_898 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 64 | chr14 | unknown | gene | 58072685 | 58109578 | + | Fgf9 | Fgf9 | P11918 | NM_013518 | TSS5958 |
| chr14 | 59030078 | 59030169 | MACS2_peak_898 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 64 | chr14 | unknown | gene | 59133039 | 59142847 | - | 1700129C05Rik | 1700129C05Rik | P5046 | NM_026461 | TSS26632 |
| chr14 | 59602439 | 59602530 | MACS2_peak_899 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 19 | chr14 | unknown | gene | 59559387 | 59597836 | - | Cdadc1 | Cdadc1 | P11682 | NM_001168535 | TSS5717 |
| chr14 | 59602439 | 59602530 | MACS2_peak_899 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 19 | chr14 | unknown | gene | 59625280 | 59630188 | + | Shisa2 | Shisa2 | P20996 | NM_145463 | TSS45 |
| chr14 | 61139133 | 61139224 | MACS2_peak_900 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 47 | chr14 | unknown | gene | 60963833 | 61046855 | - | Tnfrsf19 | Tnfrsf19 | P15270 | NM_001164155 | TSS2274 |
| chr14 | 61139133 | 61139224 | MACS2_peak_900 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 47 | chr14 | unknown | gene | 61219114 | 61258490 | - | Sgcg | Sgcg | P12281 | NM_011892 | TSS26531 |
| chr14 | 61259240 | 61259475 | MACS2_peak_901 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 58 | chr14 | unknown | gene | 61219114 | 61258490 | - | Sgcg | Sgcg | P12281 | NM_011892 | TSS26531 |
| chr14 | 61259240 | 61259475 | MACS2_peak_901 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 58 | chr14 | unknown | gene | 61292982 | 61305334 | - | 1700109G14Rik | 1700109G14Rik | | NR_033788 | TSS22956 |
| chr14 | 61950009 | 61950134 | MACS2_peak_902 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 48 | chr14 | unknown | gene | 61602835 | 61682373 | - | Dleu2 | Dleu2 | | NR_028264 | TSS18600 |
| chr14 | 61950009 | 61950134 | MACS2_peak_902 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 48 | chr14 | unknown | gene | 62276228 | 62292950 | - | Dleu7 | Dleu7 | P18486 | NM_173419 | TSS2123 |
| chr14 | 63154376 | 63154467 | MACS2_peak_903 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 77 | chr14 | unknown | gene | 63122461 | 63142329 | + | Ctsb | Ctsb | P15246 | NM_007798 | TSS22668 |
| chr14 | 63154376 | 63154467 | MACS2_peak_903 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 77 | chr14 | unknown | gene | 63182444 | 63193525 | - | Neil2 | Neil2 | P25716 | NM_201610 | TSS536 |
| chr14 | 63457346 | 63457437 | MACS2_peak_904 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 20 | chr14 | unknown | gene | 63372836 | 63417187 | - | Blk | Blk | P2481 | NM_007549 | TSS22246 |
| chr14 | 63457346 | 63457437 | MACS2_peak_904 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 20 | chr14 | unknown | gene | 63492346 | 63509092 | - | Tdh | Tdh | P18821 | NM_021480 | TSS21421 |
| chr14 | 64809272 | 64809363 | MACS2_peak_905 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 19 | chr14 | unknown | gene | 64652530 | 64806296 | + | Kif13b | Kif13b | P16782 | NM_001081177 | TSS7779 |
| chr14 | 64809272 | 64809363 | MACS2_peak_905 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 19 | chr14 | unknown | gene | 64822217 | 64949847 | - | Hmbox1 | Hmbox1 | P1859 | NM_177338 | TSS13063 |
| chr14 | 66725784 | 66725875 | MACS2_peak_906 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 48 | chr14 | unknown | gene | 66344374 | 66361134 | + | Stmn4 | Stmn4 | P14261 | NM_019675 | TSS19000 |
| chr14 | 66725784 | 66725875 | MACS2_peak_906 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 48 | chr14 | unknown | gene | 66802863 | 66868368 | - | Dpysl2 | Dpysl2 | P5271 | NM_009955 | TSS20849 |
| chr14 | 66869981 | 66870072 | MACS2_peak_907 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 47 | chr14 | unknown | gene | 66868849 | 66869443 | + | Gm5464 | Gm5464 | P26392 | NM_001034881 | TSS436 |
| chr14 | 66869981 | 66870072 | MACS2_peak_907 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 47 | chr14 | unknown | gene | 66911207 | 66917226 | + | Pnma2 | Pnma2 | P12165 | NM_175498 | TSS17155 |
| chr14 | 67061267 | 67061389 | MACS2_peak_908 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 45 | chr14 | unknown | gene | 66985239 | 67008784 | - | Bnip3l | Bnip3l | P1113 | NM_009761 | TSS24941 |
| chr14 | 67061267 | 67061389 | MACS2_peak_908 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 45 | chr14 | unknown | gene | 67233291 | 67428122 | + | Ebf2 | Ebf2 | P13855 | NM_001276387 | TSS9776 |
| chr14 | 67586794 | 67586885 | MACS2_peak_909 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 51 | chr14 | unknown | gene | 67233291 | 67428122 | + | Ebf2 | Ebf2 | P13855 | NM_001276387 | TSS9776 |
| chr14 | 67586794 | 67586885 | MACS2_peak_909 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 51 | chr14 | unknown | gene | 67676353 | 67715841 | - | Cdca2 | Cdca2 | P20992 | NM_175384 | TSS25377 |
| chr14 | 68317424 | 68317515 | MACS2_peak_910 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 23 | chr14 | unknown | gene | 68123751 | 68131371 | + | A230070E04Rik | A230070E04Rik | | NR_045897 | TSS12270 |
| chr14 | 68317424 | 68317515 | MACS2_peak_910 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 23 | chr14 | unknown | gene | 68497336 | 68533675 | - | Adam7 | Adam7 | P17002 | NM_007402 | TSS7995 |
| chr14 | 68591447 | 68591603 | MACS2_peak_911 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 51 | chr14 | unknown | gene | 68563386 | 68582046 | - | Adamdec1 | Adamdec1 | P23046 | NM_021475 | TSS26955 |
| chr14 | 68591447 | 68591603 | MACS2_peak_911 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 51 | chr14 | unknown | gene | 68604997 | 68655690 | - | Adam28 | Adam28 | | NR_102399 | TSS3398 |
| chr14 | 68819844 | 68820008 | MACS2_peak_912 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 51 | chr14 | unknown | gene | 68604997 | 68655690 | - | Adam28 | Adam28 | | NR_102399 | TSS3398 |
| chr14 | 68819844 | 68820008 | MACS2_peak_912 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 51 | chr14 | unknown | gene | 69029288 | 69038503 | + | Stc1 | Stc1 | P22489 | NM_009285 | TSS5686 |
| chr14 | 68948832 | 68948923 | MACS2_peak_913 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 30 | chr14 | unknown | gene | 68604997 | 68655690 | - | Adam28 | Adam28 | | NR_102399 | TSS3398 |
| chr14 | 68948832 | 68948923 | MACS2_peak_913 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 30 | chr14 | unknown | gene | 69029288 | 69038503 | + | Stc1 | Stc1 | P22489 | NM_009285 | TSS5686 |
| chr14 | 69231150 | 69231241 | MACS2_peak_914 | 7 | + | 3.39397 | 3.87422 | 0.75855 | 64 | chr14 | unknown | gene | 69190691 | 69192248 | + | Nkx3-1 | Nkx3-1 | P18628 | NM_010921 | TSS2408 |
| chr14 | 69231150 | 69231241 | MACS2_peak_914 | 7 | + | 3.39397 | 3.87422 | 0.75855 | 64 | chr14 | unknown | gene | 69241850 | 69284941 | - | Slc25a37 | Slc25a37 | P12258 | NM_026331 | TSS4878 |
| chr14 | 70748029 | 70748149 | MACS2_peak_915 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 75 | chr14 | unknown | gene | 70647301 | 70653084 | - | Npm2 | Npm2 | P1553 | NM_181345 | TSS2322 |
| chr14 | 70748029 | 70748149 | MACS2_peak_915 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 75 | chr14 | unknown | gene | 70774380 | 70778073 | + | Dok2 | Dok2 | P21410 | NM_010071 | TSS10177 |
| chr14 | 72603371 | 72603462 | MACS2_peak_916 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 51 | chr14 | unknown | gene | 71856708 | 71920438 | + | 4930434J06Rik | 4930434J06Rik | | NR_046274 | TSS3268 |
| chr14 | 72603371 | 72603462 | MACS2_peak_916 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 51 | chr14 | unknown | gene | 73025602 | 73026890 | + | Gm9199 | Gm9199 | | NR_027860 | TSS8021 |
| chr14 | 74996979 | 74997070 | MACS2_peak_917 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 41 | chr14 | unknown | gene | 74975085 | 74987104 | + | Gm4278 | Gm4278 | | NR_046078 | TSS20122 |
| chr14 | 74996979 | 74997070 | MACS2_peak_917 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 41 | chr14 | unknown | gene | 75004109 | 75388146 | - | Mir466f-3 | Mir466f-3 | | NR_030568 | TSS13076 |
| chr14 | 75050155 | 75050246 | MACS2_peak_918 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 5 | chr14 | unknown | gene | 52069314 | 75001122 | + | Snord58b | Snord58b | | NR_028552 | TSS22879 |
| chr14 | 75050155 | 75050246 | MACS2_peak_918 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 5 | chr14 | unknown | gene | 75084302 | 75130883 | - | Lrrc63 | Lrrc63 | P21550 | NM_027581 | TSS25720 |
| chr14 | 76147019 | 76147138 | MACS2_peak_919 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 89 | chr14 | unknown | gene | 76110890 | 76134902 | + | Nufip1 | Nufip1 | P9239 | NM_013745 | TSS22142 |
| chr14 | 76147019 | 76147138 | MACS2_peak_919 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 89 | chr14 | unknown | gene | 76415820 | 76506674 | + | Tsc22d1 | Tsc22d1 | P20917 | NM_207652 | TSS19275 |
| chr14 | 77358085 | 77358179 | MACS2_peak_920 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 18 | chr14 | unknown | gene | 77036771 | 77111604 | + | Ccdc122 | Ccdc122 | P11390 | NM_175369 | TSS15016 |
| chr14 | 77358085 | 77358179 | MACS2_peak_920 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 18 | chr14 | unknown | gene | 77479482 | 77506868 | - | Gm6994 | Gm6994 | | NR_033141 | TSS13834 |
| chr14 | 77747093 | 77747184 | MACS2_peak_921 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 38 | chr14 | unknown | gene | 77156762 | 77720944 | + | Enox1 | Enox1 | P18427 | NM_172813 | TSS26326 |
| chr14 | 77747093 | 77747184 | MACS2_peak_921 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 38 | chr14 | unknown | gene | 77793944 | 77798864 | - | Gm1587 | Gm1587 | P22965 | NM_001033440 | TSS3975 |
| chr14 | 78086679 | 78086770 | MACS2_peak_922 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 41 | chr14 | unknown | gene | 77904238 | 78001979 | + | Epsti1 | Epsti1 | P13172 | NM_029495 | TSS5187 |
| chr14 | 78086679 | 78086770 | MACS2_peak_922 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 41 | chr14 | unknown | gene | 78191372 | 78191478 | - | Mir1971 | Mir1971 | | NR_035499 | TSS18743 |
| chr14 | 78237382 | 78237501 | MACS2_peak_923 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 83 | chr14 | unknown | gene | 78191372 | 78191478 | - | Mir1971 | Mir1971 | | NR_035499 | TSS18743 |
| chr14 | 78237382 | 78237501 | MACS2_peak_923 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 83 | chr14 | unknown | gene | 78277445 | 78307889 | - | Tnfsf11 | Tnfsf11 | P10991 | NM_011613 | TSS2491 |
| chr14 | 80566008 | 80566099 | MACS2_peak_924 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 71 | chr14 | unknown | gene | 80000301 | 80021930 | + | Olfm4 | Olfm4 | P6447 | NM_001030294 | TSS3303 |
| chr14 | 80566008 | 80566099 | MACS2_peak_924 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 71 | chr14 | unknown | gene | 84443562 | 84533557 | + | Pcdh17 | Pcdh17 | P25816 | NM_001013753 | TSS21832 |
| chr14 | 81190044 | 81190135 | MACS2_peak_925 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 69 | chr14 | unknown | gene | 80000301 | 80021930 | + | Olfm4 | Olfm4 | P6447 | NM_001030294 | TSS3303 |
| chr14 | 81190044 | 81190135 | MACS2_peak_925 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 69 | chr14 | unknown | gene | 84443562 | 84533557 | + | Pcdh17 | Pcdh17 | P25816 | NM_001013753 | TSS21832 |
| chr14 | 81808266 | 81808357 | MACS2_peak_926 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 24 | chr14 | unknown | gene | 80000301 | 80021930 | + | Olfm4 | Olfm4 | P6447 | NM_001030294 | TSS3303 |

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr14 | 81808266 | 81808357 | MACS2_peak_926 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 24 | chr14 | unknown | gene | 84443562 | 84533557 | + | Pcdh17 | Pcdh17 | P25816 | NM_001013753 | TSS21832 |
| chr14 | 82032489 | 82032621 | MACS2_peak_927 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 57 | chr14 | unknown | gene | 80000301 | 80021930 | + | Olfm4 | Olfm4 | P6447 | NM_001030294 | TSS3303 |
| chr14 | 82032489 | 82032621 | MACS2_peak_927 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 57 | chr14 | unknown | gene | 84443562 | 84533557 | + | Pcdh17 | Pcdh17 | P25816 | NM_001013753 | TSS21832 |
| chr14 | 83055042 | 83055133 | MACS2_peak_928 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 12 | chr14 | unknown | gene | 80000301 | 80021930 | + | Olfm4 | Olfm4 | P6447 | NM_001030294 | TSS3303 |
| chr14 | 83055042 | 83055133 | MACS2_peak_928 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 12 | chr14 | unknown | gene | 84443562 | 84533557 | + | Pcdh17 | Pcdh17 | P25816 | NM_001013753 | TSS21832 |
| chr14 | 84886720 | 84886811 | MACS2_peak_929 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 8 | chr14 | unknown | gene | 84443562 | 84533557 | + | Pcdh17 | Pcdh17 | P25816 | NM_001013753 | TSS21832 |
| chr14 | 84886720 | 84886811 | MACS2_peak_929 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 8 | chr14 | unknown | gene | 86245969 | 86262042 | + | 4930529K09Rik | 4930529K09Rik | | NR_040457 | TSS5832 |
| chr14 | 84955820 | 84955911 | MACS2_peak_930 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 24 | chr14 | unknown | gene | 84443562 | 84533557 | + | Pcdh17 | Pcdh17 | P25816 | NM_001013753 | TSS21832 |
| chr14 | 84955820 | 84955911 | MACS2_peak_930 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 24 | chr14 | unknown | gene | 86245969 | 86262042 | + | 4930529K09Rik | 4930529K09Rik | | NR_040457 | TSS5832 |
| chr14 | 84994572 | 84994663 | MACS2_peak_931 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 55 | chr14 | unknown | gene | 84443562 | 84533557 | + | Pcdh17 | Pcdh17 | P25816 | NM_001013753 | TSS21832 |
| chr14 | 84994572 | 84994663 | MACS2_peak_931 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 55 | chr14 | unknown | gene | 86245969 | 86262042 | + | 4930529K09Rik | 4930529K09Rik | | NR_040457 | TSS5832 |
| chr14 | 85945074 | 85945278 | MACS2_peak_932 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 40 | chr14 | unknown | gene | 84443562 | 84533557 | + | Pcdh17 | Pcdh17 | P25816 | NM_001013753 | TSS21832 |
| chr14 | 85945074 | 85945278 | MACS2_peak_932 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 40 | chr14 | unknown | gene | 86245969 | 86262042 | + | 4930529K09Rik | 4930529K09Rik | | NR_040457 | TSS5832 |
| chr14 | 86207818 | 86207924 | MACS2_peak_933 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 89 | chr14 | unknown | gene | 84443562 | 84533557 | + | Pcdh17 | Pcdh17 | P25816 | NM_001013753 | TSS21832 |
| chr14 | 86207818 | 86207924 | MACS2_peak_933 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 89 | chr14 | unknown | gene | 86245969 | 86262042 | + | 4930529K09Rik | 4930529K09Rik | | NR_040457 | TSS5832 |
| chr14 | 86427263 | 86427354 | MACS2_peak_934 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 74 | chr14 | unknown | gene | 86245969 | 86262042 | + | 4930529K09Rik | 4930529K09Rik | | NR_040457 | TSS5832 |
| chr14 | 86427263 | 86427354 | MACS2_peak_934 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 74 | chr14 | unknown | gene | 86656322 | 87141114 | - | Diap3 | Diap3 | P15021 | NM_019670 | TSS11048 |
| chr14 | 86730160 | 86730312 | MACS2_peak_935 | 7 | + | 3.39397 | 3.87422 | 0.75855 | 40 | chr14 | unknown | gene | 86245969 | 86262042 | + | 4930529K09Rik | 4930529K09Rik | | NR_040457 | TSS5832 |
| chr14 | 86730160 | 86730312 | MACS2_peak_935 | 7 | + | 3.39397 | 3.87422 | 0.75855 | 40 | chr14 | unknown | gene | 87416582 | 87545508 | + | Tdrd3 | Tdrd3 | P2319 | NM_001253755 | TSS10078 |
| chr14 | 86779023 | 86779170 | MACS2_peak_936 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 77 | chr14 | unknown | gene | 86245969 | 86262042 | + | 4930529K09Rik | 4930529K09Rik | | NR_040457 | TSS5832 |
| chr14 | 86779023 | 86779170 | MACS2_peak_936 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 77 | chr14 | unknown | gene | 87416582 | 87545508 | + | Tdrd3 | Tdrd3 | P2319 | NM_001253755 | TSS10078 |
| chr14 | 87017878 | 87018015 | MACS2_peak_937 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 48 | chr14 | unknown | gene | 86245969 | 86262042 | + | 4930529K09Rik | 4930529K09Rik | | NR_040457 | TSS5832 |
| chr14 | 87017878 | 87018015 | MACS2_peak_937 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 48 | chr14 | unknown | gene | 87416582 | 87545508 | + | Tdrd3 | Tdrd3 | P2319 | NM_001253755 | TSS10078 |
| chr14 | 89196230 | 89196321 | MACS2_peak_938 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 12 | chr14 | unknown | gene | 88464746 | 88471396 | - | Pcdh20 | Pcdh20 | P4044 | NM_178685 | TSS7345 |
| chr14 | 89196230 | 89196321 | MACS2_peak_938 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 12 | chr14 | unknown | gene | 89896223 | 89899447 | + | Gm5088 | Gm5088 | | NR_002862 | TSS13589 |
| chr14 | 89940970 | 89941061 | MACS2_peak_939 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 23 | chr14 | unknown | gene | 89896223 | 89899447 | + | Gm5088 | Gm5088 | | NR_002862 | TSS13589 |
| chr14 | 89940970 | 89941061 | MACS2_peak_939 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 23 | chr14 | unknown | gene | 90126890 | 90269760 | + | 4930474H20Rik | 4930474H20Rik | | NR_045712 | TSS3637 |
| chr14 | 90221173 | 90221264 | MACS2_peak_940 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 43 | chr14 | unknown | gene | 89896223 | 89899447 | + | Gm5088 | Gm5088 | | NR_002862 | TSS13589 |
| chr14 | 90221173 | 90221264 | MACS2_peak_940 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 43 | chr14 | unknown | gene | 93013699 | 93890122 | - | Pcdh9 | Pcdh9 | P14449 | NM_001271800 | TSS20824 |
| chr14 | 90235556 | 90235647 | MACS2_peak_941 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 8 | chr14 | unknown | gene | 89896223 | 89899447 | + | Gm5088 | Gm5088 | | NR_002862 | TSS13589 |
| chr14 | 90235556 | 90235647 | MACS2_peak_941 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 8 | chr14 | unknown | gene | 93013699 | 93890122 | - | Pcdh9 | Pcdh9 | P14449 | NM_001271800 | TSS20824 |
| chr14 | 92324980 | 92325071 | MACS2_peak_942 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 28 | chr14 | unknown | gene | 90126890 | 90269760 | + | 4930474H20Rik | 4930474H20Rik | | NR_045712 | TSS3637 |
| chr14 | 92324980 | 92325071 | MACS2_peak_942 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 28 | chr14 | unknown | gene | 93013699 | 93890122 | - | Pcdh9 | Pcdh9 | P14449 | NM_001271800 | TSS20824 |
| chr14 | 93244249 | 93244347 | MACS2_peak_943 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 48 | chr14 | unknown | gene | 90126890 | 90269760 | + | 4930474H20Rik | 4930474H20Rik | | NR_045712 | TSS3637 |
| chr14 | 93244249 | 93244347 | MACS2_peak_943 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 48 | chr14 | unknown | gene | 95881265 | 95882633 | + | 4921530L21Rik | 4921530L21Rik | P26368 | NM_025733 | TSS10909 |
| chr14 | 93885342 | 93885433 | MACS2_peak_944 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 79 | chr14 | unknown | gene | 90126890 | 90269760 | + | 4930474H20Rik | 4930474H20Rik | | NR_045712 | TSS3637 |
| chr14 | 93885342 | 93885433 | MACS2_peak_944 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 79 | chr14 | unknown | gene | 95881265 | 95882633 | + | 4921530L21Rik | 4921530L21Rik | P26368 | NM_025733 | TSS10909 |
| chr14 | 95016599 | 95016690 | MACS2_peak_945 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 33 | chr14 | unknown | gene | 93013699 | 93890122 | - | Pcdh9 | Pcdh9 | P14449 | NM_001271800 | TSS20824 |
| chr14 | 95016599 | 95016690 | MACS2_peak_945 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 33 | chr14 | unknown | gene | 95881265 | 95882633 | + | 4921530L21Rik | 4921530L21Rik | P26368 | NM_025733 | TSS10909 |
| chr14 | 95662463 | 95662554 | MACS2_peak_946 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 84 | chr14 | unknown | gene | 93013699 | 93890122 | - | Pcdh9 | Pcdh9 | P14449 | NM_001271800 | TSS20824 |
| chr14 | 95662463 | 95662554 | MACS2_peak_946 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 84 | chr14 | unknown | gene | 95881265 | 95882633 | + | 4921530L21Rik | 4921530L21Rik | P26368 | NM_025733 | TSS10909 |
| chr14 | 95853269 | 95853420 | MACS2_peak_947 | 49 | + | 6.77503 | 10.04021 | 4.94691 | 69 | chr14 | unknown | gene | 93013699 | 93890122 | - | Pcdh9 | Pcdh9 | P14449 | NM_001271800 | TSS20824 |
| chr14 | 95853269 | 95853420 | MACS2_peak_947 | 49 | + | 6.77503 | 10.04021 | 4.94691 | 69 | chr14 | unknown | gene | 95881265 | 95882633 | + | 4921530L21Rik | 4921530L21Rik | P26368 | NM_025733 | TSS10909 |
| chr14 | 96574343 | 96574456 | MACS2_peak_948 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 77 | chr14 | unknown | gene | 96105264 | 96518317 | - | Klhl1 | Klhl1 | P4730 | NM_053105 | TSS12228 |
| chr14 | 96574343 | 96574456 | MACS2_peak_948 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 77 | chr14 | unknown | gene | 97786845 | 98169309 | - | Dach1 | Dach1 | P3523 | NM_001038610 | TSS14743 |
| chr14 | 97052474 | 97052565 | MACS2_peak_949 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 67 | chr14 | unknown | gene | 96105264 | 96518317 | - | Klhl1 | Klhl1 | P4730 | NM_053105 | TSS12228 |
| chr14 | 97052474 | 97052565 | MACS2_peak_949 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 67 | chr14 | unknown | gene | 97786845 | 98169309 | - | Dach1 | Dach1 | P3523 | NM_001038610 | TSS14743 |
| chr14 | 97138149 | 97138240 | MACS2_peak_950 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 40 | chr14 | unknown | gene | 96105264 | 96518317 | - | Klhl1 | Klhl1 | P4730 | NM_053105 | TSS12228 |
| chr14 | 97138149 | 97138240 | MACS2_peak_950 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 40 | chr14 | unknown | gene | 97786845 | 98169309 | - | Dach1 | Dach1 | P3523 | NM_001038610 | TSS14743 |
| chr14 | 97333333 | 97333424 | MACS2_peak_951 | 12 | + | 4.14966 | 5.12722 | 1.204 | 77 | chr14 | unknown | gene | 96105264 | 96518317 | - | Klhl1 | Klhl1 | P4730 | NM_053105 | TSS12228 |
| chr14 | 97333333 | 97333424 | MACS2_peak_951 | 12 | + | 4.14966 | 5.12722 | 1.204 | 77 | chr14 | unknown | gene | 97786845 | 98169309 | - | Dach1 | Dach1 | P3523 | NM_001038610 | TSS14743 |
| chr14 | 98771748 | 98771839 | MACS2_peak_952 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 19 | chr14 | unknown | gene | 97786845 | 98169309 | - | Dach1 | Dach1 | P3523 | NM_001038610 | TSS14743 |
| chr14 | 98771748 | 98771839 | MACS2_peak_952 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 19 | chr14 | unknown | gene | 99034543 | 99046063 | - | Mzt1 | Mzt1 | P24657 | NM_175245 | TSS2949 |
| chr14 | 100755631 | 100755722 | MACS2_peak_953 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 56 | chr14 | unknown | gene | 99870639 | 100149764 | - | Klf12 | Klf12 | P17746 | NM_010636 | TSS26738 |
| chr14 | 100755631 | 100755722 | MACS2_peak_953 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 56 | chr14 | unknown | gene | 101197689 | 101200069 | - | Prr30 | Prr30 | P17028 | NM_029680 | TSS13545 |
| chr14 | 100862534 | 100862638 | MACS2_peak_954 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 68 | chr14 | unknown | gene | 99870639 | 100149764 | - | Klf12 | Klf12 | P17746 | NM_010636 | TSS26738 |
| chr14 | 100862534 | 100862638 | MACS2_peak_954 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 68 | chr14 | unknown | gene | 101197689 | 101200069 | - | Prr30 | Prr30 | P17028 | NM_029680 | TSS13545 |
| chr14 | 100993730 | 100993821 | MACS2_peak_955 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 47 | chr14 | unknown | gene | 99870639 | 100149764 | - | Klf12 | Klf12 | P17746 | NM_010636 | TSS26738 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr14 | 100993730 | 100993821 | MACS2_peak_955 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 47 | chr14 | unknown | gene | 101197689 | 101200069 | - | Prr30 | Prr30 | P17028 | NM_029680 | TSS13545 |
| chr14 | 102329653 | 102329747 | MACS2_peak_956 | 23 | + | 5.36409 | 7.26321 | 2.37531 | 48 | chr14 | unknown | gene | 101729927 | 101933918 | + | Lmo7 | Lmo7 | P25502 | NM_201529 | TSS17991 |
| chr14 | 102329653 | 102329747 | MACS2_peak_956 | 23 | + | 5.36409 | 7.26321 | 2.37531 | 48 | chr14 | unknown | gene | 102976580 | 102982440 | - | Kctd12 | Kctd12 | P8609 | NM_177715 | TSS10350 |
| chr14 | 102670164 | 102670255 | MACS2_peak_957 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 24 | chr14 | unknown | gene | 101729927 | 101933918 | + | Lmo7 | Lmo7 | P25502 | NM_201529 | TSS17991 |
| chr14 | 102670164 | 102670255 | MACS2_peak_957 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 24 | chr14 | unknown | gene | 102976580 | 102982440 | - | Kctd12 | Kctd12 | P8609 | NM_177715 | TSS10350 |
| chr14 | 103187908 | 103188099 | MACS2_peak_958 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 117 | chr14 | unknown | gene | 103080238 | 103099509 | - | Fbxl3 | Fbxl3 | P25913 | NM_015822 | TSS6951 |
| chr14 | 103187908 | 103188099 | MACS2_peak_958 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 117 | chr14 | unknown | gene | 103513340 | 103612399 | + | Scel | Scel | P22559 | NM_022886 | TSS7944 |
| chr14 | 103291931 | 103292022 | MACS2_peak_959 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 69 | chr14 | unknown | gene | 103080238 | 103099509 | - | Fbxl3 | Fbxl3 | P25913 | NM_015822 | TSS6951 |
| chr14 | 103291931 | 103292022 | MACS2_peak_959 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 69 | chr14 | unknown | gene | 103513340 | 103612399 | + | Scel | Scel | P22559 | NM_022886 | TSS7944 |
| chr14 | 103580638 | 103580729 | MACS2_peak_960 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 11 | chr14 | unknown | gene | 103113410 | 103346517 | - | Mycbp2 | Mycbp2 | P24575 | NM_207215 | TSS1765 |
| chr14 | 103580638 | 103580729 | MACS2_peak_960 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 11 | chr14 | unknown | gene | 103650242 | 103703911 | + | Slain1 | Slain1 | P20477 | NM_198014 | TSS20726 |
| chr14 | 103877759 | 103877850 | MACS2_peak_961 | 29 | + | 5.68756 | 7.89979 | 2.96588 | 30 | chr14 | unknown | gene | 103814614 | 103844476 | - | Ednrb | Ednrb | P21634 | NM_001276296 | TSS16654 |
| chr14 | 103877759 | 103877850 | MACS2_peak_961 | 29 | + | 5.68756 | 7.89979 | 2.96588 | 30 | chr14 | unknown | gene | 103977627 | 104027142 | - | 4930432J09Rik | 4930432J09Rik | | NR_045953 | TSS6548 |
| chr14 | 103899775 | 103899944 | MACS2_peak_962 | 35 | + | 6.07165 | 8.598 | 3.58294 | 85 | chr14 | unknown | gene | 103814614 | 103844476 | - | Ednrb | Ednrb | P21634 | NM_001276296 | TSS16654 |
| chr14 | 103899775 | 103899944 | MACS2_peak_962 | 35 | + | 6.07165 | 8.598 | 3.58294 | 85 | chr14 | unknown | gene | 103977627 | 104027142 | - | 4930432J09Rik | 4930432J09Rik | | NR_045953 | TSS6548 |
| chr14 | 105417699 | 105417790 | MACS2_peak_963 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 69 | chr14 | unknown | gene | 105258672 | 105309298 | + | Ndfip2 | Ndfip2 | P20016 | NM_029561 | TSS11577 |
| chr14 | 105417699 | 105417790 | MACS2_peak_963 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 69 | chr14 | unknown | gene | 105427558 | 105437716 | + | 5430440P10Rik | 5430440P10Rik | | NR_045859 | TSS7342 |
| chr14 | 105677515 | 105677606 | MACS2_peak_964 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 32 | chr14 | unknown | gene | 105623641 | 105623770 | - | Mir6390 | Mir6390 | | NR_105814 | TSS13854 |
| chr14 | 105677515 | 105677606 | MACS2_peak_964 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 32 | chr14 | unknown | gene | 105891946 | 105896819 | - | Spry2 | Spry2 | P19077 | NM_011897 | TSS25949 |
| chr14 | 105802327 | 105802418 | MACS2_peak_965 | 16 | + | 4.811 | 6.2687 | 1.67914 | 46 | chr14 | unknown | gene | 105623641 | 105623770 | - | Mir6390 | Mir6390 | | NR_105814 | TSS13854 |
| chr14 | 105802327 | 105802418 | MACS2_peak_965 | 16 | + | 4.811 | 6.2687 | 1.67914 | 46 | chr14 | unknown | gene | 105891946 | 105896819 | - | Spry2 | Spry2 | P19077 | NM_011897 | TSS25949 |
| chr14 | 106182474 | 106182565 | MACS2_peak_966 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 83 | chr14 | unknown | gene | 106106197 | 106135862 | + | Trim52 | Trim52 | | NR_073203 | TSS7264 |
| chr14 | 106182474 | 106182565 | MACS2_peak_966 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 83 | chr14 | unknown | gene | 106417186 | 106486520 | - | 1700128A07Rik | 1700128A07Rik | | NR_045938 | TSS12527 |
| chr14 | 106376902 | 106376993 | MACS2_peak_967 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 30 | chr14 | unknown | gene | 106106197 | 106135862 | + | Trim52 | Trim52 | | NR_073203 | TSS7264 |
| chr14 | 106376902 | 106376993 | MACS2_peak_967 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 30 | chr14 | unknown | gene | 106417186 | 106486520 | - | 1700128A07Rik | 1700128A07Rik | | NR_045938 | TSS12527 |
| chr14 | 106439914 | 106440005 | MACS2_peak_968 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 25 | chr14 | unknown | gene | 106106197 | 106135862 | + | Trim52 | Trim52 | | NR_073203 | TSS7264 |
| chr14 | 106439914 | 106440005 | MACS2_peak_968 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 25 | chr14 | unknown | gene | 108909988 | 108913277 | - | Slitrk1 | Slitrk1 | P4075 | NM_199065 | TSS18315 |
| chr14 | 106982871 | 106983013 | MACS2_peak_969 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 54 | chr14 | unknown | gene | 106417186 | 106486520 | - | 1700128A07Rik | 1700128A07Rik | | NR_045938 | TSS12527 |
| chr14 | 106982871 | 106983013 | MACS2_peak_969 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 54 | chr14 | unknown | gene | 108909988 | 108913277 | - | Slitrk1 | Slitrk1 | P4075 | NM_199065 | TSS18315 |
| chr14 | 108276897 | 108276988 | MACS2_peak_970 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 31 | chr14 | unknown | gene | 106417186 | 106486520 | - | 1700128A07Rik | 1700128A07Rik | | NR_045938 | TSS12527 |
| chr14 | 108276897 | 108276988 | MACS2_peak_970 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 31 | chr14 | unknown | gene | 108909988 | 108913277 | - | Slitrk1 | Slitrk1 | P4075 | NM_199065 | TSS18315 |
| chr14 | 109111863 | 109111965 | MACS2_peak_971 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 16 | chr14 | unknown | gene | 108909988 | 108913277 | - | Slitrk1 | Slitrk1 | P4075 | NM_199065 | TSS18315 |
| chr14 | 109111863 | 109111965 | MACS2_peak_971 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 16 | chr14 | unknown | gene | 109460229 | 109490814 | + | Mir3964 | Mir3964 | | NR_039542 | TSS16332 |
| chr14 | 109874044 | 109874192 | MACS2_peak_972 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 64 | chr14 | unknown | gene | 109460229 | 109490814 | + | Mir3964 | Mir3964 | | NR_039542 | TSS16332 |
| chr14 | 109874044 | 109874192 | MACS2_peak_972 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 64 | chr14 | unknown | gene | 110748577 | 110755149 | - | Slitrk6 | Slitrk6 | P24208 | NM_175499 | TSS22542 |
| chr14 | 110036511 | 110036640 | MACS2_peak_973 | 61 | + | 7.43052 | 11.30786 | 6.16647 | 71 | chr14 | unknown | gene | 109460229 | 109490814 | + | Mir3964 | Mir3964 | | NR_039542 | TSS16332 |
| chr14 | 110036511 | 110036640 | MACS2_peak_973 | 61 | + | 7.43052 | 11.30786 | 6.16647 | 71 | chr14 | unknown | gene | 110748577 | 110755149 | - | Slitrk6 | Slitrk6 | P24208 | NM_175499 | TSS22542 |
| chr14 | 110064259 | 110064497 | MACS2_peak_974 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 89 | chr14 | unknown | gene | 109460229 | 109490814 | + | Mir3964 | Mir3964 | | NR_039542 | TSS16332 |
| chr14 | 110064259 | 110064497 | MACS2_peak_974 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 89 | chr14 | unknown | gene | 110748577 | 110755149 | - | Slitrk6 | Slitrk6 | P24208 | NM_175499 | TSS22542 |
| chr14 | 110220403 | 110220494 | MACS2_peak_975 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 59 | chr14 | unknown | gene | 109460229 | 109490814 | + | Mir3964 | Mir3964 | | NR_039542 | TSS16332 |
| chr14 | 110220403 | 110220494 | MACS2_peak_975 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 59 | chr14 | unknown | gene | 110748577 | 110755149 | - | Slitrk6 | Slitrk6 | P24208 | NM_175499 | TSS22542 |
| chr14 | 112438600 | 112438718 | MACS2_peak_976 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 75 | chr14 | unknown | gene | 112021429 | 112058438 | + | Mir466 | Mir466 | | NR_030150 | TSS1736 |
| chr14 | 112438600 | 112438718 | MACS2_peak_976 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 75 | chr14 | unknown | gene | 114831964 | 114861327 | + | 4930524C18Rik | 4930524C18Rik | | NR_045661 | TSS11682 |
| chr14 | 114051528 | 114051682 | MACS2_peak_977 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 68 | chr14 | unknown | gene | 112021429 | 112058438 | + | Mir466 | Mir466 | | NR_030150 | TSS1736 |
| chr14 | 114051528 | 114051682 | MACS2_peak_977 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 68 | chr14 | unknown | gene | 114831964 | 114861327 | + | 4930524C18Rik | 4930524C18Rik | | NR_045661 | TSS11682 |
| chr14 | 114837702 | 114837795 | MACS2_peak_978 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 14 | chr14 | unknown | gene | 112021429 | 112058438 | + | Mir466 | Mir466 | | NR_030150 | TSS1736 |
| chr14 | 114837702 | 114837795 | MACS2_peak_978 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 14 | chr14 | unknown | gene | 114940224 | 114945948 | - | 1700100I10Rik | 1700100I10Rik | | NR_126551 | TSS9173 |
| chr14 | 115529253 | 115529344 | MACS2_peak_979 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 25 | chr14 | unknown | gene | 115396550 | 115409552 | - | 4930505G20Rik | 4930505G20Rik | | NR_045761 | TSS16637 |
| chr14 | 115529253 | 115529344 | MACS2_peak_979 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 25 | chr14 | unknown | gene | 116925296 | 117975086 | + | Gpc6 | Gpc6 | P11819 | NM_001079844 | TSS17675 |
| chr14 | 116726358 | 116726501 | MACS2_peak_980 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 83 | chr14 | unknown | gene | 115092214 | 116524437 | + | Gpc5 | Gpc5 | P21154 | NM_175500 | TSS12123 |
| chr14 | 116726358 | 116726501 | MACS2_peak_980 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 83 | chr14 | unknown | gene | 116925296 | 117975086 | + | Gpc6 | Gpc6 | P11819 | NM_001079844 | TSS17675 |
| chr14 | 117332615 | 117332706 | MACS2_peak_981 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 59 | chr14 | unknown | gene | 115092214 | 116524437 | + | Gpc5 | Gpc5 | P21154 | NM_175500 | TSS12123 |
| chr14 | 117332615 | 117332706 | MACS2_peak_981 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 59 | chr14 | unknown | gene | 117953742 | 117953847 | - | Mir6239 | Mir6239 | | NR_105747 | TSS1974 |
| chr14 | 117711522 | 117711646 | MACS2_peak_982 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 74 | chr14 | unknown | gene | 115092214 | 116524437 | + | Gpc5 | Gpc5 | P21154 | NM_175500 | TSS12123 |
| chr14 | 117711522 | 117711646 | MACS2_peak_982 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 74 | chr14 | unknown | gene | 117953742 | 117953847 | - | Mir6239 | Mir6239 | | NR_105747 | TSS1974 |
| chr14 | 118787796 | 118787887 | MACS2_peak_983 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 54 | chr14 | unknown | gene | 118482691 | 118706109 | - | Abcc4 | Abcc4 | P11922 | NM_001163675 | TSS5299 |
| chr14 | 118787796 | 118787887 | MACS2_peak_983 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 54 | chr14 | unknown | gene | 118875519 | 118925470 | - | Dzip1 | Dzip1 | P20122 | NM_025943 | TSS2049 |
| chr14 | 118851742 | 118851835 | MACS2_peak_984 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 79 | chr14 | unknown | gene | 118482691 | 118706109 | - | Abcc4 | Abcc4 | P11922 | NM_001163675 | TSS5299 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr14 | 118851742 | 118851835 | MACS2_peak_984 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 79 | chr14 | unknown | gene | 118875519 | 118925470 | - | Dzip1 | Dzip1 | P20122 | NM_025943 | TSS2049 |
| chr14 | 118974488 | 118974579 | MACS2_peak_985 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 19 | chr14 | unknown | gene | 118875519 | 118925470 | - | Dzip1 | Dzip1 | P20122 | NM_025943 | TSS2049 |
| chr14 | 118974488 | 118974579 | MACS2_peak_985 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 19 | chr14 | unknown | gene | 118984984 | 119099341 | - | Uggt2 | Uggt2 | P11593 | NM_001081252 | TSS14530 |
| chr14 | 119204616 | 119204707 | MACS2_peak_986 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 42 | chr14 | unknown | gene | 118984984 | 119099341 | - | Uggt2 | Uggt2 | P11593 | NM_001081252 | TSS14530 |
| chr14 | 119204616 | 119204707 | MACS2_peak_986 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 42 | chr14 | unknown | gene | 119749226 | 119751564 | + | 1700006F04Rik | 1700006F04Rik | | NR_045621 | TSS9258 |
| chr14 | 119429001 | 119429092 | MACS2_peak_987 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 13 | chr14 | unknown | gene | 118984984 | 119099341 | - | Uggt2 | Uggt2 | P11593 | NM_001081252 | TSS14530 |
| chr14 | 119429001 | 119429092 | MACS2_peak_987 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 13 | chr14 | unknown | gene | 119749226 | 119751564 | + | 1700006F04Rik | 1700006F04Rik | | NR_045621 | TSS9258 |
| chr14 | 120705423 | 120705572 | MACS2_peak_988 | 40 | + | 6.30384 | 9.04635 | 4.00347 | 64 | chr14 | unknown | gene | 120478460 | 120503838 | + | Rap2a | Rap2a | P24113 | NM_029519 | TSS15375 |
| chr14 | 120705423 | 120705572 | MACS2_peak_988 | 40 | + | 6.30384 | 9.04635 | 4.00347 | 64 | chr14 | unknown | gene | 120911193 | 120946805 | + | Ipo5 | Ipo5 | P9948 | NM_023579 | TSS10842 |
| chr14 | 120720968 | 120721086 | MACS2_peak_989 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 30 | chr14 | unknown | gene | 120478460 | 120503838 | + | Rap2a | Rap2a | P24113 | NM_029519 | TSS15375 |
| chr14 | 120720968 | 120721086 | MACS2_peak_989 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 30 | chr14 | unknown | gene | 120911193 | 120946805 | + | Ipo5 | Ipo5 | P9948 | NM_023579 | TSS10842 |
| chr14 | 121330334 | 121330434 | MACS2_peak_990 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 55 | chr14 | unknown | gene | 121035573 | 121282391 | + | Farp1 | Farp1 | P9893 | NM_134082 | TSS12656 |
| chr14 | 121330334 | 121330434 | MACS2_peak_990 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 55 | chr14 | unknown | gene | 121459620 | 121505222 | - | Slc15a1 | Slc15a1 | P17602 | NM_053079 | TSS10852 |
| chr14 | 122371163 | 122371254 | MACS2_peak_991 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 20 | chr14 | unknown | gene | 122229904 | 122233638 | - | 1700108J01Rik | 1700108J01Rik | | NR_015532 | TSS15893 |
| chr14 | 122371163 | 122371254 | MACS2_peak_991 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 20 | chr14 | unknown | gene | 122459159 | 122465317 | - | Zic5 | Zic5 | P25427 | NM_022987 | TSS8336 |
| chr14 | 122509146 | 122509237 | MACS2_peak_992 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 23 | chr14 | unknown | gene | 122475383 | 122479243 | + | Zic2 | Zic2 | P7712 | NM_009574 | TSS1865 |
| chr14 | 122509146 | 122509237 | MACS2_peak_992 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 23 | chr14 | unknown | gene | 122534327 | 122889555 | + | Pcca | Pcca | P12108 | NM_144844 | TSS20274 |
| chr14 | 124371656 | 124371747 | MACS2_peak_993 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 30 | chr14 | unknown | gene | 123987634 | 124015684 | + | 1700024B18Rik | 1700024B18Rik | | NR_045479 | TSS9111 |
| chr15 | 3526962 | 3527104 | MACS2_peak_994 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 82 | chr15 | unknown | gene | 3280626 | 3303526 | - | Ccdc152 | Ccdc152 | P21181 | NM_001166063 | TSS14111 |
| chr15 | 3526962 | 3527104 | MACS2_peak_994 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 82 | chr15 | unknown | gene | 3963563 | 3979424 | - | Fbxo4 | Fbxo4 | P23605 | NM_134099 | TSS2309 |
| chr15 | 3988022 | 3988161 | MACS2_peak_995 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 65 | chr15 | unknown | gene | 3963563 | 3979424 | - | Fbxo4 | Fbxo4 | P23605 | NM_134099 | TSS2309 |
| chr15 | 3988022 | 3988161 | MACS2_peak_995 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 65 | chr15 | unknown | gene | 3996038 | 4015858 | + | A630020A06 | A630020A06 | | NR_045740 | TSS10991 |
| chr15 | 6424867 | 6424958 | MACS2_peak_996 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 12 | chr15 | unknown | gene | 5496317 | 5594983 | + | 5430437J10Rik | 5430437J10Rik | | NR_045274 | TSS16104 |
| chr15 | 6424867 | 6424958 | MACS2_peak_996 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 12 | chr15 | unknown | gene | 6445332 | 6498476 | + | C9 | C9 | P5425 | NM_013485 | TSS4586 |
| chr15 | 6548485 | 6548576 | MACS2_peak_997 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 69 | chr15 | unknown | gene | 6445332 | 6498476 | + | C9 | C9 | P5425 | NM_013485 | TSS4586 |
| chr15 | 6548485 | 6548576 | MACS2_peak_997 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 69 | chr15 | unknown | gene | 6579846 | 6663172 | + | Fyb | Fyb | P5495 | NM_001278269 | TSS24300 |
| chr15 | 6670050 | 6670141 | MACS2_peak_998 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 19 | chr15 | unknown | gene | 6579846 | 6663172 | + | Fyb | Fyb | P5495 | NM_001278269 | TSS24300 |
| chr15 | 6670050 | 6670141 | MACS2_peak_998 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 19 | chr15 | unknown | gene | 6708380 | 6796236 | + | Rictor | Rictor | P19559 | NM_030168 | TSS4787 |
| chr15 | 6703558 | 6703649 | MACS2_peak_999 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 25 | chr15 | unknown | gene | 6579846 | 6663172 | + | Fyb | Fyb | P5495 | NM_001278269 | TSS24300 |
| chr15 | 6703558 | 6703649 | MACS2_peak_999 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 25 | chr15 | unknown | gene | 6708380 | 6796236 | + | Rictor | Rictor | P19559 | NM_030168 | TSS4787 |
| chr15 | 7234766 | 7234857 | MACS2_peak_1000 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 5 | chr15 | unknown | gene | 7129571 | 7191169 | + | Lifr | Lifr | P12094 | NM_001113386 | TSS15010 |
| chr15 | 7234766 | 7234857 | MACS2_peak_1000 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 5 | chr15 | unknown | gene | 7810047 | 7834832 | + | Gdnf | Gdnf | P8002 | NM_001301332 | TSS5375 |
| chr15 | 7455247 | 7455338 | MACS2_peak_1001 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 8 | chr15 | unknown | gene | 7206119 | 7398084 | - | Egflam | Egflam | P25577 | NM_001289498 | TSS16646 |
| chr15 | 7455247 | 7455338 | MACS2_peak_1001 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 8 | chr15 | unknown | gene | 7810047 | 7834832 | + | Gdnf | Gdnf | P8002 | NM_001301332 | TSS5375 |
| chr15 | 7932133 | 7932224 | MACS2_peak_1002 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 30 | chr15 | unknown | gene | 7810047 | 7834832 | + | Gdnf | Gdnf | P8002 | NM_001301332 | TSS5375 |
| chr15 | 7932133 | 7932224 | MACS2_peak_1002 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 30 | chr15 | unknown | gene | 8109312 | 8157764 | + | Nup155 | Nup155 | P12769 | NM_133227 | TSS18959 |
| chr15 | 8441270 | 8441379 | MACS2_peak_1003 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 23 | chr15 | unknown | gene | 8169105 | 8270855 | + | 2410089E03Rik | 2410089E03Rik | P26423 | NM_001162906 | TSS24148 |
| chr15 | 8441270 | 8441379 | MACS2_peak_1003 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 23 | chr15 | unknown | gene | 8634123 | 8710807 | - | Slc1a3 | Slc1a3 | P14674 | NM_148938 | TSS24160 |
| chr15 | 8909027 | 8909174 | MACS2_peak_1004 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 75 | chr15 | unknown | gene | 8634123 | 8710807 | - | Slc1a3 | Slc1a3 | P14674 | NM_148938 | TSS24160 |
| chr15 | 8909027 | 8909174 | MACS2_peak_1004 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 75 | chr15 | unknown | gene | 8967948 | 9065007 | + | Ranbp3l | Ranbp3l | P25152 | NM_198024 | TSS15256 |
| chr15 | 9842230 | 9842321 | MACS2_peak_1005 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 48 | chr15 | unknown | gene | 9578192 | 9748769 | - | Spef2 | Spef2 | P10423 | NM_001305042 | TSS1552 |
| chr15 | 9842230 | 9842321 | MACS2_peak_1005 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 48 | chr15 | unknown | gene | 10177237 | 10346502 | + | Prlr | Prlr | P14979 | NM_011169 | TSS18054 |
| chr15 | 10250361 | 10250452 | MACS2_peak_1006 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 55 | chr15 | unknown | gene | 9578192 | 9748769 | - | Spef2 | Spef2 | P10423 | NM_001305042 | TSS1552 |
| chr15 | 10250361 | 10250452 | MACS2_peak_1006 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 55 | chr15 | unknown | gene | 10358578 | 10409557 | + | Agxt2 | Agxt2 | P18522 | NM_001031851 | TSS18697 |
| chr15 | 10340153 | 10340244 | MACS2_peak_1007 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 59 | chr15 | unknown | gene | 9578192 | 9748769 | - | Spef2 | Spef2 | P10423 | NM_001305042 | TSS1552 |
| chr15 | 10340153 | 10340244 | MACS2_peak_1007 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 59 | chr15 | unknown | gene | 10358578 | 10409557 | + | Agxt2 | Agxt2 | P18522 | NM_001031851 | TSS18697 |
| chr15 | 10641242 | 10641333 | MACS2_peak_1008 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 52 | chr15 | unknown | gene | 10600292 | 10611651 | + | Gm10389 | Gm10389 | | NR_033541 | TSS8071 |
| chr15 | 10641242 | 10641333 | MACS2_peak_1008 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 52 | chr15 | unknown | gene | 10714835 | 10790123 | + | 4930556M19Rik | 4930556M19Rik | | NR_045063 | TSS25468 |
| chr15 | 11506277 | 11506450 | MACS2_peak_1009 | 19 | + | 5.0267 | 6.65745 | 1.99837 | 89 | chr15 | unknown | gene | 11383662 | 11399539 | - | Tars | Tars | P7101 | NM_033074 | TSS1055 |
| chr15 | 11506277 | 11506450 | MACS2_peak_1009 | 19 | + | 5.0267 | 6.65745 | 1.99837 | 89 | chr15 | unknown | gene | 11839895 | 11907371 | - | Npr3 | Npr3 | P15473 | NM_001286395 | TSS1069 |
| chr15 | 12724523 | 12724614 | MACS2_peak_1010 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 61 | chr15 | unknown | gene | 12357053 | 12592556 | - | Pdzd2 | Pdzd2 | P16920 | NM_001081064 | TSS6674 |
| chr15 | 12724523 | 12724614 | MACS2_peak_1010 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 61 | chr15 | unknown | gene | 12808176 | 12824547 | - | 6030458C11Rik | 6030458C11Rik | P11190 | NM_029998 | TSS9176 |
| chr15 | 13490973 | 13491112 | MACS2_peak_1011 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 55 | chr15 | unknown | gene | 13034199 | 13173639 | - | Cdh6 | Cdh6 | P13598 | NM_007666 | TSS13679 |
| chr15 | 13490973 | 13491112 | MACS2_peak_1011 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 55 | chr15 | unknown | gene | 16778100 | 16856242 | + | Cdh9 | Cdh9 | P18154 | NM_009869 | TSS6675 |
| chr15 | 15136999 | 15137090 | MACS2_peak_1012 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 63 | chr15 | unknown | gene | 13034199 | 13173639 | - | Cdh6 | Cdh6 | P13598 | NM_007666 | TSS13679 |
| chr15 | 15136999 | 15137090 | MACS2_peak_1012 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 63 | chr15 | unknown | gene | 16778100 | 16856242 | + | Cdh9 | Cdh9 | P18154 | NM_009869 | TSS6675 |
| chr15 | 16152766 | 16152857 | MACS2_peak_1013 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 21 | chr15 | unknown | gene | 13034199 | 13173639 | - | Cdh6 | Cdh6 | P13598 | NM_007666 | TSS13679 |
| chr15 | 16152766 | 16152857 | MACS2_peak_1013 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 21 | chr15 | unknown | gene | 16778100 | 16856242 | + | Cdh9 | Cdh9 | P18154 | NM_009869 | TSS6675 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr15 | 16725315 | 16725406 | MACS2_peak_1014 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 87 | chr15 | unknown | gene | 13034199 | 13173639 | - | Cdh6 | Cdh6 | P13598 | NM_007666 | TSS13679 |
| chr15 | 16725315 | 16725406 | MACS2_peak_1014 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 87 | chr15 | unknown | gene | 16778100 | 16856242 | + | Cdh9 | Cdh9 | P18154 | NM_009869 | TSS6675 |
| chr15 | 18861147 | 18861238 | MACS2_peak_1015 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 60 | chr15 | unknown | gene | 18078136 | 18369627 | - | 4921515E04Rik | 4921515E04Rik |  | NR_045711 | TSS20657 |
| chr15 | 18861147 | 18861238 | MACS2_peak_1015 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 60 | chr15 | unknown | gene | 20665213 | 20666653 | - | Acot10 | Acot10 | P17751 | NM_022816 | TSS16581 |
| chr15 | 21255604 | 21255709 | MACS2_peak_1016 | 29 | + | 5.67577 | 7.86521 | 2.93324 | 75 | chr15 | unknown | gene | 20665213 | 20666653 | - | Acot10 | Acot10 | P17751 | NM_022816 | TSS16581 |
| chr15 | 21255604 | 21255709 | MACS2_peak_1016 | 29 | + | 5.67577 | 7.86521 | 2.93324 | 75 | chr15 | unknown | gene | 22713819 | 22714830 | - | Gm5803 | Gm5803 | P16733 | NM_001165971 | TSS123 |
| chr15 | 24547484 | 24547575 | MACS2_peak_1017 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 56 | chr15 | unknown | gene | 23036462 | 23474418 | - | Cdh18 | Cdh18 | P6054 | NM_001081299 | TSS15933 |
| chr15 | 24547484 | 24547575 | MACS2_peak_1017 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 56 | chr15 | unknown | gene | 25363276 | 25413764 | - | Basp1 | Basp1 | P21281 | NM_027395 | TSS6324 |
| chr15 | 25215939 | 25216070 | MACS2_peak_1018 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 82 | chr15 | unknown | gene | 23036462 | 23474418 | + | Cdh18 | Cdh18 | P6054 | NM_001081299 | TSS15933 |
| chr15 | 25215939 | 25216070 | MACS2_peak_1018 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 82 | chr15 | unknown | gene | 25363276 | 25413764 | - | Basp1 | Basp1 | P21281 | NM_027395 | TSS6324 |
| chr15 | 25235764 | 25235855 | MACS2_peak_1019 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 35 | chr15 | unknown | gene | 23036462 | 23474418 | + | Cdh18 | Cdh18 | P6054 | NM_001081299 | TSS15933 |
| chr15 | 25235764 | 25235855 | MACS2_peak_1019 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 35 | chr15 | unknown | gene | 25363276 | 25413764 | - | Basp1 | Basp1 | P21281 | NM_027395 | TSS6324 |
| chr15 | 25577395 | 25577486 | MACS2_peak_1020 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 14 | chr15 | unknown | gene | 25414191 | 25452418 | + | Gm5468 | Gm5468 |  | NR_027376 | TSS8177 |
| chr15 | 25577395 | 25577486 | MACS2_peak_1020 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 14 | chr15 | unknown | gene | 25622549 | 25812222 | + | Myo10 | Myo10 | P10279 | NM_019472 | TSS27675 |
| chr15 | 25975183 | 25975274 | MACS2_peak_1021 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 22 | chr15 | unknown | gene | 25843297 | 25972046 | + | Fam134b | Fam134b | P23531 | NM_001034851 | TSS3589 |
| chr15 | 25975183 | 25975274 | MACS2_peak_1021 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 22 | chr15 | unknown | gene | 25984365 | 25997294 | + | Zfp622 | Zfp622 | P16581 | NM_144523 | TSS16342 |
| chr15 | 26208619 | 26208710 | MACS2_peak_1022 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 7 | chr15 | unknown | gene | 25984365 | 25997294 | + | Zfp622 | Zfp622 | P16581 | NM_144523 | TSS16342 |
| chr15 | 26208619 | 26208710 | MACS2_peak_1022 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 7 | chr15 | unknown | gene | 26309071 | 26409419 | + | Mar-11 | Mar-11 | P7220 | NM_177597 | TSS7205 |
| chr15 | 26652946 | 26653037 | MACS2_peak_1023 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 34 | chr15 | unknown | gene | 26309071 | 26409419 | + | Mar-11 | Mar-11 | P7220 | NM_177597 | TSS7205 |
| chr15 | 26652946 | 26653037 | MACS2_peak_1023 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 34 | chr15 | unknown | gene | 27466676 | 27593217 | + | Ank | Ank | P10290 | NM_020332 | TSS9018 |
| chr15 | 26719569 | 26719688 | MACS2_peak_1024 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 45 | chr15 | unknown | gene | 26309071 | 26409419 | + | Mar-11 | Mar-11 | P7220 | NM_177597 | TSS7205 |
| chr15 | 26719569 | 26719688 | MACS2_peak_1024 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 45 | chr15 | unknown | gene | 27466676 | 27593217 | + | Ank | Ank | P10290 | NM_020332 | TSS9018 |
| chr15 | 26830906 | 26830997 | MACS2_peak_1025 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 33 | chr15 | unknown | gene | 26309071 | 26409419 | + | Mar-11 | Mar-11 | P7220 | NM_177597 | TSS7205 |
| chr15 | 26830906 | 26830997 | MACS2_peak_1025 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 33 | chr15 | unknown | gene | 27466676 | 27593217 | + | Ank | Ank | P10290 | NM_020332 | TSS9018 |
| chr15 | 27427785 | 27427881 | MACS2_peak_1026 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 51 | chr15 | unknown | gene | 26540458 | 26895049 | - | Fbxl7 | Fbxl7 | P146 | NM_176959 | TSS3825 |
| chr15 | 27427785 | 27427881 | MACS2_peak_1026 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 51 | chr15 | unknown | gene | 27466676 | 27593217 | + | Ank | Ank | P10290 | NM_020332 | TSS9018 |
| chr15 | 29263743 | 29263872 | MACS2_peak_1027 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 85 | chr15 | unknown | gene | 28203765 | 28470508 | + | Dnah5 | Dnah5 | P9323 | NM_133365 | TSS2085 |
| chr15 | 29263743 | 29263872 | MACS2_peak_1027 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 85 | chr15 | unknown | gene | 30172592 | 31027672 | + | Ctnnd2 | Ctnnd2 | P2989 | NM_008729 | TSS5811 |
| chr15 | 31775964 | 31776142 | MACS2_peak_1028 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 29 | chr15 | unknown | gene | 31602115 | 31617134 | + | Fam173b | Fam173b | P14356 | NM_026546 | TSS10503 |
| chr15 | 31775964 | 31776142 | MACS2_peak_1028 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 29 | chr15 | unknown | gene | 32177288 | 32178294 | + | Tas2r119 | Tas2r119 | P12197 | NM_020503 | TSS20880 |
| chr15 | 31861043 | 31861134 | MACS2_peak_1029 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 31 | chr15 | unknown | gene | 31602115 | 31617134 | + | Fam173b | Fam173b | P14356 | NM_026546 | TSS10503 |
| chr15 | 31861043 | 31861134 | MACS2_peak_1029 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 31 | chr15 | unknown | gene | 32177288 | 32178294 | + | Tas2r119 | Tas2r119 | P12197 | NM_020503 | TSS20880 |
| chr15 | 31885724 | 31885815 | MACS2_peak_1030 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 53 | chr15 | unknown | gene | 31602115 | 31617134 | + | Fam173b | Fam173b | P14356 | NM_026546 | TSS10503 |
| chr15 | 31885724 | 31885815 | MACS2_peak_1030 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 53 | chr15 | unknown | gene | 32177288 | 32178294 | + | Tas2r119 | Tas2r119 | P12197 | NM_020503 | TSS20880 |
| chr15 | 32167438 | 32167531 | MACS2_peak_1031 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 23 | chr15 | unknown | gene | 31602115 | 31617134 | + | Fam173b | Fam173b | P14356 | NM_026546 | TSS10503 |
| chr15 | 32167438 | 32167531 | MACS2_peak_1031 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 23 | chr15 | unknown | gene | 32177288 | 32178294 | + | Tas2r119 | Tas2r119 | P12197 | NM_020503 | TSS20880 |
| chr15 | 32449749 | 32449860 | MACS2_peak_1032 | 46 | + | 6.62427 | 9.68827 | 4.62121 | 35 | chr15 | unknown | gene | 32240567 | 32244662 | - | Snhg18 | Snhg18 |  | NR_038186 | TSS22283 |
| chr15 | 32449749 | 32449860 | MACS2_peak_1032 | 46 | + | 6.62427 | 9.68827 | 4.62121 | 35 | chr15 | unknown | gene | 32920722 | 33032540 | + | Sdc2 | Sdc2 | P7044 | NM_008304 | TSS347 |
| chr15 | 32923797 | 32923926 | MACS2_peak_1033 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 81 | chr15 | unknown | gene | 32244812 | 32689415 | + | Sema5a | Sema5a | P17297 | NM_009154 | TSS20395 |
| chr15 | 32923797 | 32923926 | MACS2_peak_1033 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 81 | chr15 | unknown | gene | 33083128 | 33594257 | + | Cpq | Cpq | P18718 | NM_018755 | TSS4167 |
| chr15 | 33092398 | 33092489 | MACS2_peak_1034 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 34 | chr15 | unknown | gene | 32920722 | 33032540 | + | Sdc2 | Sdc2 | P7044 | NM_008304 | TSS347 |
| chr15 | 33092398 | 33092489 | MACS2_peak_1034 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 34 | chr15 | unknown | gene | 33405208 | 33405939 | - | 1700084J12Rik | 1700084J12Rik |  | NR_033608 | TSS4978 |
| chr15 | 33290254 | 33290345 | MACS2_peak_1035 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 36 | chr15 | unknown | gene | 32920722 | 33032540 | + | Sdc2 | Sdc2 | P7044 | NM_008304 | TSS347 |
| chr15 | 33290254 | 33290345 | MACS2_peak_1035 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 36 | chr15 | unknown | gene | 33405208 | 33405939 | - | 1700084J12Rik | 1700084J12Rik |  | NR_033608 | TSS4978 |
| chr15 | 33508692 | 33508783 | MACS2_peak_1036 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 14 | chr15 | unknown | gene | 33405208 | 33405939 | - | 1700084J12Rik | 1700084J12Rik |  | NR_033608 | TSS4978 |
| chr15 | 33508692 | 33508783 | MACS2_peak_1036 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 14 | chr15 | unknown | gene | 33593880 | 33653436 | - | 4930592A05Rik | 4930592A05Rik |  | NR_045070 | TSS10450 |
| chr15 | 35080591 | 35080682 | MACS2_peak_1037 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 81 | chr15 | unknown | gene | 34837354 | 34839926 | + | Kcns2 | Kcns2 | P8012 | NM_181317 | TSS12657 |
| chr15 | 35080591 | 35080682 | MACS2_peak_1037 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 81 | chr15 | unknown | gene | 35296111 | 35302893 | + | Osr2 | Osr2 | P3619 | NM_054049 | TSS27439 |
| chr15 | 35193346 | 35193437 | MACS2_peak_1038 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 85 | chr15 | unknown | gene | 34875498 | 35155552 | - | Stk3 | Stk3 | P4140 | NM_019635 | TSS25523 |
| chr15 | 35193346 | 35193437 | MACS2_peak_1038 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 85 | chr15 | unknown | gene | 35296111 | 35302893 | + | Osr2 | Osr2 | P3619 | NM_054049 | TSS27439 |
| chr15 | 35422494 | 35422611 | MACS2_peak_1039 | 32 | + | 5.8651 | 8.25694 | 3.2954 | 71 | chr15 | unknown | gene | 35307009 | 35328535 | - | BC048602 | BC048602 |  | NR_045280 | TSS18217 |
| chr15 | 35422494 | 35422611 | MACS2_peak_1039 | 32 | + | 5.8651 | 8.25694 | 3.2954 | 71 | chr15 | unknown | gene | 35660830 | 35660918 | - | Mir599 | Mir599 |  | NR_035527 | TSS3649 |
| chr15 | 36016263 | 36016354 | MACS2_peak_1040 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 51 | chr15 | unknown | gene | 35931975 | 35938246 | - | Cox6c | Cox6c | P24590 | NM_053071 | TSS17657 |
| chr15 | 36016263 | 36016354 | MACS2_peak_1040 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 51 | chr15 | unknown | gene | 36150059 | 36164884 | - | Fbxo43 | Fbxo43 | P15986 | NM_001081253 | TSS20 |
| chr15 | 37969605 | 37969696 | MACS2_peak_1041 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 1 | chr15 | unknown | gene | 37923952 | 37960891 | - | Rrm2b | Rrm2b | P9641 | NM_199476 | TSS21603 |
| chr15 | 37969605 | 37969696 | MACS2_peak_1041 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 1 | chr15 | unknown | gene | 38219202 | 38226604 | + | Odf1 | Odf1 | P7770 | NM_008757 | TSS21768 |
| chr15 | 39884106 | 39884197 | MACS2_peak_1042 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 25 | chr15 | unknown | gene | 39768484 | 39857362 | - | Dpys | Dpys | P15680 | NM_022722 | TSS25243 |
| chr15 | 39884106 | 39884197 | MACS2_peak_1042 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 25 | chr15 | unknown | gene | 39962648 | 39967515 | + | AU022793 | AU022793 |  | NR_045719 | TSS2445 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr15 | 41214777 | 41214868 | MACS2_peak_1043 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 26 | chr15 | unknown | gene | 40655041 | 41103576 | + | Zfpm2 | Zfpm2 | P296 | NM_011766 | TSS24938 |
| chr15 | 41214777 | 41214868 | MACS2_peak_1043 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 26 | chr15 | unknown | gene | 41447481 | 41859293 | + | Oxr1 | Oxr1 | P9582 | NM_001130166 | TSS14291 |
| chr15 | 41276185 | 41276276 | MACS2_peak_1044 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 52 | chr15 | unknown | gene | 40655041 | 41103576 | + | Zfpm2 | Zfpm2 | P296 | NM_011766 | TSS24938 |
| chr15 | 41276185 | 41276276 | MACS2_peak_1044 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 52 | chr15 | unknown | gene | 41447481 | 41859293 | + | Oxr1 | Oxr1 | P9582 | NM_001130166 | TSS14291 |
| chr15 | 41471299 | 41471442 | MACS2_peak_1045 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 18 | chr15 | unknown | gene | 40655041 | 41103576 | + | Zfpm2 | Zfpm2 | P296 | NM_011766 | TSS24938 |
| chr15 | 41471299 | 41471442 | MACS2_peak_1045 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 18 | chr15 | unknown | gene | 41865292 | 41869668 | - | Abra | Abra | P20349 | NM_175456 | TSS18484 |
| chr15 | 41829410 | 41829518 | MACS2_peak_1046 | 32 | + | 5.8651 | 8.25694 | 3.2954 | 26 | chr15 | unknown | gene | 40655041 | 41103576 | + | Zfpm2 | Zfpm2 | P296 | NM_011766 | TSS24938 |
| chr15 | 41829410 | 41829518 | MACS2_peak_1046 | 32 | + | 5.8651 | 8.25694 | 3.2954 | 26 | chr15 | unknown | gene | 41865292 | 41869668 | - | Abra | Abra | P20349 | NM_175456 | TSS18484 |
| chr15 | 42089759 | 42089850 | MACS2_peak_1047 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 79 | chr15 | unknown | gene | 41865292 | 41869668 | - | Abra | Abra | P20349 | NM_175456 | TSS18484 |
| chr15 | 42089759 | 42089850 | MACS2_peak_1047 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 79 | chr15 | unknown | gene | 42424666 | 42676461 | - | Angpt1 | Angpt1 | P26273 | NM_009640 | TSS24383 |
| chr15 | 42494459 | 42494553 | MACS2_peak_1048 | 23 | + | 5.36409 | 7.26321 | 2.37531 | 43 | chr15 | unknown | gene | 41865292 | 41869668 | - | Abra | Abra | P20349 | NM_175456 | TSS18484 |
| chr15 | 42494459 | 42494553 | MACS2_peak_1048 | 23 | + | 5.36409 | 7.26321 | 2.37531 | 43 | chr15 | unknown | gene | 43020794 | 43170818 | - | Rspo2 | Rspo2 | P26079 | NM_172815 | TSS22599 |
| chr15 | 42959762 | 42959853 | MACS2_peak_1049 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 76 | chr15 | unknown | gene | 42424666 | 42676461 | - | Angpt1 | Angpt1 | P26273 | NM_009640 | TSS24383 |
| chr15 | 42959762 | 42959853 | MACS2_peak_1049 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 76 | chr15 | unknown | gene | 43020794 | 43170818 | - | Rspo2 | Rspo2 | P26079 | NM_172815 | TSS22599 |
| chr15 | 43422548 | 43422639 | MACS2_peak_1050 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 12 | chr15 | unknown | gene | 43250039 | 43282692 | - | Eif3e | Eif3e | P12313 | NM_008388 | TSS20044 |
| chr15 | 43422548 | 43422639 | MACS2_peak_1050 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 12 | chr15 | unknown | gene | 43430942 | 43477036 | - | Gm10373 | Gm10373 | | NR_046064 | TSS7577 |
| chr15 | 44321333 | 44321424 | MACS2_peak_1051 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 55 | chr15 | unknown | gene | 44196134 | 44233467 | + | Trhr | Trhr | P9999 | NM_013696 | TSS21102 |
| chr15 | 44321333 | 44321424 | MACS2_peak_1051 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 55 | chr15 | unknown | gene | 44375226 | 44427776 | - | Nudcd1 | Nudcd1 | P13069 | NM_026149 | TSS18973 |
| chr15 | 44409030 | 44409183 | MACS2_peak_1052 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 64 | chr15 | unknown | gene | 44196134 | 44233467 | + | Trhr | Trhr | P9999 | NM_013696 | TSS21102 |
| chr15 | 44409030 | 44409183 | MACS2_peak_1052 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 64 | chr15 | unknown | gene | 44428110 | 44435688 | + | Eny2 | Eny2 | P1407 | NM_175009 | TSS23472 |
| chr15 | 44639646 | 44639737 | MACS2_peak_1053 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 69 | chr15 | unknown | gene | 44457552 | 44597135 | + | Pkhd1l1 | Pkhd1l1 | P6665 | NM_138674 | TSS20392 |
| chr15 | 44639646 | 44639737 | MACS2_peak_1053 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 69 | chr15 | unknown | gene | 44671855 | 44787906 | - | Sybu | Sybu | P5502 | NM_001285843 | TSS3024 |
| chr15 | 45550731 | 45550822 | MACS2_peak_1054 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 65 | chr15 | unknown | gene | 45106283 | 45114640 | - | Kcnv1 | Kcnv1 | P14911 | NM_026200 | TSS8572 |
| chr15 | 45550731 | 45550822 | MACS2_peak_1054 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 65 | chr15 | unknown | gene | 46324584 | 46373899 | + | 1700022A22Rik | 1700022A22Rik | | NR_045509 | TSS12179 |
| chr15 | 46813402 | 46813493 | MACS2_peak_1055 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 8 | chr15 | unknown | gene | 46623304 | 46639858 | + | 4930548G14Rik | 4930548G14Rik | | NR_045811 | TSS24435 |
| chr15 | 46813402 | 46813493 | MACS2_peak_1055 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 8 | chr15 | unknown | gene | 47580637 | 48791904 | - | Csmd3 | Csmd3 | P1452 | NM_001081391 | TSS8608 |
| chr15 | 47168930 | 47169021 | MACS2_peak_1056 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 58 | chr15 | unknown | gene | 46623304 | 46639858 | + | 4930548G14Rik | 4930548G14Rik | | NR_045811 | TSS24435 |
| chr15 | 47168930 | 47169021 | MACS2_peak_1056 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 58 | chr15 | unknown | gene | 47580637 | 48791904 | - | Csmd3 | Csmd3 | P1452 | NM_001081391 | TSS8608 |
| chr15 | 47287958 | 47288176 | MACS2_peak_1057 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 52 | chr15 | unknown | gene | 46623304 | 46639858 | + | 4930548G14Rik | 4930548G14Rik | | NR_045811 | TSS24435 |
| chr15 | 47287958 | 47288176 | MACS2_peak_1057 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 52 | chr15 | unknown | gene | 47580637 | 48791904 | - | Csmd3 | Csmd3 | P1452 | NM_001081391 | TSS8608 |
| chr15 | 47517240 | 47517331 | MACS2_peak_1058 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 35 | chr15 | unknown | gene | 46623304 | 46639858 | + | 4930548G14Rik | 4930548G14Rik | | NR_045811 | TSS24435 |
| chr15 | 47517240 | 47517331 | MACS2_peak_1058 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 35 | chr15 | unknown | gene | 47580637 | 48791904 | - | Csmd3 | Csmd3 | P1452 | NM_001081391 | TSS8608 |
| chr15 | 49655850 | 49655941 | MACS2_peak_1059 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 47 | chr15 | unknown | gene | 47580637 | 48791904 | - | Csmd3 | Csmd3 | P1452 | NM_001081391 | TSS8608 |
| chr15 | 49655850 | 49655941 | MACS2_peak_1059 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 47 | chr15 | unknown | gene | 50654758 | 50890041 | - | Trps1 | Trps1 | P22326 | NM_032000 | TSS19876 |
| chr15 | 49967561 | 49967652 | MACS2_peak_1060 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 19 | chr15 | unknown | gene | 47580637 | 48791904 | - | Csmd3 | Csmd3 | P1452 | NM_001081391 | TSS8608 |
| chr15 | 49967561 | 49967652 | MACS2_peak_1060 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 19 | chr15 | unknown | gene | 50654758 | 50890041 | - | Trps1 | Trps1 | P22326 | NM_032000 | TSS19876 |
| chr15 | 50666121 | 50666258 | MACS2_peak_1061 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 34 | chr15 | unknown | gene | 47580637 | 48791904 | - | Csmd3 | Csmd3 | P1452 | NM_001081391 | TSS8608 |
| chr15 | 50666121 | 50666258 | MACS2_peak_1061 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 34 | chr15 | unknown | gene | 50889024 | 50889114 | - | Mir1907 | Mir1907 | | NR_035444 | TSS697 |
| chr15 | 50726358 | 50726476 | MACS2_peak_1062 | 7 | + | 3.33222 | 3.76219 | 0.71769 | 83 | chr15 | unknown | gene | 47580637 | 48791904 | - | Csmd3 | Csmd3 | P1452 | NM_001081391 | TSS8608 |
| chr15 | 50726358 | 50726476 | MACS2_peak_1062 | 7 | + | 3.33222 | 3.76219 | 0.71769 | 83 | chr15 | unknown | gene | 50889024 | 50889114 | - | Mir1907 | Mir1907 | | NR_035444 | TSS697 |
| chr15 | 50920945 | 50921130 | MACS2_peak_1063 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 28 | chr15 | unknown | gene | 50654758 | 50890041 | - | Trps1 | Trps1 | P22326 | NM_032000 | TSS19876 |
| chr15 | 50920945 | 50921130 | MACS2_peak_1063 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 28 | chr15 | unknown | gene | 51231639 | 51395610 | - | Gm19303 | Gm19303 | | NR_045092 | TSS8987 |
| chr15 | 51282578 | 51282742 | MACS2_peak_1064 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 21 | chr15 | unknown | gene | 50654758 | 50890041 | - | Trps1 | Trps1 | P22326 | NM_032000 | TSS19876 |
| chr15 | 51282578 | 51282742 | MACS2_peak_1064 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 21 | chr15 | unknown | gene | 51786562 | 51865457 | - | Eif3h | Eif3h | P4804 | NM_080635 | TSS16244 |
| chr15 | 51439431 | 51439522 | MACS2_peak_1065 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 45 | chr15 | unknown | gene | 51231639 | 51395610 | - | Gm19303 | Gm19303 | | NR_045092 | TSS8987 |
| chr15 | 51439431 | 51439522 | MACS2_peak_1065 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 45 | chr15 | unknown | gene | 51786562 | 51865457 | - | Eif3h | Eif3h | P4804 | NM_080635 | TSS16244 |
| chr15 | 51544519 | 51544610 | MACS2_peak_1066 | 23 | + | 5.29942 | 7.14384 | 2.32792 | 48 | chr15 | unknown | gene | 51231639 | 51395610 | - | Gm19303 | Gm19303 | | NR_045092 | TSS8987 |
| chr15 | 51544519 | 51544610 | MACS2_peak_1066 | 23 | + | 5.29942 | 7.14384 | 2.32792 | 48 | chr15 | unknown | gene | 51786562 | 51865457 | - | Eif3h | Eif3h | P4804 | NM_080635 | TSS16244 |
| chr15 | 52008793 | 52008884 | MACS2_peak_1067 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 61 | chr15 | unknown | gene | 51962603 | 51991760 | - | Rad21 | Rad21 | P24686 | NM_009009 | TSS1158 |
| chr15 | 52008793 | 52008884 | MACS2_peak_1067 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 61 | chr15 | unknown | gene | 52040106 | 52044954 | + | Aard | Aard | P16062 | NM_175503 | TSS26800 |
| chr15 | 52257380 | 52257471 | MACS2_peak_1068 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 73 | chr15 | unknown | gene | 52040106 | 52044954 | + | Aard | Aard | P16062 | NM_175503 | TSS26800 |
| chr15 | 52257380 | 52257471 | MACS2_peak_1068 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 73 | chr15 | unknown | gene | 52295552 | 52335264 | + | Slc30a8 | Slc30a8 | P9668 | NM_172816 | TSS2463 |
| chr15 | 52648419 | 52648510 | MACS2_peak_1069 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 37 | chr15 | unknown | gene | 52295552 | 52335264 | + | Slc30a8 | Slc30a8 | P9668 | NM_172816 | TSS2463 |
| chr15 | 52648419 | 52648510 | MACS2_peak_1069 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 37 | chr15 | unknown | gene | 52712444 | 52730162 | + | Med30 | Med30 | P16539 | NM_027212 | TSS2015 |
| chr15 | 52690175 | 52690270 | MACS2_peak_1070 | 25 | + | 5.43741 | 7.46771 | 2.56659 | 35 | chr15 | unknown | gene | 52295552 | 52335264 | + | Slc30a8 | Slc30a8 | P9668 | NM_172816 | TSS2463 |
| chr15 | 52690175 | 52690270 | MACS2_peak_1070 | 25 | + | 5.43741 | 7.46771 | 2.56659 | 35 | chr15 | unknown | gene | 52712444 | 52730162 | + | Med30 | Med30 | P16539 | NM_027212 | TSS2015 |
| chr15 | 53212728 | 53212845 | MACS2_peak_1071 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 63 | chr15 | unknown | gene | 52712444 | 52730162 | + | Med30 | Med30 | P16539 | NM_027212 | TSS2015 |
| chr15 | 53212728 | 53212845 | MACS2_peak_1071 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 63 | chr15 | unknown | gene | 53461800 | 53902381 | - | Samd12 | Samd12 | P1687 | NM_177225 | TSS14169 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr15 | 53254791 | 53254882 | MACS2_peak_1072 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 37 | chr15 | unknown | gene | 52712444 | 52730162 | + | Med30 | Med30 | P16539 | NM_027212 | TSS2015 |
| chr15 | 53254791 | 53254882 | MACS2_peak_1072 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 37 | chr15 | unknown | gene | 53461800 | 53902381 | - | Samd12 | Samd12 | P1687 | NM_177225 | TSS14169 |
| chr15 | 53370517 | 53370632 | MACS2_peak_1073 | 48 | + | 6.64572 | 9.88132 | 4.80476 | 47 | chr15 | unknown | gene | 53068260 | 53345363 | - | Ext1 | Ext1 | P10111 | NM_010162 | TSS2271 |
| chr15 | 53370517 | 53370632 | MACS2_peak_1073 | 48 | + | 6.64572 | 9.88132 | 4.80476 | 47 | chr15 | unknown | gene | 53461800 | 53902381 | - | Samd12 | Samd12 | P1687 | NM_177225 | TSS14169 |
| chr15 | 56046858 | 56046949 | MACS2_peak_1074 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 34 | chr15 | unknown | gene | 55639153 | 55906591 | - | Sntb1 | Sntb1 | P17594 | NM_016667 | TSS2375 |
| chr15 | 56046858 | 56046949 | MACS2_peak_1074 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 34 | chr15 | unknown | gene | 56665626 | 56694546 | - | Has2 | Has2 | P3879 | NM_008216 | TSS13533 |
| chr15 | 56495591 | 56495682 | MACS2_peak_1075 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 26 | chr15 | unknown | gene | 55639153 | 55906591 | - | Sntb1 | Sntb1 | P17594 | NM_016667 | TSS2375 |
| chr15 | 56495591 | 56495682 | MACS2_peak_1075 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 26 | chr15 | unknown | gene | 56665626 | 56694546 | - | Has2 | Has2 | P3879 | NM_008216 | TSS13533 |
| chr15 | 56643268 | 56643359 | MACS2_peak_1076 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 34 | chr15 | unknown | gene | 55639153 | 55906591 | - | Sntb1 | Sntb1 | P17594 | NM_016667 | TSS2375 |
| chr15 | 56643268 | 56643359 | MACS2_peak_1076 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 34 | chr15 | unknown | gene | 56665626 | 56694546 | - | Has2 | Has2 | P3879 | NM_008216 | TSS13533 |
| chr15 | 56797760 | 56797887 | MACS2_peak_1077 | 27 | + | 5.56793 | 7.65146 | 2.73702 | 54 | chr15 | unknown | gene | 56665626 | 56694546 | - | Has2 | Has2 | P3879 | NM_008216 | TSS13533 |
| chr15 | 56797760 | 56797887 | MACS2_peak_1077 | 27 | + | 5.56793 | 7.65146 | 2.73702 | 54 | chr15 | unknown | gene | 57243770 | 57477625 | - | Slc22a22 | Slc22a22 | P21555 | NM_172378 | TSS20018 |
| chr15 | 56975852 | 56975943 | MACS2_peak_1078 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 29 | chr15 | unknown | gene | 56665626 | 56694546 | - | Has2 | Has2 | P3879 | NM_008216 | TSS13533 |
| chr15 | 56975852 | 56975943 | MACS2_peak_1078 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 29 | chr15 | unknown | gene | 57243770 | 57477625 | - | Slc22a22 | Slc22a22 | P21555 | NM_172378 | TSS20018 |
| chr15 | 59037165 | 59037274 | MACS2_peak_1079 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 48 | chr15 | unknown | gene | 58933809 | 58939406 | + | Ndufb9 | Ndufb9 | P16146 | NM_023172 | TSS8517 |
| chr15 | 59037165 | 59037274 | MACS2_peak_1079 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 48 | chr15 | unknown | gene | 59306947 | 59312013 | + | Zfp572 | Zfp572 | | NR_045613 | TSS19404 |
| chr15 | 60899698 | 60899789 | MACS2_peak_1080 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 50 | chr15 | unknown | gene | 60822964 | 60831400 | + | 9930014A18Rik | 9930014A18Rik | | NR_030696 | TSS20412 |
| chr15 | 60899698 | 60899789 | MACS2_peak_1080 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 50 | chr15 | unknown | gene | 60917588 | 60921256 | - | A1bg | A1bg | P17517 | NM_001081067 | TSS21488 |
| chr15 | 60987205 | 60987332 | MACS2_peak_1081 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 74 | chr15 | unknown | gene | 60917588 | 60921256 | - | A1bg | A1bg | P17517 | NM_001081067 | TSS21488 |
| chr15 | 60987205 | 60987332 | MACS2_peak_1081 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 74 | chr15 | unknown | gene | 61699283 | 61774451 | - | D030024E09Rik | D030024E09Rik | | NR_040350 | TSS20389 |
| chr15 | 61922439 | 61922547 | MACS2_peak_1082 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 61 | chr15 | unknown | gene | 61699283 | 61774451 | - | D030024E09Rik | D030024E09Rik | | NR_040350 | TSS20389 |
| chr15 | 61922439 | 61922547 | MACS2_peak_1082 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 61 | chr15 | unknown | gene | 61985340 | 61989908 | + | Myc | Myc | P26346 | NM_001177352 | TSS16552 |
| chr15 | 62094558 | 62094649 | MACS2_peak_1083 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 33 | chr15 | unknown | gene | 61985340 | 61989908 | + | Myc | Myc | P26346 | NM_001177352 | TSS16552 |
| chr15 | 62094558 | 62094649 | MACS2_peak_1083 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 33 | chr15 | unknown | gene | 62217540 | 62219451 | - | H2afy3 | H2afy3 | | NR_003523 | TSS24562 |
| chr15 | 62608242 | 62608333 | MACS2_peak_1084 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 46 | chr15 | unknown | gene | 62037986 | 62250975 | + | Pvt1 | Pvt1 | | NR_003368 | TSS2371 |
| chr15 | 62608242 | 62608333 | MACS2_peak_1084 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 46 | chr15 | unknown | gene | 63414396 | 63479608 | - | Gm20740 | Gm20740 | | NR_045279 | TSS20574 |
| chr15 | 62985635 | 62985726 | MACS2_peak_1085 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 42 | chr15 | unknown | gene | 62037986 | 62250975 | + | Pvt1 | Pvt1 | | NR_003368 | TSS2371 |
| chr15 | 62985635 | 62985726 | MACS2_peak_1085 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 42 | chr15 | unknown | gene | 63414396 | 63479608 | - | Gm20740 | Gm20740 | | NR_045279 | TSS20574 |
| chr15 | 63439179 | 63439270 | MACS2_peak_1086 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 47 | chr15 | unknown | gene | 62037986 | 62250975 | + | Pvt1 | Pvt1 | | NR_003368 | TSS2371 |
| chr15 | 63439179 | 63439270 | MACS2_peak_1086 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 47 | chr15 | unknown | gene | 63775970 | 63808739 | - | Gsdmc | Gsdmc | P22206 | NM_031378 | TSS27325 |
| chr15 | 63583955 | 63584089 | MACS2_peak_1087 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 86 | chr15 | unknown | gene | 63414396 | 63479608 | - | Gm20740 | Gm20740 | | NR_045279 | TSS20574 |
| chr15 | 63583955 | 63584089 | MACS2_peak_1087 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 86 | chr15 | unknown | gene | 63775970 | 63808739 | - | Gsdmc | Gsdmc | P22206 | NM_031378 | TSS27325 |
| chr15 | 64760242 | 64760333 | MACS2_peak_1088 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 31 | chr15 | unknown | gene | 64086839 | 64382919 | - | Asap1 | Asap1 | P16408 | NM_001276462 | TSS6642 |
| chr15 | 64760242 | 64760333 | MACS2_peak_1088 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 31 | chr15 | unknown | gene | 65787040 | 65871258 | + | Efr3a | Efr3a | P1911 | NM_133766 | TSS25209 |
| chr15 | 66584457 | 66584548 | MACS2_peak_1089 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 3 | chr15 | unknown | gene | 66526211 | 66561046 | - | Tmem71 | Tmem71 | P8381 | NM_172514 | TSS10512 |
| chr15 | 66584457 | 66584548 | MACS2_peak_1089 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 3 | chr15 | unknown | gene | 66670769 | 66850607 | + | Tg | Tg | P7364 | NM_009375 | TSS8870 |
| chr15 | 66624819 | 66624914 | MACS2_peak_1090 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 20 | chr15 | unknown | gene | 66526211 | 66561046 | - | Tmem71 | Tmem71 | P8381 | NM_172514 | TSS10512 |
| chr15 | 66624819 | 66624914 | MACS2_peak_1090 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 20 | chr15 | unknown | gene | 66670769 | 66850607 | + | Tg | Tg | P7364 | NM_009375 | TSS8870 |
| chr15 | 66862000 | 66862357 | MACS2_peak_1091 | 58 | + | 4.60624 | 5.88904 | 1.68837 | 275 | chr15 | unknown | gene | 66670769 | 66850607 | + | Tg | Tg | P7364 | NM_009375 | TSS8870 |
| chr15 | 66862000 | 66862357 | MACS2_peak_1091 | 58 | + | 4.60624 | 5.88904 | 1.68837 | 275 | chr15 | unknown | gene | 66891392 | 66919454 | + | Wisp1 | Wisp1 | P25677 | NM_018865 | TSS12117 |
| chr15 | 67195720 | 67195811 | MACS2_peak_1092 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 36 | chr15 | unknown | gene | 67102874 | 67176882 | - | St3gal1 | St3gal1 | P20453 | NM_009177 | TSS19942 |
| chr15 | 67195720 | 67195811 | MACS2_peak_1092 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 36 | chr15 | unknown | gene | 67226768 | 67377094 | + | 1700012I11Rik | 1700012I11Rik | | NR_045140 | TSS6041 |
| chr15 | 67575263 | 67575354 | MACS2_peak_1093 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 41 | chr15 | unknown | gene | 67226768 | 67377094 | + | 1700012I11Rik | 1700012I11Rik | | NR_045140 | TSS6041 |
| chr15 | 67575263 | 67575354 | MACS2_peak_1093 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 41 | chr15 | unknown | gene | 68083737 | 68258686 | - | Zfat | Zfat | P21774 | NM_001145888 | TSS25639 |
| chr15 | 68221985 | 68222096 | MACS2_peak_1094 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 36 | chr15 | unknown | gene | 67226768 | 67377094 | + | 1700012I11Rik | 1700012I11Rik | | NR_045140 | TSS6041 |
| chr15 | 68221985 | 68222096 | MACS2_peak_1094 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 36 | chr15 | unknown | gene | 68337414 | 68337510 | - | Mir30b | Mir30b | | NR_029534 | TSS16089 |
| chr15 | 68566339 | 68566430 | MACS2_peak_1095 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 57 | chr15 | unknown | gene | 68341207 | 68341289 | - | Mir30d | Mir30d | | NR_029718 | TSS21459 |
| chr15 | 68566339 | 68566430 | MACS2_peak_1095 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 57 | chr15 | unknown | gene | 68928419 | 69092992 | + | Khdrbs3 | Khdrbs3 | P11381 | NM_010158 | TSS23736 |
| chr15 | 69103658 | 69103761 | MACS2_peak_1096 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 21 | chr15 | unknown | gene | 68928419 | 69092992 | + | Khdrbs3 | Khdrbs3 | P11381 | NM_010158 | TSS23736 |
| chr15 | 69103658 | 69103761 | MACS2_peak_1096 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 21 | chr15 | unknown | gene | 69270532 | 69274718 | + | 4930504C09Rik | 4930504C09Rik | | NR_130983 | TSS23153 |
| chr15 | 70746207 | 70746317 | MACS2_peak_1097 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 40 | chr15 | unknown | gene | 69924232 | 70078204 | + | Gm19782 | Gm19782 | | NR_045071 | TSS14525 |
| chr15 | 70746207 | 70746317 | MACS2_peak_1097 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 40 | chr15 | unknown | gene | 71445677 | 71727838 | - | Fam135b | Fam135b | P22515 | NM_177819 | TSS25247 |
| chr15 | 70870360 | 70870451 | MACS2_peak_1098 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 48 | chr15 | unknown | gene | 69924232 | 70078204 | + | Gm19782 | Gm19782 | | NR_045071 | TSS14525 |
| chr15 | 70870360 | 70870451 | MACS2_peak_1098 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 48 | chr15 | unknown | gene | 71445677 | 71727838 | - | Fam135b | Fam135b | P22515 | NM_177819 | TSS25247 |
| chr15 | 72097586 | 72097677 | MACS2_peak_1099 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 32 | chr15 | unknown | gene | 71798475 | 72034227 | - | Col22a1 | Col22a1 | P10950 | NM_027174 | TSS19148 |
| chr15 | 72097586 | 72097677 | MACS2_peak_1099 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 32 | chr15 | unknown | gene | 72512118 | 72546279 | - | Kcnk9 | Kcnk9 | P17040 | NM_001033876 | TSS25036 |
| chr15 | 75086294 | 75086394 | MACS2_peak_1100 | 39 | + | 5.94295 | 8.98862 | 3.94951 | 31 | chr15 | unknown | gene | 75044017 | 75048837 | - | Ly6c1 | Ly6c1 | P12542 | NM_001252056 | TSS16983 |
| chr15 | 75086294 | 75086394 | MACS2_peak_1100 | 39 | + | 5.94295 | 8.98862 | 3.94951 | 31 | chr15 | unknown | gene | 75108160 | 75111949 | - | Ly6c2 | Ly6c2 | P17452 | NM_001099217 | TSS18770 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr15 | 75086664 | 75087018 | MACS2_peak_1101 | 109 | + | 9.0366 | 16.27748 | 10.95807 | 267 | chr15 | unknown | gene | 75044017 | 75048837 | - | Ly6c1 | Ly6c1 | P12542 | NM_001252056 | TSS16983 |
| chr15 | 75086664 | 75087018 | MACS2_peak_1101 | 109 | + | 9.0366 | 16.27748 | 10.95807 | 267 | chr15 | unknown | gene | 75108160 | 75111949 | - | Ly6c2 | Ly6c2 | P17452 | NM_001099217 | TSS18770 |
| chr15 | 76555889 | 76556024 | MACS2_peak_1102 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 51 | chr15 | unknown | gene | 76538942 | 76541126 | + | Slc52a2 | Slc52a2 | P15320 | NM_029643 | TSS17322 |
| chr15 | 76555889 | 76556024 | MACS2_peak_1102 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 51 | chr15 | unknown | gene | 76576358 | 76595650 | + | Adck5 | Adck5 | P4681 | NM_172960 | TSS12585 |
| chr15 | 77151715 | 77151806 | MACS2_peak_1103 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 34 | chr15 | unknown | gene | 77084397 | 77096314 | + | 1700109K24Rik | 1700109K24Rik | | NR_108037 | TSS17068 |
| chr15 | 77151715 | 77151806 | MACS2_peak_1103 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 34 | chr15 | unknown | gene | 77388216 | 77399110 | - | Apol7a | Apol7a | P17750 | NM_029419 | TSS3881 |
| chr15 | 78351981 | 78352072 | MACS2_peak_1104 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 58 | chr15 | unknown | gene | 78325989 | 78349185 | + | Csf2rb | Csf2rb | P5100 | NM_007780 | TSS24596 |
| chr15 | 78351981 | 78352072 | MACS2_peak_1104 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 58 | chr15 | unknown | gene | 78378399 | 78395912 | - | Tex33 | Tex33 | P17110 | NM_028522 | TSS13912 |
| chr15 | 79682717 | 79682808 | MACS2_peak_1105 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 59 | chr15 | unknown | gene | 79670867 | 79672291 | + | Tomm22 | Tomm22 | P9227 | NM_172609 | TSS19095 |
| chr15 | 79682717 | 79682808 | MACS2_peak_1105 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 59 | chr15 | unknown | gene | 79690895 | 79720099 | + | Gtpbp1 | Gtpbp1 | P21965 | NM_013818 | TSS18272 |
| chr15 | 82040008 | 82040137 | MACS2_peak_1106 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 44 | chr15 | unknown | gene | 82016368 | 82039918 | + | Xrcc6 | Xrcc6 | P16285 | NM_010247 | TSS8049 |
| chr15 | 82040008 | 82040137 | MACS2_peak_1106 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 44 | chr15 | unknown | gene | 82041344 | 82047489 | - | Nhp2l1 | Nhp2l1 | P18182 | NM_011482 | TSS7122 |
| chr15 | 84969544 | 84969635 | MACS2_peak_1107 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 20 | chr15 | unknown | gene | 84951525 | 84951623 | - | Mir1249 | Mir1249 | | NR_037206 | TSS19781 |
| chr15 | 84969544 | 84969635 | MACS2_peak_1107 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 20 | chr15 | unknown | gene | 85017140 | 85022397 | + | Upk3a | Upk3a | P489 | NM_023478 | TSS22743 |
| chr15 | 86613361 | 86613469 | MACS2_peak_1108 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 46 | chr15 | unknown | gene | 86214458 | 86496941 | + | Tbc1d22a | Tbc1d22a | P16980 | NM_145476 | TSS4298 |
| chr15 | 86613361 | 86613469 | MACS2_peak_1108 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 46 | chr15 | unknown | gene | 87544298 | 87757305 | + | Fam19a5 | Fam19a5 | P2484 | NM_001252310 | TSS17122 |
| chr15 | 88740522 | 88740613 | MACS2_peak_1109 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 59 | chr15 | unknown | gene | 88687034 | 88734219 | - | Brd1 | Brd1 | P7663 | NM_001033274 | TSS16566 |
| chr15 | 88740522 | 88740613 | MACS2_peak_1109 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 59 | chr15 | unknown | gene | 88751710 | 88783237 | + | Zbed4 | Zbed4 | P12846 | NM_181412 | TSS20619 |
| chr15 | 90161855 | 90161946 | MACS2_peak_1110 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 52 | chr15 | unknown | gene | 89782392 | 89841769 | - | Syt10 | Syt10 | P21647 | NM_018803 | TSS21559 |
| chr15 | 90161855 | 90161946 | MACS2_peak_1110 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 52 | chr15 | unknown | gene | 90224310 | 90228379 | + | Alg10b | Alg10b | P8099 | NM_001033441 | TSS14657 |
| chr15 | 90540435 | 90540526 | MACS2_peak_1111 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 85 | chr15 | unknown | gene | 90224310 | 90228379 | + | Alg10b | Alg10b | P8099 | NM_001033441 | TSS14657 |
| chr15 | 90540435 | 90540526 | MACS2_peak_1111 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 85 | chr15 | unknown | gene | 90891395 | 90898476 | - | Spn-ps | Spn-ps | | NR_033583 | TSS17292 |
| chr15 | 91398508 | 91398650 | MACS2_peak_1112 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 82 | chr15 | unknown | gene | 91145870 | 91191608 | - | Abcd2 | Abcd2 | P11181 | NM_011994 | TSS22233 |
| chr15 | 91398508 | 91398650 | MACS2_peak_1112 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 82 | chr15 | unknown | gene | 91673223 | 91815535 | + | Lrrk2 | Lrrk2 | P9453 | NM_025730 | TSS23038 |
| chr15 | 93887390 | 93887481 | MACS2_peak_1113 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 62 | chr15 | unknown | gene | 93499113 | 93595891 | - | Prickle1 | Prickle1 | P9908 | NM_001033217 | TSS23053 |
| chr15 | 93887390 | 93887481 | MACS2_peak_1113 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 62 | chr15 | unknown | gene | 93904855 | 93927111 | - | 9430014N10Rik | 9430014N10Rik | | NR_045737 | TSS17373 |
| chr15 | 94522509 | 94522600 | MACS2_peak_1114 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 23 | chr15 | unknown | gene | 94270162 | 94404089 | - | Adamts20 | Adamts20 | P5436 | NM_177431 | TSS21136 |
| chr15 | 94522509 | 94522600 | MACS2_peak_1114 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 23 | chr15 | unknown | gene | 94522639 | 94543507 | - | Pus7l | Pus7l | P25272 | NM_172437 | TSS7225 |
| chr15 | 95877104 | 95877211 | MACS2_peak_1115 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 39 | chr15 | unknown | gene | 95747246 | 95751591 | - | Gm6961 | Gm6961 | | NR_131148 | TSS4160 |
| chr15 | 95877104 | 95877211 | MACS2_peak_1115 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 39 | chr15 | unknown | gene | 96051615 | 96079553 | - | D030018L15Rik | D030018L15Rik | | NR_126493 | TSS13004 |
| chr15 | 96543600 | 96543696 | MACS2_peak_1116 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 35 | chr15 | unknown | gene | 96411697 | 96460843 | - | Scaf11 | Scaf11 | P26382 | NM_028148 | TSS4859 |
| chr15 | 96543600 | 96543696 | MACS2_peak_1116 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 35 | chr15 | unknown | gene | 96571417 | 96642913 | - | Slc38a1 | Slc38a1 | P4201 | NM_134086 | TSS23340 |
| chr15 | 97135152 | 97135243 | MACS2_peak_1117 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 48 | chr15 | unknown | gene | 96994822 | 97055956 | - | Slc38a4 | Slc38a4 | P1568 | NM_027052 | TSS8747 |
| chr15 | 97135152 | 97135243 | MACS2_peak_1117 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 48 | chr15 | unknown | gene | 97244073 | 97247287 | - | Amigo2 | Amigo2 | P26735 | NM_001164602 | TSS23350 |
| chr15 | 98487512 | 98487636 | MACS2_peak_1118 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 80 | chr15 | unknown | gene | 98480399 | 98482671 | - | Lalba | Lalba | P10070 | NM_010679 | TSS4962 |
| chr15 | 98487512 | 98487636 | MACS2_peak_1118 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 80 | chr15 | unknown | gene | 98497473 | 98498406 | + | Olfr279 | Olfr279 | P26822 | NM_001001807 | TSS26513 |
| chr15 | 98987531 | 98987622 | MACS2_peak_1119 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 46 | chr15 | unknown | gene | 98949846 | 98953453 | - | Tuba1a | Tuba1a | P7531 | NM_011653 | TSS14095 |
| chr15 | 98987531 | 98987622 | MACS2_peak_1119 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 46 | chr15 | unknown | gene | 99029890 | 99038009 | + | Tuba1c | Tuba1c | P4921 | NM_009448 | TSS17060 |
| chr16 | 3116285 | 3116376 | MACS2_peak_1120 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 38 | chr16 | unknown | gene | 3592397 | 3593339 | + | Olfr161 | Olfr161 | P23523 | NM_146860 | TSS19013 |
| chr16 | 3263399 | 3263490 | MACS2_peak_1121 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 33 | chr16 | unknown | gene | 3592397 | 3593339 | + | Olfr161 | Olfr161 | P23523 | NM_146860 | TSS19013 |
| chr16 | 8227812 | 8227908 | MACS2_peak_1122 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 61 | chr16 | unknown | gene | 5884792 | 7409813 | + | Rbfox1 | Rbfox1 | P14402 | NM_021477 | TSS7767 |
| chr16 | 8227812 | 8227908 | MACS2_peak_1122 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 61 | chr16 | unknown | gene | 8409275 | 8424652 | - | Tmem114 | Tmem114 | P5063 | NM_029070 | TSS19871 |
| chr16 | 10844390 | 10844481 | MACS2_peak_1123 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 17 | chr16 | unknown | gene | 10835058 | 10839977 | + | Rmi2 | Rmi2 | P3419 | NM_001162932 | TSS6751 |
| chr16 | 10844390 | 10844481 | MACS2_peak_1123 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 17 | chr16 | unknown | gene | 10912011 | 10914797 | - | Gm21859 | Gm21859 | | NR_131135 | TSS8442 |
| chr16 | 10975059 | 10975199 | MACS2_peak_1124 | 255 | + | 16.21317 | 31.28527 | 25.58562 | 71 | chr16 | unknown | gene | 10912011 | 10914797 | - | Gm21859 | Gm21859 | | NR_131135 | TSS8442 |
| chr16 | 10975059 | 10975199 | MACS2_peak_1124 | 255 | + | 16.21317 | 31.28527 | 25.58562 | 71 | chr16 | unknown | gene | 11008897 | 11015184 | + | Gm4262 | Gm4262 | | NR_040518 | TSS10466 |
| chr16 | 14801966 | 14802057 | MACS2_peak_1125 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 60 | chr16 | unknown | gene | 14705858 | 14708296 | + | Snai2 | Snai2 | P11973 | NM_011415 | TSS10768 |
| chr16 | 14801966 | 14802057 | MACS2_peak_1125 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 60 | chr16 | unknown | gene | 14906645 | 14924142 | + | Efcab1 | Efcab1 | P2532 | NM_025769 | TSS22734 |
| chr16 | 14941337 | 14941428 | MACS2_peak_1126 | 18 | + | 4.94193 | 6.51115 | 1.87984 | 67 | chr16 | unknown | gene | 14906645 | 14924142 | + | Efcab1 | Efcab1 | P2532 | NM_025769 | TSS22734 |
| chr16 | 14941337 | 14941428 | MACS2_peak_1126 | 18 | + | 4.94193 | 6.51115 | 1.87984 | 67 | chr16 | unknown | gene | 15550985 | 15594475 | - | Ube2v2 | Ube2v2 | P8766 | NM_023585 | TSS12353 |
| chr16 | 15934439 | 15934530 | MACS2_peak_1127 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 9 | chr16 | unknown | gene | 15887285 | 15888131 | + | Cebpd | Cebpd | P15389 | NM_007679 | TSS2286 |
| chr16 | 15934439 | 15934530 | MACS2_peak_1127 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 9 | chr16 | unknown | gene | 16213344 | 16272237 | + | Pkp2 | Pkp2 | P23749 | NM_026163 | TSS2969 |
| chr16 | 16427572 | 16427685 | MACS2_peak_1128 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 44 | chr16 | unknown | gene | 16312227 | 16358865 | - | Dnm1l | Dnm1l | P1696 | NM_001276341 | TSS13008 |
| chr16 | 16427572 | 16427685 | MACS2_peak_1128 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 44 | chr16 | unknown | gene | 16673049 | 16673979 | - | Olfr19 | Olfr19 | P21172 | NM_146335 | TSS22199 |
| chr16 | 21472873 | 21472964 | MACS2_peak_1129 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 18 | chr16 | unknown | gene | 21331899 | 21333356 | - | Magef1 | Magef1 | | NR_131983 | TSS25371 |
| chr16 | 21472873 | 21472964 | MACS2_peak_1129 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 18 | chr16 | unknown | gene | 21649044 | 21694405 | - | 2510009E07Rik | 2510009E07Rik | P19930 | NM_001001881 | TSS6285 |
| chr16 | 23530284 | 23530375 | MACS2_peak_1130 | 16 | + | 4.811 | 6.2687 | 1.67914 | 28 | chr16 | unknown | gene | 23451784 | 23520550 | - | Masp1 | Masp1 | P14810 | NM_008555 | TSS17048 |
| chr16 | 23530284 | 23530375 | MACS2_peak_1130 | 16 | + | 4.811 | 6.2687 | 1.67914 | 28 | chr16 | unknown | gene | 23609918 | 23613469 | + | Rtp4 | Rtp4 | P22140 | NM_023386 | TSS5613 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr16 | 23792848 | 23792939 | MACS2_peak_1131 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 44 | chr16 | unknown | gene | 23609918 | 23613469 | + | Rtp4 | Rtp4 | P22140 | NM_023386 | TSS5613 |
| chr16 | 23792848 | 23792939 | MACS2_peak_1131 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 44 | chr16 | unknown | gene | 23889580 | 23890744 | - | Sst | Sst | P9954 | NM_009215 | TSS23661 |
| chr16 | 25967618 | 25967709 | MACS2_peak_1132 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 20 | chr16 | unknown | gene | 25683764 | 25889304 | + | Trp63 | Trp63 | P23763 | NM_001127259 | TSS10746 |
| chr16 | 25967618 | 25967709 | MACS2_peak_1132 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 20 | chr16 | unknown | gene | 26356645 | 26371626 | - | Cldn1 | Cldn1 | P17448 | NM_016674 | TSS22392 |
| chr16 | 26035480 | 26035587 | MACS2_peak_1133 | 12 | + | 4.14966 | 5.12722 | 1.204 | 65 | chr16 | unknown | gene | 25683764 | 25889304 | + | Trp63 | Trp63 | P23763 | NM_001127259 | TSS10746 |
| chr16 | 26035480 | 26035587 | MACS2_peak_1133 | 12 | + | 4.14966 | 5.12722 | 1.204 | 65 | chr16 | unknown | gene | 26356645 | 26371626 | - | Cldn1 | Cldn1 | P17448 | NM_016674 | TSS22392 |
| chr16 | 27265746 | 27265837 | MACS2_peak_1134 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 64 | chr16 | unknown | gene | 26957234 | 26991652 | - | Gmnc | Gmnc | P24605 | NM_001285916 | TSS26418 |
| chr16 | 27265746 | 27265837 | MACS2_peak_1134 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 64 | chr16 | unknown | gene | 27307640 | 27351209 | + | Ostn | Ostn | P17892 | NM_198112 | TSS16453 |
| chr16 | 28417529 | 28417656 | MACS2_peak_1135 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 51 | chr16 | unknown | gene | 27849929 | 27926128 | + | Gm10823 | Gm10823 | | NR_033475 | TSS3931 |
| chr16 | 28417529 | 28417656 | MACS2_peak_1135 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 51 | chr16 | unknown | gene | 28599934 | 28600043 | - | Mir690 | Mir690 | | NR_030463 | TSS12715 |
| chr16 | 28479568 | 28479659 | MACS2_peak_1136 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 2 | chr16 | unknown | gene | 27849929 | 27926128 | + | Gm10823 | Gm10823 | | NR_033475 | TSS3931 |
| chr16 | 28479568 | 28479659 | MACS2_peak_1136 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 2 | chr16 | unknown | gene | 28599934 | 28600043 | - | Mir690 | Mir690 | | NR_030463 | TSS12715 |
| chr16 | 28690110 | 28690201 | MACS2_peak_1137 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 58 | chr16 | unknown | gene | 28599934 | 28600043 | - | Mir690 | Mir690 | | NR_030463 | TSS12715 |
| chr16 | 28690110 | 28690201 | MACS2_peak_1137 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 58 | chr16 | unknown | gene | 28826175 | 28929663 | - | Mb21d2 | Mb21d2 | P22773 | NM_177718 | TSS4549 |
| chr16 | 28701742 | 28701833 | MACS2_peak_1138 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 4 | chr16 | unknown | gene | 28599934 | 28600043 | - | Mir690 | Mir690 | | NR_030463 | TSS12715 |
| chr16 | 28701742 | 28701833 | MACS2_peak_1138 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 4 | chr16 | unknown | gene | 28826175 | 28929663 | - | Mb21d2 | Mb21d2 | P22773 | NM_177718 | TSS4549 |
| chr16 | 31190700 | 31190791 | MACS2_peak_1139 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 8 | chr16 | unknown | gene | 30955502 | 31081335 | - | Xxylt1 | Xxylt1 | P7857 | NM_198626 | TSS24230 |
| chr16 | 31190700 | 31190791 | MACS2_peak_1139 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 8 | chr16 | unknown | gene | 31251540 | 31274970 | - | Ppp1r2 | Ppp1r2 | P11113 | NM_025800 | TSS11548 |
| chr16 | 31592292 | 31592383 | MACS2_peak_1140 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 44 | chr16 | unknown | gene | 31422296 | 31457094 | + | Bdh1 | Bdh1 | P5739 | NM_175177 | TSS7154 |
| chr16 | 31592292 | 31592383 | MACS2_peak_1140 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 44 | chr16 | unknown | gene | 31663442 | 31871781 | + | Dlg1 | Dlg1 | P462 | NM_001252435 | TSS7760 |
| chr16 | 31656718 | 31656809 | MACS2_peak_1141 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 45 | chr16 | unknown | gene | 31422296 | 31457094 | + | Bdh1 | Bdh1 | P5739 | NM_175177 | TSS7154 |
| chr16 | 31656718 | 31656809 | MACS2_peak_1141 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 45 | chr16 | unknown | gene | 31663442 | 31871781 | + | Dlg1 | Dlg1 | P462 | NM_001252435 | TSS7760 |
| chr16 | 33571777 | 33571868 | MACS2_peak_1142 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 47 | chr16 | unknown | gene | 33380774 | 33497344 | + | Zfp148 | Zfp148 | P26320 | NM_011749 | TSS19815 |
| chr16 | 33571777 | 33571868 | MACS2_peak_1142 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 47 | chr16 | unknown | gene | 33684465 | 33766810 | + | Heg1 | Heg1 | P21505 | NM_175256 | TSS22109 |
| chr16 | 33636896 | 33636987 | MACS2_peak_1143 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 54 | chr16 | unknown | gene | 33380774 | 33497344 | + | Zfp148 | Zfp148 | P26320 | NM_011749 | TSS19815 |
| chr16 | 33636896 | 33636987 | MACS2_peak_1143 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 54 | chr16 | unknown | gene | 33684465 | 33766810 | + | Heg1 | Heg1 | P21505 | NM_175256 | TSS22109 |
| chr16 | 34292598 | 34292689 | MACS2_peak_1144 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 18 | chr16 | unknown | gene | 33955011 | 33966981 | - | Umps | Umps | P6048 | NM_009471 | TSS23191 |
| chr16 | 34292598 | 34292689 | MACS2_peak_1144 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 18 | chr16 | unknown | gene | 34651210 | 34678482 | + | Ropn1 | Ropn1 | P13189 | NM_030744 | TSS14287 |
| chr16 | 34962099 | 34962190 | MACS2_peak_1145 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 22 | chr16 | unknown | gene | 34943174 | 34958994 | - | E130310I04Rik | E130310I04Rik | | NR_045723 | TSS22028 |
| chr16 | 34962099 | 34962190 | MACS2_peak_1145 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 22 | chr16 | unknown | gene | 35022420 | 35106397 | + | Hacd2 | Hacd2 | P13597 | NM_023587 | TSS3625 |
| chr16 | 35554712 | 35554835 | MACS2_peak_1146 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 68 | chr16 | unknown | gene | 35503169 | 35509419 | - | 1600019K03Rik | 1600019K03Rik | | NR_040481 | TSS4029 |
| chr16 | 35554712 | 35554835 | MACS2_peak_1146 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 68 | chr16 | unknown | gene | 35694902 | 35769241 | - | Dirc2 | Dirc2 | P4399 | NM_153550 | TSS19439 |
| chr16 | 36206191 | 36206296 | MACS2_peak_1147 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 21 | chr16 | unknown | gene | 36194479 | 36197886 | - | Gm6815 | Gm6815 | | NR_102685 | TSS14090 |
| chr16 | 36206191 | 36206296 | MACS2_peak_1147 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 21 | chr16 | unknown | gene | 36210402 | 36217788 | + | Gm5416 | Gm5416 | P9360 | NM_001082542 | TSS20236 |
| chr16 | 37005915 | 37006006 | MACS2_peak_1148 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 70 | chr16 | unknown | gene | 36966072 | 36978751 | - | Fbxo40 | Fbxo40 | P5965 | NM_001037321 | TSS15751 |
| chr16 | 37005915 | 37006006 | MACS2_peak_1148 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 70 | chr16 | unknown | gene | 37011785 | 37094614 | + | Polq | Polq | P9363 | NM_001159369 | TSS24806 |
| chr16 | 37093965 | 37094056 | MACS2_peak_1149 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 3 | chr16 | unknown | gene | 36966072 | 36978751 | - | Fbxo40 | Fbxo40 | P5965 | NM_001037321 | TSS15751 |
| chr16 | 37093965 | 37094056 | MACS2_peak_1149 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 3 | chr16 | unknown | gene | 37107309 | 37384958 | - | Stxbp5l | Stxbp5l | P1930 | NM_172440 | TSS25533 |
| chr16 | 37514023 | 37514114 | MACS2_peak_1150 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 57 | chr16 | unknown | gene | 37107309 | 37384958 | - | Stxbp5l | Stxbp5l | P1930 | NM_172440 | TSS25533 |
| chr16 | 37514023 | 37514114 | MACS2_peak_1150 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 57 | chr16 | unknown | gene | 37539893 | 37571095 | + | Rabl3 | Rabl3 | P2565 | NM_001042499 | TSS16927 |
| chr16 | 39233911 | 39234002 | MACS2_peak_1151 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 30 | chr16 | unknown | gene | 38902344 | 39025195 | + | Igsf11 | Igsf11 | P5820 | NM_170599 | TSS1773 |
| chr16 | 39233911 | 39234002 | MACS2_peak_1151 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 30 | chr16 | unknown | gene | 41533341 | 42144807 | + | Lsamp | Lsamp | P14748 | NM_175548 | TSS12217 |
| chr16 | 40504609 | 40504700 | MACS2_peak_1152 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 15 | chr16 | unknown | gene | 38902344 | 39025195 | + | Igsf11 | Igsf11 | P5820 | NM_170599 | TSS1773 |
| chr16 | 40504609 | 40504700 | MACS2_peak_1152 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 15 | chr16 | unknown | gene | 41533341 | 42144807 | + | Lsamp | Lsamp | P14748 | NM_175548 | TSS12217 |
| chr16 | 40847548 | 40847639 | MACS2_peak_1153 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 44 | chr16 | unknown | gene | 38902344 | 39025195 | + | Igsf11 | Igsf11 | P5820 | NM_170599 | TSS1773 |
| chr16 | 40847548 | 40847639 | MACS2_peak_1153 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 44 | chr16 | unknown | gene | 41533341 | 42144807 | + | Lsamp | Lsamp | P14748 | NM_175548 | TSS12217 |
| chr16 | 41050525 | 41050665 | MACS2_peak_1154 | 47 | + | 6.68747 | 9.84528 | 4.77037 | 82 | chr16 | unknown | gene | 38902344 | 39025195 | + | Igsf11 | Igsf11 | P5820 | NM_170599 | TSS1773 |
| chr16 | 41050525 | 41050665 | MACS2_peak_1154 | 47 | + | 6.68747 | 9.84528 | 4.77037 | 82 | chr16 | unknown | gene | 41533341 | 42144807 | + | Lsamp | Lsamp | P14748 | NM_175548 | TSS12217 |
| chr16 | 42695519 | 42695610 | MACS2_peak_1155 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 26 | chr16 | unknown | gene | 42248560 | 42340502 | - | Gap43 | Gap43 | P21823 | NM_008083 | TSS17593 |
| chr16 | 42695519 | 42695610 | MACS2_peak_1155 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 26 | chr16 | unknown | gene | 42725701 | 42875762 | - | 4932412D23Rik | 4932412D23Rik | | NR_040521 | TSS2001 |
| chr16 | 42970277 | 42970368 | MACS2_peak_1156 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 67 | chr16 | unknown | gene | 42884369 | 42912070 | - | Gm19522 | Gm19522 | | NR_040402 | TSS17149 |
| chr16 | 42970277 | 42970368 | MACS2_peak_1156 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 67 | chr16 | unknown | gene | 43410517 | 43420196 | - | Gm15713 | Gm15713 | | NR_046026 | TSS24728 |
| chr16 | 43669116 | 43669242 | MACS2_peak_1157 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 42 | chr16 | unknown | gene | 43648860 | 43664087 | - | Tigit | Tigit | P14143 | NM_001146325 | TSS18294 |
| chr16 | 43669116 | 43669242 | MACS2_peak_1157 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 42 | chr16 | unknown | gene | 43762241 | 43822839 | + | Drd3 | Drd3 | P5122 | NM_007877 | TSS20163 |
| chr16 | 44604689 | 44604780 | MACS2_peak_1158 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 65 | chr16 | unknown | gene | 44485044 | 44558870 | - | Boc | Boc | P5084 | NM_172506 | TSS22312 |
| chr16 | 44604689 | 44604780 | MACS2_peak_1158 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 65 | chr16 | unknown | gene | 44724300 | 44736175 | + | BC027231 | BC027231 | P17740 | NM_145972 | TSS23167 |
| chr16 | 45249645 | 45249856 | MACS2_peak_1159 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 42 | chr16 | unknown | gene | 45158828 | 45187741 | + | Atg3 | Atg3 | P24110 | NM_026402 | TSS22045 |
| chr16 | 45249645 | 45249856 | MACS2_peak_1159 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 42 | chr16 | unknown | gene | 45382134 | 45408867 | - | Cd200 | Cd200 | P26668 | NM_010818 | TSS9488 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr16 | 45741845 | 45741936 | MACS2_peak_1160 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 18 | chr16 | unknown | gene | 45711229 | 45724306 | - | Tagln3 | Tagln3 | P24483 | NM_019754 | TSS2474 |
| chr16 | 45741845 | 45741936 | MACS2_peak_1160 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 18 | chr16 | unknown | gene | 45746230 | 45844378 | - | Phldb2 | Phldb2 | P2064 | NM_153412 | TSS10026 |
| chr16 | 45763320 | 45763411 | MACS2_peak_1161 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 24 | chr16 | unknown | gene | 45729724 | 45742891 | - | Abhd10 | Abhd10 | P15968 | NM_001272070 | TSS25481 |
| chr16 | 45763320 | 45763411 | MACS2_peak_1161 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 24 | chr16 | unknown | gene | 45959260 | 46009856 | - | Plcxd2 | Plcxd2 | P25606 | NM_001134480 | TSS6730 |
| chr16 | 46456987 | 46457078 | MACS2_peak_1162 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 71 | chr16 | unknown | gene | 46152990 | 46155012 | - | Gm4737 | Gm4737 | P15373 | NM_001304528 | TSS13734 |
| chr16 | 46456987 | 46457078 | MACS2_peak_1162 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 71 | chr16 | unknown | gene | 48283734 | 48293732 | + | Dppa4 | Dppa4 | P15019 | NM_001018002 | TSS3667 |
| chr16 | 47516490 | 47516596 | MACS2_peak_1163 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 18 | chr16 | unknown | gene | 46394857 | 46496774 | - | Pvrl3 | Pvrl3 | P25289 | NM_021496 | TSS11964 |
| chr16 | 47516490 | 47516596 | MACS2_peak_1163 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 18 | chr16 | unknown | gene | 48283734 | 48293732 | + | Dppa4 | Dppa4 | P15019 | NM_001018002 | TSS3667 |
| chr16 | 48548157 | 48548248 | MACS2_peak_1164 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 81 | chr16 | unknown | gene | 48399452 | 48412416 | - | Gm5485 | Gm5485 | | NR_015373 | TSS409 |
| chr16 | 48548157 | 48548248 | MACS2_peak_1164 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 81 | chr16 | unknown | gene | 48734689 | 48771950 | - | Trat1 | Trat1 | P15074 | NM_198297 | TSS17475 |
| chr16 | 48623761 | 48623929 | MACS2_peak_1165 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 18 | chr16 | unknown | gene | 48399452 | 48412416 | - | Gm5485 | Gm5485 | | NR_015373 | TSS409 |
| chr16 | 48623761 | 48623929 | MACS2_peak_1165 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 18 | chr16 | unknown | gene | 48734689 | 48771950 | - | Trat1 | Trat1 | P15074 | NM_198297 | TSS17475 |
| chr16 | 48868994 | 48869085 | MACS2_peak_1166 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 53 | chr16 | unknown | gene | 48842551 | 48844301 | + | Retnla | Retnla | P19484 | NM_020509 | TSS2764 |
| chr16 | 48868994 | 48869085 | MACS2_peak_1166 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 53 | chr16 | unknown | gene | 48872607 | 48874344 | + | Retnlg | Retnlg | P17148 | NM_181596 | TSS13103 |
| chr16 | 49088706 | 49088797 | MACS2_peak_1167 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 67 | chr16 | unknown | gene | 48994187 | 49018545 | + | C330027C09Rik | C330027C09Rik | P15661 | NM_172616 | TSS17129 |
| chr16 | 49088706 | 49088797 | MACS2_peak_1167 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 67 | chr16 | unknown | gene | 49699293 | 49763920 | + | Ift57 | Ift57 | P12905 | NM_028680 | TSS14025 |
| chr16 | 50321985 | 50322154 | MACS2_peak_1168 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 147 | chr16 | unknown | gene | 50019657 | 50072852 | - | Gm4827 | Gm4827 | | NR_045935 | TSS12399 |
| chr16 | 50321985 | 50322154 | MACS2_peak_1168 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 147 | chr16 | unknown | gene | 50526244 | 50559459 | + | G730013B05Rik | G730013B05Rik | | NR_040380 | TSS12889 |
| chr16 | 50355689 | 50355780 | MACS2_peak_1169 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 18 | chr16 | unknown | gene | 50019657 | 50072852 | - | Gm4827 | Gm4827 | | NR_045935 | TSS12399 |
| chr16 | 50355689 | 50355780 | MACS2_peak_1169 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 18 | chr16 | unknown | gene | 50526244 | 50559459 | + | G730013B05Rik | G730013B05Rik | | NR_040380 | TSS12889 |
| chr16 | 50879206 | 50879343 | MACS2_peak_1170 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 67 | chr16 | unknown | gene | 50783408 | 50784091 | + | 1700116B05Rik | 1700116B05Rik | | NR_131005 | TSS26036 |
| chr16 | 50879206 | 50879343 | MACS2_peak_1170 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 67 | chr16 | unknown | gene | 52031548 | 52204692 | + | Cblb | Cblb | P22403 | NM_001033238 | TSS7299 |
| chr16 | 51122742 | 51122889 | MACS2_peak_1171 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 87 | chr16 | unknown | gene | 50783408 | 50784091 | + | 1700116B05Rik | 1700116B05Rik | | NR_131005 | TSS26036 |
| chr16 | 51122742 | 51122889 | MACS2_peak_1171 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 87 | chr16 | unknown | gene | 52031548 | 52204692 | + | Cblb | Cblb | P22403 | NM_001033238 | TSS7299 |
| chr16 | 51828561 | 51828652 | MACS2_peak_1172 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 33 | chr16 | unknown | gene | 50783408 | 50784091 | + | 1700116B05Rik | 1700116B05Rik | | NR_131005 | TSS26036 |
| chr16 | 51828561 | 51828652 | MACS2_peak_1172 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 33 | chr16 | unknown | gene | 52031548 | 52204692 | + | Cblb | Cblb | P22403 | NM_001033238 | TSS7299 |
| chr16 | 52574078 | 52574169 | MACS2_peak_1173 | 32 | + | 5.8651 | 8.25694 | 3.2954 | 26 | chr16 | unknown | gene | 52248995 | 52452465 | - | Alcam | Alcam | P23714 | NM_009655 | TSS3837 |
| chr16 | 52574078 | 52574169 | MACS2_peak_1173 | 32 | + | 5.8651 | 8.25694 | 3.2954 | 26 | chr16 | unknown | gene | 52799507 | 52815744 | - | 4930404A05Rik | 4930404A05Rik | | NR_040495 | TSS18927 |
| chr16 | 53029426 | 53029517 | MACS2_peak_1174 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 26 | chr16 | unknown | gene | 52799507 | 52815744 | - | 4930404A05Rik | 4930404A05Rik | | NR_040495 | TSS18927 |
| chr16 | 53029426 | 53029517 | MACS2_peak_1174 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 26 | chr16 | unknown | gene | 55225174 | 55283237 | - | Zpld1 | Zpld1 | P13986 | NM_178720 | TSS17920 |
| chr16 | 53256357 | 53256448 | MACS2_peak_1175 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 52 | chr16 | unknown | gene | 52799507 | 52815744 | - | 4930404A05Rik | 4930404A05Rik | | NR_040495 | TSS18927 |
| chr16 | 53256357 | 53256448 | MACS2_peak_1175 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 52 | chr16 | unknown | gene | 55225174 | 55283237 | - | Zpld1 | Zpld1 | P13986 | NM_178720 | TSS17920 |
| chr16 | 54097332 | 54097423 | MACS2_peak_1176 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 68 | chr16 | unknown | gene | 52799507 | 52815744 | - | 4930404A05Rik | 4930404A05Rik | | NR_040495 | TSS18927 |
| chr16 | 54097332 | 54097423 | MACS2_peak_1176 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 68 | chr16 | unknown | gene | 55225174 | 55283237 | - | Zpld1 | Zpld1 | P13986 | NM_178720 | TSS17920 |
| chr16 | 54615870 | 54615961 | MACS2_peak_1177 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 27 | chr16 | unknown | gene | 52799507 | 52815744 | - | 4930404A05Rik | 4930404A05Rik | | NR_040495 | TSS18927 |
| chr16 | 54615870 | 54615961 | MACS2_peak_1177 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 27 | chr16 | unknown | gene | 55225174 | 55283237 | - | Zpld1 | Zpld1 | P13986 | NM_178720 | TSS17920 |
| chr16 | 54637030 | 54637121 | MACS2_peak_1178 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 67 | chr16 | unknown | gene | 52799507 | 52815744 | - | 4930404A05Rik | 4930404A05Rik | | NR_040495 | TSS18927 |
| chr16 | 54637030 | 54637121 | MACS2_peak_1178 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 67 | chr16 | unknown | gene | 55225174 | 55283237 | - | Zpld1 | Zpld1 | P13986 | NM_178720 | TSS17920 |
| chr16 | 54914793 | 54914884 | MACS2_peak_1179 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 51 | chr16 | unknown | gene | 52799507 | 52815744 | - | 4930404A05Rik | 4930404A05Rik | | NR_040495 | TSS18927 |
| chr16 | 54914793 | 54914884 | MACS2_peak_1179 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 51 | chr16 | unknown | gene | 55225174 | 55283237 | - | Zpld1 | Zpld1 | P13986 | NM_178720 | TSS17920 |
| chr16 | 55196056 | 55196193 | MACS2_peak_1180 | 8 | + | 3.95075 | 4.76 | 0.89171 | 51 | chr16 | unknown | gene | 52799507 | 52815744 | - | 4930404A05Rik | 4930404A05Rik | | NR_040495 | TSS18927 |
| chr16 | 55196056 | 55196193 | MACS2_peak_1180 | 8 | + | 3.95075 | 4.76 | 0.89171 | 51 | chr16 | unknown | gene | 55225174 | 55283237 | - | Zpld1 | Zpld1 | P13986 | NM_178720 | TSS17920 |
| chr16 | 55302070 | 55302171 | MACS2_peak_1181 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 65 | chr16 | unknown | gene | 55225174 | 55283237 | - | Zpld1 | Zpld1 | P13986 | NM_178720 | TSS17920 |
| chr16 | 55302070 | 55302171 | MACS2_peak_1181 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 65 | chr16 | unknown | gene | 55494730 | 55494797 | + | Mir5118 | Mir5118 | | NR_039578 | TSS18014 |
| chr16 | 55572045 | 55572136 | MACS2_peak_1182 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 68 | chr16 | unknown | gene | 55494730 | 55494797 | + | Mir5118 | Mir5118 | | NR_039578 | TSS18014 |
| chr16 | 55572045 | 55572136 | MACS2_peak_1182 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 68 | chr16 | unknown | gene | 55811376 | 55838641 | - | Nfkbiz | Nfkbiz | P23109 | NM_001159394 | TSS4556 |
| chr16 | 57108245 | 57108336 | MACS2_peak_1183 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 37 | chr16 | unknown | gene | 57036966 | 57071346 | - | Tmem45a2 | Tmem45a2 | P9695 | NM_183281 | TSS8981 |
| chr16 | 57108245 | 57108336 | MACS2_peak_1183 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 37 | chr16 | unknown | gene | 57121713 | 57152736 | + | Tomm70a | Tomm70a | P12372 | NM_138599 | TSS25495 |
| chr16 | 57359862 | 57359953 | MACS2_peak_1184 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 7 | chr16 | unknown | gene | 57266138 | 57292851 | - | Tmem30c | Tmem30c | P17712 | NM_027651 | TSS23228 |
| chr16 | 57359862 | 57359953 | MACS2_peak_1184 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 7 | chr16 | unknown | gene | 57624255 | 57754737 | - | Col8a1 | Col8a1 | P18327 | NM_007739 | TSS7021 |
| chr16 | 57992304 | 57992395 | MACS2_peak_1185 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 55 | chr16 | unknown | gene | 57624255 | 57754737 | - | Col8a1 | Col8a1 | P18327 | NM_007739 | TSS7021 |
| chr16 | 57992304 | 57992395 | MACS2_peak_1185 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 55 | chr16 | unknown | gene | 58408534 | 58465789 | + | Dcbld2 | Dcbld2 | P13542 | NM_028523 | TSS20048 |
| chr16 | 58065715 | 58065806 | MACS2_peak_1186 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 12 | chr16 | unknown | gene | 57624255 | 57754737 | - | Col8a1 | Col8a1 | P18327 | NM_007739 | TSS7021 |
| chr16 | 58065715 | 58065806 | MACS2_peak_1186 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 12 | chr16 | unknown | gene | 58408534 | 58465789 | + | Dcbld2 | Dcbld2 | P13542 | NM_028523 | TSS20048 |
| chr16 | 59279693 | 59279784 | MACS2_peak_1187 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 38 | chr16 | unknown | gene | 59268738 | 59269665 | - | Olfr201 | Olfr201 | P15796 | NM_146994 | TSS975 |
| chr16 | 59279693 | 59279784 | MACS2_peak_1187 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 38 | chr16 | unknown | gene | 59283571 | 59284495 | - | Olfr202 | Olfr202 | P24802 | NM_146995 | TSS4088 |
| chr16 | 59497481 | 59497572 | MACS2_peak_1188 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 38 | chr16 | unknown | gene | 59471774 | 59491899 | + | Mina | Mina | P26384 | NM_025910 | TSS13592 |
| chr16 | 59497481 | 59497572 | MACS2_peak_1188 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 38 | chr16 | unknown | gene | 59613320 | 59639339 | - | Arl6 | Arl6 | P1985 | NM_019665 | TSS8165 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr16 | 59820735 | 59820863 | MACS2_peak_1189 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 48 | chr16 | unknown | gene | 59636944 | 59672993 | + | 4930547E14Rik | 4930547E14Rik | | NR_040564 | TSS1669 |
| chr16 | 59820735 | 59820863 | MACS2_peak_1189 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 48 | chr16 | unknown | gene | 62734851 | 62786682 | - | Nsun3 | Nsun3 | P405 | NM_178925 | TSS26506 |
| chr16 | 60503266 | 60503357 | MACS2_peak_1190 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 35 | chr16 | unknown | gene | 59636944 | 59672993 | + | 4930547E14Rik | 4930547E14Rik | | NR_040564 | TSS1669 |
| chr16 | 60503266 | 60503357 | MACS2_peak_1190 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 35 | chr16 | unknown | gene | 62734851 | 62786682 | - | Nsun3 | Nsun3 | P405 | NM_178925 | TSS26506 |
| chr16 | 60656891 | 60656982 | MACS2_peak_1191 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 39 | chr16 | unknown | gene | 59653482 | 60605248 | - | Epha6 | Epha6 | P25791 | NM_007938 | TSS5040 |
| chr16 | 60656891 | 60656982 | MACS2_peak_1191 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 39 | chr16 | unknown | gene | 62734851 | 62786682 | - | Nsun3 | Nsun3 | P405 | NM_178925 | TSS26506 |
| chr16 | 61558484 | 61558575 | MACS2_peak_1192 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 59 | chr16 | unknown | gene | 59653482 | 60605248 | - | Epha6 | Epha6 | P25791 | NM_007938 | TSS5040 |
| chr16 | 61558484 | 61558575 | MACS2_peak_1192 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 59 | chr16 | unknown | gene | 62734851 | 62786682 | - | Nsun3 | Nsun3 | P405 | NM_178925 | TSS26506 |
| chr16 | 62803622 | 62803713 | MACS2_peak_1193 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 42 | chr16 | unknown | gene | 62734851 | 62786682 | - | Nsun3 | Nsun3 | P405 | NM_178925 | TSS26506 |
| chr16 | 62803622 | 62803713 | MACS2_peak_1193 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 42 | chr16 | unknown | gene | 62814675 | 62822701 | + | Stx19 | Stx19 | P22387 | NM_026588 | TSS15663 |
| chr16 | 62855864 | 62855955 | MACS2_peak_1194 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 70 | chr16 | unknown | gene | 62793688 | 62846743 | - | Arl13b | Arl13b | P11325 | NM_026577 | TSS15868 |
| chr16 | 62855864 | 62855955 | MACS2_peak_1194 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 70 | chr16 | unknown | gene | 63545217 | 63864047 | - | Epha3 | Epha3 | P4762 | NM_010140 | TSS19594 |
| chr16 | 63718472 | 63718602 | MACS2_peak_1195 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 52 | chr16 | unknown | gene | 62854333 | 62928193 | + | Pros1 | Pros1 | P1504 | NM_011173 | TSS3488 |
| chr16 | 63718472 | 63718602 | MACS2_peak_1195 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 52 | chr16 | unknown | gene | 64477810 | 64478667 | - | Csnka2ip | Csnka2ip | P24814 | NM_173861 | TSS12704 |
| chr16 | 64097407 | 64097508 | MACS2_peak_1196 | 13 | + | 4.27611 | 5.31441 | 1.3392 | 86 | chr16 | unknown | gene | 63545217 | 63864047 | - | Epha3 | Epha3 | P4762 | NM_010140 | TSS19594 |
| chr16 | 64097407 | 64097508 | MACS2_peak_1196 | 13 | + | 4.27611 | 5.31441 | 1.3392 | 86 | chr16 | unknown | gene | 64477810 | 64478667 | - | Csnka2ip | Csnka2ip | P24814 | NM_173861 | TSS12704 |
| chr16 | 64207407 | 64207517 | MACS2_peak_1197 | 12 | + | 4.14966 | 5.12722 | 1.204 | 65 | chr16 | unknown | gene | 63545217 | 63864047 | - | Epha3 | Epha3 | P4762 | NM_010140 | TSS19594 |
| chr16 | 64207407 | 64207517 | MACS2_peak_1197 | 12 | + | 4.14966 | 5.12722 | 1.204 | 65 | chr16 | unknown | gene | 64477810 | 64478667 | - | Csnka2ip | Csnka2ip | P24814 | NM_173861 | TSS12704 |
| chr16 | 64462855 | 64462946 | MACS2_peak_1198 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 21 | chr16 | unknown | gene | 63545217 | 63864047 | - | Epha3 | Epha3 | P4762 | NM_010140 | TSS19594 |
| chr16 | 64462855 | 64462946 | MACS2_peak_1198 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 21 | chr16 | unknown | gene | 64477810 | 64478667 | - | Csnka2ip | Csnka2ip | P24814 | NM_173861 | TSS12704 |
| chr16 | 65556484 | 65556575 | MACS2_peak_1199 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 39 | chr16 | unknown | gene | 65520628 | 65533981 | + | Pou1f1 | Pou1f1 | P7222 | NM_008849 | TSS12031 |
| chr16 | 65556484 | 65556575 | MACS2_peak_1199 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 39 | chr16 | unknown | gene | 65815632 | 65860713 | + | Vgll3 | Vgll3 | P16323 | NM_028572 | TSS22652 |
| chr16 | 65615069 | 65615240 | MACS2_peak_1200 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 95 | chr16 | unknown | gene | 65539132 | 65562508 | - | Chmp2b | Chmp2b | P19367 | NM_026879 | TSS4401 |
| chr16 | 65615069 | 65615240 | MACS2_peak_1200 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 95 | chr16 | unknown | gene | 65815632 | 65860713 | + | Vgll3 | Vgll3 | P16323 | NM_028572 | TSS22652 |
| chr16 | 65868692 | 65868783 | MACS2_peak_1201 | 12 | + | 4.14966 | 5.12722 | 1.204 | 52 | chr16 | unknown | gene | 65815632 | 65860713 | + | Vgll3 | Vgll3 | P16323 | NM_028572 | TSS22652 |
| chr16 | 65868692 | 65868783 | MACS2_peak_1201 | 12 | + | 4.14966 | 5.12722 | 1.204 | 52 | chr16 | unknown | gene | 66655420 | 67620231 | - | Cadm2 | Cadm2 | P4171 | NM_001145977 | TSS19686 |
| chr16 | 65981746 | 65981840 | MACS2_peak_1202 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 45 | chr16 | unknown | gene | 65815632 | 65860713 | + | Vgll3 | Vgll3 | P16323 | NM_028572 | TSS22652 |
| chr16 | 65981746 | 65981840 | MACS2_peak_1202 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 45 | chr16 | unknown | gene | 66655420 | 67620231 | - | Cadm2 | Cadm2 | P4171 | NM_001145977 | TSS19686 |
| chr16 | 66632365 | 66632456 | MACS2_peak_1203 | 12 | + | 4.14966 | 5.12722 | 1.204 | 15 | chr16 | unknown | gene | 65815632 | 65860713 | + | Vgll3 | Vgll3 | P16323 | NM_028572 | TSS22652 |
| chr16 | 66632365 | 66632456 | MACS2_peak_1203 | 12 | + | 4.14966 | 5.12722 | 1.204 | 15 | chr16 | unknown | gene | 66655420 | 67620231 | - | Cadm2 | Cadm2 | P4171 | NM_001145977 | TSS19686 |
| chr16 | 67340011 | 67340102 | MACS2_peak_1204 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 29 | chr16 | unknown | gene | 66657117 | 66664626 | + | 1700010K23Rik | 1700010K23Rik | | NR_040512 | TSS23919 |
| chr16 | 67340011 | 67340102 | MACS2_peak_1204 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 29 | chr16 | unknown | gene | 69796140 | 69800381 | - | 4930428D20Rik | 4930428D20Rik | | NR_130991 | TSS15380 |
| chr16 | 68108912 | 68109003 | MACS2_peak_1205 | 12 | + | 4.14966 | 5.12722 | 1.204 | 8 | chr16 | unknown | gene | 66655420 | 67620231 | - | Cadm2 | Cadm2 | P4171 | NM_001145977 | TSS19686 |
| chr16 | 68108912 | 68109003 | MACS2_peak_1205 | 12 | + | 4.14966 | 5.12722 | 1.204 | 8 | chr16 | unknown | gene | 69796140 | 69800381 | - | 4930428D20Rik | 4930428D20Rik | | NR_130991 | TSS15380 |
| chr16 | 68381582 | 68381673 | MACS2_peak_1206 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 45 | chr16 | unknown | gene | 66655420 | 67620231 | - | Cadm2 | Cadm2 | P4171 | NM_001145977 | TSS19686 |
| chr16 | 68381582 | 68381673 | MACS2_peak_1206 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 45 | chr16 | unknown | gene | 69796140 | 69800381 | - | 4930428D20Rik | 4930428D20Rik | | NR_130991 | TSS15380 |
| chr16 | 68417063 | 68417200 | MACS2_peak_1207 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 60 | chr16 | unknown | gene | 66655420 | 67620231 | - | Cadm2 | Cadm2 | P4171 | NM_001145977 | TSS19686 |
| chr16 | 68417063 | 68417200 | MACS2_peak_1207 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 60 | chr16 | unknown | gene | 69796140 | 69800381 | - | 4930428D20Rik | 4930428D20Rik | | NR_130991 | TSS15380 |
| chr16 | 69832845 | 69832936 | MACS2_peak_1208 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 25 | chr16 | unknown | gene | 69796140 | 69800381 | - | 4930428D20Rik | 4930428D20Rik | | NR_130991 | TSS15380 |
| chr16 | 69832845 | 69832936 | MACS2_peak_1208 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 25 | chr16 | unknown | gene | 69856873 | 69863612 | - | Speer2 | Speer2 | P18502 | NM_173069 | TSS11381 |
| chr16 | 70239888 | 70239979 | MACS2_peak_1209 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 50 | chr16 | unknown | gene | 69856873 | 69863612 | - | Speer2 | Speer2 | P18502 | NM_173069 | TSS11381 |
| chr16 | 70239888 | 70239979 | MACS2_peak_1209 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 50 | chr16 | unknown | gene | 70313948 | 70569045 | + | Gbe1 | Gbe1 | P21998 | NM_028803 | TSS21509 |
| chr16 | 70644180 | 70644271 | MACS2_peak_1210 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 58 | chr16 | unknown | gene | 70616424 | 70624822 | + | D16Ertd519e | D16Ertd519e | | NR_040474 | TSS6984 |
| chr16 | 70644180 | 70644271 | MACS2_peak_1210 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 58 | chr16 | unknown | gene | 71131075 | 71139029 | + | 4931420L22Rik | 4931420L22Rik | | NR_040561 | TSS9622 |
| chr16 | 71240513 | 71240708 | MACS2_peak_1211 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 137 | chr16 | unknown | gene | 71131075 | 71139029 | + | 4931420L22Rik | 4931420L22Rik | | NR_040561 | TSS9622 |
| chr16 | 71240513 | 71240708 | MACS2_peak_1211 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 137 | chr16 | unknown | gene | 71249903 | 71267176 | + | 4930567J20Rik | 4930567J20Rik | | NR_040576 | TSS2693 |
| chr16 | 72178790 | 72178881 | MACS2_peak_1212 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 49 | chr16 | unknown | gene | 71249903 | 71267176 | + | 4930567J20Rik | 4930567J20Rik | | NR_040576 | TSS2693 |
| chr16 | 72178790 | 72178881 | MACS2_peak_1212 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 49 | chr16 | unknown | gene | 72226382 | 72234327 | - | 8030451O07Rik | 8030451O07Rik | | NR_131116 | TSS2402 |
| chr16 | 72664843 | 72664934 | MACS2_peak_1213 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 53 | chr16 | unknown | gene | 72226382 | 72234327 | - | 8030451O07Rik | 8030451O07Rik | | NR_131116 | TSS2402 |
| chr16 | 72664843 | 72664934 | MACS2_peak_1213 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 53 | chr16 | unknown | gene | 73892305 | 74410912 | - | Robo2 | Robo2 | P9504 | NM_175549 | TSS9154 |
| chr16 | 72838974 | 72839117 | MACS2_peak_1214 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 81 | chr16 | unknown | gene | 72226382 | 72234327 | - | 8030451O07Rik | 8030451O07Rik | | NR_131116 | TSS2402 |
| chr16 | 72838974 | 72839117 | MACS2_peak_1214 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 81 | chr16 | unknown | gene | 73892305 | 74410912 | - | Robo2 | Robo2 | P9504 | NM_175549 | TSS9154 |
| chr16 | 72909582 | 72909718 | MACS2_peak_1215 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 50 | chr16 | unknown | gene | 72226382 | 72234327 | - | 8030451O07Rik | 8030451O07Rik | | NR_131116 | TSS2402 |
| chr16 | 72909582 | 72909718 | MACS2_peak_1215 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 50 | chr16 | unknown | gene | 73892305 | 74410912 | - | Robo2 | Robo2 | P9504 | NM_175549 | TSS9154 |
| chr16 | 72952243 | 72952334 | MACS2_peak_1216 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 7 | chr16 | unknown | gene | 72226382 | 72234327 | - | 8030451O07Rik | 8030451O07Rik | | NR_131116 | TSS2402 |
| chr16 | 72952243 | 72952334 | MACS2_peak_1216 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 7 | chr16 | unknown | gene | 73892305 | 74410912 | - | Robo2 | Robo2 | P9504 | NM_175549 | TSS9154 |
| chr16 | 74061989 | 74062080 | MACS2_peak_1217 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 38 | chr16 | unknown | gene | 72663148 | 73044362 | + | Robo1 | Robo1 | P16562 | NM_019413 | TSS16102 |
| chr16 | 74061989 | 74062080 | MACS2_peak_1217 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 38 | chr16 | unknown | gene | 74341989 | 74342067 | - | Mir691 | Mir691 | | NR_030464 | TSS23673 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr16 | 74253177 | 74253268 | MACS2_peak_1218 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 42 | chr16 | unknown | gene | 72663148 | 73044362 | + | Robo1 | Robo1 | P16562 | NM_019413 | TSS16102 |
| chr16 | 74253177 | 74253268 | MACS2_peak_1218 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 42 | chr16 | unknown | gene | 74341989 | 74342067 | - | Mir691 | Mir691 |  | NR_030464 | TSS23673 |
| chr16 | 75079895 | 75080029 | MACS2_peak_1219 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 52 | chr16 | unknown | gene | 73892305 | 74410912 | - | Robo2 | Robo2 | P9504 | NM_175549 | TSS9154 |
| chr16 | 75079895 | 75080029 | MACS2_peak_1219 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 52 | chr16 | unknown | gene | 75540513 | 75585950 | - | Lipi | Lipi | P19244 | NM_001252513 | TSS12378 |
| chr16 | 75209839 | 75209930 | MACS2_peak_1220 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 33 | chr16 | unknown | gene | 73892305 | 74410912 | - | Robo2 | Robo2 | P9504 | NM_175549 | TSS9154 |
| chr16 | 75209839 | 75209930 | MACS2_peak_1220 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 33 | chr16 | unknown | gene | 75540513 | 75585950 | - | Lipi | Lipi | P19244 | NM_001252513 | TSS12378 |
| chr16 | 75327678 | 75327813 | MACS2_peak_1221 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 67 | chr16 | unknown | gene | 73892305 | 74410912 | - | Robo2 | Robo2 | P9504 | NM_175549 | TSS9154 |
| chr16 | 75327678 | 75327813 | MACS2_peak_1221 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 67 | chr16 | unknown | gene | 75540513 | 75585950 | - | Lipi | Lipi | P19244 | NM_001252513 | TSS12378 |
| chr16 | 76202703 | 76202821 | MACS2_peak_1222 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 79 | chr16 | unknown | gene | 76122612 | 76156086 | + | 4930578N18Rik | 4930578N18Rik |  | NR_040575 | TSS10562 |
| chr16 | 76202703 | 76202821 | MACS2_peak_1222 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 79 | chr16 | unknown | gene | 76290861 | 76373049 | - | Nrip1 | Nrip1 | P5794 | NM_173440 | TSS18238 |
| chr16 | 76246723 | 76246842 | MACS2_peak_1223 | 12 | + | 4.14966 | 5.12722 | 1.204 | 36 | chr16 | unknown | gene | 76122612 | 76156086 | + | 4930578N18Rik | 4930578N18Rik |  | NR_040575 | TSS10562 |
| chr16 | 76246723 | 76246842 | MACS2_peak_1223 | 12 | + | 4.14966 | 5.12722 | 1.204 | 36 | chr16 | unknown | gene | 76290861 | 76373049 | - | Nrip1 | Nrip1 | P5794 | NM_173440 | TSS18238 |
| chr16 | 76446255 | 76446346 | MACS2_peak_1224 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 13 | chr16 | unknown | gene | 76290861 | 76373049 | - | Nrip1 | Nrip1 | P5794 | NM_173440 | TSS18238 |
| chr16 | 76446255 | 76446346 | MACS2_peak_1224 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 13 | chr16 | unknown | gene | 77004227 | 77010881 | - | 1700041M19Rik | 1700041M19Rik |  | NR_040573 | TSS12795 |
| chr16 | 76571092 | 76571183 | MACS2_peak_1225 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 12 | chr16 | unknown | gene | 76290861 | 76373049 | - | Nrip1 | Nrip1 | P5794 | NM_173440 | TSS18238 |
| chr16 | 76571092 | 76571183 | MACS2_peak_1225 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 12 | chr16 | unknown | gene | 77004227 | 77010881 | - | 1700041M19Rik | 1700041M19Rik |  | NR_040573 | TSS12795 |
| chr16 | 76724847 | 76724938 | MACS2_peak_1226 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 16 | chr16 | unknown | gene | 76290861 | 76373049 | - | Nrip1 | Nrip1 | P5794 | NM_173440 | TSS18238 |
| chr16 | 76724847 | 76724938 | MACS2_peak_1226 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 16 | chr16 | unknown | gene | 77004227 | 77010881 | - | 1700041M19Rik | 1700041M19Rik |  | NR_040573 | TSS12795 |
| chr16 | 76757581 | 76757672 | MACS2_peak_1227 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 47 | chr16 | unknown | gene | 76290861 | 76373049 | - | Nrip1 | Nrip1 | P5794 | NM_173440 | TSS18238 |
| chr16 | 76757581 | 76757672 | MACS2_peak_1227 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 47 | chr16 | unknown | gene | 77004227 | 77010881 | - | 1700041M19Rik | 1700041M19Rik |  | NR_040573 | TSS12795 |
| chr16 | 77198122 | 77198213 | MACS2_peak_1228 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 60 | chr16 | unknown | gene | 77014068 | 77115562 | + | Usp25 | Usp25 | P20841 | NM_013918 | TSS20115 |
| chr16 | 77198122 | 77198213 | MACS2_peak_1228 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 60 | chr16 | unknown | gene | 77329327 | 77558428 | + | Mir99ahg | Mir99ahg |  | NR_015543 | TSS27093 |
| chr16 | 77243472 | 77243602 | MACS2_peak_1229 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 48 | chr16 | unknown | gene | 77014068 | 77115562 | + | Usp25 | Usp25 | P20841 | NM_013918 | TSS20115 |
| chr16 | 77243472 | 77243602 | MACS2_peak_1229 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 48 | chr16 | unknown | gene | 77329327 | 77558428 | + | Mir99ahg | Mir99ahg |  | NR_015543 | TSS27093 |
| chr16 | 77525483 | 77525574 | MACS2_peak_1230 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 46 | chr16 | unknown | gene | 77014068 | 77115562 | + | Usp25 | Usp25 | P20841 | NM_013918 | TSS20115 |
| chr16 | 77525483 | 77525574 | MACS2_peak_1230 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 46 | chr16 | unknown | gene | 77598935 | 77599000 | + | Mir99a | Mir99a |  | NR_029535 | TSS10847 |
| chr16 | 77677128 | 77677293 | MACS2_peak_1231 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 18 | chr16 | unknown | gene | 77646272 | 77646343 | + | Mir125b-2 | Mir125b-2 |  | NR_029540 | TSS22825 |
| chr16 | 77677128 | 77677293 | MACS2_peak_1231 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 18 | chr16 | unknown | gene | 78250862 | 78255454 | - | E330011O21Rik | E330011O21Rik |  | NR_045698 | TSS27431 |
| chr16 | 77872177 | 77872268 | MACS2_peak_1232 | 12 | + | 4.14966 | 5.12722 | 1.204 | 57 | chr16 | unknown | gene | 77646272 | 77646343 | + | Mir125b-2 | Mir125b-2 |  | NR_029540 | TSS22825 |
| chr16 | 77872177 | 77872268 | MACS2_peak_1232 | 12 | + | 4.14966 | 5.12722 | 1.204 | 57 | chr16 | unknown | gene | 78250862 | 78255454 | - | E330011O21Rik | E330011O21Rik |  | NR_045698 | TSS27431 |
| chr16 | 79000136 | 79000229 | MACS2_peak_1233 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 49 | chr16 | unknown | gene | 78930947 | 78950441 | + | Chodl | Chodl | P51 | NM_139134 | TSS4249 |
| chr16 | 79000136 | 79000229 | MACS2_peak_1233 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 49 | chr16 | unknown | gene | 81200696 | 81623453 | + | Ncam2 | Ncam2 | P17218 | NM_010954 | TSS8182 |
| chr16 | 81365357 | 81365496 | MACS2_peak_1234 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 68 | chr16 | unknown | gene | 78953007 | 79090917 | - | Tmprss15 | Tmprss15 | P181 | NM_008941 | TSS20800 |
| chr16 | 81365357 | 81365496 | MACS2_peak_1234 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 68 | chr16 | unknown | gene | 84371142 | 84375505 | + | 4930553E22Rik | 4930553E22Rik |  | NR_040567 | TSS20737 |
| chr16 | 81818951 | 81819152 | MACS2_peak_1235 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 60 | chr16 | unknown | gene | 81200696 | 81623453 | + | Ncam2 | Ncam2 | P17218 | NM_010954 | TSS8182 |
| chr16 | 81818951 | 81819152 | MACS2_peak_1235 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 60 | chr16 | unknown | gene | 84371142 | 84375505 | + | 4930553E22Rik | 4930553E22Rik |  | NR_040567 | TSS20737 |
| chr16 | 81891195 | 81891356 | MACS2_peak_1236 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 143 | chr16 | unknown | gene | 81200696 | 81623453 | + | Ncam2 | Ncam2 | P17218 | NM_010954 | TSS8182 |
| chr16 | 81891195 | 81891356 | MACS2_peak_1236 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 143 | chr16 | unknown | gene | 84371142 | 84375505 | + | 4930553E22Rik | 4930553E22Rik |  | NR_040567 | TSS20737 |
| chr16 | 82959118 | 82959209 | MACS2_peak_1237 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 28 | chr16 | unknown | gene | 81200696 | 81623453 | + | Ncam2 | Ncam2 | P17218 | NM_010954 | TSS8182 |
| chr16 | 82959118 | 82959209 | MACS2_peak_1237 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 28 | chr16 | unknown | gene | 84371142 | 84375505 | + | 4930553E22Rik | 4930553E22Rik |  | NR_040567 | TSS20737 |
| chr16 | 83736823 | 83736914 | MACS2_peak_1238 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 79 | chr16 | unknown | gene | 81200696 | 81623453 | + | Ncam2 | Ncam2 | P17218 | NM_010954 | TSS8182 |
| chr16 | 83736823 | 83736914 | MACS2_peak_1238 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 79 | chr16 | unknown | gene | 84371142 | 84375505 | + | 4930553E22Rik | 4930553E22Rik |  | NR_040567 | TSS20737 |
| chr16 | 84995653 | 84995744 | MACS2_peak_1239 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 14 | chr16 | unknown | gene | 84972210 | 84979451 | + | Gm10791 | Gm10791 |  | NR_045889 | TSS13549 |
| chr16 | 84995653 | 84995744 | MACS2_peak_1239 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 14 | chr16 | unknown | gene | 85456243 | 85550108 | - | Cyyr1 | Cyyr1 | P25384 | NM_144853 | TSS10150 |
| chr16 | 85288465 | 85288579 | MACS2_peak_1240 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 71 | chr16 | unknown | gene | 84954435 | 85173558 | - | App | App | P11820 | NM_007471 | TSS20828 |
| chr16 | 85288465 | 85288579 | MACS2_peak_1240 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 71 | chr16 | unknown | gene | 85456243 | 85550108 | - | Cyyr1 | Cyyr1 | P25384 | NM_144853 | TSS10150 |
| chr16 | 85627803 | 85627941 | MACS2_peak_1241 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 64 | chr16 | unknown | gene | 85456243 | 85550108 | - | Cyyr1 | Cyyr1 | P25384 | NM_144853 | TSS10150 |
| chr16 | 85627803 | 85627941 | MACS2_peak_1241 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 64 | chr16 | unknown | gene | 85793827 | 85802710 | - | Adamts1 | Adamts1 | P18276 | NM_009621 | TSS5112 |
| chr16 | 85653299 | 85653420 | MACS2_peak_1242 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 36 | chr16 | unknown | gene | 85456243 | 85550108 | - | Cyyr1 | Cyyr1 | P25384 | NM_144853 | TSS10150 |
| chr16 | 85653299 | 85653420 | MACS2_peak_1242 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 36 | chr16 | unknown | gene | 85793827 | 85802710 | - | Adamts1 | Adamts1 | P18276 | NM_009621 | TSS5112 |
| chr16 | 85759329 | 85759420 | MACS2_peak_1243 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 44 | chr16 | unknown | gene | 85456243 | 85550108 | - | Cyyr1 | Cyyr1 | P25384 | NM_144853 | TSS10150 |
| chr16 | 85759329 | 85759420 | MACS2_peak_1243 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 44 | chr16 | unknown | gene | 85793827 | 85802710 | - | Adamts1 | Adamts1 | P18276 | NM_009621 | TSS5112 |
| chr16 | 86148516 | 86148607 | MACS2_peak_1244 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 34 | chr16 | unknown | gene | 85858156 | 85900267 | - | Adamts5 | Adamts5 | P16578 | NM_011782 | TSS951 |
| chr16 | 86148516 | 86148607 | MACS2_peak_1244 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 34 | chr16 | unknown | gene | 87354184 | 87367571 | + | N6amt1 | N6amt1 | P23617 | NM_001159331 | TSS21705 |
| chr16 | 86380314 | 86380437 | MACS2_peak_1245 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 45 | chr16 | unknown | gene | 85858156 | 85900267 | - | Adamts5 | Adamts5 | P16578 | NM_011782 | TSS951 |
| chr16 | 86380314 | 86380437 | MACS2_peak_1245 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 45 | chr16 | unknown | gene | 87354184 | 87367571 | + | N6amt1 | N6amt1 | P23617 | NM_001159331 | TSS21705 |
| chr16 | 86442019 | 86442110 | MACS2_peak_1246 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 19 | chr16 | unknown | gene | 85858156 | 85900267 | - | Adamts5 | Adamts5 | P16578 | NM_011782 | TSS951 |
| chr16 | 86442019 | 86442110 | MACS2_peak_1246 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 19 | chr16 | unknown | gene | 87354184 | 87367571 | + | N6amt1 | N6amt1 | P23617 | NM_001159331 | TSS21705 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr16 | 86653602 | 86653713 | MACS2_peak_1247 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 54 | chr16 | unknown | gene | 85858156 | 85900267 | - | Adamts5 | Adamts5 | P16578 | NM_011782 | TSS951 |
| chr16 | 86653602 | 86653713 | MACS2_peak_1247 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 54 | chr16 | unknown | gene | 87354184 | 87367571 | + | N6amt1 | N6amt1 | P23617 | NM_001159331 | TSS21705 |
| chr16 | 86761998 | 86762128 | MACS2_peak_1248 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 57 | chr16 | unknown | gene | 85858156 | 85900267 | - | Adamts5 | Adamts5 | P16578 | NM_011782 | TSS951 |
| chr16 | 86761998 | 86762128 | MACS2_peak_1248 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 57 | chr16 | unknown | gene | 87354184 | 87367571 | + | N6amt1 | N6amt1 | P23617 | NM_001159331 | TSS21705 |
| chr16 | 86820794 | 86821241 | MACS2_peak_1249 | 186 | + | 12.33575 | 24.22644 | 18.67909 | 164 | chr16 | unknown | gene | 85858156 | 85900267 | - | Adamts5 | Adamts5 | P16578 | NM_011782 | TSS951 |
| chr16 | 86820794 | 86821241 | MACS2_peak_1249 | 186 | + | 12.33575 | 24.22644 | 18.67909 | 164 | chr16 | unknown | gene | 87354184 | 87367571 | + | N6amt1 | N6amt1 | P23617 | NM_001159331 | TSS21705 |
| chr16 | 88375450 | 88375541 | MACS2_peak_1250 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 12 | chr16 | unknown | gene | 87895896 | 88289702 | - | Grik1 | Grik1 | P21559 | NM_010348 | TSS27277 |
| chr16 | 88375450 | 88375541 | MACS2_peak_1250 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 12 | chr16 | unknown | gene | 88505806 | 88506839 | - | Cldn17 | Cldn17 | P22825 | NM_181490 | TSS16666 |
| chr16 | 88678269 | 88678360 | MACS2_peak_1251 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 13 | chr16 | unknown | gene | 88671045 | 88671654 | - | Krtap27-1 | Krtap27-1 | P2840 | NM_001163105 | TSS1894 |
| chr16 | 88678269 | 88678360 | MACS2_peak_1251 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 13 | chr16 | unknown | gene | 88707170 | 88707907 | - | 2310061N02Rik | 2310061N02Rik | P7633 | NM_027155 | TSS341 |
| chr16 | 92124874 | 92124965 | MACS2_peak_1252 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 30 | chr16 | unknown | gene | 92058335 | 92111925 | + | Mrps6 | Mrps6 | P10635 | NM_080456 | TSS15558 |
| chr16 | 92124874 | 92124965 | MACS2_peak_1252 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 30 | chr16 | unknown | gene | 92292388 | 92296958 | + | Kcne2 | Kcne2 | P24989 | NM_134110 | TSS19371 |
| chr16 | 93254670 | 93254761 | MACS2_peak_1253 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 28 | chr16 | unknown | gene | 92601465 | 92826074 | - | Runx1 | Runx1 | P2337 | NM_001111022 | TSS26529 |
| chr16 | 93254670 | 93254761 | MACS2_peak_1253 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 28 | chr16 | unknown | gene | 93343715 | 93359511 | - | 1810053B23Rik | 1810053B23Rik | | NR_040488 | TSS8327 |
| chr16 | 94787382 | 94787473 | MACS2_peak_1254 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 13 | chr16 | unknown | gene | 94570205 | 94692201 | + | Dyrk1a | Dyrk1a | P14577 | NM_007890 | TSS11534 |
| chr16 | 94787382 | 94787473 | MACS2_peak_1254 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 13 | chr16 | unknown | gene | 95257557 | 95296729 | + | Kcnj15 | Kcnj15 | P10761 | NM_001039056 | TSS23241 |
| chr16 | 96121901 | 96121992 | MACS2_peak_1255 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 7 | chr16 | unknown | gene | 95992091 | 96082302 | - | Brwd1 | Brwd1 | P18910 | NM_145125 | TSS12532 |
| chr16 | 96121901 | 96121992 | MACS2_peak_1255 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 7 | chr16 | unknown | gene | 96145418 | 96155952 | + | Wrb | Wrb | P19785 | NM_207301 | TSS23828 |
| chr17 | 3143222 | 3143313 | MACS2_peak_1256 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 12 | chr17 | unknown | gene | 3064317 | 3084183 | - | Pisd-ps2 | Pisd-ps2 | | NR_003519 | TSS27298 |
| chr17 | 3143222 | 3143313 | MACS2_peak_1256 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 12 | chr17 | unknown | gene | 3326572 | 3518728 | + | Tiam2 | Tiam2 | P1181 | NM_001122998 | TSS6287 |
| chr17 | 4178100 | 4178191 | MACS2_peak_1257 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 16 | chr17 | unknown | gene | 4119445 | 4122102 | - | 4930548J01Rik | 4930548J01Rik | | NR_045462 | TSS6058 |
| chr17 | 4178100 | 4178191 | MACS2_peak_1257 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 16 | chr17 | unknown | gene | 4634979 | 4637477 | + | 4930517M08Rik | 4930517M08Rik | | NR_130984 | TSS1002 |
| chr17 | 4734451 | 4734555 | MACS2_peak_1258 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 46 | chr17 | unknown | gene | 4634979 | 4637477 | + | 4930517M08Rik | 4930517M08Rik | | NR_130984 | TSS1002 |
| chr17 | 4734451 | 4734555 | MACS2_peak_1258 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 46 | chr17 | unknown | gene | 4995073 | 5343087 | + | Arid1b | Arid1b | P23579 | NM_001085355 | TSS25921 |
| chr17 | 5796019 | 5796153 | MACS2_peak_1259 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 8 | chr17 | unknown | gene | 5492599 | 5753093 | + | Zdhhc14 | Zdhhc14 | P5003 | NM_146073 | TSS10040 |
| chr17 | 5796019 | 5796153 | MACS2_peak_1259 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 8 | chr17 | unknown | gene | 5798656 | 5803242 | + | 3300005D01Rik | 3300005D01Rik | | NR_045081 | TSS24083 |
| chr17 | 5840198 | 5840289 | MACS2_peak_1260 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 6 | chr17 | unknown | gene | 5798656 | 5803242 | + | 3300005D01Rik | 3300005D01Rik | | NR_045081 | TSS24083 |
| chr17 | 5840198 | 5840289 | MACS2_peak_1260 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 6 | chr17 | unknown | gene | 5841379 | 5930617 | + | Snx9 | Snx9 | P14017 | NM_025664 | TSS7150 |
| chr17 | 6511329 | 6511420 | MACS2_peak_1261 | 23 | + | 5.29194 | 7.22295 | 2.33819 | 54 | chr17 | unknown | gene | 6439001 | 6450994 | - | Tmem181b-ps | Tmem181b-ps | | NR_033520 | TSS18148 |
| chr17 | 6511329 | 6511420 | MACS2_peak_1261 | 23 | + | 5.29194 | 7.22295 | 2.33819 | 54 | chr17 | unknown | gene | 6601670 | 6655800 | + | Dynlt1f | Dynlt1f | P15874 | NM_001166627 | TSS8515 |
| chr17 | 6698739 | 6698830 | MACS2_peak_1262 | 28 | + | 5.62289 | 7.78659 | 2.8624 | 32 | chr17 | unknown | gene | 6601778 | 6655800 | + | Dynlt1c | Dynlt1c | P15874 | NM_001166630 | TSS7848 |
| chr17 | 6698739 | 6698830 | MACS2_peak_1262 | 28 | + | 5.62289 | 7.78659 | 2.8624 | 32 | chr17 | unknown | gene | 6738130 | 6782643 | - | Ezr | Ezr | P857 | NM_009510 | TSS13585 |
| chr17 | 6712671 | 6712797 | MACS2_peak_1263 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 36 | chr17 | unknown | gene | 6601778 | 6655800 | + | Dynlt1c | Dynlt1c | P15874 | NM_001166630 | TSS7848 |
| chr17 | 6712671 | 6712797 | MACS2_peak_1263 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 36 | chr17 | unknown | gene | 6738130 | 6782643 | - | Ezr | Ezr | P857 | NM_009510 | TSS13585 |
| chr17 | 6721348 | 6721487 | MACS2_peak_1264 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 49 | chr17 | unknown | gene | 6601778 | 6655800 | + | Dynlt1c | Dynlt1c | P15874 | NM_001166630 | TSS7848 |
| chr17 | 6721348 | 6721487 | MACS2_peak_1264 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 49 | chr17 | unknown | gene | 6738130 | 6782643 | - | Ezr | Ezr | P857 | NM_009510 | TSS13585 |
| chr17 | 7271571 | 7271662 | MACS2_peak_1265 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 60 | chr17 | unknown | gene | 6954964 | 6961129 | - | Tagap1 | Tagap1 | P2771 | NM_147155 | TSS16201 |
| chr17 | 7271571 | 7271662 | MACS2_peak_1265 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 60 | chr17 | unknown | gene | 7324659 | 7345127 | + | Tcp10a | Tcp10a | P5403 | NM_011553 | TSS15035 |
| chr17 | 7654084 | 7654175 | MACS2_peak_1266 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 55 | chr17 | unknown | gene | 7363711 | 7385305 | - | Gm9992 | Gm9992 | P7174 | NM_001142539 | TSS5618 |
| chr17 | 7654084 | 7654175 | MACS2_peak_1266 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 55 | chr17 | unknown | gene | 7738567 | 7804974 | - | Fndc1 | Fndc1 | P10570 | NM_001081416 | TSS24029 |
| chr17 | 8337909 | 8338000 | MACS2_peak_1267 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 28 | chr17 | unknown | gene | 8311102 | 8326994 | + | Sft2d1 | Sft2d1 | P14312 | NM_134114 | TSS17614 |
| chr17 | 8337909 | 8338000 | MACS2_peak_1267 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 28 | chr17 | unknown | gene | 8340405 | 8341937 | + | Prr18 | Prr18 | | NR_028280 | TSS26047 |
| chr17 | 8987756 | 8987847 | MACS2_peak_1268 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 38 | chr17 | unknown | gene | 8526800 | 8981656 | + | Pde10a | Pde10a | P14093 | NM_001290707 | TSS17238 |
| chr17 | 8987756 | 8987847 | MACS2_peak_1268 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 38 | chr17 | unknown | gene | 8988332 | 9007987 | + | 1700010I14Rik | 1700010I14Rik | P2834 | NM_025851 | TSS19933 |
| chr17 | 9231726 | 9231872 | MACS2_peak_1269 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 79 | chr17 | unknown | gene | 9147718 | 9168022 | - | 6530411M01Rik | 6530411M01Rik | | NR_027881 | TSS8470 |
| chr17 | 9231726 | 9231872 | MACS2_peak_1269 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 79 | chr17 | unknown | gene | 9666496 | 9669620 | - | Pabpc6 | Pabpc6 | P21012 | NM_001163836 | TSS3409 |
| chr17 | 9435215 | 9435306 | MACS2_peak_1270 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 2 | chr17 | unknown | gene | 9147718 | 9168022 | - | 6530411M01Rik | 6530411M01Rik | | NR_027881 | TSS8470 |
| chr17 | 9435215 | 9435306 | MACS2_peak_1270 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 2 | chr17 | unknown | gene | 9666496 | 9669620 | - | Pabpc6 | Pabpc6 | P21012 | NM_001163836 | TSS3409 |
| chr17 | 9662666 | 9662757 | MACS2_peak_1271 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 16 | chr17 | unknown | gene | 9147718 | 9168022 | - | 6530411M01Rik | 6530411M01Rik | | NR_027881 | TSS8470 |
| chr17 | 9662666 | 9662757 | MACS2_peak_1271 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 16 | chr17 | unknown | gene | 9666496 | 9669620 | - | Pabpc6 | Pabpc6 | P21012 | NM_001163836 | TSS3409 |
| chr17 | 10002849 | 10002940 | MACS2_peak_1272 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 16 | chr17 | unknown | gene | 9750751 | 9775866 | - | 4930452A19Rik | 4930452A19Rik | | NR_045433 | TSS14996 |
| chr17 | 10002849 | 10002940 | MACS2_peak_1272 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 16 | chr17 | unknown | gene | 10206470 | 10318873 | - | Qk | Qk | P8044 | NM_001159517 | TSS12786 |
| chr17 | 10818287 | 10818378 | MACS2_peak_1273 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 42 | chr17 | unknown | gene | 10456215 | 10493057 | + | A230009B12Rik | A230009B12Rik | | NR_077237 | TSS2358 |
| chr17 | 10818287 | 10818378 | MACS2_peak_1273 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 42 | chr17 | unknown | gene | 10840383 | 12061653 | + | Park2 | Park2 | P20470 | NM_016694 | TSS5241 |
| chr17 | 11965930 | 11966021 | MACS2_peak_1274 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 2 | chr17 | unknown | gene | 11863069 | 11883189 | - | D17Ertd648e | D17Ertd648e | | NR_045808 | TSS19334 |
| chr17 | 11965930 | 11966021 | MACS2_peak_1274 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 2 | chr17 | unknown | gene | 12119283 | 12219079 | + | Agpat4 | Agpat4 | P24792 | NM_026644 | TSS808 |
| chr17 | 12039634 | 12039725 | MACS2_peak_1275 | 35 | + | 5.98489 | 8.51731 | 3.53253 | 26 | chr17 | unknown | gene | 11863069 | 11883189 | - | D17Ertd648e | D17Ertd648e | | NR_045808 | TSS19334 |
| chr17 | 12039634 | 12039725 | MACS2_peak_1275 | 35 | + | 5.98489 | 8.51731 | 3.53253 | 26 | chr17 | unknown | gene | 12119283 | 12219079 | + | Agpat4 | Agpat4 | P24792 | NM_026644 | TSS808 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr17 | 13587392 | 13587501 | MACS2_peak_1276 | 20 | + | 4.88639 | 6.77383 | 2.08525 | 54 | chr17 | unknown | gene | 13487020 | 13554094 | - | 2700054A10Rik | 2700054A10Rik | | NR_045436 | TSS2854 |
| chr17 | 13587392 | 13587501 | MACS2_peak_1276 | 20 | + | 4.88639 | 6.77383 | 2.08525 | 54 | chr17 | unknown | gene | 13716435 | 13761394 | - | Tcte2 | Tcte2 | P20474 | NM_022311 | TSS22864 |
| chr17 | 13590575 | 13590666 | MACS2_peak_1277 | 23 | + | 5.11378 | 7.13328 | 2.32792 | 45 | chr17 | unknown | gene | 13487020 | 13554094 | - | 2700054A10Rik | 2700054A10Rik | | NR_045436 | TSS2854 |
| chr17 | 13590575 | 13590666 | MACS2_peak_1277 | 23 | + | 5.11378 | 7.13328 | 2.32792 | 45 | chr17 | unknown | gene | 13716435 | 13761394 | - | Tcte2 | Tcte2 | P20474 | NM_022311 | TSS22864 |
| chr17 | 13654697 | 13654838 | MACS2_peak_1278 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 52 | chr17 | unknown | gene | 13487020 | 13554094 | - | 2700054A10Rik | 2700054A10Rik | | NR_045436 | TSS2854 |
| chr17 | 13654697 | 13654838 | MACS2_peak_1278 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 52 | chr17 | unknown | gene | 13716435 | 13761394 | - | Tcte2 | Tcte2 | P20474 | NM_022311 | TSS22864 |
| chr17 | 13654973 | 13655086 | MACS2_peak_1279 | 49 | + | 6.77503 | 10.04021 | 4.94691 | 59 | chr17 | unknown | gene | 13487020 | 13554094 | - | 2700054A10Rik | 2700054A10Rik | | NR_045436 | TSS2854 |
| chr17 | 13654973 | 13655086 | MACS2_peak_1279 | 49 | + | 6.77503 | 10.04021 | 4.94691 | 59 | chr17 | unknown | gene | 13716435 | 13761394 | - | Tcte2 | Tcte2 | P20474 | NM_022311 | TSS22864 |
| chr17 | 15616329 | 15616420 | MACS2_peak_1280 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 39 | chr17 | unknown | gene | 15543078 | 15563301 | - | Prdm9 | Prdm9 | P6970 | NM_144809 | TSS23638 |
| chr17 | 15616329 | 15616420 | MACS2_peak_1280 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 39 | chr17 | unknown | gene | 15631787 | 15641102 | + | 4933401D09Rik | 4933401D09Rik | | NR_045431 | TSS17983 |
| chr17 | 15977450 | 15977541 | MACS2_peak_1281 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 73 | chr17 | unknown | gene | 15806252 | 15826156 | - | Rgmb | Rgmb | P22389 | NM_178615 | TSS17069 |
| chr17 | 15977450 | 15977541 | MACS2_peak_1281 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 73 | chr17 | unknown | gene | 17064102 | 17089384 | + | Zfp960 | Zfp960 | P4605 | NM_001163919 | TSS20225 |
| chr17 | 16312627 | 16312748 | MACS2_peak_1282 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 44 | chr17 | unknown | gene | 15806252 | 15826156 | - | Rgmb | Rgmb | P22389 | NM_178615 | TSS17069 |
| chr17 | 16312627 | 16312748 | MACS2_peak_1282 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 44 | chr17 | unknown | gene | 17064102 | 17089384 | + | Zfp960 | Zfp960 | P4605 | NM_001163919 | TSS20225 |
| chr17 | 16476985 | 16477111 | MACS2_peak_1283 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 45 | chr17 | unknown | gene | 15806252 | 15826156 | - | Rgmb | Rgmb | P22389 | NM_178615 | TSS17069 |
| chr17 | 16476985 | 16477111 | MACS2_peak_1283 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 45 | chr17 | unknown | gene | 17064102 | 17089384 | + | Zfp960 | Zfp960 | P4605 | NM_001163919 | TSS20225 |
| chr17 | 29084287 | 29084477 | MACS2_peak_1284 | 58 | + | 4.60624 | 5.88904 | 1.68837 | 59 | chr17 | unknown | gene | 29057473 | 29079126 | - | Trp53cor1 | Trp53cor1 | | NR_036469 | TSS24704 |
| chr17 | 29084287 | 29084477 | MACS2_peak_1284 | 58 | + | 4.60624 | 5.88904 | 1.68837 | 59 | chr17 | unknown | gene | 29090985 | 29099393 | + | Cdkn1a | Cdkn1a | P3467 | NM_001111099 | TSS23628 |
| chr17 | 30111545 | 30111636 | MACS2_peak_1285 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 69 | chr17 | unknown | gene | 29827957 | 29887513 | - | Mdga1 | Mdga1 | P15635 | NM_001081160 | TSS12801 |
| chr17 | 30111545 | 30111636 | MACS2_peak_1285 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 69 | chr17 | unknown | gene | 30215523 | 30576287 | - | Btbd9 | Btbd9 | P13803 | NM_172618 | TSS11253 |
| chr17 | 31958563 | 31958654 | MACS2_peak_1286 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 28 | chr17 | unknown | gene | 31844249 | 31855792 | - | Sik1 | Sik1 | P1126 | NM_010831 | TSS10385 |
| chr17 | 31958563 | 31958654 | MACS2_peak_1286 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 28 | chr17 | unknown | gene | 32036161 | 32060541 | + | Rrp1b | Rrp1b | P22859 | NM_028244 | TSS24051 |
| chr17 | 33175438 | 33175529 | MACS2_peak_1287 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 13 | chr17 | unknown | gene | 33135589 | 33139683 | - | Morc2b | Morc2b | P15034 | NM_177719 | TSS19026 |
| chr17 | 33175438 | 33175529 | MACS2_peak_1287 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 13 | chr17 | unknown | gene | 33176415 | 33177363 | + | Olfr55 | Olfr55 | P10446 | NM_010998 | TSS13159 |
| chr17 | 33342528 | 33342632 | MACS2_peak_1288 | 63 | + | 7.52781 | 11.52513 | 6.36816 | 58 | chr17 | unknown | gene | 33289543 | 33303196 | + | Zfp955b | Zfp955b | P197 | NM_001142957 | TSS4882 |
| chr17 | 33342528 | 33342632 | MACS2_peak_1288 | 63 | + | 7.52781 | 11.52513 | 6.36816 | 58 | chr17 | unknown | gene | 33380178 | 33394508 | - | Zfp101 | Zfp101 | P13620 | NM_009542 | TSS12826 |
| chr17 | 35296038 | 35296132 | MACS2_peak_1289 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 5 | chr17 | unknown | gene | 35263093 | 35266870 | + | H2-D1 | H2-D1 | P17700 | NM_010380 | TSS22980 |
| chr17 | 35296038 | 35296132 | MACS2_peak_1289 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 5 | chr17 | unknown | gene | 35320557 | 35324186 | + | H2-Q1 | H2-Q1 | P9048 | NM_010390 | TSS23207 |
| chr17 | 35296278 | 35296369 | MACS2_peak_1290 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 19 | chr17 | unknown | gene | 35263093 | 35266870 | + | H2-D1 | H2-D1 | P17700 | NM_010380 | TSS22980 |
| chr17 | 35296278 | 35296369 | MACS2_peak_1290 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 19 | chr17 | unknown | gene | 35320557 | 35324186 | + | H2-Q1 | H2-Q1 | P9048 | NM_010390 | TSS23207 |
| chr17 | 35354967 | 35355106 | MACS2_peak_1291 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 48 | chr17 | unknown | gene | 35342332 | 35345706 | + | H2-Q2 | H2-Q2 | P6134 | NM_010392 | TSS17515 |
| chr17 | 35354967 | 35355106 | MACS2_peak_1291 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 48 | chr17 | unknown | gene | 35379616 | 35384674 | + | H2-Q4 | H2-Q4 | P26828 | NM_001143689 | TSS14521 |
| chr17 | 35624590 | 35624681 | MACS2_peak_1292 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 23 | chr17 | unknown | gene | 35567484 | 35568816 | + | 2300002M23Rik | 2300002M23Rik | P11818 | NM_175148 | TSS21146 |
| chr17 | 35624590 | 35624681 | MACS2_peak_1292 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 23 | chr17 | unknown | gene | 35635754 | 35643668 | - | Dpcr1 | Dpcr1 | P2339 | NM_001033366 | TSS18603 |
| chr17 | 37673060 | 37673151 | MACS2_peak_1293 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 49 | chr17 | unknown | gene | 37672024 | 37672990 | + | Olfr118 | Olfr118 | P16004 | NM_213721 | TSS14015 |
| chr17 | 37673060 | 37673151 | MACS2_peak_1293 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 49 | chr17 | unknown | gene | 37696684 | 37701637 | + | Olfr119 | Olfr119 | P22286 | NM_001011830 | TSS14841 |
| chr17 | 39847287 | 39847378 | MACS2_peak_1294 | 34 | + | 5.61404 | 8.46344 | 3.48278 | 16 | chr17 | unknown | gene | 39640956 | 39644801 | + | Esp15 | Esp15 | P22895 | NM_001244651 | TSS24665 |
| chr17 | 39847287 | 39847378 | MACS2_peak_1294 | 34 | + | 5.61404 | 8.46344 | 3.48278 | 16 | chr17 | unknown | gene | 39950519 | 39955244 | + | Esp38 | Esp38 | P15003 | NM_001256051 | TSS4969 |
| chr17 | 39847664 | 39847755 | MACS2_peak_1295 | 13 | + | 4.22853 | 5.52627 | 1.3392 | 55 | chr17 | unknown | gene | 39640956 | 39644801 | + | Esp15 | Esp15 | P22895 | NM_001244651 | TSS24665 |
| chr17 | 39847664 | 39847755 | MACS2_peak_1295 | 13 | + | 4.22853 | 5.52627 | 1.3392 | 55 | chr17 | unknown | gene | 39950519 | 39955244 | + | Esp38 | Esp38 | P15003 | NM_001256051 | TSS4969 |
| chr17 | 41548965 | 41549056 | MACS2_peak_1296 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 53 | chr17 | unknown | gene | 40934684 | 40960696 | + | Mut | Mut | P8607 | NM_008650 | TSS614 |
| chr17 | 41548965 | 41549056 | MACS2_peak_1296 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 53 | chr17 | unknown | gene | 42315946 | 42503915 | + | Ptchd4 | Ptchd4 | P11284 | NM_028474 | TSS4883 |
| chr17 | 42574958 | 42575049 | MACS2_peak_1297 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 33 | chr17 | unknown | gene | 42315946 | 42503915 | + | Ptchd4 | Ptchd4 | P11284 | NM_028474 | TSS4883 |
| chr17 | 42574958 | 42575049 | MACS2_peak_1297 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 33 | chr17 | unknown | gene | 42656886 | 42692284 | - | Adgrf4 | Adgrf4 | P3014 | NM_001289499 | TSS20156 |
| chr17 | 43376367 | 43376458 | MACS2_peak_1298 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 54 | chr17 | unknown | gene | 43270346 | 43323918 | + | Adgrf1 | Adgrf1 | P11703 | NM_133776 | TSS4273 |
| chr17 | 43376367 | 43376458 | MACS2_peak_1298 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 54 | chr17 | unknown | gene | 43389465 | 43455335 | + | Adgrf5 | Adgrf5 | P5600 | NM_001081178 | TSS18251 |
| chr17 | 44922383 | 44922474 | MACS2_peak_1299 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 29 | chr17 | unknown | gene | 44879703 | 44880288 | - | 4930564C03Rik | 4930564C03Rik | P21957 | NM_029257 | TSS22467 |
| chr17 | 44922383 | 44922474 | MACS2_peak_1299 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 29 | chr17 | unknown | gene | 45391887 | 45433435 | - | Cdc5l | Cdc5l | P18072 | NM_152810 | TSS5561 |
| chr17 | 46807073 | 46807164 | MACS2_peak_1300 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 63 | chr17 | unknown | gene | 46773906 | 46782632 | - | Rpl7l1 | Rpl7l1 | P17543 | NM_025433 | TSS13603 |
| chr17 | 46807073 | 46807164 | MACS2_peak_1300 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 63 | chr17 | unknown | gene | 46890620 | 46891715 | + | Tbcc | Tbcc | P24769 | NM_178385 | TSS13947 |
| chr17 | 49589418 | 49589509 | MACS2_peak_1301 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 27 | chr17 | unknown | gene | 49456021 | 49564337 | - | Daam2 | Daam2 | P272 | NM_001008231 | TSS5928 |
| chr17 | 49589418 | 49589509 | MACS2_peak_1301 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 27 | chr17 | unknown | gene | 49615171 | 49908793 | + | Kif6 | Kif6 | P6130 | NM_177052 | TSS25060 |
| chr17 | 49727807 | 49727898 | MACS2_peak_1302 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 15 | chr17 | unknown | gene | 49456021 | 49564337 | - | Daam2 | Daam2 | P272 | NM_001008231 | TSS5928 |
| chr17 | 49727807 | 49727898 | MACS2_peak_1302 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 15 | chr17 | unknown | gene | 49993306 | 50190497 | - | Rftn1 | Rftn1 | P25449 | NM_181397 | TSS26129 |
| chr17 | 50449680 | 50449771 | MACS2_peak_1303 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 64 | chr17 | unknown | gene | 50279392 | 50293409 | - | Dazl | Dazl | P24476 | NM_001277863 | TSS7427 |
| chr17 | 50449680 | 50449771 | MACS2_peak_1303 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 64 | chr17 | unknown | gene | 50509546 | 50687891 | + | Plcl2 | Plcl2 | P16227 | NM_013880 | TSS13258 |
| chr17 | 51682198 | 51682307 | MACS2_peak_1304 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 45 | chr17 | unknown | gene | 51277987 | 51613053 | + | Mir669a-10 | Mir669a-10 | | NR_037264 | TSS2390 |
| chr17 | 51682198 | 51682307 | MACS2_peak_1304 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 45 | chr17 | unknown | gene | 51736186 | 51833290 | - | Satb1 | Satb1 | P20397 | NM_009122 | TSS14285 |

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr17 | 53295707 | 53295798 | MACS2_peak_1305 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 31 | chr17 | unknown | gene | 52602708 | 52978312 | + | Kcnh8 | Kcnh8 | P5195 | NM_001031811 | TSS9418 |
| chr17 | 53295707 | 53295798 | MACS2_peak_1305 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 31 | chr17 | unknown | gene | 53398888 | 53463279 | - | Efhb | Efhb | P24167 | NM_172497 | TSS6140 |
| chr17 | 55768603 | 55768694 | MACS2_peak_1306 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 49 | chr17 | unknown | gene | 55652024 | 55712628 | - | Pot1b | Pot1b | P15886 | NM_028370 | TSS10933 |
| chr17 | 55768603 | 55768694 | MACS2_peak_1306 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 49 | chr17 | unknown | gene | 55864891 | 55878862 | - | Zfp119a | Zfp119a | P17649 | NM_144546 | TSS17315 |
| chr17 | 56186170 | 56186261 | MACS2_peak_1307 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 12 | chr17 | unknown | gene | 56176540 | 56183891 | - | Mydgf | Mydgf | P19777 | NM_080837 | TSS10956 |
| chr17 | 56186170 | 56186261 | MACS2_peak_1307 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 12 | chr17 | unknown | gene | 56186681 | 56218889 | - | Dpp9 | Dpp9 | P13228 | NM_172624 | TSS11732 |
| chr17 | 57456995 | 57457094 | MACS2_peak_1308 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 78 | chr17 | unknown | gene | 57279099 | 57327704 | + | Vav1 | Vav1 | P6700 | NM_001163815 | TSS22771 |
| chr17 | 57456995 | 57457094 | MACS2_peak_1308 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 78 | chr17 | unknown | gene | 57508782 | 57545314 | - | Vmn2r120 | Vmn2r120 | P19582 | NM_001104591 | TSS1880 |
| chr17 | 58318321 | 58318462 | MACS2_peak_1309 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 52 | chr17 | unknown | gene | 57508782 | 57545314 | - | Vmn2r120 | Vmn2r120 | P19582 | NM_001104591 | TSS1880 |
| chr17 | 58318321 | 58318462 | MACS2_peak_1309 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 52 | chr17 | unknown | gene | 58878807 | 58991375 | - | Pdzph1 | Pdzph1 | P420 | NM_027001 | TSS24603 |
| chr17 | 59301244 | 59301353 | MACS2_peak_1310 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 58 | chr17 | unknown | gene | 59001400 | 59013322 | - | Nudt12 | Nudt12 | P11276 | NM_026497 | TSS514 |
| chr17 | 59301244 | 59301353 | MACS2_peak_1310 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 58 | chr17 | unknown | gene | 62602956 | 62881130 | - | Efna5 | Efna5 | P10876 | NM_207654 | TSS21815 |
| chr17 | 60142273 | 60142364 | MACS2_peak_1311 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 68 | chr17 | unknown | gene | 59001400 | 59013322 | - | Nudt12 | Nudt12 | P11276 | NM_026497 | TSS514 |
| chr17 | 60142273 | 60142364 | MACS2_peak_1311 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 68 | chr17 | unknown | gene | 62602956 | 62881130 | - | Efna5 | Efna5 | P10876 | NM_207654 | TSS21815 |
| chr17 | 60825151 | 60825242 | MACS2_peak_1312 | 12 | + | 4.14966 | 5.12722 | 1.204 | 30 | chr17 | unknown | gene | 59001400 | 59013322 | - | Nudt12 | Nudt12 | P11276 | NM_026497 | TSS514 |
| chr17 | 60825151 | 60825242 | MACS2_peak_1312 | 12 | + | 4.14966 | 5.12722 | 1.204 | 30 | chr17 | unknown | gene | 62602956 | 62881130 | - | Efna5 | Efna5 | P10876 | NM_207654 | TSS21815 |
| chr17 | 61384819 | 61384911 | MACS2_peak_1313 | 43 | + | 6.46877 | 9.37984 | 4.32457 | 30 | chr17 | unknown | gene | 59001400 | 59013322 | - | Nudt12 | Nudt12 | P11276 | NM_026497 | TSS514 |
| chr17 | 61384819 | 61384911 | MACS2_peak_1313 | 43 | + | 6.46877 | 9.37984 | 4.32457 | 30 | chr17 | unknown | gene | 62602956 | 62881130 | - | Efna5 | Efna5 | P10876 | NM_207654 | TSS21815 |
| chr17 | 62377879 | 62377970 | MACS2_peak_1314 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 11 | chr17 | unknown | gene | 59001400 | 59013322 | - | Nudt12 | Nudt12 | P11276 | NM_026497 | TSS514 |
| chr17 | 62377879 | 62377970 | MACS2_peak_1314 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 11 | chr17 | unknown | gene | 62602956 | 62881130 | - | Efna5 | Efna5 | P10876 | NM_207654 | TSS21815 |
| chr17 | 62745023 | 62745114 | MACS2_peak_1315 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 22 | chr17 | unknown | gene | 59001400 | 59013322 | - | Nudt12 | Nudt12 | P11276 | NM_026497 | TSS514 |
| chr17 | 62745023 | 62745114 | MACS2_peak_1315 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 22 | chr17 | unknown | gene | 63045951 | 63500017 | - | Fbxl17 | Fbxl17 | P24453 | NM_015794 | TSS2153 |
| chr17 | 62958317 | 62958408 | MACS2_peak_1316 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 15 | chr17 | unknown | gene | 62602956 | 62881130 | - | Efna5 | Efna5 | P10876 | NM_207654 | TSS21815 |
| chr17 | 62958317 | 62958408 | MACS2_peak_1316 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 15 | chr17 | unknown | gene | 63045951 | 63500017 | - | Fbxl17 | Fbxl17 | P24453 | NM_015794 | TSS2153 |
| chr17 | 63110166 | 63110257 | MACS2_peak_1317 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 40 | chr17 | unknown | gene | 62602956 | 62881130 | - | Efna5 | Efna5 | P10876 | NM_207654 | TSS21815 |
| chr17 | 63110166 | 63110257 | MACS2_peak_1317 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 40 | chr17 | unknown | gene | 63305445 | 63312973 | - | 4930405O22Rik | 4930405O22Rik | | NR_130176 | TSS5421 |
| chr17 | 63383988 | 63384160 | MACS2_peak_1318 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 149 | chr17 | unknown | gene | 63305445 | 63312973 | - | 4930405O22Rik | 4930405O22Rik | | NR_130176 | TSS5421 |
| chr17 | 63383988 | 63384160 | MACS2_peak_1318 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 149 | chr17 | unknown | gene | 63863980 | 64139017 | + | Fer | Fer | P20502 | NM_001037997 | TSS19205 |
| chr17 | 63401045 | 63401136 | MACS2_peak_1319 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 54 | chr17 | unknown | gene | 63305445 | 63312973 | - | 4930405O22Rik | 4930405O22Rik | | NR_130176 | TSS5421 |
| chr17 | 63401045 | 63401136 | MACS2_peak_1319 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 54 | chr17 | unknown | gene | 63863980 | 64139017 | + | Fer | Fer | P20502 | NM_001037997 | TSS19205 |
| chr17 | 66408437 | 66408528 | MACS2_peak_1320 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 19 | chr17 | unknown | gene | 66123519 | 66150838 | + | Ddx11 | Ddx11 | P7536 | NM_001003919 | TSS4958 |
| chr17 | 66408437 | 66408528 | MACS2_peak_1320 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 19 | chr17 | unknown | gene | 66494511 | 66519570 | - | Rab12 | Rab12 | P25133 | NM_024448 | TSS20756 |
| chr17 | 67369262 | 67369353 | MACS2_peak_1321 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 52 | chr17 | unknown | gene | 66666847 | 67354029 | - | Ptprm | Ptprm | P26030 | NM_008984 | TSS14980 |
| chr17 | 67369262 | 67369353 | MACS2_peak_1321 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 52 | chr17 | unknown | gene | 67630964 | 67632583 | - | Lrrc30 | Lrrc30 | P26854 | NM_001033340 | TSS12702 |
| chr17 | 67741397 | 67741495 | MACS2_peak_1322 | 48 | + | 6.74627 | 9.91665 | 4.83815 | 50 | chr17 | unknown | gene | 67630964 | 67632583 | - | Lrrc30 | Lrrc30 | P26854 | NM_001033340 | TSS12702 |
| chr17 | 67741397 | 67741495 | MACS2_peak_1322 | 48 | + | 6.74627 | 9.91665 | 4.83815 | 50 | chr17 | unknown | gene | 67842707 | 68004010 | - | Arhgap28 | Arhgap28 | P1700 | NM_172964 | TSS5137 |
| chr17 | 68016058 | 68016149 | MACS2_peak_1323 | 24 | + | 5.39702 | 7.32466 | 2.43395 | 27 | chr17 | unknown | gene | 67842707 | 68004010 | - | Arhgap28 | Arhgap28 | P1700 | NM_172964 | TSS5137 |
| chr17 | 68016058 | 68016149 | MACS2_peak_1323 | 24 | + | 5.39702 | 7.32466 | 2.43395 | 27 | chr17 | unknown | gene | 68273796 | 68777961 | + | L3mbtl4 | L3mbtl4 | P3284 | NM_177278 | TSS19610 |
| chr17 | 68761239 | 68761330 | MACS2_peak_1324 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 21 | chr17 | unknown | gene | 67842707 | 68004010 | - | Arhgap28 | Arhgap28 | P1700 | NM_172964 | TSS5137 |
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| chr17 | 72465430 | 72465541 | MACS2_peak_1325 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 87 | chr17 | unknown | gene | 71769690 | 71863924 | + | Clip4 | Clip4 | P15730 | NM_175378 | TSS26733 |
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| chr17 | 73062397 | 73062488 | MACS2_peak_1326 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 52 | chr17 | unknown | gene | 72918304 | 72939444 | + | Lbh | Lbh | P7856 | NM_029999 | TSS18308 |
| chr17 | 73062397 | 73062488 | MACS2_peak_1326 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 52 | chr17 | unknown | gene | 73107984 | 73240220 | + | Lclat1 | Lclat1 | P21061 | NM_001177968 | TSS11146 |
| chr17 | 73090068 | 73090201 | MACS2_peak_1327 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 84 | chr17 | unknown | gene | 72918304 | 72939444 | + | Lbh | Lbh | P7856 | NM_029999 | TSS18308 |
| chr17 | 73090068 | 73090201 | MACS2_peak_1327 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 84 | chr17 | unknown | gene | 73107984 | 73240220 | + | Lclat1 | Lclat1 | P21061 | NM_001177968 | TSS11146 |
| chr17 | 73116193 | 73116288 | MACS2_peak_1328 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 19 | chr17 | unknown | gene | 72918304 | 72939444 | + | Lbh | Lbh | P7856 | NM_029999 | TSS18308 |
| chr17 | 73116193 | 73116288 | MACS2_peak_1328 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 19 | chr17 | unknown | gene | 73306463 | 73399296 | - | Capn13 | Capn13 | P16346 | NM_001033444 | TSS11699 |
| chr17 | 74568977 | 74569068 | MACS2_peak_1329 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 32 | chr17 | unknown | gene | 74489492 | 74499108 | + | Yipf4 | Yipf4 | P5829 | NM_026417 | TSS13600 |
| chr17 | 74568977 | 74569068 | MACS2_peak_1329 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 32 | chr17 | unknown | gene | 74717749 | 74863456 | + | Ttc27 | Ttc27 | P16079 | NM_152817 | TSS3705 |
| chr17 | 76327094 | 76327190 | MACS2_peak_1330 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 41 | chr17 | unknown | gene | 75861022 | 75889039 | + | Gm4710 | Gm4710 | | NR_033456 | TSS5471 |
| chr17 | 76327094 | 76327190 | MACS2_peak_1330 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 41 | chr17 | unknown | gene | 78200247 | 78374232 | + | Crim1 | Crim1 | P26818 | NM_015800 | TSS26579 |
| chr17 | 78227528 | 78227631 | MACS2_peak_1331 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 13 | chr17 | unknown | gene | 75861022 | 75889039 | + | Gm4710 | Gm4710 | | NR_033456 | TSS5471 |
| chr17 | 78227528 | 78227631 | MACS2_peak_1331 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 13 | chr17 | unknown | gene | 78369211 | 78418083 | - | Fez2 | Fez2 | P24382 | NM_001285949 | TSS25295 |
| chr17 | 78454530 | 78454657 | MACS2_peak_1332 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 42 | chr17 | unknown | gene | 78369211 | 78418083 | - | Fez2 | Fez2 | P24382 | NM_001285949 | TSS25295 |
| chr17 | 78454530 | 78454657 | MACS2_peak_1332 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 42 | chr17 | unknown | gene | 78508062 | 78626923 | + | Vit | Vit | P14029 | NM_028813 | TSS19797 |
| chr17 | 79756433 | 79756524 | MACS2_peak_1333 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 52 | chr17 | unknown | gene | 79706952 | 79715041 | - | Cyp1b1 | Cyp1b1 | P16948 | NM_009994 | TSS17333 |
| chr17 | 79756433 | 79756524 | MACS2_peak_1333 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 52 | chr17 | unknown | gene | 79848389 | 79896026 | - | Atl2 | Atl2 | P20379 | NM_178050 | TSS1015 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr17 | 80523475 | 80523566 | MACS2_peak_1334 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 41 | chr17 | unknown | gene | 80393751 | 80479923 | - | Sos1 | Sos1 | P12486 | NM_009231 | TSS10077 |
| chr17 | 80523475 | 80523566 | MACS2_peak_1334 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 41 | chr17 | unknown | gene | 80580512 | 80727889 | - | Map4k3 | Map4k3 | P25695 | NM_001290345 | TSS23541 |
| chr17 | 80622575 | 80622727 | MACS2_peak_1335 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 81 | chr17 | unknown | gene | 80523549 | 80563834 | - | Cdkl4 | Cdkl4 | P13323 | NM_001033443 | TSS1163 |
| chr17 | 80622575 | 80622727 | MACS2_peak_1335 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 81 | chr17 | unknown | gene | 80896792 | 80933447 | + | C230072F16Rik | C230072F16Rik | | NR_131127 | TSS22751 |
| chr17 | 81399465 | 81399556 | MACS2_peak_1336 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 13 | chr17 | unknown | gene | 81026326 | 81065060 | - | Thumpd2 | Thumpd2 | P4449 | NM_028138 | TSS6025 |
| chr17 | 81399465 | 81399556 | MACS2_peak_1336 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 13 | chr17 | unknown | gene | 83033591 | 83078225 | - | Gm19689 | Gm19689 | | NR_045094 | TSS1286 |
| chr17 | 81541795 | 81541913 | MACS2_peak_1337 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 27 | chr17 | unknown | gene | 81026326 | 81065060 | - | Thumpd2 | Thumpd2 | P4449 | NM_028138 | TSS6025 |
| chr17 | 81541795 | 81541913 | MACS2_peak_1337 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 27 | chr17 | unknown | gene | 83033591 | 83078225 | - | Gm19689 | Gm19689 | | NR_045094 | TSS1286 |
| chr17 | 82650900 | 82650991 | MACS2_peak_1338 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 28 | chr17 | unknown | gene | 81373104 | 81738387 | - | Slc8a1 | Slc8a1 | P17387 | NM_001286684 | TSS23746 |
| chr17 | 82650900 | 82650991 | MACS2_peak_1338 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 28 | chr17 | unknown | gene | 83033591 | 83078225 | - | Gm19689 | Gm19689 | | NR_045094 | TSS1286 |
| chr17 | 83110005 | 83110096 | MACS2_peak_1339 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 5 | chr17 | unknown | gene | 83033591 | 83078225 | - | Gm19689 | Gm19689 | | NR_045094 | TSS1286 |
| chr17 | 83110005 | 83110096 | MACS2_peak_1339 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 5 | chr17 | unknown | gene | 83215282 | 83224277 | + | Pkdcc | Pkdcc | P23717 | NM_134117 | TSS23374 |
| chr17 | 84061985 | 84062076 | MACS2_peak_1340 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 1 | chr17 | unknown | gene | 83998551 | 84013408 | + | 8430430B14Rik | 8430430B14Rik | | NR_130994 | TSS3993 |
| chr17 | 84061985 | 84062076 | MACS2_peak_1340 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 1 | chr17 | unknown | gene | 84078659 | 84089875 | + | 4933433H22Rik | 4933433H22Rik | | NR_045458 | TSS10248 |
| chr17 | 84493165 | 84493256 | MACS2_peak_1341 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 30 | chr17 | unknown | gene | 84190055 | 84466208 | - | Thada | Thada | P2 | NM_183021 | TSS20060 |
| chr17 | 84493165 | 84493256 | MACS2_peak_1341 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 30 | chr17 | unknown | gene | 84511894 | 84619809 | + | Plekhh2 | Plekhh2 | P4025 | NM_177606 | TSS26345 |
| chr17 | 84664369 | 84664467 | MACS2_peak_1342 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 11 | chr17 | unknown | gene | 84626498 | 84655363 | + | Dync2li1 | Dync2li1 | P3279 | NM_172256 | TSS20263 |
| chr17 | 84664369 | 84664467 | MACS2_peak_1342 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 11 | chr17 | unknown | gene | 84676301 | 84700333 | + | Abcg8 | Abcg8 | P10704 | NM_001286005 | TSS7948 |
| chr17 | 85646105 | 85646218 | MACS2_peak_1343 | 63 | + | 7.52781 | 11.52513 | 6.36816 | 60 | chr17 | unknown | gene | 85620833 | 85623919 | + | Six3 | Six3 | P9559 | NM_011381 | TSS228 |
| chr17 | 85646105 | 85646218 | MACS2_peak_1343 | 63 | + | 7.52781 | 11.52513 | 6.36816 | 60 | chr17 | unknown | gene | 85684267 | 85687952 | - | Six2 | Six2 | P25823 | NM_011380 | TSS27037 |
| chr17 | 86181417 | 86181589 | MACS2_peak_1344 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 42 | chr17 | unknown | gene | 85984664 | 86145175 | - | Srbd1 | Srbd1 | P3466 | NM_030133 | TSS4251 |
| chr17 | 86181417 | 86181589 | MACS2_peak_1344 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 42 | chr17 | unknown | gene | 86285166 | 86287178 | - | 2010106C02Rik | 2010106C02Rik | | NR_045435 | TSS26530 |
| chr17 | 86313176 | 86313279 | MACS2_peak_1345 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 79 | chr17 | unknown | gene | 86285166 | 86287178 | - | 2010106C02Rik | 2010106C02Rik | | NR_045435 | TSS26530 |
| chr17 | 86313176 | 86313279 | MACS2_peak_1345 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 79 | chr17 | unknown | gene | 86753863 | 86831102 | + | Epas1 | Epas1 | P13209 | NM_010137 | TSS14491 |
| chr17 | 86384755 | 86384949 | MACS2_peak_1346 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 50 | chr17 | unknown | gene | 86285166 | 86287178 | - | 2010106C02Rik | 2010106C02Rik | | NR_045435 | TSS26530 |
| chr17 | 86384755 | 86384949 | MACS2_peak_1346 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 50 | chr17 | unknown | gene | 86753863 | 86831102 | + | Epas1 | Epas1 | P13209 | NM_010137 | TSS14491 |
| chr17 | 87580510 | 87580601 | MACS2_peak_1347 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 53 | chr17 | unknown | gene | 87433400 | 87446795 | - | Calm2 | Calm2 | P13415 | NM_007589 | TSS3818 |
| chr17 | 87580510 | 87580601 | MACS2_peak_1347 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 53 | chr17 | unknown | gene | 87635978 | 87650469 | + | Epcam | Epcam | P3983 | NM_008532 | TSS18152 |
| chr17 | 88171870 | 88171999 | MACS2_peak_1348 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 72 | chr17 | unknown | gene | 88125511 | 88131116 | + | Gm4832 | Gm4832 | P1027 | NM_001190356 | TSS4783 |
| chr17 | 88171870 | 88171999 | MACS2_peak_1348 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 72 | chr17 | unknown | gene | 88440711 | 88486926 | + | Foxn2 | Foxn2 | P16302 | NM_180974 | TSS8932 |
| chr17 | 89401047 | 89401244 | MACS2_peak_1349 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 160 | chr17 | unknown | gene | 89379240 | 89384993 | + | Gm4719 | Gm4719 | | NR_045952 | TSS21167 |
| chr17 | 89401047 | 89401244 | MACS2_peak_1349 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 160 | chr17 | unknown | gene | 90033643 | 91092802 | - | Nrxn1 | Nrxn1 | P14666 | NM_177284 | TSS19134 |
| chr17 | 89499892 | 89500017 | MACS2_peak_1350 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 66 | chr17 | unknown | gene | 89379240 | 89384993 | + | Gm4719 | Gm4719 | | NR_045952 | TSS21167 |
| chr17 | 89499892 | 89500017 | MACS2_peak_1350 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 66 | chr17 | unknown | gene | 90033643 | 91092802 | - | Nrxn1 | Nrxn1 | P14666 | NM_177284 | TSS19134 |
| chr17 | 90363071 | 90363215 | MACS2_peak_1351 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 29 | chr17 | unknown | gene | 89379240 | 89384993 | + | Gm4719 | Gm4719 | | NR_045952 | TSS21167 |
| chr17 | 90363071 | 90363215 | MACS2_peak_1351 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 29 | chr17 | unknown | gene | 90861168 | 90867102 | + | 4930480K15Rik | 4930480K15Rik | | NR_045463 | TSS13474 |
| chr17 | 90809037 | 90809165 | MACS2_peak_1352 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 55 | chr17 | unknown | gene | 89379240 | 89384993 | + | Gm4719 | Gm4719 | | NR_045952 | TSS21167 |
| chr17 | 90809037 | 90809165 | MACS2_peak_1352 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 55 | chr17 | unknown | gene | 90861168 | 90867102 | + | 4930480K15Rik | 4930480K15Rik | | NR_045463 | TSS13474 |
| chr17 | 90863352 | 90863497 | MACS2_peak_1353 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 58 | chr17 | unknown | gene | 89379240 | 89384993 | + | Gm4719 | Gm4719 | | NR_045952 | TSS21167 |
| chr17 | 90863352 | 90863497 | MACS2_peak_1353 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 58 | chr17 | unknown | gene | 93199421 | 93204127 | + | Adcyap1 | Adcyap1 | P25710 | NM_009625 | TSS16570 |
| chr17 | 92826812 | 92826903 | MACS2_peak_1354 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 31 | chr17 | unknown | gene | 90033643 | 91092802 | - | Nrxn1 | Nrxn1 | P14666 | NM_177284 | TSS19134 |
| chr17 | 92826812 | 92826903 | MACS2_peak_1354 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 31 | chr17 | unknown | gene | 93199421 | 93204127 | + | Adcyap1 | Adcyap1 | P25710 | NM_009625 | TSS16570 |
| chr17 | 92998754 | 92998895 | MACS2_peak_1355 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 79 | chr17 | unknown | gene | 90033643 | 91092802 | - | Nrxn1 | Nrxn1 | P14666 | NM_177284 | TSS19134 |
| chr17 | 92998754 | 92998895 | MACS2_peak_1355 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 79 | chr17 | unknown | gene | 93199421 | 93204127 | + | Adcyap1 | Adcyap1 | P25710 | NM_009625 | TSS16570 |
| chr17 | 93830544 | 93830635 | MACS2_peak_1356 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 56 | chr17 | unknown | gene | 93199421 | 93204127 | + | Adcyap1 | Adcyap1 | P25710 | NM_009625 | TSS16570 |
| chr17 | 93830544 | 93830635 | MACS2_peak_1356 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 56 | chr17 | unknown | gene | 94727079 | 94749892 | - | Mettl4 | Mettl4 | P5736 | NM_176917 | TSS1519 |
| chr17 | 94876582 | 94876716 | MACS2_peak_1357 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 45 | chr17 | unknown | gene | 94759941 | 94834799 | - | Gm1976 | Gm1976 | | NR_045963 | TSS8671 |
| chr18 | 3004793 | 3004937 | MACS2_peak_1358 | 243 | + | 14.41076 | 29.98719 | 24.31233 | 74 | chr18 | unknown | gene | 3122491 | 3123412 | - | Vmn1r238 | Vmn1r238 | P20577 | NM_001167539 | TSS14177 |
| chr18 | 3005650 | 3005957 | MACS2_peak_1359 | 58 | + | 7.00658 | 11.02031 | 5.89046 | 217 | chr18 | unknown | gene | 3122491 | 3123412 | - | Vmn1r238 | Vmn1r238 | P20577 | NM_001167539 | TSS14177 |
| chr18 | 3405648 | 3405829 | MACS2_peak_1360 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 15 | chr18 | unknown | gene | 3336415 | 3366863 | + | Gm6225 | Gm6225 | | NR_033457 | TSS4267 |
| chr18 | 3405648 | 3405829 | MACS2_peak_1360 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 15 | chr18 | unknown | gene | 3507956 | 3512400 | + | Bambi | Bambi | P23311 | NM_026505 | TSS25461 |
| chr18 | 4196930 | 4197071 | MACS2_peak_1361 | 7 | + | 3.59638 | 4.22707 | 0.75855 | 69 | chr18 | unknown | gene | 4165831 | 4181974 | + | Lyzl1 | Lyzl1 | P19698 | NM_026092 | TSS13730 |
| chr18 | 4196930 | 4197071 | MACS2_peak_1361 | 7 | + | 3.59638 | 4.22707 | 0.75855 | 69 | chr18 | unknown | gene | 4331326 | 4352953 | - | Map3k8 | Map3k8 | P5674 | NM_007746 | TSS26596 |
| chr18 | 4198269 | 4198384 | MACS2_peak_1362 | 30 | + | 5.49725 | 7.99355 | 3.05202 | 36 | chr18 | unknown | gene | 4165831 | 4181974 | + | Lyzl1 | Lyzl1 | P19698 | NM_026092 | TSS13730 |
| chr18 | 4198269 | 4198384 | MACS2_peak_1362 | 30 | + | 5.49725 | 7.99355 | 3.05202 | 36 | chr18 | unknown | gene | 4331326 | 4352953 | - | Map3k8 | Map3k8 | P5674 | NM_007746 | TSS26596 |
| chr18 | 4494854 | 4494945 | MACS2_peak_1363 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 46 | chr18 | unknown | gene | 4375591 | 4396467 | + | Mtpap | Mtpap | P13696 | NM_026157 | TSS26878 |
| chr18 | 4494854 | 4494945 | MACS2_peak_1363 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 46 | chr18 | unknown | gene | 4634928 | 4680260 | + | 9430020K01Rik | 9430020K01Rik | P551 | NM_001081963 | TSS25005 |
| chr18 | 6994707 | 6994798 | MACS2_peak_1364 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 29 | chr18 | unknown | gene | 6765166 | 6788655 | + | Rab18 | Rab18 | P723 | NM_001278447 | TSS6445 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr18 | 6994707 | 6994798 | MACS2_peak_1364 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 29 | chr18 | unknown | gene | 7088232 | 7297901 | - | Armc4 | Armc4 | P10439 | NM_001081393 | TSS13776 |
| chr18 | 9047408 | 9047499 | MACS2_peak_1365 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 55 | chr18 | unknown | gene | 7868831 | 7926139 | + | Wac | Wac | P514 | NM_001282093 | TSS26115 |
| chr18 | 9047408 | 9047499 | MACS2_peak_1365 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 55 | chr18 | unknown | gene | 9212855 | 9214977 | + | Fzd8 | Fzd8 | P14720 | NM_008058 | TSS20273 |
| chr18 | 9959307 | 9959398 | MACS2_peak_1366 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 81 | chr18 | unknown | gene | 9707647 | 9877007 | + | Colec12 | Colec12 | P17562 | NM_130449 | TSS19958 |
| chr18 | 9959307 | 9959398 | MACS2_peak_1366 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 81 | chr18 | unknown | gene | 9993614 | 10029928 | - | Usp14 | Usp14 | P5589 | NM_021522 | TSS6833 |
| chr18 | 9964062 | 9964153 | MACS2_peak_1367 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 3 | chr18 | unknown | gene | 9707647 | 9877007 | + | Colec12 | Colec12 | P17562 | NM_130449 | TSS19958 |
| chr18 | 9964062 | 9964153 | MACS2_peak_1367 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 3 | chr18 | unknown | gene | 9993614 | 10029928 | - | Usp14 | Usp14 | P5589 | NM_021522 | TSS6833 |
| chr18 | 12850939 | 12851030 | MACS2_peak_1368 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 32 | chr18 | unknown | gene | 12741354 | 12755142 | + | Cabyr | Cabyr | P796 | NM_001042418 | TSS19626 |
| chr18 | 12850939 | 12851030 | MACS2_peak_1368 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 32 | chr18 | unknown | gene | 12972251 | 12990558 | + | Impact | Impact | P5960 | NM_008378 | TSS16111 |
| chr18 | 13137266 | 13137357 | MACS2_peak_1369 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 33 | chr18 | unknown | gene | 13006989 | 13022581 | + | Hrh4 | Hrh4 | P19556 | NM_153087 | TSS21154 |
| chr18 | 13137266 | 13137357 | MACS2_peak_1369 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 33 | chr18 | unknown | gene | 13687013 | 13972733 | - | Zfp521 | Zfp521 | P3897 | NM_145492 | TSS154 |
| chr18 | 13698835 | 13698926 | MACS2_peak_1370 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 28 | chr18 | unknown | gene | 13006989 | 13022581 | + | Hrh4 | Hrh4 | P19556 | NM_153087 | TSS21154 |
| chr18 | 13698835 | 13698926 | MACS2_peak_1370 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 28 | chr18 | unknown | gene | 14232305 | 14278542 | + | 8430422H06Rik | 8430422H06Rik |  | NR_045373 | TSS25160 |
| chr18 | 16752012 | 16752135 | MACS2_peak_1371 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 46 | chr18 | unknown | gene | 15452174 | 15718007 | - | Chst9 | Chst9 | P20343 | NM_199055 | TSS23161 |
| chr18 | 16752012 | 16752135 | MACS2_peak_1371 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 46 | chr18 | unknown | gene | 16816406 | 16822783 | + | Gm15328 | Gm15328 |  | NR_045399 | TSS13971 |
| chr18 | 20400694 | 20400804 | MACS2_peak_1372 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 21 | chr18 | unknown | gene | 20310872 | 20341045 | + | Dsg1a | Dsg1a | P25863 | NM_010079 | TSS26616 |
| chr18 | 20400694 | 20400804 | MACS2_peak_1372 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 21 | chr18 | unknown | gene | 20436174 | 20471603 | + | Dsg4 | Dsg4 | P19584 | NM_181564 | TSS12970 |
| chr18 | 21018505 | 21018596 | MACS2_peak_1373 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 65 | chr18 | unknown | gene | 20944624 | 20983185 | + | Rnf125 | Rnf125 | P13733 | NM_026301 | TSS15204 |
| chr18 | 21018505 | 21018596 | MACS2_peak_1373 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 65 | chr18 | unknown | gene | 21072343 | 21100058 | + | Mep1b | Mep1b | P16771 | NM_008586 | TSS15989 |
| chr18 | 21177891 | 21177982 | MACS2_peak_1374 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 9 | chr18 | unknown | gene | 21072343 | 21100058 | + | Mep1b | Mep1b | P16771 | NM_008586 | TSS15989 |
| chr18 | 21177891 | 21177982 | MACS2_peak_1374 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 9 | chr18 | unknown | gene | 21550376 | 21652368 | - | Klhl14 | Klhl14 | P25614 | NM_001081403 | TSS4664 |
| chr18 | 23854670 | 23854803 | MACS2_peak_1375 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 46 | chr18 | unknown | gene | 23774863 | 23774989 | - | Mir6360 | Mir6360 |  | NR_105778 | TSS9500 |
| chr18 | 23854670 | 23854803 | MACS2_peak_1375 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 46 | chr18 | unknown | gene | 23954687 | 23961043 | + | Zfp397 | Zfp397 | P6899 | NM_027007 | TSS2354 |
| chr18 | 24251148 | 24251275 | MACS2_peak_1376 | 7 | + | 3.33222 | 3.76219 | 0.71769 | 54 | chr18 | unknown | gene | 24104760 | 24121801 | - | Ino80c | Ino80c | P2579 | NM_172625 | TSS16914 |
| chr18 | 24251148 | 24251275 | MACS2_peak_1376 | 7 | + | 3.33222 | 3.76219 | 0.71769 | 54 | chr18 | unknown | gene | 24429109 | 24429170 | - | Mir187 | Mir187 |  | NR_029573 | TSS27148 |
| chr18 | 24333198 | 24333289 | MACS2_peak_1377 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 34 | chr18 | unknown | gene | 24205343 | 24284856 | + | Galnt1 | Galnt1 | P5137 | NM_013814 | TSS19068 |
| chr18 | 24333198 | 24333289 | MACS2_peak_1377 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 34 | chr18 | unknown | gene | 24429109 | 24429170 | - | Mir187 | Mir187 |  | NR_029573 | TSS27148 |
| chr18 | 25237861 | 25237959 | MACS2_peak_1378 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 12 | chr18 | unknown | gene | 25127222 | 25168608 | - | Tpgs2 | Tpgs2 | P12400 | NM_001142698 | TSS2932 |
| chr18 | 25237861 | 25237959 | MACS2_peak_1378 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 12 | chr18 | unknown | gene | 25477619 | 25753627 | - | Celf4 | Celf4 | P20389 | NM_001174074 | TSS15979 |
| chr18 | 25304996 | 25305087 | MACS2_peak_1379 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 31 | chr18 | unknown | gene | 25127222 | 25168608 | - | Tpgs2 | Tpgs2 | P12400 | NM_001142698 | TSS2932 |
| chr18 | 25304996 | 25305087 | MACS2_peak_1379 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 31 | chr18 | unknown | gene | 25477619 | 25753627 | - | Celf4 | Celf4 | P20389 | NM_001174074 | TSS15979 |
| chr18 | 25829357 | 25829454 | MACS2_peak_1380 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 78 | chr18 | unknown | gene | 25477619 | 25753627 | - | Celf4 | Celf4 | P20389 | NM_001174074 | TSS15979 |
| chr18 | 25829357 | 25829454 | MACS2_peak_1380 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 78 | chr18 | unknown | gene | 28560163 | 28998176 | + | 4930474G06Rik | 4930474G06Rik |  | NR_045398 | TSS5273 |
| chr18 | 31788790 | 31788881 | MACS2_peak_1381 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 56 | chr18 | unknown | gene | 31759823 | 31780755 | + | Ammecr1l | Ammecr1l | P140 | NM_153515 | TSS12734 |
| chr18 | 31788790 | 31788881 | MACS2_peak_1381 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 56 | chr18 | unknown | gene | 31789158 | 31796128 | + | Polr2d | Polr2d | P2357 | NM_027002 | TSS24476 |
| chr18 | 32942360 | 32942496 | MACS2_peak_1382 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 55 | chr18 | unknown | gene | 32880572 | 32880673 | - | Mir6361 | Mir6361 |  | NR_105779 | TSS24835 |
| chr18 | 32942360 | 32942496 | MACS2_peak_1382 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 55 | chr18 | unknown | gene | 33201420 | 33213671 | - | Stard4 | Stard4 | P12925 | NM_133774 | TSS20882 |
| chr18 | 32950996 | 32951087 | MACS2_peak_1383 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 7 | chr18 | unknown | gene | 32880572 | 32880673 | - | Mir6361 | Mir6361 |  | NR_105779 | TSS24835 |
| chr18 | 32950996 | 32951087 | MACS2_peak_1383 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 7 | chr18 | unknown | gene | 33201420 | 33213671 | - | Stard4 | Stard4 | P12925 | NM_133774 | TSS20882 |
| chr18 | 33054780 | 33054871 | MACS2_peak_1384 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 7 | chr18 | unknown | gene | 32880572 | 32880673 | - | Mir6361 | Mir6361 |  | NR_105779 | TSS24835 |
| chr18 | 33054780 | 33054871 | MACS2_peak_1384 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 7 | chr18 | unknown | gene | 33201420 | 33213671 | - | Stard4 | Stard4 | P12925 | NM_133774 | TSS20882 |
| chr18 | 33126453 | 33126610 | MACS2_peak_1385 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 67 | chr18 | unknown | gene | 32880572 | 32880673 | - | Mir6361 | Mir6361 |  | NR_105779 | TSS24835 |
| chr18 | 33126453 | 33126610 | MACS2_peak_1385 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 67 | chr18 | unknown | gene | 33201420 | 33213671 | - | Stard4 | Stard4 | P12925 | NM_133774 | TSS20882 |
| chr18 | 33544544 | 33544635 | MACS2_peak_1386 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 61 | chr18 | unknown | gene | 33464162 | 33474710 | + | Gm10549 | Gm10549 |  | NR_045415 | TSS6998 |
| chr18 | 33544544 | 33544635 | MACS2_peak_1386 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 61 | chr18 | unknown | gene | 33794891 | 33795989 | + | Epb4.1l4aos | Epb4.1l4aos |  | NR_038152 | TSS1681 |
| chr18 | 34262916 | 34263007 | MACS2_peak_1387 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 2 | chr18 | unknown | gene | 34207774 | 34221772 | - | Gm10548 | Gm10548 |  | NR_040534 | TSS153 |
| chr18 | 34262916 | 34263007 | MACS2_peak_1387 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 2 | chr18 | unknown | gene | 34331144 | 34336232 | + | Srp19 | Srp19 | P9628 | NM_025527 | TSS22234 |
| chr18 | 34381572 | 34381667 | MACS2_peak_1388 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 16 | chr18 | unknown | gene | 34344885 | 34373321 | - | Reep5 | Reep5 | P26074 | NM_007874 | TSS26925 |
| chr18 | 34381572 | 34381667 | MACS2_peak_1388 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 16 | chr18 | unknown | gene | 34409422 | 34442788 | + | Pkd2l2 | Pkd2l2 | P24878 | NM_001163004 | TSS22735 |
| chr18 | 35815105 | 35815196 | MACS2_peak_1389 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 50 | chr18 | unknown | gene | 35771558 | 35805563 | + | Ube2d2a | Ube2d2a | P10364 | NM_019912 | TSS15142 |
| chr18 | 35815105 | 35815196 | MACS2_peak_1389 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 50 | chr18 | unknown | gene | 35829817 | 35860694 | + | Cxxc5 | Cxxc5 | P9660 | NM_133687 | TSS4057 |
| chr18 | 37984944 | 37985077 | MACS2_peak_1390 | 49 | + | 6.77503 | 10.04021 | 4.94691 | 53 | chr18 | unknown | gene | 37974502 | 37974617 | - | Mir6981 | Mir6981 |  | NR_105947 | TSS16161 |
| chr18 | 37984944 | 37985077 | MACS2_peak_1390 | 49 | + | 6.77503 | 10.04021 | 4.94691 | 53 | chr18 | unknown | gene | 37990886 | 37990945 | - | Mir6980 | Mir6980 |  | NR_105946 | TSS1870 |
| chr18 | 39472468 | 39472559 | MACS2_peak_1391 | 23 | + | 5.33156 | 7.20295 | 2.32792 | 18 | chr18 | unknown | gene | 38993144 | 39371162 | + | Arhgap26 | Arhgap26 | P13409 | NM_175164 | TSS17827 |
| chr18 | 39472468 | 39472559 | MACS2_peak_1391 | 23 | + | 5.33156 | 7.20295 | 2.32792 | 18 | chr18 | unknown | gene | 39773496 | 39775570 | + | Pabpc2 | Pabpc2 | P2761 | NM_011033 | TSS19409 |
| chr18 | 39617843 | 39617950 | MACS2_peak_1392 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 82 | chr18 | unknown | gene | 39410544 | 39487232 | - | Nr3c1 | Nr3c1 | P22801 | NM_008173 | TSS6236 |
| chr18 | 39617843 | 39617950 | MACS2_peak_1392 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 82 | chr18 | unknown | gene | 39773496 | 39775570 | + | Pabpc2 | Pabpc2 | P2761 | NM_011033 | TSS19409 |
| chr18 | 40308033 | 40308314 | MACS2_peak_1393 | 74 | + | 8.11868 | 12.69111 | 7.4955 | 57 | chr18 | unknown | gene | 40256961 | 40257687 | + | 2900055J20Rik | 2900055J20Rik |  | NR_045177 | TSS22311 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr18 | 40308033 | 40308314 | MACS2_peak_1393 | 74 | + | 8.11868 | 12.69111 | 7.4955 | 57 | chr18 | unknown | gene | 41875695 | 41951175 | - | Prelid2 | Prelid2 | P18878 | NM_029942 | TSS7411 |
| chr18 | 42578132 | 42578239 | MACS2_peak_1394 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 33 | chr18 | unknown | gene | 42511486 | 42574719 | + | Tcerg1 | Tcerg1 | P11233 | NM_001039474 | TSS23438 |
| chr18 | 42578132 | 42578239 | MACS2_peak_1394 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 33 | chr18 | unknown | gene | 42645220 | 43059240 | - | Ppp2r2b | Ppp2r2b | | NR_073583 | TSS23078 |
| chr18 | 42975806 | 42976152 | MACS2_peak_1395 | 126 | + | 10.32744 | 18.04073 | 12.66113 | 191 | chr18 | unknown | gene | 42578019 | 42579611 | - | Gpr151 | Gpr151 | P15722 | NM_181543 | TSS26415 |
| chr18 | 42975806 | 42976152 | MACS2_peak_1395 | 126 | + | 10.32744 | 18.04073 | 12.66113 | 191 | chr18 | unknown | gene | 43207696 | 43315154 | + | Stk32a | Stk32a | P18065 | NM_178749 | TSS14239 |
| chr18 | 43660085 | 43660176 | MACS2_peak_1396 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 21 | chr18 | unknown | gene | 43320978 | 43438207 | - | Dpysl3 | Dpysl3 | P3608 | NM_001291455 | TSS24576 |
| chr18 | 43660085 | 43660176 | MACS2_peak_1396 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 21 | chr18 | unknown | gene | 43728068 | 43737149 | - | Spink1 | Spink1 | P17917 | NM_009258 | TSS14373 |
| chr18 | 43772194 | 43772307 | MACS2_peak_1397 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 60 | chr18 | unknown | gene | 43764300 | 43767254 | + | Scgb3a2 | Scgb3a2 | P6192 | NM_001289644 | TSS5785 |
| chr18 | 43772194 | 43772307 | MACS2_peak_1397 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 60 | chr18 | unknown | gene | 43777195 | 43792842 | - | Gm94 | Gm94 | P12886 | NM_001033280 | TSS13815 |
| chr18 | 45082591 | 45082682 | MACS2_peak_1398 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 22 | chr18 | unknown | gene | 44828664 | 44889720 | + | Ythdc2 | Ythdc2 | P24292 | NM_001163013 | TSS25484 |
| chr18 | 45082591 | 45082682 | MACS2_peak_1398 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 22 | chr18 | unknown | gene | 45560153 | 45685562 | + | Kcnn2 | Kcnn2 | P6358 | NM_080465 | TSS21409 |
| chr18 | 45737516 | 45737635 | MACS2_peak_1399 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 31 | chr18 | unknown | gene | 45560153 | 45685562 | + | Kcnn2 | Kcnn2 | P6358 | NM_080465 | TSS21409 |
| chr18 | 45737516 | 45737635 | MACS2_peak_1399 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 31 | chr18 | unknown | gene | 46165299 | 46212364 | - | Trim36 | Trim36 | P22648 | NM_001170855 | TSS23034 |
| chr18 | 46627073 | 46627164 | MACS2_peak_1400 | 13 | + | 4.55462 | 5.79642 | 1.3392 | 23 | chr18 | unknown | gene | 46597703 | 46608134 | + | Eif1a | Eif1a | P26796 | NM_010120 | TSS23957 |
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| chr18 | 48189892 | 48189983 | MACS2_peak_1401 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 37 | chr18 | unknown | gene | 47922840 | 48107980 | + | G630055G22Rik | G630055G22Rik | | NR_045404 | TSS1252 |
| chr18 | 48189892 | 48189983 | MACS2_peak_1401 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 37 | chr18 | unknown | gene | 49523288 | 49524441 | + | 1700044K03Rik | 1700044K03Rik | | NR_033785 | TSS16202 |
| chr18 | 48894564 | 48894655 | MACS2_peak_1402 | 13 | + | 4.63699 | 5.94477 | 1.394 | 15 | chr18 | unknown | gene | 47922840 | 48107980 | + | G630055G22Rik | G630055G22Rik | | NR_045404 | TSS1252 |
| chr18 | 48894564 | 48894655 | MACS2_peak_1402 | 13 | + | 4.63699 | 5.94477 | 1.394 | 15 | chr18 | unknown | gene | 49523288 | 49524441 | + | 1700044K03Rik | 1700044K03Rik | | NR_033785 | TSS16202 |
| chr18 | 49033053 | 49033179 | MACS2_peak_1403 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 45 | chr18 | unknown | gene | 47922840 | 48107980 | + | G630055G22Rik | G630055G22Rik | | NR_045404 | TSS1252 |
| chr18 | 49033053 | 49033179 | MACS2_peak_1403 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 45 | chr18 | unknown | gene | 49523288 | 49524441 | + | 1700044K03Rik | 1700044K03Rik | | NR_033785 | TSS16202 |
| chr18 | 50403595 | 50403755 | MACS2_peak_1404 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 114 | chr18 | unknown | gene | 50278368 | 50282934 | + | Fam170a | Fam170a | P9500 | NM_001004061 | TSS23145 |
| chr18 | 50403595 | 50403755 | MACS2_peak_1404 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 114 | chr18 | unknown | gene | 50567655 | 50568660 | - | Hdhd1a | Hdhd1a | P25572 | NM_026108 | TSS1453 |
| chr18 | 50932078 | 50932187 | MACS2_peak_1405 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 40 | chr18 | unknown | gene | 50567655 | 50568660 | - | Hdhd1a | Hdhd1a | P25572 | NM_026108 | TSS1453 |
| chr18 | 50932078 | 50932187 | MACS2_peak_1405 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 40 | chr18 | unknown | gene | 51117897 | 51303365 | + | Prr16 | Prr16 | P9216 | NM_001081224 | TSS13221 |
| chr18 | 51707126 | 51707276 | MACS2_peak_1406 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 80 | chr18 | unknown | gene | 51117897 | 51303365 | + | Prr16 | Prr16 | P9216 | NM_001081224 | TSS13221 |
| chr18 | 51707126 | 51707276 | MACS2_peak_1406 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 80 | chr18 | unknown | gene | 52123524 | 52123546 | - | Mir28a | Mir28a | | NR_029788 | TSS14352 |
| chr18 | 51750300 | 51750391 | MACS2_peak_1407 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 43 | chr18 | unknown | gene | 51117897 | 51303365 | + | Prr16 | Prr16 | P9216 | NM_001081224 | TSS13221 |
| chr18 | 51750300 | 51750391 | MACS2_peak_1407 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 43 | chr18 | unknown | gene | 52123524 | 52123546 | - | Mir28a | Mir28a | | NR_029788 | TSS14352 |
| chr18 | 52613501 | 52613735 | MACS2_peak_1408 | 33 | + | 5.81767 | 8.27611 | 3.31293 | 180 | chr18 | unknown | gene | 52516059 | 52529867 | - | Lox | Lox | P4983 | NM_001286182 | TSS25302 |
| chr18 | 52613501 | 52613735 | MACS2_peak_1408 | 33 | + | 5.81767 | 8.27611 | 3.31293 | 180 | chr18 | unknown | gene | 52615914 | 52639320 | + | Zfp474 | Zfp474 | P3738 | NM_025749 | TSS16125 |
| chr18 | 54197320 | 54197411 | MACS2_peak_1409 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 8 | chr18 | unknown | gene | 53862112 | 53953299 | + | Csnk1g3 | Csnk1g3 | P6339 | NM_152809 | TSS12106 |
| chr18 | 54197320 | 54197411 | MACS2_peak_1409 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 8 | chr18 | unknown | gene | 54422294 | 54453294 | + | Redrum | Redrum | | NR_040338 | TSS13416 |
| chr18 | 54900690 | 54900781 | MACS2_peak_1410 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 85 | chr18 | unknown | gene | 54611743 | 54639870 | + | 9330117O12Rik | 9330117O12Rik | | NR_045400 | TSS7599 |
| chr18 | 54900690 | 54900781 | MACS2_peak_1410 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 85 | chr18 | unknown | gene | 56432131 | 56502629 | + | Gramd3 | Gramd3 | P6020 | NM_026240 | TSS18644 |
| chr18 | 55785582 | 55785673 | MACS2_peak_1411 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 42 | chr18 | unknown | gene | 54888044 | 54990180 | - | Zfp608 | Zfp608 | P22354 | NM_175751 | TSS17762 |
| chr18 | 55785582 | 55785673 | MACS2_peak_1411 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 42 | chr18 | unknown | gene | 56432131 | 56502629 | + | Gramd3 | Gramd3 | P6020 | NM_026240 | TSS18644 |
| chr18 | 55863385 | 55863476 | MACS2_peak_1412 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 24 | chr18 | unknown | gene | 54888044 | 54990180 | - | Zfp608 | Zfp608 | P22354 | NM_175751 | TSS17762 |
| chr18 | 55863385 | 55863476 | MACS2_peak_1412 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 24 | chr18 | unknown | gene | 56432131 | 56502629 | + | Gramd3 | Gramd3 | P6020 | NM_026240 | TSS18644 |
| chr18 | 55878668 | 55878759 | MACS2_peak_1413 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 51 | chr18 | unknown | gene | 54888044 | 54990180 | - | Zfp608 | Zfp608 | P22354 | NM_175751 | TSS17762 |
| chr18 | 55878668 | 55878759 | MACS2_peak_1413 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 51 | chr18 | unknown | gene | 56432131 | 56502629 | + | Gramd3 | Gramd3 | P6020 | NM_026240 | TSS18644 |
| chr18 | 56419471 | 56419562 | MACS2_peak_1414 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 22 | chr18 | unknown | gene | 54888044 | 54990180 | - | Zfp608 | Zfp608 | P22354 | NM_175751 | TSS17762 |
| chr18 | 56419471 | 56419562 | MACS2_peak_1414 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 22 | chr18 | unknown | gene | 56432131 | 56502629 | + | Gramd3 | Gramd3 | P6020 | NM_026240 | TSS18644 |
| chr18 | 56621404 | 56621495 | MACS2_peak_1415 | 16 | + | 4.811 | 6.2687 | 1.67914 | 63 | chr18 | unknown | gene | 56588347 | 56594657 | + | Tex43 | Tex43 | P2914 | NM_026099 | TSS16623 |
| chr18 | 56621404 | 56621495 | MACS2_peak_1415 | 16 | + | 4.811 | 6.2687 | 1.67914 | 63 | chr18 | unknown | gene | 56707812 | 56752648 | + | Lmnb1 | Lmnb1 | P14500 | NM_010721 | TSS5649 |
| chr18 | 57157490 | 57157581 | MACS2_peak_1416 | 32 | + | 5.8651 | 8.25694 | 3.2954 | 63 | chr18 | unknown | gene | 56955830 | 56975379 | - | C330018D20Rik | C330018D20Rik | P11801 | NM_029909 | TSS17440 |
| chr18 | 57157490 | 57157581 | MACS2_peak_1416 | 32 | + | 5.8651 | 8.25694 | 3.2954 | 63 | chr18 | unknown | gene | 57354732 | 57389429 | + | Prrc1 | Prrc1 | P1793 | NM_028447 | TSS6250 |
| chr18 | 57940753 | 57940844 | MACS2_peak_1417 | 27 | + | 5.56793 | 7.65146 | 2.73702 | 61 | chr18 | unknown | gene | 57533825 | 57730941 | + | 1700011I03Rik | 1700011I03Rik | P6128 | NM_029290 | TSS19224 |
| chr18 | 57940753 | 57940844 | MACS2_peak_1417 | 27 | + | 5.56793 | 7.65146 | 2.73702 | 61 | chr18 | unknown | gene | 58008622 | 58209805 | - | Fbn2 | Fbn2 | P10192 | NM_010181 | TSS16020 |
| chr18 | 58659083 | 58659244 | MACS2_peak_1418 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 73 | chr18 | unknown | gene | 58556239 | 58612355 | + | Slc27a6 | Slc27a6 | P1023 | NM_001081072 | TSS21676 |
| chr18 | 58659083 | 58659244 | MACS2_peak_1418 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 73 | chr18 | unknown | gene | 58659481 | 58677911 | + | Isoc1 | Isoc1 | P5594 | NM_025478 | TSS137 |
| chr18 | 60027192 | 60027283 | MACS2_peak_1419 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 20 | chr18 | unknown | gene | 59579629 | 59579735 | + | Mir6355 | Mir6355 | | NR_105773 | TSS12017 |
| chr18 | 60027192 | 60027283 | MACS2_peak_1419 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 20 | chr18 | unknown | gene | 60212076 | 60246615 | + | Gm4951 | Gm4951 | P7761 | NM_001033767 | TSS6396 |
| chr18 | 60261680 | 60261771 | MACS2_peak_1420 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 40 | chr18 | unknown | gene | 60212076 | 60246615 | + | Gm4951 | Gm4951 | P7761 | NM_001033767 | TSS6396 |
| chr18 | 60261680 | 60261771 | MACS2_peak_1420 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 40 | chr18 | unknown | gene | 60268300 | 60273267 | - | Gm4841 | Gm4841 | P22508 | NM_001034859 | TSS10400 |
| chr18 | 60379207 | 60379315 | MACS2_peak_1421 | 32 | + | 5.82623 | 8.17465 | 3.21814 | 50 | chr18 | unknown | gene | 60293379 | 60301097 | + | F830016B08Rik | F830016B08Rik | P24153 | NM_001101475 | TSS26934 |
| chr18 | 60379207 | 60379315 | MACS2_peak_1421 | 32 | + | 5.82623 | 8.17465 | 3.21814 | 50 | chr18 | unknown | gene | 60474190 | 60501983 | - | Smim3 | Smim3 | P24826 | NM_134133 | TSS8733 |
| chr18 | 62351968 | 62352059 | MACS2_peak_1422 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 38 | chr18 | unknown | gene | 62177712 | 62179752 | - | Adrb2 | Adrb2 | P22296 | NM_007420 | TSS26350 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr18 | 62351968 | 62352059 | MACS2_peak_1422 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 38 | chr18 | unknown | gene | 62504058 | 62548743 | - | Fbxo38 | Fbxo38 | P8182 | NM_134136 | TSS15882 |
| chr18 | 63231012 | 63231103 | MACS2_peak_1423 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 53 | chr18 | unknown | gene | 62977915 | 62996960 | + | Napg | Napg | P12816 | NM_028017 | TSS11399 |
| chr18 | 63231012 | 63231103 | MACS2_peak_1423 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 53 | chr18 | unknown | gene | 63662800 | 63692173 | - | Txnl1 | Txnl1 | P12732 | NM_016792 | TSS4847 |
| chr18 | 63927065 | 63927194 | MACS2_peak_1424 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 39 | chr18 | unknown | gene | 63662800 | 63692173 | - | Txnl1 | Txnl1 | P12732 | NM_016792 | TSS4847 |
| chr18 | 63927065 | 63927194 | MACS2_peak_1424 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 39 | chr18 | unknown | gene | 64157723 | 64277180 | - | St8sia3os | St8sia3os | | NR_045366 | TSS5491 |
| chr18 | 64734031 | 64734214 | MACS2_peak_1425 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 75 | chr18 | unknown | gene | 64528978 | 64661000 | - | Atp8b1 | Atp8b1 | P10760 | NM_001001488 | TSS10526 |
| chr18 | 64734031 | 64734214 | MACS2_peak_1425 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 75 | chr18 | unknown | gene | 64887755 | 65212886 | + | Nedd4l | Nedd4l | P549 | NM_001114386 | TSS16297 |
| chr18 | 66233011 | 66233175 | MACS2_peak_1426 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 8 | chr18 | unknown | gene | 66219263 | 66219333 | - | Mir694 | Mir694 | | NR_030467 | TSS18431 |
| chr18 | 66233011 | 66233175 | MACS2_peak_1426 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 8 | chr18 | unknown | gene | 66458603 | 66463373 | + | Pmaip1 | Pmaip1 | P5740 | NM_021451 | TSS12224 |
| chr18 | 66238100 | 66238201 | MACS2_peak_1427 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 83 | chr18 | unknown | gene | 66219263 | 66219333 | - | Mir694 | Mir694 | | NR_030467 | TSS18431 |
| chr18 | 66238100 | 66238201 | MACS2_peak_1427 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 83 | chr18 | unknown | gene | 66458603 | 66463373 | + | Pmaip1 | Pmaip1 | P5740 | NM_021451 | TSS12224 |
| chr18 | 66652515 | 66652629 | MACS2_peak_1428 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 31 | chr18 | unknown | gene | 66504177 | 66511737 | + | Gm9926 | Gm9926 | | NR_040528 | TSS15572 |
| chr18 | 66652515 | 66652629 | MACS2_peak_1428 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 31 | chr18 | unknown | gene | 66857704 | 66860040 | - | Mc4r | Mc4r | P6845 | NM_016977 | TSS5287 |
| chr18 | 66709979 | 66710070 | MACS2_peak_1429 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 84 | chr18 | unknown | gene | 66504177 | 66511737 | + | Gm9926 | Gm9926 | | NR_040528 | TSS15572 |
| chr18 | 66709979 | 66710070 | MACS2_peak_1429 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 84 | chr18 | unknown | gene | 66857704 | 66860040 | - | Mc4r | Mc4r | P6845 | NM_016977 | TSS5287 |
| chr18 | 67980446 | 67980537 | MACS2_peak_1430 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 12 | chr18 | unknown | gene | 67800106 | 67884877 | + | Cep192 | Cep192 | P1149 | NM_027556 | TSS2339 |
| chr18 | 67980446 | 67980537 | MACS2_peak_1430 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 12 | chr18 | unknown | gene | 68260184 | 68300333 | - | Fam210a | Fam210a | P3031 | NM_153794 | TSS20321 |
| chr18 | 68059550 | 68059641 | MACS2_peak_1431 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 32 | chr18 | unknown | gene | 67800106 | 67884877 | + | Cep192 | Cep192 | P1149 | NM_027556 | TSS2339 |
| chr18 | 68059550 | 68059641 | MACS2_peak_1431 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 32 | chr18 | unknown | gene | 68260184 | 68300333 | - | Fam210a | Fam210a | P3031 | NM_153794 | TSS20321 |
| chr18 | 68997136 | 68997262 | MACS2_peak_1432 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 46 | chr18 | unknown | gene | 68889486 | 68951528 | - | 4930546C10Rik | 4930546C10Rik | | NR_038051 | TSS9956 |
| chr18 | 68997136 | 68997262 | MACS2_peak_1432 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 46 | chr18 | unknown | gene | 69022198 | 69022273 | - | Mir145b | Mir145b | | NR_105780 | TSS20592 |
| chr18 | 69918661 | 69918752 | MACS2_peak_1433 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 46 | chr18 | unknown | gene | 69344491 | 69687967 | + | Tcf4 | Tcf4 | P23735 | NM_013685 | TSS13285 |
| chr18 | 69918661 | 69918752 | MACS2_peak_1433 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 46 | chr18 | unknown | gene | 69925558 | 69969035 | + | Ccdc68 | Ccdc68 | P3313 | NM_201362 | TSS21806 |
| chr18 | 70086302 | 70086393 | MACS2_peak_1434 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 73 | chr18 | unknown | gene | 69925558 | 69969035 | + | Ccdc68 | Ccdc68 | P3313 | NM_201362 | TSS21806 |
| chr18 | 70086302 | 70086393 | MACS2_peak_1434 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 73 | chr18 | unknown | gene | 70240428 | 70244382 | - | Dynap | Dynap | P16732 | NM_029346 | TSS8889 |
| chr18 | 71760168 | 71760259 | MACS2_peak_1435 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 79 | chr18 | unknown | gene | 70568291 | 70626131 | + | Mbd2 | Mbd2 | P20409 | NM_010773 | TSS26627 |
| chr18 | 71760168 | 71760259 | MACS2_peak_1435 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 79 | chr18 | unknown | gene | 73572704 | 73590796 | + | Mex3c | Mex3c | P9616 | NM_001039214 | TSS20165 |
| chr18 | 74357485 | 74357576 | MACS2_peak_1436 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 78 | chr18 | unknown | gene | 74268287 | 74281951 | + | Mbd1 | Mbd1 | P24135 | NM_013594 | TSS18254 |
| chr18 | 74357485 | 74357576 | MACS2_peak_1436 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 78 | chr18 | unknown | gene | 74442618 | 74770449 | + | Myo5b | Myo5b | P7311 | NM_201600 | TSS23011 |
| chr18 | 77221853 | 77221944 | MACS2_peak_1437 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 38 | chr18 | unknown | gene | 77065207 | 77152794 | + | Pias2 | Pias2 | P5533 | NM_001164167 | TSS12271 |
| chr18 | 77221853 | 77221944 | MACS2_peak_1437 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 38 | chr18 | unknown | gene | 77281957 | 77441869 | + | Loxhd1 | Loxhd1 | P12721 | NM_172834 | TSS7300 |
| chr18 | 79868938 | 79869105 | MACS2_peak_1438 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 33 | chr18 | unknown | gene | 78750377 | 79109391 | - | Setbp1 | Setbp1 | P14107 | NM_053099 | TSS19632 |
| chr18 | 79868938 | 79869105 | MACS2_peak_1438 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 33 | chr18 | unknown | gene | 80046894 | 80117822 | + | Pard6g | Pard6g | P11778 | NM_053117 | TSS8774 |
| chr18 | 83930244 | 83930335 | MACS2_peak_1439 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 77 | chr18 | unknown | gene | 83292791 | 83325884 | - | 4921531P14Rik | 4921531P14Rik | | NR_045361 | TSS2629 |
| chr18 | 83930244 | 83930335 | MACS2_peak_1439 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 77 | chr18 | unknown | gene | 84011626 | 84085403 | - | Tshz1 | Tshz1 | P21234 | NM_001081300 | TSS21024 |
| chr18 | 83948529 | 83948679 | MACS2_peak_1440 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 70 | chr18 | unknown | gene | 83292791 | 83325884 | - | 4921531P14Rik | 4921531P14Rik | | NR_045361 | TSS2629 |
| chr18 | 83948529 | 83948679 | MACS2_peak_1440 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 70 | chr18 | unknown | gene | 84011626 | 84085403 | - | Tshz1 | Tshz1 | P21234 | NM_001081300 | TSS21024 |
| chr18 | 84927915 | 84928006 | MACS2_peak_1441 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 16 | chr18 | unknown | gene | 84851413 | 84879584 | + | Cyb5a | Cyb5a | P7414 | NM_025797 | TSS13332 |
| chr18 | 84927915 | 84928006 | MACS2_peak_1441 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 16 | chr18 | unknown | gene | 84935024 | 84981376 | + | Fbxo15 | Fbxo15 | P75 | NM_015798 | TSS2825 |
| chr18 | 85545384 | 85545484 | MACS2_peak_1442 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 70 | chr18 | unknown | gene | 84935024 | 84981376 | + | Fbxo15 | Fbxo15 | P75 | NM_015798 | TSS2825 |
| chr18 | 85545384 | 85545484 | MACS2_peak_1442 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 70 | chr18 | unknown | gene | 86394951 | 86501897 | + | Neto1 | Neto1 | P25910 | NM_144946 | TSS8420 |
| chr18 | 85978714 | 85978865 | MACS2_peak_1443 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 84 | chr18 | unknown | gene | 84935024 | 84981376 | + | Fbxo15 | Fbxo15 | P75 | NM_015798 | TSS2825 |
| chr18 | 85978714 | 85978865 | MACS2_peak_1443 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 84 | chr18 | unknown | gene | 86394951 | 86501897 | + | Neto1 | Neto1 | P25910 | NM_144946 | TSS8420 |
| chr18 | 86575969 | 86576064 | MACS2_peak_1444 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 43 | chr18 | unknown | gene | 86394951 | 86501897 | + | Neto1 | Neto1 | P25910 | NM_144946 | TSS8420 |
| chr18 | 86575969 | 86576064 | MACS2_peak_1444 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 43 | chr18 | unknown | gene | 86711109 | 86716778 | + | Cbln2 | Cbln2 | P17972 | NM_001302356 | TSS9469 |
| chr18 | 86579408 | 86579535 | MACS2_peak_1445 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 69 | chr18 | unknown | gene | 86394951 | 86501897 | + | Neto1 | Neto1 | P25910 | NM_144946 | TSS8420 |
| chr18 | 86579408 | 86579535 | MACS2_peak_1445 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 69 | chr18 | unknown | gene | 86711109 | 86716778 | + | Cbln2 | Cbln2 | P17972 | NM_001302356 | TSS9469 |
| chr18 | 86638001 | 86638092 | MACS2_peak_1446 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 85 | chr18 | unknown | gene | 86394951 | 86501897 | + | Neto1 | Neto1 | P25910 | NM_144946 | TSS8420 |
| chr18 | 86638001 | 86638092 | MACS2_peak_1446 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 85 | chr18 | unknown | gene | 86711109 | 86716778 | + | Cbln2 | Cbln2 | P17972 | NM_001302356 | TSS9469 |
| chr18 | 86872979 | 86873116 | MACS2_peak_1447 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 49 | chr18 | unknown | gene | 86711109 | 86716778 | + | Cbln2 | Cbln2 | P17972 | NM_001302356 | TSS9469 |
| chr18 | 86872979 | 86873116 | MACS2_peak_1447 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 49 | chr18 | unknown | gene | 88867879 | 88894207 | - | Socs6 | Socs6 | P19604 | NM_018821 | TSS2072 |
| chr18 | 90160575 | 90160716 | MACS2_peak_1448 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 85 | chr18 | unknown | gene | 89301134 | 89769136 | - | Dok6 | Dok6 | P1558 | NM_001039173 | TSS1458 |
| chr18 | 90160575 | 90160716 | MACS2_peak_1448 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 85 | chr18 | unknown | gene | 90510153 | 90540196 | + | Tmx3 | Tmx3 | P17359 | NM_198295 | TSS26930 |
| chr19 | 3248349 | 3248471 | MACS2_peak_1449 | 48 | + | 6.733 | 9.94597 | 4.8652 | 67 | chr19 | unknown | gene | 3153798 | 3197703 | - | 1700030N03Rik | 1700030N03Rik | | NR_045304 | TSS4739 |
| chr19 | 3248349 | 3248471 | MACS2_peak_1449 | 48 | + | 6.733 | 9.94597 | 4.8652 | 67 | chr19 | unknown | gene | 3259075 | 3282786 | - | Ighmbp2 | Ighmbp2 | P22868 | NM_009212 | TSS4089 |
| chr19 | 13232222 | 13232313 | MACS2_peak_1450 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 45 | chr19 | unknown | gene | 13190668 | 13191592 | + | Olfr1462 | Olfr1462 | P15845 | NM_146693 | TSS21515 |
| chr19 | 13232222 | 13232313 | MACS2_peak_1450 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 45 | chr19 | unknown | gene | 13234251 | 13235184 | + | Olfr1463 | Olfr1463 | P19144 | NM_001011840 | TSS10353 |
| chr19 | 14891047 | 14891138 | MACS2_peak_1451 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 78 | chr19 | unknown | gene | 14448071 | 14597412 | - | Tle4 | Tle4 | P8509 | NM_001302950 | TSS6208 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr19 | 14891047 | 14891138 | MACS2_peak_1451 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 78 | chr19 | unknown | gene | 15905122 | 15924923 | - | Psat1 | Psat1 | P4692 | NM_177420 | TSS6985 |
| chr19 | 16971115 | 16971206 | MACS2_peak_1452 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 50 | chr19 | unknown | gene | 16872315 | 16873640 | - | Foxb2 | Foxb2 | P13104 | NM_008023 | TSS13099 |
| chr19 | 16971115 | 16971206 | MACS2_peak_1452 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 50 | chr19 | unknown | gene | 17326140 | 17372844 | - | Gcnt1 | Gcnt1 | P12878 | NM_173442 | TSS20299 |
| chr19 | 17289014 | 17289105 | MACS2_peak_1453 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 12 | chr19 | unknown | gene | 16956117 | 17220814 | + | Prune2 | Prune2 | P10318 | NM_181348 | TSS23522 |
| chr19 | 17289014 | 17289105 | MACS2_peak_1453 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 12 | chr19 | unknown | gene | 17326140 | 17372844 | - | Gcnt1 | Gcnt1 | P12878 | NM_173442 | TSS20299 |
| chr19 | 18087418 | 18087509 | MACS2_peak_1454 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 77 | chr19 | unknown | gene | 17432313 | 17837152 | - | Pcsk5 | Pcsk5 | P12866 | NM_001190483 | TSS12543 |
| chr19 | 18087418 | 18087509 | MACS2_peak_1454 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 77 | chr19 | unknown | gene | 18580363 | 18631653 | - | Ostf1 | Ostf1 | P16407 | NM_017375 | TSS25049 |
| chr19 | 19033174 | 19033265 | MACS2_peak_1455 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 31 | chr19 | unknown | gene | 18749982 | 18892137 | + | Trpm6 | Trpm6 | P5211 | NM_153417 | TSS11012 |
| chr19 | 19033174 | 19033265 | MACS2_peak_1455 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 31 | chr19 | unknown | gene | 20373433 | 20390671 | - | Anxa1 | Anxa1 | P19988 | NM_010730 | TSS15466 |
| chr19 | 19618002 | 19618110 | MACS2_peak_1456 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 31 | chr19 | unknown | gene | 18930608 | 19110558 | - | Rorb | Rorb | P17471 | NM_001289921 | TSS20463 |
| chr19 | 19618002 | 19618110 | MACS2_peak_1456 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 31 | chr19 | unknown | gene | 20373433 | 20390671 | - | Anxa1 | Anxa1 | P19988 | NM_010730 | TSS15466 |
| chr19 | 20282160 | 20282257 | MACS2_peak_1457 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 31 | chr19 | unknown | gene | 18930608 | 19110558 | - | Rorb | Rorb | P17471 | NM_001289921 | TSS20463 |
| chr19 | 20282160 | 20282257 | MACS2_peak_1457 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 31 | chr19 | unknown | gene | 20373433 | 20390671 | - | Anxa1 | Anxa1 | P19988 | NM_010730 | TSS15466 |
| chr19 | 20764041 | 20764132 | MACS2_peak_1458 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 59 | chr19 | unknown | gene | 20692952 | 20727512 | - | Aldh1a7 | Aldh1a7 | P8822 | NM_011921 | TSS27212 |
| chr19 | 20764041 | 20764132 | MACS2_peak_1458 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 59 | chr19 | unknown | gene | 20783457 | 20954202 | - | Tmc1 | Tmc1 | P6294 | NM_028953 | TSS21621 |
| chr19 | 20920368 | 20920459 | MACS2_peak_1459 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 8 | chr19 | unknown | gene | 20692952 | 20727512 | - | Aldh1a7 | Aldh1a7 | P8822 | NM_011921 | TSS27212 |
| chr19 | 20920368 | 20920459 | MACS2_peak_1459 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 8 | chr19 | unknown | gene | 21104709 | 21105538 | + | 4930554I06Rik | 4930554I06Rik | | NR_126458 | TSS9882 |
| chr19 | 21603464 | 21603555 | MACS2_peak_1460 | 24 | + | 5.43036 | 7.38735 | 2.49399 | 37 | chr19 | unknown | gene | 21391306 | 21472490 | - | Gda | Gda | P7550 | NM_010266 | TSS6019 |
| chr19 | 21603464 | 21603555 | MACS2_peak_1460 | 24 | + | 5.43036 | 7.38735 | 2.49399 | 37 | chr19 | unknown | gene | 21653308 | 21684317 | + | Abhd17b | Abhd17b | P8500 | NM_146096 | TSS6180 |
| chr19 | 22256867 | 22256958 | MACS2_peak_1461 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 53 | chr19 | unknown | gene | 21778339 | 21856351 | + | Tmem2 | Tmem2 | P22066 | NM_001033759 | TSS24641 |
| chr19 | 22256867 | 22256958 | MACS2_peak_1461 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 53 | chr19 | unknown | gene | 22750604 | 22750672 | + | Mir204 | Mir204 | | NR_029591 | TSS18738 |
| chr19 | 23298920 | 23299011 | MACS2_peak_1462 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 63 | chr19 | unknown | gene | 23206440 | 23273818 | - | Smc5 | Smc5 | P3845 | NM_153808 | TSS7629 |
| chr19 | 23298920 | 23299011 | MACS2_peak_1462 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 63 | chr19 | unknown | gene | 23302608 | 23448058 | - | Mamdc2 | Mamdc2 | P12594 | NM_174857 | TSS10705 |
| chr19 | 23572672 | 23572763 | MACS2_peak_1463 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 61 | chr19 | unknown | gene | 23302608 | 23448058 | - | Mamdc2 | Mamdc2 | P12594 | NM_174857 | TSS10705 |
| chr19 | 23572672 | 23572763 | MACS2_peak_1463 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 61 | chr19 | unknown | gene | 23687399 | 23720400 | + | Ptar1 | Ptar1 | P20967 | NM_028208 | TSS15294 |
| chr19 | 23689139 | 23689250 | MACS2_peak_1464 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 47 | chr19 | unknown | gene | 23558759 | 23652726 | - | 1700028P14Rik | 1700028P14Rik | P117 | NM_026188 | TSS2747 |
| chr19 | 23689139 | 23689250 | MACS2_peak_1464 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 47 | chr19 | unknown | gene | 23758875 | 23945781 | + | Apba1 | Apba1 | P10757 | NM_177034 | TSS22609 |
| chr19 | 24084410 | 24084501 | MACS2_peak_1465 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 30 | chr19 | unknown | gene | 23972749 | 24030937 | - | Fam189a2 | Fam189a2 | P20298 | NM_001114174 | TSS17438 |
| chr19 | 24084410 | 24084501 | MACS2_peak_1465 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 30 | chr19 | unknown | gene | 24094501 | 24225026 | - | Tjp2 | Tjp2 | P6638 | NM_001198985 | TSS14385 |
| chr19 | 25607959 | 25608050 | MACS2_peak_1466 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 38 | chr19 | unknown | gene | 25505705 | 25603350 | + | Dmrt1 | Dmrt1 | P25156 | NM_015826 | TSS6463 |
| chr19 | 25607959 | 25608050 | MACS2_peak_1466 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 38 | chr19 | unknown | gene | 25610536 | 25623223 | + | Dmrt3 | Dmrt3 | P9523 | NM_177360 | TSS9852 |
| chr19 | 25935674 | 25935766 | MACS2_peak_1467 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 36 | chr19 | unknown | gene | 25672410 | 25678724 | + | Dmrt2 | Dmrt2 | P1286 | NM_145831 | TSS921 |
| chr19 | 25935674 | 25935766 | MACS2_peak_1467 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 36 | chr19 | unknown | gene | 26605159 | 26777370 | + | Smarca2 | Smarca2 | P5039 | NM_011416 | TSS10515 |
| chr19 | 26247813 | 26247904 | MACS2_peak_1468 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 14 | chr19 | unknown | gene | 25672410 | 25678724 | + | Dmrt2 | Dmrt2 | P1286 | NM_145831 | TSS921 |
| chr19 | 26247813 | 26247904 | MACS2_peak_1468 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 14 | chr19 | unknown | gene | 26605159 | 26777370 | + | Smarca2 | Smarca2 | P5039 | NM_011416 | TSS10515 |
| chr19 | 26899676 | 26899767 | MACS2_peak_1469 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 24 | chr19 | unknown | gene | 26885924 | 26888431 | + | Gm815 | Gm815 | P2439 | NM_001033407 | TSS13036 |
| chr19 | 26899676 | 26899767 | MACS2_peak_1469 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 24 | chr19 | unknown | gene | 27217019 | 27249140 | + | Vldlr | Vldlr | P21118 | NM_001161420 | TSS2518 |
| chr19 | 27445823 | 27445914 | MACS2_peak_1470 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 46 | chr19 | unknown | gene | 27430036 | 27432631 | + | C030016D13Rik | C030016D13Rik | | NR_027987 | TSS3729 |
| chr19 | 27445823 | 27445914 | MACS2_peak_1470 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 46 | chr19 | unknown | gene | 27761720 | 28011166 | - | Rfx3 | Rfx3 | P24391 | NM_001166414 | TSS18091 |
| chr19 | 28258142 | 28258233 | MACS2_peak_1471 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 49 | chr19 | unknown | gene | 27761720 | 28011166 | - | Rfx3 | Rfx3 | P24391 | NM_001166414 | TSS18091 |
| chr19 | 28258142 | 28258233 | MACS2_peak_1471 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 49 | chr19 | unknown | gene | 28258850 | 28680077 | - | Glis3 | Glis3 | P13431 | NM_175459 | TSS15378 |
| chr19 | 29015564 | 29015664 | MACS2_peak_1472 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 27 | chr19 | unknown | gene | 28963919 | 28964879 | + | Ppapdc2 | Ppapdc2 | P7768 | NM_028922 | TSS6177 |
| chr19 | 29015564 | 29015664 | MACS2_peak_1472 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 27 | chr19 | unknown | gene | 29020831 | 29047829 | - | Ak3 | Ak3 | P22930 | NM_021299 | TSS9536 |
| chr19 | 29471018 | 29471109 | MACS2_peak_1473 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 68 | chr19 | unknown | gene | 29367437 | 29385412 | + | Cd274 | Cd274 | P19758 | NM_021893 | TSS11390 |
| chr19 | 29471018 | 29471109 | MACS2_peak_1473 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 68 | chr19 | unknown | gene | 29503662 | 29521987 | - | A930007I19Rik | A930007I19Rik | | NR_015567 | TSS5636 |
| chr19 | 29528694 | 29528811 | MACS2_peak_1474 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 61 | chr19 | unknown | gene | 29503662 | 29521987 | - | A930007I19Rik | A930007I19Rik | | NR_015567 | TSS5636 |
| chr19 | 29528694 | 29528811 | MACS2_peak_1474 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 61 | chr19 | unknown | gene | 29609882 | 29648355 | - | Ermp1 | Ermp1 | P9144 | NM_001081213 | TSS1333 |
| chr19 | 29976934 | 29977025 | MACS2_peak_1475 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 65 | chr19 | unknown | gene | 29925113 | 29959041 | + | Il33 | Il33 | P25593 | NM_133775 | TSS16084 |
| chr19 | 29976934 | 29977025 | MACS2_peak_1475 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 65 | chr19 | unknown | gene | 30003789 | 30004542 | + | Trpd52l3 | Trpd52l3 | P20935 | NM_025741 | TSS13430 |
| chr19 | 30037535 | 30037626 | MACS2_peak_1476 | 12 | + | 4.14966 | 5.12722 | 1.204 | 75 | chr19 | unknown | gene | 30003789 | 30004542 | + | Trpd52l3 | Trpd52l3 | P20935 | NM_025741 | TSS13430 |
| chr19 | 30037535 | 30037626 | MACS2_peak_1476 | 12 | + | 4.14966 | 5.12722 | 1.204 | 75 | chr19 | unknown | gene | 30098440 | 30175260 | - | Gldc | Gldc | P26179 | NM_138595 | TSS2171 |
| chr19 | 30239996 | 30240087 | MACS2_peak_1477 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 10 | chr19 | unknown | gene | 30232956 | 30239524 | + | Mbl2 | Mbl2 | P20322 | NM_010776 | TSS8553 |
| chr19 | 30239996 | 30240087 | MACS2_peak_1477 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 10 | chr19 | unknown | gene | 30538875 | 30539679 | - | Ppp1r2-ps3 | Ppp1r2-ps3 | | NR_003650 | TSS5338 |
| chr19 | 30861312 | 30861407 | MACS2_peak_1478 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 38 | chr19 | unknown | gene | 30545884 | 30549379 | - | Dkk1 | Dkk1 | P4376 | NM_010051 | TSS1973 |
| chr19 | 30861312 | 30861407 | MACS2_peak_1478 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 38 | chr19 | unknown | gene | 30930385 | 30930962 | - | Gm6642 | Gm6642 | | NR_033643 | TSS2201 |
| chr19 | 31545906 | 31545997 | MACS2_peak_1479 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 47 | chr19 | unknown | gene | 31213542 | 31216396 | - | 8430431K14Rik | 8430431K14Rik | | NR_002849 | TSS25281 |
| chr19 | 31545906 | 31545997 | MACS2_peak_1479 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 47 | chr19 | unknown | gene | 31868760 | 31947510 | + | A1cf | A1cf | P1654 | NM_001081074 | TSS20760 |
| chr19 | 31754180 | 31754336 | MACS2_peak_1480 | 37 | + | 6.14712 | 8.74127 | 3.7131 | 76 | chr19 | unknown | gene | 31213542 | 31216396 | - | 8430431K14Rik | 8430431K14Rik | | NR_002849 | TSS25281 |

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr19 | 31754180 | 31754336 | MACS2_peak_1480 | 37 | + | 6.14712 | 8.74127 | 3.7131 | 76 | chr19 | unknown | gene | 31868760 | 31947510 | + | A1cf | A1cf | P1654 | NM_001081074 | TSS20760 |
| chr19 | 32075886 | 32075982 | MACS2_peak_1481 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 40 | chr19 | unknown | gene | 31868760 | 31947510 | + | A1cf | A1cf | P1654 | NM_001081074 | TSS20760 |
| chr19 | 32075886 | 32075982 | MACS2_peak_1481 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 40 | chr19 | unknown | gene | 32122726 | 32388454 | - | Sgms1 | Sgms1 | P6594 | NM_001168525 | TSS5767 |
| chr19 | 34339608 | 34339699 | MACS2_peak_1482 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 5 | chr19 | unknown | gene | 34290658 | 34327324 | + | Fas | Fas | P7087 | NM_007987 | TSS12822 |
| chr19 | 34339608 | 34339699 | MACS2_peak_1482 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 5 | chr19 | unknown | gene | 34473783 | 34475126 | - | Ch25h | Ch25h | P21072 | NM_009890 | TSS13150 |
| chr19 | 34443728 | 34443876 | MACS2_peak_1483 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 57 | chr19 | unknown | gene | 34290658 | 34327324 | + | Fas | Fas | P7087 | NM_007987 | TSS12822 |
| chr19 | 34443728 | 34443876 | MACS2_peak_1483 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 57 | chr19 | unknown | gene | 34473783 | 34475126 | - | Ch25h | Ch25h | P21072 | NM_009890 | TSS13150 |
| chr19 | 34526871 | 34526968 | MACS2_peak_1484 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 61 | chr19 | unknown | gene | 34473783 | 34475126 | - | Ch25h | Ch25h | P21072 | NM_009890 | TSS13150 |
| chr19 | 34526871 | 34526968 | MACS2_peak_1484 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 61 | chr19 | unknown | gene | 34550693 | 34574474 | + | Ifit2 | Ifit2 | P13767 | NM_008332 | TSS5881 |
| chr19 | 35056743 | 35056838 | MACS2_peak_1485 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 56 | chr19 | unknown | gene | 34922357 | 34975570 | + | Kif20b | Kif20b | P17769 | NM_183046 | TSS11851 |
| chr19 | 35056743 | 35056838 | MACS2_peak_1485 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 56 | chr19 | unknown | gene | 35958728 | 36057253 | - | Htr7 | Htr7 | P5253 | NM_008315 | TSS6269 |
| chr19 | 36044687 | 36044778 | MACS2_peak_1486 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 40 | chr19 | unknown | gene | 34922357 | 34975570 | + | Kif20b | Kif20b | P17769 | NM_183046 | TSS11851 |
| chr19 | 36044687 | 36044778 | MACS2_peak_1486 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 40 | chr19 | unknown | gene | 36083715 | 36104445 | + | Rpp30 | Rpp30 | P2035 | NM_019428 | TSS26615 |
| chr19 | 36210253 | 36210389 | MACS2_peak_1487 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 18 | chr19 | unknown | gene | 36111964 | 36119781 | - | Ankrd1 | Ankrd1 | P2130 | NM_013468 | TSS18650 |
| chr19 | 36210253 | 36210389 | MACS2_peak_1487 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 18 | chr19 | unknown | gene | 36379066 | 36455668 | + | Pcgf5 | Pcgf5 | P19396 | NM_029508 | TSS19833 |
| chr19 | 36984512 | 36984615 | MACS2_peak_1488 | 16 | + | 4.811 | 6.2687 | 1.67914 | 46 | chr19 | unknown | gene | 36917549 | 36919599 | - | Fgfbp3 | Fgfbp3 | P16753 | NM_028263 | TSS10574 |
| chr19 | 36984512 | 36984615 | MACS2_peak_1488 | 16 | + | 4.811 | 6.2687 | 1.67914 | 46 | chr19 | unknown | gene | 37021290 | 37207471 | - | Cpeb3 | Cpeb3 | P3288 | NM_198300 | TSS2237 |
| chr19 | 41481857 | 41481948 | MACS2_peak_1489 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 58 | chr19 | unknown | gene | 41274217 | 41384969 | - | Pik3ap1 | Pik3ap1 | P1818 | NM_031376 | TSS5590 |
| chr19 | 41481857 | 41481948 | MACS2_peak_1489 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 58 | chr19 | unknown | gene | 41549638 | 41559280 | + | Lcor | Lcor | P2370 | NM_172154 | TSS25482 |
| chr19 | 41564552 | 41564643 | MACS2_peak_1490 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 4 | chr19 | unknown | gene | 41549638 | 41559280 | + | Lcor | Lcor | P2370 | NM_172154 | TSS25482 |
| chr19 | 41564552 | 41564643 | MACS2_peak_1490 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 4 | chr19 | unknown | gene | 41588650 | 41588789 | + | Mir8091 | Mir8091 | | NR_106166 | TSS18379 |
| chr19 | 42069418 | 42069509 | MACS2_peak_1491 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 8 | chr19 | unknown | gene | 42052227 | 42053346 | + | 4933411K16Rik | 4933411K16Rik | P4671 | NM_025752 | TSS24373 |
| chr19 | 42069418 | 42069509 | MACS2_peak_1491 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 8 | chr19 | unknown | gene | 42074938 | 42086370 | - | Morn4 | Morn4 | P21779 | NM_198108 | TSS13252 |
| chr19 | 42127914 | 42128056 | MACS2_peak_1492 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 80 | chr19 | unknown | gene | 42090434 | 42119954 | + | Pi4k2a | Pi4k2a | P16787 | NM_145501 | TSS5796 |
| chr19 | 42127914 | 42128056 | MACS2_peak_1492 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 80 | chr19 | unknown | gene | 42147388 | 42151703 | + | Marveld1 | Marveld1 | P10470 | NM_183195 | TSS4604 |
| chr19 | 42541572 | 42541663 | MACS2_peak_1493 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 40 | chr19 | unknown | gene | 42283036 | 42431633 | - | Crtac1 | Crtac1 | P1242 | NM_145123 | TSS8852 |
| chr19 | 42541572 | 42541663 | MACS2_peak_1493 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 40 | chr19 | unknown | gene | 42592278 | 42612806 | - | Loxl4 | Loxl4 | P26013 | NM_001164311 | TSS2521 |
| chr19 | 42819804 | 42819895 | MACS2_peak_1494 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 6 | chr19 | unknown | gene | 42755195 | 42779976 | - | Hps1 | Hps1 | P20571 | NM_019424 | TSS5097 |
| chr19 | 42819804 | 42819895 | MACS2_peak_1494 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 6 | chr19 | unknown | gene | 43440435 | 43495038 | + | Cnnm1 | Cnnm1 | P6833 | NM_031396 | TSS4312 |
| chr19 | 43154647 | 43154738 | MACS2_peak_1495 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 21 | chr19 | unknown | gene | 42755195 | 42779976 | - | Hps1 | Hps1 | P20571 | NM_019424 | TSS5097 |
| chr19 | 43154647 | 43154738 | MACS2_peak_1495 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 21 | chr19 | unknown | gene | 43440435 | 43495038 | + | Cnnm1 | Cnnm1 | P6833 | NM_031396 | TSS4312 |
| chr19 | 43280309 | 43280400 | MACS2_peak_1496 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 40 | chr19 | unknown | gene | 42755195 | 42779976 | - | Hps1 | Hps1 | P20571 | NM_019424 | TSS5097 |
| chr19 | 43280309 | 43280400 | MACS2_peak_1496 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 40 | chr19 | unknown | gene | 43440435 | 43495038 | + | Cnnm1 | Cnnm1 | P6833 | NM_031396 | TSS4312 |
| chr19 | 45650005 | 45650166 | MACS2_peak_1497 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 142 | chr19 | unknown | gene | 45560614 | 45577575 | + | Dpcd | Dpcd | P19646 | NM_172639 | TSS25181 |
| chr19 | 45650005 | 45650166 | MACS2_peak_1497 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 142 | chr19 | unknown | gene | 45726554 | 45730558 | - | 4933429K18Rik | 4933429K18Rik | | NR_045307 | TSS19352 |
| chr19 | 46125757 | 46125848 | MACS2_peak_1498 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 40 | chr19 | unknown | gene | 46075846 | 46084170 | + | Nolc1 | Nolc1 | P830 | NM_001039353 | TSS17268 |
| chr19 | 46125757 | 46125848 | MACS2_peak_1498 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 40 | chr19 | unknown | gene | 46131898 | 46134802 | + | Elovl3 | Elovl3 | P9737 | NM_007703 | TSS23288 |
| chr19 | 46224962 | 46225053 | MACS2_peak_1499 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 12 | chr19 | unknown | gene | 46135685 | 46148325 | - | Pitx3 | Pitx3 | P4895 | NM_008852 | TSS1229 |
| chr19 | 46224962 | 46225053 | MACS2_peak_1499 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 12 | chr19 | unknown | gene | 46304736 | 46311894 | + | Nfkb2 | Nfkb2 | P18194 | NM_001177369 | TSS26870 |
| chr19 | 47152418 | 47152509 | MACS2_peak_1500 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 55 | chr19 | unknown | gene | 47141034 | 47144174 | - | Calhm1 | Calhm1 | P13658 | NM_001081271 | TSS5723 |
| chr19 | 47152418 | 47152509 | MACS2_peak_1500 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 55 | chr19 | unknown | gene | 47178819 | 47257655 | + | Neurl1a | Neurl1a | P11156 | NM_021360 | TSS23547 |
| chr19 | 49829809 | 49829900 | MACS2_peak_1501 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 50 | chr19 | unknown | gene | 48206024 | 48803686 | + | Sorcs3 | Sorcs3 | P9292 | NM_025696 | TSS21581 |
| chr19 | 49829809 | 49829900 | MACS2_peak_1501 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 50 | chr19 | unknown | gene | 50143300 | 50678468 | - | Sorcs1 | Sorcs1 | P23052 | NM_001252501 | TSS523 |
| chr19 | 50147579 | 50147670 | MACS2_peak_1502 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 81 | chr19 | unknown | gene | 48206024 | 48803686 | + | Sorcs3 | Sorcs3 | P9292 | NM_025696 | TSS21581 |
| chr19 | 50147579 | 50147670 | MACS2_peak_1502 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 81 | chr19 | unknown | gene | 52264322 | 52264950 | + | Ins1 | Ins1 | P6534 | NM_008386 | TSS21425 |
| chr19 | 50854084 | 50854175 | MACS2_peak_1503 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 47 | chr19 | unknown | gene | 50143300 | 50678468 | - | Sorcs1 | Sorcs1 | P23052 | NM_001252501 | TSS523 |
| chr19 | 50854084 | 50854175 | MACS2_peak_1503 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 47 | chr19 | unknown | gene | 52264322 | 52264950 | + | Ins1 | Ins1 | P6534 | NM_008386 | TSS21425 |
| chr19 | 52255412 | 52255537 | MACS2_peak_1504 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 34 | chr19 | unknown | gene | 50143300 | 50678468 | - | Sorcs1 | Sorcs1 | P23052 | NM_001252501 | TSS523 |
| chr19 | 52255412 | 52255537 | MACS2_peak_1504 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 34 | chr19 | unknown | gene | 52264322 | 52264950 | + | Ins1 | Ins1 | P6534 | NM_008386 | TSS21425 |
| chr19 | 53125372 | 53125463 | MACS2_peak_1505 | 16 | + | 4.811 | 6.2687 | 1.67914 | 55 | chr19 | unknown | gene | 53076251 | 53084392 | + | 1700054A03Rik | 1700054A03Rik | | NR_045320 | TSS26293 |
| chr19 | 53125372 | 53125463 | MACS2_peak_1505 | 16 | + | 4.811 | 6.2687 | 1.67914 | 55 | chr19 | unknown | gene | 53140442 | 53245290 | + | Add3 | Add3 | P17188 | NM_001164101 | TSS14004 |
| chr19 | 53810723 | 53810903 | MACS2_peak_1506 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 133 | chr19 | unknown | gene | 53600395 | 53644778 | + | Smc3 | Smc3 | P22028 | NM_007790 | TSS11819 |
| chr19 | 53810723 | 53810903 | MACS2_peak_1506 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 133 | chr19 | unknown | gene | 53892230 | 53929861 | + | Pdcd4 | Pdcd4 | P14800 | NM_011050 | TSS17145 |
| chr19 | 56283077 | 56283169 | MACS2_peak_1507 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 9 | chr19 | unknown | gene | 55741809 | 55931857 | + | Tcf7l2 | Tcf7l2 | P16139 | NM_001142921 | TSS25611 |
| chr19 | 56283077 | 56283169 | MACS2_peak_1507 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 9 | chr19 | unknown | gene | 56287937 | 56319635 | + | Habp2 | Habp2 | P20852 | NM_146101 | TSS22853 |
| chr19 | 57613510 | 57613601 | MACS2_peak_1508 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 41 | chr19 | unknown | gene | 57508563 | 57512788 | + | 6720468P15Rik | 6720468P15Rik | | NR_040306 | TSS10051 |
| chr19 | 57613510 | 57613601 | MACS2_peak_1508 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 41 | chr19 | unknown | gene | 58051166 | 58051236 | + | Mir5623 | Mir5623 | | NR_049196 | TSS584 |
| chr19 | 58413466 | 58413557 | MACS2_peak_1509 | 25 | + | 5.46411 | 7.45132 | 2.55202 | 56 | chr19 | unknown | gene | 58296203 | 58300348 | + | Gm10007 | Gm10007 | | NR_040449 | TSS20984 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr19 | 58413466 | 58413557 | MACS2_peak_1509 | 25 | + | 5.46411 | 7.45132 | 2.55202 | 56 | chr19 | unknown | gene | 58512001 | 58552914 | + | Ccdc172 | Ccdc172 | P7348 | NM_029372 | TSS19939 |
| chr19 | 60121738 | 60121857 | MACS2_peak_1510 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 40 | chr19 | unknown | gene | 59902883 | 59943654 | - | Rab11fip2 | Rab11fip2 | P17614 | NM_001033172 | TSS6264 |
| chr19 | 60121738 | 60121857 | MACS2_peak_1510 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 40 | chr19 | unknown | gene | 60144674 | 60162591 | + | E330013P04Rik | E330013P04Rik | | NR_026942 | TSS11478 |
| chr2 | 3050137 | 3050361 | MACS2_peak_1511 | 208 | + | 14.30284 | 26.40868 | 20.81179 | 86 | chr2 | unknown | gene | 3118387 | 3226510 | + | Fam171a1 | Fam171a1 | P23001 | NM_001081161 | TSS12738 |
| chr2 | 3964492 | 3964589 | MACS2_peak_1512 | 23 | + | 5.26766 | 7.08584 | 2.32792 | 51 | chr2 | unknown | gene | 3713457 | 3779617 | + | Fam107b | Fam107b | P11604 | NM_025626 | TSS10610 |
| chr2 | 3964492 | 3964589 | MACS2_peak_1512 | 23 | + | 5.26766 | 7.08584 | 2.32792 | 51 | chr2 | unknown | gene | 4132064 | 4141141 | - | 1700080N15Rik | 1700080N15Rik | | NR_040500 | TSS14199 |
| chr2 | 4085656 | 4085753 | MACS2_peak_1513 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 7 | chr2 | unknown | gene | 3713457 | 3779617 | + | Fam107b | Fam107b | P11604 | NM_025626 | TSS10610 |
| chr2 | 4085656 | 4085753 | MACS2_peak_1513 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 7 | chr2 | unknown | gene | 4132064 | 4141141 | - | 1700080N15Rik | 1700080N15Rik | | NR_040500 | TSS14199 |
| chr2 | 4301637 | 4301728 | MACS2_peak_1514 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 26 | chr2 | unknown | gene | 4132064 | 4141141 | - | 1700080N15Rik | 1700080N15Rik | | NR_040500 | TSS14199 |
| chr2 | 4301637 | 4301728 | MACS2_peak_1514 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 26 | chr2 | unknown | gene | 4622166 | 4651981 | - | Prpf18 | Prpf18 | P17483 | NM_026045 | TSS1899 |
| chr2 | 5262973 | 5263065 | MACS2_peak_1515 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 81 | chr2 | unknown | gene | 5137775 | 5229188 | + | Ccdc3 | Ccdc3 | P1056 | NM_028804 | TSS16083 |
| chr2 | 5262973 | 5263065 | MACS2_peak_1515 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 81 | chr2 | unknown | gene | 5293456 | 5714237 | - | Camk1d | Camk1d | P7735 | NM_001290376 | TSS15602 |
| chr2 | 5707544 | 5707635 | MACS2_peak_1516 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 31 | chr2 | unknown | gene | 5379389 | 5483389 | + | Mir466d | Mir466d | | NR_030601 | TSS19442 |
| chr2 | 5707544 | 5707635 | MACS2_peak_1516 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 31 | chr2 | unknown | gene | 5794293 | 5844908 | - | Cdc123 | Cdc123 | P20466 | NM_133837 | TSS23289 |
| chr2 | 6191181 | 6191272 | MACS2_peak_1517 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 40 | chr2 | unknown | gene | 6132868 | 6140570 | + | Gm10857 | Gm10857 | | NR_033470 | TSS5526 |
| chr2 | 6191181 | 6191272 | MACS2_peak_1517 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 40 | chr2 | unknown | gene | 6193250 | 6321611 | + | A230108P19Rik | A230108P19Rik | | NR_040333 | TSS16471 |
| chr2 | 6335686 | 6335777 | MACS2_peak_1518 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 66 | chr2 | unknown | gene | 6193250 | 6321611 | + | A230108P19Rik | A230108P19Rik | | NR_040333 | TSS16471 |
| chr2 | 6335686 | 6335777 | MACS2_peak_1518 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 66 | chr2 | unknown | gene | 6539698 | 7396198 | - | Celf2 | Celf2 | P5454 | NM_001110229 | TSS19153 |
| chr2 | 6654839 | 6654930 | MACS2_peak_1519 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 19 | chr2 | unknown | gene | 6322756 | 6441742 | + | Usp6nl | Usp6nl | P4361 | NM_001080548 | TSS24754 |
| chr2 | 6654839 | 6654930 | MACS2_peak_1519 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 19 | chr2 | unknown | gene | 6922701 | 6928722 | - | 5031426D15Rik | 5031426D15Rik | | NR_027890 | TSS225 |
| chr2 | 7246361 | 7246452 | MACS2_peak_1520 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 58 | chr2 | unknown | gene | 6922701 | 6928722 | - | 5031426D15Rik | 5031426D15Rik | | NR_027890 | TSS225 |
| chr2 | 7246361 | 7246452 | MACS2_peak_1520 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 58 | chr2 | unknown | gene | 9189514 | 9197484 | + | 1700061F12Rik | 1700061F12Rik | | NR_038180 | TSS8167 |
| chr2 | 7505585 | 7505676 | MACS2_peak_1521 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 40 | chr2 | unknown | gene | 6539698 | 7396198 | - | Celf2 | Celf2 | P5454 | NM_001110229 | TSS19153 |
| chr2 | 7505585 | 7505676 | MACS2_peak_1521 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 40 | chr2 | unknown | gene | 9189514 | 9197484 | + | 1700061F12Rik | 1700061F12Rik | | NR_038180 | TSS8167 |
| chr2 | 7913217 | 7913406 | MACS2_peak_1522 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 55 | chr2 | unknown | gene | 6539698 | 7396198 | - | Celf2 | Celf2 | P5454 | NM_001110229 | TSS19153 |
| chr2 | 7913217 | 7913406 | MACS2_peak_1522 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 55 | chr2 | unknown | gene | 9189514 | 9197484 | + | 1700061F12Rik | 1700061F12Rik | | NR_038180 | TSS8167 |
| chr2 | 8992884 | 8993043 | MACS2_peak_1523 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 90 | chr2 | unknown | gene | 6539698 | 7396198 | - | Celf2 | Celf2 | P5454 | NM_001110229 | TSS19153 |
| chr2 | 8992884 | 8993043 | MACS2_peak_1523 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 90 | chr2 | unknown | gene | 9189514 | 9197484 | + | 1700061F12Rik | 1700061F12Rik | | NR_038180 | TSS8167 |
| chr2 | 9332154 | 9332245 | MACS2_peak_1524 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 81 | chr2 | unknown | gene | 9189514 | 9197484 | + | 1700061F12Rik | 1700061F12Rik | | NR_038180 | TSS8167 |
| chr2 | 9332154 | 9332245 | MACS2_peak_1524 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 81 | chr2 | unknown | gene | 9857077 | 9878600 | - | Gata3 | Gata3 | P8393 | NM_008091 | TSS4504 |
| chr2 | 9565289 | 9565380 | MACS2_peak_1525 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 56 | chr2 | unknown | gene | 9189514 | 9197484 | + | 1700061F12Rik | 1700061F12Rik | | NR_038180 | TSS8167 |
| chr2 | 9565289 | 9565380 | MACS2_peak_1525 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 56 | chr2 | unknown | gene | 9857077 | 9878600 | - | Gata3 | Gata3 | P8393 | NM_008091 | TSS4504 |
| chr2 | 11139988 | 11140079 | MACS2_peak_1526 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 69 | chr2 | unknown | gene | 10370450 | 10590570 | + | Sfmbt2 | Sfmbt2 | P16967 | NM_001198808 | TSS24972 |
| chr2 | 11139988 | 11140079 | MACS2_peak_1526 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 69 | chr2 | unknown | gene | 11172381 | 11300125 | + | Prkcq | Prkcq | P10441 | NM_008859 | TSS828 |
| chr2 | 12052720 | 12052811 | MACS2_peak_1527 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 60 | chr2 | unknown | gene | 11777752 | 11789891 | + | Ankrd16 | Ankrd16 | P20871 | NM_177268 | TSS6148 |
| chr2 | 12052720 | 12052811 | MACS2_peak_1527 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 60 | chr2 | unknown | gene | 12106659 | 12301782 | - | Itga8 | Itga8 | P762 | NM_001001309 | TSS11488 |
| chr2 | 12300287 | 12300439 | MACS2_peak_1528 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 67 | chr2 | unknown | gene | 11777752 | 11789891 | + | Ankrd16 | Ankrd16 | P20871 | NM_177268 | TSS6148 |
| chr2 | 12300287 | 12300439 | MACS2_peak_1528 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 67 | chr2 | unknown | gene | 12301245 | 12312315 | + | E030013I19Rik | E030013I19Rik | | NR_040353 | TSS19819 |
| chr2 | 14072946 | 14073037 | MACS2_peak_1529 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 58 | chr2 | unknown | gene | 14026830 | 14055867 | - | Hacd1 | Hacd1 | P3996 | NM_013935 | TSS314 |
| chr2 | 14072946 | 14073037 | MACS2_peak_1529 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 58 | chr2 | unknown | gene | 14074111 | 14146480 | + | Stam | Stam | P3052 | NM_011484 | TSS7052 |
| chr2 | 14100488 | 14100592 | MACS2_peak_1530 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 29 | chr2 | unknown | gene | 14070332 | 14073934 | - | Stamos | Stamos | | NR_038162 | TSS24667 |
| chr2 | 14100488 | 14100592 | MACS2_peak_1530 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 29 | chr2 | unknown | gene | 14174523 | 14219436 | + | Tmem236 | Tmem236 | P6238 | NM_001081310 | TSS10097 |
| chr2 | 15013581 | 15013672 | MACS2_peak_1531 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 67 | chr2 | unknown | gene | 14604305 | 14986076 | + | Cacnb2 | Cacnb2 | P11669 | NM_023116 | TSS11906 |
| chr2 | 15013581 | 15013672 | MACS2_peak_1531 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 67 | chr2 | unknown | gene | 15055361 | 15076304 | + | Arl5b | Arl5b | P5281 | NM_029466 | TSS10104 |
| chr2 | 15551084 | 15551175 | MACS2_peak_1532 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 23 | chr2 | unknown | gene | 15055361 | 15076304 | + | Arl5b | Arl5b | P5281 | NM_029466 | TSS10104 |
| chr2 | 15551084 | 15551175 | MACS2_peak_1532 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 23 | chr2 | unknown | gene | 16356303 | 16751307 | + | Plxdc2 | Plxdc2 | P20650 | NM_026162 | TSS931 |
| chr2 | 15809705 | 15809877 | MACS2_peak_1533 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 164 | chr2 | unknown | gene | 15055361 | 15076304 | + | Arl5b | Arl5b | P5281 | NM_029466 | TSS10104 |
| chr2 | 15809705 | 15809877 | MACS2_peak_1533 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 164 | chr2 | unknown | gene | 16356303 | 16751307 | + | Plxdc2 | Plxdc2 | P20650 | NM_026162 | TSS931 |
| chr2 | 16259597 | 16259688 | MACS2_peak_1534 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 37 | chr2 | unknown | gene | 15055361 | 15076304 | + | Arl5b | Arl5b | P5281 | NM_029466 | TSS10104 |
| chr2 | 16259597 | 16259688 | MACS2_peak_1534 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 37 | chr2 | unknown | gene | 16356303 | 16751307 | + | Plxdc2 | Plxdc2 | P20650 | NM_026162 | TSS931 |
| chr2 | 16683050 | 16683175 | MACS2_peak_1535 | 72 | + | 7.85404 | 12.44522 | 7.25844 | 54 | chr2 | unknown | gene | 15055361 | 15076304 | + | Arl5b | Arl5b | P5281 | NM_029466 | TSS10104 |
| chr2 | 16683050 | 16683175 | MACS2_peak_1535 | 72 | + | 7.85404 | 12.44522 | 7.25844 | 54 | chr2 | unknown | gene | 16918677 | 17013726 | - | 4930515L03Rik | 4930515L03Rik | | NR_040632 | TSS7858 |
| chr2 | 17429341 | 17429432 | MACS2_peak_1536 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 45 | chr2 | unknown | gene | 16918677 | 17013726 | - | 4930515L03Rik | 4930515L03Rik | | NR_040632 | TSS7858 |
| chr2 | 17429341 | 17429432 | MACS2_peak_1536 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 45 | chr2 | unknown | gene | 17563513 | 17563626 | + | Mir6419 | Mir6419 | | NR_105847 | TSS21576 |
| chr2 | 17690678 | 17690816 | MACS2_peak_1537 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 57 | chr2 | unknown | gene | 17563513 | 17563626 | + | Mir6419 | Mir6419 | | NR_105847 | TSS21576 |
| chr2 | 17690678 | 17690816 | MACS2_peak_1537 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 57 | chr2 | unknown | gene | 17996421 | 17996873 | - | H2afb1 | H2afb1 | P17032 | NM_026627 | TSS15434 |
| chr2 | 18278817 | 18278908 | MACS2_peak_1538 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 9 | chr2 | unknown | gene | 18055236 | 18210812 | + | Mllt10 | Mllt10 | P5273 | NM_010804 | TSS9079 |
| chr2 | 18278817 | 18278908 | MACS2_peak_1538 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 9 | chr2 | unknown | gene | 18672461 | 18675926 | + | Commd3 | Commd3 | P17276 | NM_147778 | TSS3725 |

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr2 | 18921313 | 18921404 | MACS2_peak_1539 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 12 | chr2 | unknown | gene | 18799247 | 18801818 | - | Carlr | Carlr | | NR_131254 | TSS15849 |
| chr2 | 18921313 | 18921404 | MACS2_peak_1539 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 12 | chr2 | unknown | gene | 18998318 | 18999804 | + | 4930426L09Rik | 4930426L09Rik | | NR_024323 | TSS7579 |
| chr2 | 19036340 | 19036468 | MACS2_peak_1540 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 80 | chr2 | unknown | gene | 18998318 | 18999804 | + | 4930426L09Rik | 4930426L09Rik | | NR_024323 | TSS7579 |
| chr2 | 19036340 | 19036468 | MACS2_peak_1540 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 80 | chr2 | unknown | gene | 19199117 | 19310126 | + | Armc3 | Armc3 | P26762 | NM_001081083 | TSS6521 |
| chr2 | 19350340 | 19350441 | MACS2_peak_1541 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 54 | chr2 | unknown | gene | 19199117 | 19310126 | + | Armc3 | Armc3 | P26762 | NM_001081083 | TSS6521 |
| chr2 | 19350340 | 19350441 | MACS2_peak_1541 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 54 | chr2 | unknown | gene | 19371635 | 19394355 | + | Msrb2 | Msrb2 | P24321 | NM_029619 | TSS13717 |
| chr2 | 19716620 | 19716730 | MACS2_peak_1542 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 43 | chr2 | unknown | gene | 19658061 | 19659426 | + | Otud1 | Otud1 | P17626 | NM_027715 | TSS14668 |
| chr2 | 19716620 | 19716730 | MACS2_peak_1542 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 43 | chr2 | unknown | gene | 20289912 | 20809210 | + | Etl4 | Etl4 | P10459 | NM_001081006 | TSS4220 |
| chr2 | 20099860 | 20099951 | MACS2_peak_1543 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 72 | chr2 | unknown | gene | 19658061 | 19659426 | + | Otud1 | Otud1 | P17626 | NM_027715 | TSS14668 |
| chr2 | 20099860 | 20099951 | MACS2_peak_1543 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 72 | chr2 | unknown | gene | 20289912 | 20809210 | + | Etl4 | Etl4 | P10459 | NM_001081006 | TSS4220 |
| chr2 | 20999487 | 20999578 | MACS2_peak_1544 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 62 | chr2 | unknown | gene | 20968873 | 20970348 | + | Gm13375 | Gm13375 | | NR_033225 | TSS25235 |
| chr2 | 20999487 | 20999578 | MACS2_peak_1544 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 62 | chr2 | unknown | gene | 21180730 | 21205148 | - | Enkur | Enkur | P12666 | NM_027728 | TSS6190 |
| chr2 | 22587754 | 22587855 | MACS2_peak_1545 | 64 | + | 6.22234 | 11.59517 | 6.43608 | 67 | chr2 | unknown | gene | 22227502 | 22423370 | + | Myo3a | Myo3a | P17744 | NM_148413 | TSS25361 |
| chr2 | 22587754 | 22587855 | MACS2_peak_1545 | 64 | + | 6.22234 | 11.59517 | 6.43608 | 67 | chr2 | unknown | gene | 22622326 | 22690346 | + | Gad2 | Gad2 | P23440 | NM_008078 | TSS26215 |
| chr2 | 22587990 | 22588102 | MACS2_peak_1546 | 45 | + | 5.53097 | 9.65808 | 4.59214 | 63 | chr2 | unknown | gene | 22227502 | 22423370 | + | Myo3a | Myo3a | P17744 | NM_148413 | TSS25361 |
| chr2 | 22587990 | 22588102 | MACS2_peak_1546 | 45 | + | 5.53097 | 9.65808 | 4.59214 | 63 | chr2 | unknown | gene | 22622326 | 22690346 | + | Gad2 | Gad2 | P23440 | NM_008078 | TSS26215 |
| chr2 | 22588181 | 22588281 | MACS2_peak_1547 | 54 | + | 5.87666 | 10.61438 | 5.49998 | 38 | chr2 | unknown | gene | 22227502 | 22423370 | + | Myo3a | Myo3a | P17744 | NM_148413 | TSS25361 |
| chr2 | 22588181 | 22588281 | MACS2_peak_1547 | 54 | + | 5.87666 | 10.61438 | 5.49998 | 38 | chr2 | unknown | gene | 22622326 | 22690346 | + | Gad2 | Gad2 | P23440 | NM_008078 | TSS26215 |
| chr2 | 22588835 | 22589068 | MACS2_peak_1548 | 37 | + | 5.18529 | 8.72773 | 3.70168 | 189 | chr2 | unknown | gene | 22227502 | 22423370 | + | Myo3a | Myo3a | P17744 | NM_148413 | TSS25361 |
| chr2 | 22588835 | 22589068 | MACS2_peak_1548 | 37 | + | 5.18529 | 8.72773 | 3.70168 | 189 | chr2 | unknown | gene | 22622326 | 22690346 | + | Gad2 | Gad2 | P23440 | NM_008078 | TSS26215 |
| chr2 | 22589210 | 22589301 | MACS2_peak_1549 | 36 | + | 5.16903 | 8.70016 | 3.6758 | 54 | chr2 | unknown | gene | 22227502 | 22423370 | + | Myo3a | Myo3a | P17744 | NM_148413 | TSS25361 |
| chr2 | 22589210 | 22589301 | MACS2_peak_1549 | 36 | + | 5.16903 | 8.70016 | 3.6758 | 54 | chr2 | unknown | gene | 22622326 | 22690346 | + | Gad2 | Gad2 | P23440 | NM_008078 | TSS26215 |
| chr2 | 22589378 | 22589472 | MACS2_peak_1550 | 28 | + | 4.80934 | 7.77407 | 2.8507 | 40 | chr2 | unknown | gene | 22227502 | 22423370 | + | Myo3a | Myo3a | P17744 | NM_148413 | TSS25361 |
| chr2 | 22589378 | 22589472 | MACS2_peak_1550 | 28 | + | 4.80934 | 7.77407 | 2.8507 | 40 | chr2 | unknown | gene | 22622326 | 22690346 | + | Gad2 | Gad2 | P23440 | NM_008078 | TSS26215 |
| chr2 | 22589611 | 22589810 | MACS2_peak_1551 | 192 | + | 10.33805 | 24.84657 | 19.28542 | 118 | chr2 | unknown | gene | 22227502 | 22423370 | + | Myo3a | Myo3a | P17744 | NM_148413 | TSS25361 |
| chr2 | 22589611 | 22589810 | MACS2_peak_1551 | 192 | + | 10.33805 | 24.84657 | 19.28542 | 118 | chr2 | unknown | gene | 22622326 | 22690346 | + | Gad2 | Gad2 | P23440 | NM_008078 | TSS26215 |
| chr2 | 24051275 | 24051366 | MACS2_peak_1552 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 33 | chr2 | unknown | gene | 24002912 | 24049379 | - | Hnmt | Hnmt | P18531 | NM_080462 | TSS24296 |
| chr2 | 24051275 | 24051366 | MACS2_peak_1552 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 33 | chr2 | unknown | gene | 24071365 | 24096535 | - | Tbpl2 | Tbpl2 | | NR_110359 | TSS4554 |
| chr2 | 28529225 | 28529316 | MACS2_peak_1553 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 57 | chr2 | unknown | gene | 28496890 | 28505395 | + | Gbgt1 | Gbgt1 | P4000 | NM_139197 | TSS5623 |
| chr2 | 28529225 | 28529316 | MACS2_peak_1553 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 57 | chr2 | unknown | gene | 28555819 | 28563362 | - | Cel | Cel | P2061 | NM_009885 | TSS8057 |
| chr2 | 28635493 | 28635614 | MACS2_peak_1554 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 73 | chr2 | unknown | gene | 28609449 | 28621982 | - | Gfi1b | Gfi1b | P18973 | NM_008114 | TSS1816 |
| chr2 | 28635493 | 28635614 | MACS2_peak_1554 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 73 | chr2 | unknown | gene | 28641232 | 28687173 | + | Tsc1 | Tsc1 | P372 | NM_022887 | TSS27383 |
| chr2 | 31771512 | 31771603 | MACS2_peak_1555 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 37 | chr2 | unknown | gene | 31670736 | 31680570 | + | Exosc2 | Exosc2 | P7661 | NM_144886 | TSS17230 |
| chr2 | 31771512 | 31771603 | MACS2_peak_1555 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 37 | chr2 | unknown | gene | 31806167 | 31810518 | - | Qrfp | Qrfp | P18603 | NM_183424 | TSS10945 |
| chr2 | 34107097 | 34107188 | MACS2_peak_1556 | 23 | + | 5.26766 | 7.08584 | 2.32792 | 63 | chr2 | unknown | gene | 33729955 | 33887394 | - | Mvb12b | Mvb12b | P6686 | NM_175184 | TSS26916 |
| chr2 | 34107097 | 34107188 | MACS2_peak_1556 | 23 | + | 5.26766 | 7.08584 | 2.32792 | 63 | chr2 | unknown | gene | 34171456 | 34371920 | - | Pbx3 | Pbx3 | P7248 | NM_016768 | TSS2173 |
| chr2 | 35683315 | 35683426 | MACS2_peak_1557 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 65 | chr2 | unknown | gene | 35549533 | 35558702 | - | Gm13446 | Gm13446 | | NR_045894 | TSS26836 |
| chr2 | 35683315 | 35683426 | MACS2_peak_1557 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 65 | chr2 | unknown | gene | 35751225 | 35979624 | - | Ttll11 | Ttll11 | P15791 | NM_029774 | TSS23760 |
| chr2 | 38160255 | 38160375 | MACS2_peak_1558 | 12 | + | 4.14966 | 5.12722 | 1.204 | 79 | chr2 | unknown | gene | 37776248 | 37796672 | + | Crb2 | Crb2 | P21169 | NM_001163566 | TSS23714 |
| chr2 | 38160255 | 38160375 | MACS2_peak_1558 | 12 | + | 4.14966 | 5.12722 | 1.204 | 79 | chr2 | unknown | gene | 38339280 | 38369129 | + | Lhx2 | Lhx2 | P2139 | NM_001290646 | TSS5508 |
| chr2 | 38449449 | 38449540 | MACS2_peak_1559 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 48 | chr2 | unknown | gene | 38339280 | 38369129 | + | Lhx2 | Lhx2 | P2139 | NM_001290646 | TSS5508 |
| chr2 | 38449449 | 38449540 | MACS2_peak_1559 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 48 | chr2 | unknown | gene | 38511696 | 38585390 | + | Nek6 | Nek6 | P9098 | NM_021606 | TSS25683 |
| chr2 | 38938951 | 38939042 | MACS2_peak_1560 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 24 | chr2 | unknown | gene | 38723373 | 38926217 | - | Nr6a1 | Nr6a1 | P14987 | NM_010264 | TSS24093 |
| chr2 | 38938951 | 38939042 | MACS2_peak_1560 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 24 | chr2 | unknown | gene | 38998308 | 39001374 | + | Wdr38 | Wdr38 | P23689 | NM_029687 | TSS26598 |
| chr2 | 41305516 | 41305607 | MACS2_peak_1561 | 16 | + | 4.811 | 6.2687 | 1.67914 | 19 | chr2 | unknown | gene | 39196797 | 39226241 | - | Ppp6c | Ppp6c | P18498 | NM_024209 | TSS2707 |
| chr2 | 41305516 | 41305607 | MACS2_peak_1561 | 16 | + | 4.811 | 6.2687 | 1.67914 | 19 | chr2 | unknown | gene | 42447438 | 42447568 | - | Mir6336 | Mir6336 | | NR_105754 | TSS25204 |
| chr2 | 41704020 | 41704111 | MACS2_peak_1562 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 13 | chr2 | unknown | gene | 39196797 | 39226241 | - | Ppp6c | Ppp6c | P18498 | NM_024209 | TSS2707 |
| chr2 | 41704020 | 41704111 | MACS2_peak_1562 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 13 | chr2 | unknown | gene | 42447438 | 42447568 | - | Mir6336 | Mir6336 | | NR_105754 | TSS25204 |
| chr2 | 42197087 | 42197178 | MACS2_peak_1563 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 6 | chr2 | unknown | gene | 39196797 | 39226241 | - | Ppp6c | Ppp6c | P18498 | NM_024209 | TSS2707 |
| chr2 | 42197087 | 42197178 | MACS2_peak_1563 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 6 | chr2 | unknown | gene | 42447438 | 42447568 | - | Mir6336 | Mir6336 | | NR_105754 | TSS25204 |
| chr2 | 43580800 | 43580891 | MACS2_peak_1564 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 55 | chr2 | unknown | gene | 40596772 | 42652816 | - | Lrp1b | Lrp1b | P21516 | NM_053011 | TSS6499 |
| chr2 | 43580800 | 43580891 | MACS2_peak_1564 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 55 | chr2 | unknown | gene | 43748823 | 44394334 | + | Arhgap15 | Arhgap15 | P13611 | NM_001301831 | TSS12681 |
| chr2 | 43639151 | 43639242 | MACS2_peak_1565 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 40 | chr2 | unknown | gene | 40596772 | 42652816 | - | Lrp1b | Lrp1b | P21516 | NM_053011 | TSS6499 |
| chr2 | 43639151 | 43639242 | MACS2_peak_1565 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 40 | chr2 | unknown | gene | 43748823 | 44394334 | + | Arhgap15 | Arhgap15 | P13611 | NM_001301831 | TSS12681 |
| chr2 | 44411071 | 44411162 | MACS2_peak_1566 | 16 | + | 4.811 | 6.2687 | 1.67914 | 49 | chr2 | unknown | gene | 43748823 | 44394334 | + | Arhgap15 | Arhgap15 | P13611 | NM_001301831 | TSS12681 |
| chr2 | 44411071 | 44411162 | MACS2_peak_1566 | 16 | + | 4.811 | 6.2687 | 1.67914 | 49 | chr2 | unknown | gene | 44564411 | 44861622 | - | Gtdc1 | Gtdc1 | P24367 | NM_172662 | TSS13749 |
| chr2 | 44434884 | 44435024 | MACS2_peak_1567 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 82 | chr2 | unknown | gene | 43748823 | 44394334 | + | Arhgap15 | Arhgap15 | P13611 | NM_001301831 | TSS12681 |
| chr2 | 44434884 | 44435024 | MACS2_peak_1567 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 82 | chr2 | unknown | gene | 44564411 | 44861622 | - | Gtdc1 | Gtdc1 | P24367 | NM_172662 | TSS13749 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr2 | 44681530 | 44681621 | MACS2_peak_1568 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 37 | chr2 | unknown | gene | 43748823 | 44394334 | + | Arhgap15 | Arhgap15 | P13611 | NM_001301831 | TSS12681 |
| chr2 | 44681530 | 44681621 | MACS2_peak_1568 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 37 | chr2 | unknown | gene | 44983511 | 45113279 | - | Zeb2 | Zeb2 | P19224 | NM_015753 | TSS6070 |
| chr2 | 44966210 | 44966301 | MACS2_peak_1569 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 66 | chr2 | unknown | gene | 44564411 | 44861622 | - | Gtdc1 | Gtdc1 | P24367 | NM_172662 | TSS13749 |
| chr2 | 44966210 | 44966301 | MACS2_peak_1569 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 66 | chr2 | unknown | gene | 44983511 | 45113279 | - | Zeb2 | Zeb2 | P19224 | NM_015753 | TSS6070 |
| chr2 | 46509834 | 46509925 | MACS2_peak_1570 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 64 | chr2 | unknown | gene | 45696604 | 45698447 | + | 1700019E08Rik | 1700019E08Rik | | NR_040497 | TSS23878 |
| chr2 | 46509834 | 46509925 | MACS2_peak_1570 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 64 | chr2 | unknown | gene | 48814108 | 48899788 | + | Acvr2a | Acvr2a | P7302 | NM_007396 | TSS21826 |
| chr2 | 46734876 | 46734967 | MACS2_peak_1571 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 51 | chr2 | unknown | gene | 45696604 | 45698447 | + | 1700019E08Rik | 1700019E08Rik | | NR_040497 | TSS23878 |
| chr2 | 46734876 | 46734967 | MACS2_peak_1571 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 51 | chr2 | unknown | gene | 48814108 | 48899788 | + | Acvr2a | Acvr2a | P7302 | NM_007396 | TSS21826 |
| chr2 | 46986775 | 46986881 | MACS2_peak_1572 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 74 | chr2 | unknown | gene | 45696604 | 45698447 | + | 1700019E08Rik | 1700019E08Rik | | NR_040497 | TSS23878 |
| chr2 | 46986775 | 46986881 | MACS2_peak_1572 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 74 | chr2 | unknown | gene | 48814108 | 48899788 | + | Acvr2a | Acvr2a | P7302 | NM_007396 | TSS21826 |
| chr2 | 47342572 | 47342687 | MACS2_peak_1573 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 49 | chr2 | unknown | gene | 45696604 | 45698447 | + | 1700019E08Rik | 1700019E08Rik | | NR_040497 | TSS23878 |
| chr2 | 47342572 | 47342687 | MACS2_peak_1573 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 49 | chr2 | unknown | gene | 48814108 | 48899788 | + | Acvr2a | Acvr2a | P7302 | NM_007396 | TSS21826 |
| chr2 | 47671941 | 47672032 | MACS2_peak_1574 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 51 | chr2 | unknown | gene | 45696604 | 45698447 | + | 1700019E08Rik | 1700019E08Rik | | NR_040497 | TSS23878 |
| chr2 | 47671941 | 47672032 | MACS2_peak_1574 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 51 | chr2 | unknown | gene | 48814108 | 48899788 | + | Acvr2a | Acvr2a | P7302 | NM_007396 | TSS21826 |
| chr2 | 47774969 | 47775060 | MACS2_peak_1575 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 13 | chr2 | unknown | gene | 45696604 | 45698447 | + | 1700019E08Rik | 1700019E08Rik | | NR_040497 | TSS23878 |
| chr2 | 47774969 | 47775060 | MACS2_peak_1575 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 13 | chr2 | unknown | gene | 48814108 | 48899788 | + | Acvr2a | Acvr2a | P7302 | NM_007396 | TSS21826 |
| chr2 | 48002057 | 48002187 | MACS2_peak_1576 | 12 | + | 4.14966 | 5.12722 | 1.204 | 78 | chr2 | unknown | gene | 45696604 | 45698447 | + | 1700019E08Rik | 1700019E08Rik | | NR_040497 | TSS23878 |
| chr2 | 48002057 | 48002187 | MACS2_peak_1576 | 12 | + | 4.14966 | 5.12722 | 1.204 | 78 | chr2 | unknown | gene | 48814108 | 48899788 | + | Acvr2a | Acvr2a | P7302 | NM_007396 | TSS21826 |
| chr2 | 54118988 | 54119079 | MACS2_peak_1577 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 50 | chr2 | unknown | gene | 54084092 | 54085304 | - | Rprm | Rprm | P22550 | NM_023396 | TSS16608 |
| chr2 | 54118988 | 54119079 | MACS2_peak_1577 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 50 | chr2 | unknown | gene | 54436386 | 55112961 | + | Galnt13 | Galnt13 | P4168 | NM_173030 | TSS16797 |
| chr2 | 54542357 | 54542448 | MACS2_peak_1578 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 47 | chr2 | unknown | gene | 54084092 | 54085304 | - | Rprm | Rprm | P22550 | NM_023396 | TSS16608 |
| chr2 | 54542357 | 54542448 | MACS2_peak_1578 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 47 | chr2 | unknown | gene | 55435969 | 55595397 | + | Kcnj3 | Kcnj3 | P24398 | NM_001304810 | TSS20643 |
| chr2 | 55572056 | 55572147 | MACS2_peak_1579 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 41 | chr2 | unknown | gene | 54436386 | 55112961 | + | Galnt13 | Galnt13 | P4168 | NM_173030 | TSS16797 |
| chr2 | 55572056 | 55572147 | MACS2_peak_1579 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 41 | chr2 | unknown | gene | 56785810 | 56785907 | + | Mir195b | Mir195b | | NR_105751 | TSS21518 |
| chr2 | 56449830 | 56449930 | MACS2_peak_1580 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 21 | chr2 | unknown | gene | 55435969 | 55595397 | + | Kcnj3 | Kcnj3 | P24398 | NM_001304810 | TSS20643 |
| chr2 | 56449830 | 56449930 | MACS2_peak_1580 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 21 | chr2 | unknown | gene | 56785810 | 56785907 | + | Mir195b | Mir195b | | NR_105751 | TSS21518 |
| chr2 | 56812761 | 56812922 | MACS2_peak_1581 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 51 | chr2 | unknown | gene | 56785810 | 56785907 | + | Mir195b | Mir195b | | NR_105751 | TSS21518 |
| chr2 | 56812761 | 56812922 | MACS2_peak_1581 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 51 | chr2 | unknown | gene | 57107225 | 57124003 | - | Nr4a2 | Nr4a2 | P16834 | NM_001139509 | TSS26006 |
| chr2 | 57375450 | 57375541 | MACS2_peak_1582 | 30 | + | 5.71265 | 7.93979 | 3.00019 | 30 | chr2 | unknown | gene | 57237677 | 57367477 | + | Gpd2 | Gpd2 | P20372 | NM_001145820 | TSS12584 |
| chr2 | 57375450 | 57375541 | MACS2_peak_1582 | 30 | + | 5.71265 | 7.93979 | 3.00019 | 30 | chr2 | unknown | gene | 57998154 | 58038952 | + | Galnt5 | Galnt5 | P904 | NM_172855 | TSS6197 |
| chr2 | 57690166 | 57690257 | MACS2_peak_1583 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 16 | chr2 | unknown | gene | 57237677 | 57367477 | + | Gpd2 | Gpd2 | P20372 | NM_001145820 | TSS12584 |
| chr2 | 57690166 | 57690257 | MACS2_peak_1583 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 16 | chr2 | unknown | gene | 57998154 | 58038952 | + | Galnt5 | Galnt5 | P904 | NM_172855 | TSS6197 |
| chr2 | 58059826 | 58059917 | MACS2_peak_1584 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 31 | chr2 | unknown | gene | 58045114 | 58052716 | - | Ermn | Ermn | P2683 | NM_029972 | TSS5300 |
| chr2 | 58059826 | 58059917 | MACS2_peak_1584 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 31 | chr2 | unknown | gene | 58129138 | 58160055 | - | Cytip | Cytip | P12343 | NM_139200 | TSS18545 |
| chr2 | 59897821 | 59897912 | MACS2_peak_1585 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 20 | chr2 | unknown | gene | 59852364 | 59882606 | - | Wdsub1 | Wdsub1 | P26340 | NM_028118 | TSS4960 |
| chr2 | 59897821 | 59897912 | MACS2_peak_1585 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 20 | chr2 | unknown | gene | 59899362 | 60125740 | - | Baz2b | Baz2b | P5835 | NM_001001182 | TSS23752 |
| chr2 | 61725236 | 61725332 | MACS2_peak_1586 | 25 | + | 5.46411 | 7.45132 | 2.55202 | 26 | chr2 | unknown | gene | 61578585 | 61653555 | + | Tank | Tank | P18856 | NM_011529 | TSS12145 |
| chr2 | 61725236 | 61725332 | MACS2_peak_1586 | 25 | + | 5.46411 | 7.45132 | 2.55202 | 26 | chr2 | unknown | gene | 61804452 | 61812438 | + | Tbr1 | Tbr1 | P16947 | NM_009322 | TSS27231 |
| chr2 | 61769999 | 61770120 | MACS2_peak_1587 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 45 | chr2 | unknown | gene | 61578585 | 61653555 | + | Tank | Tank | P18856 | NM_011529 | TSS12145 |
| chr2 | 61769999 | 61770120 | MACS2_peak_1587 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 45 | chr2 | unknown | gene | 61804452 | 61812438 | + | Tbr1 | Tbr1 | P16947 | NM_009322 | TSS27231 |
| chr2 | 61908112 | 61908250 | MACS2_peak_1588 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 83 | chr2 | unknown | gene | 61804452 | 61812438 | + | Tbr1 | Tbr1 | P16947 | NM_009322 | TSS27231 |
| chr2 | 61908112 | 61908250 | MACS2_peak_1588 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 83 | chr2 | unknown | gene | 62046514 | 62324791 | + | Slc4a10 | Slc4a10 | P5691 | NM_001242380 | TSS19774 |
| chr2 | 62474427 | 62474518 | MACS2_peak_1589 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 61 | chr2 | unknown | gene | 62330072 | 62411791 | - | Dpp4 | Dpp4 | P17413 | NM_010074 | TSS6943 |
| chr2 | 62474427 | 62474518 | MACS2_peak_1589 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 61 | chr2 | unknown | gene | 62474529 | 62483653 | - | Gcg | Gcg | P10879 | NM_008100 | TSS26537 |
| chr2 | 62611671 | 62611762 | MACS2_peak_1590 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 22 | chr2 | unknown | gene | 62500935 | 62573851 | - | Fap | Fap | P25075 | NM_007986 | TSS362 |
| chr2 | 62611671 | 62611762 | MACS2_peak_1590 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 22 | chr2 | unknown | gene | 62664326 | 62691590 | + | Gca | Gca | P2048 | NM_145523 | TSS5362 |
| chr2 | 63216012 | 63216103 | MACS2_peak_1591 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 47 | chr2 | unknown | gene | 62702945 | 63184077 | - | Kcnh7 | Kcnh7 | P6083 | NM_133207 | TSS12855 |
| chr2 | 63216012 | 63216103 | MACS2_peak_1591 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 47 | chr2 | unknown | gene | 63971507 | 64098038 | - | Fign | Fign | P19719 | NM_001267846 | TSS23927 |
| chr2 | 63514945 | 63515039 | MACS2_peak_1592 | 16 | + | 4.811 | 6.2687 | 1.67914 | 71 | chr2 | unknown | gene | 62702945 | 63184077 | - | Kcnh7 | Kcnh7 | P6083 | NM_133207 | TSS12855 |
| chr2 | 63514945 | 63515039 | MACS2_peak_1592 | 16 | + | 4.811 | 6.2687 | 1.67914 | 71 | chr2 | unknown | gene | 63971507 | 64098038 | - | Fign | Fign | P19719 | NM_001267846 | TSS23927 |
| chr2 | 65515433 | 65515524 | MACS2_peak_1593 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 19 | chr2 | unknown | gene | 65364295 | 65364400 | - | Mir6337 | Mir6337 | | NR_105755 | TSS16155 |
| chr2 | 65515433 | 65515524 | MACS2_peak_1593 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 19 | chr2 | unknown | gene | 65670444 | 65764829 | + | Scn2a1 | Scn2a1 | P9237 | NM_001099298 | TSS20736 |
| chr2 | 65640147 | 65640269 | MACS2_peak_1594 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 49 | chr2 | unknown | gene | 65457117 | 65567492 | - | Scn3a | Scn3a | P4163 | NM_018732 | TSS1567 |
| chr2 | 65640147 | 65640269 | MACS2_peak_1594 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 49 | chr2 | unknown | gene | 65670444 | 65764829 | + | Scn2a1 | Scn2a1 | P9237 | NM_001099298 | TSS20736 |
| chr2 | 65867393 | 65867572 | MACS2_peak_1595 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 139 | chr2 | unknown | gene | 65670444 | 65764829 | + | Scn2a1 | Scn2a1 | P9237 | NM_001099298 | TSS20736 |
| chr2 | 65867393 | 65867572 | MACS2_peak_1595 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 139 | chr2 | unknown | gene | 66082765 | 66124793 | - | Galnt3 | Galnt3 | P20789 | NM_015736 | TSS25894 |
| chr2 | 66274290 | 66274381 | MACS2_peak_1596 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 60 | chr2 | unknown | gene | 66184326 | 66256534 | - | Ttc21b | Ttc21b | P23149 | NM_001047604 | TSS9580 |
| chr2 | 66274290 | 66274381 | MACS2_peak_1596 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 60 | chr2 | unknown | gene | 66440879 | 66547472 | + | Gm13629 | Gm13629 | | NR_033495 | TSS23660 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr2 | 66668470 | 66668561 | MACS2_peak_1597 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 37 | chr2 | unknown | gene | 66480080 | 66634962 | - | Scn9a | Scn9a | P25766 | NM_001290675 | TSS3093 |
| chr2 | 66668470 | 66668561 | MACS2_peak_1597 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 37 | chr2 | unknown | gene | 66673425 | 66784910 | - | Scn7a | Scn7a | P4427 | NM_009135 | TSS28 |
| chr2 | 69018085 | 69018176 | MACS2_peak_1598 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 55 | chr2 | unknown | gene | 68657883 | 68748369 | + | 4932414N04Rik | 4932414N04Rik | P20608 | NM_183113 | TSS14044 |
| chr2 | 69018085 | 69018176 | MACS2_peak_1598 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 55 | chr2 | unknown | gene | 69135799 | 69189133 | + | Nostrin | Nostrin | P12065 | NM_181547 | TSS10295 |
| chr2 | 69053722 | 69053901 | MACS2_peak_1599 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 39 | chr2 | unknown | gene | 68657883 | 68748369 | + | 4932414N04Rik | 4932414N04Rik | P20608 | NM_183113 | TSS14044 |
| chr2 | 69053722 | 69053901 | MACS2_peak_1599 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 39 | chr2 | unknown | gene | 69135799 | 69189133 | + | Nostrin | Nostrin | P12065 | NM_181547 | TSS10295 |
| chr2 | 69355543 | 69355663 | MACS2_peak_1600 | 123 | + | 10.43987 | 17.68996 | 12.32544 | 47 | chr2 | unknown | gene | 69238281 | 69342616 | - | Abcb11 | Abcb11 | P21313 | NM_021022 | TSS4157 |
| chr2 | 69355543 | 69355663 | MACS2_peak_1600 | 123 | + | 10.43987 | 17.68996 | 12.32544 | 47 | chr2 | unknown | gene | 69380461 | 69401457 | + | Dhrs9 | Dhrs9 | P9785 | NM_175512 | TSS11348 |
| chr2 | 69701177 | 69701268 | MACS2_peak_1601 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 40 | chr2 | unknown | gene | 69670119 | 69683599 | + | Klhl41 | Klhl41 | P16613 | NM_001081087 | TSS11288 |
| chr2 | 69701177 | 69701268 | MACS2_peak_1601 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 40 | chr2 | unknown | gene | 69723087 | 69750382 | + | Ppig | Ppig | P5807 | NM_001081086 | TSS24156 |
| chr2 | 70522621 | 70522766 | MACS2_peak_1602 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 35 | chr2 | unknown | gene | 70474922 | 70477169 | + | Sp5 | Sp5 | P1118 | NM_022435 | TSS1231 |
| chr2 | 70522621 | 70522766 | MACS2_peak_1602 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 35 | chr2 | unknown | gene | 70562163 | 70600796 | + | Gad1 | Gad1 | P24762 | NM_008077 | TSS18512 |
| chr2 | 72804108 | 72804215 | MACS2_peak_1603 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 36 | chr2 | unknown | gene | 72703509 | 72729468 | + | 8430437L04Rik | 8430437L04Rik | | NR_040503 | TSS3809 |
| chr2 | 72804108 | 72804215 | MACS2_peak_1603 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 36 | chr2 | unknown | gene | 72936431 | 72980256 | - | Sp3 | Sp3 | P1755 | NM_001098425 | TSS1979 |
| chr2 | 72921718 | 72921809 | MACS2_peak_1604 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 50 | chr2 | unknown | gene | 72745845 | 72813717 | - | 6430710C18Rik | 6430710C18Rik | | NR_102348 | TSS27581 |
| chr2 | 72921718 | 72921809 | MACS2_peak_1604 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 50 | chr2 | unknown | gene | 72936431 | 72980256 | - | Sp3 | Sp3 | P1755 | NM_001098425 | TSS1979 |
| chr2 | 73275593 | 73275684 | MACS2_peak_1605 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 42 | chr2 | unknown | gene | 73271925 | 73274558 | + | Sp9 | Sp9 | P6660 | NM_001005343 | TSS4006 |
| chr2 | 73275593 | 73275684 | MACS2_peak_1605 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 42 | chr2 | unknown | gene | 73283871 | 73312488 | - | Cir1 | Cir1 | P21792 | NM_025854 | TSS15774 |
| chr2 | 73498733 | 73498824 | MACS2_peak_1606 | 32 | + | 5.8651 | 8.25694 | 3.2954 | 12 | chr2 | unknown | gene | 73341505 | 73386480 | - | Gpr155 | Gpr155 | P26809 | NM_001276444 | TSS832 |
| chr2 | 73498733 | 73498824 | MACS2_peak_1606 | 32 | + | 5.8651 | 8.25694 | 3.2954 | 12 | chr2 | unknown | gene | 73563280 | 73580287 | - | Chrna1 | Chrna1 | P19453 | NM_007389 | TSS22522 |
| chr2 | 73624476 | 73624567 | MACS2_peak_1607 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 47 | chr2 | unknown | gene | 73596525 | 73616012 | + | Chn1os3 | Chn1os3 | | NR_040623 | TSS25369 |
| chr2 | 73624476 | 73624567 | MACS2_peak_1607 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 47 | chr2 | unknown | gene | 73816508 | 73892639 | - | Atf2 | Atf2 | P8604 | NM_009715 | TSS25026 |
| chr2 | 73910269 | 73910410 | MACS2_peak_1608 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 78 | chr2 | unknown | gene | 73816508 | 73892639 | - | Atf2 | Atf2 | P8604 | NM_009715 | TSS25026 |
| chr2 | 73910269 | 73910410 | MACS2_peak_1608 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 78 | chr2 | unknown | gene | 74298939 | 74307717 | - | 4930441J16Rik | 4930441J16Rik | | NR_040501 | TSS26310 |
| chr2 | 74384903 | 74384994 | MACS2_peak_1609 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 53 | chr2 | unknown | gene | 74298939 | 74307717 | - | 4930441J16Rik | 4930441J16Rik | | NR_040501 | TSS26310 |
| chr2 | 74384903 | 74384994 | MACS2_peak_1609 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 53 | chr2 | unknown | gene | 74514836 | 74578948 | - | Lnp | Lnp | P20110 | NM_001110209 | TSS25363 |
| chr2 | 74473233 | 74473327 | MACS2_peak_1610 | 26 | + | 5.53289 | 7.58332 | 2.67506 | 15 | chr2 | unknown | gene | 74298939 | 74307717 | - | 4930441J16Rik | 4930441J16Rik | | NR_040501 | TSS26310 |
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| chr2 | 74527593 | 74527684 | MACS2_peak_1611 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 10 | chr2 | unknown | gene | 74298939 | 74307717 | - | 4930441J16Rik | 4930441J16Rik | | NR_040501 | TSS26310 |
| chr2 | 74527593 | 74527684 | MACS2_peak_1611 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 10 | chr2 | unknown | gene | 74655615 | 74659419 | - | Evx2 | Evx2 | P4327 | NM_007967 | TSS3704 |
| chr2 | 74660527 | 74660618 | MACS2_peak_1612 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 3 | chr2 | unknown | gene | 74655615 | 74659419 | - | Evx2 | Evx2 | P4327 | NM_007967 | TSS3704 |
| chr2 | 74660527 | 74660618 | MACS2_peak_1612 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 3 | chr2 | unknown | gene | 74668309 | 74670136 | + | Hoxd13 | Hoxd13 | P21429 | NM_008275 | TSS25309 |
| chr2 | 74884803 | 74884915 | MACS2_peak_1613 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 73 | chr2 | unknown | gene | 74825811 | 74876474 | + | Mtx2 | Mtx2 | P13576 | NM_016804 | TSS15112 |
| chr2 | 74884803 | 74884915 | MACS2_peak_1613 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 73 | chr2 | unknown | gene | 75436056 | 75444179 | - | 9430019J16Rik | 9430019J16Rik | | NR_040635 | TSS19199 |
| chr2 | 75413682 | 75413773 | MACS2_peak_1614 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 24 | chr2 | unknown | gene | 74825811 | 74876474 | + | Mtx2 | Mtx2 | P13576 | NM_016804 | TSS15112 |
| chr2 | 75413682 | 75413773 | MACS2_peak_1614 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 24 | chr2 | unknown | gene | 75436056 | 75444179 | - | 9430019J16Rik | 9430019J16Rik | | NR_040635 | TSS19199 |
| chr2 | 76103914 | 76104005 | MACS2_peak_1615 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 41 | chr2 | unknown | gene | 75979105 | 75981737 | - | Ttc30a1 | Ttc30a1 | P12788 | NM_030188 | TSS439 |
| chr2 | 76103914 | 76104005 | MACS2_peak_1615 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 41 | chr2 | unknown | gene | 76353941 | 76360453 | - | Cyct | Cyct | P12736 | NM_009989 | TSS21360 |
| chr2 | 76221660 | 76221781 | MACS2_peak_1616 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 45 | chr2 | unknown | gene | 75979105 | 75981737 | - | Ttc30a1 | Ttc30a1 | P12788 | NM_030188 | TSS439 |
| chr2 | 76221660 | 76221781 | MACS2_peak_1616 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 45 | chr2 | unknown | gene | 76353941 | 76360453 | - | Cyct | Cyct | P12736 | NM_009989 | TSS21360 |
| chr2 | 76533266 | 76533357 | MACS2_peak_1617 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 54 | chr2 | unknown | gene | 76369983 | 76383767 | + | Rbm45 | Rbm45 | P7585 | NM_153405 | TSS5450 |
| chr2 | 76533266 | 76533357 | MACS2_peak_1617 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 54 | chr2 | unknown | gene | 76629936 | 76647856 | - | Prkra | Prkra | P8226 | NM_011871 | TSS17550 |
| chr2 | 77544298 | 77544389 | MACS2_peak_1618 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 17 | chr2 | unknown | gene | 77462643 | 77480938 | + | Gm13944 | Gm13944 | | NR_040368 | TSS21929 |
| chr2 | 77544298 | 77544389 | MACS2_peak_1618 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 17 | chr2 | unknown | gene | 77895652 | 77946356 | - | Cwc22 | Cwc22 | P1358 | NM_030560 | TSS24947 |
| chr2 | 77655545 | 77655647 | MACS2_peak_1619 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 34 | chr2 | unknown | gene | 77462643 | 77480938 | + | Gm13944 | Gm13944 | | NR_040368 | TSS21929 |
| chr2 | 77655545 | 77655647 | MACS2_peak_1619 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 34 | chr2 | unknown | gene | 77895652 | 77946356 | - | Cwc22 | Cwc22 | P1358 | NM_030560 | TSS24947 |
| chr2 | 78051849 | 78051940 | MACS2_peak_1620 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 58 | chr2 | unknown | gene | 77895652 | 77946356 | - | Cwc22 | Cwc22 | P1358 | NM_030560 | TSS24947 |
| chr2 | 78051849 | 78051940 | MACS2_peak_1620 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 58 | chr2 | unknown | gene | 78237546 | 78302000 | + | Gm14461 | Gm14461 | P1725 | NM_177843 | TSS18404 |
| chr2 | 78728508 | 78728697 | MACS2_peak_1621 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 40 | chr2 | unknown | gene | 78237546 | 78302000 | + | Gm14461 | Gm14461 | P1725 | NM_177843 | TSS18404 |
| chr2 | 78728508 | 78728697 | MACS2_peak_1621 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 40 | chr2 | unknown | gene | 78869046 | 78920055 | + | Ube2e3 | Ube2e3 | P13691 | NM_009454 | TSS16447 |
| chr2 | 78873735 | 78873826 | MACS2_peak_1622 | 19 | + | 5.0267 | 6.65745 | 1.99837 | 48 | chr2 | unknown | gene | 78237546 | 78302000 | + | Gm14461 | Gm14461 | P1725 | NM_177843 | TSS18404 |
| chr2 | 78873735 | 78873826 | MACS2_peak_1622 | 19 | + | 5.0267 | 6.65745 | 1.99837 | 48 | chr2 | unknown | gene | 79255425 | 79326615 | + | Itga4 | Itga4 | P9705 | NM_010576 | TSS24589 |
| chr2 | 79832830 | 79832921 | MACS2_peak_1623 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 83 | chr2 | unknown | gene | 79707779 | 79815412 | + | Ppp1r1c | Ppp1r1c | P7569 | NM_172420 | TSS16892 |
| chr2 | 79832830 | 79832921 | MACS2_peak_1623 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 83 | chr2 | unknown | gene | 79834452 | 80129412 | - | Pde1a | Pde1a | P5246 | NM_001159582 | TSS11050 |
| chr2 | 79957816 | 79957995 | MACS2_peak_1624 | 27 | + | 5.56793 | 7.65146 | 2.73702 | 51 | chr2 | unknown | gene | 79707779 | 79815412 | + | Ppp1r1c | Ppp1r1c | P7569 | NM_172420 | TSS16892 |
| chr2 | 79957816 | 79957995 | MACS2_peak_1624 | 27 | + | 5.56793 | 7.65146 | 2.73702 | 51 | chr2 | unknown | gene | 80292469 | 80293523 | + | Prdx6b | Prdx6b | P5176 | NM_177256 | TSS23723 |
| chr2 | 80411663 | 80411825 | MACS2_peak_1625 | 55 | + | 4.44162 | 5.59746 | 1.68837 | 110 | chr2 | unknown | gene | 80391363 | 80398216 | + | Gm13752 | Gm13752 | | NR_040370 | TSS7223 |
| chr2 | 80411663 | 80411825 | MACS2_peak_1625 | 55 | + | 4.44162 | 5.59746 | 1.68837 | 110 | chr2 | unknown | gene | 80411969 | 80446840 | - | Frzb | Frzb | P16178 | NM_011356 | TSS17727 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr2 | 80874967 | 80875134 | MACS2_peak_1626 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 35 | chr2 | unknown | gene | 80638811 | 80658398 | + | Nup35 | Nup35 | P6213 | NM_027091 | TSS12925 |
| chr2 | 80874967 | 80875134 | MACS2_peak_1626 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 35 | chr2 | unknown | gene | 82053657 | 82259431 | + | Zfp804a | Zfp804a | P5331 | NM_175513 | TSS22861 |
| chr2 | 81016749 | 81016840 | MACS2_peak_1627 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 27 | chr2 | unknown | gene | 80638811 | 80658398 | + | Nup35 | Nup35 | P6213 | NM_027091 | TSS12925 |
| chr2 | 81016749 | 81016840 | MACS2_peak_1627 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 27 | chr2 | unknown | gene | 82053657 | 82259431 | + | Zfp804a | Zfp804a | P5331 | NM_175513 | TSS22861 |
| chr2 | 81687769 | 81687860 | MACS2_peak_1628 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 61 | chr2 | unknown | gene | 80638811 | 80658398 | + | Nup35 | Nup35 | P6213 | NM_027091 | TSS12925 |
| chr2 | 81687769 | 81687860 | MACS2_peak_1628 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 61 | chr2 | unknown | gene | 82053657 | 82259431 | + | Zfp804a | Zfp804a | P5331 | NM_175513 | TSS22861 |
| chr2 | 81965818 | 81965915 | MACS2_peak_1629 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 58 | chr2 | unknown | gene | 80638811 | 80658398 | + | Nup35 | Nup35 | P6213 | NM_027091 | TSS12925 |
| chr2 | 81965818 | 81965915 | MACS2_peak_1629 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 58 | chr2 | unknown | gene | 82053657 | 82259431 | + | Zfp804a | Zfp804a | P5331 | NM_175513 | TSS22861 |
| chr2 | 82454687 | 82454778 | MACS2_peak_1630 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 63 | chr2 | unknown | gene | 82053657 | 82259431 | + | Zfp804a | Zfp804a | P5331 | NM_175513 | TSS22861 |
| chr2 | 82454687 | 82454778 | MACS2_peak_1630 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 63 | chr2 | unknown | gene | 83644577 | 83664010 | + | Zc3h15 | Zc3h15 | P19697 | NM_026934 | TSS1675 |
| chr2 | 87193201 | 87193376 | MACS2_peak_1631 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 87 | chr2 | unknown | gene | 87191688 | 87192645 | + | Olfr1112 | Olfr1112 | P10466 | NM_146661 | TSS8953 |
| chr2 | 87193201 | 87193376 | MACS2_peak_1631 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 87 | chr2 | unknown | gene | 87212893 | 87213874 | + | Olfr1113 | Olfr1113 | P21752 | NM_207565 | TSS11457 |
| chr2 | 88504025 | 88504116 | MACS2_peak_1632 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 30 | chr2 | unknown | gene | 88486733 | 88487669 | + | Olfr1184 | Olfr1184 | P12208 | NM_146823 | TSS15898 |
| chr2 | 88504025 | 88504116 | MACS2_peak_1632 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 30 | chr2 | unknown | gene | 88525500 | 88526496 | + | Olfr1186 | Olfr1186 | P5684 | NM_146530 | TSS1270 |
| chr2 | 89688883 | 89689006 | MACS2_peak_1633 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 56 | chr2 | unknown | gene | 89666927 | 89667884 | - | Olfr1251 | Olfr1251 | P11904 | NM_001011529 | TSS13862 |
| chr2 | 89688883 | 89689006 | MACS2_peak_1633 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 56 | chr2 | unknown | gene | 89721164 | 89722109 | - | Olfr1252 | Olfr1252 | P5272 | NM_207568 | TSS3986 |
| chr2 | 90681242 | 90681353 | MACS2_peak_1634 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 22 | chr2 | unknown | gene | 90429755 | 90580587 | - | Ptprj | Ptprj | P15371 | NM_001135657 | TSS27355 |
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| chr2 | 93851045 | 93851204 | MACS2_peak_1635 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 27 | chr2 | unknown | gene | 93833466 | 93849943 | - | Accs | Accs | P14204 | NM_183220 | TSS16004 |
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| chr2 | 94181399 | 94181490 | MACS2_peak_1636 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 73 | chr2 | unknown | gene | 94032696 | 94157869 | - | Hsd17b12 | Hsd17b12 | P7772 | NM_019657 | TSS4058 |
| chr2 | 94181399 | 94181490 | MACS2_peak_1636 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 73 | chr2 | unknown | gene | 94241363 | 94241453 | - | Mir129-2 | Mir129-2 | | NR_029752 | TSS15703 |
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| chr2 | 95920208 | 95920299 | MACS2_peak_1638 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 72 | chr2 | unknown | gene | 94411726 | 94437992 | - | Api5 | Api5 | P26713 | NM_007466 | TSS11041 |
| chr2 | 95920208 | 95920299 | MACS2_peak_1638 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 72 | chr2 | unknown | gene | 96318168 | 97630953 | + | Lrrc4c | Lrrc4c | P14779 | NM_001289743 | TSS21452 |
| chr2 | 98188496 | 98188620 | MACS2_peak_1639 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 65 | chr2 | unknown | gene | 96318168 | 97630953 | + | Lrrc4c | Lrrc4c | P14779 | NM_001289743 | TSS21452 |
| chr2 | 98188496 | 98188620 | MACS2_peak_1639 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 65 | chr2 | unknown | gene | 101560780 | 101628986 | - | B230118H07Rik | B230118H07Rik | P13791 | NM_026592 | TSS17118 |
| chr2 | 98662244 | 98662935 | MACS2_peak_1640 | 695 | + | 6.10324 | 75.94082 | 69.58165 | 473 | chr2 | unknown | gene | 96318168 | 97630953 | + | Lrrc4c | Lrrc4c | P14779 | NM_001289743 | TSS21452 |
| chr2 | 98662244 | 98662935 | MACS2_peak_1640 | 695 | + | 6.10324 | 75.94082 | 69.58165 | 473 | chr2 | unknown | gene | 101560780 | 101628986 | - | B230118H07Rik | B230118H07Rik | P13791 | NM_026592 | TSS17118 |
| chr2 | 98663820 | 98663989 | MACS2_peak_1641 | 129 | + | 3.03082 | 18.30474 | 12.91951 | 120 | chr2 | unknown | gene | 96318168 | 97630953 | + | Lrrc4c | Lrrc4c | P14779 | NM_001289743 | TSS21452 |
| chr2 | 98663820 | 98663989 | MACS2_peak_1641 | 129 | + | 3.03082 | 18.30474 | 12.91951 | 120 | chr2 | unknown | gene | 101560780 | 101628986 | - | B230118H07Rik | B230118H07Rik | P13791 | NM_026592 | TSS17118 |
| chr2 | 98665030 | 98665221 | MACS2_peak_1642 | 727 | + | 6.24601 | 79.17325 | 72.76642 | 100 | chr2 | unknown | gene | 96318168 | 97630953 | + | Lrrc4c | Lrrc4c | P14779 | NM_001289743 | TSS21452 |
| chr2 | 98665030 | 98665221 | MACS2_peak_1642 | 727 | + | 6.24601 | 79.17325 | 72.76642 | 100 | chr2 | unknown | gene | 101560780 | 101628986 | - | B230118H07Rik | B230118H07Rik | P13791 | NM_026592 | TSS17118 |
| chr2 | 98666241 | 98667322 | MACS2_peak_1643 | 768 | + | 6.42655 | 83.29155 | 76.81383 | 930 | chr2 | unknown | gene | 96318168 | 97630953 | + | Lrrc4c | Lrrc4c | P14779 | NM_001289743 | TSS21452 |
| chr2 | 98666241 | 98667322 | MACS2_peak_1643 | 768 | + | 6.42655 | 83.29155 | 76.81383 | 930 | chr2 | unknown | gene | 101560780 | 101628986 | - | B230118H07Rik | B230118H07Rik | P13791 | NM_026592 | TSS17118 |
| chr2 | 98840194 | 98840285 | MACS2_peak_1644 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 42 | chr2 | unknown | gene | 96318168 | 97630953 | + | Lrrc4c | Lrrc4c | P14779 | NM_001289743 | TSS21452 |
| chr2 | 98840194 | 98840285 | MACS2_peak_1644 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 42 | chr2 | unknown | gene | 101560780 | 101628986 | - | B230118H07Rik | B230118H07Rik | P13791 | NM_026592 | TSS17118 |
| chr2 | 100190601 | 100190692 | MACS2_peak_1645 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 57 | chr2 | unknown | gene | 96318168 | 97630953 | + | Lrrc4c | Lrrc4c | P14779 | NM_001289743 | TSS21452 |
| chr2 | 100190601 | 100190692 | MACS2_peak_1645 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 57 | chr2 | unknown | gene | 101560780 | 101628986 | - | B230118H07Rik | B230118H07Rik | P13791 | NM_026592 | TSS17118 |
| chr2 | 100341285 | 100341376 | MACS2_peak_1646 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 49 | chr2 | unknown | gene | 96318168 | 97630953 | + | Lrrc4c | Lrrc4c | P14779 | NM_001289743 | TSS21452 |
| chr2 | 100341285 | 100341376 | MACS2_peak_1646 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 49 | chr2 | unknown | gene | 101560780 | 101628986 | - | B230118H07Rik | B230118H07Rik | P13791 | NM_026592 | TSS17118 |
| chr2 | 102566823 | 102566965 | MACS2_peak_1647 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 60 | chr2 | unknown | gene | 102449365 | 102451588 | - | Fjx1 | Fjx1 | P9290 | NM_010218 | TSS21346 |
| chr2 | 102566823 | 102566965 | MACS2_peak_1647 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 60 | chr2 | unknown | gene | 102658682 | 102781534 | + | Slc1a2 | Slc1a2 | P6734 | NM_001077514 | TSS22699 |
| chr2 | 103460973 | 103461064 | MACS2_peak_1648 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 30 | chr2 | unknown | gene | 103412097 | 103449660 | + | Elf5 | Elf5 | P17937 | NM_001145813 | TSS21884 |
| chr2 | 103460973 | 103461064 | MACS2_peak_1648 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 30 | chr2 | unknown | gene | 103566309 | 103717357 | + | Abtb2 | Abtb2 | P15424 | NM_178890 | TSS3400 |
| chr2 | 104953291 | 104953382 | MACS2_peak_1649 | 26 | + | 5.49828 | 7.51662 | 2.61219 | 69 | chr2 | unknown | gene | 104830740 | 104849850 | - | Prrg4 | Prrg4 | P17577 | NM_178695 | TSS507 |
| chr2 | 104953291 | 104953382 | MACS2_peak_1649 | 26 | + | 5.49828 | 7.51662 | 2.61219 | 69 | chr2 | unknown | gene | 104999656 | 105016987 | - | Eif3m | Eif3m | P4980 | NM_145380 | TSS18812 |
| chr2 | 106466599 | 106466690 | MACS2_peak_1650 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 40 | chr2 | unknown | gene | 105966707 | 106003549 | - | Dnajc24 | Dnajc24 | | NR_033993 | TSS13207 |
| chr2 | 106466599 | 106466690 | MACS2_peak_1650 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 40 | chr2 | unknown | gene | 106693458 | 106867066 | + | Mpped2 | Mpped2 | P19835 | NM_001143683 | TSS12830 |
| chr2 | 106662968 | 106663059 | MACS2_peak_1651 | 7 | + | 3.33222 | 3.76219 | 0.71769 | 40 | chr2 | unknown | gene | 106463822 | 106523103 | - | Gm14015 | Gm14015 | | NR_040637 | TSS16547 |
| chr2 | 106662968 | 106663059 | MACS2_peak_1651 | 7 | + | 3.33222 | 3.76219 | 0.71769 | 40 | chr2 | unknown | gene | 106693458 | 106867066 | + | Mpped2 | Mpped2 | P19835 | NM_001143683 | TSS12830 |
| chr2 | 107920019 | 107920147 | MACS2_peak_1652 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 60 | chr2 | unknown | gene | 107290588 | 107296887 | + | Kcna4 | Kcna4 | P15499 | NM_021275 | TSS5747 |
| chr2 | 107920019 | 107920147 | MACS2_peak_1652 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 60 | chr2 | unknown | gene | 109092299 | 109278290 | - | Mettl15 | Mettl15 | P4949 | NM_029790 | TSS21427 |
| chr2 | 108203660 | 108203751 | MACS2_peak_1653 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 11 | chr2 | unknown | gene | 107290588 | 107296887 | + | Kcna4 | Kcna4 | P15499 | NM_021275 | TSS5747 |
| chr2 | 108203660 | 108203751 | MACS2_peak_1653 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 11 | chr2 | unknown | gene | 109092299 | 109278290 | - | Mettl15 | Mettl15 | P4949 | NM_029790 | TSS21427 |
| chr2 | 108943283 | 108943441 | MACS2_peak_1654 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 33 | chr2 | unknown | gene | 107290588 | 107296887 | + | Kcna4 | Kcna4 | P15499 | NM_021275 | TSS5747 |
| chr2 | 108943283 | 108943441 | MACS2_peak_1654 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 33 | chr2 | unknown | gene | 109092299 | 109278290 | - | Mettl15 | Mettl15 | P4949 | NM_029790 | TSS21427 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr2 | 109038264 | 109038389 | MACS2_peak_1655 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 59 | chr2 | unknown | gene | 107290588 | 107296887 | + | Kcna4 | Kcna4 | P15499 | NM_021275 | TSS5747 |
| chr2 | 109038264 | 109038389 | MACS2_peak_1655 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 59 | chr2 | unknown | gene | 109092299 | 109278290 | - | Mettl15 | Mettl15 | P4949 | NM_029790 | TSS21427 |
| chr2 | 110833392 | 110833483 | MACS2_peak_1656 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 31 | chr2 | unknown | gene | 110721493 | 110737507 | + | Muc15 | Muc15 | P11253 | NM_172979 | TSS4142 |
| chr2 | 110833392 | 110833483 | MACS2_peak_1656 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 31 | chr2 | unknown | gene | 111193253 | 111229412 | - | 4930430A15Rik | 4930430A15Rik | P20394 | NM_026248 | TSS27360 |
| chr2 | 110956860 | 110956971 | MACS2_peak_1657 | 24 | + | 5.39702 | 7.32466 | 2.43395 | 73 | chr2 | unknown | gene | 110655200 | 110950103 | - | Ano3 | Ano3 | P4480 | NM_001128103 | TSS18 |
| chr2 | 110956860 | 110956971 | MACS2_peak_1657 | 24 | + | 5.39702 | 7.32466 | 2.43395 | 73 | chr2 | unknown | gene | 111193253 | 111229412 | - | 4930430A15Rik | 4930430A15Rik | P20394 | NM_026248 | TSS27360 |
| chr2 | 111526537 | 111526628 | MACS2_peak_1658 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 8 | chr2 | unknown | gene | 111489217 | 111493815 | - | Olfr1290 | Olfr1290 | P15711 | NM_146262 | TSS4358 |
| chr2 | 111526537 | 111526628 | MACS2_peak_1658 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 8 | chr2 | unknown | gene | 111537348 | 111538287 | - | Olfr1294 | Olfr1294 | P14585 | NM_146885 | TSS10897 |
| chr2 | 111553525 | 111553640 | MACS2_peak_1659 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 47 | chr2 | unknown | gene | 111537348 | 111538287 | - | Olfr1294 | Olfr1294 | P14585 | NM_146885 | TSS10897 |
| chr2 | 111553525 | 111553640 | MACS2_peak_1659 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 47 | chr2 | unknown | gene | 111564503 | 111565442 | - | Olfr1295 | Olfr1295 | P19711 | NM_146403 | TSS10818 |
| chr2 | 111578184 | 111578275 | MACS2_peak_1660 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 25 | chr2 | unknown | gene | 111564503 | 111565442 | - | Olfr1295 | Olfr1295 | P19711 | NM_146403 | TSS10818 |
| chr2 | 111578184 | 111578275 | MACS2_peak_1660 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 25 | chr2 | unknown | gene | 111621133 | 111622072 | - | Olfr1297 | Olfr1297 | P19338 | NM_146888 | TSS3558 |
| chr2 | 111897855 | 111897946 | MACS2_peak_1661 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 44 | chr2 | unknown | gene | 111872914 | 111873853 | - | Olfr1305 | Olfr1305 | P20674 | NM_146401 | TSS12381 |
| chr2 | 111897855 | 111897946 | MACS2_peak_1661 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 44 | chr2 | unknown | gene | 111911989 | 111912928 | - | Olfr1306 | Olfr1306 | P3257 | NM_001011803 | TSS27222 |
| chr2 | 112459833 | 112459924 | MACS2_peak_1662 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 19 | chr2 | unknown | gene | 112379210 | 112412415 | + | Katnbl1 | Katnbl1 | P16137 | NM_024254 | TSS994 |
| chr2 | 112459833 | 112459924 | MACS2_peak_1662 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 19 | chr2 | unknown | gene | 112479071 | 112480769 | - | Chrm5 | Chrm5 | P4627 | NM_205783 | TSS15372 |
| chr2 | 112532867 | 112532995 | MACS2_peak_1663 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 41 | chr2 | unknown | gene | 112479071 | 112480769 | - | Chrm5 | Chrm5 | P4627 | NM_205783 | TSS15372 |
| chr2 | 112532867 | 112532995 | MACS2_peak_1663 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 41 | chr2 | unknown | gene | 112631381 | 113030331 | - | Ryr3 | Ryr3 | P11447 | NM_177652 | TSS3652 |
| chr2 | 112603791 | 112603882 | MACS2_peak_1664 | 27 | + | 5.56793 | 7.65146 | 2.73702 | 24 | chr2 | unknown | gene | 112479071 | 112480769 | - | Chrm5 | Chrm5 | P4627 | NM_205783 | TSS15372 |
| chr2 | 112603791 | 112603882 | MACS2_peak_1664 | 27 | + | 5.56793 | 7.65146 | 2.73702 | 24 | chr2 | unknown | gene | 112631381 | 113030331 | - | Ryr3 | Ryr3 | P11447 | NM_177652 | TSS3652 |
| chr2 | 113140042 | 113140133 | MACS2_peak_1665 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 62 | chr2 | unknown | gene | 112631381 | 113030331 | - | Ryr3 | Ryr3 | P11447 | NM_177652 | TSS3652 |
| chr2 | 113140042 | 113140133 | MACS2_peak_1665 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 62 | chr2 | unknown | gene | 113220186 | 113423560 | + | Mir1954 | Mir1954 |  | NR_035479 | TSS15657 |
| chr2 | 113149243 | 113149395 | MACS2_peak_1666 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 61 | chr2 | unknown | gene | 112631381 | 113030331 | - | Ryr3 | Ryr3 | P11447 | NM_177652 | TSS3652 |
| chr2 | 113149243 | 113149395 | MACS2_peak_1666 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 61 | chr2 | unknown | gene | 113220186 | 113423560 | + | Mir1954 | Mir1954 |  | NR_035479 | TSS15657 |
| chr2 | 113330384 | 113330475 | MACS2_peak_1667 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 43 | chr2 | unknown | gene | 113285731 | 113297009 | + | Tmco5b | Tmco5b | P3520 | NM_029232 | TSS14069 |
| chr2 | 113330384 | 113330475 | MACS2_peak_1667 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 43 | chr2 | unknown | gene | 113691052 | 113708550 | - | 4930533B01Rik | 4930533B01Rik |  | NR_040614 | TSS4269 |
| chr2 | 114049807 | 114049898 | MACS2_peak_1668 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 30 | chr2 | unknown | gene | 114013564 | 114032292 | + | A530058N18Rik | A530058N18Rik |  | NR_028423 | TSS10354 |
| chr2 | 114049807 | 114049898 | MACS2_peak_1668 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 30 | chr2 | unknown | gene | 114054395 | 114061502 | + | C130080G10Rik | C130080G10Rik |  | NR_028422 | TSS12047 |
| chr2 | 114224433 | 114224524 | MACS2_peak_1669 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 8 | chr2 | unknown | gene | 114193460 | 114201432 | - | Zfp770 | Zfp770 | P815 | NM_175466 | TSS8894 |
| chr2 | 114224433 | 114224524 | MACS2_peak_1669 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 8 | chr2 | unknown | gene | 114516417 | 114654853 | - | Dph6 | Dph6 | P2383 | NM_025675 | TSS2223 |
| chr2 | 114389030 | 114389121 | MACS2_peak_1670 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 21 | chr2 | unknown | gene | 114193460 | 114201432 | - | Zfp770 | Zfp770 | P815 | NM_175466 | TSS8894 |
| chr2 | 114389030 | 114389121 | MACS2_peak_1670 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 21 | chr2 | unknown | gene | 114516417 | 114654853 | - | Dph6 | Dph6 | P2383 | NM_025675 | TSS2223 |
| chr2 | 114624188 | 114624279 | MACS2_peak_1671 | 22 | + | 5.20528 | 6.973 | 2.25118 | 16 | chr2 | unknown | gene | 114193460 | 114201432 | - | Zfp770 | Zfp770 | P815 | NM_175466 | TSS8894 |
| chr2 | 114624188 | 114624279 | MACS2_peak_1671 | 22 | + | 5.20528 | 6.973 | 2.25118 | 16 | chr2 | unknown | gene | 115329265 | 115344280 | - | 4930528P14Rik | 4930528P14Rik |  | NR_040516 | TSS14948 |
| chr2 | 114793464 | 114793555 | MACS2_peak_1672 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 35 | chr2 | unknown | gene | 114516417 | 114654853 | - | Dph6 | Dph6 | P2383 | NM_025675 | TSS2223 |
| chr2 | 114793464 | 114793555 | MACS2_peak_1672 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 35 | chr2 | unknown | gene | 115329265 | 115344280 | - | 4930528P14Rik | 4930528P14Rik |  | NR_040516 | TSS14948 |
| chr2 | 115397001 | 115397092 | MACS2_peak_1673 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 47 | chr2 | unknown | gene | 115329265 | 115344280 | - | 4930528P14Rik | 4930528P14Rik |  | NR_040516 | TSS14948 |
| chr2 | 115397001 | 115397092 | MACS2_peak_1673 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 47 | chr2 | unknown | gene | 115493512 | 115512201 | - | 3110099E03Rik | 3110099E03Rik |  | NR_030712 | TSS11735 |
| chr2 | 115531695 | 115531786 | MACS2_peak_1674 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 15 | chr2 | unknown | gene | 115493512 | 115512201 | - | 3110099E03Rik | 3110099E03Rik |  | NR_030712 | TSS11735 |
| chr2 | 115531695 | 115531786 | MACS2_peak_1674 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 15 | chr2 | unknown | gene | 115581715 | 115777031 | + | BC052040 | BC052040 | P9181 | NM_207264 | TSS23020 |
| chr2 | 115702092 | 115702183 | MACS2_peak_1675 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 23 | chr2 | unknown | gene | 115638724 | 115638813 | + | Mir1951 | Mir1951 |  | NR_035476 | TSS18086 |
| chr2 | 115702092 | 115702183 | MACS2_peak_1675 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 23 | chr2 | unknown | gene | 115861263 | 116064813 | - | Meis2 | Meis2 | P26205 | NM_001159568 | TSS5313 |
| chr2 | 115766065 | 115766199 | MACS2_peak_1676 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 81 | chr2 | unknown | gene | 115638724 | 115638813 | + | Mir1951 | Mir1951 |  | NR_035476 | TSS18086 |
| chr2 | 115766065 | 115766199 | MACS2_peak_1676 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 81 | chr2 | unknown | gene | 115861263 | 116064813 | - | Meis2 | Meis2 | P26205 | NM_001159568 | TSS5313 |
| chr2 | 115802724 | 115802857 | MACS2_peak_1677 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 46 | chr2 | unknown | gene | 115581715 | 115777031 | + | BC052040 | BC052040 | P9181 | NM_207264 | TSS23020 |
| chr2 | 115802724 | 115802857 | MACS2_peak_1677 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 46 | chr2 | unknown | gene | 115861263 | 116064813 | - | Meis2 | Meis2 | P26205 | NM_001159568 | TSS5313 |
| chr2 | 115845357 | 115845469 | MACS2_peak_1678 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 50 | chr2 | unknown | gene | 115581715 | 115777031 | + | BC052040 | BC052040 | P9181 | NM_207264 | TSS23020 |
| chr2 | 115845357 | 115845469 | MACS2_peak_1678 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 50 | chr2 | unknown | gene | 115861263 | 116064813 | - | Meis2 | Meis2 | P26205 | NM_001159568 | TSS5313 |
| chr2 | 115929953 | 115930044 | MACS2_peak_1679 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 43 | chr2 | unknown | gene | 115581715 | 115777031 | + | BC052040 | BC052040 | P9181 | NM_207264 | TSS23020 |
| chr2 | 115929953 | 115930044 | MACS2_peak_1679 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 43 | chr2 | unknown | gene | 116074547 | 116076096 | - | 2810405F15Rik | 2810405F15Rik |  | NR_033447 | TSS7356 |
| chr2 | 116090189 | 116090362 | MACS2_peak_1680 | 12 | + | 4.14966 | 5.12722 | 1.204 | 155 | chr2 | unknown | gene | 116074547 | 116076096 | - | 2810405F15Rik | 2810405F15Rik |  | NR_033447 | TSS7356 |
| chr2 | 116090189 | 116090362 | MACS2_peak_1680 | 12 | + | 4.14966 | 5.12722 | 1.204 | 155 | chr2 | unknown | gene | 116878690 | 116892311 | + | Tmco5 | Tmco5 | P21587 | NM_026104 | TSS15264 |
| chr2 | 116885524 | 116885615 | MACS2_peak_1681 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 39 | chr2 | unknown | gene | 116074547 | 116076096 | - | 2810405F15Rik | 2810405F15Rik |  | NR_033447 | TSS7356 |
| chr2 | 116885524 | 116885615 | MACS2_peak_1681 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 39 | chr2 | unknown | gene | 116900151 | 116912791 | + | D330050G23Rik | D330050G23Rik |  | NR_040335 | TSS16763 |
| chr2 | 117145476 | 117145567 | MACS2_peak_1682 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 30 | chr2 | unknown | gene | 116900151 | 116912791 | + | D330050G23Rik | D330050G23Rik |  | NR_040335 | TSS16763 |
| chr2 | 117145476 | 117145567 | MACS2_peak_1682 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 30 | chr2 | unknown | gene | 117185126 | 117185226 | + | Mir674 | Mir674 |  | NR_030440 | TSS17156 |
| chr2 | 117445093 | 117445205 | MACS2_peak_1683 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 77 | chr2 | unknown | gene | 117279992 | 117342709 | - | Rasgrp1 | Rasgrp1 | P4451 | NM_011246 | TSS6373 |
| chr2 | 117445093 | 117445205 | MACS2_peak_1683 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 77 | chr2 | unknown | gene | 117804648 | 117812802 | - | Gm13985 | Gm13985 |  | NR_126427 | TSS11901 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr2 | 117731758 | 117731949 | MACS2_peak_1684 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 32 | chr2 | unknown | gene | 117279992 | 117342709 | - | Rasgrp1 | Rasgrp1 | P4451 | NM_011246 | TSS6373 |
| chr2 | 117731758 | 117731949 | MACS2_peak_1684 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 32 | chr2 | unknown | gene | 117804648 | 117812802 | - | Gm13985 | Gm13985 | | NR_126427 | TSS11901 |
| chr2 | 118013658 | 118013749 | MACS2_peak_1685 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 48 | chr2 | unknown | gene | 117821927 | 117909136 | + | 4930412B13Rik | 4930412B13Rik | | NR_040631 | TSS3462 |
| chr2 | 118013658 | 118013749 | MACS2_peak_1685 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 48 | chr2 | unknown | gene | 118111921 | 118125029 | + | Thbs1 | Thbs1 | P21703 | NM_011580 | TSS4561 |
| chr2 | 118029712 | 118029803 | MACS2_peak_1686 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 57 | chr2 | unknown | gene | 117821927 | 117909136 | + | 4930412B13Rik | 4930412B13Rik | | NR_040631 | TSS3462 |
| chr2 | 118029712 | 118029803 | MACS2_peak_1686 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 57 | chr2 | unknown | gene | 118111921 | 118125029 | + | Thbs1 | Thbs1 | P21703 | NM_011580 | TSS4561 |
| chr2 | 118660639 | 118660730 | MACS2_peak_1687 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 13 | chr2 | unknown | gene | 118598210 | 118641319 | + | Bub1b | Bub1b | P17675 | NM_009773 | TSS19116 |
| chr2 | 118660639 | 118660730 | MACS2_peak_1687 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 13 | chr2 | unknown | gene | 118663576 | 118696574 | + | Pak6 | Pak6 | P25605 | NM_001033254 | TSS13973 |
| chr2 | 119046616 | 119046707 | MACS2_peak_1688 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 31 | chr2 | unknown | gene | 119034789 | 119038759 | + | Rpusd2 | Rpusd2 | P17802 | NM_173450 | TSS27322 |
| chr2 | 119046616 | 119046707 | MACS2_peak_1688 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 31 | chr2 | unknown | gene | 119047118 | 119104077 | + | Casc5 | Casc5 | P12440 | NM_029617 | TSS7325 |
| chr2 | 119455588 | 119455701 | MACS2_peak_1689 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 34 | chr2 | unknown | gene | 119351241 | 119353590 | + | Chac1 | Chac1 | P7084 | NM_026929 | TSS20881 |
| chr2 | 119455588 | 119455701 | MACS2_peak_1689 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 34 | chr2 | unknown | gene | 119519403 | 119547627 | - | Exd1 | Exd1 | P9451 | NM_172857 | TSS15520 |
| chr2 | 119727072 | 119727163 | MACS2_peak_1690 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 24 | chr2 | unknown | gene | 119655450 | 119662798 | - | Ndufaf1 | Ndufaf1 | P2655 | NM_027175 | TSS21906 |
| chr2 | 119727072 | 119727163 | MACS2_peak_1690 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 24 | chr2 | unknown | gene | 119742336 | 119750867 | + | Itpka | Itpka | P8764 | NM_146125 | TSS226 |
| chr2 | 120094485 | 120094576 | MACS2_peak_1691 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 63 | chr2 | unknown | gene | 120027482 | 120043032 | + | Gm28042 | Gm28042 | | NR_104353 | TSS10116 |
| chr2 | 120094485 | 120094576 | MACS2_peak_1691 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 63 | chr2 | unknown | gene | 120166411 | 120244907 | - | Pla2g4e | Pla2g4e | P1738 | NM_177845 | TSS13556 |
| chr2 | 123096196 | 123096354 | MACS2_peak_1692 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 151 | chr2 | unknown | gene | 122765358 | 122809338 | + | Sqrdl | Sqrdl | P19350 | NM_001162503 | TSS23635 |
| chr2 | 123096196 | 123096354 | MACS2_peak_1692 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 151 | chr2 | unknown | gene | 124089968 | 124665309 | + | Sema6d | Sema6d | P23889 | NM_001290997 | TSS4577 |
| chr2 | 123526072 | 123526163 | MACS2_peak_1693 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 51 | chr2 | unknown | gene | 122765358 | 122809338 | + | Sqrdl | Sqrdl | P19350 | NM_001162503 | TSS23635 |
| chr2 | 123526072 | 123526163 | MACS2_peak_1693 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 51 | chr2 | unknown | gene | 124089968 | 124665309 | + | Sema6d | Sema6d | P23889 | NM_001290997 | TSS4577 |
| chr2 | 123931850 | 123931950 | MACS2_peak_1694 | 45 | + | 6.59824 | 9.65189 | 4.58689 | 55 | chr2 | unknown | gene | 122765358 | 122809338 | + | Sqrdl | Sqrdl | P19350 | NM_001162503 | TSS23635 |
| chr2 | 123931850 | 123931950 | MACS2_peak_1694 | 45 | + | 6.59824 | 9.65189 | 4.58689 | 55 | chr2 | unknown | gene | 124089968 | 124665309 | + | Sema6d | Sema6d | P23889 | NM_001290997 | TSS4577 |
| chr2 | 125847318 | 125847409 | MACS2_peak_1695 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 40 | chr2 | unknown | gene | 125736985 | 125782622 | - | Secisbp2l | Secisbp2l | P3787 | NM_177608 | TSS16974 |
| chr2 | 125847318 | 125847409 | MACS2_peak_1695 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 40 | chr2 | unknown | gene | 125859108 | 125983262 | + | Galk2 | Galk2 | P10552 | NM_175154 | TSS10012 |
| chr2 | 126147835 | 126147985 | MACS2_peak_1696 | 189 | + | 13.04591 | 24.4735 | 18.9217 | 76 | chr2 | unknown | gene | 126034657 | 126089561 | + | Fgf7 | Fgf7 | P11613 | NM_008008 | TSS9413 |
| chr2 | 126147835 | 126147985 | MACS2_peak_1696 | 189 | + | 13.04591 | 24.4735 | 18.9217 | 76 | chr2 | unknown | gene | 126152140 | 126164974 | + | Dtwd1 | Dtwd1 | P1409 | NM_026981 | TSS26308 |
| chr2 | 126721023 | 126721114 | MACS2_peak_1697 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 36 | chr2 | unknown | gene | 126628906 | 126676337 | - | Gabpb1 | Gabpb1 | P17688 | NM_001271469 | TSS10237 |
| chr2 | 126721023 | 126721114 | MACS2_peak_1697 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 36 | chr2 | unknown | gene | 126761049 | 126783287 | - | Usp50 | Usp50 | P3163 | NM_029163 | TSS21029 |
| chr2 | 127887186 | 127887316 | MACS2_peak_1698 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 59 | chr2 | unknown | gene | 127800199 | 127831745 | - | Bub1 | Bub1 | P15444 | NM_009772 | TSS21157 |
| chr2 | 127887186 | 127887316 | MACS2_peak_1698 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 59 | chr2 | unknown | gene | 128126037 | 128158329 | + | Bcl2l11 | Bcl2l11 | P16594 | NM_207680 | TSS7857 |
| chr2 | 128097077 | 128097185 | MACS2_peak_1699 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 41 | chr2 | unknown | gene | 127800199 | 127831745 | - | Bub1 | Bub1 | P15444 | NM_009772 | TSS21157 |
| chr2 | 128097077 | 128097185 | MACS2_peak_1699 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 41 | chr2 | unknown | gene | 128126037 | 128158329 | + | Bcl2l11 | Bcl2l11 | P16594 | NM_207680 | TSS7857 |
| chr2 | 128339772 | 128339869 | MACS2_peak_1700 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 70 | chr2 | unknown | gene | 128126037 | 128158329 | + | Bcl2l11 | Bcl2l11 | P16594 | NM_207680 | TSS7857 |
| chr2 | 128339772 | 128339869 | MACS2_peak_1700 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 70 | chr2 | unknown | gene | 128610082 | 128687395 | - | Anapc1 | Anapc1 | P222 | NM_008569 | TSS25052 |
| chr2 | 128344587 | 128344678 | MACS2_peak_1701 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 20 | chr2 | unknown | gene | 128126037 | 128158329 | + | Bcl2l11 | Bcl2l11 | P16594 | NM_207680 | TSS7857 |
| chr2 | 128344587 | 128344678 | MACS2_peak_1701 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 20 | chr2 | unknown | gene | 128610082 | 128687395 | - | Anapc1 | Anapc1 | P222 | NM_008569 | TSS25052 |
| chr2 | 130205343 | 130205434 | MACS2_peak_1702 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 49 | chr2 | unknown | gene | 130171635 | 130179236 | - | Snrpb | Snrpb | P12733 | NM_009225 | TSS21856 |
| chr2 | 130205343 | 130205434 | MACS2_peak_1702 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 49 | chr2 | unknown | gene | 130274411 | 130279223 | + | Nop56 | Nop56 | P22614 | NM_024193 | TSS1638 |
| chr2 | 130506366 | 130506515 | MACS2_peak_1703 | 44 | + | 6.51136 | 9.46827 | 4.41032 | 70 | chr2 | unknown | gene | 130424319 | 130443658 | + | Vps16 | Vps16 | P15902 | NM_030559 | TSS10356 |
| chr2 | 130506366 | 130506515 | MACS2_peak_1703 | 44 | + | 6.51136 | 9.46827 | 4.41032 | 70 | chr2 | unknown | gene | 130543790 | 130563749 | - | 4930473A02Rik | 4930473A02Rik | | NR_040348 | TSS18917 |
| chr2 | 131789678 | 131789769 | MACS2_peak_1704 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 53 | chr2 | unknown | gene | 131142468 | 131604824 | - | Mir3098 | Mir3098 | | NR_037281 | TSS25198 |
| chr2 | 131789678 | 131789769 | MACS2_peak_1704 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 53 | chr2 | unknown | gene | 131820005 | 131847656 | - | 5330413P13Rik | 5330413P13Rik | | NR_029381 | TSS17680 |
| chr2 | 131799931 | 131800057 | MACS2_peak_1705 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 81 | chr2 | unknown | gene | 131142468 | 131604824 | - | Mir3098 | Mir3098 | | NR_037281 | TSS25198 |
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| chr2 | 133755811 | 133755930 | MACS2_peak_1706 | 12 | + | 4.14966 | 5.12722 | 1.204 | 35 | chr2 | unknown | gene | 133564707 | 133564794 | + | Mir3090 | Mir3090 | | NR_037273 | TSS19479 |
| chr2 | 133755811 | 133755930 | MACS2_peak_1706 | 12 | + | 4.14966 | 5.12722 | 1.204 | 35 | chr2 | unknown | gene | 134497360 | 134554332 | - | Hao1 | Hao1 | P10788 | NM_010403 | TSS5168 |
| chr2 | 134388910 | 134389014 | MACS2_peak_1707 | 24 | + | 5.43036 | 7.38735 | 2.49399 | 67 | chr2 | unknown | gene | 133564707 | 133564794 | + | Mir3090 | Mir3090 | | NR_037273 | TSS19479 |
| chr2 | 134388910 | 134389014 | MACS2_peak_1707 | 24 | + | 5.43036 | 7.38735 | 2.49399 | 67 | chr2 | unknown | gene | 134497360 | 134554332 | - | Hao1 | Hao1 | P10788 | NM_010403 | TSS5168 |
| chr2 | 134675945 | 134676044 | MACS2_peak_1708 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 73 | chr2 | unknown | gene | 134594501 | 134644005 | - | Tmx4 | Tmx4 | P26526 | NM_029148 | TSS25697 |
| chr2 | 134675945 | 134676044 | MACS2_peak_1708 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 73 | chr2 | unknown | gene | 134786163 | 135472280 | + | Plcb1 | Plcb1 | P17988 | NM_019677 | TSS15844 |
| chr2 | 134681649 | 134681740 | MACS2_peak_1709 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 28 | chr2 | unknown | gene | 134594501 | 134644005 | - | Tmx4 | Tmx4 | P26526 | NM_029148 | TSS25697 |
| chr2 | 134681649 | 134681740 | MACS2_peak_1709 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 28 | chr2 | unknown | gene | 134786163 | 135472280 | + | Plcb1 | Plcb1 | P17988 | NM_019677 | TSS15844 |
| chr2 | 135326150 | 135326249 | MACS2_peak_1710 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 80 | chr2 | unknown | gene | 135169572 | 135215616 | - | 4930545L23Rik | 4930545L23Rik | | NR_040517 | TSS18902 |
| chr2 | 135326150 | 135326249 | MACS2_peak_1710 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 80 | chr2 | unknown | gene | 135405829 | 135405850 | + | Mir3963 | Mir3963 | | NR_039540 | TSS16229 |
| chr2 | 135837332 | 135837477 | MACS2_peak_1711 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 70 | chr2 | unknown | gene | 135580529 | 135583220 | - | 9630028H03Rik | 9630028H03Rik | | NR_015544 | TSS12764 |
| chr2 | 135837332 | 135837477 | MACS2_peak_1711 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 70 | chr2 | unknown | gene | 136057926 | 136069191 | + | Lamp5 | Lamp5 | P21708 | NM_029530 | TSS17808 |
| chr2 | 136993912 | 136994003 | MACS2_peak_1712 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 39 | chr2 | unknown | gene | 136873780 | 136891406 | - | Mkks | Mkks | P26116 | NM_021527 | TSS575 |
| chr2 | 136993912 | 136994003 | MACS2_peak_1712 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 39 | chr2 | unknown | gene | 137081450 | 137116257 | - | Jag1 | Jag1 | P16815 | NM_013822 | TSS15805 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr2 | 137752443 | 137752534 | MACS2_peak_1713 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 41 | chr2 | unknown | gene | 137081450 | 137116257 | - | Jag1 | Jag1 | P16815 | NM_013822 | TSS15805 |
| chr2 | 137752443 | 137752534 | MACS2_peak_1713 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 41 | chr2 | unknown | gene | 138256583 | 138284490 | + | Btbd3 | Btbd3 | P3988 | NM_001025431 | TSS24206 |
| chr2 | 137757362 | 137757528 | MACS2_peak_1714 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 83 | chr2 | unknown | gene | 137081450 | 137116257 | - | Jag1 | Jag1 | P16815 | NM_013822 | TSS15805 |
| chr2 | 137757362 | 137757528 | MACS2_peak_1714 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 83 | chr2 | unknown | gene | 138256583 | 138284490 | + | Btbd3 | Btbd3 | P3988 | NM_001025431 | TSS24206 |
| chr2 | 138502997 | 138503152 | MACS2_peak_1715 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 89 | chr2 | unknown | gene | 138256583 | 138284490 | + | Btbd3 | Btbd3 | P3988 | NM_001025431 | TSS24206 |
| chr2 | 138502997 | 138503152 | MACS2_peak_1715 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 89 | chr2 | unknown | gene | 138819928 | 138820007 | + | Mir1952 | Mir1952 | | NR_035477 | TSS25212 |
| chr2 | 138667359 | 138667450 | MACS2_peak_1716 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 46 | chr2 | unknown | gene | 138256583 | 138284490 | + | Btbd3 | Btbd3 | P3988 | NM_001025431 | TSS24206 |
| chr2 | 138667359 | 138667450 | MACS2_peak_1716 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 46 | chr2 | unknown | gene | 138819928 | 138820007 | + | Mir1952 | Mir1952 | | NR_035477 | TSS25212 |
| chr2 | 139043050 | 139043141 | MACS2_peak_1717 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 74 | chr2 | unknown | gene | 138819928 | 138820007 | + | Mir1952 | Mir1952 | | NR_035477 | TSS25212 |
| chr2 | 139043050 | 139043141 | MACS2_peak_1717 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 74 | chr2 | unknown | gene | 139493919 | 139636814 | + | Sptlc3 | Sptlc3 | P20031 | NM_175467 | TSS22926 |
| chr2 | 140474121 | 140474223 | MACS2_peak_1718 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 32 | chr2 | unknown | gene | 140229857 | 140389632 | - | Sel1l2 | Sel1l2 | P16318 | NM_001033296 | TSS18253 |
| chr2 | 140474121 | 140474223 | MACS2_peak_1718 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 32 | chr2 | unknown | gene | 140658197 | 140671476 | - | Flrt3 | Flrt3 | P2636 | NM_178382 | TSS10989 |
| chr2 | 140934304 | 140934541 | MACS2_peak_1719 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 227 | chr2 | unknown | gene | 140658197 | 140671476 | - | Flrt3 | Flrt3 | P2636 | NM_178382 | TSS10989 |
| chr2 | 140934304 | 140934541 | MACS2_peak_1719 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 227 | chr2 | unknown | gene | 142618344 | 142901371 | - | Kif16b | Kif16b | P10827 | NM_001081133 | TSS13418 |
| chr2 | 141496687 | 141496778 | MACS2_peak_1720 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 49 | chr2 | unknown | gene | 140658197 | 140671476 | - | Flrt3 | Flrt3 | P2636 | NM_178382 | TSS10989 |
| chr2 | 141496687 | 141496778 | MACS2_peak_1720 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 49 | chr2 | unknown | gene | 142618344 | 142901371 | - | Kif16b | Kif16b | P10827 | NM_001081133 | TSS13418 |
| chr2 | 142071117 | 142071254 | MACS2_peak_1721 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 90 | chr2 | unknown | gene | 140658197 | 140671476 | - | Flrt3 | Flrt3 | P2636 | NM_178382 | TSS10989 |
| chr2 | 142071117 | 142071254 | MACS2_peak_1721 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 90 | chr2 | unknown | gene | 142618344 | 142901371 | - | Kif16b | Kif16b | P10827 | NM_001081133 | TSS13418 |
| chr2 | 142458181 | 142458292 | MACS2_peak_1722 | 24 | + | 5.39702 | 7.32466 | 2.43395 | 74 | chr2 | unknown | gene | 140395429 | 142390050 | + | Macrod2 | Macrod2 | P20499 | NM_001013802 | TSS3329 |
| chr2 | 142458181 | 142458292 | MACS2_peak_1722 | 24 | + | 5.39702 | 7.32466 | 2.43395 | 74 | chr2 | unknown | gene | 142618344 | 142901371 | - | Kif16b | Kif16b | P10827 | NM_001081133 | TSS13418 |
| chr2 | 142582297 | 142582388 | MACS2_peak_1723 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 20 | chr2 | unknown | gene | 140395429 | 142390050 | + | Macrod2 | Macrod2 | P20499 | NM_001013802 | TSS3329 |
| chr2 | 142582297 | 142582388 | MACS2_peak_1723 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 20 | chr2 | unknown | gene | 142618344 | 142901371 | - | Kif16b | Kif16b | P10827 | NM_001081133 | TSS13418 |
| chr2 | 143033378 | 143033469 | MACS2_peak_1724 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 51 | chr2 | unknown | gene | 142902964 | 142903572 | + | Kif16bos | Kif16bos | | NR_131921 | TSS11181 |
| chr2 | 143033378 | 143033469 | MACS2_peak_1724 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 51 | chr2 | unknown | gene | 143063068 | 143071555 | + | Snrpb2 | Snrpb2 | P14724 | NM_021335 | TSS3146 |
| chr2 | 144562779 | 144562870 | MACS2_peak_1725 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 6 | chr2 | unknown | gene | 144542264 | 144550778 | - | Rbbp9 | Rbbp9 | P9255 | NM_015754 | TSS3308 |
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| chr2 | 145387265 | 145387356 | MACS2_peak_1726 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 65 | chr2 | unknown | gene | 144823665 | 144824213 | + | Scp2d1 | Scp2d1 | P23894 | NM_025490 | TSS23883 |
| chr2 | 145387265 | 145387356 | MACS2_peak_1726 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 65 | chr2 | unknown | gene | 145549454 | 145554853 | - | Gm14092 | Gm14092 | P2277 | NM_001037929 | TSS27039 |
| chr2 | 145866378 | 145866513 | MACS2_peak_1727 | 44 | + | 6.55451 | 9.55892 | 4.49773 | 66 | chr2 | unknown | gene | 145701194 | 145753672 | + | BC039771 | BC039771 | | NR_033220 | TSS19915 |
| chr2 | 145866378 | 145866513 | MACS2_peak_1727 | 44 | + | 6.55451 | 9.55892 | 4.49773 | 66 | chr2 | unknown | gene | 145903240 | 145915889 | + | Naa20 | Naa20 | P2560 | NM_026425 | TSS13325 |
| chr2 | 147040426 | 147040572 | MACS2_peak_1728 | 56 | + | 7.18752 | 10.78892 | 5.67026 | 73 | chr2 | unknown | gene | 146855888 | 146970060 | + | Kiz | Kiz | P3453 | NM_001033298 | TSS21209 |
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| chr2 | 148151568 | 148151699 | MACS2_peak_1729 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 54 | chr2 | unknown | gene | 148042876 | 148046969 | - | Foxa2 | Foxa2 | P1878 | NM_001291065 | TSS1609 |
| chr2 | 148151568 | 148151699 | MACS2_peak_1729 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 54 | chr2 | unknown | gene | 148395376 | 148396628 | + | Sstr4 | Sstr4 | P15096 | NM_009219 | TSS7958 |
| chr2 | 148236341 | 148236447 | MACS2_peak_1730 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 86 | chr2 | unknown | gene | 148042876 | 148046969 | - | Foxa2 | Foxa2 | P1878 | NM_001291065 | TSS1609 |
| chr2 | 148236341 | 148236447 | MACS2_peak_1730 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 86 | chr2 | unknown | gene | 148395376 | 148396628 | + | Sstr4 | Sstr4 | P15096 | NM_009219 | TSS7958 |
| chr2 | 148294445 | 148294536 | MACS2_peak_1731 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 34 | chr2 | unknown | gene | 148042876 | 148046969 | - | Foxa2 | Foxa2 | P1878 | NM_001291065 | TSS1609 |
| chr2 | 148294445 | 148294536 | MACS2_peak_1731 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 34 | chr2 | unknown | gene | 148395376 | 148396628 | + | Sstr4 | Sstr4 | P15096 | NM_009219 | TSS7958 |
| chr2 | 148337065 | 148337232 | MACS2_peak_1732 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 78 | chr2 | unknown | gene | 148042876 | 148046969 | - | Foxa2 | Foxa2 | P1878 | NM_001291065 | TSS1609 |
| chr2 | 148337065 | 148337232 | MACS2_peak_1732 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 78 | chr2 | unknown | gene | 148395376 | 148396628 | + | Sstr4 | Sstr4 | P15096 | NM_009219 | TSS7958 |
| chr2 | 148643466 | 148643557 | MACS2_peak_1733 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 62 | chr2 | unknown | gene | 148436650 | 148443424 | - | Cd93 | Cd93 | P15080 | NM_010740 | TSS4631 |
| chr2 | 148643466 | 148643557 | MACS2_peak_1733 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 62 | chr2 | unknown | gene | 148672614 | 148675763 | + | Nxt1 | Nxt1 | P18661 | NM_019761 | TSS9381 |
| chr2 | 148778790 | 148778907 | MACS2_peak_1734 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 49 | chr2 | unknown | gene | 148768617 | 148771403 | - | Cst11 | Cst11 | P418 | NM_030059 | TSS3155 |
| chr2 | 148778790 | 148778907 | MACS2_peak_1734 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 49 | chr2 | unknown | gene | 148782008 | 148785827 | + | 8030411F24Rik | 8030411F24Rik | P2393 | NM_030135 | TSS21243 |
| chr2 | 149091771 | 149091862 | MACS2_peak_1735 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 46 | chr2 | unknown | gene | 148871731 | 148875377 | - | Cst3 | Cst3 | P7600 | NM_009976 | TSS20111 |
| chr2 | 149091771 | 149091862 | MACS2_peak_1735 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 46 | chr2 | unknown | gene | 149405248 | 149410053 | + | Cst10 | Cst10 | P6017 | NM_021405 | TSS24675 |
| chr2 | 150416758 | 150416849 | MACS2_peak_1736 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 22 | chr2 | unknown | gene | 150310936 | 150362644 | - | 3300002I08Rik | 3300002I08Rik | P20931 | NM_027017 | TSS19554 |
| chr2 | 150416758 | 150416849 | MACS2_peak_1736 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 22 | chr2 | unknown | gene | 150470990 | 150484982 | - | Zfp345 | Zfp345 | P4677 | NM_001034900 | TSS4551 |
| chr2 | 153018719 | 153018854 | MACS2_peak_1737 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 85 | chr2 | unknown | gene | 153008889 | 153015320 | - | Pdrg1 | Pdrg1 | P23344 | NM_178939 | TSS29 |
| chr2 | 153018719 | 153018854 | MACS2_peak_1737 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 85 | chr2 | unknown | gene | 153031851 | 153054970 | + | Xkr7 | Xkr7 | P86 | NM_001011732 | TSS20003 |
| chr2 | 153172757 | 153172848 | MACS2_peak_1738 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 63 | chr2 | unknown | gene | 153108467 | 153151149 | + | Hck | Hck | P24953 | NM_010407 | TSS22414 |
| chr2 | 153172757 | 153172848 | MACS2_peak_1738 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 63 | chr2 | unknown | gene | 153222369 | 153225316 | - | Tspyl3 | Tspyl3 | P18565 | NM_198617 | TSS26827 |
| chr2 | 154849055 | 154849231 | MACS2_peak_1739 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 90 | chr2 | unknown | gene | 154657025 | 154694008 | + | Chmp4b | Chmp4b | P19163 | NM_029362 | TSS5678 |
| chr2 | 154849055 | 154849231 | MACS2_peak_1739 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 90 | chr2 | unknown | gene | 154871409 | 154892704 | - | Eif2s2 | Eif2s2 | P12038 | NM_026030 | TSS11714 |
| chr2 | 155873599 | 155873787 | MACS2_peak_1740 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 51 | chr2 | unknown | gene | 155829182 | 155834848 | - | Fam83c | Fam83c | P9193 | NM_027788 | TSS21526 |
| chr2 | 155873599 | 155873787 | MACS2_peak_1740 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 51 | chr2 | unknown | gene | 155941024 | 155945055 | - | Gdf5 | Gdf5 | P18013 | NM_008109 | TSS25232 |
| chr2 | 157668074 | 157668165 | MACS2_peak_1741 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 54 | chr2 | unknown | gene | 157556361 | 157566361 | - | Blcap | Blcap | P5026 | NM_016916 | TSS18096 |
| chr2 | 157668074 | 157668165 | MACS2_peak_1741 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 54 | chr2 | unknown | gene | 157737400 | 157890993 | + | Ctnnbl1 | Ctnnbl1 | P15652 | NM_025680 | TSS3375 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr2 | 160672199 | 160672290 | MACS2_peak_1742 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 17 | chr2 | unknown | gene | 160363676 | 160366676 | - | Mafb | Mafb | P2851 | NM_010658 | TSS19528 |
| chr2 | 160672199 | 160672290 | MACS2_peak_1742 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 17 | chr2 | unknown | gene | 160731309 | 160775368 | + | Plcg1 | Plcg1 | P25950 | NM_021280 | TSS18999 |
| chr2 | 161076145 | 161076297 | MACS2_peak_1743 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 82 | chr2 | unknown | gene | 160906437 | 160912171 | - | Emilin3 | Emilin3 | P7783 | NM_001291145 | TSS22630 |
| chr2 | 161076145 | 161076297 | MACS2_peak_1743 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 82 | chr2 | unknown | gene | 161521987 | 162660899 | - | Ptprt | Ptprt | P10613 | NM_001291149 | TSS4858 |
| chr2 | 161697313 | 161697404 | MACS2_peak_1744 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 86 | chr2 | unknown | gene | 160946977 | 161109086 | - | Chd6 | Chd6 | P11659 | NM_173368 | TSS23834 |
| chr2 | 161697313 | 161697404 | MACS2_peak_1744 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 86 | chr2 | unknown | gene | 162390812 | 162393946 | + | Ptprtos | Ptprtos |  | NR_040617 | TSS25163 |
| chr2 | 161777723 | 161777850 | MACS2_peak_1745 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 71 | chr2 | unknown | gene | 160946977 | 161109086 | - | Chd6 | Chd6 | P11659 | NM_173368 | TSS23834 |
| chr2 | 161777723 | 161777850 | MACS2_peak_1745 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 71 | chr2 | unknown | gene | 162390812 | 162393946 | + | Ptprtos | Ptprtos |  | NR_040617 | TSS25163 |
| chr2 | 162242864 | 162242955 | MACS2_peak_1746 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 74 | chr2 | unknown | gene | 160946977 | 161109086 | - | Chd6 | Chd6 | P11659 | NM_173368 | TSS23834 |
| chr2 | 162242864 | 162242955 | MACS2_peak_1746 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 74 | chr2 | unknown | gene | 162390812 | 162393946 | + | Ptprtos | Ptprtos |  | NR_040617 | TSS25163 |
| chr2 | 162281367 | 162281458 | MACS2_peak_1747 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 15 | chr2 | unknown | gene | 160946977 | 161109086 | - | Chd6 | Chd6 | P11659 | NM_173368 | TSS23834 |
| chr2 | 162281367 | 162281458 | MACS2_peak_1747 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 15 | chr2 | unknown | gene | 162390812 | 162393946 | + | Ptprtos | Ptprtos |  | NR_040617 | TSS25163 |
| chr2 | 162828144 | 162828237 | MACS2_peak_1748 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 26 | chr2 | unknown | gene | 162661162 | 162675204 | + | 9430021M05Rik | 9430021M05Rik |  | NR_033569 | TSS6459 |
| chr2 | 162828144 | 162828237 | MACS2_peak_1748 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 26 | chr2 | unknown | gene | 162931507 | 162934757 | + | Srsf6 | Srsf6 | P3585 | NM_026499 | TSS6323 |
| chr2 | 164698580 | 164698692 | MACS2_peak_1749 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 84 | chr2 | unknown | gene | 164685106 | 164686990 | + | Wfdc13 | Wfdc13 | P1449 | NM_001012704 | TSS21740 |
| chr2 | 164698580 | 164698692 | MACS2_peak_1749 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 84 | chr2 | unknown | gene | 164715304 | 164717983 | + | Spint5 | Spint5 | P24547 | NM_001040055 | TSS11710 |
| chr2 | 166332932 | 166333134 | MACS2_peak_1750 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 56 | chr2 | unknown | gene | 166273907 | 166294831 | + | Gm11468 | Gm11468 |  | NR_033467 | TSS22411 |
| chr2 | 166332932 | 166333134 | MACS2_peak_1750 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 56 | chr2 | unknown | gene | 166447450 | 166458770 | + | 5031425F14Rik | 5031425F14Rik |  | NR_015558 | TSS23031 |
| chr2 | 171796048 | 171796139 | MACS2_peak_1751 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 14 | chr2 | unknown | gene | 170731806 | 170879238 | + | Dok5 | Dok5 | P14875 | NM_029761 | TSS6483 |
| chr2 | 171796048 | 171796139 | MACS2_peak_1751 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 14 | chr2 | unknown | gene | 171956878 | 171962799 | - | 1700028P15Rik | 1700028P15Rik |  | NR_040509 | TSS6807 |
| chr2 | 171909148 | 171909243 | MACS2_peak_1752 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 29 | chr2 | unknown | gene | 170731806 | 170879238 | + | Dok5 | Dok5 | P14875 | NM_029761 | TSS6483 |
| chr2 | 171909148 | 171909243 | MACS2_peak_1752 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 29 | chr2 | unknown | gene | 171956878 | 171962799 | - | 1700028P15Rik | 1700028P15Rik |  | NR_040509 | TSS6807 |
| chr2 | 173350321 | 173350476 | MACS2_peak_1753 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 85 | chr2 | unknown | gene | 173224464 | 173276184 | - | Pmepa1 | Pmepa1 | P14494 | NM_022995 | TSS23042 |
| chr2 | 173350321 | 173350476 | MACS2_peak_1753 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 85 | chr2 | unknown | gene | 173522591 | 173528344 | + | 1700021F07Rik | 1700021F07Rik | P21538 | NM_028158 | TSS27178 |
| chr2 | 173694752 | 173694902 | MACS2_peak_1754 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 36 | chr2 | unknown | gene | 173579319 | 173659539 | - | Ppp4r1l-ps | Ppp4r1l-ps |  | NR_027957 | TSS12798 |
| chr2 | 173694752 | 173694902 | MACS2_peak_1754 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 36 | chr2 | unknown | gene | 173701029 | 173701148 | - | Mir6340 | Mir6340 |  | NR_105758 | TSS4153 |
| chr2 | 179877623 | 179877714 | MACS2_peak_1755 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 25 | chr2 | unknown | gene | 179414935 | 179416774 | + | 4930591A17Rik | 4930591A17Rik | P16968 | NM_026596 | TSS1662 |
| chr2 | 179877623 | 179877714 | MACS2_peak_1755 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 25 | chr2 | unknown | gene | 179912145 | 179976646 | - | Taf4a | Taf4a | P9366 | NM_001081092 | TSS4617 |
| chr2 | 181917800 | 181917927 | MACS2_peak_1756 | 27 | + | 5.55967 | 7.67698 | 2.76031 | 41 | chr2 | unknown | gene | 181864359 | 181868331 | + | Polr3k | Polr3k | P20200 | NM_025901 | TSS12071 |
| chr2 | 181917800 | 181917927 | MACS2_peak_1756 | 27 | + | 5.55967 | 7.67698 | 2.76031 | 41 | chr2 | unknown | gene | 181991225 | 182001087 | + | Gm14496 | Gm14496 | P11683 | NM_001205282 | TSS3160 |
| chr2 | 181930211 | 181930302 | MACS2_peak_1757 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 53 | chr2 | unknown | gene | 181864359 | 181868331 | + | Polr3k | Polr3k | P20200 | NM_025901 | TSS12071 |
| chr2 | 181930211 | 181930302 | MACS2_peak_1757 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 53 | chr2 | unknown | gene | 181991225 | 182001087 | + | Gm14496 | Gm14496 | P11683 | NM_001205282 | TSS3160 |
| chr3 | 4140454 | 4140545 | MACS2_peak_1758 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 10 | chr3 | unknown | gene | 3508029 | 3657176 | + | Hnf4g | Hnf4g | P23309 | NM_013920 | TSS5455 |
| chr3 | 4140454 | 4140545 | MACS2_peak_1758 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 10 | chr3 | unknown | gene | 4798707 | 4814911 | + | 1110015O18Rik | 1110015O18Rik |  | NR_045272 | TSS9879 |
| chr3 | 4641844 | 4641935 | MACS2_peak_1759 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 58 | chr3 | unknown | gene | 3508029 | 3657176 | + | Hnf4g | Hnf4g | P23309 | NM_013920 | TSS5455 |
| chr3 | 4641844 | 4641935 | MACS2_peak_1759 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 58 | chr3 | unknown | gene | 4798707 | 4814911 | + | 1110015O18Rik | 1110015O18Rik |  | NR_045272 | TSS9879 |
| chr3 | 7433083 | 7433179 | MACS2_peak_1760 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 56 | chr3 | unknown | gene | 6615412 | 6620392 | - | 1700008P02Rik | 1700008P02Rik | P11871 | NM_027048 | TSS10147 |
| chr3 | 7433083 | 7433179 | MACS2_peak_1760 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 56 | chr3 | unknown | gene | 7503425 | 7551548 | + | Zc2hc1a | Zc2hc1a | P2128 | NM_173181 | TSS17108 |
| chr3 | 9323890 | 9323981 | MACS2_peak_1761 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 47 | chr3 | unknown | gene | 9250566 | 9281033 | + | Zbtb10 | Zbtb10 | P25245 | NM_177660 | TSS3324 |
| chr3 | 9323890 | 9323981 | MACS2_peak_1761 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 47 | chr3 | unknown | gene | 9403077 | 9413903 | + | C030034L19Rik | C030034L19Rik |  | NR_015499 | TSS569 |
| chr3 | 9851991 | 9852082 | MACS2_peak_1762 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 46 | chr3 | unknown | gene | 9687481 | 9833679 | - | Pag1 | Pag1 | P4571 | NM_001195031 | TSS1398 |
| chr3 | 9851991 | 9852082 | MACS2_peak_1762 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 46 | chr3 | unknown | gene | 10012584 | 10016120 | + | Fabp5 | Fabp5 | P3858 | NM_010634 | TSS23676 |
| chr3 | 11095299 | 11095390 | MACS2_peak_1763 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 36 | chr3 | unknown | gene | 10417816 | 10440130 | - | Snx16 | Snx16 | P782 | NM_001127191 | TSS1294 |
| chr3 | 11095299 | 11095390 | MACS2_peak_1763 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 36 | chr3 | unknown | gene | 11823228 | 11844359 | - | Gm10745 | Gm10745 |  | NR_040751 | TSS14522 |
| chr3 | 11546450 | 11546587 | MACS2_peak_1764 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 65 | chr3 | unknown | gene | 10417816 | 10440130 | - | Snx16 | Snx16 | P782 | NM_001127191 | TSS1294 |
| chr3 | 11546450 | 11546587 | MACS2_peak_1764 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 65 | chr3 | unknown | gene | 11823228 | 11844359 | - | Gm10745 | Gm10745 |  | NR_040751 | TSS14522 |
| chr3 | 18213452 | 18213570 | MACS2_peak_1765 | 12 | + | 4.14966 | 5.12722 | 1.204 | 33 | chr3 | unknown | gene | 18054324 | 18055855 | + | Bhlhe22 | Bhlhe22 | P19192 | NM_021560 | TSS12013 |
| chr3 | 18213452 | 18213570 | MACS2_peak_1765 | 12 | + | 4.14966 | 5.12722 | 1.204 | 33 | chr3 | unknown | gene | 18468284 | 18480477 | - | 4930433B08Rik | 4930433B08Rik |  | NR_040544 | TSS25323 |
| chr3 | 18487848 | 18487994 | MACS2_peak_1766 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 62 | chr3 | unknown | gene | 18468284 | 18480477 | - | 4930433B08Rik | 4930433B08Rik |  | NR_040544 | TSS25323 |
| chr3 | 18487848 | 18487994 | MACS2_peak_1766 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 62 | chr3 | unknown | gene | 19132143 | 19163065 | - | Armc1 | Armc1 | P16337 | NM_028840 | TSS9112 |
| chr3 | 18725707 | 18725804 | MACS2_peak_1767 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 27 | chr3 | unknown | gene | 18468284 | 18480477 | - | 4930433B08Rik | 4930433B08Rik |  | NR_040544 | TSS25323 |
| chr3 | 18725707 | 18725804 | MACS2_peak_1767 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 27 | chr3 | unknown | gene | 19132143 | 19163065 | - | Armc1 | Armc1 | P16337 | NM_028840 | TSS9112 |
| chr3 | 18990833 | 18990964 | MACS2_peak_1768 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 86 | chr3 | unknown | gene | 18468284 | 18480477 | - | 4930433B08Rik | 4930433B08Rik |  | NR_040544 | TSS25323 |
| chr3 | 18990833 | 18990964 | MACS2_peak_1768 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 86 | chr3 | unknown | gene | 19132143 | 19163065 | - | Armc1 | Armc1 | P16337 | NM_028840 | TSS9112 |
| chr3 | 20127652 | 20127743 | MACS2_peak_1769 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 4 | chr3 | unknown | gene | 20057810 | 20118491 | + | Hltf | Hltf | P24999 | NM_009210 | TSS25458 |
| chr3 | 20127652 | 20127743 | MACS2_peak_1769 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 4 | chr3 | unknown | gene | 20215615 | 20242171 | - | Cpa3 | Cpa3 | P7379 | NM_007753 | TSS12073 |
| chr3 | 20353617 | 20353754 | MACS2_peak_1770 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 58 | chr3 | unknown | gene | 20249483 | 20275650 | - | Cpb1 | Cpb1 | P6662 | NM_029706 | TSS16868 |
| chr3 | 20353617 | 20353754 | MACS2_peak_1770 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 58 | chr3 | unknown | gene | 22076651 | 22210427 | + | Tbl1xr1 | Tbl1xr1 | P20296 | NM_030732 | TSS14625 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr3 | 20537403 | 20537494 | MACS2_peak_1771 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 65 | chr3 | unknown | gene | 20314472 | 20367177 | - | Agtr1b | Agtr1b | P8831 | NM_175086 | TSS12111 |
| chr3 | 20537403 | 20537494 | MACS2_peak_1771 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 65 | chr3 | unknown | gene | 22076651 | 22210427 | + | Tbl1xr1 | Tbl1xr1 | P20296 | NM_030732 | TSS14625 |
| chr3 | 20894318 | 20894409 | MACS2_peak_1772 | 24 | + | 5.43036 | 7.38735 | 2.49399 | 43 | chr3 | unknown | gene | 20314472 | 20367177 | - | Agtr1b | Agtr1b | P8831 | NM_175086 | TSS12111 |
| chr3 | 20894318 | 20894409 | MACS2_peak_1772 | 24 | + | 5.43036 | 7.38735 | 2.49399 | 43 | chr3 | unknown | gene | 22076651 | 22210427 | + | Tbl1xr1 | Tbl1xr1 | P20296 | NM_030732 | TSS14625 |
| chr3 | 21633904 | 21634032 | MACS2_peak_1773 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 41 | chr3 | unknown | gene | 20314472 | 20367177 | - | Agtr1b | Agtr1b | P8831 | NM_175086 | TSS12111 |
| chr3 | 21633904 | 21634032 | MACS2_peak_1773 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 41 | chr3 | unknown | gene | 22076651 | 22210427 | + | Tbl1xr1 | Tbl1xr1 | P20296 | NM_030732 | TSS14625 |
| chr3 | 24423228 | 24423319 | MACS2_peak_1774 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 18 | chr3 | unknown | gene | 22251369 | 22251607 | + | Rprl2 | Rprl2 | | NR_004439 | TSS14506 |
| chr3 | 24423228 | 24423319 | MACS2_peak_1774 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 18 | chr3 | unknown | gene | 25431840 | 26331909 | - | Nlgn1 | Nlgn1 | P24436 | NM_138666 | TSS7432 |
| chr3 | 26082828 | 26082919 | MACS2_peak_1775 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 2 | chr3 | unknown | gene | 22251369 | 22251607 | + | Rprl2 | Rprl2 | | NR_004439 | TSS14506 |
| chr3 | 26082828 | 26082919 | MACS2_peak_1775 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 2 | chr3 | unknown | gene | 26637630 | 26983042 | + | Spata16 | Spata16 | P10104 | NM_027583 | TSS19110 |
| chr3 | 26506756 | 26506873 | MACS2_peak_1776 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 73 | chr3 | unknown | gene | 25431840 | 26331909 | - | Nlgn1 | Nlgn1 | P24436 | NM_138666 | TSS7432 |
| chr3 | 26506756 | 26506873 | MACS2_peak_1776 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 73 | chr3 | unknown | gene | 26637630 | 26983042 | + | Spata16 | Spata16 | P10104 | NM_027583 | TSS19110 |
| chr3 | 27621016 | 27621107 | MACS2_peak_1777 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 7 | chr3 | unknown | gene | 27584899 | 27584995 | - | Mir3092 | Mir3092 | | NR_037275 | TSS5360 |
| chr3 | 27621016 | 27621107 | MACS2_peak_1777 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 7 | chr3 | unknown | gene | 27866064 | 27896343 | - | Tmem212 | Tmem212 | P14255 | NM_001164437 | TSS3306 |
| chr3 | 28197179 | 28197270 | MACS2_peak_1778 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 62 | chr3 | unknown | gene | 27938679 | 28131738 | + | Pld1 | Pld1 | P3156 | NM_001164056 | TSS24315 |
| chr3 | 28197179 | 28197270 | MACS2_peak_1778 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 62 | chr3 | unknown | gene | 28263213 | 28667982 | + | Tnik | Tnik | P9473 | NM_001163009 | TSS16372 |
| chr3 | 29753009 | 29753100 | MACS2_peak_1779 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 20 | chr3 | unknown | gene | 29082576 | 29690412 | + | Egfem1 | Egfem1 | P6141 | NM_001167748 | TSS16564 |
| chr3 | 29753009 | 29753100 | MACS2_peak_1779 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 20 | chr3 | unknown | gene | 29891016 | 29924191 | + | Mannr | Mannr | | NR_110437 | TSS15660 |
| chr3 | 30229854 | 30229945 | MACS2_peak_1780 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 64 | chr3 | unknown | gene | 29891016 | 29924191 | + | Mannr | Mannr | | NR_110437 | TSS15660 |
| chr3 | 30229854 | 30229945 | MACS2_peak_1780 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 64 | chr3 | unknown | gene | 30597072 | 30599849 | - | Actrt3 | Actrt3 | P26898 | NM_029690 | TSS15715 |
| chr3 | 30257225 | 30257316 | MACS2_peak_1781 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 85 | chr3 | unknown | gene | 29891016 | 29924191 | + | Mannr | Mannr | | NR_110437 | TSS15660 |
| chr3 | 30257225 | 30257316 | MACS2_peak_1781 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 85 | chr3 | unknown | gene | 30597072 | 30599849 | - | Actrt3 | Actrt3 | P26898 | NM_029690 | TSS15715 |
| chr3 | 30321935 | 30322081 | MACS2_peak_1782 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 87 | chr3 | unknown | gene | 29891016 | 29924191 | + | Mannr | Mannr | | NR_110437 | TSS15660 |
| chr3 | 30321935 | 30322081 | MACS2_peak_1782 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 87 | chr3 | unknown | gene | 30597072 | 30599849 | - | Actrt3 | Actrt3 | P26898 | NM_029690 | TSS15715 |
| chr3 | 30467337 | 30467428 | MACS2_peak_1783 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 25 | chr3 | unknown | gene | 29891016 | 29924191 | + | Mannr | Mannr | | NR_110437 | TSS15660 |
| chr3 | 30467337 | 30467428 | MACS2_peak_1783 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 25 | chr3 | unknown | gene | 30597072 | 30599849 | - | Actrt3 | Actrt3 | P26898 | NM_029690 | TSS15715 |
| chr3 | 31097122 | 31097319 | MACS2_peak_1784 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 108 | chr3 | unknown | gene | 30995770 | 31050277 | + | Prkci | Prkci | P6693 | NM_008857 | TSS22381 |
| chr3 | 31097122 | 31097319 | MACS2_peak_1784 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 108 | chr3 | unknown | gene | 31149919 | 31163308 | + | Cldn11 | Cldn11 | P11144 | NM_008770 | TSS8132 |
| chr3 | 31644186 | 31644277 | MACS2_peak_1785 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 31 | chr3 | unknown | gene | 31202855 | 31310319 | - | Slc7a14 | Slc7a14 | P24967 | NM_172861 | TSS15415 |
| chr3 | 31644186 | 31644277 | MACS2_peak_1785 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 31 | chr3 | unknown | gene | 31902702 | 32198359 | + | Kcnmb2 | Kcnmb2 | P3198 | NM_028231 | TSS18511 |
| chr3 | 34843662 | 34843753 | MACS2_peak_1786 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 30 | chr3 | unknown | gene | 34772074 | 34782346 | + | Gm38509 | Gm38509 | | NR_110488 | TSS5625 |
| chr3 | 34843662 | 34843753 | MACS2_peak_1786 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 30 | chr3 | unknown | gene | 34922544 | 34922651 | - | Mir6378 | Mir6378 | | NR_105799 | TSS25006 |
| chr3 | 35274200 | 35274321 | MACS2_peak_1787 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 78 | chr3 | unknown | gene | 34922544 | 34922651 | - | Mir6378 | Mir6378 | | NR_105799 | TSS25006 |
| chr3 | 35274200 | 35274321 | MACS2_peak_1787 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 78 | chr3 | unknown | gene | 35597151 | 35666163 | - | Gm6639 | Gm6639 | | NR_040748 | TSS13259 |
| chr3 | 35628512 | 35628603 | MACS2_peak_1788 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 49 | chr3 | unknown | gene | 34922544 | 34922651 | - | Mir6378 | Mir6378 | | NR_105799 | TSS25006 |
| chr3 | 35628512 | 35628603 | MACS2_peak_1788 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 49 | chr3 | unknown | gene | 35754137 | 35855186 | + | Atp11b | Atp11b | P4419 | NM_029570 | TSS10223 |
| chr3 | 37938100 | 37938191 | MACS2_peak_1789 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 58 | chr3 | unknown | gene | 37714189 | 37724360 | - | Gm5148 | Gm5148 | P15151 | NM_198657 | TSS26891 |
| chr3 | 37938100 | 37938191 | MACS2_peak_1789 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 58 | chr3 | unknown | gene | 38203150 | 38208119 | - | 5430434I15Rik | 5430434I15Rik | | NR_040541 | TSS2593 |
| chr3 | 38515398 | 38515489 | MACS2_peak_1790 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 45 | chr3 | unknown | gene | 38449260 | 38484816 | - | Ankrd50 | Ankrd50 | P24813 | NM_001167883 | TSS6784 |
| chr3 | 38515398 | 38515489 | MACS2_peak_1790 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 45 | chr3 | unknown | gene | 38886939 | 39010842 | + | Fat4 | Fat4 | P9376 | NM_183221 | TSS3388 |
| chr3 | 39829581 | 39829672 | MACS2_peak_1791 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 53 | chr3 | unknown | gene | 38886939 | 39010842 | + | Fat4 | Fat4 | P9376 | NM_183221 | TSS3388 |
| chr3 | 39829581 | 39829672 | MACS2_peak_1791 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 53 | chr3 | unknown | gene | 40504864 | 40522912 | - | 1700017G19Rik | 1700017G19Rik | | NR_040445 | TSS15098 |
| chr3 | 40160123 | 40160216 | MACS2_peak_1792 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 39 | chr3 | unknown | gene | 38886939 | 39010842 | + | Fat4 | Fat4 | P9376 | NM_183221 | TSS3388 |
| chr3 | 40160123 | 40160216 | MACS2_peak_1792 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 39 | chr3 | unknown | gene | 40504864 | 40522912 | - | 1700017G19Rik | 1700017G19Rik | | NR_040445 | TSS15098 |
| chr3 | 40413817 | 40413908 | MACS2_peak_1793 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 24 | chr3 | unknown | gene | 38886939 | 39010842 | + | Fat4 | Fat4 | P9376 | NM_183221 | TSS3388 |
| chr3 | 40413817 | 40413908 | MACS2_peak_1793 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 24 | chr3 | unknown | gene | 40504864 | 40522912 | - | 1700017G19Rik | 1700017G19Rik | | NR_040445 | TSS15098 |
| chr3 | 40744591 | 40744682 | MACS2_peak_1794 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 20 | chr3 | unknown | gene | 40708870 | 40725068 | + | Slc25a31 | Slc25a31 | P9345 | NM_178386 | TSS13091 |
| chr3 | 40744591 | 40744682 | MACS2_peak_1794 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 20 | chr3 | unknown | gene | 40745612 | 40789389 | + | Hspa4l | Hspa4l | P6068 | NM_011020 | TSS19361 |
| chr3 | 41419363 | 41419454 | MACS2_peak_1795 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 55 | chr3 | unknown | gene | 41066325 | 41082994 | - | Pgrmc2 | Pgrmc2 | P20555 | NM_027558 | TSS13761 |
| chr3 | 41419363 | 41419454 | MACS2_peak_1795 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 55 | chr3 | unknown | gene | 41487680 | 41493199 | - | Platr4 | Platr4 | | NR_040385 | TSS11395 |
| chr3 | 41955366 | 41955457 | MACS2_peak_1796 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 38 | chr3 | unknown | gene | 41742614 | 41758627 | + | D3Ertd751e | D3Ertd751e | P8678 | NM_001291048 | TSS1387 |
| chr3 | 41955366 | 41955457 | MACS2_peak_1796 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 38 | chr3 | unknown | gene | 45280438 | 45378260 | - | 2610316D01Rik | 2610316D01Rik | | NR_045172 | TSS12157 |
| chr3 | 42360677 | 42360768 | MACS2_peak_1797 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 30 | chr3 | unknown | gene | 41742614 | 41758627 | + | D3Ertd751e | D3Ertd751e | P8678 | NM_001291048 | TSS1387 |
| chr3 | 42360677 | 42360768 | MACS2_peak_1797 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 30 | chr3 | unknown | gene | 45280438 | 45378260 | - | 2610316D01Rik | 2610316D01Rik | | NR_045172 | TSS12157 |
| chr3 | 42727627 | 42727718 | MACS2_peak_1798 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 16 | chr3 | unknown | gene | 41742614 | 41758627 | + | D3Ertd751e | D3Ertd751e | P8678 | NM_001291048 | TSS1387 |
| chr3 | 42727627 | 42727718 | MACS2_peak_1798 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 16 | chr3 | unknown | gene | 45280438 | 45378260 | - | 2610316D01Rik | 2610316D01Rik | | NR_045172 | TSS12157 |
| chr3 | 44143653 | 44143744 | MACS2_peak_1799 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 2 | chr3 | unknown | gene | 41742614 | 41758627 | + | D3Ertd751e | D3Ertd751e | P8678 | NM_001291048 | TSS1387 |
| chr3 | 44143653 | 44143744 | MACS2_peak_1799 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 2 | chr3 | unknown | gene | 45280438 | 45378260 | - | 2610316D01Rik | 2610316D01Rik | | NR_045172 | TSS12157 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr3 | 45665997 | 45666099 | MACS2_peak_1800 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 26 | chr3 | unknown | gene | 45416583 | 45439309 | - | 1700027H10Rik | 1700027H10Rik | | NR_040594 | TSS7350 |
| chr3 | 45665997 | 45666099 | MACS2_peak_1800 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 26 | chr3 | unknown | gene | 46442196 | 46447941 | - | Pabpc4l | Pabpc4l | P286 | NM_001101479 | TSS27125 |
| chr3 | 46181703 | 46181794 | MACS2_peak_1801 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 23 | chr3 | unknown | gene | 45416583 | 45439309 | - | 1700027H10Rik | 1700027H10Rik | | NR_040594 | TSS7350 |
| chr3 | 46181703 | 46181794 | MACS2_peak_1801 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 23 | chr3 | unknown | gene | 46442196 | 46447941 | - | Pabpc4l | Pabpc4l | P286 | NM_001101479 | TSS27125 |
| chr3 | 47664825 | 47664916 | MACS2_peak_1802 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 74 | chr3 | unknown | gene | 46900667 | 46900782 | - | Mir6379 | Mir6379 | | NR_105800 | TSS20364 |
| chr3 | 47664825 | 47664916 | MACS2_peak_1802 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 74 | chr3 | unknown | gene | 48026011 | 48026759 | - | Gm7977 | Gm7977 | | NR_040408 | TSS13373 |
| chr3 | 47913985 | 47914076 | MACS2_peak_1803 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 5 | chr3 | unknown | gene | 46900667 | 46900782 | - | Mir6379 | Mir6379 | | NR_105800 | TSS20364 |
| chr3 | 47913985 | 47914076 | MACS2_peak_1803 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 5 | chr3 | unknown | gene | 48026011 | 48026759 | - | Gm7977 | Gm7977 | | NR_040408 | TSS13373 |
| chr3 | 48661000 | 48661091 | MACS2_peak_1804 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 11 | chr3 | unknown | gene | 48605730 | 48609100 | - | 1700018B24Rik | 1700018B24Rik | | NR_003617 | TSS2341 |
| chr3 | 48661000 | 48661091 | MACS2_peak_1804 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 11 | chr3 | unknown | gene | 49743295 | 49756864 | - | Pcdh18 | Pcdh18 | P19061 | NM_130448 | TSS4468 |
| chr3 | 49470173 | 49470264 | MACS2_peak_1805 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 57 | chr3 | unknown | gene | 48605730 | 48609100 | - | 1700018B24Rik | 1700018B24Rik | | NR_003617 | TSS2341 |
| chr3 | 49470173 | 49470264 | MACS2_peak_1805 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 57 | chr3 | unknown | gene | 49743295 | 49756864 | - | Pcdh18 | Pcdh18 | P19061 | NM_130448 | TSS4468 |
| chr3 | 49471667 | 49471758 | MACS2_peak_1806 | 32 | + | 5.82623 | 8.17465 | 3.21814 | 53 | chr3 | unknown | gene | 48605730 | 48609100 | - | 1700018B24Rik | 1700018B24Rik | | NR_003617 | TSS2341 |
| chr3 | 49471667 | 49471758 | MACS2_peak_1806 | 32 | + | 5.82623 | 8.17465 | 3.21814 | 53 | chr3 | unknown | gene | 49743295 | 49756864 | - | Pcdh18 | Pcdh18 | P19061 | NM_130448 | TSS4468 |
| chr3 | 49642618 | 49642797 | MACS2_peak_1807 | 12 | + | 4.14966 | 5.12722 | 1.204 | 90 | chr3 | unknown | gene | 48605730 | 48609100 | - | 1700018B24Rik | 1700018B24Rik | | NR_003617 | TSS2341 |
| chr3 | 49642618 | 49642797 | MACS2_peak_1807 | 12 | + | 4.14966 | 5.12722 | 1.204 | 90 | chr3 | unknown | gene | 49743295 | 49756864 | - | Pcdh18 | Pcdh18 | P19061 | NM_130448 | TSS4468 |
| chr3 | 50129175 | 50129267 | MACS2_peak_1808 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 24 | chr3 | unknown | gene | 49743295 | 49756864 | - | Pcdh18 | Pcdh18 | P19061 | NM_130448 | TSS4468 |
| chr3 | 50129175 | 50129267 | MACS2_peak_1808 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 24 | chr3 | unknown | gene | 50364935 | 50443261 | - | Slc7a11 | Slc7a11 | P16916 | NM_011990 | TSS23041 |
| chr3 | 52247466 | 52247576 | MACS2_peak_1809 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 68 | chr3 | unknown | gene | 51687612 | 52104143 | - | Maml3 | Maml3 | P24484 | NM_001004176 | TSS21152 |
| chr3 | 52247466 | 52247576 | MACS2_peak_1809 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 68 | chr3 | unknown | gene | 52268336 | 52350109 | + | Foxo1 | Foxo1 | P25437 | NM_019739 | TSS18132 |
| chr3 | 53160977 | 53161068 | MACS2_peak_1810 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 30 | chr3 | unknown | gene | 52982122 | 53017198 | - | Cog6 | Cog6 | P24144 | NM_026225 | TSS7653 |
| chr3 | 53160977 | 53161068 | MACS2_peak_1810 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 30 | chr3 | unknown | gene | 53451995 | 53463143 | - | Nhlrc3 | Nhlrc3 | P9373 | NM_172501 | TSS14868 |
| chr3 | 53676335 | 53676426 | MACS2_peak_1811 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 40 | chr3 | unknown | gene | 53513937 | 53657084 | - | Frem2 | Frem2 | P5346 | NM_172862 | TSS19440 |
| chr3 | 53676335 | 53676426 | MACS2_peak_1811 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 40 | chr3 | unknown | gene | 53853375 | 53863750 | - | Ufm1 | Ufm1 | P20659 | NM_026435 | TSS7058 |
| chr3 | 54474327 | 54474418 | MACS2_peak_1812 | 35 | + | 5.98489 | 8.51731 | 3.53253 | 24 | chr3 | unknown | gene | 54361106 | 54390299 | + | Postn | Postn | P21062 | NM_001198765 | TSS9398 |
| chr3 | 54474327 | 54474418 | MACS2_peak_1812 | 35 | + | 5.98489 | 8.51731 | 3.53253 | 24 | chr3 | unknown | gene | 54693104 | 54716651 | + | Supt20 | Supt20 | P4879 | NM_019995 | TSS4474 |
| chr3 | 56575468 | 56575759 | MACS2_peak_1813 | 76 | + | 8.19616 | 12.86681 | 7.66366 | 211 | chr3 | unknown | gene | 55625197 | 56183235 | - | Nbea | Nbea | P4077 | NM_030595 | TSS13818 |
| chr3 | 56575468 | 56575759 | MACS2_peak_1813 | 76 | + | 8.19616 | 12.86681 | 7.66366 | 211 | chr3 | unknown | gene | 57287063 | 57301919 | - | Tm4sf1 | Tm4sf1 | P7845 | NM_008536 | TSS19035 |
| chr3 | 57269680 | 57269771 | MACS2_peak_1814 | 12 | + | 4.14966 | 5.12722 | 1.204 | 47 | chr3 | unknown | gene | 55625197 | 56183235 | - | Nbea | Nbea | P4077 | NM_030595 | TSS13818 |
| chr3 | 57269680 | 57269771 | MACS2_peak_1814 | 12 | + | 4.14966 | 5.12722 | 1.204 | 47 | chr3 | unknown | gene | 57287063 | 57301919 | - | Tm4sf1 | Tm4sf1 | P7845 | NM_008536 | TSS19035 |
| chr3 | 57532519 | 57532616 | MACS2_peak_1815 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 31 | chr3 | unknown | gene | 57425409 | 57441091 | + | Tm4sf4 | Tm4sf4 | P14515 | NM_145539 | TSS20879 |
| chr3 | 57532519 | 57532616 | MACS2_peak_1815 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 31 | chr3 | unknown | gene | 57616608 | 57616722 | + | Mir6377 | Mir6377 | | NR_105797 | TSS10528 |
| chr3 | 57553556 | 57553647 | MACS2_peak_1816 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 27 | chr3 | unknown | gene | 57425409 | 57441091 | + | Tm4sf4 | Tm4sf4 | P14515 | NM_145539 | TSS20879 |
| chr3 | 57553556 | 57553647 | MACS2_peak_1816 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 27 | chr3 | unknown | gene | 57616608 | 57616722 | + | Mir6377 | Mir6377 | | NR_105797 | TSS10528 |
| chr3 | 58564602 | 58564693 | MACS2_peak_1817 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 71 | chr3 | unknown | gene | 58525820 | 58557186 | + | Eif2a | Eif2a | P19254 | NM_001005509 | TSS19486 |
| chr3 | 58564602 | 58564693 | MACS2_peak_1817 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 71 | chr3 | unknown | gene | 58576657 | 58593546 | + | Selt | Selt | P3856 | NM_001040396 | TSS8086 |
| chr3 | 59135143 | 59135260 | MACS2_peak_1818 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 40 | chr3 | unknown | gene | 59096447 | 59101821 | - | Gpr171 | Gpr171 | P21183 | NM_173398 | TSS5186 |
| chr3 | 59135143 | 59135260 | MACS2_peak_1818 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 40 | chr3 | unknown | gene | 59146295 | 59153628 | - | F630111L10Rik | F630111L10Rik | | NR_045641 | TSS18469 |
| chr3 | 59167648 | 59167739 | MACS2_peak_1819 | 21 | + | 5.11444 | 6.81116 | 2.12135 | 28 | chr3 | unknown | gene | 59146295 | 59153628 | - | F630111L10Rik | F630111L10Rik | | NR_045641 | TSS18469 |
| chr3 | 59167648 | 59167739 | MACS2_peak_1819 | 21 | + | 5.11444 | 6.81116 | 2.12135 | 28 | chr3 | unknown | gene | 59178913 | 59195104 | - | Gpr87 | Gpr87 | P7191 | NM_001302203 | TSS5905 |
| chr3 | 59460448 | 59460539 | MACS2_peak_1820 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 81 | chr3 | unknown | gene | 59316734 | 59344256 | - | Igsf10 | Igsf10 | P13683 | NM_001162884 | TSS2619 |
| chr3 | 59460448 | 59460539 | MACS2_peak_1820 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 81 | chr3 | unknown | gene | 59729785 | 59752333 | + | Gm5538 | Gm5538 | P13525 | NM_001101531 | TSS10335 |
| chr3 | 60265256 | 60265359 | MACS2_peak_1821 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 65 | chr3 | unknown | gene | 60081868 | 60087006 | + | Sucnr1 | Sucnr1 | P20278 | NM_032400 | TSS8333 |
| chr3 | 60265256 | 60265359 | MACS2_peak_1821 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 65 | chr3 | unknown | gene | 60472829 | 60629748 | + | Mbnl1 | Mbnl1 | P6030 | NM_001253713 | TSS8916 |
| chr3 | 60301614 | 60301749 | MACS2_peak_1822 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 86 | chr3 | unknown | gene | 60081868 | 60087006 | + | Sucnr1 | Sucnr1 | P20278 | NM_032400 | TSS8333 |
| chr3 | 60301614 | 60301749 | MACS2_peak_1822 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 86 | chr3 | unknown | gene | 60472829 | 60629748 | + | Mbnl1 | Mbnl1 | P6030 | NM_001253713 | TSS8916 |
| chr3 | 60527705 | 60527796 | MACS2_peak_1823 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 21 | chr3 | unknown | gene | 60081868 | 60087006 | + | Sucnr1 | Sucnr1 | P20278 | NM_032400 | TSS8333 |
| chr3 | 60527705 | 60527796 | MACS2_peak_1823 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 21 | chr3 | unknown | gene | 61002784 | 61008982 | + | P2ry1 | P2ry1 | P3128 | NM_008772 | TSS27685 |
| chr3 | 60785017 | 60785168 | MACS2_peak_1824 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 68 | chr3 | unknown | gene | 60472829 | 60629748 | + | Mbnl1 | Mbnl1 | P6030 | NM_001253713 | TSS8916 |
| chr3 | 60785017 | 60785168 | MACS2_peak_1824 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 68 | chr3 | unknown | gene | 61002784 | 61008982 | + | P2ry1 | P2ry1 | P3128 | NM_008772 | TSS27685 |
| chr3 | 60833734 | 60833849 | MACS2_peak_1825 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 59 | chr3 | unknown | gene | 60472829 | 60629748 | + | Mbnl1 | Mbnl1 | P6030 | NM_001253713 | TSS8916 |
| chr3 | 60833734 | 60833849 | MACS2_peak_1825 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 59 | chr3 | unknown | gene | 61002784 | 61008982 | + | P2ry1 | P2ry1 | P3128 | NM_008772 | TSS27685 |
| chr3 | 61298879 | 61298970 | MACS2_peak_1826 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 56 | chr3 | unknown | gene | 61002784 | 61008982 | + | P2ry1 | P2ry1 | P3128 | NM_008772 | TSS27685 |
| chr3 | 61298879 | 61298970 | MACS2_peak_1826 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 56 | chr3 | unknown | gene | 61364506 | 61365608 | + | Rap2b | Rap2b | P23578 | NM_028712 | TSS3617 |
| chr3 | 62538526 | 62538617 | MACS2_peak_1827 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 21 | chr3 | unknown | gene | 62468641 | 62506939 | - | Dhx36 | Dhx36 | P11606 | NM_028136 | TSS17213 |
| chr3 | 62538526 | 62538617 | MACS2_peak_1827 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 21 | chr3 | unknown | gene | 63295434 | 63380332 | + | Mme | Mme | P12593 | NM_001289462 | TSS3172 |
| chr3 | 64298312 | 64298403 | MACS2_peak_1828 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 47 | chr3 | unknown | gene | 64258960 | 64287411 | - | Vmn2r3 | Vmn2r3 | P20832 | NM_001104614 | TSS21000 |
| chr3 | 64298312 | 64298403 | MACS2_peak_1828 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 47 | chr3 | unknown | gene | 64388620 | 64410048 | - | Vmn2r4 | Vmn2r4 | P3912 | NM_001104615 | TSS12332 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr3 | 65236189 | 65236280 | MACS2_peak_1829 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 34 | chr3 | unknown | gene | 64632862 | 64844743 | - | Vmn2r-ps11 | Vmn2r-ps11 | | NR_003962 | TSS12993 |
| chr3 | 65236189 | 65236280 | MACS2_peak_1829 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 34 | chr3 | unknown | gene | 65324019 | 65349429 | - | A730090N16Rik | A730090N16Rik | | NR_040390 | TSS24951 |
| chr3 | 65489133 | 65489224 | MACS2_peak_1830 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 8 | chr3 | unknown | gene | 65379656 | 65392537 | - | Ssr3 | Ssr3 | P8848 | NM_026155 | TSS13264 |
| chr3 | 65489133 | 65489224 | MACS2_peak_1830 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 8 | chr3 | unknown | gene | 65527484 | 65529414 | - | 4931440P22Rik | 4931440P22Rik | | NR_027955 | TSS13970 |
| chr3 | 65585951 | 65586042 | MACS2_peak_1831 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 38 | chr3 | unknown | gene | 65528446 | 65553565 | + | Tiparp | Tiparp | P21070 | NM_178892 | TSS13633 |
| chr3 | 65585951 | 65586042 | MACS2_peak_1831 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 38 | chr3 | unknown | gene | 65659287 | 65659426 | + | Mir8120 | Mir8120 | | NR_106200 | TSS13877 |
| chr3 | 65629656 | 65629747 | MACS2_peak_1832 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 21 | chr3 | unknown | gene | 65528446 | 65553565 | + | Tiparp | Tiparp | P21070 | NM_178892 | TSS13633 |
| chr3 | 65629656 | 65629747 | MACS2_peak_1832 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 21 | chr3 | unknown | gene | 65659287 | 65659426 | + | Mir8120 | Mir8120 | | NR_106200 | TSS13877 |
| chr3 | 69045467 | 69045590 | MACS2_peak_1833 | 23 | + | 5.36409 | 7.26321 | 2.37531 | 56 | chr3 | unknown | gene | 69035293 | 69044742 | - | Trim59 | Trim59 | P18830 | NM_025863 | TSS10633 |
| chr3 | 69045467 | 69045590 | MACS2_peak_1833 | 23 | + | 5.36409 | 7.26321 | 2.37531 | 56 | chr3 | unknown | gene | 69072220 | 69126800 | - | Kpna4 | Kpna4 | P24956 | NM_008467 | TSS1832 |
| chr3 | 70214609 | 70214700 | MACS2_peak_1834 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 78 | chr3 | unknown | gene | 70007612 | 70028125 | + | Otol1 | Otol1 | P20772 | NM_001018031 | TSS14655 |
| chr3 | 70214609 | 70214700 | MACS2_peak_1834 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 78 | chr3 | unknown | gene | 70772378 | 70807291 | - | Gm6634 | Gm6634 | | NR_040556 | TSS16807 |
| chr3 | 71485496 | 71485587 | MACS2_peak_1835 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 13 | chr3 | unknown | gene | 70772378 | 70807291 | - | Gm6634 | Gm6634 | | NR_040556 | TSS16807 |
| chr3 | 71485496 | 71485587 | MACS2_peak_1835 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 13 | chr3 | unknown | gene | 72888559 | 72966866 | - | Sis | Sis | P5862 | NM_001081137 | TSS21392 |
| chr3 | 72111673 | 72111764 | MACS2_peak_1836 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 59 | chr3 | unknown | gene | 70772378 | 70807291 | - | Gm6634 | Gm6634 | | NR_040556 | TSS16807 |
| chr3 | 72111673 | 72111764 | MACS2_peak_1836 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 59 | chr3 | unknown | gene | 72888559 | 72966866 | - | Sis | Sis | P5862 | NM_001081137 | TSS21392 |
| chr3 | 72221080 | 72221205 | MACS2_peak_1837 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 76 | chr3 | unknown | gene | 70772378 | 70807291 | - | Gm6634 | Gm6634 | | NR_040556 | TSS16807 |
| chr3 | 72221080 | 72221205 | MACS2_peak_1837 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 76 | chr3 | unknown | gene | 72888559 | 72966866 | - | Sis | Sis | P5862 | NM_001081137 | TSS21392 |
| chr3 | 73770493 | 73770584 | MACS2_peak_1838 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 2 | chr3 | unknown | gene | 73635808 | 73708415 | - | Bche | Bche | P22204 | NM_009738 | TSS25637 |
| chr3 | 73770493 | 73770584 | MACS2_peak_1838 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 2 | chr3 | unknown | gene | 74009218 | 74017277 | - | Gm20356 | Gm20356 | | NR_040450 | TSS10042 |
| chr3 | 74745666 | 74745757 | MACS2_peak_1839 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 11 | chr3 | unknown | gene | 74009218 | 74017277 | - | Gm20356 | Gm20356 | | NR_040450 | TSS10042 |
| chr3 | 74745666 | 74745757 | MACS2_peak_1839 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 11 | chr3 | unknown | gene | 75037906 | 75143723 | - | Zbbx | Zbbx | P22363 | NM_172515 | TSS771 |
| chr3 | 74875303 | 74875394 | MACS2_peak_1840 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 56 | chr3 | unknown | gene | 74009218 | 74017277 | - | Gm20356 | Gm20356 | | NR_040450 | TSS10042 |
| chr3 | 74875303 | 74875394 | MACS2_peak_1840 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 56 | chr3 | unknown | gene | 75037906 | 75143723 | - | Zbbx | Zbbx | P22363 | NM_172515 | TSS771 |
| chr3 | 76073723 | 76073814 | MACS2_peak_1841 | 12 | + | 4.14966 | 5.12722 | 1.204 | 10 | chr3 | unknown | gene | 75876182 | 75956298 | - | Golim4 | Golim4 | P6330 | NM_001291069 | TSS26435 |
| chr3 | 76073723 | 76073814 | MACS2_peak_1841 | 12 | + | 4.14966 | 5.12722 | 1.204 | 10 | chr3 | unknown | gene | 76074560 | 76708177 | + | Fstl5 | Fstl5 | P17230 | NM_178673 | TSS26244 |
| chr3 | 76285720 | 76285811 | MACS2_peak_1842 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 18 | chr3 | unknown | gene | 75876182 | 75956298 | - | Golim4 | Golim4 | P6330 | NM_001291069 | TSS26435 |
| chr3 | 76285720 | 76285811 | MACS2_peak_1842 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 18 | chr3 | unknown | gene | 79062528 | 79145824 | - | Rapgef2 | Rapgef2 | P15847 | NM_001099624 | TSS27352 |
| chr3 | 76371455 | 76371546 | MACS2_peak_1843 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 56 | chr3 | unknown | gene | 75876182 | 75956298 | - | Golim4 | Golim4 | P6330 | NM_001291069 | TSS26435 |
| chr3 | 76371455 | 76371546 | MACS2_peak_1843 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 56 | chr3 | unknown | gene | 79062528 | 79145824 | - | Rapgef2 | Rapgef2 | P15847 | NM_001099624 | TSS27352 |
| chr3 | 77304465 | 77304556 | MACS2_peak_1844 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 34 | chr3 | unknown | gene | 76074560 | 76708177 | + | Fstl5 | Fstl5 | P17230 | NM_178673 | TSS26244 |
| chr3 | 77304465 | 77304556 | MACS2_peak_1844 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 34 | chr3 | unknown | gene | 79062528 | 79145824 | - | Rapgef2 | Rapgef2 | P15847 | NM_001099624 | TSS27352 |
| chr3 | 80838250 | 80838360 | MACS2_peak_1845 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 30 | chr3 | unknown | gene | 80684935 | 80802384 | - | Gria2 | Gria2 | P20764 | NM_001083806 | TSS2324 |
| chr3 | 80838250 | 80838360 | MACS2_peak_1845 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 30 | chr3 | unknown | gene | 80843598 | 80913660 | - | Glrb | Glrb | P14466 | NM_001281969 | TSS5746 |
| chr3 | 81343272 | 81343392 | MACS2_peak_1846 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 58 | chr3 | unknown | gene | 81036415 | 81212578 | + | Pdgfc | Pdgfc | P18673 | NM_019971 | TSS7869 |
| chr3 | 81343272 | 81343392 | MACS2_peak_1846 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 58 | chr3 | unknown | gene | 81932615 | 81954260 | + | Ctso | Ctso | P13549 | NM_177662 | TSS8662 |
| chr3 | 81712896 | 81712987 | MACS2_peak_1847 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 64 | chr3 | unknown | gene | 81036415 | 81212578 | + | Pdgfc | Pdgfc | P18673 | NM_019971 | TSS7869 |
| chr3 | 81712896 | 81712987 | MACS2_peak_1847 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 64 | chr3 | unknown | gene | 81932615 | 81954260 | + | Ctso | Ctso | P13549 | NM_177662 | TSS8662 |
| chr3 | 81821039 | 81821170 | MACS2_peak_1848 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 79 | chr3 | unknown | gene | 81036415 | 81212578 | + | Pdgfc | Pdgfc | P18673 | NM_019971 | TSS7869 |
| chr3 | 81821039 | 81821170 | MACS2_peak_1848 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 79 | chr3 | unknown | gene | 81932615 | 81954260 | + | Ctso | Ctso | P13549 | NM_177662 | TSS8662 |
| chr3 | 83852029 | 83852130 | MACS2_peak_1849 | 30 | + | 5.71265 | 7.93979 | 3.00019 | 42 | chr3 | unknown | gene | 83836271 | 83841608 | - | Tlr2 | Tlr2 | P8908 | NM_011905 | TSS17540 |
| chr3 | 83852029 | 83852130 | MACS2_peak_1849 | 30 | + | 5.71265 | 7.93979 | 3.00019 | 42 | chr3 | unknown | gene | 83898286 | 84040100 | - | D930015E06Rik | D930015E06Rik | P16013 | NM_172681 | TSS17037 |
| chr3 | 84574870 | 84575077 | MACS2_peak_1850 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 151 | chr3 | unknown | gene | 84442195 | 84480439 | - | Fhdc1 | Fhdc1 | P21051 | NM_001033301 | TSS26282 |
| chr3 | 84574870 | 84575077 | MACS2_peak_1850 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 151 | chr3 | unknown | gene | 84593573 | 84595319 | + | Tigd4 | Tigd4 | P22625 | NM_207278 | TSS9285 |
| chr3 | 84905950 | 84906059 | MACS2_peak_1851 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 20 | chr3 | unknown | gene | 84666191 | 84701939 | + | Tmem154 | Tmem154 | P17068 | NM_177260 | TSS22240 |
| chr3 | 84905950 | 84906059 | MACS2_peak_1851 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 20 | chr3 | unknown | gene | 84965055 | 84965363 | - | Dear1 | Dear1 | P18265 | NM_001040461 | TSS5433 |
| chr3 | 85003985 | 85004120 | MACS2_peak_1852 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 45 | chr3 | unknown | gene | 84815576 | 84977541 | + | Fbxw7 | Fbxw7 | P25340 | NM_001177773 | TSS18859 |
| chr3 | 85003985 | 85004120 | MACS2_peak_1852 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 45 | chr3 | unknown | gene | 85317518 | 85332027 | + | 1700036G14Rik | 1700036G14Rik | | NR_040542 | TSS25955 |
| chr3 | 85920597 | 85920688 | MACS2_peak_1853 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 31 | chr3 | unknown | gene | 85869845 | 85887518 | - | Glt28d2 | Glt28d2 | P7285 | NM_177130 | TSS10767 |
| chr3 | 85920597 | 85920688 | MACS2_peak_1853 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 31 | chr3 | unknown | gene | 85993809 | 86002491 | - | Prss48 | Prss48 | P8179 | NM_001001650 | TSS18176 |
| chr3 | 86264003 | 86264094 | MACS2_peak_1854 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 84 | chr3 | unknown | gene | 86137939 | 86142569 | - | Rps3a1 | Rps3a1 | P2947 | NM_016959 | TSS12990 |
| chr3 | 86264003 | 86264094 | MACS2_peak_1854 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 84 | chr3 | unknown | gene | 86545580 | 86547691 | - | Mab21l2 | Mab21l2 | P7465 | NM_011839 | TSS20759 |
| chr3 | 86505293 | 86505384 | MACS2_peak_1855 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 25 | chr3 | unknown | gene | 86137939 | 86142569 | - | Rps3a1 | Rps3a1 | P2947 | NM_016959 | TSS12990 |
| chr3 | 86505293 | 86505384 | MACS2_peak_1855 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 25 | chr3 | unknown | gene | 86545580 | 86547691 | - | Mab21l2 | Mab21l2 | P7465 | NM_011839 | TSS20759 |
| chr3 | 86699262 | 86699353 | MACS2_peak_1856 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 65 | chr3 | unknown | gene | 86545580 | 86547691 | - | Mab21l2 | Mab21l2 | P7465 | NM_011839 | TSS20759 |
| chr3 | 86699262 | 86699353 | MACS2_peak_1856 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 65 | chr3 | unknown | gene | 86786149 | 86920170 | - | Dclk2 | Dclk2 | P165 | NM_027539 | TSS27015 |
| chr3 | 87202369 | 87202460 | MACS2_peak_1857 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 33 | chr3 | unknown | gene | 87078591 | 87174747 | - | Kirrel | Kirrel | P10802 | NM_001170985 | TSS3044 |
| chr3 | 87202369 | 87202460 | MACS2_peak_1857 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 33 | chr3 | unknown | gene | 87250964 | 87263475 | - | Fcrls | Fcrls | P19017 | NM_030707 | TSS14335 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr3 | 87422761 | 87422910 | MACS2_peak_1858 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 73 | chr3 | unknown | gene | 87376386 | 87391291 | + | Fcrl1 | Fcrl1 | P26196 | NM_153090 | TSS17734 |
| chr3 | 87422761 | 87422910 | MACS2_peak_1858 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 73 | chr3 | unknown | gene | 87435781 | 87500678 | + | Fcrl5 | Fcrl5 | P25735 | NM_183222 | TSS6117 |
| chr3 | 88305881 | 88305989 | MACS2_peak_1859 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 61 | chr3 | unknown | gene | 88282759 | 88296838 | - | Tsacc | Tsacc | P6118 | NM_029801 | TSS9734 |
| chr3 | 88305881 | 88305989 | MACS2_peak_1859 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 61 | chr3 | unknown | gene | 88325022 | 88328368 | + | Glmp | Glmp | P20981 | NM_020003 | TSS10411 |
| chr3 | 92221508 | 92221599 | MACS2_peak_1860 | 12 | + | 4.2291 | 5.23562 | 1.28645 | 38 | chr3 | unknown | gene | 92134993 | 92142754 | - | Lelp1 | Lelp1 | P314 | NM_027042 | TSS24607 |
| chr3 | 92221508 | 92221599 | MACS2_peak_1860 | 12 | + | 4.2291 | 5.23562 | 1.28645 | 38 | chr3 | unknown | gene | 92285303 | 92288839 | + | Sprr2a3 | Sprr2a3 | P9484 | NM_001309382 | TSS12954 |
| chr3 | 95821597 | 95821737 | MACS2_peak_1861 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 78 | chr3 | unknown | gene | 95759872 | 95818751 | - | Rprd2 | Rprd2 | P20292 | NM_001081293 | TSS22295 |
| chr3 | 95821597 | 95821737 | MACS2_peak_1861 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 78 | chr3 | unknown | gene | 95830621 | 95855753 | - | Prpf3 | Prpf3 | P21069 | NM_027541 | TSS10590 |
| chr3 | 96044514 | 96045042 | MACS2_peak_1862 | 225 | + | 13.31164 | 28.1401 | 22.50508 | 346 | chr3 | unknown | gene | 95988835 | 95995797 | - | Plekho1 | Plekho1 | P12464 | NM_023320 | TSS8962 |
| chr3 | 96044514 | 96045042 | MACS2_peak_1862 | 225 | + | 13.31164 | 28.1401 | 22.50508 | 346 | chr3 | unknown | gene | 96080595 | 96148402 | + | Mir1946b | Mir1946b | | NR_035496 | TSS3599 |
| chr3 | 97796225 | 97796316 | MACS2_peak_1863 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 50 | chr3 | unknown | gene | 97690508 | 97690562 | - | Mir7225 | Mir7225 | | NR_106084 | TSS2279 |
| chr3 | 97796225 | 97796316 | MACS2_peak_1863 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 50 | chr3 | unknown | gene | 97901226 | 97921270 | + | Sec22b | Sec22b | P21364 | NM_011342 | TSS2638 |
| chr3 | 97974947 | 97975048 | MACS2_peak_1864 | 38 | + | 6.17742 | 8.88798 | 3.85613 | 38 | chr3 | unknown | gene | 97930172 | 97966786 | + | Gm5544 | Gm5544 | P5638 | NM_001033779 | TSS24049 |
| chr3 | 97974947 | 97975048 | MACS2_peak_1864 | 38 | + | 6.17742 | 8.88798 | 3.85613 | 38 | chr3 | unknown | gene | 98013537 | 98147444 | + | Notch2 | Notch2 | P12363 | NM_010928 | TSS13367 |
| chr3 | 99083973 | 99084064 | MACS2_peak_1865 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 73 | chr3 | unknown | gene | 99049821 | 99053742 | + | Gm12440 | Gm12440 | | NR_110516 | TSS5149 |
| chr3 | 99083973 | 99084064 | MACS2_peak_1865 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 73 | chr3 | unknown | gene | 99141089 | 99216907 | + | Wars2 | Wars2 | P16441 | NM_027462 | TSS6777 |
| chr3 | 99552148 | 99552300 | MACS2_peak_1866 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 69 | chr3 | unknown | gene | 99253759 | 99352623 | + | Tbx15 | Tbx15 | P4759 | NM_009323 | TSS22722 |
| chr3 | 99552148 | 99552300 | MACS2_peak_1866 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 69 | chr3 | unknown | gene | 99885416 | 100143322 | + | Spag17 | Spag17 | P6133 | NM_028892 | TSS2097 |
| chr3 | 101235175 | 101235266 | MACS2_peak_1867 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 32 | chr3 | unknown | gene | 101040235 | 101110140 | - | Ptgfrn | Ptgfrn | P4041 | NM_011197 | TSS764 |
| chr3 | 101235175 | 101235266 | MACS2_peak_1867 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 32 | chr3 | unknown | gene | 101275907 | 101287879 | - | Cd2 | Cd2 | P10981 | NM_013486 | TSS12671 |
| chr3 | 102311869 | 102311980 | MACS2_peak_1868 | 49 | + | 6.83013 | 10.07655 | 4.98053 | 73 | chr3 | unknown | gene | 102262404 | 102288771 | + | A230001M10Rik | A230001M10Rik | | NR_040391 | TSS1374 |
| chr3 | 102311869 | 102311980 | MACS2_peak_1868 | 49 | + | 6.83013 | 10.07655 | 4.98053 | 73 | chr3 | unknown | gene | 102469918 | 102520848 | + | Ngf | Ngf | P8982 | NM_001112698 | TSS10456 |
| chr3 | 102630750 | 102630841 | MACS2_peak_1869 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 44 | chr3 | unknown | gene | 102469918 | 102520848 | + | Ngf | Ngf | P8982 | NM_001112698 | TSS10456 |
| chr3 | 102630750 | 102630841 | MACS2_peak_1869 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 44 | chr3 | unknown | gene | 102720230 | 102735417 | - | Tspan2os | Tspan2os | | NR_040588 | TSS18427 |
| chr3 | 102853160 | 102853331 | MACS2_peak_1870 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 86 | chr3 | unknown | gene | 102777397 | 102782714 | - | Tshb | Tshb | P25408 | NM_001165939 | TSS21659 |
| chr3 | 102853160 | 102853331 | MACS2_peak_1870 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 86 | chr3 | unknown | gene | 102939657 | 102964133 | - | Nr1h5 | Nr1h5 | P8075 | NM_198658 | TSS14330 |
| chr3 | 104216033 | 104216124 | MACS2_peak_1871 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 57 | chr3 | unknown | gene | 103968109 | 104007008 | + | Phtf1 | Phtf1 | P5926 | NM_001163467 | TSS8305 |
| chr3 | 104216033 | 104216124 | MACS2_peak_1871 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 57 | chr3 | unknown | gene | 104453982 | 104511691 | - | Lrig2 | Lrig2 | P25447 | NM_001025067 | TSS16049 |
| chr3 | 106075243 | 106075334 | MACS2_peak_1872 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 66 | chr3 | unknown | gene | 105996956 | 106014605 | - | Pifo | Pifo | P14283 | NM_001200028 | TSS8414 |
| chr3 | 106075243 | 106075334 | MACS2_peak_1872 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 66 | chr3 | unknown | gene | 106113381 | 106132017 | + | Chia1 | Chia1 | P9745 | NM_023186 | TSS17019 |
| chr3 | 106215411 | 106215504 | MACS2_peak_1873 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 8 | chr3 | unknown | gene | 106147553 | 106167521 | - | Chil3 | Chil3 | P15551 | NM_009892 | TSS27437 |
| chr3 | 106215411 | 106215504 | MACS2_peak_1873 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 8 | chr3 | unknown | gene | 106387383 | 106406031 | - | Chil6 | Chil6 | P214 | NM_178412 | TSS334 |
| chr3 | 106559284 | 106559375 | MACS2_peak_1874 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 6 | chr3 | unknown | gene | 106502259 | 106547802 | - | Cept1 | Cept1 | P23389 | NM_001293694 | TSS20995 |
| chr3 | 106559284 | 106559375 | MACS2_peak_1874 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 6 | chr3 | unknown | gene | 106684986 | 106735848 | + | Lrif1 | Lrif1 | P7908 | NM_001039478 | TSS4449 |
| chr3 | 107033177 | 107033279 | MACS2_peak_1875 | 32 | + | 5.8651 | 8.25694 | 3.2954 | 54 | chr3 | unknown | gene | 106821606 | 106822557 | - | Olfr266 | Olfr266 | P12825 | NM_146489 | TSS8869 |
| chr3 | 107033177 | 107033279 | MACS2_peak_1875 | 32 | + | 5.8651 | 8.25694 | 3.2954 | 54 | chr3 | unknown | gene | 107036161 | 107038009 | + | Kcna3 | Kcna3 | P6212 | NM_008418 | TSS15370 |
| chr3 | 108283211 | 108283325 | MACS2_peak_1876 | 16 | + | 4.811 | 6.2687 | 1.67914 | 39 | chr3 | unknown | gene | 108256925 | 108279812 | + | Psma5 | Psma5 | P13247 | NM_011967 | TSS9568 |
| chr3 | 108283211 | 108283325 | MACS2_peak_1876 | 16 | + | 4.811 | 6.2687 | 1.67914 | 39 | chr3 | unknown | gene | 108284063 | 108357243 | + | Sort1 | Sort1 | P8378 | NM_019972 | TSS714 |
| chr3 | 108751355 | 108751446 | MACS2_peak_1877 | 27 | + | 5.56793 | 7.65146 | 2.73702 | 43 | chr3 | unknown | gene | 108678637 | 108722299 | - | Gpsm2 | Gpsm2 | P21230 | NM_029522 | TSS7865 |
| chr3 | 108751355 | 108751446 | MACS2_peak_1877 | 27 | + | 5.56793 | 7.65146 | 2.73702 | 43 | chr3 | unknown | gene | 108793179 | 108840468 | - | Stxbp3 | Stxbp3 | P19760 | NM_011504 | TSS18201 |
| chr3 | 109011070 | 109011161 | MACS2_peak_1878 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 69 | chr3 | unknown | gene | 108940083 | 108960338 | + | Henmt1 | Henmt1 | P6672 | NM_025723 | TSS15653 |
| chr3 | 109011070 | 109011161 | MACS2_peak_1878 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 69 | chr3 | unknown | gene | 109080498 | 109116512 | + | Slc25a54 | Slc25a54 | P21796 | NM_029054 | TSS24425 |
| chr3 | 109078631 | 109078722 | MACS2_peak_1879 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 11 | chr3 | unknown | gene | 108970996 | 109027321 | - | Fam102b | Fam102b | P24941 | NM_001163567 | TSS7068 |
| chr3 | 109078631 | 109078722 | MACS2_peak_1879 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 11 | chr3 | unknown | gene | 109080498 | 109116512 | + | Slc25a54 | Slc25a54 | P21796 | NM_029054 | TSS24425 |
| chr3 | 109664252 | 109664343 | MACS2_peak_1880 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 47 | chr3 | unknown | gene | 109123148 | 109166510 | + | Slc25a24 | Slc25a24 | P16602 | NM_172685 | TSS3786 |
| chr3 | 109664252 | 109664343 | MACS2_peak_1880 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 47 | chr3 | unknown | gene | 109780049 | 110143472 | - | Ntng1 | Ntng1 | P7874 | NM_001163350 | TSS17437 |
| chr3 | 109822737 | 109822828 | MACS2_peak_1881 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 66 | chr3 | unknown | gene | 109340682 | 109683609 | + | Vav3 | Vav3 | P15067 | NM_020505 | TSS8495 |
| chr3 | 109822737 | 109822828 | MACS2_peak_1881 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 66 | chr3 | unknown | gene | 110246103 | 110250971 | - | Prmt6 | Prmt6 | | NR_024139 | TSS27382 |
| chr3 | 110971210 | 110971317 | MACS2_peak_1882 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 62 | chr3 | unknown | gene | 110246103 | 110250971 | - | Prmt6 | Prmt6 | | NR_024139 | TSS27382 |
| chr3 | 110971210 | 110971317 | MACS2_peak_1882 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 62 | chr3 | unknown | gene | 111881902 | 112082001 | + | Gm6602 | Gm6602 | | NR_045362 | TSS14437 |
| chr3 | 111670906 | 111670997 | MACS2_peak_1883 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 22 | chr3 | unknown | gene | 110246103 | 110250971 | - | Prmt6 | Prmt6 | | NR_024139 | TSS27382 |
| chr3 | 111670906 | 111670997 | MACS2_peak_1883 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 22 | chr3 | unknown | gene | 111881902 | 112082001 | + | Gm6602 | Gm6602 | | NR_045362 | TSS14437 |
| chr3 | 114216745 | 114216836 | MACS2_peak_1884 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 19 | chr3 | unknown | gene | 113605066 | 113630054 | - | Rnpc3 | Rnpc3 | P17097 | NM_026043 | TSS10836 |
| chr3 | 114216745 | 114216836 | MACS2_peak_1884 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 19 | chr3 | unknown | gene | 114863252 | 115027151 | + | Mir669b | Mir669b | | NR_030469 | TSS23813 |
| chr3 | 115051048 | 115051312 | MACS2_peak_1885 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 58 | chr3 | unknown | gene | 114863252 | 115027151 | + | Mir669b | Mir669b | | NR_030469 | TSS23813 |
| chr3 | 115051048 | 115051312 | MACS2_peak_1885 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 58 | chr3 | unknown | gene | 115710432 | 115715055 | - | S1pr1 | S1pr1 | P1364 | NM_007901 | TSS17893 |
| chr3 | 115146626 | 115146731 | MACS2_peak_1886 | 49 | + | 6.77503 | 10.04021 | 4.94691 | 44 | chr3 | unknown | gene | 114904077 | 115122857 | + | Olfm3 | Olfm3 | P13646 | NM_153458 | TSS13548 |
| chr3 | 115146626 | 115146731 | MACS2_peak_1886 | 49 | + | 6.77503 | 10.04021 | 4.94691 | 44 | chr3 | unknown | gene | 115710432 | 115715055 | - | S1pr1 | S1pr1 | P1364 | NM_007901 | TSS17893 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr3 | 115755219 | 115755365 | MACS2_peak_1887 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 57 | chr3 | unknown | gene | 115710432 | 115715055 | - | S1pr1 | S1pr1 | P1364 | NM_007901 | TSS17893 |
| chr3 | 115755219 | 115755365 | MACS2_peak_1887 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 57 | chr3 | unknown | gene | 115881578 | 115888059 | - | A930005H10Rik | A930005H10Rik | | NR_027894 | TSS5900 |
| chr3 | 115774094 | 115774185 | MACS2_peak_1888 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 38 | chr3 | unknown | gene | 115710432 | 115715055 | - | S1pr1 | S1pr1 | P1364 | NM_007901 | TSS17893 |
| chr3 | 115774094 | 115774185 | MACS2_peak_1888 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 38 | chr3 | unknown | gene | 115881578 | 115888059 | - | A930005H10Rik | A930005H10Rik | | NR_027894 | TSS5900 |
| chr3 | 115783877 | 115783968 | MACS2_peak_1889 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 36 | chr3 | unknown | gene | 115710432 | 115715055 | - | S1pr1 | S1pr1 | P1364 | NM_007901 | TSS17893 |
| chr3 | 115783877 | 115783968 | MACS2_peak_1889 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 36 | chr3 | unknown | gene | 115881578 | 115888059 | - | A930005H10Rik | A930005H10Rik | | NR_027894 | TSS5900 |
| chr3 | 116036587 | 116036678 | MACS2_peak_1890 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 80 | chr3 | unknown | gene | 116007448 | 116027498 | + | Extl2 | Extl2 | P8309 | NM_001163515 | TSS21866 |
| chr3 | 116036587 | 116036678 | MACS2_peak_1890 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 80 | chr3 | unknown | gene | 116110019 | 116129367 | - | Vcam1 | Vcam1 | P3504 | NM_011693 | TSS13715 |
| chr3 | 116603125 | 116603228 | MACS2_peak_1891 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 20 | chr3 | unknown | gene | 116562972 | 116581285 | + | Lrrc39 | Lrrc39 | P24959 | NM_027321 | TSS9987 |
| chr3 | 116603125 | 116603228 | MACS2_peak_1891 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 20 | chr3 | unknown | gene | 116631166 | 116662478 | - | Hiat1 | Hiat1 | P2979 | NM_008246 | TSS13742 |
| chr3 | 116943014 | 116943135 | MACS2_peak_1892 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 31 | chr3 | unknown | gene | 116859566 | 116903161 | + | Frrs1 | Frrs1 | P22804 | NM_001113478 | TSS18889 |
| chr3 | 116943014 | 116943135 | MACS2_peak_1892 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 31 | chr3 | unknown | gene | 116968266 | 116984406 | + | 4930455H04Rik | 4930455H04Rik | | NR_040596 | TSS22939 |
| chr3 | 117441630 | 117441721 | MACS2_peak_1893 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 14 | chr3 | unknown | gene | 117319145 | 117360248 | - | Lppr4 | Lppr4 | P15567 | NM_177664 | TSS2222 |
| chr3 | 117441630 | 117441721 | MACS2_peak_1893 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 14 | chr3 | unknown | gene | 117575226 | 117686648 | + | Lppr5 | Lppr5 | P22202 | NM_001305451 | TSS1619 |
| chr3 | 117565565 | 117565656 | MACS2_peak_1894 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 33 | chr3 | unknown | gene | 117319145 | 117360248 | - | Lppr4 | Lppr4 | P15567 | NM_177664 | TSS2222 |
| chr3 | 117565565 | 117565656 | MACS2_peak_1894 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 33 | chr3 | unknown | gene | 117575226 | 117686648 | + | Lppr5 | Lppr5 | P22202 | NM_001305451 | TSS1619 |
| chr3 | 117703045 | 117703136 | MACS2_peak_1895 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 29 | chr3 | unknown | gene | 117575226 | 117686648 | + | Lppr5 | Lppr5 | P22202 | NM_001305451 | TSS1619 |
| chr3 | 117703045 | 117703136 | MACS2_peak_1895 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 29 | chr3 | unknown | gene | 117781496 | 117868905 | - | Snx7 | Snx7 | P8595 | NM_029655 | TSS5272 |
| chr3 | 117725335 | 117725442 | MACS2_peak_1896 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 79 | chr3 | unknown | gene | 117575226 | 117686648 | + | Lppr5 | Lppr5 | P22202 | NM_001305451 | TSS1619 |
| chr3 | 117725335 | 117725442 | MACS2_peak_1896 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 79 | chr3 | unknown | gene | 117781496 | 117868905 | - | Snx7 | Snx7 | P8595 | NM_029655 | TSS5272 |
| chr3 | 118274304 | 118274395 | MACS2_peak_1897 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 48 | chr3 | unknown | gene | 117781496 | 117868905 | - | Snx7 | Snx7 | P8595 | NM_029655 | TSS5272 |
| chr3 | 118274304 | 118274395 | MACS2_peak_1897 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 48 | chr3 | unknown | gene | 118433856 | 118433929 | + | Mir137 | Mir137 | | NR_029551 | TSS12339 |
| chr3 | 118829913 | 118830018 | MACS2_peak_1898 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 21 | chr3 | unknown | gene | 118433856 | 118433929 | + | Mir137 | Mir137 | | NR_029551 | TSS12339 |
| chr3 | 118829913 | 118830018 | MACS2_peak_1898 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 21 | chr3 | unknown | gene | 119718741 | 119783209 | - | Ptbp2 | Ptbp2 | P22552 | NM_019550 | TSS11547 |
| chr3 | 121226210 | 121226315 | MACS2_peak_1899 | 45 | + | 6.59824 | 9.65189 | 4.58689 | 78 | chr3 | unknown | gene | 121155401 | 121171676 | - | Rwdd3 | Rwdd3 | P2000 | NM_025637 | TSS6512 |
| chr3 | 121226210 | 121226315 | MACS2_peak_1899 | 45 | + | 6.59824 | 9.65189 | 4.58689 | 78 | chr3 | unknown | gene | 121291816 | 121361786 | + | Alg14 | Alg14 | P8031 | NM_024178 | TSS13365 |
| chr3 | 121959466 | 121959578 | MACS2_peak_1900 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 69 | chr3 | unknown | gene | 121758909 | 121815118 | - | Abcd3 | Abcd3 | P4539 | NM_008991 | TSS5118 |
| chr3 | 121959466 | 121959578 | MACS2_peak_1900 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 69 | chr3 | unknown | gene | 122044459 | 122179833 | + | Abca4 | Abca4 | P5416 | NM_007378 | TSS2613 |
| chr3 | 122683295 | 122683386 | MACS2_peak_1901 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 67 | chr3 | unknown | gene | 122538718 | 122619553 | - | Fnbp1l | Fnbp1l | P21524 | NM_153118 | TSS8721 |
| chr3 | 122683295 | 122683386 | MACS2_peak_1901 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 67 | chr3 | unknown | gene | 122729157 | 122855332 | + | Pde5a | Pde5a | P23040 | NM_153422 | TSS20372 |
| chr3 | 122757707 | 122757798 | MACS2_peak_1902 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 25 | chr3 | unknown | gene | 122538718 | 122619553 | - | Fnbp1l | Fnbp1l | P21524 | NM_153118 | TSS8721 |
| chr3 | 122757707 | 122757798 | MACS2_peak_1902 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 25 | chr3 | unknown | gene | 122795090 | 122801980 | - | 4930447N08Rik | 4930447N08Rik | | NR_045168 | TSS11266 |
| chr3 | 122766420 | 122766557 | MACS2_peak_1903 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 59 | chr3 | unknown | gene | 122538718 | 122619553 | - | Fnbp1l | Fnbp1l | P21524 | NM_153118 | TSS8721 |
| chr3 | 122766420 | 122766557 | MACS2_peak_1903 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 59 | chr3 | unknown | gene | 122795090 | 122801980 | - | 4930447N08Rik | 4930447N08Rik | | NR_045168 | TSS11266 |
| chr3 | 123027907 | 123028024 | MACS2_peak_1904 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 42 | chr3 | unknown | gene | 122933600 | 122984447 | - | Usp53 | Usp53 | P24284 | NM_133857 | TSS10823 |
| chr3 | 123027907 | 123028024 | MACS2_peak_1904 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 42 | chr3 | unknown | gene | 123076518 | 123236007 | - | Synpo2 | Synpo2 | P6762 | NM_080451 | TSS5716 |
| chr3 | 123335133 | 123335224 | MACS2_peak_1905 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 59 | chr3 | unknown | gene | 123076518 | 123236007 | - | Synpo2 | Synpo2 | P6762 | NM_080451 | TSS5716 |
| chr3 | 123335133 | 123335224 | MACS2_peak_1905 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 59 | chr3 | unknown | gene | 123368294 | 123385827 | - | Mettl14 | Mettl14 | P2316 | NM_201638 | TSS1415 |
| chr3 | 124114509 | 124114600 | MACS2_peak_1906 | 16 | + | 4.811 | 6.2687 | 1.67914 | 55 | chr3 | unknown | gene | 123526165 | 123690852 | - | Ndst3 | Ndst3 | | NR_121616 | TSS5782 |
| chr3 | 124114509 | 124114600 | MACS2_peak_1906 | 16 | + | 4.811 | 6.2687 | 1.67914 | 55 | chr3 | unknown | gene | 124321036 | 124322284 | + | Tram1l1 | Tram1l1 | P10136 | NM_146140 | TSS15617 |
| chr3 | 124778071 | 124778162 | MACS2_peak_1907 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 28 | chr3 | unknown | gene | 124565890 | 124581091 | - | 1700003H04Rik | 1700003H04Rik | | NR_015460 | TSS18655 |
| chr3 | 124778071 | 124778162 | MACS2_peak_1907 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 28 | chr3 | unknown | gene | 125404090 | 125724770 | + | Ndst4 | Ndst4 | P7126 | NM_022565 | TSS25989 |
| chr3 | 127012072 | 127012201 | MACS2_peak_1908 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 47 | chr3 | unknown | gene | 126921606 | 126998452 | - | Ank2 | Ank2 | P19808 | NM_001034168 | TSS3310 |
| chr3 | 127012072 | 127012201 | MACS2_peak_1908 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 47 | chr3 | unknown | gene | 127161304 | 127168290 | + | LOC100862268 | LOC100862268 | | NR_105030 | TSS23395 |
| chr3 | 128093715 | 128093806 | MACS2_peak_1909 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 64 | chr3 | unknown | gene | 127916170 | 127955220 | + | 9830132P13Rik | 9830132P13Rik | | NR_040552 | TSS12029 |
| chr3 | 128093715 | 128093806 | MACS2_peak_1909 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 64 | chr3 | unknown | gene | 128117014 | 128231605 | - | D030025E07Rik | D030025E07Rik | | NR_045704 | TSS9486 |
| chr3 | 128185111 | 128185202 | MACS2_peak_1910 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 24 | chr3 | unknown | gene | 127916170 | 127955220 | + | 9830132P13Rik | 9830132P13Rik | | NR_040552 | TSS12029 |
| chr3 | 128185111 | 128185202 | MACS2_peak_1910 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 24 | chr3 | unknown | gene | 129199877 | 129218897 | + | Pitx2 | Pitx2 | P16281 | NM_001286942 | TSS25682 |
| chr3 | 128233981 | 128234072 | MACS2_peak_1911 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 48 | chr3 | unknown | gene | 128117014 | 128231605 | - | D030025E07Rik | D030025E07Rik | | NR_045704 | TSS9486 |
| chr3 | 128233981 | 128234072 | MACS2_peak_1911 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 48 | chr3 | unknown | gene | 129199877 | 129218897 | + | Pitx2 | Pitx2 | P16281 | NM_001286942 | TSS25682 |
| chr3 | 128435412 | 128435503 | MACS2_peak_1912 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 39 | chr3 | unknown | gene | 128117014 | 128231605 | - | D030025E07Rik | D030025E07Rik | | NR_045704 | TSS9486 |
| chr3 | 128435412 | 128435503 | MACS2_peak_1912 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 39 | chr3 | unknown | gene | 129199877 | 129218897 | + | Pitx2 | Pitx2 | P16281 | NM_001286942 | TSS25682 |
| chr3 | 128891159 | 128891302 | MACS2_peak_1913 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 75 | chr3 | unknown | gene | 128117014 | 128231605 | - | D030025E07Rik | D030025E07Rik | | NR_045704 | TSS9486 |
| chr3 | 128891159 | 128891302 | MACS2_peak_1913 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 75 | chr3 | unknown | gene | 129199877 | 129218897 | + | Pitx2 | Pitx2 | P16281 | NM_001286942 | TSS25682 |
| chr3 | 129110815 | 129110906 | MACS2_peak_1914 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 28 | chr3 | unknown | gene | 128117014 | 128231605 | - | D030025E07Rik | D030025E07Rik | | NR_045704 | TSS9486 |
| chr3 | 129110815 | 129110906 | MACS2_peak_1914 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 28 | chr3 | unknown | gene | 129199877 | 129218897 | + | Pitx2 | Pitx2 | P16281 | NM_001286942 | TSS25682 |
| chr3 | 129836909 | 129837000 | MACS2_peak_1915 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 48 | chr3 | unknown | gene | 129824911 | 129831396 | - | Gar1 | Gar1 | P12883 | NM_026578 | TSS1178 |
| chr3 | 129836909 | 129837000 | MACS2_peak_1915 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 48 | chr3 | unknown | gene | 129878605 | 129894956 | + | Pla2g12a | Pla2g12a | P13454 | NM_023196 | TSS6725 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr3 | 130303316 | 130303449 | MACS2_peak_1916 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 60 | chr3 | unknown | gene | 129983184 | 130060668 | - | Sec24b | Sec24b | P13926 | NM_207209 | TSS16620 |
| chr3 | 130303316 | 130303449 | MACS2_peak_1916 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 60 | chr3 | unknown | gene | 130617447 | 130634677 | + | Etnppl | Etnppl | P23053 | NM_001163587 | TSS21868 |
| chr3 | 132086871 | 132086976 | MACS2_peak_1917 | 16 | + | 4.811 | 6.2687 | 1.67914 | 52 | chr3 | unknown | gene | 131564767 | 131643102 | + | Papss1 | Papss1 | P2473 | NM_001289479 | TSS11979 |
| chr3 | 132086871 | 132086976 | MACS2_peak_1917 | 16 | + | 4.811 | 6.2687 | 1.67914 | 52 | chr3 | unknown | gene | 132630190 | 132644631 | + | Gm5549 | Gm5549 | P18517 | NM_001270430 | TSS15060 |
| chr3 | 132096859 | 132096988 | MACS2_peak_1918 | 16 | + | 4.811 | 6.2687 | 1.67914 | 51 | chr3 | unknown | gene | 131564767 | 131643102 | + | Papss1 | Papss1 | P2473 | NM_001289479 | TSS11979 |
| chr3 | 132096859 | 132096988 | MACS2_peak_1918 | 16 | + | 4.811 | 6.2687 | 1.67914 | 51 | chr3 | unknown | gene | 132630190 | 132644631 | + | Gm5549 | Gm5549 | P18517 | NM_001270430 | TSS15060 |
| chr3 | 133511159 | 133511283 | MACS2_peak_1919 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 48 | chr3 | unknown | gene | 133310109 | 133377875 | + | Ppa2 | Ppa2 | P16906 | NM_001293641 | TSS19609 |
| chr3 | 133511159 | 133511283 | MACS2_peak_1919 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 48 | chr3 | unknown | gene | 134236494 | 134258097 | + | Cxxc4 | Cxxc4 | P21862 | NM_001004367 | TSS24684 |
| chr3 | 133876105 | 133876196 | MACS2_peak_1920 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 69 | chr3 | unknown | gene | 133463676 | 133544390 | - | Tet2 | Tet2 | P1237 | NM_001040400 | TSS20832 |
| chr3 | 133876105 | 133876196 | MACS2_peak_1920 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 69 | chr3 | unknown | gene | 134236494 | 134258097 | + | Cxxc4 | Cxxc4 | P21862 | NM_001004367 | TSS24684 |
| chr3 | 133884208 | 133884299 | MACS2_peak_1921 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 20 | chr3 | unknown | gene | 133463676 | 133544390 | - | Tet2 | Tet2 | P1237 | NM_001040400 | TSS20832 |
| chr3 | 133884208 | 133884299 | MACS2_peak_1921 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 20 | chr3 | unknown | gene | 134236494 | 134258097 | + | Cxxc4 | Cxxc4 | P21862 | NM_001004367 | TSS24684 |
| chr3 | 133970097 | 133970248 | MACS2_peak_1922 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 65 | chr3 | unknown | gene | 133463676 | 133544390 | - | Tet2 | Tet2 | P1237 | NM_001040400 | TSS20832 |
| chr3 | 133970097 | 133970248 | MACS2_peak_1922 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 65 | chr3 | unknown | gene | 134236494 | 134258097 | + | Cxxc4 | Cxxc4 | P21862 | NM_001004367 | TSS24684 |
| chr3 | 134367381 | 134367472 | MACS2_peak_1923 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 38 | chr3 | unknown | gene | 134236494 | 134258097 | + | Cxxc4 | Cxxc4 | P21862 | NM_001004367 | TSS24684 |
| chr3 | 134367381 | 134367472 | MACS2_peak_1923 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 38 | chr3 | unknown | gene | 134404142 | 134423635 | - | 4930539C22Rik | 4930539C22Rik | | NR_040600 | TSS25373 |
| chr3 | 135041433 | 135041524 | MACS2_peak_1924 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 83 | chr3 | unknown | gene | 134829006 | 134932442 | + | Tacr3 | Tacr3 | P10010 | NM_021382 | TSS4462 |
| chr3 | 135041433 | 135041524 | MACS2_peak_1924 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 83 | chr3 | unknown | gene | 135212562 | 135273239 | + | Cenpe | Cenpe | P3883 | NM_173762 | TSS25648 |
| chr3 | 135338327 | 135338418 | MACS2_peak_1925 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 12 | chr3 | unknown | gene | 135281220 | 135304221 | + | Bdh2 | Bdh2 | P10218 | NM_001172055 | TSS9526 |
| chr3 | 135338327 | 135338418 | MACS2_peak_1925 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 12 | chr3 | unknown | gene | 135348036 | 135397808 | + | Slc9b1 | Slc9b1 | P8148 | NM_028946 | TSS12962 |
| chr3 | 135623371 | 135623482 | MACS2_peak_1926 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 70 | chr3 | unknown | gene | 135485610 | 135570439 | + | Manba | Manba | P3132 | NM_027288 | TSS505 |
| chr3 | 135623371 | 135623482 | MACS2_peak_1926 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 70 | chr3 | unknown | gene | 135825278 | 135886954 | + | Slc39a8 | Slc39a8 | P10612 | NM_026228 | TSS25239 |
| chr3 | 136563794 | 136563944 | MACS2_peak_1927 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 87 | chr3 | unknown | gene | 136435269 | 136449349 | - | 1700030L20Rik | 1700030L20Rik | | NR_040592 | TSS7853 |
| chr3 | 136563794 | 136563944 | MACS2_peak_1927 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 87 | chr3 | unknown | gene | 136670065 | 136935225 | + | Ppp3ca | Ppp3ca | P558 | NM_001293622 | TSS1376 |
| chr3 | 136752301 | 136752433 | MACS2_peak_1928 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 79 | chr3 | unknown | gene | 136435269 | 136449349 | - | 1700030L20Rik | 1700030L20Rik | | NR_040592 | TSS7853 |
| chr3 | 136752301 | 136752433 | MACS2_peak_1928 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 79 | chr3 | unknown | gene | 137341077 | 137431069 | + | Emcn | Emcn | P21935 | NM_016885 | TSS14575 |
| chr3 | 137158814 | 137158920 | MACS2_peak_1929 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 6 | chr3 | unknown | gene | 136670065 | 136935225 | + | Ppp3ca | Ppp3ca | P558 | NM_001293622 | TSS1376 |
| chr3 | 137158814 | 137158920 | MACS2_peak_1929 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 6 | chr3 | unknown | gene | 137341077 | 137431069 | + | Emcn | Emcn | P21935 | NM_016885 | TSS14575 |
| chr3 | 137362341 | 137362445 | MACS2_peak_1930 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 18 | chr3 | unknown | gene | 136670065 | 136935225 | + | Ppp3ca | Ppp3ca | P558 | NM_001293622 | TSS1376 |
| chr3 | 137362341 | 137362445 | MACS2_peak_1930 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 18 | chr3 | unknown | gene | 137550044 | 137552622 | - | Gm4861 | Gm4861 | P7300 | NM_177665 | TSS5644 |
| chr3 | 137861306 | 137861398 | MACS2_peak_1931 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 52 | chr3 | unknown | gene | 137623671 | 137626456 | + | Ddit4l | Ddit4l | P954 | NM_030143 | TSS3803 |
| chr3 | 137861306 | 137861398 | MACS2_peak_1931 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 52 | chr3 | unknown | gene | 137864486 | 137866447 | + | H2afz | H2afz | P16548 | NM_016750 | TSS19152 |
| chr3 | 138568762 | 138568853 | MACS2_peak_1932 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 51 | chr3 | unknown | gene | 138526190 | 138555504 | + | Eif4e | Eif4e | P14114 | NM_007917 | TSS9703 |
| chr3 | 138568762 | 138568853 | MACS2_peak_1932 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 51 | chr3 | unknown | gene | 138711534 | 138726984 | - | 4930425O10Rik | 4930425O10Rik | | NR_040545 | TSS11654 |
| chr3 | 139018925 | 139019016 | MACS2_peak_1933 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 68 | chr3 | unknown | gene | 138742207 | 138902444 | + | Tspan5 | Tspan5 | P26853 | NM_019571 | TSS3293 |
| chr3 | 139018925 | 139019016 | MACS2_peak_1933 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 68 | chr3 | unknown | gene | 139205892 | 139709173 | + | Stpg2 | Stpg2 | P3486 | NM_198659 | TSS1007 |
| chr3 | 139193451 | 139193542 | MACS2_peak_1934 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 17 | chr3 | unknown | gene | 138925896 | 139075039 | - | Rap1gds1 | Rap1gds1 | P10883 | NM_145544 | TSS19880 |
| chr3 | 139193451 | 139193542 | MACS2_peak_1934 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 17 | chr3 | unknown | gene | 139205892 | 139709173 | + | Stpg2 | Stpg2 | P3486 | NM_198659 | TSS1007 |
| chr3 | 139558515 | 139558606 | MACS2_peak_1935 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 67 | chr3 | unknown | gene | 138925896 | 139075039 | - | Rap1gds1 | Rap1gds1 | P10883 | NM_145544 | TSS19880 |
| chr3 | 139558515 | 139558606 | MACS2_peak_1935 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 67 | chr3 | unknown | gene | 140028248 | 140028370 | + | Mir7j | Mir7j | | NR_105798 | TSS23071 |
| chr3 | 139900099 | 139900236 | MACS2_peak_1936 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 88 | chr3 | unknown | gene | 139205892 | 139709173 | + | Stpg2 | Stpg2 | P3486 | NM_198659 | TSS1007 |
| chr3 | 139900099 | 139900236 | MACS2_peak_1936 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 88 | chr3 | unknown | gene | 140028248 | 140028370 | + | Mir7j | Mir7j | | NR_105798 | TSS23071 |
| chr3 | 140629985 | 140630076 | MACS2_peak_1937 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 52 | chr3 | unknown | gene | 140028248 | 140028370 | + | Mir7j | Mir7j | | NR_105798 | TSS23071 |
| chr3 | 140629985 | 140630076 | MACS2_peak_1937 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 52 | chr3 | unknown | gene | 141210003 | 141211745 | - | Pdha2 | Pdha2 | P12158 | NM_008811 | TSS20810 |
| chr3 | 141887662 | 141887787 | MACS2_peak_1938 | 31 | + | 5.82147 | 8.1379 | 3.18452 | 61 | chr3 | unknown | gene | 141465563 | 141828572 | + | Unc5c | Unc5c | P17506 | NM_001293561 | TSS145 |
| chr3 | 141887662 | 141887787 | MACS2_peak_1938 | 31 | + | 5.82147 | 8.1379 | 3.18452 | 61 | chr3 | unknown | gene | 142239584 | 142395696 | - | Pdlim5 | Pdlim5 | P5604 | NM_001190856 | TSS18329 |
| chr3 | 142161313 | 142161404 | MACS2_peak_1939 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 43 | chr3 | unknown | gene | 141465563 | 141828572 | + | Unc5c | Unc5c | P17506 | NM_001293561 | TSS145 |
| chr3 | 142161313 | 142161404 | MACS2_peak_1939 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 43 | chr3 | unknown | gene | 142239584 | 142395696 | - | Pdlim5 | Pdlim5 | P5604 | NM_001190856 | TSS18329 |
| chr3 | 142191770 | 142191886 | MACS2_peak_1940 | 113 | + | 9.93641 | 16.71535 | 11.38262 | 44 | chr3 | unknown | gene | 141837135 | 142169228 | - | Bmpr1b | Bmpr1b | P9823 | NM_001277216 | TSS22091 |
| chr3 | 142191770 | 142191886 | MACS2_peak_1940 | 113 | + | 9.93641 | 16.71535 | 11.38262 | 44 | chr3 | unknown | gene | 142239584 | 142395696 | - | Pdlim5 | Pdlim5 | P5604 | NM_001190856 | TSS18329 |
| chr3 | 142358767 | 142358858 | MACS2_peak_1941 | 16 | + | 4.811 | 6.2687 | 1.67914 | 35 | chr3 | unknown | gene | 141837135 | 142169228 | - | Bmpr1b | Bmpr1b | P9823 | NM_001277216 | TSS22091 |
| chr3 | 142358767 | 142358858 | MACS2_peak_1941 | 16 | + | 4.811 | 6.2687 | 1.67914 | 35 | chr3 | unknown | gene | 142496933 | 142521162 | + | Gbp5 | Gbp5 | P20262 | NM_153564 | TSS4185 |
| chr3 | 143265896 | 143265987 | MACS2_peak_1942 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 85 | chr3 | unknown | gene | 143243054 | 143257996 | + | A830019L24Rik | A830019L24Rik | | NR_040551 | TSS26044 |
| chr3 | 143265896 | 143265987 | MACS2_peak_1942 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 85 | chr3 | unknown | gene | 143670891 | 143712143 | - | Gm6260 | Gm6260 | | NR_040405 | TSS18590 |
| chr3 | 143386723 | 143386814 | MACS2_peak_1943 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 18 | chr3 | unknown | gene | 143243054 | 143257996 | + | A830019L24Rik | A830019L24Rik | | NR_040551 | TSS26044 |
| chr3 | 143386723 | 143386814 | MACS2_peak_1943 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 18 | chr3 | unknown | gene | 143670891 | 143712143 | - | Gm6260 | Gm6260 | | NR_040405 | TSS18590 |
| chr3 | 144206739 | 144206923 | MACS2_peak_1944 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 123 | chr3 | unknown | gene | 144188529 | 144205255 | - | Lmo4 | Lmo4 | P25810 | NM_010723 | TSS8164 |
| chr3 | 144206739 | 144206923 | MACS2_peak_1944 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 123 | chr3 | unknown | gene | 144431106 | 144569857 | - | Hs2st1 | Hs2st1 | P18092 | NM_011828 | TSS16378 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr3 | 144827595 | 144827706 | MACS2_peak_1945 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 84 | chr3 | unknown | gene | 144796558 | 144819469 | - | Clca3a2 | Clca3a2 | P16990 | NM_030601 | TSS19490 |
| chr3 | 144827595 | 144827706 | MACS2_peak_1945 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 84 | chr3 | unknown | gene | 144879321 | 144896011 | - | Clca4c-ps | Clca4c-ps | | NR_126537 | TSS25861 |
| chr3 | 146598454 | 146598545 | MACS2_peak_1946 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 20 | chr3 | unknown | gene | 146506345 | 146521396 | - | Rpf1 | Rpf1 | P5952 | NM_027371 | TSS8416 |
| chr3 | 146598454 | 146598545 | MACS2_peak_1946 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 20 | chr3 | unknown | gene | 146641931 | 146651715 | + | Gm16325 | Gm16325 | | NR_045949 | TSS18083 |
| chr3 | 147091575 | 147091666 | MACS2_peak_1947 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 6 | chr3 | unknown | gene | 146852366 | 146979751 | + | Ttll7 | Ttll7 | P18159 | NM_001302957 | TSS20242 |
| chr3 | 147091575 | 147091666 | MACS2_peak_1947 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 6 | chr3 | unknown | gene | 148815585 | 148954635 | - | Adgrl2 | Adgrl2 | P13408 | NM_001081298 | TSS18937 |
| chr3 | 148030594 | 148030685 | MACS2_peak_1948 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 24 | chr3 | unknown | gene | 146852366 | 146979751 | + | Ttll7 | Ttll7 | P18159 | NM_001302957 | TSS20242 |
| chr3 | 148030594 | 148030685 | MACS2_peak_1948 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 24 | chr3 | unknown | gene | 148815585 | 148954635 | - | Adgrl2 | Adgrl2 | P13408 | NM_001081298 | TSS18937 |
| chr3 | 148197302 | 148197398 | MACS2_peak_1949 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 80 | chr3 | unknown | gene | 146852366 | 146979751 | + | Ttll7 | Ttll7 | P18159 | NM_001302957 | TSS20242 |
| chr3 | 148197302 | 148197398 | MACS2_peak_1949 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 80 | chr3 | unknown | gene | 148815585 | 148954635 | - | Adgrl2 | Adgrl2 | P13408 | NM_001081298 | TSS18937 |
| chr3 | 148463153 | 148463267 | MACS2_peak_1950 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 45 | chr3 | unknown | gene | 146852366 | 146979751 | + | Ttll7 | Ttll7 | P18159 | NM_001302957 | TSS20242 |
| chr3 | 148463153 | 148463267 | MACS2_peak_1950 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 45 | chr3 | unknown | gene | 148815585 | 148954635 | - | Adgrl2 | Adgrl2 | P13408 | NM_001081298 | TSS18937 |
| chr3 | 148967158 | 148967249 | MACS2_peak_1951 | 20 | + | 5.05561 | 6.70783 | 2.03509 | 21 | chr3 | unknown | gene | 148815585 | 148954635 | - | Adgrl2 | Adgrl2 | P13408 | NM_001081298 | TSS18937 |
| chr3 | 148967158 | 148967249 | MACS2_peak_1951 | 20 | + | 5.05561 | 6.70783 | 2.03509 | 21 | chr3 | unknown | gene | 149274736 | 149279980 | + | Gm1653 | Gm1653 | | NR_040591 | TSS15629 |
| chr3 | 148999764 | 148999855 | MACS2_peak_1952 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 60 | chr3 | unknown | gene | 148815585 | 148954635 | - | Adgrl2 | Adgrl2 | P13408 | NM_001081298 | TSS18937 |
| chr3 | 148999764 | 148999855 | MACS2_peak_1952 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 60 | chr3 | unknown | gene | 149274736 | 149279980 | + | Gm1653 | Gm1653 | | NR_040591 | TSS15629 |
| chr3 | 149240582 | 149240673 | MACS2_peak_1953 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 14 | chr3 | unknown | gene | 148815585 | 148954635 | - | Adgrl2 | Adgrl2 | P13408 | NM_001081298 | TSS18937 |
| chr3 | 149240582 | 149240673 | MACS2_peak_1953 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 14 | chr3 | unknown | gene | 149274736 | 149279980 | + | Gm1653 | Gm1653 | | NR_040591 | TSS15629 |
| chr3 | 150937246 | 150937415 | MACS2_peak_1954 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 10 | chr3 | unknown | gene | 149274736 | 149279980 | + | Gm1653 | Gm1653 | | NR_040591 | TSS15629 |
| chr3 | 150937246 | 150937415 | MACS2_peak_1954 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 10 | chr3 | unknown | gene | 151437881 | 151543296 | + | Adgrl4 | Adgrl4 | P14425 | NM_133222 | TSS25425 |
| chr3 | 151434380 | 151434471 | MACS2_peak_1955 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 48 | chr3 | unknown | gene | 149274736 | 149279980 | + | Gm1653 | Gm1653 | | NR_040591 | TSS15629 |
| chr3 | 151434380 | 151434471 | MACS2_peak_1955 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 48 | chr3 | unknown | gene | 151437881 | 151543296 | + | Adgrl4 | Adgrl4 | P14425 | NM_133222 | TSS25425 |
| chr3 | 152017440 | 152017599 | MACS2_peak_1956 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 35 | chr3 | unknown | gene | 151798609 | 151837528 | - | Ptgfr | Ptgfr | P19111 | NM_008966 | TSS25689 |
| chr3 | 152017440 | 152017599 | MACS2_peak_1956 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 35 | chr3 | unknown | gene | 152093840 | 152165887 | - | Gipc2 | Gipc2 | P12884 | NM_016867 | TSS14874 |
| chr3 | 152072074 | 152072180 | MACS2_peak_1957 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 40 | chr3 | unknown | gene | 151798609 | 151837528 | - | Ptgfr | Ptgfr | P19111 | NM_008966 | TSS25689 |
| chr3 | 152072074 | 152072180 | MACS2_peak_1957 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 40 | chr3 | unknown | gene | 152093840 | 152165887 | - | Gipc2 | Gipc2 | P12884 | NM_016867 | TSS14874 |
| chr3 | 153549763 | 153549854 | MACS2_peak_1958 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 21 | chr3 | unknown | gene | 153296501 | 153298649 | - | 1700012D16Rik | 1700012D16Rik | | NR_126464 | TSS17673 |
| chr3 | 153549763 | 153549854 | MACS2_peak_1958 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 21 | chr3 | unknown | gene | 153789304 | 153792087 | - | 5730460C07Rik | 5730460C07Rik | | NR_045801 | TSS1806 |
| chr3 | 153945411 | 153945518 | MACS2_peak_1959 | 40 | + | 6.30384 | 9.04635 | 4.00347 | 59 | chr3 | unknown | gene | 153922352 | 153944425 | - | Acadm | Acadm | P20398 | NM_007382 | TSS2449 |
| chr3 | 153945411 | 153945518 | MACS2_peak_1959 | 40 | + | 6.30384 | 9.04635 | 4.00347 | 59 | chr3 | unknown | gene | 153973435 | 154270086 | + | Slc44a5 | Slc44a5 | P19606 | NM_001081263 | TSS422 |
| chr3 | 154712524 | 154712615 | MACS2_peak_1960 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 13 | chr3 | unknown | gene | 154596710 | 154622258 | + | Cryz | Cryz | P14397 | NM_009968 | TSS16790 |
| chr3 | 154712524 | 154712615 | MACS2_peak_1960 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 13 | chr3 | unknown | gene | 154786290 | 155055306 | - | Tnni3k | Tnni3k | P19982 | NM_177066 | TSS4124 |
| chr3 | 155165679 | 155165833 | MACS2_peak_1961 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 79 | chr3 | unknown | gene | 155084918 | 155093356 | - | Fpgt | Fpgt | P15909 | NM_029330 | TSS7827 |
| chr3 | 155165679 | 155165833 | MACS2_peak_1961 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 79 | chr3 | unknown | gene | 155976353 | 156008592 | + | 9330178D15Rik | 9330178D15Rik | | NR_040553 | TSS23888 |
| chr3 | 155570858 | 155571016 | MACS2_peak_1962 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 23 | chr3 | unknown | gene | 155093433 | 155193767 | + | Lrriq3 | Lrriq3 | P16666 | NM_028938 | TSS6877 |
| chr3 | 155570858 | 155571016 | MACS2_peak_1962 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 23 | chr3 | unknown | gene | 155976353 | 156008592 | + | 9330178D15Rik | 9330178D15Rik | | NR_040553 | TSS23888 |
| chr3 | 156685070 | 156685195 | MACS2_peak_1963 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 44 | chr3 | unknown | gene | 156546752 | 156561746 | - | 4930570G19Rik | 4930570G19Rik | | NR_040399 | TSS1530 |
| chr3 | 156685070 | 156685195 | MACS2_peak_1963 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 44 | chr3 | unknown | gene | 157534396 | 157546738 | + | Zranb2 | Zranb2 | P24982 | NM_017381 | TSS15513 |
| chr3 | 158325229 | 158325320 | MACS2_peak_1964 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 15 | chr3 | unknown | gene | 158036681 | 158066218 | + | Lrrc40 | Lrrc40 | P13093 | NM_024194 | TSS20668 |
| chr3 | 158325229 | 158325320 | MACS2_peak_1964 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 15 | chr3 | unknown | gene | 159076363 | 159308080 | + | Gm20752 | Gm20752 | | NR_040750 | TSS17204 |
| chr3 | 159268678 | 159268791 | MACS2_peak_1965 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 83 | chr3 | unknown | gene | 158082894 | 158562221 | - | Lrrc7 | Lrrc7 | P10952 | NM_001291452 | TSS24092 |
| chr3 | 159268678 | 159268791 | MACS2_peak_1965 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 83 | chr3 | unknown | gene | 159495432 | 159529139 | + | Depdc1a | Depdc1a | P26694 | NM_001172092 | TSS4207 |
| chr3 | 159494109 | 159494200 | MACS2_peak_1966 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 53 | chr3 | unknown | gene | 159076363 | 159308080 | + | Gm20752 | Gm20752 | | NR_040750 | TSS17204 |
| chr3 | 159494109 | 159494200 | MACS2_peak_1966 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 53 | chr3 | unknown | gene | 159495432 | 159529139 | + | Depdc1a | Depdc1a | P26694 | NM_001172092 | TSS4207 |
| chr4 | 3090065 | 3090178 | MACS2_peak_1967 | 58 | + | 7.13224 | 10.94419 | 5.81828 | 63 | chr4 | unknown | gene | 3172082 | 3173003 | + | Vmn1r2 | Vmn1r2 | P11212 | NM_001167534 | TSS16062 |
| chr4 | 3939901 | 3940046 | MACS2_peak_1968 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 72 | chr4 | unknown | gene | 3901157 | 3938405 | - | Plag1 | Plag1 | P19678 | NM_019969 | TSS5291 |
| chr4 | 3939901 | 3940046 | MACS2_peak_1968 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 72 | chr4 | unknown | gene | 3995941 | 4019663 | - | Sdr16c5 | Sdr16c5 | P22548 | NM_181989 | TSS16 |
| chr4 | 4137166 | 4137266 | MACS2_peak_1969 | 30 | + | 5.71265 | 7.93979 | 3.00019 | 56 | chr4 | unknown | gene | 4056665 | 4077514 | - | Sdr16c6 | Sdr16c6 | P19502 | NM_001080710 | TSS4511 |
| chr4 | 4137166 | 4137266 | MACS2_peak_1969 | 30 | + | 5.71265 | 7.93979 | 3.00019 | 56 | chr4 | unknown | gene | 4527773 | 4528719 | - | Gm11780 | Gm11780 | P788 | NM_001277919 | TSS10199 |
| chr4 | 4756923 | 4757014 | MACS2_peak_1970 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 26 | chr4 | unknown | gene | 4527773 | 4528719 | - | Gm11780 | Gm11780 | P788 | NM_001277919 | TSS10199 |
| chr4 | 4756923 | 4757014 | MACS2_peak_1970 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 26 | chr4 | unknown | gene | 4764350 | 4793103 | - | Impad1 | Impad1 | P8077 | NM_177730 | TSS22924 |
| chr4 | 6780422 | 6780513 | MACS2_peak_1971 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 73 | chr4 | unknown | gene | 6396207 | 6454043 | - | Nsmaf | Nsmaf | P2487 | NM_010945 | TSS2727 |
| chr4 | 6780422 | 6780513 | MACS2_peak_1971 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 73 | chr4 | unknown | gene | 7560687 | 7573801 | + | 8430436N08Rik | 8430436N08Rik | | NR_040645 | TSS26306 |
| chr4 | 7566279 | 7566408 | MACS2_peak_1972 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 77 | chr4 | unknown | gene | 6687385 | 6990491 | - | Tox | Tox | P12450 | NM_145711 | TSS17767 |
| chr4 | 7566279 | 7566408 | MACS2_peak_1972 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 77 | chr4 | unknown | gene | 8141492 | 8238954 | - | Car8 | Car8 | P10273 | NM_007592 | TSS11741 |
| chr4 | 8577463 | 8577554 | MACS2_peak_1973 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 24 | chr4 | unknown | gene | 8141492 | 8238954 | - | Car8 | Car8 | P10273 | NM_007592 | TSS11741 |
| chr4 | 8577463 | 8577554 | MACS2_peak_1973 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 24 | chr4 | unknown | gene | 8690405 | 8866655 | + | Chd7 | Chd7 | P5576 | NM_001277149 | TSS18326 |
| chr4 | 8622452 | 8622543 | MACS2_peak_1974 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 21 | chr4 | unknown | gene | 8535643 | 8606503 | + | Rab2a | Rab2a | P19927 | NM_021518 | TSS13273 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr4 | 8622452 | 8622543 | MACS2_peak_1974 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 21 | chr4 | unknown | gene | 8690405 | 8866655 | + | Chd7 | Chd7 | P5576 | NM_001277149 | TSS18326 |
| chr4 | 8676171 | 8676262 | MACS2_peak_1975 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 36 | chr4 | unknown | gene | 8535643 | 8606503 | + | Rab2a | Rab2a | P19927 | NM_021518 | TSS13273 |
| chr4 | 8676171 | 8676262 | MACS2_peak_1975 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 36 | chr4 | unknown | gene | 8690405 | 8866655 | + | Chd7 | Chd7 | P5576 | NM_001277149 | TSS18326 |
| chr4 | 8737089 | 8737180 | MACS2_peak_1976 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 10 | chr4 | unknown | gene | 8535643 | 8606503 | + | Rab2a | Rab2a | P19927 | NM_021518 | TSS13273 |
| chr4 | 8737089 | 8737180 | MACS2_peak_1976 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 10 | chr4 | unknown | gene | 9269316 | 9449477 | + | Clvs1 | Clvs1 | P24581 | NM_028940 | TSS5773 |
| chr4 | 9435230 | 9435321 | MACS2_peak_1977 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 34 | chr4 | unknown | gene | 8690405 | 8866655 | + | Chd7 | Chd7 | P5576 | NM_001277149 | TSS18326 |
| chr4 | 9435230 | 9435321 | MACS2_peak_1977 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 34 | chr4 | unknown | gene | 9449084 | 9669344 | - | Asph | Asph | P3391 | NM_023066 | TSS23677 |
| chr4 | 9959425 | 9959516 | MACS2_peak_1978 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 53 | chr4 | unknown | gene | 9915964 | 9917397 | - | 4930448K20Rik | 4930448K20Rik | | NR_004448 | TSS16277 |
| chr4 | 9959425 | 9959516 | MACS2_peak_1978 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 53 | chr4 | unknown | gene | 10508030 | 10797802 | - | 1700123O12Rik | 1700123O12Rik | | NR_045185 | TSS26404 |
| chr4 | 10601346 | 10601473 | MACS2_peak_1979 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 37 | chr4 | unknown | gene | 9915964 | 9917397 | - | 4930448K20Rik | 4930448K20Rik | | NR_004448 | TSS16277 |
| chr4 | 10601346 | 10601473 | MACS2_peak_1979 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 37 | chr4 | unknown | gene | 10874497 | 10898052 | + | 2610301B20Rik | 2610301B20Rik | P11837 | NM_026005 | TSS25122 |
| chr4 | 11747872 | 11747963 | MACS2_peak_1980 | 12 | + | 4.14966 | 5.12722 | 1.204 | 19 | chr4 | unknown | gene | 11704446 | 11713753 | + | Gem | Gem | P12557 | NM_010276 | TSS16322 |
| chr4 | 11747872 | 11747963 | MACS2_peak_1980 | 12 | + | 4.14966 | 5.12722 | 1.204 | 19 | chr4 | unknown | gene | 11758156 | 11817074 | + | Cdh17 | Cdh17 | P10491 | NM_019753 | TSS3013 |
| chr4 | 12858097 | 12858188 | MACS2_peak_1981 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 74 | chr4 | unknown | gene | 12153721 | 12171930 | - | Fam92a | Fam92a | P9507 | NM_026558 | TSS17526 |
| chr4 | 12858097 | 12858188 | MACS2_peak_1981 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 74 | chr4 | unknown | gene | 12906836 | 12980518 | + | Triqk | Triqk | P25064 | NM_173746 | TSS14950 |
| chr4 | 13163159 | 13163250 | MACS2_peak_1982 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 32 | chr4 | unknown | gene | 12906836 | 12980518 | + | Triqk | Triqk | P25064 | NM_173746 | TSS14950 |
| chr4 | 13163159 | 13163250 | MACS2_peak_1982 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 32 | chr4 | unknown | gene | 13743301 | 13889887 | + | Runx1t1 | Runx1t1 | P7736 | NM_001111026 | TSS21583 |
| chr4 | 13603361 | 13603452 | MACS2_peak_1983 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 36 | chr4 | unknown | gene | 12906836 | 12980518 | + | Triqk | Triqk | P25064 | NM_173746 | TSS14950 |
| chr4 | 13603361 | 13603452 | MACS2_peak_1983 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 36 | chr4 | unknown | gene | 13743301 | 13889887 | + | Runx1t1 | Runx1t1 | P7736 | NM_001111026 | TSS21583 |
| chr4 | 14387809 | 14387905 | MACS2_peak_1984 | 23 | + | 5.33156 | 7.20295 | 2.32792 | 41 | chr4 | unknown | gene | 14212011 | 14291309 | - | Gm2560 | Gm2560 | | NR_131155 | TSS10588 |
| chr4 | 14387809 | 14387905 | MACS2_peak_1984 | 23 | + | 5.33156 | 7.20295 | 2.32792 | 41 | chr4 | unknown | gene | 14505196 | 14621778 | - | Slc26a7 | Slc26a7 | P24963 | NM_145947 | TSS13797 |
| chr4 | 14592657 | 14592788 | MACS2_peak_1985 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 59 | chr4 | unknown | gene | 14212011 | 14291309 | - | Gm2560 | Gm2560 | | NR_131155 | TSS10588 |
| chr4 | 14592657 | 14592788 | MACS2_peak_1985 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 59 | chr4 | unknown | gene | 14665753 | 14796045 | - | Lrrc69 | Lrrc69 | P5311 | NM_028499 | TSS7291 |
| chr4 | 15885256 | 15885359 | MACS2_peak_1986 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 34 | chr4 | unknown | gene | 15265819 | 15283350 | + | Tmem64 | Tmem64 | P18047 | NM_181401 | TSS16204 |
| chr4 | 15885256 | 15885359 | MACS2_peak_1986 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 34 | chr4 | unknown | gene | 15917239 | 15945351 | - | Decr1 | Decr1 | P5115 | NM_026172 | TSS18860 |
| chr4 | 16099515 | 16099606 | MACS2_peak_1987 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 70 | chr4 | unknown | gene | 15997120 | 16013730 | - | Osgin2 | Osgin2 | P9800 | NM_145950 | TSS1922 |
| chr4 | 16099515 | 16099606 | MACS2_peak_1987 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 70 | chr4 | unknown | gene | 16123374 | 16163396 | - | Ripk2 | Ripk2 | P25206 | NM_138952 | TSS26090 |
| chr4 | 16114356 | 16114447 | MACS2_peak_1988 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 3 | chr4 | unknown | gene | 15997120 | 16013730 | - | Osgin2 | Osgin2 | P9800 | NM_145950 | TSS1922 |
| chr4 | 16114356 | 16114447 | MACS2_peak_1988 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 3 | chr4 | unknown | gene | 16123374 | 16163396 | - | Ripk2 | Ripk2 | P25206 | NM_138952 | TSS26090 |
| chr4 | 16494308 | 16494399 | MACS2_peak_1989 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 13 | chr4 | unknown | gene | 16164109 | 16266225 | + | A530072M11Rik | A530072M11Rik | | NR_045765 | TSS22998 |
| chr4 | 16494308 | 16494399 | MACS2_peak_1989 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 13 | chr4 | unknown | gene | 17853481 | 18116221 | + | Mmp16 | Mmp16 | P24591 | NM_019724 | TSS3264 |
| chr4 | 18286609 | 18286714 | MACS2_peak_1990 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 72 | chr4 | unknown | gene | 17853481 | 18116221 | + | Mmp16 | Mmp16 | P24591 | NM_019724 | TSS3264 |
| chr4 | 18286609 | 18286714 | MACS2_peak_1990 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 72 | chr4 | unknown | gene | 19280849 | 19508083 | + | Cngb3 | Cngb3 | P19166 | NM_013927 | TSS1020 |
| chr4 | 19158134 | 19158225 | MACS2_peak_1991 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 9 | chr4 | unknown | gene | 17853481 | 18116221 | + | Mmp16 | Mmp16 | P24591 | NM_019724 | TSS3264 |
| chr4 | 19158134 | 19158225 | MACS2_peak_1991 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 9 | chr4 | unknown | gene | 19280849 | 19508083 | + | Cngb3 | Cngb3 | P19166 | NM_013927 | TSS1020 |
| chr4 | 20470869 | 20470960 | MACS2_peak_1992 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 53 | chr4 | unknown | gene | 20042051 | 20065861 | + | Ggh | Ggh | P11836 | NM_010281 | TSS23468 |
| chr4 | 20470869 | 20470960 | MACS2_peak_1992 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 53 | chr4 | unknown | gene | 21677479 | 21685798 | - | Prdm13 | Prdm13 | P2114 | NM_001080771 | TSS2420 |
| chr4 | 23642089 | 23642180 | MACS2_peak_1993 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 20 | chr4 | unknown | gene | 22490547 | 22493126 | + | Pnky | Pnky | | NR_131335 | TSS24488 |
| chr4 | 23642089 | 23642180 | MACS2_peak_1993 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 20 | chr4 | unknown | gene | 24496461 | 24602646 | + | Mms22l | Mms22l | P21425 | NM_199467 | TSS4748 |
| chr4 | 23922186 | 23922390 | MACS2_peak_1994 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 31 | chr4 | unknown | gene | 22490547 | 22493126 | + | Pnky | Pnky | | NR_131335 | TSS24488 |
| chr4 | 23922186 | 23922390 | MACS2_peak_1994 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 31 | chr4 | unknown | gene | 24496461 | 24602646 | + | Mms22l | Mms22l | P21425 | NM_199467 | TSS4748 |
| chr4 | 24038508 | 24038675 | MACS2_peak_1995 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 12 | chr4 | unknown | gene | 22490547 | 22493126 | + | Pnky | Pnky | | NR_131335 | TSS24488 |
| chr4 | 24038508 | 24038675 | MACS2_peak_1995 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 12 | chr4 | unknown | gene | 24496461 | 24602646 | + | Mms22l | Mms22l | P21425 | NM_199467 | TSS4748 |
| chr4 | 24665211 | 24665302 | MACS2_peak_1996 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 24 | chr4 | unknown | gene | 24496461 | 24602646 | + | Mms22l | Mms22l | P21425 | NM_199467 | TSS4748 |
| chr4 | 24665211 | 24665302 | MACS2_peak_1996 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 24 | chr4 | unknown | gene | 24898082 | 24901975 | + | Ndufaf4 | Ndufaf4 | P3658 | NM_026742 | TSS20342 |
| chr4 | 25585369 | 25585460 | MACS2_peak_1997 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 19 | chr4 | unknown | gene | 25248585 | 25281752 | - | Ufl1 | Ufl1 | P20305 | NM_026194 | TSS13534 |
| chr4 | 25585369 | 25585460 | MACS2_peak_1997 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 19 | chr4 | unknown | gene | 25609332 | 25800003 | - | Fut9 | Fut9 | P26872 | NM_010243 | TSS2669 |
| chr4 | 25632307 | 25632398 | MACS2_peak_1998 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 49 | chr4 | unknown | gene | 25248585 | 25281752 | - | Ufl1 | Ufl1 | P20305 | NM_026194 | TSS13534 |
| chr4 | 25632307 | 25632398 | MACS2_peak_1998 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 49 | chr4 | unknown | gene | 26324505 | 26346652 | - | Manea | Manea | P26047 | NM_172865 | TSS14669 |
| chr4 | 26308937 | 26309028 | MACS2_peak_1999 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 37 | chr4 | unknown | gene | 25609332 | 25800003 | - | Fut9 | Fut9 | P26872 | NM_010243 | TSS2669 |
| chr4 | 26308937 | 26309028 | MACS2_peak_1999 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 37 | chr4 | unknown | gene | 26324505 | 26346652 | - | Manea | Manea | P26047 | NM_172865 | TSS14669 |
| chr4 | 26771689 | 26771780 | MACS2_peak_2000 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 41 | chr4 | unknown | gene | 26635819 | 26705449 | - | 4930548K13Rik | 4930548K13Rik | | NR_040656 | TSS19471 |
| chr4 | 26771689 | 26771780 | MACS2_peak_2000 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 41 | chr4 | unknown | gene | 28813130 | 28964003 | + | Epha7 | Epha7 | P17077 | NM_001290434 | TSS24844 |
| chr4 | 26888543 | 26888634 | MACS2_peak_2001 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 59 | chr4 | unknown | gene | 26635819 | 26705449 | - | 4930548K13Rik | 4930548K13Rik | | NR_040656 | TSS19471 |
| chr4 | 26888543 | 26888634 | MACS2_peak_2001 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 59 | chr4 | unknown | gene | 28813130 | 28964003 | + | Epha7 | Epha7 | P17077 | NM_001290434 | TSS24844 |
| chr4 | 27103005 | 27103096 | MACS2_peak_2002 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 77 | chr4 | unknown | gene | 26635819 | 26705449 | - | 4930548K13Rik | 4930548K13Rik | | NR_040656 | TSS19471 |
| chr4 | 27103005 | 27103096 | MACS2_peak_2002 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 77 | chr4 | unknown | gene | 28813130 | 28964003 | + | Epha7 | Epha7 | P17077 | NM_001290434 | TSS24844 |
| chr4 | 27449513 | 27449604 | MACS2_peak_2003 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 21 | chr4 | unknown | gene | 26635819 | 26705449 | - | 4930548K13Rik | 4930548K13Rik | | NR_040656 | TSS19471 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr4 | 27449513 | 27449604 | MACS2_peak_2003 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 21 | chr4 | unknown | gene | 28813130 | 28964003 | + | Epha7 | Epha7 | P17077 | NM_001290434 | TSS24844 |
| chr4 | 27721799 | 27721890 | MACS2_peak_2004 | 12 | + | 4.14966 | 5.12722 | 1.204 | 33 | chr4 | unknown | gene | 26635819 | 26705449 | - | 4930548K13Rik | 4930548K13Rik | | NR_040656 | TSS19471 |
| chr4 | 27721799 | 27721890 | MACS2_peak_2004 | 12 | + | 4.14966 | 5.12722 | 1.204 | 33 | chr4 | unknown | gene | 28813130 | 28964003 | + | Epha7 | Epha7 | P17077 | NM_001290434 | TSS24844 |
| chr4 | 28081530 | 28081621 | MACS2_peak_2005 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 49 | chr4 | unknown | gene | 26635819 | 26705449 | - | 4930548K13Rik | 4930548K13Rik | | NR_040656 | TSS19471 |
| chr4 | 28081530 | 28081621 | MACS2_peak_2005 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 49 | chr4 | unknown | gene | 28813130 | 28964003 | + | Epha7 | Epha7 | P17077 | NM_001290434 | TSS24844 |
| chr4 | 28176904 | 28177038 | MACS2_peak_2006 | 173 | + | 12.58611 | 22.85786 | 17.35208 | 58 | chr4 | unknown | gene | 26635819 | 26705449 | - | 4930548K13Rik | 4930548K13Rik | | NR_040656 | TSS19471 |
| chr4 | 28176904 | 28177038 | MACS2_peak_2006 | 173 | + | 12.58611 | 22.85786 | 17.35208 | 58 | chr4 | unknown | gene | 28813130 | 28964003 | + | Epha7 | Epha7 | P17077 | NM_001290434 | TSS24844 |
| chr4 | 28931334 | 28931425 | MACS2_peak_2007 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 36 | chr4 | unknown | gene | 26635819 | 26705449 | - | 4930548K13Rik | 4930548K13Rik | | NR_040656 | TSS19471 |
| chr4 | 28931334 | 28931425 | MACS2_peak_2007 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 36 | chr4 | unknown | gene | 30664595 | 30855744 | + | 4930556G01Rik | 4930556G01Rik | | NR_040655 | TSS11637 |
| chr4 | 29166870 | 29166961 | MACS2_peak_2008 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 22 | chr4 | unknown | gene | 28813130 | 28964003 | + | Epha7 | Epha7 | P17077 | NM_001290434 | TSS24844 |
| chr4 | 29166870 | 29166961 | MACS2_peak_2008 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 22 | chr4 | unknown | gene | 30664595 | 30855744 | + | 4930556G01Rik | 4930556G01Rik | | NR_040655 | TSS11637 |
| chr4 | 31119099 | 31119190 | MACS2_peak_2009 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 41 | chr4 | unknown | gene | 30664595 | 30855744 | + | 4930556G01Rik | 4930556G01Rik | | NR_040655 | TSS11637 |
| chr4 | 31119099 | 31119190 | MACS2_peak_2009 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 41 | chr4 | unknown | gene | 31964106 | 32019681 | + | Map3k7 | Map3k7 | P9393 | NM_172688 | TSS23094 |
| chr4 | 31223126 | 31223217 | MACS2_peak_2010 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 80 | chr4 | unknown | gene | 30664595 | 30855744 | + | 4930556G01Rik | 4930556G01Rik | | NR_040655 | TSS11637 |
| chr4 | 31223126 | 31223217 | MACS2_peak_2010 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 80 | chr4 | unknown | gene | 31964106 | 32019681 | + | Map3k7 | Map3k7 | P9393 | NM_172688 | TSS23094 |
| chr4 | 31468378 | 31468469 | MACS2_peak_2011 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 13 | chr4 | unknown | gene | 30664595 | 30855744 | + | 4930556G01Rik | 4930556G01Rik | | NR_040655 | TSS11637 |
| chr4 | 31468378 | 31468469 | MACS2_peak_2011 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 13 | chr4 | unknown | gene | 31964106 | 32019681 | + | Map3k7 | Map3k7 | P9393 | NM_172688 | TSS23094 |
| chr4 | 31538364 | 31538455 | MACS2_peak_2012 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 14 | chr4 | unknown | gene | 30664595 | 30855744 | + | 4930556G01Rik | 4930556G01Rik | | NR_040655 | TSS11637 |
| chr4 | 31538364 | 31538455 | MACS2_peak_2012 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 14 | chr4 | unknown | gene | 31964106 | 32019681 | + | Map3k7 | Map3k7 | P9393 | NM_172688 | TSS23094 |
| chr4 | 31928665 | 31928758 | MACS2_peak_2013 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 26 | chr4 | unknown | gene | 30664595 | 30855744 | + | 4930556G01Rik | 4930556G01Rik | | NR_040655 | TSS11637 |
| chr4 | 31928665 | 31928758 | MACS2_peak_2013 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 26 | chr4 | unknown | gene | 31964106 | 32019681 | + | Map3k7 | Map3k7 | P9393 | NM_172688 | TSS23094 |
| chr4 | 32560888 | 32561020 | MACS2_peak_2014 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 81 | chr4 | unknown | gene | 31964106 | 32019681 | + | Map3k7 | Map3k7 | P9393 | NM_172688 | TSS23094 |
| chr4 | 32560888 | 32561020 | MACS2_peak_2014 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 81 | chr4 | unknown | gene | 32600864 | 32602382 | - | Gja10 | Gja10 | P2671 | NM_010289 | TSS22703 |
| chr4 | 33892261 | 33892354 | MACS2_peak_2015 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 61 | chr4 | unknown | gene | 33310310 | 33500414 | + | Rngtt | Rngtt | P501 | NM_011884 | TSS9935 |
| chr4 | 33892261 | 33892354 | MACS2_peak_2015 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 61 | chr4 | unknown | gene | 33924631 | 33945035 | + | Cnr1 | Cnr1 | P5494 | NM_007726 | TSS11690 |
| chr4 | 35152941 | 35153056 | MACS2_peak_2016 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 41 | chr4 | unknown | gene | 34909788 | 34911481 | - | Platr9 | Platr9 | | NR_040652 | TSS9267 |
| chr4 | 35152941 | 35153056 | MACS2_peak_2016 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 41 | chr4 | unknown | gene | 35191281 | 35225880 | - | 3110043O21Rik | 3110043O21Rik | P26667 | NM_001081343 | TSS524 |
| chr4 | 36688898 | 36689022 | MACS2_peak_2017 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 69 | chr4 | unknown | gene | 36668509 | 36668586 | - | Mir873a | Mir873a | | NR_030605 | TSS12173 |
| chr4 | 36688898 | 36689022 | MACS2_peak_2017 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 69 | chr4 | unknown | gene | 39450292 | 39451446 | + | 1700009N14Rik | 1700009N14Rik | P21445 | NM_001081095 | TSS9061 |
| chr4 | 37547738 | 37547885 | MACS2_peak_2018 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 80 | chr4 | unknown | gene | 35706647 | 36951744 | - | Lingo2 | Lingo2 | P21991 | NM_001166000 | TSS8386 |
| chr4 | 37547738 | 37547885 | MACS2_peak_2018 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 80 | chr4 | unknown | gene | 39450292 | 39451446 | + | 1700009N14Rik | 1700009N14Rik | P21445 | NM_001081095 | TSS9061 |
| chr4 | 38847189 | 38847292 | MACS2_peak_2019 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 29 | chr4 | unknown | gene | 35706647 | 36951744 | - | Lingo2 | Lingo2 | P21991 | NM_001166000 | TSS8386 |
| chr4 | 38847189 | 38847292 | MACS2_peak_2019 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 29 | chr4 | unknown | gene | 39450292 | 39451446 | + | 1700009N14Rik | 1700009N14Rik | P21445 | NM_001081095 | TSS9061 |
| chr4 | 39675313 | 39675404 | MACS2_peak_2020 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 6 | chr4 | unknown | gene | 39450292 | 39451446 | + | 1700009N14Rik | 1700009N14Rik | P21445 | NM_001081095 | TSS9061 |
| chr4 | 39675313 | 39675404 | MACS2_peak_2020 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 6 | chr4 | unknown | gene | 40143264 | 40197667 | + | Aco1 | Aco1 | P5199 | NM_007386 | TSS3761 |
| chr4 | 42214806 | 42214931 | MACS2_peak_2021 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 58 | chr4 | unknown | gene | 41769469 | 41774176 | - | Ccl27a | Ccl27a | P9814 | NM_001048179 | TSS24130 |
| chr4 | 42214806 | 42214931 | MACS2_peak_2021 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 58 | chr4 | unknown | gene | 42848070 | 42853826 | - | Fam205a1 | Fam205a1 | P20700 | NM_001277167 | TSS9711 |
| chr4 | 42587206 | 42587297 | MACS2_peak_2022 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 60 | chr4 | unknown | gene | 41889794 | 42233950 | + | Gm3893 | Gm3893 | | NR_033506 | TSS17262 |
| chr4 | 42587206 | 42587297 | MACS2_peak_2022 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 60 | chr4 | unknown | gene | 42848070 | 42853826 | - | Fam205a1 | Fam205a1 | P20700 | NM_001277167 | TSS9711 |
| chr4 | 43559995 | 43560086 | MACS2_peak_2023 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 15 | chr4 | unknown | gene | 43513725 | 43523354 | - | Tpm2 | Tpm2 | P21456 | NM_001277876 | TSS14664 |
| chr4 | 43559995 | 43560086 | MACS2_peak_2023 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 15 | chr4 | unknown | gene | 43562633 | 43566797 | + | Creb3 | Creb3 | P21009 | NM_013497 | TSS138 |
| chr4 | 44303554 | 44303645 | MACS2_peak_2024 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 37 | chr4 | unknown | gene | 44221194 | 44221267 | - | Mir5106 | Mir5106 | | NR_039565 | TSS2891 |
| chr4 | 44303554 | 44303645 | MACS2_peak_2024 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 37 | chr4 | unknown | gene | 44531505 | 44710408 | - | Pax5 | Pax5 | P9440 | NM_008782 | TSS7090 |
| chr4 | 49912295 | 49912386 | MACS2_peak_2025 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 3 | chr4 | unknown | gene | 49661610 | 49845081 | - | Grin3a | Grin3a | P6208 | NM_001033351 | TSS24931 |
| chr4 | 49912295 | 49912386 | MACS2_peak_2025 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 3 | chr4 | unknown | gene | 51216677 | 51229928 | + | Cylc2 | Cylc2 | P15920 | NM_001162865 | TSS20011 |
| chr4 | 51445160 | 51445251 | MACS2_peak_2026 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 25 | chr4 | unknown | gene | 51216677 | 51229928 | + | Cylc2 | Cylc2 | P15920 | NM_001162865 | TSS20011 |
| chr4 | 51445160 | 51445251 | MACS2_peak_2026 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 25 | chr4 | unknown | gene | 51968093 | 52051110 | - | C630028M04Rik | C630028M04Rik | | NR_040668 | TSS7444 |
| chr4 | 51513392 | 51513483 | MACS2_peak_2027 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 30 | chr4 | unknown | gene | 51216677 | 51229928 | + | Cylc2 | Cylc2 | P15920 | NM_001162865 | TSS20011 |
| chr4 | 51513392 | 51513483 | MACS2_peak_2027 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 30 | chr4 | unknown | gene | 51968093 | 52051110 | - | C630028M04Rik | C630028M04Rik | | NR_040668 | TSS7444 |
| chr4 | 51538105 | 51538196 | MACS2_peak_2028 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 17 | chr4 | unknown | gene | 51216677 | 51229928 | + | Cylc2 | Cylc2 | P15920 | NM_001162865 | TSS20011 |
| chr4 | 51538105 | 51538196 | MACS2_peak_2028 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 17 | chr4 | unknown | gene | 51968093 | 52051110 | - | C630028M04Rik | C630028M04Rik | | NR_040668 | TSS7444 |
| chr4 | 52735846 | 52735937 | MACS2_peak_2029 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 29 | chr4 | unknown | gene | 52596273 | 52612160 | + | Toporsl | Toporsl | P5128 | NM_026652 | TSS15241 |
| chr4 | 52735846 | 52735937 | MACS2_peak_2029 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 29 | chr4 | unknown | gene | 52814603 | 52828269 | + | 4930552N02Rik | 4930552N02Rik | | NR_040661 | TSS22936 |
| chr4 | 52778698 | 52778789 | MACS2_peak_2030 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 41 | chr4 | unknown | gene | 52596273 | 52612160 | + | Toporsl | Toporsl | P5128 | NM_026652 | TSS15241 |
| chr4 | 52778698 | 52778789 | MACS2_peak_2030 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 41 | chr4 | unknown | gene | 52814603 | 52828269 | + | 4930552N02Rik | 4930552N02Rik | | NR_040661 | TSS22936 |
| chr4 | 53346943 | 53347034 | MACS2_peak_2031 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 41 | chr4 | unknown | gene | 53261355 | 53270232 | - | AI427809 | AI427809 | | NR_033140 | TSS6584 |
| chr4 | 53346943 | 53347034 | MACS2_peak_2031 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 41 | chr4 | unknown | gene | 53440412 | 53621609 | + | Slc44a1 | Slc44a1 | P6395 | NM_133891 | TSS22187 |
| chr4 | 53355473 | 53355564 | MACS2_peak_2032 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 49 | chr4 | unknown | gene | 53261355 | 53270232 | - | AI427809 | AI427809 | | NR_033140 | TSS6584 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr4 | 53355473 | 53355564 | MACS2_peak_2032 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 49 | chr4 | unknown | gene | 53440412 | 53621609 | + | Slc44a1 | Slc44a1 | P6395 | NM_133891 | TSS22187 |
| chr4 | 53523988 | 53524079 | MACS2_peak_2033 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 29 | chr4 | unknown | gene | 53261355 | 53270232 | - | AI427809 | AI427809 | | NR_033140 | TSS6584 |
| chr4 | 53523988 | 53524079 | MACS2_peak_2033 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 29 | chr4 | unknown | gene | 53631470 | 53701163 | + | Fsd1l | Fsd1l | P3012 | NM_176966 | TSS19431 |
| chr4 | 53632800 | 53632891 | MACS2_peak_2034 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 20 | chr4 | unknown | gene | 53440412 | 53621609 | + | Slc44a1 | Slc44a1 | P6395 | NM_133891 | TSS22187 |
| chr4 | 53632800 | 53632891 | MACS2_peak_2034 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 20 | chr4 | unknown | gene | 53714181 | 53761387 | + | Fktn | Fktn | P449 | NM_139309 | TSS21967 |
| chr4 | 54088245 | 54088336 | MACS2_peak_2035 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 9 | chr4 | unknown | gene | 53826044 | 53860100 | + | Tmem38b | Tmem38b | P26830 | NM_028053 | TSS19008 |
| chr4 | 54088245 | 54088336 | MACS2_peak_2035 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 9 | chr4 | unknown | gene | 54947944 | 55080873 | + | Zfp462 | Zfp462 | P21832 | NM_172867 | TSS23198 |
| chr4 | 54408677 | 54408768 | MACS2_peak_2036 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 29 | chr4 | unknown | gene | 53826044 | 53860100 | + | Tmem38b | Tmem38b | P26830 | NM_028053 | TSS19008 |
| chr4 | 54408677 | 54408768 | MACS2_peak_2036 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 29 | chr4 | unknown | gene | 54947944 | 55080873 | + | Zfp462 | Zfp462 | P21832 | NM_172867 | TSS23198 |
| chr4 | 54465044 | 54465135 | MACS2_peak_2037 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 25 | chr4 | unknown | gene | 53826044 | 53860100 | + | Tmem38b | Tmem38b | P26830 | NM_028053 | TSS19008 |
| chr4 | 54465044 | 54465135 | MACS2_peak_2037 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 25 | chr4 | unknown | gene | 54947944 | 55080873 | + | Zfp462 | Zfp462 | P21832 | NM_172867 | TSS23198 |
| chr4 | 54785306 | 54785397 | MACS2_peak_2038 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 28 | chr4 | unknown | gene | 53826044 | 53860100 | + | Tmem38b | Tmem38b | P26830 | NM_028053 | TSS19008 |
| chr4 | 54785306 | 54785397 | MACS2_peak_2038 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 28 | chr4 | unknown | gene | 54947944 | 55080873 | + | Zfp462 | Zfp462 | P21832 | NM_172867 | TSS23198 |
| chr4 | 54793744 | 54793835 | MACS2_peak_2039 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 33 | chr4 | unknown | gene | 53826044 | 53860100 | + | Tmem38b | Tmem38b | P26830 | NM_028053 | TSS19008 |
| chr4 | 54793744 | 54793835 | MACS2_peak_2039 | 30 | + | 5.75002 | 8.01616 | 3.07128 | 33 | chr4 | unknown | gene | 54947944 | 55080873 | + | Zfp462 | Zfp462 | P21832 | NM_172867 | TSS23198 |
| chr4 | 56281459 | 56281570 | MACS2_peak_2040 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 55 | chr4 | unknown | gene | 55527136 | 55531871 | - | Klf4 | Klf4 | P2411 | NM_010637 | TSS2813 |
| chr4 | 56281459 | 56281570 | MACS2_peak_2040 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 55 | chr4 | unknown | gene | 56740004 | 56741356 | - | Actl7b | Actl7b | P1186 | NM_025271 | TSS13406 |
| chr4 | 57389886 | 57389977 | MACS2_peak_2041 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 18 | chr4 | unknown | gene | 57359791 | 57364292 | - | 1700042G15Rik | 1700042G15Rik | | NR_038179 | TSS23973 |
| chr4 | 57389886 | 57389977 | MACS2_peak_2041 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 18 | chr4 | unknown | gene | 57568247 | 57710187 | + | Palm2 | Palm2 | P14869 | NM_172868 | TSS9042 |
| chr4 | 58305814 | 58305967 | MACS2_peak_2042 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 70 | chr4 | unknown | gene | 58042795 | 58206376 | - | Svep1 | Svep1 | P21294 | NM_022814 | TSS7002 |
| chr4 | 58305814 | 58305967 | MACS2_peak_2042 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 70 | chr4 | unknown | gene | 58435251 | 58553491 | - | Lpar1 | Lpar1 | P21331 | NM_001290486 | TSS27485 |
| chr4 | 58636288 | 58636379 | MACS2_peak_2043 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 20 | chr4 | unknown | gene | 58435251 | 58553491 | - | Lpar1 | Lpar1 | P21331 | NM_001290486 | TSS27485 |
| chr4 | 58636288 | 58636379 | MACS2_peak_2043 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 20 | chr4 | unknown | gene | 58784778 | 58785720 | - | Olfr267 | Olfr267 | P7610 | NM_146920 | TSS1110 |
| chr4 | 58850182 | 58850273 | MACS2_peak_2044 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 9 | chr4 | unknown | gene | 58784778 | 58785720 | - | Olfr267 | Olfr267 | P7610 | NM_146920 | TSS1110 |
| chr4 | 58850182 | 58850273 | MACS2_peak_2044 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 9 | chr4 | unknown | gene | 58943627 | 58957906 | + | Zkscan16 | Zkscan16 | P22726 | NM_001099323 | TSS18479 |
| chr4 | 59550188 | 59550279 | MACS2_peak_2045 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 25 | chr4 | unknown | gene | 59471867 | 59549155 | - | Ptbp3 | Ptbp3 | P6270 | NM_144904 | TSS4997 |
| chr4 | 59550188 | 59550279 | MACS2_peak_2045 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 25 | chr4 | unknown | gene | 59581562 | 59617747 | + | Hsdl2 | Hsdl2 | P19270 | NM_001301367 | TSS17794 |
| chr4 | 61807778 | 61807869 | MACS2_peak_2046 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 37 | chr4 | unknown | gene | 61778327 | 61782158 | - | Mup19 | Mup19 | P13605 | NM_001135127 | TSS26149 |
| chr4 | 61807778 | 61807869 | MACS2_peak_2046 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 37 | chr4 | unknown | gene | 61831318 | 61835122 | - | Mup5 | Mup5 | P21561 | NM_008649 | TSS4791 |
| chr4 | 62366587 | 62366713 | MACS2_peak_2047 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 37 | chr4 | unknown | gene | 62300341 | 62360422 | - | Fkbp15 | Fkbp15 | P12103 | NM_001045528 | TSS294 |
| chr4 | 62366587 | 62366713 | MACS2_peak_2047 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 37 | chr4 | unknown | gene | 62394588 | 62408623 | - | Cdc26 | Cdc26 | P1320 | NM_139291 | TSS23381 |
| chr4 | 62378585 | 62378686 | MACS2_peak_2048 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 45 | chr4 | unknown | gene | 62300341 | 62360422 | - | Fkbp15 | Fkbp15 | P12103 | NM_001045528 | TSS294 |
| chr4 | 62378585 | 62378686 | MACS2_peak_2048 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 45 | chr4 | unknown | gene | 62394588 | 62408623 | - | Cdc26 | Cdc26 | P1320 | NM_139291 | TSS23381 |
| chr4 | 62967264 | 62967355 | MACS2_peak_2049 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 44 | chr4 | unknown | gene | 62559846 | 62702245 | + | Rgs3 | Rgs3 | P23603 | NM_019492 | TSS22261 |
| chr4 | 62967264 | 62967355 | MACS2_peak_2049 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 44 | chr4 | unknown | gene | 63143278 | 63154055 | - | Ambp | Ambp | P13340 | NM_007443 | TSS22556 |
| chr4 | 63028979 | 63029070 | MACS2_peak_2050 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 34 | chr4 | unknown | gene | 62559846 | 62702245 | + | Rgs3 | Rgs3 | P23603 | NM_019492 | TSS22261 |
| chr4 | 63028979 | 63029070 | MACS2_peak_2050 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 34 | chr4 | unknown | gene | 63143278 | 63154055 | - | Ambp | Ambp | P13340 | NM_007443 | TSS22556 |
| chr4 | 63029838 | 63029958 | MACS2_peak_2051 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 37 | chr4 | unknown | gene | 62559846 | 62702245 | + | Rgs3 | Rgs3 | P23603 | NM_019492 | TSS22261 |
| chr4 | 63029838 | 63029958 | MACS2_peak_2051 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 37 | chr4 | unknown | gene | 63143278 | 63154055 | - | Ambp | Ambp | P13340 | NM_007443 | TSS22556 |
| chr4 | 63834404 | 63834525 | MACS2_peak_2052 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 57 | chr4 | unknown | gene | 63724602 | 63745084 | - | Tnfsf15 | Tnfsf15 | P25525 | NM_177371 | TSS13959 |
| chr4 | 63834404 | 63834525 | MACS2_peak_2052 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 57 | chr4 | unknown | gene | 63959784 | 64047015 | - | Tnc | Tnc | P110 | NM_011607 | TSS14000 |
| chr4 | 64085568 | 64085659 | MACS2_peak_2053 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 56 | chr4 | unknown | gene | 63959784 | 64047015 | - | Tnc | Tnc | P110 | NM_011607 | TSS14000 |
| chr4 | 64085568 | 64085659 | MACS2_peak_2053 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 56 | chr4 | unknown | gene | 65124173 | 65351725 | + | Pappa | Pappa | P1292 | NM_021362 | TSS7146 |
| chr4 | 64226235 | 64226326 | MACS2_peak_2054 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 20 | chr4 | unknown | gene | 63959784 | 64047015 | - | Tnc | Tnc | P110 | NM_011607 | TSS14000 |
| chr4 | 64226235 | 64226326 | MACS2_peak_2054 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 20 | chr4 | unknown | gene | 65124173 | 65351725 | + | Pappa | Pappa | P1292 | NM_021362 | TSS7146 |
| chr4 | 64327168 | 64327259 | MACS2_peak_2055 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 58 | chr4 | unknown | gene | 63959784 | 64047015 | - | Tnc | Tnc | P110 | NM_011607 | TSS14000 |
| chr4 | 64327168 | 64327259 | MACS2_peak_2055 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 58 | chr4 | unknown | gene | 65124173 | 65351725 | + | Pappa | Pappa | P1292 | NM_021362 | TSS7146 |
| chr4 | 64497888 | 64498103 | MACS2_peak_2056 | 328 | + | 17.68053 | 38.69132 | 32.85984 | 144 | chr4 | unknown | gene | 63959784 | 64047015 | - | Tnc | Tnc | P110 | NM_011607 | TSS14000 |
| chr4 | 64497888 | 64498103 | MACS2_peak_2056 | 328 | + | 17.68053 | 38.69132 | 32.85984 | 144 | chr4 | unknown | gene | 65124173 | 65351725 | + | Pappa | Pappa | P1292 | NM_021362 | TSS7146 |
| chr4 | 67016675 | 67016766 | MACS2_peak_2057 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 49 | chr4 | unknown | gene | 66827810 | 66841479 | + | Tlr4 | Tlr4 | P5231 | NM_021297 | TSS2746 |
| chr4 | 67016675 | 67016766 | MACS2_peak_2057 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 49 | chr4 | unknown | gene | 68761371 | 68954397 | - | Brinp1 | Brinp1 | P13461 | NM_019967 | TSS26927 |
| chr4 | 68046139 | 68046245 | MACS2_peak_2058 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 50 | chr4 | unknown | gene | 66827810 | 66841479 | + | Tlr4 | Tlr4 | P5231 | NM_021297 | TSS2746 |
| chr4 | 68046139 | 68046245 | MACS2_peak_2058 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 50 | chr4 | unknown | gene | 68761371 | 68954397 | - | Brinp1 | Brinp1 | P13461 | NM_019967 | TSS26927 |
| chr4 | 68302291 | 68302382 | MACS2_peak_2059 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 38 | chr4 | unknown | gene | 66827810 | 66841479 | + | Tlr4 | Tlr4 | P5231 | NM_021297 | TSS2746 |
| chr4 | 68302291 | 68302382 | MACS2_peak_2059 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 38 | chr4 | unknown | gene | 68761371 | 68954397 | - | Brinp1 | Brinp1 | P13461 | NM_019967 | TSS26927 |
| chr4 | 68901372 | 68901463 | MACS2_peak_2060 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 39 | chr4 | unknown | gene | 66827810 | 66841479 | + | Tlr4 | Tlr4 | P5231 | NM_021297 | TSS2746 |
| chr4 | 68901372 | 68901463 | MACS2_peak_2060 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 39 | chr4 | unknown | gene | 70223023 | 70410267 | - | Cdk5rap2 | Cdk5rap2 | P8937 | NM_145990 | TSS12323 |
| chr4 | 68990578 | 68990669 | MACS2_peak_2061 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 28 | chr4 | unknown | gene | 68761371 | 68954397 | - | Brinp1 | Brinp1 | P13461 | NM_019967 | TSS26927 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr4 | 68990578 | 68990669 | MACS2_peak_2061 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 28 | chr4 | unknown | gene | 70223023 | 70410267 | - | Cdk5rap2 | Cdk5rap2 | P8937 | NM_145990 | TSS12323 |
| chr4 | 69120779 | 69120870 | MACS2_peak_2062 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 39 | chr4 | unknown | gene | 68761371 | 68954397 | - | Brinp1 | Brinp1 | P13461 | NM_019967 | TSS26927 |
| chr4 | 69120779 | 69120870 | MACS2_peak_2062 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 39 | chr4 | unknown | gene | 70223023 | 70410267 | - | Cdk5rap2 | Cdk5rap2 | P8937 | NM_145990 | TSS12323 |
| chr4 | 69135365 | 69135456 | MACS2_peak_2063 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 37 | chr4 | unknown | gene | 68761371 | 68954397 | - | Brinp1 | Brinp1 | P13461 | NM_019967 | TSS26927 |
| chr4 | 69135365 | 69135456 | MACS2_peak_2063 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 37 | chr4 | unknown | gene | 70223023 | 70410267 | - | Cdk5rap2 | Cdk5rap2 | P8937 | NM_145990 | TSS12323 |
| chr4 | 69485253 | 69485344 | MACS2_peak_2064 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 32 | chr4 | unknown | gene | 68761371 | 68954397 | - | Brinp1 | Brinp1 | P13461 | NM_019967 | TSS26927 |
| chr4 | 69485253 | 69485344 | MACS2_peak_2064 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 32 | chr4 | unknown | gene | 70223023 | 70410267 | - | Cdk5rap2 | Cdk5rap2 | P8937 | NM_145990 | TSS12323 |
| chr4 | 70378114 | 70378274 | MACS2_peak_2065 | 695 | + | 30.41291 | 75.94997 | 69.59044 | 89 | chr4 | unknown | gene | 68761371 | 68954397 | - | Brinp1 | Brinp1 | P13461 | NM_019967 | TSS26927 |
| chr4 | 70378114 | 70378274 | MACS2_peak_2065 | 695 | + | 30.41291 | 75.94997 | 69.59044 | 89 | chr4 | unknown | gene | 70431926 | 70534822 | - | Megf9 | Megf9 | P17598 | NM_172694 | TSS11744 |
| chr4 | 71553711 | 71553923 | MACS2_peak_2066 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 88 | chr4 | unknown | gene | 70431926 | 70534822 | - | Megf9 | Megf9 | P17598 | NM_172694 | TSS11744 |
| chr4 | 71553711 | 71553923 | MACS2_peak_2066 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 88 | chr4 | unknown | gene | 72109944 | 72200005 | - | Tle1 | Tle1 | P14889 | NM_001285529 | TSS4530 |
| chr4 | 72134160 | 72134251 | MACS2_peak_2067 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 78 | chr4 | unknown | gene | 70431926 | 70534822 | - | Megf9 | Megf9 | P17598 | NM_172694 | TSS11744 |
| chr4 | 72134160 | 72134251 | MACS2_peak_2067 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 78 | chr4 | unknown | gene | 72201243 | 72203930 | + | C630043F03Rik | C630043F03Rik |  | NR_027923 | TSS22488 |
| chr4 | 73036795 | 73037007 | MACS2_peak_2068 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 67 | chr4 | unknown | gene | 72850582 | 72852569 | - | Aldoart1 | Aldoart1 | P7353 | NM_001199270 | TSS20543 |
| chr4 | 73036795 | 73037007 | MACS2_peak_2068 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 67 | chr4 | unknown | gene | 73401031 | 73404955 | - | Gm11487 | Gm11487 | P11153 | NM_001013393 | TSS24740 |
| chr4 | 74425033 | 74425124 | MACS2_peak_2069 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 83 | chr4 | unknown | gene | 74242496 | 74404997 | + | Kdm4c | Kdm4c | P10708 | NM_001172095 | TSS5484 |
| chr4 | 74425033 | 74425124 | MACS2_peak_2069 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 83 | chr4 | unknown | gene | 75277353 | 75278251 | - | Tmem261 | Tmem261 | P4830 | NM_025849 | TSS16193 |
| chr4 | 74843218 | 74843309 | MACS2_peak_2070 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 61 | chr4 | unknown | gene | 74242496 | 74404997 | + | Kdm4c | Kdm4c | P10708 | NM_001172095 | TSS5484 |
| chr4 | 74843218 | 74843309 | MACS2_peak_2070 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 61 | chr4 | unknown | gene | 75277353 | 75278251 | - | Tmem261 | Tmem261 | P4830 | NM_025849 | TSS16193 |
| chr4 | 75388237 | 75388328 | MACS2_peak_2071 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 37 | chr4 | unknown | gene | 75277353 | 75278251 | - | Tmem261 | Tmem261 | P4830 | NM_025849 | TSS16193 |
| chr4 | 75388237 | 75388328 | MACS2_peak_2071 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 37 | chr4 | unknown | gene | 75941236 | 78211895 | - | Ptprd | Ptprd | P23881 | NM_011211 | TSS2071 |
| chr4 | 75615595 | 75615686 | MACS2_peak_2072 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 10 | chr4 | unknown | gene | 75277353 | 75278251 | - | Tmem261 | Tmem261 | P4830 | NM_025849 | TSS16193 |
| chr4 | 75615595 | 75615686 | MACS2_peak_2072 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 10 | chr4 | unknown | gene | 75941236 | 78211895 | - | Ptprd | Ptprd | P23881 | NM_011211 | TSS2071 |
| chr4 | 76400317 | 76400408 | MACS2_peak_2073 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 5 | chr4 | unknown | gene | 75277353 | 75278251 | - | Tmem261 | Tmem261 | P4830 | NM_025849 | TSS16193 |
| chr4 | 76400317 | 76400408 | MACS2_peak_2073 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 5 | chr4 | unknown | gene | 78594046 | 78597484 | + | A430085M09Rik | A430085M09Rik |  | NR_131142 | TSS22671 |
| chr4 | 79283896 | 79283987 | MACS2_peak_2074 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 31 | chr4 | unknown | gene | 78594046 | 78597484 | + | A430085M09Rik | A430085M09Rik |  | NR_131142 | TSS22671 |
| chr4 | 79283896 | 79283987 | MACS2_peak_2074 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 31 | chr4 | unknown | gene | 80834212 | 80850884 | + | Tyrp1 | Tyrp1 | P14407 | NM_001282015 | TSS21512 |
| chr4 | 80002897 | 80002988 | MACS2_peak_2075 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 31 | chr4 | unknown | gene | 78594046 | 78597484 | + | A430085M09Rik | A430085M09Rik |  | NR_131142 | TSS22671 |
| chr4 | 80002897 | 80002988 | MACS2_peak_2075 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 31 | chr4 | unknown | gene | 80834212 | 80850884 | + | Tyrp1 | Tyrp1 | P14407 | NM_001282015 | TSS21512 |
| chr4 | 80942763 | 80942878 | MACS2_peak_2076 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 77 | chr4 | unknown | gene | 80834212 | 80850884 | + | Tyrp1 | Tyrp1 | P14407 | NM_001282015 | TSS21512 |
| chr4 | 80942763 | 80942878 | MACS2_peak_2076 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 77 | chr4 | unknown | gene | 81278498 | 81442815 | - | Mpdz | Mpdz | P11259 | NM_001305286 | TSS24658 |
| chr4 | 81367595 | 81367686 | MACS2_peak_2077 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 19 | chr4 | unknown | gene | 80910685 | 80953937 | + | Lurap1l | Lurap1l | P11622 | NM_026821 | TSS12868 |
| chr4 | 81367595 | 81367686 | MACS2_peak_2077 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 19 | chr4 | unknown | gene | 81476308 | 81487013 | - | Mir466h | Mir466h |  | NR_030570 | TSS16584 |
| chr4 | 81580319 | 81580442 | MACS2_peak_2078 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 40 | chr4 | unknown | gene | 81476308 | 81487013 | - | Mir466h | Mir466h |  | NR_030570 | TSS16584 |
| chr4 | 81580319 | 81580442 | MACS2_peak_2078 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 40 | chr4 | unknown | gene | 82065379 | 82102807 | + | Gm5860 | Gm5860 |  | NR_040659 | TSS6091 |
| chr4 | 82166473 | 82166564 | MACS2_peak_2079 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 45 | chr4 | unknown | gene | 82065379 | 82102807 | + | Gm5860 | Gm5860 |  | NR_040659 | TSS6091 |
| chr4 | 82166473 | 82166564 | MACS2_peak_2079 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 45 | chr4 | unknown | gene | 82290172 | 82504760 | - | Nfib | Nfib | P10498 | NM_008687 | TSS15263 |
| chr4 | 82273380 | 82273500 | MACS2_peak_2080 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 81 | chr4 | unknown | gene | 82065379 | 82102807 | + | Gm5860 | Gm5860 |  | NR_040659 | TSS6091 |
| chr4 | 82273380 | 82273500 | MACS2_peak_2080 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 81 | chr4 | unknown | gene | 82290172 | 82504760 | - | Nfib | Nfib | P10498 | NM_008687 | TSS15263 |
| chr4 | 82357768 | 82357890 | MACS2_peak_2081 | 24 | + | 5.39702 | 7.32466 | 2.43395 | 53 | chr4 | unknown | gene | 82065379 | 82102807 | + | Gm5860 | Gm5860 |  | NR_040659 | TSS6091 |
| chr4 | 82357768 | 82357890 | MACS2_peak_2081 | 24 | + | 5.39702 | 7.32466 | 2.43395 | 53 | chr4 | unknown | gene | 82798737 | 82859661 | - | Zdhhc21 | Zdhhc21 | P10425 | NM_026647 | TSS6967 |
| chr4 | 82485266 | 82485357 | MACS2_peak_2082 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 26 | chr4 | unknown | gene | 82065379 | 82102807 | + | Gm5860 | Gm5860 |  | NR_040659 | TSS6091 |
| chr4 | 82485266 | 82485357 | MACS2_peak_2082 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 26 | chr4 | unknown | gene | 82798737 | 82859661 | - | Zdhhc21 | Zdhhc21 | P10425 | NM_026647 | TSS6967 |
| chr4 | 82590033 | 82590142 | MACS2_peak_2083 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 32 | chr4 | unknown | gene | 82290172 | 82504760 | - | Nfib | Nfib | P10498 | NM_008687 | TSS15263 |
| chr4 | 82590033 | 82590142 | MACS2_peak_2083 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 32 | chr4 | unknown | gene | 82798737 | 82859661 | - | Zdhhc21 | Zdhhc21 | P10425 | NM_026647 | TSS6967 |
| chr4 | 84454268 | 84454359 | MACS2_peak_2084 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 54 | chr4 | unknown | gene | 84042039 | 84044879 | - | 6030471H07Rik | 6030471H07Rik |  | NR_130998 | TSS10589 |
| chr4 | 84454268 | 84454359 | MACS2_peak_2084 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 54 | chr4 | unknown | gene | 84884308 | 85130743 | + | Cntln | Cntln | P8162 | NM_177385 | TSS23572 |
| chr4 | 84938146 | 84938237 | MACS2_peak_2085 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 43 | chr4 | unknown | gene | 84272541 | 84674977 | - | Bnc2 | Bnc2 | P1433 | NM_172870 | TSS16404 |
| chr4 | 84938146 | 84938237 | MACS2_peak_2085 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 43 | chr4 | unknown | gene | 85205455 | 85387753 | + | Sh3gl2 | Sh3gl2 | P22823 | NM_019535 | TSS14464 |
| chr4 | 85076375 | 85076541 | MACS2_peak_2086 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 78 | chr4 | unknown | gene | 84272541 | 84674977 | - | Bnc2 | Bnc2 | P1433 | NM_172870 | TSS16404 |
| chr4 | 85076375 | 85076541 | MACS2_peak_2086 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 78 | chr4 | unknown | gene | 85205455 | 85387753 | + | Sh3gl2 | Sh3gl2 | P22823 | NM_019535 | TSS14464 |
| chr4 | 85316895 | 85316986 | MACS2_peak_2087 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 36 | chr4 | unknown | gene | 84884308 | 85130743 | + | Cntln | Cntln | P8162 | NM_177385 | TSS23572 |
| chr4 | 85316895 | 85316986 | MACS2_peak_2087 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 36 | chr4 | unknown | gene | 86053914 | 86425948 | + | Adamtsl1 | Adamtsl1 | P25637 | NM_029967 | TSS19339 |
| chr4 | 86294869 | 86294997 | MACS2_peak_2088 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 47 | chr4 | unknown | gene | 85205455 | 85387753 | + | Sh3gl2 | Sh3gl2 | P22823 | NM_019535 | TSS14464 |
| chr4 | 86294869 | 86294997 | MACS2_peak_2088 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 47 | chr4 | unknown | gene | 86444697 | 86558015 | - | Saxo1 | Saxo1 | P16619 | NM_001081096 | TSS18957 |
| chr4 | 86496841 | 86496932 | MACS2_peak_2089 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 13 | chr4 | unknown | gene | 86053914 | 86425948 | + | Adamtsl1 | Adamtsl1 | P25637 | NM_029967 | TSS19339 |
| chr4 | 86496841 | 86496932 | MACS2_peak_2089 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 13 | chr4 | unknown | gene | 86558443 | 86559804 | + | Saxo1os | Saxo1os |  | NR_131920 | TSS18089 |
| chr4 | 87369319 | 87369436 | MACS2_peak_2090 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 27 | chr4 | unknown | gene | 86983125 | 87230540 | - | Slc24a2 | Slc24a2 | P448 | NM_172426 | TSS2910 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr4 | 87369319 | 87369436 | MACS2_peak_2090 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 27 | chr4 | unknown | gene | 87769924 | 88033095 | - | Mllt3 | Mllt3 | P15263 | NM_001286158 | TSS20856 |
| chr4 | 87388322 | 87388413 | MACS2_peak_2091 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 30 | chr4 | unknown | gene | 86983125 | 87230540 | - | Slc24a2 | Slc24a2 | P448 | NM_172426 | TSS2910 |
| chr4 | 87388322 | 87388413 | MACS2_peak_2091 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 30 | chr4 | unknown | gene | 87769924 | 88033095 | - | Mllt3 | Mllt3 | P15263 | NM_001286158 | TSS20856 |
| chr4 | 87588443 | 87588560 | MACS2_peak_2092 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 64 | chr4 | unknown | gene | 86983125 | 87230540 | - | Slc24a2 | Slc24a2 | P448 | NM_172426 | TSS2910 |
| chr4 | 87588443 | 87588560 | MACS2_peak_2092 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 64 | chr4 | unknown | gene | 87769924 | 88033095 | - | Mllt3 | Mllt3 | P15263 | NM_001286158 | TSS20856 |
| chr4 | 88519045 | 88519144 | MACS2_peak_2093 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 74 | chr4 | unknown | gene | 88412929 | 88438870 | - | Hacd4 | Hacd4 | P25528 | NM_025760 | TSS24960 |
| chr4 | 88519045 | 88519144 | MACS2_peak_2093 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 74 | chr4 | unknown | gene | 88522024 | 88522774 | - | Ifnb1 | Ifnb1 | P18497 | NM_010510 | TSS20581 |
| chr4 | 88746617 | 88746779 | MACS2_peak_2094 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 131 | chr4 | unknown | gene | 88718291 | 88722002 | - | Klhl9 | Klhl9 | P416 | NM_172871 | TSS2063 |
| chr4 | 88746617 | 88746779 | MACS2_peak_2094 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 131 | chr4 | unknown | gene | 88754867 | 88755416 | + | Gm13271 | Gm13271 | P23716 | NM_001085528 | TSS5965 |
| chr4 | 88759760 | 88759851 | MACS2_peak_2095 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 47 | chr4 | unknown | gene | 88757843 | 88758380 | + | Gm13286 | Gm13286 | P11949 | NM_001243150 | TSS2122 |
| chr4 | 88759760 | 88759851 | MACS2_peak_2095 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 47 | chr4 | unknown | gene | 88760773 | 88761322 | + | Gm13283 | Gm13283 | P20749 | NM_001085531 | TSS4607 |
| chr4 | 89587356 | 89587447 | MACS2_peak_2096 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 61 | chr4 | unknown | gene | 89306288 | 89310797 | - | Cdkn2b | Cdkn2b | P14520 | NM_007670 | TSS16437 |
| chr4 | 89587356 | 89587447 | MACS2_peak_2096 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 61 | chr4 | unknown | gene | 89688197 | 89692277 | + | Dmrta1 | Dmrta1 | P5958 | NM_175647 | TSS11715 |
| chr4 | 90484224 | 90484339 | MACS2_peak_2097 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 42 | chr4 | unknown | gene | 90359624 | 90361314 | - | Gm12633 | Gm12633 | | NR_033610 | TSS10963 |
| chr4 | 90484224 | 90484339 | MACS2_peak_2097 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 42 | chr4 | unknown | gene | 91250766 | 91399984 | - | Elavl2 | Elavl2 | P1705 | NM_207685 | TSS22317 |
| chr4 | 92048217 | 92048308 | MACS2_peak_2098 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 66 | chr4 | unknown | gene | 91250766 | 91399984 | - | Elavl2 | Elavl2 | P1705 | NM_207685 | TSS22317 |
| chr4 | 92048217 | 92048308 | MACS2_peak_2098 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 66 | chr4 | unknown | gene | 92144317 | 92146978 | - | Izumo3 | Izumo3 | P1438 | NM_027034 | TSS6374 |
| chr4 | 92318622 | 92318713 | MACS2_peak_2099 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 4 | chr4 | unknown | gene | 92144317 | 92146978 | - | Izumo3 | Izumo3 | P1438 | NM_027034 | TSS6374 |
| chr4 | 92318622 | 92318713 | MACS2_peak_2099 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 4 | chr4 | unknown | gene | 93334147 | 93335420 | - | Tusc1 | Tusc1 | P25513 | NM_026954 | TSS10668 |
| chr4 | 92771718 | 92771809 | MACS2_peak_2100 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 39 | chr4 | unknown | gene | 92144317 | 92146978 | - | Izumo3 | Izumo3 | P1438 | NM_027034 | TSS6374 |
| chr4 | 92771718 | 92771809 | MACS2_peak_2100 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 39 | chr4 | unknown | gene | 93334147 | 93335420 | - | Tusc1 | Tusc1 | P25513 | NM_026954 | TSS10668 |
| chr4 | 93794967 | 93795058 | MACS2_peak_2101 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 61 | chr4 | unknown | gene | 93334147 | 93335420 | - | Tusc1 | Tusc1 | P25513 | NM_026954 | TSS10668 |
| chr4 | 93794967 | 93795058 | MACS2_peak_2101 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 61 | chr4 | unknown | gene | 94500078 | 94556704 | - | Caap1 | Caap1 | P23136 | NM_026368 | TSS18563 |
| chr4 | 95175681 | 95175772 | MACS2_peak_2102 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 61 | chr4 | unknown | gene | 95049035 | 95051271 | - | Jun | Jun | P7027 | NM_010591 | TSS22596 |
| chr4 | 95175681 | 95175772 | MACS2_peak_2102 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 61 | chr4 | unknown | gene | 95557506 | 95926804 | + | Fggy | Fggy | P15562 | NM_001113412 | TSS9660 |
| chr4 | 96343412 | 96343503 | MACS2_peak_2103 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 40 | chr4 | unknown | gene | 96099317 | 96141042 | - | Cyp2j12 | Cyp2j12 | P2029 | NM_001100182 | TSS3636 |
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| chr4 | 96878899 | 96878990 | MACS2_peak_2104 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 60 | chr4 | unknown | gene | 96723886 | 96785160 | - | Gm12695 | Gm12695 | P13558 | NM_001081284 | TSS9056 |
| chr4 | 96878899 | 96878990 | MACS2_peak_2104 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 60 | chr4 | unknown | gene | 97567874 | 97584591 | - | E130114P18Rik | E130114P18Rik | | NR_015513 | TSS1919 |
| chr4 | 96933896 | 96934016 | MACS2_peak_2105 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 30 | chr4 | unknown | gene | 96723886 | 96785160 | - | Gm12695 | Gm12695 | P13558 | NM_001081284 | TSS9056 |
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| chr4 | 97595074 | 97595165 | MACS2_peak_2106 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 20 | chr4 | unknown | gene | 97567874 | 97584591 | - | E130114P18Rik | E130114P18Rik | | NR_015513 | TSS1919 |
| chr4 | 97595074 | 97595165 | MACS2_peak_2106 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 20 | chr4 | unknown | gene | 98355369 | 98383236 | - | Tm2d1 | Tm2d1 | P17490 | NM_053157 | TSS18671 |
| chr4 | 98560628 | 98560719 | MACS2_peak_2107 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 39 | chr4 | unknown | gene | 98355369 | 98383236 | - | Tm2d1 | Tm2d1 | P17490 | NM_053157 | TSS18671 |
| chr4 | 98560628 | 98560719 | MACS2_peak_2107 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 39 | chr4 | unknown | gene | 98726753 | 98738116 | + | L1td1 | L1td1 | P4990 | NM_001081202 | TSS25064 |
| chr4 | 98649826 | 98649917 | MACS2_peak_2108 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 74 | chr4 | unknown | gene | 98355369 | 98383236 | - | Tm2d1 | Tm2d1 | P17490 | NM_053157 | TSS18671 |
| chr4 | 98649826 | 98649917 | MACS2_peak_2108 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 74 | chr4 | unknown | gene | 98726753 | 98738116 | + | L1td1 | L1td1 | P4990 | NM_001081202 | TSS25064 |
| chr4 | 98910068 | 98910159 | MACS2_peak_2109 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 24 | chr4 | unknown | gene | 98754891 | 98817537 | - | Kank4 | Kank4 | P6829 | NM_172872 | TSS17419 |
| chr4 | 98910068 | 98910159 | MACS2_peak_2109 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 24 | chr4 | unknown | gene | 98923809 | 98934805 | + | Usp1 | Usp1 | P26525 | NM_001301414 | TSS10587 |
| chr4 | 99088780 | 99088909 | MACS2_peak_2110 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 73 | chr4 | unknown | gene | 99030954 | 99038002 | + | Angptl3 | Angptl3 | P9653 | NM_013913 | TSS6994 |
| chr4 | 99088780 | 99088909 | MACS2_peak_2110 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 73 | chr4 | unknown | gene | 99193933 | 99258564 | + | Atg4c | Atg4c | P15561 | NM_175029 | TSS22273 |
| chr4 | 99173096 | 99173236 | MACS2_peak_2111 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 82 | chr4 | unknown | gene | 98936658 | 99120762 | - | Dock7 | Dock7 | P137 | NM_026082 | TSS26743 |
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| chr4 | 99658744 | 99658961 | MACS2_peak_2112 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 148 | chr4 | unknown | gene | 99656298 | 99658034 | + | Foxd3 | Foxd3 | P6033 | NM_010425 | TSS21061 |
| chr4 | 99658744 | 99658961 | MACS2_peak_2112 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 148 | chr4 | unknown | gene | 99715629 | 99762068 | + | Alg6 | Alg6 | P20043 | NM_001081264 | TSS22513 |
| chr4 | 99817046 | 99817137 | MACS2_peak_2113 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 78 | chr4 | unknown | gene | 99715629 | 99762068 | + | Alg6 | Alg6 | P20043 | NM_001081264 | TSS22513 |
| chr4 | 99817046 | 99817137 | MACS2_peak_2113 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 78 | chr4 | unknown | gene | 99829499 | 99912610 | + | Efcab7 | Efcab7 | P5480 | NM_145549 | TSS3277 |
| chr4 | 100033575 | 100033666 | MACS2_peak_2114 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 71 | chr4 | unknown | gene | 99929450 | 99986764 | + | Pgm2 | Pgm2 | P18898 | NM_028132 | TSS18667 |
| chr4 | 100033575 | 100033666 | MACS2_peak_2114 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 71 | chr4 | unknown | gene | 100095790 | 100442245 | + | Ror1 | Ror1 | P1360 | NM_013845 | TSS7409 |
| chr4 | 100123876 | 100123967 | MACS2_peak_2115 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 8 | chr4 | unknown | gene | 99929450 | 99986764 | + | Pgm2 | Pgm2 | P18898 | NM_028132 | TSS18667 |
| chr4 | 100123876 | 100123967 | MACS2_peak_2115 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 8 | chr4 | unknown | gene | 100478866 | 100550002 | + | Ube2u | Ube2u | P8293 | NM_001033773 | TSS5946 |
| chr4 | 102393025 | 102393116 | MACS2_peak_2116 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 59 | chr4 | unknown | gene | 101986839 | 101990014 | + | Gm12789 | Gm12789 | P693 | NM_001085520 | TSS5487 |
| chr4 | 102393025 | 102393116 | MACS2_peak_2116 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 59 | chr4 | unknown | gene | 102760134 | 102970079 | + | Sgip1 | Sgip1 | P18932 | NM_001285860 | TSS25341 |
| chr4 | 102488579 | 102488670 | MACS2_peak_2117 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 4 | chr4 | unknown | gene | 101986839 | 101990014 | + | Gm12789 | Gm12789 | P693 | NM_001085520 | TSS5487 |
| chr4 | 102488579 | 102488670 | MACS2_peak_2117 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 4 | chr4 | unknown | gene | 102760134 | 102970079 | + | Sgip1 | Sgip1 | P18932 | NM_001285860 | TSS25341 |
| chr4 | 104528778 | 104528881 | MACS2_peak_2118 | 37 | + | 6.18557 | 8.81513 | 3.78456 | 16 | chr4 | unknown | gene | 103382499 | 103492188 | + | Gm12718 | Gm12718 | | NR_040673 | TSS27421 |
| chr4 | 104528778 | 104528881 | MACS2_peak_2118 | 37 | + | 6.18557 | 8.81513 | 3.78456 | 16 | chr4 | unknown | gene | 104766316 | 104804160 | + | C8b | C8b | P18442 | NM_133882 | TSS12811 |
| chr4 | 105146697 | 105146823 | MACS2_peak_2119 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 54 | chr4 | unknown | gene | 105029649 | 105109798 | - | Prkaa2 | Prkaa2 | P24508 | NM_178143 | TSS2757 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr4 | 105146697 | 105146823 | MACS2_peak_2119 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 54 | chr4 | unknown | gene | 105157346 | 105231022 | + | Ppap2b | Ppap2b | P16128 | NM_080555 | TSS6914 |
| chr4 | 105532517 | 105532608 | MACS2_peak_2120 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 30 | chr4 | unknown | gene | 105157346 | 105231022 | + | Ppap2b | Ppap2b | P16128 | NM_080555 | TSS6914 |
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| chr4 | 108074563 | 108074713 | MACS2_peak_2122 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 78 | chr4 | unknown | gene | 108014792 | 108032090 | - | Podn | Podn | P3638 | NM_172874 | TSS8676 |
| chr4 | 108074563 | 108074713 | MACS2_peak_2122 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 78 | chr4 | unknown | gene | 108087356 | 108087449 | + | Mir6397 | Mir6397 | | NR_105823 | TSS16869 |
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| chr4 | 108213840 | 108213965 | MACS2_peak_2123 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 49 | chr4 | unknown | gene | 108227754 | 108300920 | - | Zyg11b | Zyg11b | P8721 | NM_001033634 | TSS22089 |
| chr4 | 109151294 | 109151385 | MACS2_peak_2124 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 28 | chr4 | unknown | gene | 109000804 | 109061130 | + | Nrd1 | Nrd1 | P7002 | NM_146150 | TSS20047 |
| chr4 | 109151294 | 109151385 | MACS2_peak_2124 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 28 | chr4 | unknown | gene | 109218412 | 109254001 | + | Calr4 | Calr4 | P18337 | NM_001285895 | TSS10706 |
| chr4 | 109684553 | 109684644 | MACS2_peak_2125 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 25 | chr4 | unknown | gene | 109660875 | 109666756 | - | Cdkn2c | Cdkn2c | P26521 | NM_001301368 | TSS4265 |
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| chr4 | 109834620 | 109834739 | MACS2_peak_2126 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 61 | chr4 | unknown | gene | 109978024 | 109982653 | + | Dmrta2 | Dmrta2 | P15497 | NM_172296 | TSS21463 |
| chr4 | 113612925 | 113613016 | MACS2_peak_2127 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 46 | chr4 | unknown | gene | 112804615 | 113286973 | - | Skint6 | Skint6 | P19782 | NM_001103199 | TSS24809 |
| chr4 | 113612925 | 113613016 | MACS2_peak_2127 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 46 | chr4 | unknown | gene | 114163383 | 114244886 | + | Skint11 | Skint11 | P5836 | NM_177669 | TSS27194 |
| chr4 | 113767789 | 113767916 | MACS2_peak_2128 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 41 | chr4 | unknown | gene | 112804615 | 113286973 | - | Skint6 | Skint6 | P19782 | NM_001103199 | TSS24809 |
| chr4 | 113767789 | 113767916 | MACS2_peak_2128 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 41 | chr4 | unknown | gene | 114163383 | 114244886 | + | Skint11 | Skint11 | P5836 | NM_177669 | TSS27194 |
| chr4 | 114082743 | 114082848 | MACS2_peak_2129 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 73 | chr4 | unknown | gene | 113477890 | 113999503 | - | Skint5 | Skint5 | P18784 | NM_001167878 | TSS15443 |
| chr4 | 114082743 | 114082848 | MACS2_peak_2129 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 73 | chr4 | unknown | gene | 114163383 | 114244886 | + | Skint11 | Skint11 | P5836 | NM_177669 | TSS27194 |
| chr4 | 114729432 | 114729523 | MACS2_peak_2130 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 10 | chr4 | unknown | gene | 114406723 | 114610129 | + | Trabd2b | Trabd2b | P6690 | NM_001085549 | TSS23566 |
| chr4 | 114729432 | 114729523 | MACS2_peak_2130 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 10 | chr4 | unknown | gene | 114821719 | 114856166 | + | Gm12830 | Gm12830 | | NR_033617 | TSS16598 |
| chr4 | 118547230 | 118547337 | MACS2_peak_2131 | 25 | + | 5.43741 | 7.46771 | 2.56659 | 21 | chr4 | unknown | gene | 118540940 | 118543726 | - | Tmem125 | Tmem125 | P4324 | NM_172383 | TSS5511 |
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| chr4 | 118547419 | 118547570 | MACS2_peak_2132 | 17 | + | 4.83325 | 6.32651 | 1.72807 | 70 | chr4 | unknown | gene | 118540940 | 118543726 | - | Tmem125 | Tmem125 | P4324 | NM_172383 | TSS5511 |
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| chr4 | 118547666 | 118547758 | MACS2_peak_2133 | 17 | + | 4.83325 | 6.32651 | 1.72807 | 58 | chr4 | unknown | gene | 118540940 | 118543726 | - | Tmem125 | Tmem125 | P4324 | NM_172383 | TSS5511 |
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| chr4 | 120003830 | 120003922 | MACS2_peak_2134 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 49 | chr4 | unknown | gene | 119656602 | 119658855 | - | Guca2b | Guca2b | P164 | NM_008191 | TSS16266 |
| chr4 | 120003830 | 120003922 | MACS2_peak_2134 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 49 | chr4 | unknown | gene | 120161423 | 120166730 | + | Edn2 | Edn2 | P11261 | NM_007902 | TSS25766 |
| chr4 | 121220921 | 121221012 | MACS2_peak_2135 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 28 | chr4 | unknown | gene | 121145372 | 121188358 | - | Rlf | Rlf | P13183 | NM_001081013 | TSS11144 |
| chr4 | 121220921 | 121221012 | MACS2_peak_2135 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 28 | chr4 | unknown | gene | 121316315 | 121324893 | - | Gm12888 | Gm12888 | P14245 | NM_001033791 | TSS5609 |
| chr4 | 121325862 | 121325953 | MACS2_peak_2136 | 32 | + | 5.82623 | 8.17465 | 3.21814 | 32 | chr4 | unknown | gene | 121316315 | 121324893 | - | Gm12888 | Gm12888 | P14245 | NM_001033791 | TSS5609 |
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| chr4 | 123421774 | 123421865 | MACS2_peak_2137 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 73 | chr4 | unknown | gene | 123403600 | 123410707 | - | D830031N03Rik | D830031N03Rik | P8660 | NM_001167918 | TSS22727 |
| chr4 | 123421774 | 123421865 | MACS2_peak_2137 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 73 | chr4 | unknown | gene | 123616419 | 123616521 | + | Mir6398 | Mir6398 | | NR_105824 | TSS21564 |
| chr4 | 124616327 | 124616418 | MACS2_peak_2138 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 59 | chr4 | unknown | gene | 124569178 | 124575538 | + | 4933407E24Rik | 4933407E24Rik | | NR_045819 | TSS12158 |
| chr4 | 124616327 | 124616418 | MACS2_peak_2138 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 59 | chr4 | unknown | gene | 124657645 | 124659056 | + | Pou3f1 | Pou3f1 | P24100 | NM_011141 | TSS2929 |
| chr4 | 126261889 | 126261987 | MACS2_peak_2139 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 64 | chr4 | unknown | gene | 126232167 | 126256062 | - | Map7d1 | Map7d1 | P16891 | NM_001145970 | TSS15841 |
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| chr4 | 129384643 | 129384738 | MACS2_peak_2140 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 33 | chr4 | unknown | gene | 129353631 | 129378028 | - | Zbtb8a | Zbtb8a | P11498 | NM_028603 | TSS24127 |
| chr4 | 129384643 | 129384738 | MACS2_peak_2140 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 33 | chr4 | unknown | gene | 129425764 | 129440818 | - | Zbtb8b | Zbtb8b | P15529 | NM_153541 | TSS19780 |
| chr4 | 129740602 | 129740693 | MACS2_peak_2141 | 24 | + | 5.43036 | 7.38735 | 2.49399 | 52 | chr4 | unknown | gene | 129676354 | 129696718 | - | Tmem39b | Tmem39b | P21202 | NM_199305 | TSS7439 |
| chr4 | 129740602 | 129740693 | MACS2_peak_2141 | 24 | + | 5.43036 | 7.38735 | 2.49399 | 52 | chr4 | unknown | gene | 129820478 | 129847822 | + | Ptp4a2 | Ptp4a2 | P24535 | NM_008974 | TSS12058 |
| chr4 | 132270303 | 132270394 | MACS2_peak_2142 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 65 | chr4 | unknown | gene | 132270078 | 132270186 | - | Rnu11 | Rnu11 | | NR_002865 | TSS14629 |
| chr4 | 132270303 | 132270394 | MACS2_peak_2142 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 65 | chr4 | unknown | gene | 132274374 | 132292662 | + | Taf12 | Taf12 | P5951 | NM_025579 | TSS15414 |
| chr4 | 132906099 | 132906246 | MACS2_peak_2143 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 70 | chr4 | unknown | gene | 132854063 | 132884365 | - | Stx12 | Stx12 | P18897 | NM_133887 | TSS26076 |
| chr4 | 132906099 | 132906246 | MACS2_peak_2143 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 70 | chr4 | unknown | gene | 132974094 | 133000343 | + | Fgr | Fgr | P20742 | NM_010208 | TSS12753 |
| chr4 | 134453583 | 134453674 | MACS2_peak_2144 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 28 | chr4 | unknown | gene | 134448764 | 134450171 | - | 1700021N21Rik | 1700021N21Rik | | NR_045800 | TSS19606 |
| chr4 | 134453583 | 134453674 | MACS2_peak_2144 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 28 | chr4 | unknown | gene | 134468319 | 134473403 | + | Stmn1 | Stmn1 | P12606 | NM_019641 | TSS15030 |
| chr4 | 138798116 | 138798262 | MACS2_peak_2145 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 78 | chr4 | unknown | gene | 138775734 | 138780393 | + | Pla2g2d | Pla2g2d | P8434 | NM_011109 | TSS20933 |
| chr4 | 138798116 | 138798262 | MACS2_peak_2145 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 78 | chr4 | unknown | gene | 138799246 | 138863469 | - | Pla2g5 | Pla2g5 | P15769 | NM_001122954 | TSS7621 |
| chr4 | 142827164 | 142827255 | MACS2_peak_2146 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 19 | chr4 | unknown | gene | 142102389 | 142239192 | - | Kazn | Kazn | P6635 | NM_144531 | TSS25996 |
| chr4 | 142827164 | 142827255 | MACS2_peak_2146 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 19 | chr4 | unknown | gene | 143107390 | 143212709 | - | Prdm2 | Prdm2 | P23539 | NM_001081355 | TSS26637 |
| chr4 | 144999914 | 145000040 | MACS2_peak_2147 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 63 | chr4 | unknown | gene | 144892826 | 144927219 | + | Dhrs3 | Dhrs3 | P13656 | NM_001172424 | TSS5398 |
| chr4 | 144999914 | 145000040 | MACS2_peak_2147 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 63 | chr4 | unknown | gene | 145212367 | 145246801 | - | Tnfrsf1b | Tnfrsf1b | P2701 | NM_011610 | TSS5180 |
| chr4 | 145416595 | 145416744 | MACS2_peak_2148 | 9 | + | 3.947 | 4.7755 | 0.90681 | 82 | chr4 | unknown | gene | 145268975 | 145315084 | - | Tnfrsf8 | Tnfrsf8 | P20261 | NM_009401 | TSS11118 |

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr4 | 145416595 | 145416744 | MACS2_peak_2148 | 9 | + | 3.947 | 4.7755 | 0.90681 | 82 | chr4 | unknown | gene | 145464209 | 145467961 | + | Smarca5-ps | Smarca5-ps | | NR_002888 | TSS2975 |
| chr4 | 145440274 | 145440383 | MACS2_peak_2149 | 12 | + | 4.03859 | 5.23273 | 1.28421 | 21 | chr4 | unknown | gene | 145268975 | 145315084 | - | Tnfrsf8 | Tnfrsf8 | P20261 | NM_009401 | TSS11118 |
| chr4 | 145440274 | 145440383 | MACS2_peak_2149 | 12 | + | 4.03859 | 5.23273 | 1.28421 | 21 | chr4 | unknown | gene | 145464209 | 145467961 | + | Smarca5-ps | Smarca5-ps | | NR_002888 | TSS2975 |
| chr4 | 146268006 | 146268097 | MACS2_peak_2150 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 35 | chr4 | unknown | gene | 146156826 | 146196977 | + | Zfp600 | Zfp600 | P21220 | NM_001177546 | TSS18133 |
| chr4 | 146268006 | 146268097 | MACS2_peak_2150 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 35 | chr4 | unknown | gene | 146449029 | 146467545 | + | Gm13251 | Gm13251 | P1170 | NM_001085522 | TSS6579 |
| chr4 | 146427052 | 146427206 | MACS2_peak_2151 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 73 | chr4 | unknown | gene | 146156826 | 146196977 | + | Zfp600 | Zfp600 | P21220 | NM_001177546 | TSS18133 |
| chr4 | 146427052 | 146427206 | MACS2_peak_2151 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 73 | chr4 | unknown | gene | 146449029 | 146467545 | + | Gm13251 | Gm13251 | P1170 | NM_001085522 | TSS6579 |
| chr4 | 146460791 | 146460920 | MACS2_peak_2152 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 53 | chr4 | unknown | gene | 146156826 | 146196977 | + | Zfp600 | Zfp600 | P21220 | NM_001177546 | TSS18133 |
| chr4 | 146460791 | 146460920 | MACS2_peak_2152 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 53 | chr4 | unknown | gene | 146501999 | 146537957 | + | Gm13247 | Gm13247 | P6598 | NM_001243138 | TSS25471 |
| chr4 | 146464749 | 146464840 | MACS2_peak_2153 | 21 | + | 5.14436 | 6.86416 | 2.16038 | 59 | chr4 | unknown | gene | 146156826 | 146196977 | + | Zfp600 | Zfp600 | P21220 | NM_001177546 | TSS18133 |
| chr4 | 146464749 | 146464840 | MACS2_peak_2153 | 21 | + | 5.14436 | 6.86416 | 2.16038 | 59 | chr4 | unknown | gene | 146501999 | 146537957 | + | Gm13247 | Gm13247 | P6598 | NM_001243138 | TSS25471 |
| chr4 | 146891866 | 146891957 | MACS2_peak_2154 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 10 | chr4 | unknown | gene | 146519038 | 146546873 | - | 1700095A21Rik | 1700095A21Rik | | NR_045468 | TSS2259 |
| chr4 | 146891866 | 146891957 | MACS2_peak_2154 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 10 | chr4 | unknown | gene | 147021849 | 147059114 | + | Rex2 | Rex2 | P13098 | NM_001177767 | TSS24579 |
| chr4 | 146925280 | 146925371 | MACS2_peak_2155 | 13 | + | 4.32419 | 5.39568 | 1.3392 | 17 | chr4 | unknown | gene | 146519038 | 146546873 | - | 1700095A21Rik | 1700095A21Rik | | NR_045468 | TSS2259 |
| chr4 | 146925280 | 146925371 | MACS2_peak_2155 | 13 | + | 4.32419 | 5.39568 | 1.3392 | 17 | chr4 | unknown | gene | 147021849 | 147059114 | + | Rex2 | Rex2 | P13098 | NM_001177767 | TSS24579 |
| chr4 | 146973973 | 146974064 | MACS2_peak_2156 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 23 | chr4 | unknown | gene | 146519038 | 146546873 | - | 1700095A21Rik | 1700095A21Rik | | NR_045468 | TSS2259 |
| chr4 | 146973973 | 146974064 | MACS2_peak_2156 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 23 | chr4 | unknown | gene | 147021849 | 147059114 | + | Rex2 | Rex2 | P13098 | NM_001177767 | TSS24579 |
| chr4 | 147403415 | 147403506 | MACS2_peak_2157 | 13 | + | 4.55763 | 5.87087 | 1.3392 | 69 | chr4 | unknown | gene | 147063365 | 147068436 | - | 4933438K21Rik | 4933438K21Rik | | NR_045446 | TSS26777 |
| chr4 | 147403415 | 147403506 | MACS2_peak_2157 | 13 | + | 4.55763 | 5.87087 | 1.3392 | 69 | chr4 | unknown | gene | 147553276 | 147584236 | + | Gm13154 | Gm13154 | P18732 | NM_001014397 | TSS2922 |
| chr4 | 147452892 | 147452983 | MACS2_peak_2158 | 14 | + | 4.62963 | 5.98833 | 1.43589 | 15 | chr4 | unknown | gene | 147063365 | 147068436 | - | 4933438K21Rik | 4933438K21Rik | | NR_045446 | TSS26777 |
| chr4 | 147452892 | 147452983 | MACS2_peak_2158 | 14 | + | 4.62963 | 5.98833 | 1.43589 | 15 | chr4 | unknown | gene | 147553276 | 147584236 | + | Gm13154 | Gm13154 | P18732 | NM_001014397 | TSS2922 |
| chr4 | 147458869 | 147458967 | MACS2_peak_2159 | 12 | + | 4.20597 | 5.19712 | 1.2614 | 64 | chr4 | unknown | gene | 147063365 | 147068436 | - | 4933438K21Rik | 4933438K21Rik | | NR_045446 | TSS26777 |
| chr4 | 147458869 | 147458967 | MACS2_peak_2159 | 12 | + | 4.20597 | 5.19712 | 1.2614 | 64 | chr4 | unknown | gene | 147553276 | 147584236 | + | Gm13154 | Gm13154 | P18732 | NM_001014397 | TSS2922 |
| chr4 | 147497867 | 147497958 | MACS2_peak_2160 | 13 | + | 4.55763 | 5.87087 | 1.3392 | 21 | chr4 | unknown | gene | 147063365 | 147068436 | - | 4933438K21Rik | 4933438K21Rik | | NR_045446 | TSS26777 |
| chr4 | 147497867 | 147497958 | MACS2_peak_2160 | 13 | + | 4.55763 | 5.87087 | 1.3392 | 21 | chr4 | unknown | gene | 147553276 | 147584236 | + | Gm13154 | Gm13154 | P18732 | NM_001014397 | TSS2922 |
| chr4 | 147543612 | 147543703 | MACS2_peak_2161 | 16 | + | 4.811 | 6.2687 | 1.67914 | 32 | chr4 | unknown | gene | 147175865 | 147513294 | + | Gm13152 | Gm13152 | P4565 | NM_001039209 | TSS5527 |
| chr4 | 147543612 | 147543703 | MACS2_peak_2161 | 16 | + | 4.811 | 6.2687 | 1.67914 | 32 | chr4 | unknown | gene | 147553276 | 147584236 | + | Gm13154 | Gm13154 | P18732 | NM_001014397 | TSS2922 |
| chr4 | 147776603 | 147776694 | MACS2_peak_2162 | 35 | + | 6.0346 | 8.52848 | 3.54349 | 55 | chr4 | unknown | gene | 147674224 | 147702631 | - | Zfp534 | Zfp534 | P19939 | NM_001127188 | TSS16240 |
| chr4 | 147776603 | 147776694 | MACS2_peak_2162 | 35 | + | 6.0346 | 8.52848 | 3.54349 | 55 | chr4 | unknown | gene | 147821776 | 147822202 | - | Rps19-ps3 | Rps19-ps3 | | NR_033639 | TSS10552 |
| chr4 | 147849555 | 147849646 | MACS2_peak_2163 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 48 | chr4 | unknown | gene | 147822985 | 147848280 | - | Zfp933 | Zfp933 | P18881 | NM_198619 | TSS3597 |
| chr4 | 147849555 | 147849646 | MACS2_peak_2163 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 48 | chr4 | unknown | gene | 147860777 | 147868719 | - | Miip | Miip | P4447 | NM_001025365 | TSS7194 |
| chr4 | 150373679 | 150373770 | MACS2_peak_2164 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 80 | chr4 | unknown | gene | 150237196 | 150248555 | + | Eno1 | Eno1 | P3965 | NM_023119 | TSS4291 |
| chr4 | 150373679 | 150373770 | MACS2_peak_2164 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 80 | chr4 | unknown | gene | 150629395 | 150652174 | - | Slc45a1 | Slc45a1 | P19603 | NM_173774 | TSS23255 |
| chr4 | 151511346 | 151511472 | MACS2_peak_2165 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 69 | chr4 | unknown | gene | 151089569 | 151091140 | + | Gm13090 | Gm13090 | P13518 | NM_001308446 | TSS2529 |
| chr4 | 151511346 | 151511472 | MACS2_peak_2165 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 69 | chr4 | unknown | gene | 151933719 | 151980728 | + | Dnajc11 | Dnajc11 | P632 | NM_172704 | TSS27263 |
| chr4 | 152611870 | 152611961 | MACS2_peak_2166 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 29 | chr4 | unknown | gene | 152478141 | 152562778 | + | Nphp4 | Nphp4 | P2513 | NM_153424 | TSS12214 |
| chr4 | 152611870 | 152611961 | MACS2_peak_2166 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 29 | chr4 | unknown | gene | 152697539 | 152700922 | + | Gm833 | Gm833 | | NR_033138 | TSS21255 |
| chr4 | 153341856 | 153341947 | MACS2_peak_2167 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 40 | chr4 | unknown | gene | 152697539 | 152700922 | + | Gm833 | Gm833 | | NR_033138 | TSS21255 |
| chr4 | 153341856 | 153341947 | MACS2_peak_2167 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 40 | chr4 | unknown | gene | 153373220 | 153482157 | - | Ajap1 | Ajap1 | P21943 | NM_001099299 | TSS11821 |
| chr4 | 154908629 | 154908720 | MACS2_peak_2168 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 71 | chr4 | unknown | gene | 154896429 | 154899005 | - | Fam213b | Fam213b | P23629 | NM_025582 | TSS9522 |
| chr4 | 154908629 | 154908720 | MACS2_peak_2168 | 28 | + | 5.63936 | 7.79234 | 2.86435 | 71 | chr4 | unknown | gene | 154922209 | 154928046 | - | Tnfrsf14 | Tnfrsf14 | P26321 | NM_178931 | TSS22597 |
| chr4 | 155282400 | 155282491 | MACS2_peak_2169 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 10 | chr4 | unknown | gene | 155249965 | 155256207 | + | Faap20 | Faap20 | P6515 | NM_001190445 | TSS8935 |
| chr4 | 155282400 | 155282491 | MACS2_peak_2169 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 10 | chr4 | unknown | gene | 155384978 | 155397962 | - | Gabrd | Gabrd | P17726 | NM_008072 | TSS9686 |
| chr4 | 155493086 | 155493275 | MACS2_peak_2170 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 39 | chr4 | unknown | gene | 155469113 | 155470530 | + | Tmem52 | Tmem52 | P18734 | NM_027161 | TSS1092 |
| chr4 | 155493086 | 155493275 | MACS2_peak_2170 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 39 | chr4 | unknown | gene | 155562391 | 155589475 | + | Nadk | Nadk | P24267 | NM_138671 | TSS190 |
| chr4_GL456216_random | 49137 | 49363 | MACS2_peak_2171 | 63 | + | 7.52781 | 11.52513 | 6.36816 | 62 | chr4_GL456216_random | unknown | gene | 15880 | 35436 | + | Dhrsx | Dhrsx | P8960 | NM_001033326 | TSS865 |
| chr5 | 3695468 | 3695559 | MACS2_peak_2172 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 19 | chr5 | unknown | gene | 3657003 | 3679160 | + | Tmbim7 | Tmbim7 | P24482 | NM_029141 | TSS19085 |
| chr5 | 3695468 | 3695559 | MACS2_peak_2172 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 19 | chr5 | unknown | gene | 3803164 | 3840942 | + | Krit1 | Krit1 | P6791 | NM_001170552 | TSS10234 |
| chr5 | 3850346 | 3850437 | MACS2_peak_2173 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 53 | chr5 | unknown | gene | 3803164 | 3840942 | + | Krit1 | Krit1 | P6791 | NM_001170552 | TSS10234 |
| chr5 | 3850346 | 3850437 | MACS2_peak_2173 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 53 | chr5 | unknown | gene | 3890580 | 3893933 | - | Mterf1a | Mterf1a | P1607 | NM_001013023 | TSS25917 |
| chr5 | 5628755 | 5628874 | MACS2_peak_2174 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 86 | chr5 | unknown | gene | 5573798 | 5576203 | + | Gm8773 | Gm8773 | | NR_033499 | TSS15503 |
| chr5 | 5628755 | 5628874 | MACS2_peak_2174 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 86 | chr5 | unknown | gene | 5664828 | 5694568 | - | Steap2 | Steap2 | P25382 | NM_001285471 | TSS8205 |
| chr5 | 5665521 | 5665612 | MACS2_peak_2175 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 53 | chr5 | unknown | gene | 5580981 | 5664030 | - | Cfap69 | Cfap69 | P5931 | NM_172447 | TSS18687 |
| chr5 | 5665521 | 5665612 | MACS2_peak_2175 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 53 | chr5 | unknown | gene | 5736321 | 5749317 | - | Steap1 | Steap1 | P4945 | NM_027399 | TSS14259 |
| chr5 | 5944814 | 5945252 | MACS2_peak_2176 | 526 | + | 21.38855 | 58.73455 | 52.634 | 350 | chr5 | unknown | gene | 5736321 | 5749317 | - | Steap1 | Steap1 | P4945 | NM_027399 | TSS14259 |
| chr5 | 5944814 | 5945252 | MACS2_peak_2176 | 526 | + | 21.38855 | 58.73455 | 52.634 | 350 | chr5 | unknown | gene | 6769029 | 7344378 | - | Zfp804b | Zfp804b | P7407 | NM_001163223 | TSS5775 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr5 | 8788726 | 8788817 | MACS2_peak_2177 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 57 | chr5 | unknown | gene | 8660091 | 8747561 | + | Abcb1a | Abcb1a | P21492 | NM_011076 | TSS18516 |
| chr5 | 8788726 | 8788817 | MACS2_peak_2177 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 57 | chr5 | unknown | gene | 8798146 | 8865950 | + | Abcb1b | Abcb1b | P12115 | NM_011075 | TSS8628 |
| chr5 | 8943558 | 8943649 | MACS2_peak_2178 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 60 | chr5 | unknown | gene | 8798146 | 8865950 | + | Abcb1b | Abcb1b | P12115 | NM_011075 | TSS8628 |
| chr5 | 8943558 | 8943649 | MACS2_peak_2178 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 60 | chr5 | unknown | gene | 8966047 | 8997146 | - | Crot | Crot | P6607 | NM_023733 | TSS13886 |
| chr5 | 13204207 | 13204298 | MACS2_peak_2179 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 47 | chr5 | unknown | gene | 12383165 | 12585302 | + | Sema3d | Sema3d | P1599 | NM_028882 | TSS26775 |
| chr5 | 13204207 | 13204298 | MACS2_peak_2179 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 47 | chr5 | unknown | gene | 13396783 | 13599603 | + | Sema3a | Sema3a | P21804 | NM_001243072 | TSS4378 |
| chr5 | 13375591 | 13375702 | MACS2_peak_2180 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 35 | chr5 | unknown | gene | 12383165 | 12585302 | + | Sema3d | Sema3d | P1599 | NM_028882 | TSS26775 |
| chr5 | 13375591 | 13375702 | MACS2_peak_2180 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 35 | chr5 | unknown | gene | 13396783 | 13599603 | + | Sema3a | Sema3a | P21804 | NM_001243072 | TSS4378 |
| chr5 | 13685630 | 13685721 | MACS2_peak_2181 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 4 | chr5 | unknown | gene | 13396783 | 13599603 | + | Sema3a | Sema3a | P21804 | NM_001243072 | TSS4378 |
| chr5 | 13685630 | 13685721 | MACS2_peak_2181 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 4 | chr5 | unknown | gene | 13791618 | 13796453 | + | Speer3 | Speer3 | P9618 | NM_027650 | TSS5655 |
| chr5 | 14107603 | 14107704 | MACS2_peak_2182 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 58 | chr5 | unknown | gene | 13791618 | 13796453 | + | Speer3 | Speer3 | P9618 | NM_027650 | TSS5655 |
| chr5 | 14107603 | 14107704 | MACS2_peak_2182 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 58 | chr5 | unknown | gene | 14514917 | 14858886 | + | Pclo | Pclo | P25021 | NM_001110796 | TSS3719 |
| chr5 | 14900132 | 14900233 | MACS2_peak_2183 | 33 | + | 5.89082 | 8.26333 | 3.30064 | 53 | chr5 | unknown | gene | 14514917 | 14858886 | + | Pclo | Pclo | P25021 | NM_001110796 | TSS3719 |
| chr5 | 14900132 | 14900233 | MACS2_peak_2183 | 33 | + | 5.89082 | 8.26333 | 3.30064 | 53 | chr5 | unknown | gene | 14910123 | 14914829 | - | Gm9758 | Gm9758 | P13847 | NM_198666 | TSS10206 |
| chr5 | 14954247 | 14954339 | MACS2_peak_2184 | 25 | + | 4.99708 | 7.48111 | 2.5796 | 34 | chr5 | unknown | gene | 14933630 | 14938406 | - | Speer4e | Speer4e | P23290 | NM_001122661 | TSS16120 |
| chr5 | 14954247 | 14954339 | MACS2_peak_2184 | 25 | + | 4.99708 | 7.48111 | 2.5796 | 34 | chr5 | unknown | gene | 14974496 | 14978875 | - | Gm10354 | Gm10354 | P10829 | NM_001281514 | TSS35 |
| chr5 | 15019419 | 15019510 | MACS2_peak_2185 | 13 | + | 4.22853 | 5.52627 | 1.3392 | 35 | chr5 | unknown | gene | 14974496 | 14978875 | - | Gm10354 | Gm10354 | P10829 | NM_001281514 | TSS35 |
| chr5 | 15019419 | 15019510 | MACS2_peak_2185 | 13 | + | 4.22853 | 5.52627 | 1.3392 | 35 | chr5 | unknown | gene | 15028949 | 15032938 | - | Gm17019 | Gm17019 | P20522 | NM_182957 | TSS8860 |
| chr5 | 15524082 | 15524173 | MACS2_peak_2186 | 15 | + | 4.62392 | 6.14334 | 1.57372 | 57 | chr5 | unknown | gene | 15028949 | 15032938 | - | Gm17019 | Gm17019 | P20522 | NM_182957 | TSS8860 |
| chr5 | 15524082 | 15524173 | MACS2_peak_2186 | 15 | + | 4.62392 | 6.14334 | 1.57372 | 57 | chr5 | unknown | gene | 15619098 | 15623510 | + | Speer4d | Speer4d | P8800 | NM_025759 | TSS25374 |
| chr5 | 15680119 | 15680219 | MACS2_peak_2187 | 30 | + | 5.31962 | 7.9949 | 3.05309 | 60 | chr5 | unknown | gene | 15652287 | 15657059 | - | 4930572O03Rik | 4930572O03Rik | | NR_073011 | TSS18901 |
| chr5 | 15680119 | 15680219 | MACS2_peak_2187 | 30 | + | 5.31962 | 7.9949 | 3.05309 | 60 | chr5 | unknown | gene | 15680709 | 15714596 | + | Speer4cos | Speer4cos | | NR_001585 | TSS5030 |
| chr5 | 15764898 | 15764989 | MACS2_peak_2188 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 28 | chr5 | unknown | gene | 15680709 | 15714596 | + | Speer4cos | Speer4cos | | NR_001585 | TSS5030 |
| chr5 | 15764898 | 15764989 | MACS2_peak_2188 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 28 | chr5 | unknown | gene | 15863927 | 15883766 | - | 4930519H02Rik | 4930519H02Rik | | NR_045974 | TSS15229 |
| chr5 | 16325512 | 16325603 | MACS2_peak_2189 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 72 | chr5 | unknown | gene | 15863927 | 15883766 | - | 4930519H02Rik | 4930519H02Rik | | NR_045974 | TSS15229 |
| chr5 | 16325512 | 16325603 | MACS2_peak_2189 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 72 | chr5 | unknown | gene | 16553494 | 16618993 | + | Hgf | Hgf | P13764 | NM_001289460 | TSS1063 |
| chr5 | 16953403 | 16953494 | MACS2_peak_2190 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 24 | chr5 | unknown | gene | 16553494 | 16618993 | + | Hgf | Hgf | P13764 | NM_001289460 | TSS1063 |
| chr5 | 16953403 | 16953494 | MACS2_peak_2190 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 24 | chr5 | unknown | gene | 17476121 | 17480485 | + | Speer4f1 | Speer4f1 | P12916 | NM_027609 | TSS18001 |
| chr5 | 17006392 | 17006487 | MACS2_peak_2191 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 47 | chr5 | unknown | gene | 16553494 | 16618993 | + | Hgf | Hgf | P13764 | NM_001289460 | TSS1063 |
| chr5 | 17006392 | 17006487 | MACS2_peak_2191 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 47 | chr5 | unknown | gene | 17476121 | 17480485 | + | Speer4f1 | Speer4f1 | P12916 | NM_027609 | TSS18001 |
| chr5 | 17147472 | 17147563 | MACS2_peak_2192 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 16 | chr5 | unknown | gene | 16553494 | 16618993 | + | Hgf | Hgf | P13764 | NM_001289460 | TSS1063 |
| chr5 | 17147472 | 17147563 | MACS2_peak_2192 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 16 | chr5 | unknown | gene | 17476121 | 17480485 | + | Speer4f1 | Speer4f1 | P12916 | NM_027609 | TSS18001 |
| chr5 | 17463122 | 17463255 | MACS2_peak_2193 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 76 | chr5 | unknown | gene | 16553494 | 16618993 | + | Hgf | Hgf | P13764 | NM_001289460 | TSS1063 |
| chr5 | 17463122 | 17463255 | MACS2_peak_2193 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 76 | chr5 | unknown | gene | 17476121 | 17480485 | + | Speer4f1 | Speer4f1 | P12916 | NM_027609 | TSS18001 |
| chr5 | 17493518 | 17493615 | MACS2_peak_2194 | 23 | + | 5.26766 | 7.08584 | 2.32792 | 25 | chr5 | unknown | gene | 17476121 | 17480485 | + | Speer4f1 | Speer4f1 | P12916 | NM_027609 | TSS18001 |
| chr5 | 17493518 | 17493615 | MACS2_peak_2194 | 23 | + | 5.26766 | 7.08584 | 2.32792 | 25 | chr5 | unknown | gene | 17574815 | 17727756 | + | Sema3c | Sema3c | P11992 | NM_013657 | TSS6280 |
| chr5 | 17621284 | 17621375 | MACS2_peak_2195 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 46 | chr5 | unknown | gene | 17476121 | 17480485 | + | Speer4f1 | Speer4f1 | P12916 | NM_027609 | TSS18001 |
| chr5 | 17621284 | 17621375 | MACS2_peak_2195 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 46 | chr5 | unknown | gene | 17781689 | 17888959 | - | Cd36 | Cd36 | P24294 | NM_001159555 | TSS26893 |
| chr5 | 17823004 | 17823101 | MACS2_peak_2196 | 16 | + | 4.811 | 6.2687 | 1.67914 | 11 | chr5 | unknown | gene | 17574815 | 17727756 | + | Sema3c | Sema3c | P11992 | NM_013657 | TSS6280 |
| chr5 | 17823004 | 17823101 | MACS2_peak_2196 | 16 | + | 4.811 | 6.2687 | 1.67914 | 11 | chr5 | unknown | gene | 17962569 | 18019668 | + | Gnat3 | Gnat3 | P21397 | NM_001081143 | TSS22723 |
| chr5 | 17882838 | 17883089 | MACS2_peak_2197 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 161 | chr5 | unknown | gene | 17574815 | 17727756 | + | Sema3c | Sema3c | P11992 | NM_013657 | TSS6280 |
| chr5 | 17882838 | 17883089 | MACS2_peak_2197 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 161 | chr5 | unknown | gene | 17962569 | 18019668 | + | Gnat3 | Gnat3 | P21397 | NM_001081143 | TSS22723 |
| chr5 | 18414923 | 18415072 | MACS2_peak_2198 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 60 | chr5 | unknown | gene | 18265134 | 18360169 | - | Gnai1 | Gnai1 | P26292 | NM_010305 | TSS11236 |
| chr5 | 18414923 | 18415072 | MACS2_peak_2198 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 60 | chr5 | unknown | gene | 19202367 | 19226555 | - | 4921504A21Rik | 4921504A21Rik | | NR_102341 | TSS331 |
| chr5 | 19590133 | 19590224 | MACS2_peak_2199 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 30 | chr5 | unknown | gene | 19202367 | 19226555 | - | 4921504A21Rik | 4921504A21Rik | | NR_102341 | TSS331 |
| chr5 | 19590133 | 19590224 | MACS2_peak_2199 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 30 | chr5 | unknown | gene | 20758663 | 20882124 | - | Phtf2 | Phtf2 | P19763 | NM_172992 | TSS4431 |
| chr5 | 19930593 | 19930684 | MACS2_peak_2200 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 4 | chr5 | unknown | gene | 19202367 | 19226555 | - | 4921504A21Rik | 4921504A21Rik | | NR_102341 | TSS331 |
| chr5 | 19930593 | 19930684 | MACS2_peak_2200 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 4 | chr5 | unknown | gene | 20758663 | 20882124 | - | Phtf2 | Phtf2 | P19763 | NM_172992 | TSS4431 |
| chr5 | 20596397 | 20596488 | MACS2_peak_2201 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 36 | chr5 | unknown | gene | 19202367 | 19226555 | - | 4921504A21Rik | 4921504A21Rik | | NR_102341 | TSS331 |
| chr5 | 20596397 | 20596488 | MACS2_peak_2201 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 36 | chr5 | unknown | gene | 20758663 | 20882124 | - | Phtf2 | Phtf2 | P19763 | NM_172992 | TSS4431 |
| chr5 | 20614197 | 20614288 | MACS2_peak_2202 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 10 | chr5 | unknown | gene | 19202367 | 19226555 | - | 4921504A21Rik | 4921504A21Rik | | NR_102341 | TSS331 |
| chr5 | 20614197 | 20614288 | MACS2_peak_2202 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 10 | chr5 | unknown | gene | 20758663 | 20882124 | - | Phtf2 | Phtf2 | P19763 | NM_172992 | TSS4431 |
| chr5 | 21661667 | 21661758 | MACS2_peak_2203 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 12 | chr5 | unknown | gene | 21645983 | 21661618 | + | Armc10 | Armc10 | P14543 | NM_026034 | TSS2282 |
| chr5 | 21661667 | 21661758 | MACS2_peak_2203 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 12 | chr5 | unknown | gene | 21662902 | 21701345 | - | Napepld | Napepld | P6409 | NM_178728 | TSS10366 |
| chr5 | 22110954 | 22111045 | MACS2_peak_2204 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 23 | chr5 | unknown | gene | 21809000 | 21865604 | - | Slc26a5 | Slc26a5 | P9405 | NM_001289787 | TSS18838 |
| chr5 | 22110954 | 22111045 | MACS2_peak_2204 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 23 | chr5 | unknown | gene | 22486488 | 22550263 | - | Orc5 | Orc5 | P861 | NM_011959 | TSS11060 |
| chr5 | 23595774 | 23595914 | MACS2_peak_2205 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 68 | chr5 | unknown | gene | 23434428 | 23503047 | + | Kmt2e | Kmt2e | P17179 | NM_026984 | TSS23962 |
| chr5 | 23595774 | 23595914 | MACS2_peak_2205 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 68 | chr5 | unknown | gene | 23692260 | 23712667 | - | AI506816 | AI506816 | | NR_015554 | TSS19049 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr5 | 25958126 | 25958217 | MACS2_peak_2206 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 20 | chr5 | unknown | gene | 25949796 | 25954344 | - | Gm21671 | Gm21671 | P13621 | NM_001281516 | TSS7782 |
| chr5 | 25958126 | 25958217 | MACS2_peak_2206 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 20 | chr5 | unknown | gene | 26000171 | 26004727 | - | Gm1979 | Gm1979 | P17774 | NM_001281519 | TSS10496 |
| chr5 | 28218889 | 28218980 | MACS2_peak_2207 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 71 | chr5 | unknown | gene | 28165695 | 28170435 | + | En2 | En2 | P2312 | NM_010134 | TSS13405 |
| chr5 | 28218889 | 28218980 | MACS2_peak_2207 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 71 | chr5 | unknown | gene | 28317188 | 28413616 | + | Rbm33 | Rbm33 | P13112 | NM_028234 | TSS1313 |
| chr5 | 30550263 | 30550440 | MACS2_peak_2208 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 40 | chr5 | unknown | gene | 30485583 | 30545779 | - | Cib4 | Cib4 | P18284 | NM_028483 | TSS22230 |
| chr5 | 30550263 | 30550440 | MACS2_peak_2208 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 40 | chr5 | unknown | gene | 30573986 | 30588619 | - | Gm9899 | Gm9899 | | NR_040427 | TSS19563 |
| chr5 | 30615929 | 30616043 | MACS2_peak_2209 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 26 | chr5 | unknown | gene | 30573986 | 30588619 | - | Gm9899 | Gm9899 | | NR_040427 | TSS19563 |
| chr5 | 30615929 | 30616043 | MACS2_peak_2209 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 26 | chr5 | unknown | gene | 30647935 | 30648015 | + | Mir5625 | Mir5625 | | NR_049199 | TSS8482 |
| chr5 | 31177705 | 31177796 | MACS2_peak_2210 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 44 | chr5 | unknown | gene | 31140662 | 31154251 | - | Mpv17 | Mpv17 | P16953 | NM_001294322 | TSS15207 |
| chr5 | 31177705 | 31177796 | MACS2_peak_2210 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 44 | chr5 | unknown | gene | 31187557 | 31193023 | - | Eif2b4 | Eif2b4 | P10752 | NM_010122 | TSS22019 |
| chr5 | 33352798 | 33352889 | MACS2_peak_2211 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 16 | chr5 | unknown | gene | 33247722 | 33274818 | - | Ctbp1 | Ctbp1 | P19550 | NM_001198860 | TSS17195 |
| chr5 | 33352798 | 33352889 | MACS2_peak_2211 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 16 | chr5 | unknown | gene | 33378695 | 33414891 | + | Uvssa | Uvssa | P2864 | NM_001081101 | TSS17013 |
| chr5 | 33554986 | 33555137 | MACS2_peak_2212 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 127 | chr5 | unknown | gene | 33430733 | 33434090 | - | Nkx1-1 | Nkx1-1 | P11250 | NM_011320 | TSS8787 |
| chr5 | 33554986 | 33555137 | MACS2_peak_2212 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 127 | chr5 | unknown | gene | 33600352 | 33629635 | - | Fam53a | Fam53a | P14739 | NM_178390 | TSS16059 |
| chr5 | 34107225 | 34107316 | MACS2_peak_2213 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 30 | chr5 | unknown | gene | 33995983 | 34001147 | + | Nat8l | Nat8l | P915 | NM_001001985 | TSS16245 |
| chr5 | 34107225 | 34107316 | MACS2_peak_2213 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 30 | chr5 | unknown | gene | 34118739 | 34135339 | + | 4930557J02Rik | 4930557J02Rik | | NR_040703 | TSS8457 |
| chr5 | 34401690 | 34401781 | MACS2_peak_2214 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 37 | chr5 | unknown | gene | 34336249 | 34351380 | + | Rnf4 | Rnf4 | P23755 | NM_011278 | TSS9273 |
| chr5 | 34401690 | 34401781 | MACS2_peak_2214 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 37 | chr5 | unknown | gene | 34496095 | 34513897 | - | Tnip2 | Tnip2 | P16878 | NM_139064 | TSS17838 |
| chr5 | 35892444 | 35892535 | MACS2_peak_2215 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 51 | chr5 | unknown | gene | 35757879 | 35883419 | + | Ablim2 | Ablim2 | P17728 | NM_001177700 | TSS4746 |
| chr5 | 35892444 | 35892535 | MACS2_peak_2215 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 51 | chr5 | unknown | gene | 35893318 | 35999725 | + | Afap1 | Afap1 | P12597 | NM_027373 | TSS4488 |
| chr5 | 36630632 | 36630775 | MACS2_peak_2216 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 88 | chr5 | unknown | gene | 36490603 | 36586226 | - | Tbc1d14 | Tbc1d14 | P50 | NM_001113364 | TSS15711 |
| chr5 | 36630632 | 36630775 | MACS2_peak_2216 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 88 | chr5 | unknown | gene | 36747373 | 36748645 | - | Bloc1s4 | Bloc1s4 | P12493 | NM_133724 | TSS7155 |
| chr5 | 37788869 | 37788960 | MACS2_peak_2217 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 41 | chr5 | unknown | gene | 37735518 | 37739295 | + | Cytl1 | Cytl1 | P19132 | NM_001081106 | TSS12049 |
| chr5 | 37788869 | 37788960 | MACS2_peak_2217 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 41 | chr5 | unknown | gene | 37820490 | 37824333 | - | Msx1 | Msx1 | P19817 | NM_010835 | TSS25767 |
| chr5 | 38752667 | 38752780 | MACS2_peak_2218 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 46 | chr5 | unknown | gene | 38668483 | 38684826 | - | Zfp518b | Zfp518b | P14602 | NM_001177902 | TSS13846 |
| chr5 | 38752667 | 38752780 | MACS2_peak_2218 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 46 | chr5 | unknown | gene | 39461748 | 39603574 | - | 4930513D17Rik | 4930513D17Rik | | NR_045416 | TSS2141 |
| chr5 | 38997517 | 38997608 | MACS2_peak_2219 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 23 | chr5 | unknown | gene | 38706456 | 38876693 | - | Clnk | Clnk | P20071 | NM_013748 | TSS9370 |
| chr5 | 38997517 | 38997608 | MACS2_peak_2219 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 23 | chr5 | unknown | gene | 39461748 | 39603574 | - | 4930513D17Rik | 4930513D17Rik | | NR_045416 | TSS2141 |
| chr5 | 42401770 | 42401861 | MACS2_peak_2220 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 76 | chr5 | unknown | gene | 42067959 | 42216784 | + | Gm16223 | Gm16223 | | NR_131130 | TSS11802 |
| chr5 | 42401770 | 42401861 | MACS2_peak_2220 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 76 | chr5 | unknown | gene | 43151685 | 43235354 | - | Gm7854 | Gm7854 | | NR_028417 | TSS2780 |
| chr5 | 43540514 | 43540605 | MACS2_peak_2221 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 11 | chr5 | unknown | gene | 43233462 | 43285946 | + | Cpeb2 | Cpeb2 | P21327 | NM_175937 | TSS12421 |
| chr5 | 43540514 | 43540605 | MACS2_peak_2221 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 11 | chr5 | unknown | gene | 43662378 | 43740854 | + | Cc2d2a | Cc2d2a | P1614 | NM_172274 | TSS10536 |
| chr5 | 43767536 | 43767627 | MACS2_peak_2222 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 59 | chr5 | unknown | gene | 43662378 | 43740854 | + | Cc2d2a | Cc2d2a | P1614 | NM_172274 | TSS10536 |
| chr5 | 43767536 | 43767627 | MACS2_peak_2222 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 59 | chr5 | unknown | gene | 43818892 | 43842102 | + | Bst1 | Bst1 | P23887 | NM_009763 | TSS23977 |
| chr5 | 44299539 | 44299762 | MACS2_peak_2223 | 25 | + | 5.46411 | 7.45132 | 2.55202 | 67 | chr5 | unknown | gene | 44175161 | 44226603 | - | Tapt1 | Tapt1 | P18972 | NM_173764 | TSS17378 |
| chr5 | 44299539 | 44299762 | MACS2_peak_2223 | 25 | + | 5.46411 | 7.45132 | 2.55202 | 67 | chr5 | unknown | gene | 44472132 | 44799493 | - | Ldb2 | Ldb2 | P25621 | NM_001286348 | TSS21824 |
| chr5 | 46968322 | 46968453 | MACS2_peak_2224 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 75 | chr5 | unknown | gene | 45926821 | 45932409 | - | 4930405L22Rik | 4930405L22Rik | | NR_110478 | TSS18142 |
| chr5 | 46968322 | 46968453 | MACS2_peak_2224 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 75 | chr5 | unknown | gene | 47983154 | 48304241 | + | Slit2 | Slit2 | P7849 | NM_001291228 | TSS22733 |
| chr5 | 47060125 | 47060216 | MACS2_peak_2225 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 8 | chr5 | unknown | gene | 45926821 | 45932409 | - | 4930405L22Rik | 4930405L22Rik | | NR_110478 | TSS18142 |
| chr5 | 47060125 | 47060216 | MACS2_peak_2225 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 8 | chr5 | unknown | gene | 47983154 | 48304241 | + | Slit2 | Slit2 | P7849 | NM_001291228 | TSS22733 |
| chr5 | 47291929 | 47292020 | MACS2_peak_2226 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 9 | chr5 | unknown | gene | 45926821 | 45932409 | - | 4930405L22Rik | 4930405L22Rik | | NR_110478 | TSS18142 |
| chr5 | 47291929 | 47292020 | MACS2_peak_2226 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 9 | chr5 | unknown | gene | 47983154 | 48304241 | + | Slit2 | Slit2 | P7849 | NM_001291228 | TSS22733 |
| chr5 | 47902260 | 47902394 | MACS2_peak_2227 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 56 | chr5 | unknown | gene | 45926821 | 45932409 | - | 4930405L22Rik | 4930405L22Rik | | NR_110478 | TSS18142 |
| chr5 | 47902260 | 47902394 | MACS2_peak_2227 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 56 | chr5 | unknown | gene | 47983154 | 48304241 | + | Slit2 | Slit2 | P7849 | NM_001291228 | TSS22733 |
| chr5 | 48041523 | 48041614 | MACS2_peak_2228 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 48 | chr5 | unknown | gene | 45926821 | 45932409 | - | 4930405L22Rik | 4930405L22Rik | | NR_110478 | TSS18142 |
| chr5 | 48041523 | 48041614 | MACS2_peak_2228 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 48 | chr5 | unknown | gene | 48223941 | 48224051 | + | Mir218-1 | Mir218-1 | | NR_029798 | TSS14072 |
| chr5 | 48049801 | 48049892 | MACS2_peak_2229 | 16 | + | 4.811 | 6.2687 | 1.67914 | 34 | chr5 | unknown | gene | 45926821 | 45932409 | - | 4930405L22Rik | 4930405L22Rik | | NR_110478 | TSS18142 |
| chr5 | 48049801 | 48049892 | MACS2_peak_2229 | 16 | + | 4.811 | 6.2687 | 1.67914 | 34 | chr5 | unknown | gene | 48223941 | 48224051 | + | Mir218-1 | Mir218-1 | | NR_029798 | TSS14072 |
| chr5 | 48775566 | 48775657 | MACS2_peak_2230 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 35 | chr5 | unknown | gene | 48395572 | 48414294 | + | 5730480H06Rik | 5730480H06Rik | | NR_045500 | TSS7991 |
| chr5 | 48775566 | 48775657 | MACS2_peak_2230 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 35 | chr5 | unknown | gene | 49959950 | 50058775 | - | Adgra2 | Adgra2 | P17993 | NM_133911 | TSS13772 |
| chr5 | 48845724 | 48845815 | MACS2_peak_2231 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 5 | chr5 | unknown | gene | 48395572 | 48414294 | + | 5730480H06Rik | 5730480H06Rik | | NR_045500 | TSS7991 |
| chr5 | 48845724 | 48845815 | MACS2_peak_2231 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 5 | chr5 | unknown | gene | 49959950 | 50058775 | - | Adgra2 | Adgra2 | P17993 | NM_133911 | TSS13772 |
| chr5 | 50967519 | 50967610 | MACS2_peak_2232 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 63 | chr5 | unknown | gene | 50252761 | 50252868 | + | Mir8117 | Mir8117 | | NR_106197 | TSS24440 |
| chr5 | 50967519 | 50967610 | MACS2_peak_2232 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 63 | chr5 | unknown | gene | 51454248 | 51553782 | - | Ppargc1a | Ppargc1a | P6244 | NM_008904 | TSS12435 |
| chr5 | 51720743 | 51720888 | MACS2_peak_2233 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 34 | chr5 | unknown | gene | 51454248 | 51553782 | - | Ppargc1a | Ppargc1a | P6244 | NM_008904 | TSS12435 |
| chr5 | 51720743 | 51720888 | MACS2_peak_2233 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 34 | chr5 | unknown | gene | 52135901 | 52136017 | - | Mir6417 | Mir6417 | | NR_105845 | TSS7682 |
| chr5 | 51967543 | 51967655 | MACS2_peak_2234 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 87 | chr5 | unknown | gene | 51454248 | 51553782 | - | Ppargc1a | Ppargc1a | P6244 | NM_008904 | TSS12435 |
| chr5 | 51967543 | 51967655 | MACS2_peak_2234 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 87 | chr5 | unknown | gene | 52135901 | 52136017 | - | Mir6417 | Mir6417 | | NR_105845 | TSS7682 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr5 | 52655093 | 52655234 | MACS2_peak_2235 | 57 | + | 7.23484 | 10.88753 | 5.76525 | 74 | chr5 | unknown | gene | 52607549 | 52619011 | - | 8030423F21Rik | 8030423F21Rik | | NR_045738 | TSS22951 |
| chr5 | 52655093 | 52655234 | MACS2_peak_2235 | 57 | + | 7.23484 | 10.88753 | 5.76525 | 74 | chr5 | unknown | gene | 52741573 | 52767756 | + | Pi4k2b | Pi4k2b | P21563 | NM_028744 | TSS7912 |
| chr5 | 52751881 | 52751972 | MACS2_peak_2236 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 46 | chr5 | unknown | gene | 52643406 | 52669688 | - | Sepsecs | Sepsecs | P14004 | NM_172490 | TSS14722 |
| chr5 | 52751881 | 52751972 | MACS2_peak_2236 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 46 | chr5 | unknown | gene | 52775408 | 52823687 | + | Zcchc4 | Zcchc4 | P24447 | NM_001309445 | TSS11374 |
| chr5 | 53171863 | 53171954 | MACS2_peak_2237 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 65 | chr5 | unknown | gene | 53049352 | 53069630 | + | Slc34a2 | Slc34a2 | P5491 | NM_011402 | TSS15590 |
| chr5 | 53171863 | 53171954 | MACS2_peak_2237 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 65 | chr5 | unknown | gene | 53267105 | 53277934 | + | Smim20 | Smim20 | P26449 | NM_001145433 | TSS19435 |
| chr5 | 53429379 | 53429476 | MACS2_peak_2238 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 12 | chr5 | unknown | gene | 53267105 | 53277934 | + | Smim20 | Smim20 | P26449 | NM_001145433 | TSS19435 |
| chr5 | 53429379 | 53429476 | MACS2_peak_2238 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 12 | chr5 | unknown | gene | 53555778 | 53653620 | + | Rbpj | Rbpj | P20252 | NM_001080928 | TSS15482 |
| chr5 | 56186952 | 56187079 | MACS2_peak_2239 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 56 | chr5 | unknown | gene | 54349991 | 54358542 | + | Gm10440 | Gm10440 | | NR_038045 | TSS7093 |
| chr5 | 56186952 | 56187079 | MACS2_peak_2239 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 56 | chr5 | unknown | gene | 57570083 | 57717919 | - | 4932441J04Rik | 4932441J04Rik | | NR_015588 | TSS27545 |
| chr5 | 57401202 | 57401293 | MACS2_peak_2240 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 17 | chr5 | unknown | gene | 54349991 | 54358542 | + | Gm10440 | Gm10440 | | NR_038045 | TSS7093 |
| chr5 | 57401202 | 57401293 | MACS2_peak_2240 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 17 | chr5 | unknown | gene | 57570083 | 57717919 | - | 4932441J04Rik | 4932441J04Rik | | NR_015588 | TSS27545 |
| chr5 | 57865799 | 57865890 | MACS2_peak_2241 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 21 | chr5 | unknown | gene | 57570083 | 57717919 | - | 4932441J04Rik | 4932441J04Rik | | NR_015588 | TSS27545 |
| chr5 | 57865799 | 57865890 | MACS2_peak_2241 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 21 | chr5 | unknown | gene | 58443239 | 58452998 | - | 4930459L07Rik | 4930459L07Rik | | NR_046190 | TSS18113 |
| chr5 | 58019248 | 58019339 | MACS2_peak_2242 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 57 | chr5 | unknown | gene | 57570083 | 57717919 | - | 4932441J04Rik | 4932441J04Rik | | NR_015588 | TSS27545 |
| chr5 | 58019248 | 58019339 | MACS2_peak_2242 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 57 | chr5 | unknown | gene | 58443239 | 58452998 | - | 4930459L07Rik | 4930459L07Rik | | NR_046190 | TSS18113 |
| chr5 | 58314954 | 58315093 | MACS2_peak_2243 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 54 | chr5 | unknown | gene | 57718020 | 58129351 | + | Pcdh7 | Pcdh7 | P25906 | NM_018764 | TSS14436 |
| chr5 | 58314954 | 58315093 | MACS2_peak_2243 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 54 | chr5 | unknown | gene | 58443239 | 58452998 | - | 4930459L07Rik | 4930459L07Rik | | NR_046190 | TSS18113 |
| chr5 | 59446075 | 59446216 | MACS2_peak_2244 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 68 | chr5 | unknown | gene | 58443239 | 58452998 | - | 4930459L07Rik | 4930459L07Rik | | NR_046190 | TSS18113 |
| chr5 | 59446075 | 59446216 | MACS2_peak_2244 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 68 | chr5 | unknown | gene | 59963118 | 59986002 | - | 4933402J10Rik | 4933402J10Rik | | NR_040682 | TSS15950 |
| chr5 | 61124174 | 61124278 | MACS2_peak_2245 | 26 | + | 5.49828 | 7.51662 | 2.61219 | 70 | chr5 | unknown | gene | 59963118 | 59986002 | - | 4933402J10Rik | 4933402J10Rik | | NR_040682 | TSS15950 |
| chr5 | 61124174 | 61124278 | MACS2_peak_2245 | 26 | + | 5.49828 | 7.51662 | 2.61219 | 70 | chr5 | unknown | gene | 61808842 | 61810425 | + | G6pd2 | G6pd2 | P3326 | NM_019468 | TSS25457 |
| chr5 | 61605934 | 61606049 | MACS2_peak_2246 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 48 | chr5 | unknown | gene | 59963118 | 59986002 | - | 4933402J10Rik | 4933402J10Rik | | NR_040682 | TSS15950 |
| chr5 | 61605934 | 61606049 | MACS2_peak_2246 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 48 | chr5 | unknown | gene | 61808842 | 61810425 | + | G6pd2 | G6pd2 | P3326 | NM_019468 | TSS25457 |
| chr5 | 62811395 | 62811486 | MACS2_peak_2247 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 25 | chr5 | unknown | gene | 62602445 | 62766177 | - | Arap2 | Arap2 | P18291 | NM_178407 | TSS19853 |
| chr5 | 62811395 | 62811486 | MACS2_peak_2247 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 25 | chr5 | unknown | gene | 62813822 | 62888282 | + | Dthd1 | Dthd1 | P17113 | NM_001170705 | TSS21500 |
| chr5 | 62894504 | 62894595 | MACS2_peak_2248 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 74 | chr5 | unknown | gene | 62813822 | 62888282 | + | Dthd1 | Dthd1 | P17113 | NM_001170705 | TSS21500 |
| chr5 | 62894504 | 62894595 | MACS2_peak_2248 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 74 | chr5 | unknown | gene | 63649102 | 63808303 | + | Nwd2 | Nwd2 | P18764 | NM_177006 | TSS20916 |
| chr5 | 64300620 | 64300711 | MACS2_peak_2249 | 35 | + | 5.98489 | 8.51731 | 3.53253 | 58 | chr5 | unknown | gene | 64092949 | 64127879 | + | Pgm1 | Pgm1 | P2320 | NM_025700 | TSS12453 |
| chr5 | 64300620 | 64300711 | MACS2_peak_2249 | 35 | + | 5.98489 | 8.51731 | 3.53253 | 58 | chr5 | unknown | gene | 64454812 | 64467942 | - | 1700027F09Rik | 1700027F09Rik | | NR_040681 | TSS24091 |
| chr5 | 65682729 | 65682821 | MACS2_peak_2250 | 45 | + | 6.59824 | 9.65189 | 4.58689 | 32 | chr5 | unknown | gene | 65537260 | 65594949 | + | Ube2k | Ube2k | P18408 | NM_016786 | TSS26072 |
| chr5 | 65682729 | 65682821 | MACS2_peak_2250 | 45 | + | 6.59824 | 9.65189 | 4.58689 | 32 | chr5 | unknown | gene | 65763520 | 65826650 | + | N4bp2 | N4bp2 | P20042 | NM_001024917 | TSS10953 |
| chr5 | 66269906 | 66270037 | MACS2_peak_2251 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 75 | chr5 | unknown | gene | 66166606 | 66191335 | - | 1700126H18Rik | 1700126H18Rik | | NR_040695 | TSS9317 |
| chr5 | 66269906 | 66270037 | MACS2_peak_2251 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 75 | chr5 | unknown | gene | 66298724 | 66618817 | - | Apbb2 | Apbb2 | P13115 | NM_009686 | TSS26884 |
| chr5 | 67807581 | 67807672 | MACS2_peak_2252 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 58 | chr5 | unknown | gene | 67607882 | 67611475 | + | Shisa3 | Shisa3 | P12015 | NM_001033415 | TSS25673 |
| chr5 | 67807581 | 67807672 | MACS2_peak_2252 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 58 | chr5 | unknown | gene | 67933611 | 67943081 | - | 4930425K10Rik | 4930425K10Rik | | NR_038182 | TSS18304 |
| chr5 | 68128878 | 68128969 | MACS2_peak_2253 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 80 | chr5 | unknown | gene | 67941668 | 67976956 | + | Gm5108 | Gm5108 | P25327 | NM_001256184 | TSS15074 |
| chr5 | 68128878 | 68128969 | MACS2_peak_2253 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 80 | chr5 | unknown | gene | 69109284 | 69341301 | - | Kctd8 | Kctd8 | P4198 | NM_175519 | TSS20151 |
| chr5 | 68256301 | 68256392 | MACS2_peak_2254 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 20 | chr5 | unknown | gene | 68031834 | 68166271 | + | Grxcr1 | Grxcr1 | P6078 | NM_001018019 | TSS9096 |
| chr5 | 68256301 | 68256392 | MACS2_peak_2254 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 20 | chr5 | unknown | gene | 69109284 | 69341301 | - | Kctd8 | Kctd8 | P4198 | NM_175519 | TSS20151 |
| chr5 | 68864146 | 68864281 | MACS2_peak_2255 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 21 | chr5 | unknown | gene | 68031834 | 68166271 | + | Grxcr1 | Grxcr1 | P6078 | NM_001018019 | TSS9096 |
| chr5 | 68864146 | 68864281 | MACS2_peak_2255 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 21 | chr5 | unknown | gene | 69109284 | 69341301 | - | Kctd8 | Kctd8 | P4198 | NM_175519 | TSS20151 |
| chr5 | 70181021 | 70181153 | MACS2_peak_2256 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 88 | chr5 | unknown | gene | 69575001 | 69592285 | - | Gnpda2 | Gnpda2 | P18273 | NM_001038015 | TSS21877 |
| chr5 | 70181021 | 70181153 | MACS2_peak_2256 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 88 | chr5 | unknown | gene | 70751046 | 70842219 | - | Gabrg1 | Gabrg1 | P6404 | NM_010252 | TSS13574 |
| chr5 | 70549482 | 70549573 | MACS2_peak_2257 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 60 | chr5 | unknown | gene | 69575001 | 69592285 | - | Gnpda2 | Gnpda2 | P18273 | NM_001038015 | TSS21877 |
| chr5 | 70549482 | 70549573 | MACS2_peak_2257 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 60 | chr5 | unknown | gene | 70751046 | 70842219 | - | Gabrg1 | Gabrg1 | P6404 | NM_010252 | TSS13574 |
| chr5 | 72460567 | 72460658 | MACS2_peak_2258 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 62 | chr5 | unknown | gene | 72203328 | 72297246 | + | Atp10d | Atp10d | | NR_003966 | TSS26662 |
| chr5 | 72460567 | 72460658 | MACS2_peak_2258 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 62 | chr5 | unknown | gene | 72513303 | 72559645 | - | Nfxl1 | Nfxl1 | P6687 | NM_133921 | TSS5801 |
| chr5 | 74174148 | 74174306 | MACS2_peak_2259 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 121 | chr5 | unknown | gene | 74093082 | 74094336 | + | Dancr | Dancr | | NR_015531 | TSS16993 |
| chr5 | 74174148 | 74174306 | MACS2_peak_2259 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 121 | chr5 | unknown | gene | 74195325 | 74198579 | + | Rasl11b | Rasl11b | P5294 | NM_026878 | TSS16656 |
| chr5 | 74695687 | 74695778 | MACS2_peak_2260 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 24 | chr5 | unknown | gene | 74535481 | 74595986 | + | Fip1l1 | Fip1l1 | P2068 | NM_024183 | TSS12888 |
| chr5 | 74695687 | 74695778 | MACS2_peak_2260 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 24 | chr5 | unknown | gene | 74949193 | 74966368 | + | Gm6116 | Gm6116 | | NR_045866 | TSS8942 |
| chr5 | 75313813 | 75313904 | MACS2_peak_2261 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 50 | chr5 | unknown | gene | 75152290 | 75195100 | + | Pdgfra | Pdgfra | P15206 | NM_011058 | TSS7232 |
| chr5 | 75313813 | 75313904 | MACS2_peak_2261 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 50 | chr5 | unknown | gene | 75574986 | 75654545 | + | Kit | Kit | P7210 | NM_001122733 | TSS11910 |
| chr5 | 75912608 | 75912699 | MACS2_peak_2262 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 71 | chr5 | unknown | gene | 75574986 | 75654545 | + | Kit | Kit | P7210 | NM_001122733 | TSS11910 |
| chr5 | 75912608 | 75912699 | MACS2_peak_2262 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 71 | chr5 | unknown | gene | 75933269 | 75978168 | - | Kdr | Kdr | P15430 | NM_010612 | TSS13661 |
| chr5 | 75917900 | 75917991 | MACS2_peak_2263 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 32 | chr5 | unknown | gene | 75574986 | 75654545 | + | Kit | Kit | P7210 | NM_001122733 | TSS11910 |
| chr5 | 75917900 | 75917991 | MACS2_peak_2263 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 32 | chr5 | unknown | gene | 75933269 | 75978168 | - | Kdr | Kdr | P15430 | NM_010612 | TSS13661 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr5 | 76141384 | 76141475 | MACS2_peak_2264 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 58 | chr5 | unknown | gene | 75933269 | 75978168 | - | Kdr | Kdr | P15430 | NM_010612 | TSS13661 |
| chr5 | 76141384 | 76141475 | MACS2_peak_2264 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 58 | chr5 | unknown | gene | 76183879 | 76208586 | + | Tmem165 | Tmem165 | P18624 | NM_011626 | TSS1763 |
| chr5 | 76303324 | 76303431 | MACS2_peak_2265 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 40 | chr5 | unknown | gene | 76183879 | 76208586 | + | Tmem165 | Tmem165 | P18624 | NM_011626 | TSS1763 |
| chr5 | 76303324 | 76303431 | MACS2_peak_2265 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 40 | chr5 | unknown | gene | 76312145 | 76331018 | - | Pdcl2 | Pdcl2 | P2537 | NM_023508 | TSS24651 |
| chr5 | 77474720 | 77474829 | MACS2_peak_2266 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 74 | chr5 | unknown | gene | 77465487 | 77468857 | + | 1700017L05Rik | 1700017L05Rik | | NR_131050 | TSS21881 |
| chr5 | 77474720 | 77474829 | MACS2_peak_2266 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 74 | chr5 | unknown | gene | 78929669 | 79515904 | - | Mir669m-1 | Mir669m-1 | | NR_035474 | TSS18856 |
| chr5 | 77661852 | 77661943 | MACS2_peak_2267 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 29 | chr5 | unknown | gene | 77465487 | 77468857 | + | 1700017L05Rik | 1700017L05Rik | | NR_131050 | TSS21881 |
| chr5 | 77661852 | 77661943 | MACS2_peak_2267 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 29 | chr5 | unknown | gene | 78929669 | 79515904 | - | Mir669m-1 | Mir669m-1 | | NR_035474 | TSS18856 |
| chr5 | 77728246 | 77728337 | MACS2_peak_2268 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 26 | chr5 | unknown | gene | 77465487 | 77468857 | + | 1700017L05Rik | 1700017L05Rik | | NR_131050 | TSS21881 |
| chr5 | 77728246 | 77728337 | MACS2_peak_2268 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 26 | chr5 | unknown | gene | 78929669 | 79515904 | - | Mir669m-1 | Mir669m-1 | | NR_035474 | TSS18856 |
| chr5 | 78439166 | 78439257 | MACS2_peak_2269 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 67 | chr5 | unknown | gene | 77465487 | 77468857 | + | 1700017L05Rik | 1700017L05Rik | | NR_131050 | TSS21881 |
| chr5 | 78439166 | 78439257 | MACS2_peak_2269 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 67 | chr5 | unknown | gene | 78929669 | 79515904 | - | Mir669m-1 | Mir669m-1 | | NR_035474 | TSS18856 |
| chr5 | 79236334 | 79236425 | MACS2_peak_2270 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 17 | chr5 | unknown | gene | 77465487 | 77468857 | + | 1700017L05Rik | 1700017L05Rik | | NR_131050 | TSS21881 |
| chr5 | 79236334 | 79236425 | MACS2_peak_2270 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 17 | chr5 | unknown | gene | 81021592 | 81795063 | + | Adgrl3 | Adgrl3 | P13016 | NM_198702 | TSS16963 |
| chr5 | 79487228 | 79487346 | MACS2_peak_2271 | 26 | + | 5.49828 | 7.51662 | 2.61219 | 60 | chr5 | unknown | gene | 77465487 | 77468857 | + | 1700017L05Rik | 1700017L05Rik | | NR_131050 | TSS21881 |
| chr5 | 79487228 | 79487346 | MACS2_peak_2271 | 26 | + | 5.49828 | 7.51662 | 2.61219 | 60 | chr5 | unknown | gene | 81021592 | 81795063 | + | Adgrl3 | Adgrl3 | P13016 | NM_198702 | TSS16963 |
| chr5 | 80083122 | 80083213 | MACS2_peak_2272 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 27 | chr5 | unknown | gene | 78929669 | 79515904 | - | Mir669m-1 | Mir669m-1 | | NR_035474 | TSS18856 |
| chr5 | 80083122 | 80083213 | MACS2_peak_2272 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 27 | chr5 | unknown | gene | 81021592 | 81795063 | + | Adgrl3 | Adgrl3 | P13016 | NM_198702 | TSS16963 |
| chr5 | 80185278 | 80185369 | MACS2_peak_2273 | 12 | + | 4.14966 | 5.12722 | 1.204 | 30 | chr5 | unknown | gene | 78929669 | 79515904 | - | Mir669m-1 | Mir669m-1 | | NR_035474 | TSS18856 |
| chr5 | 80185278 | 80185369 | MACS2_peak_2273 | 12 | + | 4.14966 | 5.12722 | 1.204 | 30 | chr5 | unknown | gene | 81021592 | 81795063 | + | Adgrl3 | Adgrl3 | P13016 | NM_198702 | TSS16963 |
| chr5 | 80233035 | 80233126 | MACS2_peak_2274 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 4 | chr5 | unknown | gene | 78929669 | 79515904 | - | Mir669m-1 | Mir669m-1 | | NR_035474 | TSS18856 |
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| chr5 | 80488727 | 80488818 | MACS2_peak_2275 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 31 | chr5 | unknown | gene | 78929669 | 79515904 | - | Mir669m-1 | Mir669m-1 | | NR_035474 | TSS18856 |
| chr5 | 80488727 | 80488818 | MACS2_peak_2275 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 31 | chr5 | unknown | gene | 81021592 | 81795063 | + | Adgrl3 | Adgrl3 | P13016 | NM_198702 | TSS16963 |
| chr5 | 81342022 | 81342136 | MACS2_peak_2276 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 26 | chr5 | unknown | gene | 78929669 | 79515904 | - | Mir669m-1 | Mir669m-1 | | NR_035474 | TSS18856 |
| chr5 | 81342022 | 81342136 | MACS2_peak_2276 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 26 | chr5 | unknown | gene | 82798943 | 82799065 | - | Mir1187 | Mir1187 | | NR_035415 | TSS10061 |
| chr5 | 81412681 | 81412828 | MACS2_peak_2277 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 58 | chr5 | unknown | gene | 78929669 | 79515904 | - | Mir669m-1 | Mir669m-1 | | NR_035474 | TSS18856 |
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| chr5 | 81783109 | 81783382 | MACS2_peak_2278 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 141 | chr5 | unknown | gene | 78929669 | 79515904 | - | Mir669m-1 | Mir669m-1 | | NR_035474 | TSS18856 |
| chr5 | 81783109 | 81783382 | MACS2_peak_2278 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 141 | chr5 | unknown | gene | 82798943 | 82799065 | - | Mir1187 | Mir1187 | | NR_035415 | TSS10061 |
| chr5 | 82008813 | 82008904 | MACS2_peak_2279 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 26 | chr5 | unknown | gene | 81021592 | 81795063 | + | Adgrl3 | Adgrl3 | P13016 | NM_198702 | TSS16963 |
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| chr5 | 82713536 | 82713627 | MACS2_peak_2280 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 23 | chr5 | unknown | gene | 81021592 | 81795063 | + | Adgrl3 | Adgrl3 | P13016 | NM_198702 | TSS16963 |
| chr5 | 82713536 | 82713627 | MACS2_peak_2280 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 23 | chr5 | unknown | gene | 82798943 | 82799065 | - | Mir1187 | Mir1187 | | NR_035415 | TSS10061 |
| chr5 | 83484151 | 83484242 | MACS2_peak_2281 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 49 | chr5 | unknown | gene | 83278121 | 83355000 | - | Tecrl | Tecrl | P13298 | NM_153801 | TSS11846 |
| chr5 | 83484151 | 83484242 | MACS2_peak_2281 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 49 | chr5 | unknown | gene | 84054764 | 84416505 | - | Epha5 | Epha5 | P11228 | NM_007937 | TSS1694 |
| chr5 | 84836993 | 84837123 | MACS2_peak_2282 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 87 | chr5 | unknown | gene | 84054764 | 84416505 | - | Epha5 | Epha5 | P11228 | NM_007937 | TSS1694 |
| chr5 | 84836993 | 84837123 | MACS2_peak_2282 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 87 | chr5 | unknown | gene | 86012024 | 86065345 | - | Cenpc1 | Cenpc1 | P24048 | NM_007683 | TSS25624 |
| chr5 | 86391525 | 86391621 | MACS2_peak_2283 | 32 | + | 5.8651 | 8.25694 | 3.2954 | 60 | chr5 | unknown | gene | 86302853 | 86373352 | - | Tmprss11d | Tmprss11d | P4094 | NM_145561 | TSS20087 |
| chr5 | 86391525 | 86391621 | MACS2_peak_2283 | 32 | + | 5.8651 | 8.25694 | 3.2954 | 60 | chr5 | unknown | gene | 86410409 | 86468855 | - | Tmprss11a | Tmprss11a | P17902 | NM_001033233 | TSS12877 |
| chr5 | 86438824 | 86438957 | MACS2_peak_2284 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 90 | chr5 | unknown | gene | 86302853 | 86373352 | - | Tmprss11d | Tmprss11d | P4094 | NM_145561 | TSS20087 |
| chr5 | 86438824 | 86438957 | MACS2_peak_2284 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 90 | chr5 | unknown | gene | 86485876 | 86518504 | - | Tmprss11g | Tmprss11g | P19655 | NM_177162 | TSS20549 |
| chr5 | 88781062 | 88781153 | MACS2_peak_2285 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 51 | chr5 | unknown | gene | 88720870 | 88756172 | + | Mob1b | Mob1b | P8746 | NM_026735 | TSS16837 |
| chr5 | 88781062 | 88781153 | MACS2_peak_2285 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 51 | chr5 | unknown | gene | 88887259 | 89235612 | + | Slc4a4 | Slc4a4 | P23496 | NM_001136260 | TSS6692 |
| chr5 | 89151087 | 89151223 | MACS2_peak_2286 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 54 | chr5 | unknown | gene | 88765012 | 88781246 | + | Dck | Dck | P13775 | NM_007832 | TSS8446 |
| chr5 | 89151087 | 89151223 | MACS2_peak_2286 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 54 | chr5 | unknown | gene | 89417510 | 89457718 | - | Gc | Gc | P2229 | NM_008096 | TSS20399 |
| chr5 | 89166459 | 89166550 | MACS2_peak_2287 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 38 | chr5 | unknown | gene | 88765012 | 88781246 | + | Dck | Dck | P13775 | NM_007832 | TSS8446 |
| chr5 | 89166459 | 89166550 | MACS2_peak_2287 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 38 | chr5 | unknown | gene | 89417510 | 89457718 | - | Gc | Gc | P2229 | NM_008096 | TSS20399 |
| chr5 | 89495091 | 89495182 | MACS2_peak_2288 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 52 | chr5 | unknown | gene | 89417510 | 89457718 | - | Gc | Gc | P2229 | NM_008096 | TSS20399 |
| chr5 | 89495091 | 89495182 | MACS2_peak_2288 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 52 | chr5 | unknown | gene | 89527428 | 89583466 | + | Npffr2 | Npffr2 | P19235 | NM_133192 | TSS17588 |
| chr5 | 90690159 | 90690269 | MACS2_peak_2289 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 89 | chr5 | unknown | gene | 90603075 | 90640487 | - | Rassf6 | Rassf6 | P24529 | NM_028478 | TSS3530 |
| chr5 | 90690159 | 90690269 | MACS2_peak_2289 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 89 | chr5 | unknown | gene | 90759297 | 90760513 | + | Cxcl5 | Cxcl5 | P8345 | NM_009141 | TSS20069 |
| chr5 | 91205242 | 91205334 | MACS2_peak_2290 | 30 | + | 5.71265 | 7.93979 | 3.00019 | 43 | chr5 | unknown | gene | 91139614 | 91148432 | + | Areg | Areg | P22454 | NM_009704 | TSS12861 |
| chr5 | 91205242 | 91205334 | MACS2_peak_2290 | 30 | + | 5.71265 | 7.93979 | 3.00019 | 43 | chr5 | unknown | gene | 91257570 | 91283076 | - | Gm19619 | Gm19619 | | NR_040428 | TSS27478 |
| chr5 | 91351643 | 91351734 | MACS2_peak_2291 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 21 | chr5 | unknown | gene | 91257570 | 91283076 | - | Gm19619 | Gm19619 | | NR_040428 | TSS27478 |
| chr5 | 91351643 | 91351734 | MACS2_peak_2291 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 21 | chr5 | unknown | gene | 91357260 | 91402721 | - | Btc | Btc | P25414 | NM_007568 | TSS14624 |
| chr5 | 91940474 | 91940565 | MACS2_peak_2292 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 83 | chr5 | unknown | gene | 91766241 | 91767300 | - | 1700063O14Rik | 1700063O14Rik | | NR_045383 | TSS19379 |
| chr5 | 91940474 | 91940565 | MACS2_peak_2292 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 83 | chr5 | unknown | gene | 91948841 | 91962719 | - | Rchy1 | Rchy1 | P16760 | NM_026557 | TSS4069 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr5 | 93096119 | 93096289 | MACS2_peak_2293 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 88 | chr5 | unknown | gene | 93041122 | 93044858 | - | Sowahb | Sowahb | P14798 | NM_175270 | TSS4258 |
| chr5 | 93096119 | 93096289 | MACS2_peak_2293 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 88 | chr5 | unknown | gene | 93181932 | 93206495 | - | Ccni | Ccni | P12282 | NM_017367 | TSS2706 |
| chr5 | 93206912 | 93207003 | MACS2_peak_2294 | 22 | + | 5.23629 | 7.0289 | 2.291 | 17 | chr5 | unknown | gene | 93181932 | 93206495 | - | Ccni | Ccni | P12282 | NM_017367 | TSS2706 |
| chr5 | 93206912 | 93207003 | MACS2_peak_2294 | 22 | + | 5.23629 | 7.0289 | 2.291 | 17 | chr5 | unknown | gene | 93267572 | 93274997 | + | Ccng2 | Ccng2 | P5230 | NM_007635 | TSS12268 |
| chr5 | 95864997 | 95865178 | MACS2_peak_2295 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 14 | chr5 | unknown | gene | 95456805 | 95484671 | + | D5Ertd577e | D5Ertd577e | P18238 | NM_177187 | TSS26849 |
| chr5 | 95864997 | 95865178 | MACS2_peak_2295 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 14 | chr5 | unknown | gene | 95956938 | 95960268 | + | Cxcl13 | Cxcl13 | P14937 | NM_018866 | TSS16789 |
| chr5 | 96069638 | 96069825 | MACS2_peak_2296 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 60 | chr5 | unknown | gene | 95956938 | 95960268 | + | Cxcl13 | Cxcl13 | P14937 | NM_018866 | TSS16789 |
| chr5 | 96069638 | 96069825 | MACS2_peak_2296 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 60 | chr5 | unknown | gene | 96070332 | 96161990 | - | Cnot6l | Cnot6l | P22242 | NM_001285514 | TSS26744 |
| chr5 | 96708361 | 96708452 | MACS2_peak_2297 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 72 | chr5 | unknown | gene | 96210114 | 96264337 | + | Mrpl1 | Mrpl1 | P14890 | NM_001039084 | TSS27453 |
| chr5 | 96708361 | 96708452 | MACS2_peak_2297 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 72 | chr5 | unknown | gene | 96793384 | 96845560 | + | Anxa3 | Anxa3 | P13759 | NM_013470 | TSS18478 |
| chr5 | 97103938 | 97104029 | MACS2_peak_2298 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 26 | chr5 | unknown | gene | 96997688 | 97088136 | + | Bmp2k | Bmp2k | P20226 | NM_080708 | TSS25756 |
| chr5 | 97103938 | 97104029 | MACS2_peak_2298 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 26 | chr5 | unknown | gene | 97382208 | 97392297 | - | Naa11 | Naa11 | P10954 | NM_001033191 | TSS16341 |
| chr5 | 97348666 | 97348811 | MACS2_peak_2299 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 77 | chr5 | unknown | gene | 97082328 | 97111443 | - | Paqr3 | Paqr3 | P13199 | NM_198422 | TSS25977 |
| chr5 | 97348666 | 97348811 | MACS2_peak_2299 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 77 | chr5 | unknown | gene | 97382208 | 97392297 | - | Naa11 | Naa11 | P10954 | NM_001033191 | TSS16341 |
| chr5 | 98565900 | 98565991 | MACS2_peak_2300 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 34 | chr5 | unknown | gene | 98475555 | 98475664 | - | Mir703 | Mir703 | | NR_030484 | TSS7189 |
| chr5 | 98565900 | 98565991 | MACS2_peak_2300 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 34 | chr5 | unknown | gene | 98854438 | 98879929 | + | Bmp3 | Bmp3 | P253 | NM_173404 | TSS25615 |
| chr5 | 99074226 | 99074317 | MACS2_peak_2301 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 41 | chr5 | unknown | gene | 98929772 | 99037079 | - | Prkg2 | Prkg2 | P2943 | NM_008926 | TSS14715 |
| chr5 | 99074226 | 99074317 | MACS2_peak_2301 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 41 | chr5 | unknown | gene | 99217419 | 99252927 | - | Rasgef1b | Rasgef1b | P20831 | NM_181318 | TSS640 |
| chr5 | 99337392 | 99337483 | MACS2_peak_2302 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 22 | chr5 | unknown | gene | 99217419 | 99252927 | - | Rasgef1b | Rasgef1b | P20831 | NM_181318 | TSS640 |
| chr5 | 99337392 | 99337483 | MACS2_peak_2302 | 7 | + | 3.41507 | 3.91313 | 0.75855 | 22 | chr5 | unknown | gene | 99730853 | 99753973 | - | Gm38413 | Gm38413 | | NR_131054 | TSS2759 |
| chr5 | 99880463 | 99880582 | MACS2_peak_2303 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 48 | chr5 | unknown | gene | 99730853 | 99753973 | - | Gm38413 | Gm38413 | | NR_131054 | TSS2759 |
| chr5 | 99880463 | 99880582 | MACS2_peak_2303 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 48 | chr5 | unknown | gene | 99955934 | 99978624 | - | Hnrnpd | Hnrnpd | P8593 | NM_001077265 | TSS23864 |
| chr5 | 103396996 | 103397087 | MACS2_peak_2304 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 29 | chr5 | unknown | gene | 103230374 | 103299029 | - | 4930429D17Rik | 4930429D17Rik | | NR_040699 | TSS9783 |
| chr5 | 103396996 | 103397087 | MACS2_peak_2304 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 29 | chr5 | unknown | gene | 103425191 | 103597785 | + | Ptpn13 | Ptpn13 | P2733 | NM_011204 | TSS3633 |
| chr5 | 103744839 | 103744930 | MACS2_peak_2305 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 61 | chr5 | unknown | gene | 103648586 | 103655732 | - | 1700016H13Rik | 1700016H13Rik | P184 | NM_028824 | TSS14212 |
| chr5 | 103744839 | 103744930 | MACS2_peak_2305 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 61 | chr5 | unknown | gene | 103754161 | 103850823 | + | Aff1 | Aff1 | P2599 | NM_133919 | TSS12835 |
| chr5 | 103878423 | 103878560 | MACS2_peak_2306 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 48 | chr5 | unknown | gene | 103754161 | 103850823 | + | Aff1 | Aff1 | P2599 | NM_133919 | TSS12835 |
| chr5 | 103878423 | 103878560 | MACS2_peak_2306 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 48 | chr5 | unknown | gene | 103955441 | 103977315 | - | Hsd17b13 | Hsd17b13 | P648 | NM_198030 | TSS10491 |
| chr5 | 103948032 | 103948123 | MACS2_peak_2307 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 10 | chr5 | unknown | gene | 103862049 | 103911229 | - | Klhl8 | Klhl8 | P5712 | NM_178741 | TSS4765 |
| chr5 | 103948032 | 103948123 | MACS2_peak_2307 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 10 | chr5 | unknown | gene | 103955441 | 103977315 | - | Hsd17b13 | Hsd17b13 | P648 | NM_198030 | TSS10491 |
| chr5 | 107190138 | 107190229 | MACS2_peak_2308 | 7 | + | 3.39397 | 3.87422 | 0.75855 | 11 | chr5 | unknown | gene | 106964321 | 106983355 | + | Cdc7 | Cdc7 | P25765 | NM_009863 | TSS12598 |
| chr5 | 107190138 | 107190229 | MACS2_peak_2308 | 7 | + | 3.39397 | 3.87422 | 0.75855 | 11 | chr5 | unknown | gene | 107331193 | 107385526 | + | Brdt | Brdt | P3723 | NM_001079873 | TSS14147 |
| chr5 | 107228472 | 107228563 | MACS2_peak_2309 | 30 | + | 5.71265 | 7.93979 | 3.00019 | 55 | chr5 | unknown | gene | 106964321 | 106983355 | + | Cdc7 | Cdc7 | P25765 | NM_009863 | TSS12598 |
| chr5 | 107228472 | 107228563 | MACS2_peak_2309 | 30 | + | 5.71265 | 7.93979 | 3.00019 | 55 | chr5 | unknown | gene | 107331193 | 107385526 | + | Brdt | Brdt | P3723 | NM_001079873 | TSS14147 |
| chr5 | 108596999 | 108597092 | MACS2_peak_2310 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 4 | chr5 | unknown | gene | 108518553 | 108550027 | - | Cplx1 | Cplx1 | P3361 | NM_007756 | TSS23887 |
| chr5 | 108596999 | 108597092 | MACS2_peak_2310 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 4 | chr5 | unknown | gene | 108629809 | 108646505 | + | Tmem175 | Tmem175 | P7764 | NM_001163532 | TSS9697 |
| chr5 | 109312188 | 109312279 | MACS2_peak_2311 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 37 | chr5 | unknown | gene | 109286268 | 109297556 | - | Vmn2r15 | Vmn2r15 | P8100 | NM_001104626 | TSS17151 |
| chr5 | 109312188 | 109312279 | MACS2_peak_2311 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 37 | chr5 | unknown | gene | 109330380 | 109364481 | + | Vmn2r16 | Vmn2r16 | P23817 | NM_001104627 | TSS9072 |
| chr5 | 114173053 | 114173208 | MACS2_peak_2312 | 279 | + | 17.07534 | 33.71909 | 27.9675 | 75 | chr5 | unknown | gene | 114130434 | 114138376 | + | Ung | Ung | P26647 | NM_001040691 | TSS19091 |
| chr5 | 114173053 | 114173208 | MACS2_peak_2312 | 279 | + | 17.07534 | 33.71909 | 27.9675 | 75 | chr5 | unknown | gene | 114254163 | 114273761 | - | Foxn4 | Foxn4 | P3696 | NM_148935 | TSS2717 |
| chr5 | 114889040 | 114889137 | MACS2_peak_2313 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 28 | chr5 | unknown | gene | 114853713 | 114882865 | + | 4930519G04Rik | 4930519G04Rik | P20004 | NM_026263 | TSS20914 |
| chr5 | 114889040 | 114889137 | MACS2_peak_2313 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 28 | chr5 | unknown | gene | 114896933 | 114911367 | + | Oasl2 | Oasl2 | P12412 | NM_011854 | TSS8800 |
| chr5 | 114922437 | 114922545 | MACS2_peak_2314 | 63 | + | 7.52781 | 11.52513 | 6.36816 | 65 | chr5 | unknown | gene | 114896933 | 114911367 | + | Oasl2 | Oasl2 | P12412 | NM_011854 | TSS8800 |
| chr5 | 114922437 | 114922545 | MACS2_peak_2314 | 63 | + | 7.52781 | 11.52513 | 6.36816 | 65 | chr5 | unknown | gene | 114923239 | 114937418 | + | Oasl1 | Oasl1 | P20383 | NM_145209 | TSS14746 |
| chr5 | 116345166 | 116345257 | MACS2_peak_2315 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 41 | chr5 | unknown | gene | 116312359 | 116318274 | + | B230112J18Rik | B230112J18Rik | | NR_110475 | TSS18198 |
| chr5 | 116345166 | 116345257 | MACS2_peak_2315 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 41 | chr5 | unknown | gene | 116408490 | 116422479 | - | Hspb8 | Hspb8 | P26689 | NM_030704 | TSS19689 |
| chr5 | 118930334 | 118930428 | MACS2_peak_2316 | 35 | + | 5.98489 | 8.51731 | 3.53253 | 27 | chr5 | unknown | gene | 118560718 | 118762833 | + | Med13l | Med13l | P12300 | NM_172424 | TSS14340 |
| chr5 | 118930334 | 118930428 | MACS2_peak_2316 | 35 | + | 5.98489 | 8.51731 | 3.53253 | 27 | chr5 | unknown | gene | 118952338 | 118961261 | + | 4930413E15Rik | 4930413E15Rik | | NR_040694 | TSS4255 |
| chr5 | 129908323 | 129908414 | MACS2_peak_2317 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 3 | chr5 | unknown | gene | 129895722 | 129903482 | + | Zbed5 | Zbed5 | P21871 | NM_183088 | TSS265 |
| chr5 | 129908323 | 129908414 | MACS2_peak_2317 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 3 | chr5 | unknown | gene | 129908539 | 129911281 | + | Nupr1l | Nupr1l | P2861 | NM_026916 | TSS9200 |
| chr5 | 131519692 | 131519831 | MACS2_peak_2318 | 59 | + | 7.33138 | 11.09226 | 5.95913 | 51 | chr5 | unknown | gene | 130874950 | 131306600 | - | Wbscr17 | Wbscr17 | P18120 | NM_145218 | TSS946 |
| chr5 | 131519692 | 131519831 | MACS2_peak_2318 | 59 | + | 7.33138 | 11.09226 | 5.95913 | 51 | chr5 | unknown | gene | 131880268 | 131883768 | + | 4930563F08Rik | 4930563F08Rik | | NR_040704 | TSS3072 |
| chr5 | 132285006 | 132285097 | MACS2_peak_2319 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 75 | chr5 | unknown | gene | 131880268 | 131883768 | + | 4930563F08Rik | 4930563F08Rik | | NR_040704 | TSS3072 |
| chr5 | 132285006 | 132285097 | MACS2_peak_2319 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 75 | chr5 | unknown | gene | 134099747 | 134138294 | + | Gatsl2 | Gatsl2 | P74 | NM_030719 | TSS14686 |
| chr5 | 132498025 | 132498116 | MACS2_peak_2320 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 23 | chr5 | unknown | gene | 131880268 | 131883768 | + | 4930563F08Rik | 4930563F08Rik | | NR_040704 | TSS3072 |
| chr5 | 132498025 | 132498116 | MACS2_peak_2320 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 23 | chr5 | unknown | gene | 134099747 | 134138294 | + | Gatsl2 | Gatsl2 | P74 | NM_030719 | TSS14686 |
| chr5 | 133283159 | 133283250 | MACS2_peak_2321 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 19 | chr5 | unknown | gene | 131437681 | 132541823 | - | Auts2 | Auts2 | P20420 | NM_177047 | TSS7483 |
| chr5 | 133283159 | 133283250 | MACS2_peak_2321 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 19 | chr5 | unknown | gene | 134099747 | 134138294 | + | Gatsl2 | Gatsl2 | P74 | NM_030719 | TSS14686 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr5 | 134630584 | 134630675 | MACS2_peak_2322 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 50 | chr5 | unknown | gene | 134600102 | 134615025 | - | Lat2 | Lat2 | P4277 | NM_020044 | TSS24266 |
| chr5 | 134630584 | 134630675 | MACS2_peak_2322 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 50 | chr5 | unknown | gene | 134656038 | 134688395 | - | Limk1 | Limk1 | P24527 | NM_010717 | TSS19108 |
| chr5 | 135307810 | 135307907 | MACS2_peak_2323 | 44 | + | 6.55451 | 9.55892 | 4.49773 | 65 | chr5 | unknown | gene | 135248937 | 135251029 | - | Fzd9 | Fzd9 | P23808 | NM_010246 | TSS10791 |
| chr5 | 135307810 | 135307907 | MACS2_peak_2323 | 44 | + | 6.55451 | 9.55892 | 4.49773 | 65 | chr5 | unknown | gene | 135353295 | 135367654 | + | Trim50 | Trim50 | P10593 | NM_178240 | TSS20630 |
| chr5 | 135309004 | 135309095 | MACS2_peak_2324 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 61 | chr5 | unknown | gene | 135248937 | 135251029 | - | Fzd9 | Fzd9 | P23808 | NM_010246 | TSS10791 |
| chr5 | 135309004 | 135309095 | MACS2_peak_2324 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 61 | chr5 | unknown | gene | 135353295 | 135367654 | + | Trim50 | Trim50 | P10593 | NM_178240 | TSS20630 |
| chr5 | 135714043 | 135714134 | MACS2_peak_2325 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 49 | chr5 | unknown | gene | 135632653 | 135643378 | + | Rhbdd2 | Rhbdd2 | P10790 | NM_146002 | TSS15182 |
| chr5 | 135714043 | 135714134 | MACS2_peak_2325 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 49 | chr5 | unknown | gene | 135735489 | 135744128 | - | Tmem120a | Tmem120a | P14605 | NM_172541 | TSS16011 |
| chr5 | 136570870 | 136570995 | MACS2_peak_2326 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 61 | chr5 | unknown | gene | 136248134 | 136567240 | - | Cux1 | Cux1 | P6842 | NM_001291240 | TSS526 |
| chr5 | 136570870 | 136570995 | MACS2_peak_2326 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 61 | chr5 | unknown | gene | 136693145 | 136700953 | + | Myl10 | Myl10 | P4252 | NM_021611 | TSS13080 |
| chr5 | 136890271 | 136890362 | MACS2_peak_2327 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 28 | chr5 | unknown | gene | 136741763 | 136883007 | - | Col26a1 | Col26a1 | P3304 | NM_024474 | TSS26453 |
| chr5 | 136890271 | 136890362 | MACS2_peak_2327 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 28 | chr5 | unknown | gene | 136908149 | 136912973 | + | Ift22 | Ift22 | P18235 | NM_026073 | TSS11872 |
| chr5 | 138597647 | 138597738 | MACS2_peak_2328 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 21 | chr5 | unknown | gene | 138561839 | 138564660 | - | 1700123K08Rik | 1700123K08Rik | P25898 | NM_029693 | TSS23540 |
| chr5 | 138597647 | 138597738 | MACS2_peak_2328 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 21 | chr5 | unknown | gene | 138603651 | 138619743 | - | Zfp68 | Zfp68 | P14390 | NM_013844 | TSS15557 |
| chr5 | 138618000 | 138618125 | MACS2_peak_2329 | 38 | + | 6.2245 | 8.89055 | 3.85809 | 50 | chr5 | unknown | gene | 138561839 | 138564660 | - | 1700123K08Rik | 1700123K08Rik | P25898 | NM_029693 | TSS23540 |
| chr5 | 138618000 | 138618125 | MACS2_peak_2329 | 38 | + | 6.2245 | 8.89055 | 3.85809 | 50 | chr5 | unknown | gene | 138622858 | 138647897 | + | A430033K04Rik | A430033K04Rik | P23818 | NM_183025 | TSS23781 |
| chr5 | 140740556 | 140740647 | MACS2_peak_2330 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 15 | chr5 | unknown | gene | 140705010 | 140718597 | + | Brat1 | Brat1 | P22305 | NM_181066 | TSS16100 |
| chr5 | 140740556 | 140740647 | MACS2_peak_2330 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 15 | chr5 | unknown | gene | 140759943 | 140830296 | - | Gna12 | Gna12 | P15772 | NM_010302 | TSS1375 |
| chr5 | 142770596 | 142770687 | MACS2_peak_2331 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 56 | chr5 | unknown | gene | 142702100 | 142721490 | + | Slc29a4 | Slc29a4 | P12384 | NM_146257 | TSS14973 |
| chr5 | 142770596 | 142770687 | MACS2_peak_2331 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 56 | chr5 | unknown | gene | 142871788 | 142895238 | - | Fbxl18 | Fbxl18 | P20592 | NM_001033312 | TSS13265 |
| chr5 | 145757700 | 145757791 | MACS2_peak_2332 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 85 | chr5 | unknown | gene | 145558663 | 145720049 | - | Cyp3a41a | Cyp3a41a | P3795 | NM_017396 | TSS4629 |
| chr5 | 145757700 | 145757791 | MACS2_peak_2332 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 85 | chr5 | unknown | gene | 145773982 | 145805789 | - | Cyp3a44 | Cyp3a44 | P23535 | NM_177380 | TSS4974 |
| chr5 | 147063456 | 147063547 | MACS2_peak_2333 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 67 | chr5 | unknown | gene | 146951572 | 146963797 | - | Mtif3 | Mtif3 | P4595 | NM_001256102 | TSS15123 |
| chr5 | 147063456 | 147063547 | MACS2_peak_2333 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 67 | chr5 | unknown | gene | 147077345 | 147110927 | + | Polr1d | Polr1d | P18299 | NM_009087 | TSS9448 |
| chr5 | 151058366 | 151058505 | MACS2_peak_2334 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 59 | chr5 | unknown | gene | 150952606 | 150991854 | + | Kl | Kl | P12187 | NM_013823 | TSS1291 |
| chr5 | 151058366 | 151058505 | MACS2_peak_2334 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 59 | chr5 | unknown | gene | 151368674 | 151414083 | + | 1700028E10Rik | 1700028E10Rik | | NR_045700 | TSS19631 |
| chr6 | 4040472 | 4040563 | MACS2_peak_2335 | 16 | + | 4.811 | 6.2687 | 1.67914 | 48 | chr6 | unknown | gene | 4003986 | 4008160 | + | Gng11 | Gng11 | P11561 | NM_025331 | TSS25202 |
| chr6 | 4040472 | 4040563 | MACS2_peak_2335 | 16 | + | 4.811 | 6.2687 | 1.67914 | 48 | chr6 | unknown | gene | 4076903 | 4086795 | - | Bet1 | Bet1 | P12603 | NM_009748 | TSS20038 |
| chr6 | 4582979 | 4583105 | MACS2_peak_2336 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 88 | chr6 | unknown | gene | 4505696 | 4540662 | + | Col1a2 | Col1a2 | P1408 | NM_007743 | TSS9712 |
| chr6 | 4582979 | 4583105 | MACS2_peak_2336 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 88 | chr6 | unknown | gene | 4601065 | 4642118 | + | Casd1 | Casd1 | P645 | NM_145398 | TSS6248 |
| chr6 | 4613210 | 4613372 | MACS2_peak_2337 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 73 | chr6 | unknown | gene | 4505696 | 4540662 | + | Col1a2 | Col1a2 | P1408 | NM_007743 | TSS9712 |
| chr6 | 4613210 | 4613372 | MACS2_peak_2337 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 73 | chr6 | unknown | gene | 4674349 | 4747088 | - | Sgce | Sgce | P26612 | NM_001130191 | TSS13334 |
| chr6 | 4970835 | 4970926 | MACS2_peak_2338 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 48 | chr6 | unknown | gene | 4747305 | 4757240 | + | Peg10 | Peg10 | P6168 | NM_001040611 | TSS7383 |
| chr6 | 4970835 | 4970926 | MACS2_peak_2338 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 48 | chr6 | unknown | gene | 5168089 | 5193749 | - | Pon1 | Pon1 | P23410 | NM_011134 | TSS21181 |
| chr6 | 5185277 | 5185368 | MACS2_peak_2339 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 14 | chr6 | unknown | gene | 4903319 | 5159752 | + | Ppp1r9a | Ppp1r9a | P12416 | NM_181595 | TSS23356 |
| chr6 | 5185277 | 5185368 | MACS2_peak_2339 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 14 | chr6 | unknown | gene | 5220851 | 5256226 | - | Pon3 | Pon3 | P3113 | NM_173006 | TSS25984 |
| chr6 | 5988604 | 5988695 | MACS2_peak_2340 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 18 | chr6 | unknown | gene | 5963896 | 5977393 | - | 1700019G24Rik | 1700019G24Rik | | NR_040255 | TSS11652 |
| chr6 | 5988604 | 5988695 | MACS2_peak_2340 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 18 | chr6 | unknown | gene | 6041217 | 6217010 | - | Slc25a13 | Slc25a13 | P19600 | NM_001177572 | TSS16585 |
| chr6 | 7383687 | 7383778 | MACS2_peak_2341 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 18 | chr6 | unknown | gene | 6956017 | 7039057 | + | Sdhaf3 | Sdhaf3 | P24303 | NM_001077713 | TSS19070 |
| chr6 | 7383687 | 7383778 | MACS2_peak_2341 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 18 | chr6 | unknown | gene | 7555070 | 7562432 | + | Tac1 | Tac1 | P6227 | NM_009311 | TSS24581 |
| chr6 | 8275389 | 8275487 | MACS2_peak_2342 | 39 | + | 6.26392 | 8.9676 | 3.93029 | 22 | chr6 | unknown | gene | 8255935 | 8259098 | - | Rpa3 | Rpa3 | P10618 | NM_026632 | TSS18164 |
| chr6 | 8275389 | 8275487 | MACS2_peak_2342 | 39 | + | 6.26392 | 8.9676 | 3.93029 | 22 | chr6 | unknown | gene | 8507058 | 8509161 | - | A430035B10Rik | A430035B10Rik | | NR_040452 | TSS15753 |
| chr6 | 9539308 | 9539399 | MACS2_peak_2343 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 63 | chr6 | unknown | gene | 8950018 | 9247846 | + | Nxph1 | Nxph1 | P1268 | NM_008751 | TSS25891 |
| chr6 | 9539308 | 9539399 | MACS2_peak_2343 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 63 | chr6 | unknown | gene | 10971467 | 10974378 | - | AA545190 | AA545190 | | NR_033776 | TSS3143 |
| chr6 | 11091899 | 11091990 | MACS2_peak_2344 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 15 | chr6 | unknown | gene | 10971467 | 10974378 | - | AA545190 | AA545190 | | NR_033776 | TSS3143 |
| chr6 | 11091899 | 11091990 | MACS2_peak_2344 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 15 | chr6 | unknown | gene | 11900372 | 11907365 | - | Ndufa4 | Ndufa4 | P3827 | NM_010886 | TSS9131 |
| chr6 | 12861863 | 12861995 | MACS2_peak_2345 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 68 | chr6 | unknown | gene | 12311607 | 12748953 | - | Thsd7a | Thsd7a | P9364 | NM_001164805 | TSS19444 |
| chr6 | 12861863 | 12861995 | MACS2_peak_2345 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 68 | chr6 | unknown | gene | 13069758 | 13084326 | + | Tmem106b | Tmem106b | P20413 | NM_027992 | TSS10143 |
| chr6 | 13176058 | 13176149 | MACS2_peak_2346 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 35 | chr6 | unknown | gene | 13069758 | 13084326 | + | Tmem106b | Tmem106b | P20413 | NM_027992 | TSS10143 |
| chr6 | 13176058 | 13176149 | MACS2_peak_2346 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 35 | chr6 | unknown | gene | 13185610 | 13224863 | - | Vwde | Vwde | P21302 | NM_001013757 | TSS16565 |
| chr6 | 13354007 | 13354131 | MACS2_peak_2347 | 38 | + | 6.2245 | 8.89055 | 3.85809 | 69 | chr6 | unknown | gene | 13185610 | 13224863 | - | Vwde | Vwde | P21302 | NM_001013757 | TSS16565 |
| chr6 | 13354007 | 13354131 | MACS2_peak_2347 | 38 | + | 6.2245 | 8.89055 | 3.85809 | 69 | chr6 | unknown | gene | 13413336 | 13415996 | + | 1700016P04Rik | 1700016P04Rik | | NR_038149 | TSS22023 |
| chr6 | 14043518 | 14043632 | MACS2_peak_2348 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 31 | chr6 | unknown | gene | 13871568 | 13896421 | + | 1110019D14Rik | 1110019D14Rik | | NR_045995 | TSS14241 |
| chr6 | 14043518 | 14043632 | MACS2_peak_2348 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 31 | chr6 | unknown | gene | 14713821 | 14755246 | - | Ppp1r3a | Ppp1r3a | P19269 | NM_080464 | TSS9178 |
| chr6 | 14278430 | 14278521 | MACS2_peak_2349 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 40 | chr6 | unknown | gene | 13871568 | 13896421 | + | 1110019D14Rik | 1110019D14Rik | | NR_045995 | TSS14241 |
| chr6 | 14278430 | 14278521 | MACS2_peak_2349 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 40 | chr6 | unknown | gene | 14713821 | 14755246 | - | Ppp1r3a | Ppp1r3a | P19269 | NM_080464 | TSS9178 |
| chr6 | 14836720 | 14836811 | MACS2_peak_2350 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 31 | chr6 | unknown | gene | 14713821 | 14755246 | - | Ppp1r3a | Ppp1r3a | P19269 | NM_080464 | TSS9178 |
| chr6 | 14836720 | 14836811 | MACS2_peak_2350 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 31 | chr6 | unknown | gene | 14901348 | 15438021 | + | Foxp2 | Foxp2 | P21413 | NM_053242 | TSS10171 |

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr6 | 14925596 | 14925687 | MACS2_peak_2351 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 28 | chr6 | unknown | gene | 14713821 | 14755246 | - | Ppp1r3a | Ppp1r3a | P19269 | NM_080464 | TSS9178 |
| chr6 | 14925596 | 14925687 | MACS2_peak_2351 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 28 | chr6 | unknown | gene | 15720660 | 15799865 | + | Mdfic | Mdfic | P14027 | NM_175088 | TSS4576 |
| chr6 | 15051736 | 15051827 | MACS2_peak_2352 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 9 | chr6 | unknown | gene | 14713821 | 14755246 | - | Ppp1r3a | Ppp1r3a | P19269 | NM_080464 | TSS9178 |
| chr6 | 15051736 | 15051827 | MACS2_peak_2352 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 9 | chr6 | unknown | gene | 15720660 | 15799865 | + | Mdfic | Mdfic | P14027 | NM_175088 | TSS4576 |
| chr6 | 15067852 | 15068010 | MACS2_peak_2353 | 7 | + | 3.85827 | 4.59669 | 0.75855 | 73 | chr6 | unknown | gene | 14713821 | 14755246 | - | Ppp1r3a | Ppp1r3a | P19269 | NM_080464 | TSS9178 |
| chr6 | 15067852 | 15068010 | MACS2_peak_2353 | 7 | + | 3.85827 | 4.59669 | 0.75855 | 73 | chr6 | unknown | gene | 15720660 | 15799865 | + | Mdfic | Mdfic | P14027 | NM_175088 | TSS4576 |
| chr6 | 15176726 | 15176817 | MACS2_peak_2354 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 39 | chr6 | unknown | gene | 14713821 | 14755246 | - | Ppp1r3a | Ppp1r3a | P19269 | NM_080464 | TSS9178 |
| chr6 | 15176726 | 15176817 | MACS2_peak_2354 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 39 | chr6 | unknown | gene | 15720660 | 15799865 | + | Mdfic | Mdfic | P14027 | NM_175088 | TSS4576 |
| chr6 | 15489492 | 15489583 | MACS2_peak_2355 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 25 | chr6 | unknown | gene | 14901348 | 15438021 | + | Foxp2 | Foxp2 | P21413 | NM_053242 | TSS10171 |
| chr6 | 15489492 | 15489583 | MACS2_peak_2355 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 25 | chr6 | unknown | gene | 15720660 | 15799865 | + | Mdfic | Mdfic | P14027 | NM_175088 | TSS4576 |
| chr6 | 15828071 | 15828174 | MACS2_peak_2356 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 51 | chr6 | unknown | gene | 15720660 | 15799865 | + | Mdfic | Mdfic | P14027 | NM_175088 | TSS4576 |
| chr6 | 15828071 | 15828174 | MACS2_peak_2356 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 51 | chr6 | unknown | gene | 16833380 | 16898441 | - | Tfec | Tfec | P13026 | NM_031198 | TSS3429 |
| chr6 | 16275789 | 16275925 | MACS2_peak_2357 | 26 | + | 5.49828 | 7.51662 | 2.61219 | 72 | chr6 | unknown | gene | 15720660 | 15799865 | + | Mdfic | Mdfic | P14027 | NM_175088 | TSS4576 |
| chr6 | 16275789 | 16275925 | MACS2_peak_2357 | 26 | + | 5.49828 | 7.51662 | 2.61219 | 72 | chr6 | unknown | gene | 16833380 | 16898441 | - | Tfec | Tfec | P13026 | NM_031198 | TSS3429 |
| chr6 | 16278691 | 16278782 | MACS2_peak_2358 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 24 | chr6 | unknown | gene | 15720660 | 15799865 | + | Mdfic | Mdfic | P14027 | NM_175088 | TSS4576 |
| chr6 | 16278691 | 16278782 | MACS2_peak_2358 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 24 | chr6 | unknown | gene | 16833380 | 16898441 | - | Tfec | Tfec | P13026 | NM_031198 | TSS3429 |
| chr6 | 16804283 | 16804397 | MACS2_peak_2359 | 25 | + | 5.46411 | 7.45132 | 2.55202 | 25 | chr6 | unknown | gene | 15720660 | 15799865 | + | Mdfic | Mdfic | P14027 | NM_175088 | TSS4576 |
| chr6 | 16804283 | 16804397 | MACS2_peak_2359 | 25 | + | 5.46411 | 7.45132 | 2.55202 | 25 | chr6 | unknown | gene | 16833380 | 16898441 | - | Tfec | Tfec | P13026 | NM_031198 | TSS3429 |
| chr6 | 17595073 | 17595164 | MACS2_peak_2360 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 3 | chr6 | unknown | gene | 17463956 | 17571823 | + | Met | Met | P18766 | NM_008591 | TSS27139 |
| chr6 | 17595073 | 17595164 | MACS2_peak_2360 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 3 | chr6 | unknown | gene | 17637097 | 17665435 | + | Capza2 | Capza2 | P4182 | NM_007604 | TSS1212 |
| chr6 | 17856655 | 17856746 | MACS2_peak_2361 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 15 | chr6 | unknown | gene | 17637097 | 17665435 | + | Capza2 | Capza2 | P4182 | NM_007604 | TSS1212 |
| chr6 | 17856655 | 17856746 | MACS2_peak_2361 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 15 | chr6 | unknown | gene | 17988939 | 18030287 | - | Wnt2 | Wnt2 | P13497 | NM_023653 | TSS20140 |
| chr6 | 18037126 | 18037217 | MACS2_peak_2362 | 8 | + | 3.92722 | 4.71804 | 0.85326 | 71 | chr6 | unknown | gene | 17988939 | 18030287 | - | Wnt2 | Wnt2 | P13497 | NM_023653 | TSS20140 |
| chr6 | 18037126 | 18037217 | MACS2_peak_2362 | 8 | + | 3.92722 | 4.71804 | 0.85326 | 71 | chr6 | unknown | gene | 18050963 | 18109036 | - | Asz1 | Asz1 | P5710 | NM_023729 | TSS5748 |
| chr6 | 19567025 | 19567122 | MACS2_peak_2363 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 13 | chr6 | unknown | gene | 19555341 | 19555461 | + | Mir6370 | Mir6370 | | NR_105789 | TSS5873 |
| chr6 | 19567025 | 19567122 | MACS2_peak_2363 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 13 | chr6 | unknown | gene | 21216108 | 21727342 | + | Kcnd2 | Kcnd2 | P3633 | NM_019697 | TSS11703 |
| chr6 | 20010048 | 20010139 | MACS2_peak_2364 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 54 | chr6 | unknown | gene | 19555341 | 19555461 | + | Mir6370 | Mir6370 | | NR_105789 | TSS5873 |
| chr6 | 20010048 | 20010139 | MACS2_peak_2364 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 54 | chr6 | unknown | gene | 21216108 | 21727342 | + | Kcnd2 | Kcnd2 | P3633 | NM_019697 | TSS11703 |
| chr6 | 21370630 | 21370733 | MACS2_peak_2365 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 65 | chr6 | unknown | gene | 19555341 | 19555461 | + | Mir6370 | Mir6370 | | NR_105789 | TSS5873 |
| chr6 | 21370630 | 21370733 | MACS2_peak_2365 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 65 | chr6 | unknown | gene | 21771394 | 21852515 | - | Tspan12 | Tspan12 | P17953 | NM_173007 | TSS27261 |
| chr6 | 22039045 | 22039136 | MACS2_peak_2366 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 31 | chr6 | unknown | gene | 21949614 | 21973699 | + | Ing3 | Ing3 | P26591 | NM_023626 | TSS10418 |
| chr6 | 22039045 | 22039136 | MACS2_peak_2366 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 31 | chr6 | unknown | gene | 22288226 | 22298231 | + | Wnt16 | Wnt16 | P18710 | NM_053116 | TSS19328 |
| chr6 | 23045582 | 23045685 | MACS2_peak_2367 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 50 | chr6 | unknown | gene | 22306521 | 22356081 | - | Fam3c | Fam3c | P22253 | NM_138587 | TSS3676 |
| chr6 | 23045582 | 23045685 | MACS2_peak_2367 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 50 | chr6 | unknown | gene | 23072172 | 23132986 | - | Aass | Aass | P10762 | NM_013930 | TSS15968 |
| chr6 | 24114351 | 24114442 | MACS2_peak_2368 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 33 | chr6 | unknown | gene | 23969160 | 23970060 | - | Tas2r118 | Tas2r118 | P15721 | NM_207022 | TSS20781 |
| chr6 | 24114351 | 24114442 | MACS2_peak_2368 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 33 | chr6 | unknown | gene | 24444864 | 24515067 | - | Iqub | Iqub | P17619 | NM_172535 | TSS5553 |
| chr6 | 24751392 | 24751530 | MACS2_peak_2369 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 83 | chr6 | unknown | gene | 24733244 | 24743791 | + | Hyal6 | Hyal6 | P4708 | NM_028920 | TSS16461 |
| chr6 | 24751392 | 24751530 | MACS2_peak_2369 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 83 | chr6 | unknown | gene | 24791187 | 24800802 | + | Spam1 | Spam1 | P3203 | NM_001079875 | TSS1431 |
| chr6 | 28543562 | 28543653 | MACS2_peak_2370 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 46 | chr6 | unknown | gene | 28442333 | 28449340 | - | Pax4 | Pax4 | P22361 | NM_011038 | TSS8958 |
| chr6 | 28543562 | 28543653 | MACS2_peak_2370 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 46 | chr6 | unknown | gene | 28828125 | 28831614 | - | Lrrc4 | Lrrc4 | P25244 | NM_138682 | TSS19768 |
| chr6 | 29592493 | 29592614 | MACS2_peak_2371 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 83 | chr6 | unknown | gene | 29526624 | 29536785 | + | Irf5 | Irf5 | P23868 | NM_012057 | TSS1297 |
| chr6 | 29592493 | 29592614 | MACS2_peak_2371 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 83 | chr6 | unknown | gene | 29694213 | 29717638 | + | Tspan33 | Tspan33 | P15120 | NM_146173 | TSS1884 |
| chr6 | 30380510 | 30380601 | MACS2_peak_2372 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 55 | chr6 | unknown | gene | 30211289 | 30304104 | - | Ube2h | Ube2h | P15311 | NM_001169577 | TSS2205 |
| chr6 | 30380510 | 30380601 | MACS2_peak_2372 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 55 | chr6 | unknown | gene | 30401908 | 30450696 | + | Klhdc10 | Klhdc10 | P7378 | NM_029742 | TSS16523 |
| chr6 | 30514589 | 30514703 | MACS2_peak_2373 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 53 | chr6 | unknown | gene | 30481232 | 30509687 | - | Tmem209 | Tmem209 | P23733 | NM_178625 | TSS25731 |
| chr6 | 30514589 | 30514703 | MACS2_peak_2373 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 53 | chr6 | unknown | gene | 30541641 | 30564425 | + | Cpa2 | Cpa2 | P9182 | NM_001024698 | TSS27073 |
| chr6 | 30820771 | 30820862 | MACS2_peak_2374 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 79 | chr6 | unknown | gene | 30733505 | 30747169 | + | Mest | Mest | P25114 | NM_001252293 | TSS12743 |
| chr6 | 30820771 | 30820862 | MACS2_peak_2374 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 79 | chr6 | unknown | gene | 30896980 | 30915573 | - | Tsga13 | Tsga13 | P9031 | NM_054073 | TSS718 |
| chr6 | 31021666 | 31021757 | MACS2_peak_2375 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 8 | chr6 | unknown | gene | 30956020 | 30958697 | - | Klf14 | Klf14 | P26455 | NM_001135093 | TSS24975 |
| chr6 | 31021666 | 31021757 | MACS2_peak_2375 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 8 | chr6 | unknown | gene | 31062659 | 31062747 | - | Mir29a | Mir29a | | NR_029744 | TSS4224 |
| chr6 | 33224097 | 33224188 | MACS2_peak_2376 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 59 | chr6 | unknown | gene | 32792226 | 33060080 | - | Chchd3 | Chchd3 | P4896 | NM_025336 | TSS4857 |
| chr6 | 33224097 | 33224188 | MACS2_peak_2376 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 59 | chr6 | unknown | gene | 33249149 | 33972151 | + | Exoc4 | Exoc4 | P26454 | NM_009148 | TSS8585 |
| chr6 | 34754825 | 34754916 | MACS2_peak_2377 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 69 | chr6 | unknown | gene | 34476355 | 34504449 | + | Bpgm | Bpgm | P4264 | NM_007563 | TSS8209 |
| chr6 | 34754825 | 34754916 | MACS2_peak_2377 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 69 | chr6 | unknown | gene | 34780431 | 34857903 | + | Agbl3 | Agbl3 | P18147 | NM_001289657 | TSS21149 |
| chr6 | 36417224 | 36417315 | MACS2_peak_2378 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 12 | chr6 | unknown | gene | 36333137 | 36388234 | - | 9330158H04Rik | 9330158H04Rik | | NR_015589 | TSS16569 |
| chr6 | 36417224 | 36417315 | MACS2_peak_2378 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 12 | chr6 | unknown | gene | 36421741 | 36421825 | + | Mir490 | Mir490 | | NR_030524 | TSS2535 |
| chr6 | 36444853 | 36444944 | MACS2_peak_2379 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 67 | chr6 | unknown | gene | 36421741 | 36421825 | + | Mir490 | Mir490 | | NR_030524 | TSS2535 |
| chr6 | 36444853 | 36444944 | MACS2_peak_2379 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 67 | chr6 | unknown | gene | 36715662 | 36811361 | - | Ptn | Ptn | P18375 | NM_008973 | TSS4290 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr6 | 36854805 | 36854896 | MACS2_peak_2380 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 7 | chr6 | unknown | gene | 36715662 | 36811361 | - | Ptn | Ptn | P18375 | NM_008973 | TSS4290 |
| chr6 | 36854805 | 36854896 | MACS2_peak_2380 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 7 | chr6 | unknown | gene | 37331020 | 37441800 | - | Creb3l2 | Creb3l2 | P23711 | NM_178661 | TSS4325 |
| chr6 | 37030624 | 37030855 | MACS2_peak_2381 | 25 | + | 5.46411 | 7.45132 | 2.55202 | 178 | chr6 | unknown | gene | 36715662 | 36811361 | - | Ptn | Ptn | P18375 | NM_008973 | TSS4290 |
| chr6 | 37030624 | 37030855 | MACS2_peak_2381 | 25 | + | 5.46411 | 7.45132 | 2.55202 | 178 | chr6 | unknown | gene | 37331020 | 37441800 | - | Creb3l2 | Creb3l2 | P23711 | NM_178661 | TSS4325 |
| chr6 | 37095209 | 37095317 | MACS2_peak_2382 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 57 | chr6 | unknown | gene | 36715662 | 36811361 | - | Ptn | Ptn | P18375 | NM_008973 | TSS4290 |
| chr6 | 37095209 | 37095317 | MACS2_peak_2382 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 57 | chr6 | unknown | gene | 37331020 | 37441800 | - | Creb3l2 | Creb3l2 | P23711 | NM_178661 | TSS4325 |
| chr6 | 37442655 | 37442746 | MACS2_peak_2383 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 55 | chr6 | unknown | gene | 37331020 | 37441800 | - | Creb3l2 | Creb3l2 | P23711 | NM_178661 | TSS4325 |
| chr6 | 37442655 | 37442746 | MACS2_peak_2383 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 55 | chr6 | unknown | gene | 37530172 | 37567166 | + | Akr1d1 | Akr1d1 | P20696 | NM_145364 | TSS23532 |
| chr6 | 39791469 | 39791560 | MACS2_peak_2384 | 35 | + | 5.98489 | 8.51731 | 3.53253 | 43 | chr6 | unknown | gene | 39603236 | 39725295 | - | Braf | Braf | P21265 | NM_139294 | TSS17853 |
| chr6 | 39791469 | 39791560 | MACS2_peak_2384 | 35 | + | 5.98489 | 8.51731 | 3.53253 | 43 | chr6 | unknown | gene | 39801806 | 39810936 | - | Mrps33 | Mrps33 | P4184 | NM_001010930 | TSS2146 |
| chr6 | 43102229 | 43102320 | MACS2_peak_2385 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 10 | chr6 | unknown | gene | 42955499 | 42956432 | + | Olfr444 | Olfr444 | P26465 | NM_146656 | TSS2873 |
| chr6 | 43102229 | 43102320 | MACS2_peak_2385 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 10 | chr6 | unknown | gene | 43115743 | 43116676 | + | Olfr441 | Olfr441 | P242 | NM_146655 | TSS13693 |
| chr6 | 43343686 | 43343797 | MACS2_peak_2386 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 57 | chr6 | unknown | gene | 43303673 | 43309526 | - | Nobox | Nobox | P26367 | NM_130869 | TSS21317 |
| chr6 | 43343686 | 43343797 | MACS2_peak_2386 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 57 | chr6 | unknown | gene | 43345006 | 43666175 | - | Tpk1 | Tpk1 | P25783 | NM_013861 | TSS26289 |
| chr6 | 43692232 | 43692323 | MACS2_peak_2387 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 52 | chr6 | unknown | gene | 43345006 | 43666175 | - | Tpk1 | Tpk1 | P25783 | NM_013861 | TSS26289 |
| chr6 | 43692232 | 43692323 | MACS2_peak_2387 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 52 | chr6 | unknown | gene | 45060060 | 47298614 | + | Cntnap2 | Cntnap2 | P16224 | NM_001004357 | TSS11679 |
| chr6 | 45777323 | 45777471 | MACS2_peak_2388 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 70 | chr6 | unknown | gene | 43345006 | 43666175 | - | Tpk1 | Tpk1 | P25783 | NM_013861 | TSS26289 |
| chr6 | 45777323 | 45777471 | MACS2_peak_2388 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 70 | chr6 | unknown | gene | 47454323 | 47525634 | + | Cul1 | Cul1 | P8949 | NM_012042 | TSS2174 |
| chr6 | 45864553 | 45864644 | MACS2_peak_2389 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 22 | chr6 | unknown | gene | 43345006 | 43666175 | - | Tpk1 | Tpk1 | P25783 | NM_013861 | TSS26289 |
| chr6 | 45864553 | 45864644 | MACS2_peak_2389 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 22 | chr6 | unknown | gene | 47454323 | 47525634 | + | Cul1 | Cul1 | P8949 | NM_012042 | TSS2174 |
| chr6 | 45920190 | 45920281 | MACS2_peak_2390 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 19 | chr6 | unknown | gene | 43345006 | 43666175 | - | Tpk1 | Tpk1 | P25783 | NM_013861 | TSS26289 |
| chr6 | 45920190 | 45920281 | MACS2_peak_2390 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 19 | chr6 | unknown | gene | 47454323 | 47525634 | + | Cul1 | Cul1 | P8949 | NM_012042 | TSS2174 |
| chr6 | 47357449 | 47357540 | MACS2_peak_2391 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 44 | chr6 | unknown | gene | 45060060 | 47298614 | + | Cntnap2 | Cntnap2 | P16224 | NM_001004357 | TSS11679 |
| chr6 | 47357449 | 47357540 | MACS2_peak_2391 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 44 | chr6 | unknown | gene | 47454323 | 47525634 | + | Cul1 | Cul1 | P8949 | NM_012042 | TSS2174 |
| chr6 | 47485028 | 47485119 | MACS2_peak_2392 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 46 | chr6 | unknown | gene | 45060060 | 47298614 | + | Cntnap2 | Cntnap2 | P16224 | NM_001004357 | TSS11679 |
| chr6 | 47485028 | 47485119 | MACS2_peak_2392 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 46 | chr6 | unknown | gene | 47530273 | 47595030 | - | Ezh2 | Ezh2 | P17121 | NM_001146689 | TSS6297 |
| chr6 | 49418995 | 49419086 | MACS2_peak_2393 | 12 | + | 4.14966 | 5.12722 | 1.204 | 43 | chr6 | unknown | gene | 49367738 | 49388885 | + | Fam221a | Fam221a | P19064 | NM_172727 | TSS2980 |
| chr6 | 49418995 | 49419086 | MACS2_peak_2393 | 12 | + | 4.14966 | 5.12722 | 1.204 | 43 | chr6 | unknown | gene | 49822728 | 49829327 | + | Npy | Npy | P1344 | NM_023456 | TSS521 |
| chr6 | 52361162 | 52361272 | MACS2_peak_2394 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 28 | chr6 | unknown | gene | 52313497 | 52317099 | + | Evx1 | Evx1 | P15415 | NM_007966 | TSS8653 |
| chr6 | 52361162 | 52361272 | MACS2_peak_2394 | 7 | + | 3.47996 | 4.03501 | 0.75855 | 28 | chr6 | unknown | gene | 52492450 | 52500085 | + | 1700094M24Rik | 1700094M24Rik |  | NR_046049 | TSS4369 |
| chr6 | 52518910 | 52519077 | MACS2_peak_2395 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 77 | chr6 | unknown | gene | 52492450 | 52500085 | + | 1700094M24Rik | 1700094M24Rik |  | NR_046049 | TSS4369 |
| chr6 | 52518910 | 52519077 | MACS2_peak_2395 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 77 | chr6 | unknown | gene | 52546229 | 52640248 | - | Hibadh | Hibadh | P10497 | NM_145567 | TSS21428 |
| chr6 | 52765012 | 52765103 | MACS2_peak_2396 | 27 | + | 5.56793 | 7.65146 | 2.73702 | 44 | chr6 | unknown | gene | 52546229 | 52640248 | - | Hibadh | Hibadh | P10497 | NM_145567 | TSS21428 |
| chr6 | 52765012 | 52765103 | MACS2_peak_2396 | 27 | + | 5.56793 | 7.65146 | 2.73702 | 44 | chr6 | unknown | gene | 52768067 | 53068567 | - | Jazf1 | Jazf1 | P17739 | NM_001168277 | TSS929 |
| chr6 | 53154580 | 53154671 | MACS2_peak_2397 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 60 | chr6 | unknown | gene | 52768067 | 53068567 | - | Jazf1 | Jazf1 | P17739 | NM_001168277 | TSS929 |
| chr6 | 53154580 | 53154671 | MACS2_peak_2397 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 60 | chr6 | unknown | gene | 53221163 | 53226599 | + | Gm4872 | Gm4872 |  | NR_073371 | TSS6762 |
| chr6 | 53738729 | 53738820 | MACS2_peak_2398 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 7 | chr6 | unknown | gene | 53573373 | 53694087 | + | Creb5 | Creb5 | P12082 | NM_172728 | TSS7993 |
| chr6 | 53738729 | 53738820 | MACS2_peak_2398 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 7 | chr6 | unknown | gene | 53815467 | 53820235 | - | Tril | Tril | P20581 | NM_025817 | TSS7495 |
| chr6 | 53781775 | 53781891 | MACS2_peak_2399 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 49 | chr6 | unknown | gene | 53573373 | 53694087 | + | Creb5 | Creb5 | P12082 | NM_172728 | TSS7993 |
| chr6 | 53781775 | 53781891 | MACS2_peak_2399 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 49 | chr6 | unknown | gene | 53815467 | 53820235 | - | Tril | Tril | P20581 | NM_025817 | TSS7495 |
| chr6 | 53782759 | 53782850 | MACS2_peak_2400 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 31 | chr6 | unknown | gene | 53573373 | 53694087 | + | Creb5 | Creb5 | P12082 | NM_172728 | TSS7993 |
| chr6 | 53782759 | 53782850 | MACS2_peak_2400 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 31 | chr6 | unknown | gene | 53815467 | 53820235 | - | Tril | Tril | P20581 | NM_025817 | TSS7495 |
| chr6 | 53923622 | 53923713 | MACS2_peak_2401 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 12 | chr6 | unknown | gene | 53815467 | 53820235 | - | Tril | Tril | P20581 | NM_025817 | TSS7495 |
| chr6 | 53923622 | 53923713 | MACS2_peak_2401 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 12 | chr6 | unknown | gene | 53978690 | 54017383 | + | 4921529L05Rik | 4921529L05Rik |  | NR_110484 | TSS22740 |
| chr6 | 54028990 | 54029081 | MACS2_peak_2402 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 57 | chr6 | unknown | gene | 53978690 | 54017383 | + | 4921529L05Rik | 4921529L05Rik |  | NR_110484 | TSS22740 |
| chr6 | 54028990 | 54029081 | MACS2_peak_2402 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 57 | chr6 | unknown | gene | 54039931 | 54300244 | + | Chn2 | Chn2 | P23737 | NM_001163640 | TSS14487 |
| chr6 | 56240149 | 56240276 | MACS2_peak_2403 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 65 | chr6 | unknown | gene | 56017514 | 56031556 | + | Ppp1r17 | Ppp1r17 | P10814 | NM_011153 | TSS20430 |
| chr6 | 56240149 | 56240276 | MACS2_peak_2403 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 65 | chr6 | unknown | gene | 56701062 | 56704668 | - | Lsm5 | Lsm5 | P21243 | NM_025520 | TSS8539 |
| chr6 | 56751311 | 56751402 | MACS2_peak_2404 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 22 | chr6 | unknown | gene | 56701062 | 56704668 | - | Lsm5 | Lsm5 | P21243 | NM_025520 | TSS8539 |
| chr6 | 56751311 | 56751402 | MACS2_peak_2404 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 22 | chr6 | unknown | gene | 56777524 | 56797813 | - | Kbtbd2 | Kbtbd2 | P8114 | NM_145958 | TSS22579 |
| chr6 | 56922727 | 56922818 | MACS2_peak_2405 | 9 | + | 3.97456 | 4.80277 | 0.93007 | 9 | chr6 | unknown | gene | 56832058 | 56878210 | + | Fkbp9 | Fkbp9 | P20040 | NM_012056 | TSS11942 |
| chr6 | 56922727 | 56922818 | MACS2_peak_2405 | 9 | + | 3.97456 | 4.80277 | 0.93007 | 9 | chr6 | unknown | gene | 56956512 | 56957406 | + | Vmn1r4 | Vmn1r4 | P737 | NM_134176 | TSS23507 |
| chr6 | 58655891 | 58655982 | MACS2_peak_2406 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 54 | chr6 | unknown | gene | 58471966 | 58472878 | - | Vmn1r31 | Vmn1r31 | P12902 | NM_001166729 | TSS10344 |
| chr6 | 58655891 | 58655982 | MACS2_peak_2406 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 54 | chr6 | unknown | gene | 58833699 | 58918921 | + | Herc3 | Herc3 | P3497 | NM_028705 | TSS4583 |
| chr6 | 58954884 | 58955003 | MACS2_peak_2407 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 74 | chr6 | unknown | gene | 58833699 | 58918921 | + | Herc3 | Herc3 | P3497 | NM_028705 | TSS4583 |
| chr6 | 58954884 | 58955003 | MACS2_peak_2407 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 74 | chr6 | unknown | gene | 59208869 | 59211727 | + | Tigd2 | Tigd2 | P3567 | NM_001081145 | TSS12847 |
| chr6 | 61147464 | 61147555 | MACS2_peak_2408 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 9 | chr6 | unknown | gene | 60944316 | 60988619 | + | Mmrn1 | Mmrn1 | P13889 | NM_001163507 | TSS10517 |
| chr6 | 61147464 | 61147555 | MACS2_peak_2408 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 9 | chr6 | unknown | gene | 61175603 | 61180810 | - | A730020E08Rik | A730020E08Rik |  | NR_040287 | TSS26261 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr6 | 61696427 | 61696570 | MACS2_peak_2409 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 67 | chr6 | unknown | gene | 61175603 | 61180810 | - | A730020E08Rik | A730020E08Rik | | NR_040287 | TSS26261 |
| chr6 | 61696427 | 61696570 | MACS2_peak_2409 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 67 | chr6 | unknown | gene | 63256856 | 64666279 | + | Grid2 | Grid2 | P25004 | NM_008167 | TSS11224 |
| chr6 | 61997102 | 61997260 | MACS2_peak_2410 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 69 | chr6 | unknown | gene | 61175603 | 61180810 | - | A730020E08Rik | A730020E08Rik | | NR_040287 | TSS26261 |
| chr6 | 61997102 | 61997260 | MACS2_peak_2410 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 69 | chr6 | unknown | gene | 63256856 | 64666279 | + | Grid2 | Grid2 | P25004 | NM_008167 | TSS11224 |
| chr6 | 62054485 | 62054576 | MACS2_peak_2411 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 10 | chr6 | unknown | gene | 61175603 | 61180810 | - | A730020E08Rik | A730020E08Rik | | NR_040287 | TSS26261 |
| chr6 | 62054485 | 62054576 | MACS2_peak_2411 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 10 | chr6 | unknown | gene | 63256856 | 64666279 | + | Grid2 | Grid2 | P25004 | NM_008167 | TSS11224 |
| chr6 | 62066244 | 62066382 | MACS2_peak_2412 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 84 | chr6 | unknown | gene | 61175603 | 61180810 | - | A730020E08Rik | A730020E08Rik | | NR_040287 | TSS26261 |
| chr6 | 62066244 | 62066382 | MACS2_peak_2412 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 84 | chr6 | unknown | gene | 63256856 | 64666279 | + | Grid2 | Grid2 | P25004 | NM_008167 | TSS11224 |
| chr6 | 63316180 | 63316271 | MACS2_peak_2413 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 36 | chr6 | unknown | gene | 61180324 | 62380267 | + | Ccser1 | Ccser1 | P23277 | NM_001164316 | TSS24502 |
| chr6 | 63316180 | 63316271 | MACS2_peak_2413 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 36 | chr6 | unknown | gene | 64729145 | 64730378 | + | Atoh1 | Atoh1 | P2801 | NM_007500 | TSS1592 |
| chr6 | 64002996 | 64003087 | MACS2_peak_2414 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 36 | chr6 | unknown | gene | 61180324 | 62380267 | + | Ccser1 | Ccser1 | P23277 | NM_001164316 | TSS24502 |
| chr6 | 64002996 | 64003087 | MACS2_peak_2414 | 7 | + | 3.69031 | 4.45654 | 0.75855 | 36 | chr6 | unknown | gene | 64729145 | 64730378 | + | Atoh1 | Atoh1 | P2801 | NM_007500 | TSS1592 |
| chr6 | 64251967 | 64252058 | MACS2_peak_2415 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 36 | chr6 | unknown | gene | 61180324 | 62380267 | + | Ccser1 | Ccser1 | P23277 | NM_001164316 | TSS24502 |
| chr6 | 64251967 | 64252058 | MACS2_peak_2415 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 36 | chr6 | unknown | gene | 64729145 | 64730378 | + | Atoh1 | Atoh1 | P2801 | NM_007500 | TSS1592 |
| chr6 | 64746252 | 64746343 | MACS2_peak_2416 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 75 | chr6 | unknown | gene | 64729145 | 64730378 | + | Atoh1 | Atoh1 | P2801 | NM_007500 | TSS1592 |
| chr6 | 64746252 | 64746343 | MACS2_peak_2416 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 75 | chr6 | unknown | gene | 65042666 | 65114362 | + | Smarcad1 | Smarcad1 | P22347 | NM_007958 | TSS1226 |
| chr6 | 65673966 | 65674057 | MACS2_peak_2417 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 44 | chr6 | unknown | gene | 65590397 | 65631108 | + | Tnip3 | Tnip3 | P23705 | NM_001001495 | TSS12195 |
| chr6 | 65673966 | 65674057 | MACS2_peak_2417 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 44 | chr6 | unknown | gene | 65778961 | 65936134 | + | Prdm5 | Prdm5 | P8695 | NM_027547 | TSS18208 |
| chr6 | 65841170 | 65841333 | MACS2_peak_2418 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 76 | chr6 | unknown | gene | 65671610 | 65704445 | + | Ndnf | Ndnf | P21667 | NM_172399 | TSS20794 |
| chr6 | 65841170 | 65841333 | MACS2_peak_2418 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 76 | chr6 | unknown | gene | 65952570 | 65953364 | + | 4930544G11Rik | 4930544G11Rik | P9923 | NM_001161773 | TSS14028 |
| chr6 | 65895570 | 65895661 | MACS2_peak_2419 | 7 | + | 3.39397 | 3.87422 | 0.75855 | 52 | chr6 | unknown | gene | 65671610 | 65704445 | + | Ndnf | Ndnf | P21667 | NM_172399 | TSS20794 |
| chr6 | 65895570 | 65895661 | MACS2_peak_2419 | 7 | + | 3.39397 | 3.87422 | 0.75855 | 52 | chr6 | unknown | gene | 65952570 | 65953364 | + | 4930544G11Rik | 4930544G11Rik | P9923 | NM_001161773 | TSS14028 |
| chr6 | 67284355 | 67284475 | MACS2_peak_2420 | 26 | + | 5.53289 | 7.58332 | 2.67506 | 49 | chr6 | unknown | gene | 67266978 | 67283959 | + | Serbp1 | Serbp1 | P24607 | NM_001113566 | TSS3112 |
| chr6 | 67284355 | 67284475 | MACS2_peak_2420 | 26 | + | 5.53289 | 7.58332 | 2.67506 | 49 | chr6 | unknown | gene | 67292017 | 67376137 | - | Il12rb2 | Il12rb2 | P11557 | NM_008354 | TSS3377 |
| chr6 | 67908065 | 67908221 | MACS2_peak_2421 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 83 | chr6 | unknown | gene | 67565233 | 67565699 | - | 4930515G16Rik | 4930515G16Rik | | NR_003100 | TSS21315 |
| chr6 | 67908065 | 67908221 | MACS2_peak_2421 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 83 | chr6 | unknown | gene | 69326936 | 69327174 | - | Rprl1 | Rprl1 | | NR_004434 | TSS7210 |
| chr6 | 69409942 | 69410033 | MACS2_peak_2422 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 51 | chr6 | unknown | gene | 69326936 | 69327174 | - | Rprl1 | Rprl1 | | NR_004434 | TSS7210 |
| chr6 | 69409942 | 69410033 | MACS2_peak_2422 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 51 | chr6 | unknown | gene | 70765719 | 70792149 | - | Rpia | Rpia | P14704 | NM_009075 | TSS25762 |
| chr6 | 71635156 | 71635247 | MACS2_peak_2423 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 13 | chr6 | unknown | gene | 71588969 | 71632917 | - | Kdm3a | Kdm3a | P14914 | NM_001038695 | TSS18028 |
| chr6 | 71635156 | 71635247 | MACS2_peak_2423 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 13 | chr6 | unknown | gene | 71707680 | 71807801 | + | Reep1 | Reep1 | P276 | NM_178608 | TSS13246 |
| chr6 | 72438564 | 72438704 | MACS2_peak_2424 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 116 | chr6 | unknown | gene | 72414307 | 72430156 | + | Ggcx | Ggcx | P24461 | NM_019802 | TSS13441 |
| chr6 | 72438564 | 72438704 | MACS2_peak_2424 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 116 | chr6 | unknown | gene | 72544390 | 72562875 | + | Capg | Capg | P2787 | NM_007599 | TSS5053 |
| chr6 | 75552833 | 75552924 | MACS2_peak_2425 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 36 | chr6 | unknown | gene | 73436964 | 73471021 | - | 1700065L07Rik | 1700065L07Rik | | NR_108032 | TSS24243 |
| chr6 | 75552833 | 75552924 | MACS2_peak_2425 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 36 | chr6 | unknown | gene | 76881636 | 77979667 | - | Ctnna2 | Ctnna2 | P12318 | NM_009819 | TSS13308 |
| chr6 | 76250548 | 76250639 | MACS2_peak_2426 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 22 | chr6 | unknown | gene | 73436964 | 73471021 | - | 1700065L07Rik | 1700065L07Rik | | NR_108032 | TSS24243 |
| chr6 | 76250548 | 76250639 | MACS2_peak_2426 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 22 | chr6 | unknown | gene | 76881636 | 77979667 | - | Ctnna2 | Ctnna2 | P12318 | NM_009819 | TSS13308 |
| chr6 | 79923882 | 79924026 | MACS2_peak_2427 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 60 | chr6 | unknown | gene | 79818030 | 79818364 | + | Gm20594 | Gm20594 | P17058 | NM_001190732 | TSS13292 |
| chr6 | 79923882 | 79924026 | MACS2_peak_2427 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 60 | chr6 | unknown | gene | 80018876 | 80809189 | + | Lrrtm4 | Lrrtm4 | P147 | NM_001134743 | TSS27203 |
| chr6 | 80238929 | 80239020 | MACS2_peak_2428 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 24 | chr6 | unknown | gene | 79818030 | 79818364 | + | Gm20594 | Gm20594 | P17058 | NM_001190732 | TSS13292 |
| chr6 | 80238929 | 80239020 | MACS2_peak_2428 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 24 | chr6 | unknown | gene | 81895589 | 81895663 | - | Mir7232 | Mir7232 | | NR_106091 | TSS17875 |
| chr6 | 80599846 | 80599988 | MACS2_peak_2429 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 64 | chr6 | unknown | gene | 79818030 | 79818364 | + | Gm20594 | Gm20594 | P17058 | NM_001190732 | TSS13292 |
| chr6 | 80599846 | 80599988 | MACS2_peak_2429 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 64 | chr6 | unknown | gene | 81895589 | 81895663 | - | Mir7232 | Mir7232 | | NR_106091 | TSS17875 |
| chr6 | 80842808 | 80842899 | MACS2_peak_2430 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 17 | chr6 | unknown | gene | 80018876 | 80809189 | + | Lrrtm4 | Lrrtm4 | P147 | NM_001134743 | TSS27203 |
| chr6 | 80842808 | 80842899 | MACS2_peak_2430 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 17 | chr6 | unknown | gene | 81895589 | 81895663 | - | Mir7232 | Mir7232 | | NR_106091 | TSS17875 |
| chr6 | 81113027 | 81113118 | MACS2_peak_2431 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 50 | chr6 | unknown | gene | 80018876 | 80809189 | + | Lrrtm4 | Lrrtm4 | P147 | NM_001134743 | TSS27203 |
| chr6 | 81113027 | 81113118 | MACS2_peak_2431 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 50 | chr6 | unknown | gene | 81895589 | 81895663 | - | Mir7232 | Mir7232 | | NR_106091 | TSS17875 |
| chr6 | 82268994 | 82269150 | MACS2_peak_2432 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 55 | chr6 | unknown | gene | 82041627 | 82092164 | + | Eva1a | Eva1a | P6120 | NM_145570 | TSS14898 |
| chr6 | 82268994 | 82269150 | MACS2_peak_2432 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 55 | chr6 | unknown | gene | 82402474 | 82557218 | + | Tacr1 | Tacr1 | P1863 | NM_009313 | TSS9559 |
| chr6 | 83121486 | 83121577 | MACS2_peak_2433 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 50 | chr6 | unknown | gene | 83119043 | 83121271 | - | Wbp1 | Wbp1 | P15264 | NM_016757 | TSS10000 |
| chr6 | 83121486 | 83121577 | MACS2_peak_2433 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 50 | chr6 | unknown | gene | 83121827 | 83125029 | - | Ino80b | Ino80b | P6566 | NM_023547 | TSS896 |
| chr6 | 83572318 | 83572409 | MACS2_peak_2434 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 14 | chr6 | unknown | gene | 83512908 | 83536251 | - | Actg2 | Actg2 | P26019 | NM_009610 | TSS23154 |
| chr6 | 83572318 | 83572409 | MACS2_peak_2434 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 14 | chr6 | unknown | gene | 83644541 | 83656032 | - | Clec4f | Clec4f | P8057 | NM_016751 | TSS11396 |
| chr6 | 83911298 | 83911389 | MACS2_peak_2435 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 18 | chr6 | unknown | gene | 83806058 | 83831741 | - | Paip2b | Paip2b | P7532 | NM_146169 | TSS17776 |
| chr6 | 83911298 | 83911389 | MACS2_peak_2435 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 18 | chr6 | unknown | gene | 83914352 | 83986623 | + | Zfp638 | Zfp638 | P14234 | NM_001166371 | TSS20568 |
| chr6 | 85024461 | 85024552 | MACS2_peak_2436 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 35 | chr6 | unknown | gene | 84571413 | 84593908 | - | Cyp26b1 | Cyp26b1 | P11035 | NM_175475 | TSS8908 |
| chr6 | 85024461 | 85024552 | MACS2_peak_2436 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 35 | chr6 | unknown | gene | 85076140 | 85077126 | + | Npm3-ps1 | Npm3-ps1 | | NR_002702 | TSS17132 |
| chr6 | 85557967 | 85558058 | MACS2_peak_2437 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 37 | chr6 | unknown | gene | 85511121 | 85513397 | - | Egr4 | Egr4 | P18358 | NM_020596 | TSS9417 |
| chr6 | 85557967 | 85558058 | MACS2_peak_2437 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 37 | chr6 | unknown | gene | 85587530 | 85702638 | + | Alms1 | Alms1 | P25228 | NM_145223 | TSS21494 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr6 | 91374961 | 91375052 | MACS2_peak_2438 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 20 | chr6 | unknown | gene | 91212763 | 91271879 | + | Fbln2 | Fbln2 | P12455 | NM_001081437 | TSS14752 |
| chr6 | 91374961 | 91375052 | MACS2_peak_2438 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 20 | chr6 | unknown | gene | 91430459 | 91440854 | - | 4930471M09Rik | 4930471M09Rik | | NR_045980 | TSS14774 |
| chr6 | 91980672 | 91980771 | MACS2_peak_2439 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 19 | chr6 | unknown | gene | 91904232 | 91950640 | + | 4930590J08Rik | 4930590J08Rik | P12970 | NM_198668 | TSS13963 |
| chr6 | 91980672 | 91980771 | MACS2_peak_2439 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 19 | chr6 | unknown | gene | 91987109 | 92074606 | + | Fgd5 | Fgd5 | P968 | NM_172731 | TSS21220 |
| chr6 | 93290525 | 93290616 | MACS2_peak_2440 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 7 | chr6 | unknown | gene | 92940581 | 93111749 | + | 9530026P05Rik | 9530026P05Rik | | NR_015530 | TSS27081 |
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| chr6 | 93816735 | 93816826 | MACS2_peak_2441 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 57 | chr6 | unknown | gene | 92940581 | 93111749 | + | 9530026P05Rik | 9530026P05Rik | | NR_015530 | TSS27081 |
| chr6 | 93816735 | 93816826 | MACS2_peak_2441 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 57 | chr6 | unknown | gene | 94132922 | 94237442 | - | 4930511A08Rik | 4930511A08Rik | | NR_130996 | TSS6953 |
| chr6 | 93896401 | 93896492 | MACS2_peak_2442 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 63 | chr6 | unknown | gene | 92940581 | 93111749 | + | 9530026P05Rik | 9530026P05Rik | | NR_015530 | TSS27081 |
| chr6 | 93896401 | 93896492 | MACS2_peak_2442 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 63 | chr6 | unknown | gene | 94132922 | 94237442 | - | 4930511A08Rik | 4930511A08Rik | | NR_130996 | TSS6953 |
| chr6 | 95383034 | 95383125 | MACS2_peak_2443 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 35 | chr6 | unknown | gene | 95290573 | 95333993 | - | AY512915 | AY512915 | | NR_033559 | TSS16183 |
| chr6 | 95383034 | 95383125 | MACS2_peak_2443 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 35 | chr6 | unknown | gene | 95473008 | 95718775 | - | Suclg2 | Suclg2 | P23710 | NM_011507 | TSS2789 |
| chr6 | 98580441 | 98580532 | MACS2_peak_2444 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 39 | chr6 | unknown | gene | 98238013 | 98342754 | - | Gm765 | Gm765 | P5802 | NM_001128092 | TSS26462 |
| chr6 | 98580441 | 98580532 | MACS2_peak_2444 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 39 | chr6 | unknown | gene | 98925341 | 99435345 | - | Foxp1 | Foxp1 | P22100 | NM_053202 | TSS15797 |
| chr6 | 99040007 | 99040127 | MACS2_peak_2445 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 35 | chr6 | unknown | gene | 98238013 | 98342754 | - | Gm765 | Gm765 | P5802 | NM_001128092 | TSS26462 |
| chr6 | 99040007 | 99040127 | MACS2_peak_2445 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 35 | chr6 | unknown | gene | 99625136 | 99666752 | - | Eif4e3 | Eif4e3 | P22024 | NM_025829 | TSS3081 |
| chr6 | 99064155 | 99064346 | MACS2_peak_2446 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 57 | chr6 | unknown | gene | 98238013 | 98342754 | - | Gm765 | Gm765 | P5802 | NM_001128092 | TSS26462 |
| chr6 | 99064155 | 99064346 | MACS2_peak_2446 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 57 | chr6 | unknown | gene | 99625136 | 99666752 | - | Eif4e3 | Eif4e3 | P22024 | NM_025829 | TSS3081 |
| chr6 | 100511364 | 100511455 | MACS2_peak_2447 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 3 | chr6 | unknown | gene | 100228564 | 100287277 | - | Rybp | Rybp | P2183 | NM_019743 | TSS7376 |
| chr6 | 100511364 | 100511455 | MACS2_peak_2447 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 3 | chr6 | unknown | gene | 100527399 | 100533426 | + | 1700049E22Rik | 1700049E22Rik | | NR_040525 | TSS13006 |
| chr6 | 101778274 | 101778365 | MACS2_peak_2448 | 15 | + | 4.70395 | 6.11067 | 1.54175 | 57 | chr6 | unknown | gene | 101149606 | 101377888 | - | Pdzrn3 | Pdzrn3 | P14864 | NM_018884 | TSS430 |
| chr6 | 101778274 | 101778365 | MACS2_peak_2448 | 15 | + | 4.70395 | 6.11067 | 1.54175 | 57 | chr6 | unknown | gene | 102163305 | 102464583 | - | Cntn3 | Cntn3 | P2719 | NM_008779 | TSS6327 |
| chr6 | 102026482 | 102026573 | MACS2_peak_2449 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 43 | chr6 | unknown | gene | 101774248 | 101801982 | + | Gm9871 | Gm9871 | | NR_027989 | TSS22466 |
| chr6 | 102026482 | 102026573 | MACS2_peak_2449 | 27 | + | 5.60342 | 7.72112 | 2.79954 | 43 | chr6 | unknown | gene | 102163305 | 102464583 | - | Cntn3 | Cntn3 | P2719 | NM_008779 | TSS6327 |
| chr6 | 103649019 | 103649332 | MACS2_peak_2450 | 2177 | + | 43.96769 | 225.5578 | 217.71306 | 185 | chr6 | unknown | gene | 102794383 | 102794485 | + | Mir6373 | Mir6373 | | NR_105792 | TSS8192 |
| chr6 | 103649019 | 103649332 | MACS2_peak_2450 | 2177 | + | 43.96769 | 225.5578 | 217.71306 | 185 | chr6 | unknown | gene | 104493043 | 104863227 | + | Cntn6 | Cntn6 | P641 | NM_017383 | TSS22266 |
| chr6 | 105182444 | 105182539 | MACS2_peak_2451 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 24 | chr6 | unknown | gene | 104493043 | 104863227 | + | Cntn6 | Cntn6 | P641 | NM_017383 | TSS22266 |
| chr6 | 105182444 | 105182539 | MACS2_peak_2451 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 24 | chr6 | unknown | gene | 105481265 | 105492668 | - | Gm19757 | Gm19757 | | NR_040297 | TSS6348 |
| chr6 | 105858300 | 105858454 | MACS2_peak_2452 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 75 | chr6 | unknown | gene | 105481265 | 105492668 | - | Gm19757 | Gm19757 | | NR_040297 | TSS6348 |
| chr6 | 105858300 | 105858454 | MACS2_peak_2452 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 75 | chr6 | unknown | gene | 106710378 | 106749037 | - | Il5ra | Il5ra | P19015 | NM_008370 | TSS5735 |
| chr6 | 108548440 | 108548531 | MACS2_peak_2453 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 52 | chr6 | unknown | gene | 108489742 | 108489803 | + | Mir7661 | Mir7661 | | NR_106121 | TSS16511 |
| chr6 | 108548440 | 108548531 | MACS2_peak_2453 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 52 | chr6 | unknown | gene | 108577035 | 108660934 | - | 0610040F04Rik | 0610040F04Rik | | NR_104577 | TSS21164 |
| chr6 | 109264864 | 109264955 | MACS2_peak_2454 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 65 | chr6 | unknown | gene | 108828640 | 108855556 | + | Edem1 | Edem1 | P2437 | NM_138677 | TSS12466 |
| chr6 | 109264864 | 109264955 | MACS2_peak_2454 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 65 | chr6 | unknown | gene | 110645597 | 111566067 | + | Grm7 | Grm7 | P26891 | NM_177328 | TSS14737 |
| chr6 | 109754079 | 109754207 | MACS2_peak_2455 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 87 | chr6 | unknown | gene | 108828640 | 108855556 | + | Edem1 | Edem1 | P2437 | NM_138677 | TSS12466 |
| chr6 | 109754079 | 109754207 | MACS2_peak_2455 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 87 | chr6 | unknown | gene | 110645597 | 111566067 | + | Grm7 | Grm7 | P26891 | NM_177328 | TSS14737 |
| chr6 | 110046441 | 110046599 | MACS2_peak_2456 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 30 | chr6 | unknown | gene | 108828640 | 108855556 | + | Edem1 | Edem1 | P2437 | NM_138677 | TSS12466 |
| chr6 | 110046441 | 110046599 | MACS2_peak_2456 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 30 | chr6 | unknown | gene | 110645597 | 111566067 | + | Grm7 | Grm7 | P26891 | NM_177328 | TSS14737 |
| chr6 | 110994295 | 110994390 | MACS2_peak_2457 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 22 | chr6 | unknown | gene | 108828640 | 108855556 | + | Edem1 | Edem1 | P2437 | NM_138677 | TSS12466 |
| chr6 | 110994295 | 110994390 | MACS2_peak_2457 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 22 | chr6 | unknown | gene | 112210707 | 112212518 | + | 1700054K19Rik | 1700054K19Rik | | NR_027865 | TSS27674 |
| chr6 | 114565401 | 114565552 | MACS2_peak_2458 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 76 | chr6 | unknown | gene | 114397935 | 114481226 | + | Hrh1 | Hrh1 | P717 | NM_008285 | TSS26646 |
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| chr6 | 114782440 | 114782531 | MACS2_peak_2459 | 12 | + | 4.14966 | 5.12722 | 1.204 | 13 | chr6 | unknown | gene | 114397935 | 114481226 | + | Hrh1 | Hrh1 | P717 | NM_008285 | TSS26646 |
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| chr6 | 117040586 | 117040677 | MACS2_peak_2460 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 22 | chr6 | unknown | gene | 116692724 | 116716577 | - | Tmem72 | Tmem72 | P12170 | NM_178768 | TSS6673 |
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| chr6 | 119598896 | 119598987 | MACS2_peak_2461 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 31 | chr6 | unknown | gene | 119432530 | 119544347 | - | Wnt5b | Wnt5b | P25942 | NM_009525 | TSS13478 |
| chr6 | 119598896 | 119598987 | MACS2_peak_2461 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 31 | chr6 | unknown | gene | 119848192 | 119849016 | + | 3110021A11Rik | 3110021A11Rik | | NR_030776 | TSS264 |
| chr6 | 120111501 | 120111637 | MACS2_peak_2462 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 78 | chr6 | unknown | gene | 119923968 | 120037632 | - | Wnk1 | Wnk1 | P9425 | NM_001199084 | TSS24953 |
| chr6 | 120111501 | 120111637 | MACS2_peak_2462 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 78 | chr6 | unknown | gene | 120203809 | 120294559 | - | B4galnt3 | B4galnt3 | P13068 | NM_198884 | TSS8388 |
| chr6 | 120872535 | 120872626 | MACS2_peak_2463 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 74 | chr6 | unknown | gene | 120795243 | 120822620 | - | Atp6v1e1 | Atp6v1e1 | P3992 | NM_007510 | TSS25594 |
| chr6 | 120872535 | 120872626 | MACS2_peak_2463 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 74 | chr6 | unknown | gene | 120893118 | 120916820 | - | Bid | Bid | P22351 | NM_007544 | TSS13880 |
| chr6 | 122448612 | 122448703 | MACS2_peak_2464 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 57 | chr6 | unknown | gene | 122317730 | 122340227 | - | Phc1 | Phc1 | P15292 | NM_007905 | TSS17918 |
| chr6 | 122448612 | 122448703 | MACS2_peak_2464 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 57 | chr6 | unknown | gene | 122453608 | 122486305 | - | Rimklb | Rimklb | P5748 | NM_027664 | TSS8793 |
| chr6 | 126947556 | 126947647 | MACS2_peak_2465 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 65 | chr6 | unknown | gene | 126923418 | 126939510 | - | Rad51ap1 | Rad51ap1 | P17444 | NM_009013 | TSS20229 |
| chr6 | 126947556 | 126947647 | MACS2_peak_2465 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 65 | chr6 | unknown | gene | 127015541 | 127024157 | + | Fgf6 | Fgf6 | P23315 | NM_010204 | TSS6246 |
| chr6 | 127158203 | 127158317 | MACS2_peak_2466 | 40 | + | 6.30384 | 9.04635 | 4.00347 | 57 | chr6 | unknown | gene | 127125708 | 127150773 | - | Ccnd2 | Ccnd2 | P17319 | NM_009829 | TSS11085 |
| chr6 | 127158203 | 127158317 | MACS2_peak_2466 | 40 | + | 6.30384 | 9.04635 | 4.00347 | 57 | chr6 | unknown | gene | 127296185 | 127307967 | - | Gm38404 | Gm38404 | | NR_073373 | TSS11314 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr6 | 127349778 | 127349900 | MACS2_peak_2467 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 83 | chr6 | unknown | gene | 127296185 | 127307967 | - | Gm38404 | Gm38404 |  | NR_073373 | TSS11314 |
| chr6 | 127349778 | 127349900 | MACS2_peak_2467 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 83 | chr6 | unknown | gene | 127453722 | 127491735 | + | Parp11 | Parp11 | P1929 | NM_181402 | TSS26145 |
| chr6 | 128897769 | 128897860 | MACS2_peak_2468 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 67 | chr6 | unknown | gene | 128887586 | 128896550 | + | Clec2i | Clec2i | P19511 | NM_001289707 | TSS6203 |
| chr6 | 128897769 | 128897860 | MACS2_peak_2468 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 67 | chr6 | unknown | gene | 128931792 | 128974895 | - | Mir7649 | Mir7649 |  | NR_106107 | TSS13247 |
| chr6 | 130692402 | 130692493 | MACS2_peak_2469 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 18 | chr6 | unknown | gene | 130363917 | 130386874 | - | Klra1 | Klra1 | P26461 | NM_016659 | TSS236 |
| chr6 | 130692402 | 130692493 | MACS2_peak_2469 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 18 | chr6 | unknown | gene | 131219234 | 131247362 | - | Klra2 | Klra2 | P1134 | NM_001170851 | TSS9373 |
| chr6 | 130830931 | 130831022 | MACS2_peak_2470 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 43 | chr6 | unknown | gene | 130363917 | 130386874 | - | Klra1 | Klra1 | P26461 | NM_016659 | TSS236 |
| chr6 | 130830931 | 130831022 | MACS2_peak_2470 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 43 | chr6 | unknown | gene | 131219234 | 131247362 | - | Klra2 | Klra2 | P1134 | NM_001170851 | TSS9373 |
| chr6 | 131377493 | 131377632 | MACS2_peak_2471 | 63 | + | 7.52781 | 11.52513 | 6.36816 | 69 | chr6 | unknown | gene | 131299143 | 131312982 | - | Styk1 | Styk1 | P4064 | NM_172891 | TSS8514 |
| chr6 | 131377493 | 131377632 | MACS2_peak_2471 | 63 | + | 7.52781 | 11.52513 | 6.36816 | 69 | chr6 | unknown | gene | 131543761 | 131553705 | + | 5430401F13Rik | 5430401F13Rik | P17620 | NM_001244628 | TSS19261 |
| chr6 | 134912268 | 134912414 | MACS2_peak_2472 | 46 | + | 3.91441 | 4.69531 | 1.17619 | 43 | chr6 | unknown | gene | 134897960 | 134900785 | + | 2810454H06Rik | 2810454H06Rik |  | NR_029441 | TSS9260 |
| chr6 | 134912268 | 134912414 | MACS2_peak_2472 | 46 | + | 3.91441 | 4.69531 | 1.17619 | 43 | chr6 | unknown | gene | 134920400 | 134925525 | + | Cdkn1b | Cdkn1b | P11926 | NM_009875 | TSS2008 |
| chr6 | 134941163 | 134941307 | MACS2_peak_2473 | 36 | + | 3.29017 | 3.68739 | 0.76206 | 95 | chr6 | unknown | gene | 134920400 | 134925525 | + | Cdkn1b | Cdkn1b | P11926 | NM_009875 | TSS2008 |
| chr6 | 134941163 | 134941307 | MACS2_peak_2473 | 36 | + | 3.29017 | 3.68739 | 0.76206 | 95 | chr6 | unknown | gene | 134982000 | 134984325 | + | Apold1 | Apold1 | P7612 | NM_001109914 | TSS8886 |
| chr6 | 135385533 | 135385624 | MACS2_peak_2474 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 27 | chr6 | unknown | gene | 135362930 | 135381140 | + | Emp1 | Emp1 | P11192 | NM_010128 | TSS17064 |
| chr6 | 135385533 | 135385624 | MACS2_peak_2474 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 27 | chr6 | unknown | gene | 135658912 | 135683391 | + | 4930425L21Rik | 4930425L21Rik |  | NR_126088 | TSS4018 |
| chr6 | 135575869 | 135576020 | MACS2_peak_2475 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 90 | chr6 | unknown | gene | 135362930 | 135381140 | + | Emp1 | Emp1 | P11192 | NM_010128 | TSS17064 |
| chr6 | 135575869 | 135576020 | MACS2_peak_2475 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 90 | chr6 | unknown | gene | 135658912 | 135683391 | + | 4930425L21Rik | 4930425L21Rik |  | NR_126088 | TSS4018 |
| chr6 | 136827007 | 136827106 | MACS2_peak_2476 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 16 | chr6 | unknown | gene | 136808247 | 136808729 | + | H2afj | H2afj | P19087 | NM_177688 | TSS21702 |
| chr6 | 136827007 | 136827106 | MACS2_peak_2476 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 16 | chr6 | unknown | gene | 136828842 | 136840507 | + | BC049715 | BC049715 | P1085 | NM_178776 | TSS5143 |
| chr6 | 136856635 | 136856726 | MACS2_peak_2477 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 72 | chr6 | unknown | gene | 136828842 | 136840507 | + | BC049715 | BC049715 | P1085 | NM_178776 | TSS5143 |
| chr6 | 136856635 | 136856726 | MACS2_peak_2477 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 72 | chr6 | unknown | gene | 136872434 | 136875730 | - | Mgp | Mgp | P11077 | NM_008597 | TSS5769 |
| chr6 | 138283078 | 138283169 | MACS2_peak_2478 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 66 | chr6 | unknown | gene | 138140536 | 138156378 | + | Mgst1 | Mgst1 | P20692 | NM_019946 | TSS7313 |
| chr6 | 138283078 | 138283169 | MACS2_peak_2478 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 66 | chr6 | unknown | gene | 138364480 | 138581968 | - | Lmo3 | Lmo3 | P18849 | NM_207222 | TSS24486 |
| chr6 | 138833562 | 138833653 | MACS2_peak_2479 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 47 | chr6 | unknown | gene | 138657091 | 138658444 | - | Igbp1b | Igbp1b | P24524 | NM_015777 | TSS46 |
| chr6 | 138833562 | 138833653 | MACS2_peak_2479 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 47 | chr6 | unknown | gene | 139315596 | 139322576 | - | 4922502N22Rik | 4922502N22Rik |  | NR_045149 | TSS6718 |
| chr6 | 139178033 | 139178124 | MACS2_peak_2480 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 37 | chr6 | unknown | gene | 138657091 | 138658444 | - | Igbp1b | Igbp1b | P24524 | NM_015777 | TSS46 |
| chr6 | 139178033 | 139178124 | MACS2_peak_2480 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 37 | chr6 | unknown | gene | 139315596 | 139322576 | - | 4922502N22Rik | 4922502N22Rik |  | NR_045149 | TSS6718 |
| chr6 | 139475795 | 139475886 | MACS2_peak_2481 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 27 | chr6 | unknown | gene | 139315596 | 139322576 | - | 4922502N22Rik | 4922502N22Rik |  | NR_045149 | TSS6718 |
| chr6 | 139475795 | 139475886 | MACS2_peak_2481 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 27 | chr6 | unknown | gene | 139493181 | 139501874 | - | Rergl | Rergl | P4340 | NM_001128090 | TSS19481 |
| chr6 | 139738805 | 139738896 | MACS2_peak_2482 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 14 | chr6 | unknown | gene | 139493181 | 139501874 | - | Rergl | Rergl | P4340 | NM_001128090 | TSS19481 |
| chr6 | 139738805 | 139738896 | MACS2_peak_2482 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 14 | chr6 | unknown | gene | 139989721 | 140041417 | - | Plcz1 | Plcz1 | P15779 | NM_054066 | TSS12928 |
| chr6 | 139895759 | 139895917 | MACS2_peak_2483 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 81 | chr6 | unknown | gene | 139493181 | 139501874 | - | Rergl | Rergl | P4340 | NM_001128090 | TSS19481 |
| chr6 | 139895759 | 139895917 | MACS2_peak_2483 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 81 | chr6 | unknown | gene | 139989721 | 140041417 | - | Plcz1 | Plcz1 | P15779 | NM_054066 | TSS12928 |
| chr6 | 139908941 | 139909081 | MACS2_peak_2484 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 56 | chr6 | unknown | gene | 139493181 | 139501874 | - | Rergl | Rergl | P4340 | NM_001128090 | TSS19481 |
| chr6 | 139908941 | 139909081 | MACS2_peak_2484 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 56 | chr6 | unknown | gene | 139989721 | 140041417 | - | Plcz1 | Plcz1 | P15779 | NM_054066 | TSS12928 |
| chr6 | 141042106 | 141042270 | MACS2_peak_2485 | 16 | + | 4.811 | 6.2687 | 1.67914 | 79 | chr6 | unknown | gene | 140622662 | 140677418 | + | Aebp2 | Aebp2 | P17923 | NM_178803 | TSS11551 |
| chr6 | 141042106 | 141042270 | MACS2_peak_2485 | 16 | + | 4.811 | 6.2687 | 1.67914 | 79 | chr6 | unknown | gene | 141249268 | 141498893 | + | Pde3a | Pde3a | P570 | NM_018779 | TSS23603 |
| chr6 | 141064383 | 141064524 | MACS2_peak_2486 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 57 | chr6 | unknown | gene | 140622662 | 140677418 | + | Aebp2 | Aebp2 | P17923 | NM_178803 | TSS11551 |
| chr6 | 141064383 | 141064524 | MACS2_peak_2486 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 57 | chr6 | unknown | gene | 141249268 | 141498893 | + | Pde3a | Pde3a | P570 | NM_018779 | TSS23603 |
| chr6 | 141184836 | 141184972 | MACS2_peak_2487 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 64 | chr6 | unknown | gene | 140622662 | 140677418 | + | Aebp2 | Aebp2 | P17923 | NM_178803 | TSS11551 |
| chr6 | 141184836 | 141184972 | MACS2_peak_2487 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 64 | chr6 | unknown | gene | 141249268 | 141498893 | + | Pde3a | Pde3a | P570 | NM_018779 | TSS23603 |
| chr6 | 141341562 | 141341653 | MACS2_peak_2488 | 23 | + | 5.36409 | 7.26321 | 2.37531 | 41 | chr6 | unknown | gene | 140622662 | 140677418 | + | Aebp2 | Aebp2 | P17923 | NM_178803 | TSS11551 |
| chr6 | 141341562 | 141341653 | MACS2_peak_2488 | 23 | + | 5.36409 | 7.26321 | 2.37531 | 41 | chr6 | unknown | gene | 141524385 | 141569528 | + | Slco1c1 | Slco1c1 | P1748 | NM_001177772 | TSS17871 |
| chr6 | 142807952 | 142808053 | MACS2_peak_2489 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 18 | chr6 | unknown | gene | 142785780 | 142804390 | - | Gm766 | Gm766 | P25927 | NM_001145390 | TSS17285 |
| chr6 | 142807952 | 142808053 | MACS2_peak_2489 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 18 | chr6 | unknown | gene | 142814230 | 142833494 | + | Gm7457 | Gm7457 |  | NR_045707 | TSS5877 |
| chr6 | 143570755 | 143570900 | MACS2_peak_2490 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 56 | chr6 | unknown | gene | 143245887 | 143297879 | + | D6Ertd474e | D6Ertd474e |  | NR_027803 | TSS1850 |
| chr6 | 143570755 | 143570900 | MACS2_peak_2490 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 56 | chr6 | unknown | gene | 143593352 | 143651288 | - | 1700060C16Rik | 1700060C16Rik |  | NR_045732 | TSS7746 |
| chr6 | 143848224 | 143848315 | MACS2_peak_2491 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 26 | chr6 | unknown | gene | 143593352 | 143651288 | - | 1700060C16Rik | 1700060C16Rik |  | NR_045732 | TSS7746 |
| chr6 | 143848224 | 143848315 | MACS2_peak_2491 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 26 | chr6 | unknown | gene | 144672867 | 144693832 | + | Sox5os3 | Sox5os3 |  | NR_040519 | TSS6684 |
| chr6 | 143851631 | 143851722 | MACS2_peak_2492 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 37 | chr6 | unknown | gene | 143593352 | 143651288 | - | 1700060C16Rik | 1700060C16Rik |  | NR_045732 | TSS7746 |
| chr6 | 143851631 | 143851722 | MACS2_peak_2492 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 37 | chr6 | unknown | gene | 144672867 | 144693832 | + | Sox5os3 | Sox5os3 |  | NR_040519 | TSS6684 |
| chr6 | 144674520 | 144674620 | MACS2_peak_2493 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 55 | chr6 | unknown | gene | 143828424 | 144209368 | - | Sox5 | Sox5 | P3263 | NM_001243163 | TSS1623 |
| chr6 | 144674520 | 144674620 | MACS2_peak_2493 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 55 | chr6 | unknown | gene | 144993834 | 145075894 | - | Bcat1 | Bcat1 | P15824 | NM_007532 | TSS25956 |
| chr6 | 146719884 | 146719975 | MACS2_peak_2494 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 38 | chr6 | unknown | gene | 146657217 | 146665403 | + | 4930479D17Rik | 4930479D17Rik |  | NR_046277 | TSS23519 |
| chr6 | 146719884 | 146719975 | MACS2_peak_2494 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 38 | chr6 | unknown | gene | 146724929 | 146775721 | + | Stk38l | Stk38l | P7215 | NM_172734 | TSS16369 |
| chr6 | 146912715 | 146912806 | MACS2_peak_2495 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 15 | chr6 | unknown | gene | 146850109 | 146871345 | + | Smco2 | Smco2 | P6941 | NM_027059 | TSS4855 |
| chr6 | 146912715 | 146912806 | MACS2_peak_2495 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 15 | chr6 | unknown | gene | 146951300 | 146954421 | - | 1700034J05Rik | 1700034J05Rik | P26495 | NM_001164236 | TSS14792 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr6 | 148349608 | 148349699 | MACS2_peak_2496 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 33 | chr6 | unknown | gene | 148212287 | 148235663 | + | 4732416N19Rik | 4732416N19Rik | | NR_015615 | TSS5295 |
| chr6 | 148349608 | 148349699 | MACS2_peak_2496 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 33 | chr6 | unknown | gene | 148354655 | 148355596 | + | Rps4l | Rps4l | | NR_003634 | TSS25965 |
| chr6 | 148820259 | 148820350 | MACS2_peak_2497 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 57 | chr6 | unknown | gene | 148659977 | 148678000 | - | 4930528G23Rik | 4930528G23Rik | | NR_131024 | TSS12084 |
| chr6 | 148820259 | 148820350 | MACS2_peak_2497 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 57 | chr6 | unknown | gene | 148842491 | 148896237 | - | Caprin2 | Caprin2 | P1860 | NM_001301351 | TSS20836 |
| chr6 | 149073042 | 149073137 | MACS2_peak_2498 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 41 | chr6 | unknown | gene | 148921058 | 148946432 | - | Fam60a | Fam60a | P4262 | NM_019643 | TSS24025 |
| chr6 | 149073042 | 149073137 | MACS2_peak_2498 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 41 | chr6 | unknown | gene | 149141512 | 149150685 | + | Mettl20 | Mettl20 | P26756 | NM_001252095 | TSS3332 |
| chr6 | 149378722 | 149378821 | MACS2_peak_2499 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 57 | chr6 | unknown | gene | 149309413 | 149334749 | + | 2810474O19Rik | 2810474O19Rik | P22830 | NM_001289661 | TSS720 |
| chr6 | 149378722 | 149378821 | MACS2_peak_2499 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 57 | chr6 | unknown | gene | 149408983 | 149556664 | + | Bicd1 | Bicd1 | P21357 | NM_001112796 | TSS4648 |
| chr7 | 6395025 | 6395116 | MACS2_peak_2500 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 58 | chr7 | unknown | gene | 6363307 | 6379491 | + | Zfp78 | Zfp78 | P11149 | NM_001025163 | TSS1293 |
| chr7 | 6395025 | 6395116 | MACS2_peak_2500 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 58 | chr7 | unknown | gene | 6415174 | 6429390 | + | Gm16532 | Gm16532 | P6783 | NM_001134752 | TSS14431 |
| chr7 | 6936898 | 6936989 | MACS2_peak_2501 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 13 | chr7 | unknown | gene | 6803586 | 6803670 | + | Mir3099 | Mir3099 | | NR_037213 | TSS17015 |
| chr7 | 6936898 | 6936989 | MACS2_peak_2501 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 13 | chr7 | unknown | gene | 6955685 | 6976662 | - | Zim3 | Zim3 | | NR_036631 | TSS10072 |
| chr7 | 12493773 | 12493864 | MACS2_peak_2502 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 56 | chr7 | unknown | gene | 12415148 | 12422488 | - | Zfp551 | Zfp551 | P4112 | NM_001033820 | TSS6016 |
| chr7 | 12493773 | 12493864 | MACS2_peak_2502 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 56 | chr7 | unknown | gene | 12512550 | 12556053 | + | 2900092C05Rik | 2900092C05Rik | P862 | NM_028434 | TSS17141 |
| chr7 | 16964402 | 16964493 | MACS2_peak_2503 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 55 | chr7 | unknown | gene | 16959794 | 16962036 | + | Pnmal1 | Pnmal1 | P5402 | NM_001007569 | TSS19900 |
| chr7 | 16964402 | 16964493 | MACS2_peak_2503 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 55 | chr7 | unknown | gene | 16994587 | 16996645 | + | Ccdc8 | Ccdc8 | P17205 | NM_001101535 | TSS25229 |
| chr7 | 26779927 | 26780037 | MACS2_peak_2504 | 78 | + | 8.28059 | 13.05121 | 7.84118 | 37 | chr7 | unknown | gene | 26757141 | 26771414 | + | Cyp2b19 | Cyp2b19 | P3160 | NM_007814 | TSS18461 |
| chr7 | 26779927 | 26780037 | MACS2_peak_2504 | 78 | + | 8.28059 | 13.05121 | 7.84118 | 37 | chr7 | unknown | gene | 26808926 | 26820829 | + | Cyp2g1 | Cyp2g1 | P21381 | NM_013809 | TSS23795 |
| chr7 | 27751027 | 27751118 | MACS2_peak_2505 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 14 | chr7 | unknown | gene | 27731408 | 27750023 | + | Zfp60 | Zfp60 | P26282 | NM_029531 | TSS22182 |
| chr7 | 27751027 | 27751118 | MACS2_peak_2505 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 14 | chr7 | unknown | gene | 27765672 | 27770972 | + | Gm10046 | Gm10046 | | NR_033484 | TSS13415 |
| chr7 | 30094801 | 30094922 | MACS2_peak_2506 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 65 | chr7 | unknown | gene | 30077336 | 30090510 | - | Zfp566 | Zfp566 | P23065 | NM_152814 | TSS19402 |
| chr7 | 30094801 | 30094922 | MACS2_peak_2506 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 65 | chr7 | unknown | gene | 30095075 | 30105900 | + | Zfp260 | Zfp260 | P13582 | NM_011981 | TSS11388 |
| chr7 | 30665295 | 30665400 | MACS2_peak_2507 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 89 | chr7 | unknown | gene | 30653707 | 30664928 | - | Haus5 | Haus5 | P9295 | NM_027999 | TSS788 |
| chr7 | 30665295 | 30665400 | MACS2_peak_2507 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 89 | chr7 | unknown | gene | 30670721 | 30671605 | - | Pmis2 | Pmis2 | | NR_027849 | TSS16363 |
| chr7 | 30850211 | 30850309 | MACS2_peak_2508 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 84 | chr7 | unknown | gene | 30818356 | 30823775 | - | Ffar2 | Ffar2 | P9232 | NM_001168509 | TSS16410 |
| chr7 | 30850211 | 30850309 | MACS2_peak_2508 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 84 | chr7 | unknown | gene | 30854329 | 30856178 | - | Ffar3 | Ffar3 | P9215 | NM_001033316 | TSS4874 |
| chr7 | 36788020 | 36788126 | MACS2_peak_2509 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 42 | chr7 | unknown | gene | 36698117 | 36771833 | + | Tshz3 | Tshz3 | P22337 | NM_172298 | TSS16177 |
| chr7 | 36788020 | 36788126 | MACS2_peak_2509 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 42 | chr7 | unknown | gene | 37479108 | 37769752 | - | Zfp536 | Zfp536 | P11114 | NM_172385 | TSS15826 |
| chr7 | 37035716 | 37035851 | MACS2_peak_2510 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 68 | chr7 | unknown | gene | 36698117 | 36771833 | + | Tshz3 | Tshz3 | P22337 | NM_172298 | TSS16177 |
| chr7 | 37035716 | 37035851 | MACS2_peak_2510 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 68 | chr7 | unknown | gene | 37479108 | 37769752 | - | Zfp536 | Zfp536 | P11114 | NM_172385 | TSS15826 |
| chr7 | 38009156 | 38009247 | MACS2_peak_2511 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 75 | chr7 | unknown | gene | 37479108 | 37769752 | - | Zfp536 | Zfp536 | P11114 | NM_172385 | TSS15826 |
| chr7 | 38009156 | 38009247 | MACS2_peak_2511 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 75 | chr7 | unknown | gene | 38097983 | 38107490 | - | Ccne1 | Ccne1 | P6673 | NM_007633 | TSS14895 |
| chr7 | 39190624 | 39190721 | MACS2_peak_2512 | 63 | + | 7.52781 | 11.52513 | 6.36816 | 52 | chr7 | unknown | gene | 38762405 | 38770304 | - | Gm21276 | Gm21276 | | NR_073038 | TSS4385 |
| chr7 | 39190624 | 39190721 | MACS2_peak_2512 | 63 | + | 7.52781 | 11.52513 | 6.36816 | 52 | chr7 | unknown | gene | 39407293 | 39413013 | - | Gm5114 | Gm5114 | P6059 | NM_177890 | TSS11698 |
| chr7 | 41189482 | 41189573 | MACS2_peak_2513 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 51 | chr7 | unknown | gene | 41060616 | 41089843 | - | 1700110I07Rik | 1700110I07Rik | | NR_131068 | TSS27278 |
| chr7 | 41189482 | 41189573 | MACS2_peak_2513 | 17 | + | 4.87194 | 6.38592 | 1.77838 | 51 | chr7 | unknown | gene | 41284326 | 41289869 | + | Gm5592 | Gm5592 | P3656 | NM_001033782 | TSS24253 |
| chr7 | 41199895 | 41199986 | MACS2_peak_2514 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 24 | chr7 | unknown | gene | 41060616 | 41089843 | - | 1700110I07Rik | 1700110I07Rik | | NR_131068 | TSS27278 |
| chr7 | 41199895 | 41199986 | MACS2_peak_2514 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 24 | chr7 | unknown | gene | 41284326 | 41289869 | + | Gm5592 | Gm5592 | P3656 | NM_001033782 | TSS24253 |
| chr7 | 42004329 | 42004435 | MACS2_peak_2515 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 30 | chr7 | unknown | gene | 41836880 | 41872670 | - | Vmn2r58 | Vmn2r58 | P11308 | NM_001105055 | TSS13322 |
| chr7 | 42004329 | 42004435 | MACS2_peak_2515 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 30 | chr7 | unknown | gene | 42011791 | 42058981 | - | Vmn2r59 | Vmn2r59 | P5903 | NM_001105056 | TSS6896 |
| chr7 | 44816871 | 44816962 | MACS2_peak_2516 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 14 | chr7 | unknown | gene | 44812255 | 44816658 | - | Atf5 | Atf5 | | NR_033136 | TSS25121 |
| chr7 | 44816871 | 44816962 | MACS2_peak_2516 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 14 | chr7 | unknown | gene | 44836287 | 44840705 | + | Il4i1 | Il4i1 | P924 | NM_010215 | TSS4907 |
| chr7 | 45623678 | 45623790 | MACS2_peak_2517 | 76 | + | 8.17358 | 12.81159 | 7.61239 | 39 | chr7 | unknown | gene | 45617605 | 45619757 | + | Fut1 | Fut1 | P25179 | NM_001271981 | TSS4268 |
| chr7 | 45623678 | 45623790 | MACS2_peak_2517 | 76 | + | 8.17358 | 12.81159 | 7.61239 | 39 | chr7 | unknown | gene | 45627536 | 45638884 | + | Rasip1 | Rasip1 | P22492 | NM_028544 | TSS4300 |
| chr7 | 46516313 | 46516404 | MACS2_peak_2518 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 47 | chr7 | unknown | gene | 46396467 | 46437336 | + | Kcnc1 | Kcnc1 | P7356 | NM_001112739 | TSS15562 |
| chr7 | 46516313 | 46516404 | MACS2_peak_2518 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 47 | chr7 | unknown | gene | 46644640 | 46672537 | - | Tph1 | Tph1 | P25091 | NM_001136084 | TSS10472 |
| chr7 | 47003298 | 47003408 | MACS2_peak_2519 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 22 | chr7 | unknown | gene | 46976631 | 46987803 | + | Gm9999 | Gm9999 | | NR_033461 | TSS898 |
| chr7 | 47003298 | 47003408 | MACS2_peak_2519 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 22 | chr7 | unknown | gene | 47050639 | 47053852 | + | Tmem86a | Tmem86a | P18707 | NM_026436 | TSS26111 |
| chr7 | 49045909 | 49046000 | MACS2_peak_2520 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 58 | chr7 | unknown | gene | 48866428 | 48881041 | - | E2f8 | E2f8 | P4022 | NM_001013368 | TSS7870 |
| chr7 | 49045909 | 49046000 | MACS2_peak_2520 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 58 | chr7 | unknown | gene | 49631498 | 49636715 | - | Dbx1 | Dbx1 | P6820 | NM_001005232 | TSS26213 |
| chr7 | 50976213 | 50976304 | MACS2_peak_2521 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 51 | chr7 | unknown | gene | 49975349 | 50862949 | + | Nell1 | Nell1 | P6900 | NM_001037906 | TSS2383 |
| chr7 | 50976213 | 50976304 | MACS2_peak_2521 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 51 | chr7 | unknown | gene | 51511028 | 51593845 | + | Ano5 | Ano5 | | NR_073508 | TSS20679 |
| chr7 | 51570844 | 51570998 | MACS2_peak_2522 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 121 | chr7 | unknown | gene | 49975349 | 50862949 | + | Nell1 | Nell1 | P6900 | NM_001037906 | TSS2383 |
| chr7 | 51570844 | 51570998 | MACS2_peak_2522 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 121 | chr7 | unknown | gene | 51621829 | 51669360 | + | Slc17a6 | Slc17a6 | P6475 | NM_080853 | TSS25509 |
| chr7 | 56347798 | 56347889 | MACS2_peak_2523 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 58 | chr7 | unknown | gene | 56050154 | 56231132 | + | Herc2 | Herc2 | P9248 | NM_010418 | TSS13210 |
| chr7 | 56347798 | 56347889 | MACS2_peak_2523 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 58 | chr7 | unknown | gene | 56724241 | 57386773 | - | Gabrg3 | Gabrg3 | P22510 | NM_008074 | TSS17889 |
| chr7 | 57995915 | 57996018 | MACS2_peak_2524 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 57 | chr7 | unknown | gene | 57590517 | 57824759 | + | Gabrb3 | Gabrb3 | P7588 | NM_001038701 | TSS19310 |
| chr7 | 57995915 | 57996018 | MACS2_peak_2524 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 57 | chr7 | unknown | gene | 58658201 | 58828737 | + | Atp10a | Atp10a | P2828 | NM_009728 | TSS27166 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr7 | 58737029 | 58737120 | MACS2_peak_2525 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 53 | chr7 | unknown | gene | 57590517 | 57824759 | + | Gabrb3 | Gabrb3 | P7588 | NM_001038701 | TSS19310 |
| chr7 | 58737029 | 58737120 | MACS2_peak_2525 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 53 | chr7 | unknown | gene | 59228749 | 59304930 | + | Ube3a | Ube3a | P5406 | NM_173010 | TSS7578 |
| chr7 | 59243155 | 59243300 | MACS2_peak_2526 | 53 | + | 7.00427 | 10.41695 | 5.30875 | 71 | chr7 | unknown | gene | 58658201 | 58828737 | + | Atp10a | Atp10a | P2828 | NM_009728 | TSS27166 |
| chr7 | 59243155 | 59243300 | MACS2_peak_2526 | 53 | + | 7.00427 | 10.41695 | 5.30875 | 71 | chr7 | unknown | gene | 59307923 | 59324149 | - | C230091D08Rik | C230091D08Rik | | NR_015479 | TSS18561 |
| chr7 | 59767490 | 59767581 | MACS2_peak_2527 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 29 | chr7 | unknown | gene | 59675989 | 59751580 | - | Snord116l2 | Snord116l2 | | NR_033779 | TSS3891 |
| chr7 | 59767490 | 59767581 | MACS2_peak_2527 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 29 | chr7 | unknown | gene | 59969576 | 59974431 | - | Snhg14 | Snhg14 | | NR_015456 | TSS15238 |
| chr7 | 59769912 | 59770019 | MACS2_peak_2528 | 49 | + | 6.78794 | 9.9958 | 4.9135 | 55 | chr7 | unknown | gene | 59675989 | 59751580 | - | Snord116l2 | Snord116l2 | | NR_033779 | TSS3891 |
| chr7 | 59769912 | 59770019 | MACS2_peak_2528 | 49 | + | 6.78794 | 9.9958 | 4.9135 | 55 | chr7 | unknown | gene | 59969576 | 59974431 | - | Snhg14 | Snhg14 | | NR_015456 | TSS15238 |
| chr7 | 59977089 | 59977220 | MACS2_peak_2529 | 63 | + | 7.52781 | 11.52513 | 6.36816 | 58 | chr7 | unknown | gene | 59969576 | 59974431 | - | Snhg14 | Snhg14 | | NR_015456 | TSS15238 |
| chr7 | 59977089 | 59977220 | MACS2_peak_2529 | 63 | + | 7.52781 | 11.52513 | 6.36816 | 58 | chr7 | unknown | gene | 59978810 | 59978856 | - | Snord64 | Snord64 | | NR_028529 | TSS15391 |
| chr7 | 64483669 | 64483760 | MACS2_peak_2530 | 13 | + | 4.58138 | 5.9095 | 1.36391 | 33 | chr7 | unknown | gene | 64392770 | 64411987 | + | Mcee | Mcee | P22810 | NM_028626 | TSS8431 |
| chr7 | 64483669 | 64483760 | MACS2_peak_2530 | 13 | + | 4.58138 | 5.9095 | 1.36391 | 33 | chr7 | unknown | gene | 64501705 | 64753142 | + | Apba2 | Apba2 | P24626 | NM_007461 | TSS16142 |
| chr7 | 65494533 | 65494708 | MACS2_peak_2531 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 118 | chr7 | unknown | gene | 65296164 | 65370836 | - | Tjp1 | Tjp1 | P12079 | NM_009386 | TSS25419 |
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| chr7 | 66462923 | 66463014 | MACS2_peak_2532 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 29 | chr7 | unknown | gene | 66390892 | 66427412 | - | Aldh1a3 | Aldh1a3 | P3903 | NM_053080 | TSS10904 |
| chr7 | 66462923 | 66463014 | MACS2_peak_2532 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 29 | chr7 | unknown | gene | 66644566 | 66689561 | - | Asb7 | Asb7 | | NR_003961 | TSS17038 |
| chr7 | 67934668 | 67934792 | MACS2_peak_2533 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 48 | chr7 | unknown | gene | 67784537 | 67803496 | - | 4833412C05Rik | 4833412C05Rik | | NR_045954 | TSS20559 |
| chr7 | 67934668 | 67934792 | MACS2_peak_2533 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 48 | chr7 | unknown | gene | 67952256 | 68226401 | + | Igf1r | Igf1r | P5980 | NM_010513 | TSS16231 |
| chr7 | 68763322 | 68763413 | MACS2_peak_2534 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 75 | chr7 | unknown | gene | 68736993 | 68749066 | - | Arrdc4 | Arrdc4 | P24809 | NM_001042592 | TSS1911 |
| chr7 | 68763322 | 68763413 | MACS2_peak_2534 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 75 | chr7 | unknown | gene | 69496093 | 69499689 | + | 4930402F11Rik | 4930402F11Rik | | NR_045940 | TSS19812 |
| chr7 | 69508098 | 69508189 | MACS2_peak_2535 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 55 | chr7 | unknown | gene | 69496093 | 69499689 | + | 4930402F11Rik | 4930402F11Rik | | NR_045940 | TSS19812 |
| chr7 | 69508098 | 69508189 | MACS2_peak_2535 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 55 | chr7 | unknown | gene | 70178867 | 70337852 | - | Gm29683 | Gm29683 | | NR_131145 | TSS26075 |
| chr7 | 69685946 | 69686037 | MACS2_peak_2536 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 29 | chr7 | unknown | gene | 69496093 | 69499689 | + | 4930402F11Rik | 4930402F11Rik | | NR_045940 | TSS19812 |
| chr7 | 69685946 | 69686037 | MACS2_peak_2536 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 29 | chr7 | unknown | gene | 70178867 | 70337852 | - | Gm29683 | Gm29683 | | NR_131145 | TSS26075 |
| chr7 | 69906329 | 69906420 | MACS2_peak_2537 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 37 | chr7 | unknown | gene | 69496093 | 69499689 | + | 4930402F11Rik | 4930402F11Rik | | NR_045940 | TSS19812 |
| chr7 | 69906329 | 69906420 | MACS2_peak_2537 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 37 | chr7 | unknown | gene | 70178867 | 70337852 | - | Gm29683 | Gm29683 | | NR_131145 | TSS26075 |
| chr7 | 70277880 | 70277984 | MACS2_peak_2538 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 16 | chr7 | unknown | gene | 69496093 | 69499689 | + | 4930402F11Rik | 4930402F11Rik | | NR_045940 | TSS19812 |
| chr7 | 70277880 | 70277984 | MACS2_peak_2538 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 16 | chr7 | unknown | gene | 70351949 | 70366135 | - | Nr2f2 | Nr2f2 | P26338 | NM_009697 | TSS23226 |
| chr7 | 71093283 | 71093374 | MACS2_peak_2539 | 19 | + | 4.96987 | 6.55914 | 1.92611 | 39 | chr7 | unknown | gene | 70365382 | 70411146 | + | B130024G19Rik | B130024G19Rik | | NR_045850 | TSS17160 |
| chr7 | 71093283 | 71093374 | MACS2_peak_2539 | 19 | + | 4.96987 | 6.55914 | 1.92611 | 39 | chr7 | unknown | gene | 71909694 | 71939191 | + | 4930441H08Rik | 4930441H08Rik | | NR_130995 | TSS453 |
| chr7 | 71132336 | 71132429 | MACS2_peak_2540 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 76 | chr7 | unknown | gene | 70365382 | 70411146 | + | B130024G19Rik | B130024G19Rik | | NR_045850 | TSS17160 |
| chr7 | 71132336 | 71132429 | MACS2_peak_2540 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 76 | chr7 | unknown | gene | 71909694 | 71939191 | + | 4930441H08Rik | 4930441H08Rik | | NR_130995 | TSS453 |
| chr7 | 71474891 | 71474982 | MACS2_peak_2541 | 22 | + | 5.23629 | 7.0289 | 2.291 | 39 | chr7 | unknown | gene | 70365382 | 70411146 | + | B130024G19Rik | B130024G19Rik | | NR_045850 | TSS17160 |
| chr7 | 71474891 | 71474982 | MACS2_peak_2541 | 22 | + | 5.23629 | 7.0289 | 2.291 | 39 | chr7 | unknown | gene | 71909694 | 71939191 | + | 4930441H08Rik | 4930441H08Rik | | NR_130995 | TSS453 |
| chr7 | 71670256 | 71670347 | MACS2_peak_2542 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 22 | chr7 | unknown | gene | 70365382 | 70411146 | + | B130024G19Rik | B130024G19Rik | | NR_045850 | TSS17160 |
| chr7 | 71670256 | 71670347 | MACS2_peak_2542 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 22 | chr7 | unknown | gene | 71909694 | 71939191 | + | 4930441H08Rik | 4930441H08Rik | | NR_130995 | TSS453 |
| chr7 | 71910113 | 71910204 | MACS2_peak_2543 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 29 | chr7 | unknown | gene | 70365382 | 70411146 | + | B130024G19Rik | B130024G19Rik | | NR_045850 | TSS17160 |
| chr7 | 71910113 | 71910204 | MACS2_peak_2543 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 29 | chr7 | unknown | gene | 71947526 | 71962018 | - | Gm36633 | Gm36633 | | NR_126483 | TSS27005 |
| chr7 | 72180322 | 72180413 | MACS2_peak_2544 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 44 | chr7 | unknown | gene | 71961174 | 72027317 | + | 1700011C11Rik | 1700011C11Rik | | NR_126462 | TSS8724 |
| chr7 | 72180322 | 72180413 | MACS2_peak_2544 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 44 | chr7 | unknown | gene | 73097751 | 73102068 | - | Gm6567 | Gm6567 | | NR_046024 | TSS13284 |
| chr7 | 72276851 | 72276952 | MACS2_peak_2545 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 33 | chr7 | unknown | gene | 71961174 | 72027317 | + | 1700011C11Rik | 1700011C11Rik | | NR_126462 | TSS8724 |
| chr7 | 72276851 | 72276952 | MACS2_peak_2545 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 33 | chr7 | unknown | gene | 73097751 | 73102068 | - | Gm6567 | Gm6567 | | NR_046024 | TSS13284 |
| chr7 | 72807210 | 72807355 | MACS2_peak_2546 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 62 | chr7 | unknown | gene | 72077829 | 72306595 | - | Mctp2 | Mctp2 | P6283 | NM_001024703 | TSS3535 |
| chr7 | 72807210 | 72807355 | MACS2_peak_2546 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 62 | chr7 | unknown | gene | 73097751 | 73102068 | - | Gm6567 | Gm6567 | | NR_046024 | TSS13284 |
| chr7 | 74080339 | 74080431 | MACS2_peak_2547 | 35 | + | 5.98489 | 8.51731 | 3.53253 | 22 | chr7 | unknown | gene | 73939119 | 74013494 | - | St8sia2 | St8sia2 | P25809 | NM_009181 | TSS12286 |
| chr7 | 74080339 | 74080431 | MACS2_peak_2547 | 35 | + | 5.98489 | 8.51731 | 3.53253 | 22 | chr7 | unknown | gene | 74275417 | 74554590 | - | Slco3a1 | Slco3a1 | P20902 | NM_001038643 | TSS10265 |
| chr7 | 74173065 | 74173241 | MACS2_peak_2548 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 127 | chr7 | unknown | gene | 73939119 | 74013494 | - | St8sia2 | St8sia2 | P25809 | NM_009181 | TSS12286 |
| chr7 | 74173065 | 74173241 | MACS2_peak_2548 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 127 | chr7 | unknown | gene | 74275417 | 74554590 | - | Slco3a1 | Slco3a1 | P20902 | NM_001038643 | TSS10265 |
| chr7 | 74296072 | 74296163 | MACS2_peak_2549 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 81 | chr7 | unknown | gene | 73939119 | 74013494 | - | St8sia2 | St8sia2 | P25809 | NM_009181 | TSS12286 |
| chr7 | 74296072 | 74296163 | MACS2_peak_2549 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 81 | chr7 | unknown | gene | 75030210 | 75075166 | + | 4930533N22Rik | 4930533N22Rik | | NR_131122 | TSS12040 |
| chr7 | 76842962 | 76843069 | MACS2_peak_2550 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 24 | chr7 | unknown | gene | 75848337 | 75874130 | + | Klhl25 | Klhl25 | P24118 | NM_001122780 | TSS6806 |
| chr7 | 76842962 | 76843069 | MACS2_peak_2550 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 24 | chr7 | unknown | gene | 78192113 | 78577783 | - | Ntrk3 | Ntrk3 | P10851 | NM_008746 | TSS22794 |
| chr7 | 77256248 | 77256339 | MACS2_peak_2551 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 18 | chr7 | unknown | gene | 76229886 | 77124698 | + | Agbl1 | Agbl1 | P4015 | NM_001199224 | TSS21874 |
| chr7 | 77256248 | 77256339 | MACS2_peak_2551 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 18 | chr7 | unknown | gene | 78192113 | 78577783 | - | Ntrk3 | Ntrk3 | P10851 | NM_008746 | TSS22794 |
| chr7 | 77677835 | 77677926 | MACS2_peak_2552 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 74 | chr7 | unknown | gene | 76229886 | 77124698 | + | Agbl1 | Agbl1 | P4015 | NM_001199224 | TSS21874 |
| chr7 | 77677835 | 77677926 | MACS2_peak_2552 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 74 | chr7 | unknown | gene | 78192113 | 78577783 | - | Ntrk3 | Ntrk3 | P10851 | NM_008746 | TSS22794 |
| chr7 | 77972846 | 77972941 | MACS2_peak_2553 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 12 | chr7 | unknown | gene | 76229886 | 77124698 | + | Agbl1 | Agbl1 | P4015 | NM_001199224 | TSS21874 |
| chr7 | 77972846 | 77972941 | MACS2_peak_2553 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 12 | chr7 | unknown | gene | 78192113 | 78577783 | - | Ntrk3 | Ntrk3 | P10851 | NM_008746 | TSS22794 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr7 | 78110950 | 78111041 | MACS2_peak_2554 | 16 | + | 4.811 | 6.2687 | 1.67914 | 72 | chr7 | unknown | gene | 76229886 | 77124698 | + | Agbl1 | Agbl1 | P4015 | NM_001199224 | TSS21874 |
| chr7 | 78110950 | 78111041 | MACS2_peak_2554 | 16 | + | 4.811 | 6.2687 | 1.67914 | 72 | chr7 | unknown | gene | 78192113 | 78577783 | - | Ntrk3 | Ntrk3 | P10851 | NM_008746 | TSS22794 |
| chr7 | 78202181 | 78202332 | MACS2_peak_2555 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 63 | chr7 | unknown | gene | 76229886 | 77124698 | + | Agbl1 | Agbl1 | P4015 | NM_001199224 | TSS21874 |
| chr7 | 78202181 | 78202332 | MACS2_peak_2555 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 63 | chr7 | unknown | gene | 78581065 | 78718220 | - | E430016F16Rik | E430016F16Rik |  | NR_015542 | TSS2976 |
| chr7 | 78769359 | 78769506 | MACS2_peak_2556 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 44 | chr7 | unknown | gene | 78581065 | 78718220 | - | E430016F16Rik | E430016F16Rik |  | NR_015542 | TSS2976 |
| chr7 | 78769359 | 78769506 | MACS2_peak_2556 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 44 | chr7 | unknown | gene | 78775340 | 78783028 | - | Mrpl46 | Mrpl46 | P2307 | NM_023331 | TSS15176 |
| chr7 | 84115637 | 84115728 | MACS2_peak_2557 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 14 | chr7 | unknown | gene | 83932856 | 84086505 | - | Cemip | Cemip | P16956 | NM_030728 | TSS15745 |
| chr7 | 84115637 | 84115728 | MACS2_peak_2557 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 14 | chr7 | unknown | gene | 84246274 | 84409885 | - | Arnt2 | Arnt2 | P7832 | NM_007488 | TSS4098 |
| chr7 | 84146181 | 84146272 | MACS2_peak_2558 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 31 | chr7 | unknown | gene | 83932856 | 84086505 | - | Cemip | Cemip | P16956 | NM_030728 | TSS15745 |
| chr7 | 84146181 | 84146272 | MACS2_peak_2558 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 31 | chr7 | unknown | gene | 84246274 | 84409885 | - | Arnt2 | Arnt2 | P7832 | NM_007488 | TSS4098 |
| chr7 | 86085058 | 86085149 | MACS2_peak_2559 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 25 | chr7 | unknown | gene | 85951866 | 85961482 | - | Vmn2r74 | Vmn2r74 | P15334 | NM_001105187 | TSS15730 |
| chr7 | 86085058 | 86085149 | MACS2_peak_2559 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 25 | chr7 | unknown | gene | 86148041 | 86171724 | - | Vmn2r75 | Vmn2r75 | P19229 | NM_001102578 | TSS16614 |
| chr7 | 87082494 | 87082647 | MACS2_peak_2560 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 70 | chr7 | unknown | gene | 86996464 | 87037968 | + | Vmn2r79 | Vmn2r79 | P6969 | NM_001105190 | TSS102 |
| chr7 | 87082494 | 87082647 | MACS2_peak_2560 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 70 | chr7 | unknown | gene | 87246648 | 87396891 | + | Nox4 | Nox4 | P26570 | NM_001285835 | TSS23788 |
| chr7 | 88268208 | 88268299 | MACS2_peak_2561 | 8 | + | 3.82409 | 4.7186 | 0.85377 | 33 | chr7 | unknown | gene | 87584167 | 88130869 | + | Grm5 | Grm5 | P11854 | NM_001081414 | TSS9795 |
| chr7 | 88268208 | 88268299 | MACS2_peak_2561 | 8 | + | 3.82409 | 4.7186 | 0.85377 | 33 | chr7 | unknown | gene | 88278092 | 88309902 | + | Ctsc | Ctsc | P26238 | NM_009982 | TSS18831 |
| chr7 | 88745260 | 88745410 | MACS2_peak_2562 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 81 | chr7 | unknown | gene | 88430272 | 88490760 | + | Rab38 | Rab38 | P13885 | NM_028238 | TSS22272 |
| chr7 | 88745260 | 88745410 | MACS2_peak_2562 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 81 | chr7 | unknown | gene | 89139720 | 89338588 | - | Tmem135 | Tmem135 | P10464 | NM_028343 | TSS7876 |
| chr7 | 90109833 | 90109942 | MACS2_peak_2563 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 34 | chr7 | unknown | gene | 90029158 | 90049071 | + | E230029C05Rik | E230029C05Rik |  | NR_110365 | TSS17447 |
| chr7 | 90109833 | 90109942 | MACS2_peak_2563 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 34 | chr7 | unknown | gene | 90124835 | 90129936 | - | 2310010J17Rik | 2310010J17Rik |  | NR_046006 | TSS17940 |
| chr7 | 91486011 | 91486102 | MACS2_peak_2564 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 6 | chr7 | unknown | gene | 90468828 | 90475975 | - | Tmem126b | Tmem126b | P17710 | NM_026734 | TSS18951 |
| chr7 | 91486011 | 91486102 | MACS2_peak_2564 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 6 | chr7 | unknown | gene | 92092205 | 92119511 | - | 4930567K12Rik | 4930567K12Rik |  | NR_131016 | TSS9790 |
| chr7 | 92126942 | 92127033 | MACS2_peak_2565 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 18 | chr7 | unknown | gene | 92092205 | 92119511 | - | 4930567K12Rik | 4930567K12Rik |  | NR_131016 | TSS9790 |
| chr7 | 92126942 | 92127033 | MACS2_peak_2565 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 18 | chr7 | unknown | gene | 92561148 | 92581856 | + | Ccdc90b | Ccdc90b | P10687 | NM_001162918 | TSS1640 |
| chr7 | 92356702 | 92356828 | MACS2_peak_2566 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 69 | chr7 | unknown | gene | 92092205 | 92119511 | - | 4930567K12Rik | 4930567K12Rik |  | NR_131016 | TSS9790 |
| chr7 | 92356702 | 92356828 | MACS2_peak_2566 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 69 | chr7 | unknown | gene | 92561148 | 92581856 | + | Ccdc90b | Ccdc90b | P10687 | NM_001162918 | TSS1640 |
| chr7 | 92852833 | 92852924 | MACS2_peak_2567 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 27 | chr7 | unknown | gene | 92741713 | 92835939 | + | Rab30 | Rab30 | P8827 | NM_029494 | TSS12280 |
| chr7 | 92852833 | 92852924 | MACS2_peak_2567 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 27 | chr7 | unknown | gene | 92857526 | 92874232 | - | Ddias | Ddias | P10294 | NM_001080995 | TSS4565 |
| chr7 | 96152886 | 96152977 | MACS2_peak_2568 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 30 | chr7 | unknown | gene | 93079878 | 93081275 | + | Fam181b | Fam181b | P13878 | NM_021427 | TSS12906 |
| chr7 | 96152886 | 96152977 | MACS2_peak_2568 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 30 | chr7 | unknown | gene | 96210636 | 96906591 | + | Tenm4 | Tenm4 | P18472 | NM_011858 | TSS3204 |
| chr7 | 96639862 | 96640023 | MACS2_peak_2569 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 76 | chr7 | unknown | gene | 96339482 | 96341964 | - | Gm15412 | Gm15412 |  | NR_046043 | TSS18587 |
| chr7 | 96639862 | 96640023 | MACS2_peak_2569 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 76 | chr7 | unknown | gene | 96791432 | 96801549 | - | Gm15413 | Gm15413 |  | NR_045874 | TSS14357 |
| chr7 | 97405188 | 97405279 | MACS2_peak_2570 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 86 | chr7 | unknown | gene | 97371616 | 97391759 | + | Alg8 | Alg8 | P24142 | NM_199035 | TSS13256 |
| chr7 | 97405188 | 97405279 | MACS2_peak_2570 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 86 | chr7 | unknown | gene | 97412956 | 97417503 | - | Thrsp | Thrsp | P26113 | NM_009381 | TSS18905 |
| chr7 | 100229509 | 100229600 | MACS2_peak_2571 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 9 | chr7 | unknown | gene | 100176669 | 100184489 | + | Kcne3 | Kcne3 | P15046 | NM_001190869 | TSS8740 |
| chr7 | 100229509 | 100229600 | MACS2_peak_2571 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 9 | chr7 | unknown | gene | 100264543 | 100265561 | + | Gpx2-ps1 | Gpx2-ps1 |  | NR_033563 | TSS68 |
| chr7 | 100351665 | 100351756 | MACS2_peak_2572 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 69 | chr7 | unknown | gene | 100285519 | 100318980 | + | P4ha3 | P4ha3 | P17587 | NM_177161 | TSS2645 |
| chr7 | 100351665 | 100351756 | MACS2_peak_2572 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 69 | chr7 | unknown | gene | 100372232 | 100469528 | + | C2cd3 | C2cd3 | P24540 | NM_001017985 | TSS9993 |
| chr7 | 105090857 | 105090948 | MACS2_peak_2573 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 62 | chr7 | unknown | gene | 105085717 | 105086665 | + | Olfr679 | Olfr679 | P20367 | NM_147044 | TSS8129 |
| chr7 | 105090857 | 105090948 | MACS2_peak_2573 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 62 | chr7 | unknown | gene | 105121458 | 105122406 | + | Olfr681 | Olfr681 | P6684 | NM_207557 | TSS18509 |
| chr7 | 108762406 | 108762497 | MACS2_peak_2574 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 45 | chr7 | unknown | gene | 108754857 | 108755787 | + | Olfr513 | Olfr513 | P19127 | NM_146723 | TSS19064 |
| chr7 | 108762406 | 108762497 | MACS2_peak_2574 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 45 | chr7 | unknown | gene | 108825064 | 108825997 | - | Olfr514 | Olfr514 | P8731 | NM_146726 | TSS14302 |
| chr7 | 112074465 | 112074630 | MACS2_peak_2575 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 82 | chr7 | unknown | gene | 111471660 | 111779547 | - | Galnt18 | Galnt18 | P19239 | NM_173739 | TSS12785 |
| chr7 | 112074465 | 112074630 | MACS2_peak_2575 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 82 | chr7 | unknown | gene | 112116018 | 112159057 | - | Dkk3 | Dkk3 | P15188 | NM_015814 | TSS7552 |
| chr7 | 114395955 | 114396046 | MACS2_peak_2576 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 15 | chr7 | unknown | gene | 114264549 | 114276003 | - | Psma1 | Psma1 | P6351 | NM_011965 | TSS25549 |
| chr7 | 114395955 | 114396046 | MACS2_peak_2576 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 15 | chr7 | unknown | gene | 114415253 | 114536248 | + | Pde3b | Pde3b | P17240 | NM_011055 | TSS22465 |
| chr7 | 115752982 | 115753073 | MACS2_peak_2577 | 24 | + | 5.43036 | 7.38735 | 2.49399 | 39 | chr7 | unknown | gene | 114948649 | 114983967 | + | A730082K24Rik | A730082K24Rik |  | NR_040317 | TSS27657 |
| chr7 | 115752982 | 115753073 | MACS2_peak_2577 | 24 | + | 5.43036 | 7.38735 | 2.49399 | 39 | chr7 | unknown | gene | 116081761 | 116093149 | - | 1700003G18Rik | 1700003G18Rik |  | NR_029433 | TSS21272 |
| chr7 | 115869729 | 115869820 | MACS2_peak_2578 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 56 | chr7 | unknown | gene | 114948649 | 114983967 | + | A730082K24Rik | A730082K24Rik |  | NR_040317 | TSS27657 |
| chr7 | 115869729 | 115869820 | MACS2_peak_2578 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 56 | chr7 | unknown | gene | 116081761 | 116093149 | - | 1700003G18Rik | 1700003G18Rik |  | NR_029433 | TSS21272 |
| chr7 | 118234872 | 118235003 | MACS2_peak_2579 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 63 | chr7 | unknown | gene | 118118889 | 118129504 | - | Arl6ip1 | Arl6ip1 | P19231 | NM_019419 | TSS20661 |
| chr7 | 118234872 | 118235003 | MACS2_peak_2579 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 63 | chr7 | unknown | gene | 118243906 | 118245551 | + | 4930583K01Rik | 4930583K01Rik |  | NR_027879 | TSS26397 |
| chr7 | 119791855 | 119791946 | MACS2_peak_2580 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 38 | chr7 | unknown | gene | 119760922 | 119784360 | + | Acsm3 | Acsm3 | P22712 | NM_212442 | TSS3266 |
| chr7 | 119791855 | 119791946 | MACS2_peak_2580 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 38 | chr7 | unknown | gene | 119794129 | 119848791 | + | 2610020H08Rik | 2610020H08Rik | P6143 | NM_028129 | TSS11365 |
| chr7 | 119798750 | 119798852 | MACS2_peak_2581 | 35 | + | 5.98489 | 8.51731 | 3.53253 | 49 | chr7 | unknown | gene | 119783825 | 119793940 | - | Eri2 | Eri2 | P22042 | NM_027698 | TSS5740 |
| chr7 | 119798750 | 119798852 | MACS2_peak_2581 | 35 | + | 5.98489 | 8.51731 | 3.53253 | 49 | chr7 | unknown | gene | 119853162 | 119895745 | - | Dcun1d3 | Dcun1d3 | P23498 | NM_173408 | TSS1835 |
| chr7 | 120700109 | 120700237 | MACS2_peak_2582 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 40 | chr7 | unknown | gene | 120659295 | 120670196 | - | Pdzd9 | Pdzd9 | P16513 | NM_001040136 | TSS2156 |
| chr7 | 120700109 | 120700237 | MACS2_peak_2582 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 40 | chr7 | unknown | gene | 120739556 | 120805540 | + | Vwa3a | Vwa3a | P18179 | NM_177697 | TSS16187 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr7 | 122126421 | 122126512 | MACS2_peak_2583 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 10 | chr7 | unknown | gene | 122088043 | 122101822 | - | Ndufab1 | Ndufab1 | P13244 | NM_028177 | TSS18888 |
| chr7 | 122126421 | 122126512 | MACS2_peak_2583 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 10 | chr7 | unknown | gene | 122133040 | 122148154 | + | Dctn5 | Dctn5 | P19767 | NM_021608 | TSS26295 |
| chr7 | 122269178 | 122269269 | MACS2_peak_2584 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 32 | chr7 | unknown | gene | 122219495 | 122222175 | + | Chp2 | Chp2 | P13617 | NM_027363 | TSS16374 |
| chr7 | 122269178 | 122269269 | MACS2_peak_2584 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 32 | chr7 | unknown | gene | 122289124 | 122627814 | + | Prkcb | Prkcb | P26021 | NM_008855 | TSS24200 |
| chr7 | 122564668 | 122564791 | MACS2_peak_2585 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 46 | chr7 | unknown | gene | 122219495 | 122222175 | + | Chp2 | Chp2 | P13617 | NM_027363 | TSS16374 |
| chr7 | 122564668 | 122564791 | MACS2_peak_2585 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 46 | chr7 | unknown | gene | 122671743 | 122768846 | + | Cacng3 | Cacng3 | P23592 | NM_019430 | TSS3732 |
| chr7 | 122867851 | 122868031 | MACS2_peak_2586 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 50 | chr7 | unknown | gene | 122671743 | 122768846 | + | Cacng3 | Cacng3 | P23592 | NM_019430 | TSS3732 |
| chr7 | 122867851 | 122868031 | MACS2_peak_2586 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 50 | chr7 | unknown | gene | 122969057 | 122970459 | - | 4930413G21Rik | 4930413G21Rik | | NR_045614 | TSS16944 |
| chr7 | 123164882 | 123164973 | MACS2_peak_2587 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 6 | chr7 | unknown | gene | 122970563 | 123002144 | + | Rbbp6 | Rbbp6 | P18163 | NM_175023 | TSS16509 |
| chr7 | 123164882 | 123164973 | MACS2_peak_2587 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 6 | chr7 | unknown | gene | 123214865 | 123273203 | + | Slc5a11 | Slc5a11 | P14496 | NM_146198 | TSS13197 |
| chr7 | 123432923 | 123433014 | MACS2_peak_2588 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 12 | chr7 | unknown | gene | 123377981 | 123430155 | + | Lcmt1 | Lcmt1 | P5492 | NM_025304 | TSS26324 |
| chr7 | 123432923 | 123433014 | MACS2_peak_2588 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 12 | chr7 | unknown | gene | 123462293 | 123467456 | + | Aqp8 | Aqp8 | P16278 | NM_001109045 | TSS3968 |
| chr7 | 124791751 | 124791850 | MACS2_peak_2589 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 44 | chr7 | unknown | gene | 124625669 | 124708935 | - | 3100003L05Rik | 3100003L05Rik | | NR_045907 | TSS3359 |
| chr7 | 124791751 | 124791850 | MACS2_peak_2589 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 44 | chr7 | unknown | gene | 125331781 | 125349786 | - | 4933440M02Rik | 4933440M02Rik | | NR_045804 | TSS5189 |
| chr7 | 124793507 | 124793598 | MACS2_peak_2590 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 3 | chr7 | unknown | gene | 124625669 | 124708935 | - | 3100003L05Rik | 3100003L05Rik | | NR_045907 | TSS3359 |
| chr7 | 124793507 | 124793598 | MACS2_peak_2590 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 3 | chr7 | unknown | gene | 125331781 | 125349786 | - | 4933440M02Rik | 4933440M02Rik | | NR_045804 | TSS5189 |
| chr7 | 127498258 | 127498401 | MACS2_peak_2591 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 72 | chr7 | unknown | gene | 127485220 | 127490283 | + | Fbrs | Fbrs | P9658 | NM_010183 | TSS13639 |
| chr7 | 127498258 | 127498401 | MACS2_peak_2591 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 72 | chr7 | unknown | gene | 127510437 | 127512869 | - | 1700008J07Rik | 1700008J07Rik | | NR_024331 | TSS17109 |
| chr7 | 128282736 | 128282827 | MACS2_peak_2592 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 34 | chr7 | unknown | gene | 128265696 | 128272187 | + | Slc5a2 | Slc5a2 | P21024 | NM_133254 | TSS23229 |
| chr7 | 128282736 | 128282827 | MACS2_peak_2592 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 34 | chr7 | unknown | gene | 128288368 | 128288435 | - | Mir3103 | Mir3103 | | NR_037290 | TSS5119 |
| chr7 | 128321414 | 128321552 | MACS2_peak_2593 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 86 | chr7 | unknown | gene | 128271378 | 128298083 | - | BC017158 | BC017158 | P975 | NM_145590 | TSS25571 |
| chr7 | 128321414 | 128321552 | MACS2_peak_2593 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 86 | chr7 | unknown | gene | 128373624 | 128418114 | - | Rgs10 | Rgs10 | P3630 | NM_026418 | TSS11220 |
| chr7 | 128639780 | 128639923 | MACS2_peak_2594 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 84 | chr7 | unknown | gene | 128523582 | 128546396 | + | Bag3 | Bag3 | P2835 | NM_013863 | TSS26569 |
| chr7 | 128639780 | 128639923 | MACS2_peak_2594 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 84 | chr7 | unknown | gene | 128696458 | 128740190 | - | Mcmbp | Mcmbp | P16830 | NM_145955 | TSS20696 |
| chr7 | 134227955 | 134228046 | MACS2_peak_2595 | 13 | + | 4.52781 | 5.74876 | 1.3392 | 5 | chr7 | unknown | gene | 133883198 | 134224877 | - | Adam12 | Adam12 | P17919 | NM_007400 | TSS10389 |
| chr7 | 134227955 | 134228046 | MACS2_peak_2595 | 13 | + | 4.52781 | 5.74876 | 1.3392 | 5 | chr7 | unknown | gene | 134266261 | 134376828 | - | D7Ertd443e | D7Ertd443e | P13171 | NM_001081331 | TSS8878 |
| chr7 | 135633725 | 135633816 | MACS2_peak_2596 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 15 | chr7 | unknown | gene | 135566161 | 135566282 | + | Mir1962 | Mir1962 | | NR_035488 | TSS13783 |
| chr7 | 135633725 | 135633816 | MACS2_peak_2596 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 15 | chr7 | unknown | gene | 135648456 | 135652314 | - | 5830432E09Rik | 5830432E09Rik | | NR_015548 | TSS6182 |
| chr7 | 137308148 | 137308239 | MACS2_peak_2597 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 43 | chr7 | unknown | gene | 137234682 | 137242609 | + | Gm10578 | Gm10578 | | NR_045885 | TSS4736 |
| chr7 | 137308148 | 137308239 | MACS2_peak_2597 | 18 | + | 4.90299 | 6.44649 | 1.82743 | 43 | chr7 | unknown | gene | 137375568 | 137410708 | - | 9430038I01Rik | 9430038I01Rik | P9736 | NM_029886 | TSS17094 |
| chr7 | 141042026 | 141042190 | MACS2_peak_2598 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 39 | chr7 | unknown | gene | 141015811 | 141016858 | - | Ifitm6 | Ifitm6 | P9794 | NM_001033632 | TSS1517 |
| chr7 | 141042026 | 141042190 | MACS2_peak_2598 | 7 | + | 3.54736 | 4.16538 | 0.75855 | 39 | chr7 | unknown | gene | 141061273 | 141072119 | + | B4galnt4 | B4galnt4 | P12319 | NM_177897 | TSS9445 |
| chr7 | 143034153 | 143034244 | MACS2_peak_2599 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 10 | chr7 | unknown | gene | 143005045 | 143018739 | + | Tspan32 | Tspan32 | P12498 | NM_001128080 | TSS15529 |
| chr7 | 143034153 | 143034244 | MACS2_peak_2599 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 10 | chr7 | unknown | gene | 143052749 | 143067374 | + | Cd81 | Cd81 | P3446 | NM_133655 | TSS10021 |
| chr8 | 5472518 | 5472628 | MACS2_peak_2600 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 46 | chr8 | unknown | gene | 5085622 | 5105183 | - | Slc10a2 | Slc10a2 | P6545 | NM_011388 | TSS3799 |
| chr8 | 5472518 | 5472628 | MACS2_peak_2600 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 46 | chr8 | unknown | gene | 8617438 | 8660614 | - | Efnb2 | Efnb2 | P15397 | NM_010111 | TSS4968 |
| chr8 | 7597597 | 7597688 | MACS2_peak_2601 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 43 | chr8 | unknown | gene | 5085622 | 5105183 | - | Slc10a2 | Slc10a2 | P6545 | NM_011388 | TSS3799 |
| chr8 | 7597597 | 7597688 | MACS2_peak_2601 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 43 | chr8 | unknown | gene | 8617438 | 8660614 | - | Efnb2 | Efnb2 | P15397 | NM_010111 | TSS4968 |
| chr8 | 7854142 | 7854233 | MACS2_peak_2602 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 22 | chr8 | unknown | gene | 5085622 | 5105183 | - | Slc10a2 | Slc10a2 | P6545 | NM_011388 | TSS3799 |
| chr8 | 7854142 | 7854233 | MACS2_peak_2602 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 22 | chr8 | unknown | gene | 8617438 | 8660614 | - | Efnb2 | Efnb2 | P15397 | NM_010111 | TSS4968 |
| chr8 | 8105742 | 8105833 | MACS2_peak_2603 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 73 | chr8 | unknown | gene | 5085622 | 5105183 | - | Slc10a2 | Slc10a2 | P6545 | NM_011388 | TSS3799 |
| chr8 | 8105742 | 8105833 | MACS2_peak_2603 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 73 | chr8 | unknown | gene | 8617438 | 8660614 | - | Efnb2 | Efnb2 | P15397 | NM_010111 | TSS4968 |
| chr8 | 9342079 | 9342170 | MACS2_peak_2604 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 40 | chr8 | unknown | gene | 9144668 | 9149050 | + | 4930453L07Rik | 4930453L07Rik | | NR_073360 | TSS4733 |
| chr8 | 9342079 | 9342170 | MACS2_peak_2604 | 33 | + | 5.90449 | 8.3414 | 3.37031 | 40 | chr8 | unknown | gene | 9970019 | 9976323 | - | Lig4 | Lig4 | P20961 | NM_176953 | TSS5768 |
| chr8 | 10929617 | 10929708 | MACS2_peak_2605 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 52 | chr8 | unknown | gene | 10924426 | 10928457 | - | 3930402G23Rik | 3930402G23Rik | | NR_030715 | TSS24547 |
| chr8 | 10929617 | 10929708 | MACS2_peak_2605 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 52 | chr8 | unknown | gene | 10986963 | 11008430 | - | Irs2 | Irs2 | P3234 | NM_001081212 | TSS27618 |
| chr8 | 14695721 | 14695812 | MACS2_peak_2606 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 48 | chr8 | unknown | gene | 14027564 | 14090262 | - | Erich1 | Erich1 | P6879 | NM_001034862 | TSS13594 |
| chr8 | 14695721 | 14695812 | MACS2_peak_2606 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 48 | chr8 | unknown | gene | 14888535 | 14896854 | + | Cln8 | Cln8 | P5049 | NM_012000 | TSS12574 |
| chr8 | 17618200 | 17618291 | MACS2_peak_2607 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 41 | chr8 | unknown | gene | 15892544 | 17534974 | - | Csmd1 | Csmd1 | P16147 | NM_053171 | TSS5234 |
| chr8 | 17618200 | 17618291 | MACS2_peak_2607 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 41 | chr8 | unknown | gene | 18595172 | 18801461 | + | Mcph1 | Mcph1 | P19676 | NM_173189 | TSS12947 |
| chr8 | 17649535 | 17649626 | MACS2_peak_2608 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 46 | chr8 | unknown | gene | 15892544 | 17534974 | - | Csmd1 | Csmd1 | P16147 | NM_053171 | TSS5234 |
| chr8 | 17649535 | 17649626 | MACS2_peak_2608 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 46 | chr8 | unknown | gene | 18595172 | 18801461 | + | Mcph1 | Mcph1 | P19676 | NM_173189 | TSS12947 |
| chr8 | 19727984 | 19728080 | MACS2_peak_2609 | 44 | + | 5.64717 | 9.50196 | 4.44324 | 54 | chr8 | unknown | gene | 19495096 | 19497696 | + | Defb7 | Defb7 | P14313 | NM_139220 | TSS16329 |
| chr8 | 19727984 | 19728080 | MACS2_peak_2609 | 44 | + | 5.64717 | 9.50196 | 4.44324 | 54 | chr8 | unknown | gene | 19729575 | 20639412 | + | Gm21119 | Gm21119 | P10259 | NM_001270553 | TSS4326 |
| chr8 | 19799952 | 19800043 | MACS2_peak_2610 | 30 | + | 5.66765 | 8.02745 | 3.08206 | 52 | chr8 | unknown | gene | 19729575 | 19752236 | + | 4930467E23Rik | 4930467E23Rik | P4192 | NM_001039553 | TSS4326 |
| chr8 | 19799952 | 19800043 | MACS2_peak_2610 | 30 | + | 5.66765 | 8.02745 | 3.08206 | 52 | chr8 | unknown | gene | 20268285 | 20297432 | - | 6820431F20Rik | 6820431F20Rik | | NR_030708 | TSS6068 |
| chr8 | 19934380 | 19934506 | MACS2_peak_2611 | 27 | + | 5.30427 | 7.68694 | 2.76995 | 52 | chr8 | unknown | gene | 19729575 | 19752236 | + | 4930467E23Rik | 4930467E23Rik | P4192 | NM_001039553 | TSS4326 |
| chr8 | 19934380 | 19934506 | MACS2_peak_2611 | 27 | + | 5.30427 | 7.68694 | 2.76995 | 52 | chr8 | unknown | gene | 20268285 | 20297432 | - | 6820431F20Rik | 6820431F20Rik | | NR_030708 | TSS6068 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr8 | 20524497 | 20524588 | MACS2_peak_2612 | 17 | + | 4.47883 | 6.38315 | 1.77838 | 32 | chr8 | unknown | gene | 20385781 | 20424814 | - | 2610005L07Rik | 2610005L07Rik | | NR_028428 | TSS19140 |
| chr8 | 20524497 | 20524588 | MACS2_peak_2612 | 17 | + | 4.47883 | 6.38315 | 1.77838 | 32 | chr8 | unknown | gene | 20876498 | 20889113 | + | Gm21944 | Gm21944 | | NR_002880 | TSS7601 |
| chr8 | 20592166 | 20592264 | MACS2_peak_2613 | 13 | + | 3.6846 | 5.33702 | 1.3392 | 13 | chr8 | unknown | gene | 20385781 | 20424814 | - | 2610005L07Rik | 2610005L07Rik | | NR_028428 | TSS19140 |
| chr8 | 20592166 | 20592264 | MACS2_peak_2613 | 13 | + | 3.6846 | 5.33702 | 1.3392 | 13 | chr8 | unknown | gene | 20876498 | 20889113 | + | Gm21944 | Gm21944 | | NR_002880 | TSS7601 |
| chr8 | 20834809 | 20834970 | MACS2_peak_2614 | 31 | + | 5.40687 | 8.13371 | 3.18112 | 86 | chr8 | unknown | gene | 19729575 | 20639412 | + | Gm21119 | Gm21119 | P10259 | NM_001270553 | TSS4326 |
| chr8 | 20834809 | 20834970 | MACS2_peak_2614 | 31 | + | 5.40687 | 8.13371 | 3.18112 | 86 | chr8 | unknown | gene | 20876498 | 20889113 | + | Gm21944 | Gm21944 | | NR_002880 | TSS7601 |
| chr8 | 20945052 | 20945205 | MACS2_peak_2615 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 90 | chr8 | unknown | gene | 20943693 | 20944710 | - | AY761185 | AY761185 | P24479 | NM_001012640 | TSS1972 |
| chr8 | 20945052 | 20945205 | MACS2_peak_2615 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 90 | chr8 | unknown | gene | 21025544 | 21026423 | + | Defa21 | Defa21 | P20133 | NM_183253 | TSS11202 |
| chr8 | 20956296 | 20956387 | MACS2_peak_2616 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 20 | chr8 | unknown | gene | 20943693 | 20944710 | - | AY761185 | AY761185 | P24479 | NM_001012640 | TSS1972 |
| chr8 | 20956296 | 20956387 | MACS2_peak_2616 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 20 | chr8 | unknown | gene | 21025544 | 21026423 | + | Defa21 | Defa21 | P20133 | NM_183253 | TSS11202 |
| chr8 | 21011094 | 21011201 | MACS2_peak_2617 | 20 | + | 4.97265 | 6.69923 | 2.03091 | 60 | chr8 | unknown | gene | 20943693 | 20944710 | - | AY761185 | AY761185 | P24479 | NM_001012640 | TSS1972 |
| chr8 | 21011094 | 21011201 | MACS2_peak_2617 | 20 | + | 4.97265 | 6.69923 | 2.03091 | 60 | chr8 | unknown | gene | 21025544 | 21026423 | + | Defa21 | Defa21 | P20133 | NM_183253 | TSS11202 |
| chr8 | 22871057 | 22871148 | MACS2_peak_2618 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 46 | chr8 | unknown | gene | 22787353 | 22805654 | - | Ap3m2 | Ap3m2 | P22205 | NM_001122820 | TSS14857 |
| chr8 | 22871057 | 22871148 | MACS2_peak_2618 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 46 | chr8 | unknown | gene | 22974835 | 23150497 | + | Ank1 | Ank1 | P19514 | NM_001110783 | TSS9035 |
| chr8 | 23809876 | 23809998 | MACS2_peak_2619 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 68 | chr8 | unknown | gene | 23411501 | 23446488 | + | Sfrp1 | Sfrp1 | P15232 | NM_013834 | TSS2481 |
| chr8 | 23809876 | 23809998 | MACS2_peak_2619 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 68 | chr8 | unknown | gene | 24437615 | 24438896 | - | 1810011O10Rik | 1810011O10Rik | P11053 | NM_026931 | TSS9739 |
| chr8 | 24738962 | 24739053 | MACS2_peak_2620 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 52 | chr8 | unknown | gene | 24677233 | 24725756 | - | Adam3 | Adam3 | P4035 | NM_009619 | TSS2656 |
| chr8 | 24738962 | 24739053 | MACS2_peak_2620 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 52 | chr8 | unknown | gene | 24836142 | 24948795 | - | Adam32 | Adam32 | P15128 | NM_001293693 | TSS13391 |
| chr8 | 26732447 | 26732538 | MACS2_peak_2621 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 42 | chr8 | unknown | gene | 26158168 | 26162799 | + | Thap1 | Thap1 | P2253 | NM_199042 | TSS4509 |
| chr8 | 26732447 | 26732538 | MACS2_peak_2621 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 42 | chr8 | unknown | gene | 26814596 | 26824423 | - | 2310008N11Rik | 2310008N11Rik | | NR_045904 | TSS8694 |
| chr8 | 28096622 | 28096713 | MACS2_peak_2622 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 65 | chr8 | unknown | gene | 28083193 | 28084853 | - | Gm8096 | Gm8096 | | NR_033590 | TSS9167 |
| chr8 | 28096622 | 28096713 | MACS2_peak_2622 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 65 | chr8 | unknown | gene | 28646716 | 29219338 | - | Unc5d | Unc5d | P13570 | NM_153135 | TSS9752 |
| chr8 | 28690958 | 28691049 | MACS2_peak_2623 | 13 | + | 4.27611 | 5.31441 | 1.3392 | 79 | chr8 | unknown | gene | 28083193 | 28084853 | - | Gm8096 | Gm8096 | | NR_033590 | TSS9167 |
| chr8 | 28690958 | 28691049 | MACS2_peak_2623 | 13 | + | 4.27611 | 5.31441 | 1.3392 | 79 | chr8 | unknown | gene | 30568394 | 30575573 | + | 4933433F19Rik | 4933433F19Rik | | NR_045856 | TSS20276 |
| chr8 | 31130504 | 31130617 | MACS2_peak_2624 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 64 | chr8 | unknown | gene | 31111845 | 31128693 | + | Rnf122 | Rnf122 | P12581 | NM_175136 | TSS20075 |
| chr8 | 31130504 | 31130617 | MACS2_peak_2624 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 64 | chr8 | unknown | gene | 31150315 | 31161873 | + | Tti2 | Tti2 | P24017 | NM_001199988 | TSS16848 |
| chr8 | 31446466 | 31446557 | MACS2_peak_2625 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 55 | chr8 | unknown | gene | 31367748 | 31382438 | + | 7420700N18Rik | 7420700N18Rik | | NR_046272 | TSS19930 |
| chr8 | 31446466 | 31446557 | MACS2_peak_2625 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 55 | chr8 | unknown | gene | 31818027 | 31918203 | - | Nrg1 | Nrg1 | P2133 | NM_178591 | TSS17977 |
| chr8 | 34156391 | 34156484 | MACS2_peak_2626 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 38 | chr8 | unknown | gene | 34135571 | 34146700 | - | Leprotl1 | Leprotl1 | P17235 | NM_026609 | TSS15234 |
| chr8 | 34156391 | 34156484 | MACS2_peak_2626 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 38 | chr8 | unknown | gene | 34166621 | 34166712 | - | Mir6395 | Mir6395 | | NR_105820 | TSS25057 |
| chr8 | 34916187 | 34916278 | MACS2_peak_2627 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 87 | chr8 | unknown | gene | 34807609 | 34818783 | + | Dusp4 | Dusp4 | P9535 | NM_176933 | TSS13232 |
| chr8 | 34916187 | 34916278 | MACS2_peak_2627 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 87 | chr8 | unknown | gene | 35375740 | 35384863 | + | Ppp1r3b | Ppp1r3b | P25742 | NM_177741 | TSS25128 |
| chr8 | 35440074 | 35440249 | MACS2_peak_2628 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 53 | chr8 | unknown | gene | 35375740 | 35384863 | + | Ppp1r3b | Ppp1r3b | P25742 | NM_177741 | TSS25128 |
| chr8 | 35440074 | 35440249 | MACS2_peak_2628 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 53 | chr8 | unknown | gene | 35465264 | 35495367 | - | Eri1 | Eri1 | P5679 | NM_026067 | TSS10332 |
| chr8 | 35496572 | 35496663 | MACS2_peak_2629 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 38 | chr8 | unknown | gene | 35465264 | 35495367 | - | Eri1 | Eri1 | P5679 | NM_026067 | TSS10332 |
| chr8 | 35496572 | 35496663 | MACS2_peak_2629 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 38 | chr8 | unknown | gene | 35582502 | 35589020 | - | Gm16793 | Gm16793 | | NR_040376 | TSS25117 |
| chr8 | 35677385 | 35677476 | MACS2_peak_2630 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 16 | chr8 | unknown | gene | 35587797 | 35676763 | + | Mfhas1 | Mfhas1 | P8282 | NM_001081279 | TSS13050 |
| chr8 | 35677385 | 35677476 | MACS2_peak_2630 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 16 | chr8 | unknown | gene | 35824708 | 35826332 | - | Cldn23 | Cldn23 | P8260 | NM_027998 | TSS10972 |
| chr8 | 36727551 | 36727642 | MACS2_peak_2631 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 40 | chr8 | unknown | gene | 36489190 | 36512588 | + | 6430573F11Rik | 6430573F11Rik | P2287 | NM_176952 | TSS18520 |
| chr8 | 36727551 | 36727642 | MACS2_peak_2631 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 40 | chr8 | unknown | gene | 36985572 | 37024238 | - | G630064G18Rik | G630064G18Rik | | NR_126063 | TSS64 |
| chr8 | 36935723 | 36935855 | MACS2_peak_2632 | 12 | + | 4.14966 | 5.12722 | 1.204 | 76 | chr8 | unknown | gene | 36489190 | 36512588 | + | 6430573F11Rik | 6430573F11Rik | P2287 | NM_176952 | TSS18520 |
| chr8 | 36935723 | 36935855 | MACS2_peak_2632 | 12 | + | 4.14966 | 5.12722 | 1.204 | 76 | chr8 | unknown | gene | 36985572 | 37024238 | - | G630064G18Rik | G630064G18Rik | | NR_126063 | TSS64 |
| chr8 | 37977028 | 37977176 | MACS2_peak_2633 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 78 | chr8 | unknown | gene | 36985572 | 37024238 | - | G630064G18Rik | G630064G18Rik | | NR_126063 | TSS64 |
| chr8 | 37977028 | 37977176 | MACS2_peak_2633 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 78 | chr8 | unknown | gene | 38252132 | 38252202 | - | Mir383 | Mir383 | | NR_029884 | TSS19174 |
| chr8 | 38415792 | 38415883 | MACS2_peak_2634 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 27 | chr8 | unknown | gene | 38252132 | 38252202 | - | Mir383 | Mir383 | | NR_029884 | TSS19174 |
| chr8 | 38415792 | 38415883 | MACS2_peak_2634 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 27 | chr8 | unknown | gene | 39005866 | 39130817 | + | Tusc3 | Tusc3 | P4562 | NM_030254 | TSS279 |
| chr8 | 39036618 | 39036724 | MACS2_peak_2635 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 31 | chr8 | unknown | gene | 37522553 | 38660763 | - | Sgcz | Sgcz | P18619 | NM_145841 | TSS21178 |
| chr8 | 39036618 | 39036724 | MACS2_peak_2635 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 31 | chr8 | unknown | gene | 39297979 | 39368268 | + | Gm6213 | Gm6213 | | NR_044988 | TSS4195 |
| chr8 | 39563069 | 39563330 | MACS2_peak_2636 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 184 | chr8 | unknown | gene | 39297979 | 39368268 | + | Gm6213 | Gm6213 | | NR_044988 | TSS4195 |
| chr8 | 39563069 | 39563330 | MACS2_peak_2636 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 184 | chr8 | unknown | gene | 39581699 | 39642620 | - | Msr1 | Msr1 | P8703 | NM_001113326 | TSS4205 |
| chr8 | 39677150 | 39677241 | MACS2_peak_2637 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 44 | chr8 | unknown | gene | 39581699 | 39642620 | - | Msr1 | Msr1 | P8703 | NM_001113326 | TSS4205 |
| chr8 | 39677150 | 39677241 | MACS2_peak_2637 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 44 | chr8 | unknown | gene | 40279165 | 40286707 | - | Fgf20 | Fgf20 | P13302 | NM_030610 | TSS6746 |
| chr8 | 40192142 | 40192233 | MACS2_peak_2638 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 48 | chr8 | unknown | gene | 39581699 | 39642620 | - | Msr1 | Msr1 | P8703 | NM_001113326 | TSS4205 |
| chr8 | 40192142 | 40192233 | MACS2_peak_2638 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 48 | chr8 | unknown | gene | 40279165 | 40286707 | - | Fgf20 | Fgf20 | P13302 | NM_030610 | TSS6746 |
| chr8 | 40970377 | 40970468 | MACS2_peak_2639 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 26 | chr8 | unknown | gene | 40862366 | 40916534 | + | Slc7a2 | Slc7a2 | P11041 | NM_007514 | TSS6897 |
| chr8 | 40970377 | 40970468 | MACS2_peak_2639 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 26 | chr8 | unknown | gene | 40990911 | 41133726 | - | Mtus1 | Mtus1 | P3353 | NM_001286413 | TSS9762 |
| chr8 | 41373713 | 41373804 | MACS2_peak_2640 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 30 | chr8 | unknown | gene | 41239758 | 41332008 | + | Pcm1 | Pcm1 | P22006 | NM_023662 | TSS8983 |
| chr8 | 41373713 | 41373804 | MACS2_peak_2640 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 30 | chr8 | unknown | gene | 41397453 | 41416961 | - | Frg1 | Frg1 | P26041 | NM_013522 | TSS10320 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr8 | 42183525 | 42183616 | MACS2_peak_2641 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 47 | chr8 | unknown | gene | 41827266 | 42046202 | + | 2810404M03Rik | 2810404M03Rik | | NR_045497 | TSS11143 |
| chr8 | 42183525 | 42183616 | MACS2_peak_2641 | 10 | + | 4.02307 | 4.89082 | 1.00781 | 47 | chr8 | unknown | gene | 43129806 | 43141392 | - | Triml1 | Triml1 | P17788 | NM_177742 | TSS1827 |
| chr8 | 42886403 | 42886494 | MACS2_peak_2642 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 65 | chr8 | unknown | gene | 41827266 | 42046202 | + | 2810404M03Rik | 2810404M03Rik | | NR_045497 | TSS11143 |
| chr8 | 42886403 | 42886494 | MACS2_peak_2642 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 65 | chr8 | unknown | gene | 43129806 | 43141392 | - | Triml1 | Triml1 | P17788 | NM_177742 | TSS1827 |
| chr8 | 44369518 | 44369609 | MACS2_peak_2643 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 54 | chr8 | unknown | gene | 43673657 | 43699491 | - | Gm5347 | Gm5347 | P1849 | NM_001079931 | TSS26691 |
| chr8 | 44369518 | 44369609 | MACS2_peak_2643 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 54 | chr8 | unknown | gene | 44950207 | 45051409 | + | Fat1 | Fat1 | P22964 | NM_001081286 | TSS3945 |
| chr8 | 44645622 | 44645713 | MACS2_peak_2644 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 27 | chr8 | unknown | gene | 43673657 | 43699491 | - | Gm5347 | Gm5347 | P1849 | NM_001079931 | TSS26691 |
| chr8 | 44645622 | 44645713 | MACS2_peak_2644 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 27 | chr8 | unknown | gene | 44950207 | 45051409 | + | Fat1 | Fat1 | P22964 | NM_001081286 | TSS3945 |
| chr8 | 45627077 | 45627168 | MACS2_peak_2645 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 31 | chr8 | unknown | gene | 45395664 | 45410539 | - | Tlr3 | Tlr3 | P10701 | NM_126166 | TSS19806 |
| chr8 | 45627077 | 45627168 | MACS2_peak_2645 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 31 | chr8 | unknown | gene | 45723324 | 45819297 | - | Sorbs2os | Sorbs2os | | NR_045739 | TSS4603 |
| chr8 | 45943383 | 45943474 | MACS2_peak_2646 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 22 | chr8 | unknown | gene | 45885484 | 45919014 | + | Pdlim3 | Pdlim3 | P18806 | NM_016798 | TSS7689 |
| chr8 | 45943383 | 45943474 | MACS2_peak_2646 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 22 | chr8 | unknown | gene | 45953605 | 45973603 | - | 1700029J07Rik | 1700029J07Rik | P12738 | NM_001033148 | TSS8696 |
| chr8 | 47409877 | 47410079 | MACS2_peak_2647 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 61 | chr8 | unknown | gene | 47180047 | 47352348 | - | Stox2 | Stox2 | P2650 | NM_001114311 | TSS11416 |
| chr8 | 47409877 | 47410079 | MACS2_peak_2647 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 61 | chr8 | unknown | gene | 47490127 | 47533470 | - | Trappc11 | Trappc11 | P21874 | NM_177240 | TSS2234 |
| chr8 | 47734739 | 47734905 | MACS2_peak_2648 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 89 | chr8 | unknown | gene | 47709343 | 47713770 | - | Cdkn2aip | Cdkn2aip | P4755 | NM_172407 | TSS19231 |
| chr8 | 47734739 | 47734905 | MACS2_peak_2648 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 89 | chr8 | unknown | gene | 47822142 | 47822805 | + | Cldn24 | Cldn24 | P24446 | NM_001111318 | TSS23743 |
| chr8 | 48573059 | 48573150 | MACS2_peak_2649 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 37 | chr8 | unknown | gene | 48099091 | 48140421 | + | Dctd | Dctd | P12516 | NM_001161516 | TSS3585 |
| chr8 | 48573059 | 48573150 | MACS2_peak_2649 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 37 | chr8 | unknown | gene | 50368111 | 50416089 | + | Gm2516 | Gm2516 | | NR_046067 | TSS3412 |
| chr8 | 49550573 | 49550718 | MACS2_peak_2650 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 58 | chr8 | unknown | gene | 48225664 | 48674641 | - | Tenm3 | Tenm3 | P3902 | NM_001145937 | TSS491 |
| chr8 | 49550573 | 49550718 | MACS2_peak_2650 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 58 | chr8 | unknown | gene | 50368111 | 50416089 | + | Gm2516 | Gm2516 | | NR_046067 | TSS3412 |
| chr8 | 50295211 | 50295302 | MACS2_peak_2651 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 63 | chr8 | unknown | gene | 48225664 | 48674641 | - | Tenm3 | Tenm3 | P3902 | NM_001145937 | TSS491 |
| chr8 | 50295211 | 50295302 | MACS2_peak_2651 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 63 | chr8 | unknown | gene | 50368111 | 50416089 | + | Gm2516 | Gm2516 | | NR_046067 | TSS3412 |
| chr8 | 50656034 | 50656125 | MACS2_peak_2652 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 59 | chr8 | unknown | gene | 50368111 | 50416089 | + | Gm2516 | Gm2516 | | NR_046067 | TSS3412 |
| chr8 | 50656034 | 50656125 | MACS2_peak_2652 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 59 | chr8 | unknown | gene | 53511701 | 53523276 | + | Aga | Aga | P203 | NM_001005847 | TSS14537 |
| chr8 | 50684326 | 50684417 | MACS2_peak_2653 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 45 | chr8 | unknown | gene | 50368111 | 50416089 | + | Gm2516 | Gm2516 | | NR_046067 | TSS3412 |
| chr8 | 50684326 | 50684417 | MACS2_peak_2653 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 45 | chr8 | unknown | gene | 53511701 | 53523276 | + | Aga | Aga | P203 | NM_001005847 | TSS14537 |
| chr8 | 51153372 | 51153463 | MACS2_peak_2654 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 7 | chr8 | unknown | gene | 50368111 | 50416089 | + | Gm2516 | Gm2516 | | NR_046067 | TSS3412 |
| chr8 | 51153372 | 51153463 | MACS2_peak_2654 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 7 | chr8 | unknown | gene | 53511701 | 53523276 | + | Aga | Aga | P203 | NM_001005847 | TSS14537 |
| chr8 | 51774540 | 51774636 | MACS2_peak_2655 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 7 | chr8 | unknown | gene | 50368111 | 50416089 | + | Gm2516 | Gm2516 | | NR_046067 | TSS3412 |
| chr8 | 51774540 | 51774636 | MACS2_peak_2655 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 7 | chr8 | unknown | gene | 53511701 | 53523276 | + | Aga | Aga | P203 | NM_001005847 | TSS14537 |
| chr8 | 52112652 | 52112743 | MACS2_peak_2656 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 40 | chr8 | unknown | gene | 50368111 | 50416089 | + | Gm2516 | Gm2516 | | NR_046067 | TSS3412 |
| chr8 | 52112652 | 52112743 | MACS2_peak_2656 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 40 | chr8 | unknown | gene | 53511701 | 53523276 | + | Aga | Aga | P203 | NM_001005847 | TSS14537 |
| chr8 | 52426135 | 52426226 | MACS2_peak_2657 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 6 | chr8 | unknown | gene | 50368111 | 50416089 | + | Gm2516 | Gm2516 | | NR_046067 | TSS3412 |
| chr8 | 52426135 | 52426226 | MACS2_peak_2657 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 6 | chr8 | unknown | gene | 53511701 | 53523276 | + | Aga | Aga | P203 | NM_001005847 | TSS14537 |
| chr8 | 52678218 | 52678309 | MACS2_peak_2658 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 19 | chr8 | unknown | gene | 50368111 | 50416089 | + | Gm2516 | Gm2516 | | NR_046067 | TSS3412 |
| chr8 | 52678218 | 52678309 | MACS2_peak_2658 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 19 | chr8 | unknown | gene | 53511701 | 53523276 | + | Aga | Aga | P203 | NM_001005847 | TSS14537 |
| chr8 | 53840815 | 53840920 | MACS2_peak_2659 | 26 | + | 5.49828 | 7.51662 | 2.61219 | 68 | chr8 | unknown | gene | 53586866 | 53638911 | - | Neil3 | Neil3 | P10413 | NM_146208 | TSS11249 |
| chr8 | 53840815 | 53840920 | MACS2_peak_2659 | 26 | + | 5.49828 | 7.51662 | 2.61219 | 68 | chr8 | unknown | gene | 54077531 | 54186068 | + | Vegfc | Vegfc | P18663 | NM_009506 | TSS24819 |
| chr8 | 55081965 | 55082056 | MACS2_peak_2660 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 51 | chr8 | unknown | gene | 54779433 | 55058929 | + | Gpm6a | Gpm6a | P19032 | NM_001253754 | TSS10807 |
| chr8 | 55081965 | 55082056 | MACS2_peak_2660 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 51 | chr8 | unknown | gene | 55870911 | 55906964 | - | Adam29 | Adam29 | P19000 | NM_175939 | TSS21970 |
| chr8 | 57257639 | 57257730 | MACS2_peak_2661 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 23 | chr8 | unknown | gene | 56551133 | 56591623 | + | Fbxo8 | Fbxo8 | P9836 | NM_015791 | TSS2115 |
| chr8 | 57257639 | 57257730 | MACS2_peak_2661 | 11 | + | 4.09808 | 5.02969 | 1.12528 | 23 | chr8 | unknown | gene | 57304413 | 57320859 | - | LOC102636514 | LOC102636514 | | NR_110474 | TSS15565 |
| chr8 | 57669085 | 57669176 | MACS2_peak_2662 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 73 | chr8 | unknown | gene | 57651752 | 57663430 | + | AW046200 | AW046200 | | NR_040698 | TSS11720 |
| chr8 | 57669085 | 57669176 | MACS2_peak_2662 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 73 | chr8 | unknown | gene | 57774051 | 58911474 | - | Galntl6 | Galntl6 | P3094 | NM_175032 | TSS23377 |
| chr8 | 58112405 | 58112543 | MACS2_peak_2663 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 55 | chr8 | unknown | gene | 57651752 | 57663430 | + | AW046200 | AW046200 | | NR_040698 | TSS11720 |
| chr8 | 58112405 | 58112543 | MACS2_peak_2663 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 55 | chr8 | unknown | gene | 58698848 | 58700796 | - | Gm15881 | Gm15881 | P366 | NM_001177534 | TSS26843 |
| chr8 | 59069096 | 59069187 | MACS2_peak_2664 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 35 | chr8 | unknown | gene | 58911754 | 58913205 | + | BC030500 | BC030500 | P26412 | NM_173411 | TSS26322 |
| chr8 | 59069096 | 59069187 | MACS2_peak_2664 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 35 | chr8 | unknown | gene | 59825648 | 59844721 | + | 4930470O06Rik | 4930470O06Rik | | NR_126087 | TSS12202 |
| chr8 | 59675414 | 59675555 | MACS2_peak_2665 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 52 | chr8 | unknown | gene | 58911754 | 58913205 | + | BC030500 | BC030500 | P26412 | NM_173411 | TSS26322 |
| chr8 | 59675414 | 59675555 | MACS2_peak_2665 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 52 | chr8 | unknown | gene | 59825648 | 59844721 | + | 4930470O06Rik | 4930470O06Rik | | NR_126087 | TSS12202 |
| chr8 | 60670805 | 60670896 | MACS2_peak_2666 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 23 | chr8 | unknown | gene | 60506123 | 60545264 | + | Aadat | Aadat | P12773 | NM_011834 | TSS3938 |
| chr8 | 60670805 | 60670896 | MACS2_peak_2666 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 23 | chr8 | unknown | gene | 60890450 | 60907468 | + | 2700029M09Rik | 2700029M09Rik | P1997 | NM_028299 | TSS13583 |
| chr8 | 60978419 | 60978510 | MACS2_peak_2667 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 79 | chr8 | unknown | gene | 60890450 | 60907468 | + | 2700029M09Rik | 2700029M09Rik | P1997 | NM_028299 | TSS13583 |
| chr8 | 60978419 | 60978510 | MACS2_peak_2667 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 79 | chr8 | unknown | gene | 60993192 | 61130157 | + | Nek1 | Nek1 | P17940 | NM_001293638 | TSS8928 |
| chr8 | 62223355 | 62223446 | MACS2_peak_2668 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 27 | chr8 | unknown | gene | 62057041 | 62123028 | - | Anxa10 | Anxa10 | P11216 | NM_001136089 | TSS9145 |
| chr8 | 62223355 | 62223446 | MACS2_peak_2668 | 14 | + | 4.66511 | 5.99612 | 1.4409 | 27 | chr8 | unknown | gene | 62951231 | 63355381 | + | Spock3 | Spock3 | P10608 | NM_001252620 | TSS11671 |
| chr8 | 63784939 | 63785030 | MACS2_peak_2669 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 52 | chr8 | unknown | gene | 62951231 | 63355381 | + | Spock3 | Spock3 | P10608 | NM_001252620 | TSS11671 |
| chr8 | 63784939 | 63785030 | MACS2_peak_2669 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 52 | chr8 | unknown | gene | 63924693 | 63952170 | - | Sgol2b | Sgol2b | P20533 | NM_001195687 | TSS7530 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr8 | 65364654 | 65364745 | MACS2_peak_2670 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 49 | chr8 | unknown | gene | 65085614 | 65129537 | - | BC030870 | BC030870 | | NR_033217 | TSS18956 |
| chr8 | 65364654 | 65364745 | MACS2_peak_2670 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 49 | chr8 | unknown | gene | 65618039 | 66468530 | + | Mar-01 | Mar-01 | P25424 | NM_001293784 | TSS17479 |
| chr8 | 66103128 | 66103249 | MACS2_peak_2671 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 90 | chr8 | unknown | gene | 65085614 | 65129537 | - | BC030870 | BC030870 | | NR_033217 | TSS18956 |
| chr8 | 66103128 | 66103249 | MACS2_peak_2671 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 90 | chr8 | unknown | gene | 66476345 | 66486414 | - | Tma16 | Tma16 | P840 | NM_025465 | TSS10431 |
| chr8 | 66270503 | 66270594 | MACS2_peak_2672 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 23 | chr8 | unknown | gene | 65085614 | 65129537 | - | BC030870 | BC030870 | | NR_033217 | TSS18956 |
| chr8 | 66270503 | 66270594 | MACS2_peak_2672 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 23 | chr8 | unknown | gene | 66476345 | 66486414 | - | Tma16 | Tma16 | P840 | NM_025465 | TSS10431 |
| chr8 | 67396984 | 67397075 | MACS2_peak_2673 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 23 | chr8 | unknown | gene | 66860216 | 66889518 | + | Naf1 | Naf1 | P18503 | NM_001163564 | TSS24721 |
| chr8 | 67396984 | 67397075 | MACS2_peak_2673 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 23 | chr8 | unknown | gene | 67490757 | 67491846 | + | Nat1 | Nat1 | P24974 | NM_008673 | TSS10511 |
| chr8 | 67806358 | 67806449 | MACS2_peak_2674 | 12 | + | 4.14966 | 5.12722 | 1.204 | 32 | chr8 | unknown | gene | 67523853 | 67548343 | + | Nat3 | Nat3 | P23553 | NM_008674 | TSS23174 |
| chr8 | 67806358 | 67806449 | MACS2_peak_2674 | 12 | + | 4.14966 | 5.12722 | 1.204 | 32 | chr8 | unknown | gene | 68276527 | 68346746 | + | Sh2d4a | Sh2d4a | P8980 | NM_028182 | TSS15485 |
| chr8 | 68733213 | 68733389 | MACS2_peak_2675 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 89 | chr8 | unknown | gene | 68368458 | 68375710 | + | 1700125H03Rik | 1700125H03Rik | | NR_038181 | TSS14845 |
| chr8 | 68733213 | 68733389 | MACS2_peak_2675 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 89 | chr8 | unknown | gene | 68793928 | 68827433 | + | Ints10 | Ints10 | P8105 | NM_001293791 | TSS12205 |
| chr8 | 68906534 | 68906664 | MACS2_peak_2676 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 58 | chr8 | unknown | gene | 68880554 | 68904506 | + | Lpl | Lpl | P12469 | NM_008509 | TSS22511 |
| chr8 | 68906534 | 68906664 | MACS2_peak_2676 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 58 | chr8 | unknown | gene | 69037707 | 69089222 | - | Slc18a1 | Slc18a1 | P5347 | NM_153054 | TSS7237 |
| chr8 | 69189581 | 69189672 | MACS2_peak_2677 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 20 | chr8 | unknown | gene | 69135502 | 69140953 | - | Lzts1 | Lzts1 | P10036 | NM_199364 | TSS13703 |
| chr8 | 69189581 | 69189672 | MACS2_peak_2677 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 20 | chr8 | unknown | gene | 69209045 | 69228980 | + | Zfp930 | Zfp930 | P20538 | NM_001013379 | TSS14647 |
| chr8 | 69543384 | 69543600 | MACS2_peak_2678 | 13 | + | 4.47739 | 5.9134 | 1.36721 | 43 | chr8 | unknown | gene | 69371024 | 69395544 | - | Gm10033 | Gm10033 | | NR_038043 | TSS16253 |
| chr8 | 69543384 | 69543600 | MACS2_peak_2678 | 13 | + | 4.47739 | 5.9134 | 1.36721 | 43 | chr8 | unknown | gene | 69610653 | 69625548 | - | Zfp868 | Zfp868 | P14612 | NM_001045553 | TSS17864 |
| chr8 | 69584223 | 69584314 | MACS2_peak_2679 | 12 | + | 4.12946 | 5.19036 | 1.25487 | 40 | chr8 | unknown | gene | 69371024 | 69395544 | - | Gm10033 | Gm10033 | | NR_038043 | TSS16253 |
| chr8 | 69584223 | 69584314 | MACS2_peak_2679 | 12 | + | 4.12946 | 5.19036 | 1.25487 | 40 | chr8 | unknown | gene | 69610653 | 69625548 | - | Zfp868 | Zfp868 | P14612 | NM_001045553 | TSS17864 |
| chr8 | 70537717 | 70537808 | MACS2_peak_2680 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 50 | chr8 | unknown | gene | 70527742 | 70534953 | + | Fkbp8 | Fkbp8 | P24377 | NM_001111066 | TSS9881 |
| chr8 | 70537717 | 70537808 | MACS2_peak_2680 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 50 | chr8 | unknown | gene | 70539674 | 70591614 | + | Ell | Ell | P17140 | NM_007924 | TSS12315 |
| chr8 | 70996540 | 70996631 | MACS2_peak_2681 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 45 | chr8 | unknown | gene | 70925524 | 70925618 | + | Mir1969 | Mir1969 | | NR_035495 | TSS25339 |
| chr8 | 70996540 | 70996631 | MACS2_peak_2681 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 45 | chr8 | unknown | gene | 71006727 | 71026755 | - | 1700026F02Rik | 1700026F02Rik | | NR_045487 | TSS23621 |
| chr8 | 71882613 | 71882704 | MACS2_peak_2682 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 71 | chr8 | unknown | gene | 71708386 | 71725681 | - | Fcho1 | Fcho1 | | NR_028267 | TSS4438 |
| chr8 | 71882613 | 71882704 | MACS2_peak_2682 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 71 | chr8 | unknown | gene | 71908605 | 71914998 | + | Zfp882 | Zfp882 | P12941 | NM_001166645 | TSS14819 |
| chr8 | 73203527 | 73203618 | MACS2_peak_2683 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 21 | chr8 | unknown | gene | 73016511 | 73016591 | + | Mir28b | Mir28b | | NR_039551 | TSS17700 |
| chr8 | 73203527 | 73203618 | MACS2_peak_2683 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 21 | chr8 | unknown | gene | 74873173 | 74892951 | + | Isx | Isx | P12804 | NM_027837 | TSS14621 |
| chr8 | 74146435 | 74146584 | MACS2_peak_2684 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 32 | chr8 | unknown | gene | 72814598 | 73352556 | - | Large | Large | P26850 | NM_010687 | TSS5849 |
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| chr8 | 75937633 | 75937771 | MACS2_peak_2685 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 19 | chr8 | unknown | gene | 75213943 | 75222248 | + | Rasd2 | Rasd2 | P4128 | NM_029182 | TSS9424 |
| chr8 | 75937633 | 75937771 | MACS2_peak_2685 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 19 | chr8 | unknown | gene | 76749086 | 76900173 | - | Gm10649 | Gm10649 | | NR_028579 | TSS17209 |
| chr8 | 76794964 | 76795055 | MACS2_peak_2686 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 46 | chr8 | unknown | gene | 75448693 | 75984295 | + | 1700007B14Rik | 1700007B14Rik | P17374 | NM_027944 | TSS26717 |
| chr8 | 76794964 | 76795055 | MACS2_peak_2686 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 46 | chr8 | unknown | gene | 76902507 | 77242530 | + | Nr3c2 | Nr3c2 | P5719 | NM_001083906 | TSS486 |
| chr8 | 77611172 | 77611263 | MACS2_peak_2687 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 57 | chr8 | unknown | gene | 77595977 | 77610225 | - | Tmem184c | Tmem184c | P5134 | NM_145599 | TSS6174 |
| chr8 | 77611172 | 77611263 | MACS2_peak_2687 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 57 | chr8 | unknown | gene | 77624171 | 77628956 | + | 1700092C02Rik | 1700092C02Rik | | NR_045467 | TSS15103 |
| chr8 | 77658719 | 77658810 | MACS2_peak_2688 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 48 | chr8 | unknown | gene | 77624171 | 77628956 | + | 1700092C02Rik | 1700092C02Rik | | NR_045467 | TSS15103 |
| chr8 | 77658719 | 77658810 | MACS2_peak_2688 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 48 | chr8 | unknown | gene | 77663028 | 77724452 | - | Ednra | Ednra | P25779 | NM_010332 | TSS20309 |
| chr8 | 78028787 | 78028878 | MACS2_peak_2689 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 68 | chr8 | unknown | gene | 77663028 | 77724452 | - | Ednra | Ednra | P25779 | NM_010332 | TSS20309 |
| chr8 | 78028787 | 78028878 | MACS2_peak_2689 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 68 | chr8 | unknown | gene | 78213341 | 78393683 | + | Ttc29 | Ttc29 | P11138 | NM_183096 | TSS3861 |
| chr8 | 78563271 | 78563366 | MACS2_peak_2690 | 40 | + | 6.34428 | 9.12687 | 4.08077 | 49 | chr8 | unknown | gene | 78505268 | 78508928 | - | Rbmxl1 | Rbmxl1 | P21983 | NM_001252089 | TSS26218 |
| chr8 | 78563271 | 78563366 | MACS2_peak_2690 | 40 | + | 6.34428 | 9.12687 | 4.08077 | 49 | chr8 | unknown | gene | 78804867 | 78821152 | - | Lsm6 | Lsm6 | P7408 | NM_030145 | TSS17184 |
| chr8 | 79999411 | 79999502 | MACS2_peak_2691 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 68 | chr8 | unknown | gene | 79711819 | 79775162 | + | Anapc10 | Anapc10 | P22281 | NM_026904 | TSS4200 |
| chr8 | 79999411 | 79999502 | MACS2_peak_2691 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 68 | chr8 | unknown | gene | 80494044 | 80509474 | + | Gypa | Gypa | P17224 | NM_010369 | TSS11639 |
| chr8 | 80033454 | 80033545 | MACS2_peak_2692 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 60 | chr8 | unknown | gene | 79711819 | 79775162 | + | Anapc10 | Anapc10 | P22281 | NM_026904 | TSS4200 |
| chr8 | 80033454 | 80033545 | MACS2_peak_2692 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 60 | chr8 | unknown | gene | 80494044 | 80509474 | + | Gypa | Gypa | P17224 | NM_010369 | TSS11639 |
| chr8 | 80785293 | 80785454 | MACS2_peak_2693 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 111 | chr8 | unknown | gene | 80699942 | 80739096 | - | Smarca5 | Smarca5 | P19680 | NM_053124 | TSS14124 |
| chr8 | 80785293 | 80785454 | MACS2_peak_2693 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 111 | chr8 | unknown | gene | 80980732 | 81014436 | - | Usp38 | Usp38 | P10370 | NM_027554 | TSS6824 |
| chr8 | 80861872 | 80861963 | MACS2_peak_2694 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 47 | chr8 | unknown | gene | 80699942 | 80739096 | - | Smarca5 | Smarca5 | P19680 | NM_053124 | TSS14124 |
| chr8 | 80861872 | 80861963 | MACS2_peak_2694 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 47 | chr8 | unknown | gene | 80980732 | 81014436 | - | Usp38 | Usp38 | P10370 | NM_027554 | TSS6824 |
| chr8 | 80914651 | 80914765 | MACS2_peak_2695 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 71 | chr8 | unknown | gene | 80764430 | 80879603 | - | Gab1 | Gab1 | P18070 | NM_001301298 | TSS13780 |
| chr8 | 80914651 | 80914765 | MACS2_peak_2695 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 71 | chr8 | unknown | gene | 80980732 | 81014436 | - | Usp38 | Usp38 | P10370 | NM_027554 | TSS6824 |
| chr8 | 81492040 | 81492131 | MACS2_peak_2696 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 46 | chr8 | unknown | gene | 80980732 | 81014436 | - | Usp38 | Usp38 | P10370 | NM_027554 | TSS6824 |
| chr8 | 81492040 | 81492131 | MACS2_peak_2696 | 7 | + | 3.59376 | 4.25757 | 0.75855 | 46 | chr8 | unknown | gene | 82331623 | 82402586 | - | Il15 | Il15 | P26270 | NM_008357 | TSS9984 |
| chr8 | 81521251 | 81521342 | MACS2_peak_2697 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 62 | chr8 | unknown | gene | 80980732 | 81014436 | - | Usp38 | Usp38 | P10370 | NM_027554 | TSS6824 |
| chr8 | 81521251 | 81521342 | MACS2_peak_2697 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 62 | chr8 | unknown | gene | 82331623 | 82402586 | - | Il15 | Il15 | P26270 | NM_008357 | TSS9984 |
| chr8 | 81536677 | 81536768 | MACS2_peak_2698 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 58 | chr8 | unknown | gene | 80980732 | 81014436 | - | Usp38 | Usp38 | P10370 | NM_027554 | TSS6824 |
| chr8 | 81536677 | 81536768 | MACS2_peak_2698 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 58 | chr8 | unknown | gene | 82331623 | 82402586 | - | Il15 | Il15 | P26270 | NM_008357 | TSS9984 |

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr8 | 81817187 | 81817300 | MACS2_peak_2699 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 58 | chr8 | unknown | gene | 80980732 | 81014436 | - | Usp38 | Usp38 | P10370 | NM_027554 | TSS6824 |
| chr8 | 81817187 | 81817300 | MACS2_peak_2699 | 10 | + | 4.04776 | 4.93617 | 1.04625 | 58 | chr8 | unknown | gene | 82331623 | 82402586 | - | Il15 | Il15 | P26270 | NM_008357 | TSS9984 |
| chr8 | 82296198 | 82296289 | MACS2_peak_2700 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 26 | chr8 | unknown | gene | 81342561 | 82122735 | + | Inpp4b | Inpp4b | P26740 | NM_001024617 | TSS2456 |
| chr8 | 82296198 | 82296289 | MACS2_peak_2700 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 26 | chr8 | unknown | gene | 82331623 | 82402586 | - | Il15 | Il15 | P26270 | NM_008357 | TSS9984 |
| chr8 | 82732685 | 82732776 | MACS2_peak_2701 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 26 | chr8 | unknown | gene | 82331623 | 82402586 | - | Il15 | Il15 | P26270 | NM_008357 | TSS9984 |
| chr8 | 82732685 | 82732776 | MACS2_peak_2701 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 26 | chr8 | unknown | gene | 82763619 | 82774126 | - | Zfp330 | Zfp330 | P14517 | NM_145600 | TSS27592 |
| chr8 | 86007381 | 86007473 | MACS2_peak_2702 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 21 | chr8 | unknown | gene | 85717556 | 85840738 | - | Itfg1 | Itfg1 | P5904 | NM_028007 | TSS13982 |
| chr8 | 86007381 | 86007473 | MACS2_peak_2702 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 21 | chr8 | unknown | gene | 86504840 | 86566557 | - | Abcc12 | Abcc12 | P15305 | NM_172912 | TSS12025 |
| chr8 | 86495211 | 86495302 | MACS2_peak_2703 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 56 | chr8 | unknown | gene | 85841001 | 86059442 | + | Phkb | Phkb | P6044 | NM_199446 | TSS24934 |
| chr8 | 86495211 | 86495302 | MACS2_peak_2703 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 56 | chr8 | unknown | gene | 86504840 | 86566557 | - | Abcc12 | Abcc12 | P15305 | NM_172912 | TSS12025 |
| chr8 | 88219198 | 88219289 | MACS2_peak_2704 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 19 | chr8 | unknown | gene | 88137884 | 88170981 | + | Heatr3 | Heatr3 | P9956 | NM_172757 | TSS10678 |
| chr8 | 88219198 | 88219289 | MACS2_peak_2704 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 19 | chr8 | unknown | gene | 88272402 | 88327818 | + | Adcy7 | Adcy7 | P19418 | NM_007406 | TSS7009 |
| chr8 | 88368539 | 88368630 | MACS2_peak_2705 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 44 | chr8 | unknown | gene | 88332310 | 88361954 | - | Brd7 | Brd7 | P22724 | NM_012047 | TSS3075 |
| chr8 | 88368539 | 88368630 | MACS2_peak_2705 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 44 | chr8 | unknown | gene | 88521343 | 88592152 | + | Nkd1 | Nkd1 | P16241 | NM_027280 | TSS27281 |
| chr8 | 88522055 | 88522146 | MACS2_peak_2706 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 30 | chr8 | unknown | gene | 88332310 | 88361954 | - | Brd7 | Brd7 | P22724 | NM_012047 | TSS3075 |
| chr8 | 88522055 | 88522146 | MACS2_peak_2706 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 30 | chr8 | unknown | gene | 88626827 | 88636128 | - | Snx20 | Snx20 | P5800 | NM_027840 | TSS11246 |
| chr8 | 88706248 | 88706426 | MACS2_peak_2707 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 17 | chr8 | unknown | gene | 88647346 | 88688474 | + | Nod2 | Nod2 | P3030 | NM_145857 | TSS11005 |
| chr8 | 88706248 | 88706426 | MACS2_peak_2707 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 17 | chr8 | unknown | gene | 89024734 | 89024831 | + | Mir8110 | Mir8110 | | NR_106190 | TSS25462 |
| chr8 | 89570153 | 89570244 | MACS2_peak_2708 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 3 | chr8 | unknown | gene | 89027242 | 89044162 | - | Sall1 | Sall1 | P2680 | NM_021390 | TSS18836 |
| chr8 | 89570153 | 89570244 | MACS2_peak_2708 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 3 | chr8 | unknown | gene | 90247111 | 90347949 | - | Tox3 | Tox3 | P10737 | NM_172913 | TSS23188 |
| chr8 | 90057511 | 90057671 | MACS2_peak_2709 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 26 | chr8 | unknown | gene | 89027242 | 89044162 | - | Sall1 | Sall1 | P2680 | NM_021390 | TSS18836 |
| chr8 | 90057511 | 90057671 | MACS2_peak_2709 | 15 | + | 4.75156 | 6.15633 | 1.58089 | 26 | chr8 | unknown | gene | 90247111 | 90347949 | - | Tox3 | Tox3 | P10737 | NM_172913 | TSS23188 |
| chr8 | 90993376 | 90993467 | MACS2_peak_2710 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 41 | chr8 | unknown | gene | 90247111 | 90347949 | - | Tox3 | Tox3 | P10737 | NM_172913 | TSS23188 |
| chr8 | 90993376 | 90993467 | MACS2_peak_2710 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 41 | chr8 | unknown | gene | 91070056 | 91122446 | + | Rbl2 | Rbl2 | P17718 | NM_001282001 | TSS4002 |
| chr8 | 92312333 | 92312427 | MACS2_peak_2711 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 35 | chr8 | unknown | gene | 91798510 | 91801240 | - | Irx3 | Irx3 | P17458 | NM_001253822 | TSS13624 |
| chr8 | 92312333 | 92312427 | MACS2_peak_2711 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 35 | chr8 | unknown | gene | 92326030 | 92356120 | - | Crnde | Crnde | | NR_033641 | TSS20565 |
| chr8 | 92355173 | 92355331 | MACS2_peak_2712 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 71 | chr8 | unknown | gene | 91798510 | 91801240 | - | Irx3 | Irx3 | P17458 | NM_001253822 | TSS13624 |
| chr8 | 92355173 | 92355331 | MACS2_peak_2712 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 71 | chr8 | unknown | gene | 92357795 | 92360896 | + | Irx5 | Irx5 | P15720 | NM_018826 | TSS23180 |
| chr8 | 92892499 | 92892590 | MACS2_peak_2713 | 27 | + | 5.56793 | 7.65146 | 2.73702 | 27 | chr8 | unknown | gene | 92827327 | 92852665 | + | Mmp2 | Mmp2 | P25523 | NM_008610 | TSS17409 |
| chr8 | 92892499 | 92892590 | MACS2_peak_2713 | 27 | + | 5.56793 | 7.65146 | 2.73702 | 27 | chr8 | unknown | gene | 92901394 | 92902228 | + | Capns2 | Capns2 | P26539 | NM_027112 | TSS17773 |
| chr8 | 93706973 | 93707064 | MACS2_peak_2714 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 44 | chr8 | unknown | gene | 93499212 | 93535707 | - | Ces5a | Ces5a | P22590 | NM_001003951 | TSS24026 |
| chr8 | 93706973 | 93707064 | MACS2_peak_2714 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 44 | chr8 | unknown | gene | 93810837 | 93969388 | + | Gnao1 | Gnao1 | P10368 | NM_001113384 | TSS27264 |
| chr8 | 95762333 | 95762424 | MACS2_peak_2715 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 29 | chr8 | unknown | gene | 95753150 | 95753214 | - | Mir7073 | Mir7073 | | NR_106041 | TSS21729 |
| chr8 | 95762333 | 95762424 | MACS2_peak_2715 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 29 | chr8 | unknown | gene | 95806829 | 95821728 | + | 4930513N10Rik | 4930513N10Rik | | NR_015574 | TSS12853 |
| chr8 | 96723176 | 96723267 | MACS2_peak_2716 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 58 | chr8 | unknown | gene | 96545953 | 96545973 | - | Mir28c | Mir28c | | NR_039538 | TSS18626 |
| chr8 | 96723176 | 96723267 | MACS2_peak_2716 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 58 | chr8 | unknown | gene | 99011886 | 99032741 | + | Gm15679 | Gm15679 | | NR_110579 | TSS20284 |
| chr8 | 96740253 | 96740344 | MACS2_peak_2717 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 80 | chr8 | unknown | gene | 96545953 | 96545973 | - | Mir28c | Mir28c | | NR_039538 | TSS18626 |
| chr8 | 96740253 | 96740344 | MACS2_peak_2717 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 80 | chr8 | unknown | gene | 99011886 | 99032741 | + | Gm15679 | Gm15679 | | NR_110579 | TSS20284 |
| chr8 | 96775514 | 96775622 | MACS2_peak_2718 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 24 | chr8 | unknown | gene | 96545953 | 96545973 | - | Mir28c | Mir28c | | NR_039538 | TSS18626 |
| chr8 | 96775514 | 96775622 | MACS2_peak_2718 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 24 | chr8 | unknown | gene | 99011886 | 99032741 | + | Gm15679 | Gm15679 | | NR_110579 | TSS20284 |
| chr8 | 97121310 | 97121483 | MACS2_peak_2719 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 90 | chr8 | unknown | gene | 96545953 | 96545973 | - | Mir28c | Mir28c | | NR_039538 | TSS18626 |
| chr8 | 97121310 | 97121483 | MACS2_peak_2719 | 7 | + | 3.6414 | 4.35447 | 0.75855 | 90 | chr8 | unknown | gene | 99011886 | 99032741 | + | Gm15679 | Gm15679 | | NR_110579 | TSS20284 |
| chr8 | 97967801 | 97967938 | MACS2_peak_2720 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 52 | chr8 | unknown | gene | 96545953 | 96545973 | - | Mir28c | Mir28c | | NR_039538 | TSS18626 |
| chr8 | 97967801 | 97967938 | MACS2_peak_2720 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 52 | chr8 | unknown | gene | 99011886 | 99032741 | + | Gm15679 | Gm15679 | | NR_110579 | TSS20284 |
| chr8 | 98678551 | 98678702 | MACS2_peak_2721 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 69 | chr8 | unknown | gene | 96545953 | 96545973 | - | Mir28c | Mir28c | | NR_039538 | TSS18626 |
| chr8 | 98678551 | 98678702 | MACS2_peak_2721 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 69 | chr8 | unknown | gene | 99011886 | 99032741 | + | Gm15679 | Gm15679 | | NR_110579 | TSS20284 |
| chr8 | 99346406 | 99346545 | MACS2_peak_2722 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 88 | chr8 | unknown | gene | 99011886 | 99032741 | + | Gm15679 | Gm15679 | | NR_110579 | TSS20284 |
| chr8 | 99346406 | 99346545 | MACS2_peak_2722 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 88 | chr8 | unknown | gene | 102632994 | 102785111 | - | Cdh11 | Cdh11 | P16687 | NM_009866 | TSS22894 |
| chr8 | 99836673 | 99836764 | MACS2_peak_2723 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 76 | chr8 | unknown | gene | 99024470 | 99416471 | - | Cdh8 | Cdh8 | P25850 | NM_001285913 | TSS22006 |
| chr8 | 99836673 | 99836764 | MACS2_peak_2723 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 76 | chr8 | unknown | gene | 102632994 | 102785111 | - | Cdh11 | Cdh11 | P16687 | NM_009866 | TSS22894 |
| chr8 | 100013901 | 100014063 | MACS2_peak_2724 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 131 | chr8 | unknown | gene | 99024470 | 99416471 | - | Cdh8 | Cdh8 | P25850 | NM_001285913 | TSS22006 |
| chr8 | 100013901 | 100014063 | MACS2_peak_2724 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 131 | chr8 | unknown | gene | 102632994 | 102785111 | - | Cdh11 | Cdh11 | P16687 | NM_009866 | TSS22894 |
| chr8 | 100181464 | 100181555 | MACS2_peak_2725 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 75 | chr8 | unknown | gene | 99024470 | 99416471 | - | Cdh8 | Cdh8 | P25850 | NM_001285913 | TSS22006 |
| chr8 | 100181464 | 100181555 | MACS2_peak_2725 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 75 | chr8 | unknown | gene | 102632994 | 102785111 | - | Cdh11 | Cdh11 | P16687 | NM_009866 | TSS22894 |
| chr8 | 101471628 | 101471745 | MACS2_peak_2726 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 48 | chr8 | unknown | gene | 99024470 | 99416471 | - | Cdh8 | Cdh8 | P25850 | NM_001285913 | TSS22006 |
| chr8 | 101471628 | 101471745 | MACS2_peak_2726 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 48 | chr8 | unknown | gene | 102632994 | 102785111 | - | Cdh11 | Cdh11 | P16687 | NM_009866 | TSS22894 |
| chr8 | 101547129 | 101547220 | MACS2_peak_2727 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 17 | chr8 | unknown | gene | 99024470 | 99416471 | - | Cdh8 | Cdh8 | P25850 | NM_001285913 | TSS22006 |
| chr8 | 101547129 | 101547220 | MACS2_peak_2727 | 13 | + | 4.28449 | 5.39087 | 1.3392 | 17 | chr8 | unknown | gene | 102632994 | 102785111 | - | Cdh11 | Cdh11 | P16687 | NM_009866 | TSS22894 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr8 | 101602348 | 101602439 | MACS2_peak_2728 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 20 | chr8 | unknown | gene | 99024470 | 99416471 | - | Cdh8 | Cdh8 | P25850 | NM_001285913 | TSS22006 |
| chr8 | 101602348 | 101602439 | MACS2_peak_2728 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 20 | chr8 | unknown | gene | 102632994 | 102785111 | - | Cdh11 | Cdh11 | P16687 | NM_009866 | TSS22894 |
| chr8 | 102120272 | 102120363 | MACS2_peak_2729 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 61 | chr8 | unknown | gene | 99024470 | 99416471 | - | Cdh8 | Cdh8 | P25850 | NM_001285913 | TSS22006 |
| chr8 | 102120272 | 102120363 | MACS2_peak_2729 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 61 | chr8 | unknown | gene | 102632994 | 102785111 | - | Cdh11 | Cdh11 | P16687 | NM_009866 | TSS22894 |
| chr8 | 102553677 | 102553768 | MACS2_peak_2730 | 27 | + | 5.56793 | 7.65146 | 2.73702 | 55 | chr8 | unknown | gene | 99024470 | 99416471 | - | Cdh8 | Cdh8 | P25850 | NM_001285913 | TSS22006 |
| chr8 | 102553677 | 102553768 | MACS2_peak_2730 | 27 | + | 5.56793 | 7.65146 | 2.73702 | 55 | chr8 | unknown | gene | 102632994 | 102785111 | - | Cdh11 | Cdh11 | P16687 | NM_009866 | TSS22894 |
| chr8 | 104567859 | 104567974 | MACS2_peak_2731 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 32 | chr8 | unknown | gene | 104534699 | 104549679 | + | Car7 | Car7 | P21918 | NM_001301164 | TSS21349 |
| chr8 | 104567859 | 104567974 | MACS2_peak_2731 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 32 | chr8 | unknown | gene | 104591467 | 104595119 | + | Pdp2 | Pdp2 | P26099 | NM_001024606 | TSS1066 |
| chr8 | 107521328 | 107521419 | MACS2_peak_2732 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 18 | chr8 | unknown | gene | 107412488 | 107425028 | - | Nob1 | Nob1 | P23996 | NM_026277 | TSS12376 |
| chr8 | 107521328 | 107521419 | MACS2_peak_2732 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 18 | chr8 | unknown | gene | 107551243 | 107551313 | + | Mir140 | Mir140 | | NR_029553 | TSS2064 |
| chr8 | 108138319 | 108138410 | MACS2_peak_2733 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 52 | chr8 | unknown | gene | 107580379 | 107588352 | - | Psmd7 | Psmd7 | P6257 | NM_010817 | TSS3188 |
| chr8 | 108138319 | 108138410 | MACS2_peak_2733 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 52 | chr8 | unknown | gene | 108553251 | 108584677 | - | Lncbate1 | Lncbate1 | | NR_077224 | TSS25253 |
| chr8 | 109185017 | 109185108 | MACS2_peak_2734 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 35 | chr8 | unknown | gene | 108714643 | 108957102 | + | Zfhx3 | Zfhx3 | P12911 | NM_007496 | TSS2370 |
| chr8 | 109185017 | 109185108 | MACS2_peak_2734 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 35 | chr8 | unknown | gene | 109339799 | 109340908 | - | Gm1943 | Gm1943 | | NR_002928 | TSS9234 |
| chr8 | 109707368 | 109707497 | MACS2_peak_2735 | 57 | + | 7.23484 | 10.88753 | 5.76525 | 58 | chr8 | unknown | gene | 109671320 | 109693294 | - | Ist1 | Ist1 | P18723 | NM_028018 | TSS10666 |
| chr8 | 109707368 | 109707497 | MACS2_peak_2735 | 57 | + | 7.23484 | 10.88753 | 5.76525 | 58 | chr8 | unknown | gene | 109726450 | 109737739 | - | Atxn1l | Atxn1l | P5160 | NM_001080930 | TSS9450 |
| chr8 | 109778033 | 109778124 | MACS2_peak_2736 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 46 | chr8 | unknown | gene | 109726450 | 109737739 | - | Atxn1l | Atxn1l | P5160 | NM_001080930 | TSS9450 |
| chr8 | 109778033 | 109778124 | MACS2_peak_2736 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 46 | chr8 | unknown | gene | 109778582 | 109860195 | + | Ap1g1 | Ap1g1 | P25411 | NM_009677 | TSS3485 |
| chr8 | 110698450 | 110698558 | MACS2_peak_2737 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 42 | chr8 | unknown | gene | 110266976 | 110610057 | + | Hydin | Hydin | P24603 | NM_172916 | TSS27192 |
| chr8 | 110698450 | 110698558 | MACS2_peak_2737 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 42 | chr8 | unknown | gene | 110721483 | 110739077 | + | Mtss1l | Mtss1l | P20152 | NM_198625 | TSS27214 |
| chr8 | 114181922 | 114182020 | MACS2_peak_2738 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 41 | chr8 | unknown | gene | 114133573 | 114152016 | + | Nudt7 | Nudt7 | P15288 | NM_024446 | TSS8204 |
| chr8 | 114181922 | 114182020 | MACS2_peak_2738 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 41 | chr8 | unknown | gene | 114205639 | 114371745 | + | Vat1l | Vat1l | P12790 | NM_173016 | TSS23512 |
| chr8 | 115462895 | 115463038 | MACS2_peak_2739 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 36 | chr8 | unknown | gene | 114439651 | 115351826 | + | Wwox | Wwox | P15466 | NM_019573 | TSS22944 |
| chr8 | 115462895 | 115463038 | MACS2_peak_2739 | 7 | + | 3.50214 | 4.07747 | 0.75855 | 36 | chr8 | unknown | gene | 115703252 | 115706863 | - | Maf | Maf | P8749 | NM_001025577 | TSS24766 |
| chr8 | 116298762 | 116298896 | MACS2_peak_2740 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 49 | chr8 | unknown | gene | 115703252 | 115706863 | - | Maf | Maf | P8749 | NM_001025577 | TSS24766 |
| chr8 | 116298762 | 116298896 | MACS2_peak_2740 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 49 | chr8 | unknown | gene | 116505014 | 116515723 | + | Dynlrb2 | Dynlrb2 | P16432 | NM_029297 | TSS8630 |
| chr8 | 120265075 | 120265193 | MACS2_peak_2741 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 70 | chr8 | unknown | gene | 120204433 | 120228230 | - | A330074K22Rik | A330074K22Rik | | NR_110496 | TSS8479 |
| chr8 | 120265075 | 120265193 | MACS2_peak_2741 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 70 | chr8 | unknown | gene | 120488865 | 120578603 | + | Gse1 | Gse1 | P14416 | NM_198671 | TSS13617 |
| chr8 | 121384897 | 121384988 | MACS2_peak_2742 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 68 | chr8 | unknown | gene | 121127684 | 121128972 | + | Foxl1 | Foxl1 | P20754 | NM_008024 | TSS77 |
| chr8 | 121384897 | 121384988 | MACS2_peak_2742 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 68 | chr8 | unknown | gene | 121530783 | 121541755 | - | 1700018B08Rik | 1700018B08Rik | P2466 | NM_029597 | TSS17974 |
| chr8 | 125783428 | 125783519 | MACS2_peak_2743 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 62 | chr8 | unknown | gene | 125734202 | 125747766 | + | Ntpcr | Ntpcr | P12637 | NM_025636 | TSS10599 |
| chr8 | 125783428 | 125783519 | MACS2_peak_2743 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 62 | chr8 | unknown | gene | 125910449 | 125944983 | + | BC021891 | BC021891 | P26663 | NM_145608 | TSS16340 |
| chr8 | 126505845 | 126505945 | MACS2_peak_2744 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 79 | chr8 | unknown | gene | 126426651 | 126475065 | - | Gm17296 | Gm17296 | P6856 | NM_001159907 | TSS24430 |
| chr8 | 126505845 | 126505945 | MACS2_peak_2744 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 79 | chr8 | unknown | gene | 126588295 | 126593436 | - | Irf2bp2 | Irf2bp2 | P10605 | NM_001164598 | TSS15683 |
| chr8 | 126589754 | 126589877 | MACS2_peak_2745 | 40 | + | 6.34428 | 9.12687 | 4.08077 | 64 | chr8 | unknown | gene | 126426651 | 126475065 | - | Gm17296 | Gm17296 | P6856 | NM_001159907 | TSS24430 |
| chr8 | 126589754 | 126589877 | MACS2_peak_2745 | 40 | + | 6.34428 | 9.12687 | 4.08077 | 64 | chr8 | unknown | gene | 126930663 | 126945724 | - | Tomm20 | Tomm20 | P19501 | NM_024214 | TSS1463 |
| chr8 | 126716120 | 126716269 | MACS2_peak_2746 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 58 | chr8 | unknown | gene | 126588295 | 126593436 | - | Irf2bp2 | Irf2bp2 | P10605 | NM_001164598 | TSS15683 |
| chr8 | 126716120 | 126716269 | MACS2_peak_2746 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 58 | chr8 | unknown | gene | 126930663 | 126945724 | - | Tomm20 | Tomm20 | P19501 | NM_024214 | TSS1463 |
| chr8 | 127294014 | 127294141 | MACS2_peak_2747 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 59 | chr8 | unknown | gene | 126947172 | 126971039 | - | Rbm34 | Rbm34 | P24696 | NM_172762 | TSS22179 |
| chr8 | 127294014 | 127294141 | MACS2_peak_2747 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 59 | chr8 | unknown | gene | 128278147 | 128278225 | - | Mir21c | Mir21c | | NR_105822 | TSS15218 |
| chr8 | 128591128 | 128591233 | MACS2_peak_2748 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 42 | chr8 | unknown | gene | 128359072 | 128502814 | + | Nrp1 | Nrp1 | P13825 | NM_008737 | TSS306 |
| chr8 | 128591128 | 128591233 | MACS2_peak_2748 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 42 | chr8 | unknown | gene | 128685653 | 128732088 | + | Itgb1 | Itgb1 | P19774 | NM_010578 | TSS1958 |
| chr8 | 128760359 | 128760450 | MACS2_peak_2749 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 32 | chr8 | unknown | gene | 128685653 | 128732088 | + | Itgb1 | Itgb1 | P19774 | NM_010578 | TSS1958 |
| chr8 | 128760359 | 128760450 | MACS2_peak_2749 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 32 | chr8 | unknown | gene | 128980018 | 129065492 | - | Ccdc7a | Ccdc7a | P11663 | NM_029061 | TSS870 |
| chr8 | 128788378 | 128788530 | MACS2_peak_2750 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 29 | chr8 | unknown | gene | 128685653 | 128732088 | + | Itgb1 | Itgb1 | P19774 | NM_010578 | TSS1958 |
| chr8 | 128788378 | 128788530 | MACS2_peak_2750 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 29 | chr8 | unknown | gene | 128980018 | 129065492 | - | Ccdc7a | Ccdc7a | P11663 | NM_029061 | TSS870 |
| chr9 | 3000048 | 3000166 | MACS2_peak_2751 | 268 | + | 4.31217 | 32.58075 | 26.85464 | 49 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3000278 | 3000646 | MACS2_peak_2752 | 791 | + | 7.22313 | 85.62823 | 79.12994 | 274 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3000898 | 3001044 | MACS2_peak_2753 | 638 | + | 6.33687 | 70.08575 | 63.84557 | 75 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3001132 | 3001526 | MACS2_peak_2754 | 610 | + | 6.07619 | 67.21635 | 61.0295 | 307 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3002053 | 3002241 | MACS2_peak_2755 | 549 | + | 5.44959 | 61.02723 | 54.90676 | 69 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3002709 | 3002808 | MACS2_peak_2756 | 194 | + | 3.37727 | 25.04905 | 19.48411 | 47 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3003336 | 3003500 | MACS2_peak_2757 | 444 | + | 4.65923 | 50.45076 | 44.44417 | 72 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3004576 | 3004782 | MACS2_peak_2758 | 143 | + | 2.91362 | 19.81483 | 14.38821 | 153 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3006425 | 3006518 | MACS2_peak_2759 | 102 | + | 2.87329 | 15.50016 | 10.20518 | 61 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3006710 | 3006884 | MACS2_peak_2760 | 703 | + | 6.30325 | 76.73692 | 70.36445 | 105 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3007129 | 3007299 | MACS2_peak_2761 | 190 | + | 3.5903 | 24.65013 | 19.09399 | 49 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3007566 | 3007667 | MACS2_peak_2762 | 241 | + | 3.94452 | 29.77361 | 24.10547 | 55 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr9 | 3009312 | 3009490 | MACS2_peak_2763 | 197 | + | 3.61065 | 25.31427 | 19.74244 | 45 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3009755 | 3009876 | MACS2_peak_2764 | 204 | + | 3.72185 | 26.01473 | 20.42742 | 67 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3009980 | 3010084 | MACS2_peak_2765 | 257 | + | 4.03822 | 31.42678 | 25.722 | 54 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3012297 | 3012398 | MACS2_peak_2766 | 117 | + | 3.10367 | 17.13571 | 11.79182 | 51 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3012767 | 3013070 | MACS2_peak_2767 | 187 | + | 3.66732 | 24.30104 | 18.75268 | 54 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3013208 | 3013329 | MACS2_peak_2768 | 211 | + | 3.81066 | 26.75807 | 21.15343 | 66 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3013434 | 3013538 | MACS2_peak_2769 | 240 | + | 3.96919 | 29.71242 | 24.0448 | 64 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3014066 | 3014347 | MACS2_peak_2770 | 487 | + | 5.28374 | 54.83652 | 48.77288 | 72 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3014778 | 3014881 | MACS2_peak_2771 | 136 | + | 3.24892 | 19.09775 | 13.68721 | 51 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3015300 | 3015425 | MACS2_peak_2772 | 104 | + | 2.94465 | 15.70682 | 10.40611 | 42 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3017936 | 3018031 | MACS2_peak_2773 | 31 | + | 2.188 | 8.04859 | 3.10211 | 36 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3018509 | 3018693 | MACS2_peak_2774 | 206 | + | 3.6369 | 26.28447 | 20.69021 | 71 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3020190 | 3020315 | MACS2_peak_2775 | 374 | + | 4.38512 | 43.34284 | 37.44786 | 64 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3020464 | 3020569 | MACS2_peak_2776 | 231 | + | 3.64496 | 28.8392 | 23.18979 | 51 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3020848 | 3021018 | MACS2_peak_2777 | 430 | + | 4.53718 | 49.0848 | 43.09553 | 75 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3022483 | 3022613 | MACS2_peak_2778 | 135 | + | 2.93344 | 18.91851 | 13.51209 | 57 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3023534 | 3023722 | MACS2_peak_2779 | 139 | + | 2.93998 | 19.34879 | 13.93214 | 55 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3024077 | 3024207 | MACS2_peak_2780 | 458 | + | 4.5877 | 51.91546 | 45.88755 | 69 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3024435 | 3024654 | MACS2_peak_2781 | 216 | + | 3.37207 | 27.23965 | 21.62712 | 71 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3025031 | 3025140 | MACS2_peak_2782 | 221 | + | 3.40311 | 27.79615 | 22.17232 | 55 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3025491 | 3025965 | MACS2_peak_2783 | 432 | + | 4.58421 | 49.29115 | 43.29876 | 64 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3027132 | 3027236 | MACS2_peak_2784 | 161 | + | 3.1099 | 21.58795 | 16.11161 | 57 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3027561 | 3027657 | MACS2_peak_2785 | 53 | + | 2.3175 | 10.43537 | 5.32647 | 34 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3028071 | 3028173 | MACS2_peak_2786 | 244 | + | 3.5085 | 30.09322 | 24.41648 | 58 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3028530 | 3028629 | MACS2_peak_2787 | 124 | + | 2.81856 | 17.80584 | 12.43829 | 56 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3028777 | 3028869 | MACS2_peak_2788 | 154 | + | 3.03625 | 20.86201 | 15.40738 | 48 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3029699 | 3029813 | MACS2_peak_2789 | 159 | + | 3.15882 | 21.45147 | 15.97912 | 69 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3031229 | 3031339 | MACS2_peak_2790 | 269 | + | 3.82384 | 32.6642 | 26.93571 | 59 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3031685 | 3031797 | MACS2_peak_2791 | 200 | + | 3.44156 | 25.67154 | 20.0904 | 59 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3032107 | 3032205 | MACS2_peak_2792 | 50 | + | 2.35195 | 10.10457 | 5.00662 | 40 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3032412 | 3032705 | MACS2_peak_2793 | 279 | + | 3.93211 | 33.75181 | 27.99887 | 206 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3032851 | 3032952 | MACS2_peak_2794 | 231 | + | 3.69008 | 28.77293 | 23.12416 | 62 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3034380 | 3034504 | MACS2_peak_2795 | 93 | + | 2.86889 | 14.57841 | 9.31988 | 57 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3034608 | 3034704 | MACS2_peak_2796 | 208 | + | 3.7699 | 26.41822 | 20.82088 | 48 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3034846 | 3035251 | MACS2_peak_2797 | 373 | + | 4.92764 | 43.28294 | 37.39045 | 68 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3035363 | 3035457 | MACS2_peak_2798 | 160 | + | 3.52814 | 21.49539 | 16.02238 | 51 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3036004 | 3036104 | MACS2_peak_2799 | 205 | + | 4.00734 | 26.13633 | 20.54618 | 54 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3037350 | 3037457 | MACS2_peak_2800 | 292 | + | 5.09681 | 35.01278 | 29.23613 | 57 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3037871 | 3037983 | MACS2_peak_2801 | 104 | + | 3.70285 | 15.70355 | 10.403 | 55 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 3038099 | 3038241 | MACS2_peak_2802 | 207 | + | 4.8748 | 26.29556 | 20.70099 | 72 | chr9 | unknown | gene | 3038668 | 3038743 | - | Mir101c | Mir101c | | NR_039546 | TSS6828 |
| chr9 | 6264210 | 6264301 | MACS2_peak_2803 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 46 | chr9 | unknown | gene | 5345475 | 5373034 | + | Casp12 | Casp12 | P25602 | NM_009808 | TSS23596 |
| chr9 | 6264210 | 6264301 | MACS2_peak_2803 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 46 | chr9 | unknown | gene | 6265027 | 6266367 | - | Ddi1 | Ddi1 | P15164 | NM_027942 | TSS7278 |
| chr9 | 7670904 | 7670995 | MACS2_peak_2804 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 76 | chr9 | unknown | gene | 7571457 | 7581393 | + | Mmp27 | Mmp27 | P4784 | NM_001030289 | TSS24362 |
| chr9 | 7670904 | 7670995 | MACS2_peak_2804 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 76 | chr9 | unknown | gene | 7692110 | 7699357 | + | Mmp7 | Mmp7 | P11907 | NM_010810 | TSS16796 |
| chr9 | 8710696 | 8710787 | MACS2_peak_2805 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 41 | chr9 | unknown | gene | 8544141 | 8680565 | + | Trpc6 | Trpc6 | P4912 | NM_001282087 | TSS4366 |
| chr9 | 8710696 | 8710787 | MACS2_peak_2805 | 7 | + | 3.74056 | 4.56432 | 0.75855 | 41 | chr9 | unknown | gene | 8899832 | 8965138 | + | Pgr | Pgr | P5028 | NM_008829 | TSS6356 |
| chr9 | 9104751 | 9104890 | MACS2_peak_2806 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 56 | chr9 | unknown | gene | 8899832 | 8965138 | + | Pgr | Pgr | P5028 | NM_008829 | TSS6356 |
| chr9 | 9104751 | 9104890 | MACS2_peak_2806 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 56 | chr9 | unknown | gene | 9236287 | 9260885 | + | Gm16833 | Gm16833 | | NR_045754 | TSS3972 |
| chr9 | 10116620 | 10116736 | MACS2_peak_2807 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 63 | chr9 | unknown | gene | 9894430 | 9894521 | + | Mir6237 | Mir6237 | | NR_105745 | TSS2166 |
| chr9 | 10116620 | 10116736 | MACS2_peak_2807 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 63 | chr9 | unknown | gene | 13091266 | 13105855 | - | 4930568E12Rik | 4930568E12Rik | | NR_040755 | TSS13021 |
| chr9 | 10704315 | 10704419 | MACS2_peak_2808 | 46 | + | 6.64256 | 9.7473 | 4.67773 | 31 | chr9 | unknown | gene | 9894430 | 9894521 | + | Mir6237 | Mir6237 | | NR_105745 | TSS2166 |
| chr9 | 10704315 | 10704419 | MACS2_peak_2808 | 46 | + | 6.64256 | 9.7473 | 4.67773 | 31 | chr9 | unknown | gene | 13091266 | 13105855 | - | 4930568E12Rik | 4930568E12Rik | | NR_040755 | TSS13021 |
| chr9 | 10897368 | 10897459 | MACS2_peak_2809 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 63 | chr9 | unknown | gene | 9894430 | 9894521 | + | Mir6237 | Mir6237 | | NR_105745 | TSS2166 |
| chr9 | 10897368 | 10897459 | MACS2_peak_2809 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 63 | chr9 | unknown | gene | 13091266 | 13105855 | - | 4930568E12Rik | 4930568E12Rik | | NR_040755 | TSS13021 |
| chr9 | 13534350 | 13534491 | MACS2_peak_2810 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 19 | chr9 | unknown | gene | 13431360 | 13432740 | + | Phxr4 | Phxr4 | | NR_028271 | TSS9897 |
| chr9 | 13534350 | 13534491 | MACS2_peak_2810 | 13 | + | 4.25683 | 5.33568 | 1.3392 | 19 | chr9 | unknown | gene | 13619988 | 13706604 | + | Maml2 | Maml2 | P16580 | NM_001013813 | TSS1906 |
| chr9 | 14037586 | 14037677 | MACS2_peak_2811 | 13 | + | 4.60921 | 5.8944 | 1.34955 | 14 | chr9 | unknown | gene | 13827726 | 13844118 | + | Fam76b | Fam76b | P10813 | NM_176836 | TSS21001 |
| chr9 | 14037586 | 14037677 | MACS2_peak_2811 | 13 | + | 4.60921 | 5.8944 | 1.34955 | 14 | chr9 | unknown | gene | 14276300 | 14325706 | + | Sesn3 | Sesn3 | P12566 | NM_030261 | TSS17744 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr9 | 14307931 | 14308034 | MACS2_peak_2812 | 30 | + | 5.71265 | 7.93979 | 3.00019 | 80 | chr9 | unknown | gene | 13827726 | 13844118 | + | Fam76b | Fam76b | P10813 | NM_176836 | TSS21001 |
| chr9 | 14307931 | 14308034 | MACS2_peak_2812 | 30 | + | 5.71265 | 7.93979 | 3.00019 | 80 | chr9 | unknown | gene | 14353989 | 14380970 | - | Endod1 | Endod1 | P3781 | NM_028013 | TSS24783 |
| chr9 | 16281806 | 16281897 | MACS2_peak_2813 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 21 | chr9 | unknown | gene | 15862613 | 15874460 | - | Mtnr1b | Mtnr1b | P20000 | NM_145712 | TSS3811 |
| chr9 | 16281806 | 16281897 | MACS2_peak_2813 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 21 | chr9 | unknown | gene | 18292266 | 18312921 | + | Chordc1 | Chordc1 | P10374 | NM_025844 | TSS7019 |
| chr9 | 16565599 | 16565727 | MACS2_peak_2814 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 60 | chr9 | unknown | gene | 15910192 | 16378225 | - | Fat3 | Fat3 | P22893 | NM_001080814 | TSS10830 |
| chr9 | 16565599 | 16565727 | MACS2_peak_2814 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 60 | chr9 | unknown | gene | 18292266 | 18312921 | + | Chordc1 | Chordc1 | P10374 | NM_025844 | TSS7019 |
| chr9 | 16721483 | 16721574 | MACS2_peak_2815 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 64 | chr9 | unknown | gene | 15910192 | 16378225 | - | Fat3 | Fat3 | P22893 | NM_001080814 | TSS10830 |
| chr9 | 16721483 | 16721574 | MACS2_peak_2815 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 64 | chr9 | unknown | gene | 18292266 | 18312921 | + | Chordc1 | Chordc1 | P10374 | NM_025844 | TSS7019 |
| chr9 | 17144936 | 17145029 | MACS2_peak_2816 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 43 | chr9 | unknown | gene | 15910192 | 16378225 | - | Fat3 | Fat3 | P22893 | NM_001080814 | TSS10830 |
| chr9 | 17144936 | 17145029 | MACS2_peak_2816 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 43 | chr9 | unknown | gene | 18292266 | 18312921 | + | Chordc1 | Chordc1 | P10374 | NM_025844 | TSS7019 |
| chr9 | 18815083 | 18815174 | MACS2_peak_2817 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 23 | chr9 | unknown | gene | 18754691 | 18755633 | - | Olfr24 | Olfr24 | P88 | NM_146606 | TSS3108 |
| chr9 | 18815083 | 18815174 | MACS2_peak_2817 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 23 | chr9 | unknown | gene | 18815353 | 18816292 | - | Olfr828 | Olfr828 | P6727 | NM_146605 | TSS297 |
| chr9 | 24117683 | 24117850 | MACS2_peak_2818 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 62 | chr9 | unknown | gene | 23223075 | 23484032 | + | Bmper | Bmper | P8867 | NM_028472 | TSS699 |
| chr9 | 24117683 | 24117850 | MACS2_peak_2818 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 62 | chr9 | unknown | gene | 24411778 | 24503130 | - | Dpy19l1 | Dpy19l1 | P8696 | NM_172920 | TSS16196 |
| chr9 | 24223287 | 24223378 | MACS2_peak_2819 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 42 | chr9 | unknown | gene | 23223075 | 23484032 | + | Bmper | Bmper | P8867 | NM_028472 | TSS699 |
| chr9 | 24223287 | 24223378 | MACS2_peak_2819 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 42 | chr9 | unknown | gene | 24411778 | 24503130 | - | Dpy19l1 | Dpy19l1 | P8696 | NM_172920 | TSS16196 |
| chr9 | 24321428 | 24321519 | MACS2_peak_2820 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 30 | chr9 | unknown | gene | 24098017 | 24313813 | + | Npsr1 | Npsr1 | P24158 | NM_175678 | TSS26956 |
| chr9 | 24321428 | 24321519 | MACS2_peak_2820 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 30 | chr9 | unknown | gene | 24411778 | 24503130 | - | Dpy19l1 | Dpy19l1 | P8696 | NM_172920 | TSS16196 |
| chr9 | 24541969 | 24542194 | MACS2_peak_2821 | 1082 | + | 35.64373 | 114.92446 | 108.21293 | 135 | chr9 | unknown | gene | 24411778 | 24503130 | - | Dpy19l1 | Dpy19l1 | P8696 | NM_172920 | TSS16196 |
| chr9 | 24541969 | 24542194 | MACS2_peak_2821 | 1082 | + | 35.64373 | 114.92446 | 108.21293 | 135 | chr9 | unknown | gene | 24557047 | 24696163 | - | Dpy19l2 | Dpy19l2 | P858 | NM_001166207 | TSS1089 |
| chr9 | 24663001 | 24663092 | MACS2_peak_2822 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 33 | chr9 | unknown | gene | 24625203 | 24625677 | + | Cypt9 | Cypt9 | P15715 | NM_001039942 | TSS25046 |
| chr9 | 24663001 | 24663092 | MACS2_peak_2822 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 33 | chr9 | unknown | gene | 24720811 | 24773845 | - | Tbx20 | Tbx20 | P7360 | NM_194263 | TSS15225 |
| chr9 | 25095898 | 25095989 | MACS2_peak_2823 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 77 | chr9 | unknown | gene | 24720811 | 24773845 | - | Tbx20 | Tbx20 | P7360 | NM_194263 | TSS15225 |
| chr9 | 25095898 | 25095989 | MACS2_peak_2823 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 77 | chr9 | unknown | gene | 25108129 | 25150966 | - | Herpud2 | Herpud2 | P19847 | NM_020586 | TSS6857 |
| chr9 | 27651739 | 27651870 | MACS2_peak_2824 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 58 | chr9 | unknown | gene | 27396806 | 27401711 | + | Spata19 | Spata19 | P13958 | NM_029299 | TSS6852 |
| chr9 | 27651739 | 27651870 | MACS2_peak_2824 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 58 | chr9 | unknown | gene | 27791268 | 28920187 | + | Opcml | Opcml | P2963 | NM_177906 | TSS16268 |
| chr9 | 29385861 | 29386063 | MACS2_peak_2825 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 123 | chr9 | unknown | gene | 27791268 | 28920187 | + | Opcml | Opcml | P2963 | NM_177906 | TSS16268 |
| chr9 | 29385861 | 29386063 | MACS2_peak_2825 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 123 | chr9 | unknown | gene | 30427328 | 30464418 | + | Snx19 | Snx19 | P21135 | NM_028874 | TSS19702 |
| chr9 | 29660381 | 29660472 | MACS2_peak_2826 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 27 | chr9 | unknown | gene | 27791268 | 28920187 | + | Opcml | Opcml | P2963 | NM_177906 | TSS16268 |
| chr9 | 29660381 | 29660472 | MACS2_peak_2826 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 27 | chr9 | unknown | gene | 30427328 | 30464418 | + | Snx19 | Snx19 | P21135 | NM_028874 | TSS19702 |
| chr9 | 30198255 | 30198346 | MACS2_peak_2827 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 61 | chr9 | unknown | gene | 28995963 | 29962926 | - | Ntm | Ntm | P979 | NM_172290 | TSS22236 |
| chr9 | 30198255 | 30198346 | MACS2_peak_2827 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 61 | chr9 | unknown | gene | 30427328 | 30464418 | + | Snx19 | Snx19 | P21135 | NM_028874 | TSS19702 |
| chr9 | 31162823 | 31162914 | MACS2_peak_2828 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 33 | chr9 | unknown | gene | 31088589 | 31131626 | - | St14 | St14 | P24059 | NM_011176 | TSS24507 |
| chr9 | 31162823 | 31162914 | MACS2_peak_2828 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 33 | chr9 | unknown | gene | 31271400 | 31275275 | + | Gm7244 | Gm7244 | P22444 | NM_001101597 | TSS17267 |
| chr9 | 32219325 | 32219488 | MACS2_peak_2829 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 83 | chr9 | unknown | gene | 31846043 | 31913091 | - | Barx2 | Barx2 | P5544 | NM_013800 | TSS4980 |
| chr9 | 32219325 | 32219488 | MACS2_peak_2829 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 83 | chr9 | unknown | gene | 32314782 | 32344237 | - | Kcnj5 | Kcnj5 | P967 | NM_010605 | TSS12162 |
| chr9 | 32872159 | 32872250 | MACS2_peak_2830 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 38 | chr9 | unknown | gene | 32696041 | 32754425 | + | Ets1 | Ets1 | P24160 | NM_001038642 | TSS22918 |
| chr9 | 32872159 | 32872250 | MACS2_peak_2830 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 38 | chr9 | unknown | gene | 32904068 | 32928966 | - | Gm27162 | Gm27162 | | NR_131058 | TSS16502 |
| chr9 | 33871967 | 33872058 | MACS2_peak_2831 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 46 | chr9 | unknown | gene | 32904068 | 32928966 | - | Gm27162 | Gm27162 | | NR_131058 | TSS16502 |
| chr9 | 33871967 | 33872058 | MACS2_peak_2831 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 46 | chr9 | unknown | gene | 34042370 | 34059019 | + | 7630403G23Rik | 7630403G23Rik | | NR_040744 | TSS13709 |
| chr9 | 34007355 | 34007446 | MACS2_peak_2832 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 40 | chr9 | unknown | gene | 32904068 | 32928966 | - | Gm27162 | Gm27162 | | NR_131058 | TSS16502 |
| chr9 | 34007355 | 34007446 | MACS2_peak_2832 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 40 | chr9 | unknown | gene | 34042370 | 34059019 | + | 7630403G23Rik | 7630403G23Rik | | NR_040744 | TSS13709 |
| chr9 | 34037687 | 34037778 | MACS2_peak_2833 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 86 | chr9 | unknown | gene | 32904068 | 32928966 | - | Gm27162 | Gm27162 | | NR_131058 | TSS16502 |
| chr9 | 34037687 | 34037778 | MACS2_peak_2833 | 12 | + | 4.17595 | 5.17759 | 1.24227 | 86 | chr9 | unknown | gene | 34042370 | 34059019 | + | 7630403G23Rik | 7630403G23Rik | | NR_040744 | TSS13709 |
| chr9 | 35305195 | 35305613 | MACS2_peak_2834 | 1940 | + | 31.85544 | 201.49117 | 194.00475 | 300 | chr9 | unknown | gene | 35281104 | 35285423 | + | 4933422A05Rik | 4933422A05Rik | | NR_040715 | TSS4700 |
| chr9 | 35305195 | 35305613 | MACS2_peak_2834 | 1940 | + | 31.85544 | 201.49117 | 194.00475 | 300 | chr9 | unknown | gene | 35452075 | 35504220 | + | Cdon | Cdon | P22890 | NM_021339 | TSS12638 |
| chr9 | 36250390 | 36250481 | MACS2_peak_2835 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 21 | chr9 | unknown | gene | 36134286 | 36135630 | - | Gm3434 | Gm3434 | | NR_030729 | TSS9168 |
| chr9 | 36250390 | 36250481 | MACS2_peak_2835 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 21 | chr9 | unknown | gene | 36431883 | 36434938 | + | Gm7257 | Gm7257 | P8248 | NM_001167586 | TSS26122 |
| chr9 | 39108000 | 39108156 | MACS2_peak_2836 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 85 | chr9 | unknown | gene | 39077795 | 39078743 | - | Olfr938 | Olfr938 | P10696 | NM_146438 | TSS17133 |
| chr9 | 39108000 | 39108156 | MACS2_peak_2836 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 85 | chr9 | unknown | gene | 39128166 | 39145037 | + | Olfr27 | Olfr27 | P19933 | NM_146829 | TSS11039 |
| chr9 | 41603127 | 41603234 | MACS2_peak_2837 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 50 | chr9 | unknown | gene | 41581925 | 41582002 | + | Mir125b-1 | Mir125b-1 | | NR_029822 | TSS1762 |
| chr9 | 41603127 | 41603234 | MACS2_peak_2837 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 50 | chr9 | unknown | gene | 41968488 | 42124113 | - | Sorl1 | Sorl1 | P19076 | NM_011436 | TSS8817 |
| chr9 | 42017799 | 42017890 | MACS2_peak_2838 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 20 | chr9 | unknown | gene | 41376525 | 41615183 | + | 3110039I08Rik | 3110039I08Rik | | NR_040725 | TSS19993 |
| chr9 | 42017799 | 42017890 | MACS2_peak_2838 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 20 | chr9 | unknown | gene | 42182237 | 42209231 | - | 4930546K05Rik | 4930546K05Rik | | NR_040754 | TSS1797 |
| chr9 | 42225706 | 42225797 | MACS2_peak_2839 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 67 | chr9 | unknown | gene | 42182237 | 42209231 | - | 4930546K05Rik | 4930546K05Rik | | NR_040754 | TSS1797 |
| chr9 | 42225706 | 42225797 | MACS2_peak_2839 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 67 | chr9 | unknown | gene | 42254176 | 42264300 | - | Sc5d | Sc5d | P11972 | NM_172769 | TSS1455 |
| chr9 | 46119938 | 46120029 | MACS2_peak_2840 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 14 | chr9 | unknown | gene | 45965310 | 45984871 | - | Pafah1b2 | Pafah1b2 | P15678 | NM_008775 | TSS9304 |
| chr9 | 46119938 | 46120029 | MACS2_peak_2840 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 14 | chr9 | unknown | gene | 46228629 | 46230402 | + | Apoa1 | Apoa1 | P5646 | NM_009692 | TSS19230 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr9 | 46913549 | 46913640 | MACS2_peak_2841 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 64 | chr9 | unknown | gene | 46303360 | 46319986 | - | 4931429L15Rik | 4931429L15Rik | P25585 | NM_183104 | TSS11788 |
| chr9 | 46913549 | 46913640 | MACS2_peak_2841 | 17 | + | 4.84128 | 6.32668 | 1.72807 | 64 | chr9 | unknown | gene | 46998740 | 47003338 | + | Gm4791 | Gm4791 | P13113 | NM_001243258 | TSS3456 |
| chr9 | 46930543 | 46930634 | MACS2_peak_2842 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 64 | chr9 | unknown | gene | 46913602 | 46927366 | + | 2900052N01Rik | 2900052N01Rik | | NR_015605 | TSS11098 |
| chr9 | 46930543 | 46930634 | MACS2_peak_2842 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 64 | chr9 | unknown | gene | 46998740 | 47003338 | + | Gm4791 | Gm4791 | P13113 | NM_001243258 | TSS3456 |
| chr9 | 47520371 | 47520462 | MACS2_peak_2843 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 46 | chr9 | unknown | gene | 46998740 | 47003338 | + | Gm4791 | Gm4791 | P13113 | NM_001243258 | TSS3456 |
| chr9 | 47520371 | 47520462 | MACS2_peak_2843 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 46 | chr9 | unknown | gene | 47530351 | 47850390 | + | Cadm1 | Cadm1 | P7718 | NM_207676 | TSS13135 |
| chr9 | 49639717 | 49639808 | MACS2_peak_2844 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 38 | chr9 | unknown | gene | 49518287 | 49568025 | + | Gm11149 | Gm11149 | | NR_029465 | TSS3898 |
| chr9 | 49639717 | 49639808 | MACS2_peak_2844 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 38 | chr9 | unknown | gene | 50232522 | 50233182 | - | 2310003N18Rik | 2310003N18Rik | | NR_131161 | TSS3460 |
| chr9 | 49780504 | 49780595 | MACS2_peak_2845 | 12 | + | 4.14966 | 5.12722 | 1.204 | 14 | chr9 | unknown | gene | 49518287 | 49568025 | + | Gm11149 | Gm11149 | | NR_029465 | TSS3898 |
| chr9 | 49780504 | 49780595 | MACS2_peak_2845 | 12 | + | 4.14966 | 5.12722 | 1.204 | 14 | chr9 | unknown | gene | 50232522 | 50233182 | - | 2310003N18Rik | 2310003N18Rik | | NR_131161 | TSS3460 |
| chr9 | 50032848 | 50032939 | MACS2_peak_2846 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 56 | chr9 | unknown | gene | 49502145 | 49798729 | - | Ncam1 | Ncam1 | P20559 | NM_001081445 | TSS6845 |
| chr9 | 50032848 | 50032939 | MACS2_peak_2846 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 56 | chr9 | unknown | gene | 50232522 | 50233182 | - | 2310003N18Rik | 2310003N18Rik | | NR_131161 | TSS3460 |
| chr9 | 50921592 | 50921683 | MACS2_peak_2847 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 62 | chr9 | unknown | gene | 50856923 | 50892748 | + | Ppp2r1b | Ppp2r1b | P5214 | NM_001286553 | TSS23317 |
| chr9 | 50921592 | 50921683 | MACS2_peak_2847 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 62 | chr9 | unknown | gene | 51056779 | 51076970 | - | Layn | Layn | P810 | NM_001033534 | TSS21610 |
| chr9 | 51944578 | 51944669 | MACS2_peak_2848 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 29 | chr9 | unknown | gene | 51914428 | 51927003 | + | 4933407I05Rik | 4933407I05Rik | | NR_040731 | TSS18526 |
| chr9 | 51944578 | 51944669 | MACS2_peak_2848 | 13 | + | 4.31251 | 5.44742 | 1.3392 | 29 | chr9 | unknown | gene | 52002060 | 52048705 | - | Gm6981 | Gm6981 | | NR_023357 | TSS12517 |
| chr9 | 51988895 | 51988986 | MACS2_peak_2849 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 43 | chr9 | unknown | gene | 51943024 | 51963467 | - | Fdx1 | Fdx1 | P15172 | NM_007996 | TSS17112 |
| chr9 | 51988895 | 51988986 | MACS2_peak_2849 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 43 | chr9 | unknown | gene | 52002060 | 52048705 | - | Gm6981 | Gm6981 | | NR_023357 | TSS12517 |
| chr9 | 52186021 | 52186183 | MACS2_peak_2850 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 89 | chr9 | unknown | gene | 52111984 | 52168111 | - | Zc3h12c | Zc3h12c | P5417 | NM_001162921 | TSS10566 |
| chr9 | 52186021 | 52186183 | MACS2_peak_2850 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 89 | chr9 | unknown | gene | 52673031 | 52679780 | - | AI593442 | AI593442 | P13196 | NM_001286641 | TSS12712 |
| chr9 | 52974207 | 52974298 | MACS2_peak_2851 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 38 | chr9 | unknown | gene | 52679862 | 52798772 | + | Gm1715 | Gm1715 | | NR_045333 | TSS7942 |
| chr9 | 52974207 | 52974298 | MACS2_peak_2851 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 38 | chr9 | unknown | gene | 53098453 | 53248003 | - | Ddx10 | Ddx10 | P6107 | NM_029936 | TSS11918 |
| chr9 | 53643539 | 53643630 | MACS2_peak_2852 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 42 | chr9 | unknown | gene | 53580521 | 53610275 | - | Acat1 | Acat1 | P1120 | NM_144784 | TSS22772 |
| chr9 | 53643539 | 53643630 | MACS2_peak_2852 | 23 | + | 5.20137 | 7.06174 | 2.31103 | 42 | chr9 | unknown | gene | 53684109 | 53706115 | - | Rab39 | Rab39 | P24563 | NM_175562 | TSS23242 |
| chr9 | 54167747 | 54167838 | MACS2_peak_2853 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 64 | chr9 | unknown | gene | 54025605 | 54068270 | - | Tnfaip8l3 | Tnfaip8l3 | P4610 | NM_001033535 | TSS16109 |
| chr9 | 54167747 | 54167838 | MACS2_peak_2853 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 64 | chr9 | unknown | gene | 54268579 | 54301570 | - | Gldnos | Gldnos | | NR_045805 | TSS13950 |
| chr9 | 61442772 | 61442863 | MACS2_peak_2854 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 22 | chr9 | unknown | gene | 61372365 | 61416716 | + | Tle3 | Tle3 | P10606 | NM_009389 | TSS15495 |
| chr9 | 61442772 | 61442863 | MACS2_peak_2854 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 22 | chr9 | unknown | gene | 61913282 | 61914428 | - | Rplp1 | Rplp1 | P26601 | NM_018853 | TSS2675 |
| chr9 | 62227846 | 62227941 | MACS2_peak_2855 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 32 | chr9 | unknown | gene | 62122517 | 62122594 | - | Mir5133 | Mir5133 | | NR_039595 | TSS16935 |
| chr9 | 62227846 | 62227941 | MACS2_peak_2855 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 32 | chr9 | unknown | gene | 62242595 | 62244100 | - | A730043L09Rik | A730043L09Rik | | NR_040769 | TSS17868 |
| chr9 | 64233192 | 64233283 | MACS2_peak_2856 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 36 | chr9 | unknown | gene | 64179296 | 64182270 | + | Snapc5 | Snapc5 | P21192 | NM_183316 | TSS14856 |
| chr9 | 64233192 | 64233283 | MACS2_peak_2856 | 7 | + | 3.61742 | 4.30541 | 0.75855 | 36 | chr9 | unknown | gene | 64235200 | 64235940 | + | Uchl4 | Uchl4 | P13135 | NM_033607 | TSS18281 |
| chr9 | 65201524 | 65201615 | MACS2_peak_2857 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 22 | chr9 | unknown | gene | 65141188 | 65185334 | + | Igdcc3 | Igdcc3 | P14876 | NM_008988 | TSS9202 |
| chr9 | 65201524 | 65201615 | MACS2_peak_2857 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 22 | chr9 | unknown | gene | 65214689 | 65237989 | + | Parp16 | Parp16 | P22153 | NM_177460 | TSS6210 |
| chr9 | 65296556 | 65296647 | MACS2_peak_2858 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 65 | chr9 | unknown | gene | 65265179 | 65280377 | + | Cilp | Cilp | P9228 | NM_173385 | TSS8841 |
| chr9 | 65296556 | 65296647 | MACS2_peak_2858 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 65 | chr9 | unknown | gene | 65346067 | 65358717 | + | Pdcd7 | Pdcd7 | P5828 | NM_016688 | TSS16793 |
| chr9 | 65386484 | 65386575 | MACS2_peak_2859 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 58 | chr9 | unknown | gene | 65361059 | 65380294 | + | Ubap1l | Ubap1l | P25375 | NM_001111145 | TSS17042 |
| chr9 | 65386484 | 65386575 | MACS2_peak_2859 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 58 | chr9 | unknown | gene | 65388683 | 65391652 | - | Kbtbd13 | Kbtbd13 | P6730 | NM_028974 | TSS6103 |
| chr9 | 67041976 | 67042067 | MACS2_peak_2860 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 14 | chr9 | unknown | gene | 66955392 | 66975391 | - | Lactb | Lactb | P3654 | NM_030717 | TSS9544 |
| chr9 | 67041976 | 67042067 | MACS2_peak_2860 | 20 | + | 5.03127 | 6.70315 | 2.03091 | 14 | chr9 | unknown | gene | 67133560 | 67163788 | + | Gm19299 | Gm19299 | | NR_045748 | TSS907 |
| chr9 | 67491764 | 67491855 | MACS2_peak_2861 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 54 | chr9 | unknown | gene | 67236659 | 67236726 | - | Mir190a | Mir190a | | NR_029576 | TSS14932 |
| chr9 | 67491764 | 67491855 | MACS2_peak_2861 | 13 | + | 4.22952 | 5.28177 | 1.31871 | 54 | chr9 | unknown | gene | 67727716 | 67727780 | - | Mir7241 | Mir7241 | | NR_106100 | TSS5435 |
| chr9 | 67608479 | 67608570 | MACS2_peak_2862 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 79 | chr9 | unknown | gene | 67217084 | 67559703 | - | Tln2 | Tln2 | P13227 | NM_001081242 | TSS3985 |
| chr9 | 67608479 | 67608570 | MACS2_peak_2862 | 21 | + | 5.13196 | 6.91269 | 2.19729 | 79 | chr9 | unknown | gene | 67727716 | 67727780 | - | Mir7241 | Mir7241 | | NR_106100 | TSS5435 |
| chr9 | 69319593 | 69319684 | MACS2_peak_2863 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 19 | chr9 | unknown | gene | 68765345 | 68773322 | + | 9530091C08Rik | 9530091C08Rik | | NR_033299 | TSS7274 |
| chr9 | 69319593 | 69319684 | MACS2_peak_2863 | 7 | + | 3.57041 | 4.21091 | 0.75855 | 19 | chr9 | unknown | gene | 69397997 | 69432169 | + | Ice2 | Ice2 | P7436 | NM_145618 | TSS9494 |
| chr9 | 71556236 | 71556327 | MACS2_peak_2864 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 31 | chr9 | unknown | gene | 71478436 | 71485796 | - | Polr2m | Polr2m | P26258 | NM_001164793 | TSS24909 |
| chr9 | 71556236 | 71556327 | MACS2_peak_2864 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 31 | chr9 | unknown | gene | 71626506 | 71771602 | - | Cgnl1 | Cgnl1 | P12330 | NM_026599 | TSS16137 |
| chr9 | 72107536 | 72107627 | MACS2_peak_2865 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 3 | chr9 | unknown | gene | 71963440 | 71963460 | + | Mir378a | Mir378a | | NR_029879 | TSS20606 |
| chr9 | 72107536 | 72107627 | MACS2_peak_2865 | 7 | + | 3.45805 | 3.99349 | 0.75855 | 3 | chr9 | unknown | gene | 72274898 | 72362507 | + | Zfp280d | Zfp280d | P12351 | NM_146224 | TSS7837 |
| chr9 | 72552799 | 72552890 | MACS2_peak_2866 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 33 | chr9 | unknown | gene | 72518249 | 72531858 | - | 4930509E16Rik | 4930509E16Rik | | NR_045735 | TSS7316 |
| chr9 | 72552799 | 72552890 | MACS2_peak_2866 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 33 | chr9 | unknown | gene | 72662346 | 72747228 | + | Nedd4 | Nedd4 | P4723 | NM_010890 | TSS22345 |
| chr9 | 75050088 | 75050223 | MACS2_peak_2867 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 68 | chr9 | unknown | gene | 74953052 | 75031668 | + | Fam214a | Fam214a | P10735 | NM_001113283 | TSS11905 |
| chr9 | 75050088 | 75050223 | MACS2_peak_2867 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 68 | chr9 | unknown | gene | 75071205 | 75217993 | + | Myo5a | Myo5a | P11842 | NM_010864 | TSS20555 |
| chr9 | 76376030 | 76376195 | MACS2_peak_2868 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 136 | chr9 | unknown | gene | 76225879 | 76323504 | - | Hcrtr2 | Hcrtr2 | P9378 | NM_198962 | TSS25978 |
| chr9 | 76376030 | 76376195 | MACS2_peak_2868 | 18 | + | 4.93444 | 6.50843 | 1.87805 | 136 | chr9 | unknown | gene | 76490704 | 76545783 | - | Fam83b | Fam83b | P3387 | NM_001045518 | TSS23694 |
| chr9 | 76576796 | 76576887 | MACS2_peak_2869 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 65 | chr9 | unknown | gene | 76490704 | 76545783 | - | Fam83b | Fam83b | P3387 | NM_001045518 | TSS23694 |
| chr9 | 76576796 | 76576887 | MACS2_peak_2869 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 65 | chr9 | unknown | gene | 76951697 | 77045700 | - | Tinag | Tinag | P8013 | NM_012033 | TSS19237 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr9 | 76726014 | 76726105 | MACS2_peak_2870 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 67 | chr9 | unknown | gene | 76490704 | 76545783 | - | Fam83b | Fam83b | P3387 | NM_001045518 | TSS23694 |
| chr9 | 76726014 | 76726105 | MACS2_peak_2870 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 67 | chr9 | unknown | gene | 76951697 | 77045700 | - | Tinag | Tinag | P8013 | NM_012033 | TSS19237 |
| chr9 | 81304155 | 81304246 | MACS2_peak_2871 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 47 | chr9 | unknown | gene | 80313329 | 80465289 | - | Impg1 | Impg1 | P6210 | NM_022016 | TSS11109 |
| chr9 | 81304155 | 81304246 | MACS2_peak_2871 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 47 | chr9 | unknown | gene | 81631391 | 81632552 | - | Htr1b | Htr1b | P21366 | NM_010482 | TSS22749 |
| chr9 | 81480884 | 81480975 | MACS2_peak_2872 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 4 | chr9 | unknown | gene | 80313329 | 80465289 | - | Impg1 | Impg1 | P6210 | NM_022016 | TSS11109 |
| chr9 | 81480884 | 81480975 | MACS2_peak_2872 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 4 | chr9 | unknown | gene | 81631391 | 81632552 | - | Htr1b | Htr1b | P21366 | NM_010482 | TSS22749 |
| chr9 | 81497959 | 81498097 | MACS2_peak_2873 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 74 | chr9 | unknown | gene | 80313329 | 80465289 | - | Impg1 | Impg1 | P6210 | NM_022016 | TSS11109 |
| chr9 | 81497959 | 81498097 | MACS2_peak_2873 | 7 | + | 3.43643 | 3.95288 | 0.75855 | 74 | chr9 | unknown | gene | 81631391 | 81632552 | - | Htr1b | Htr1b | P21366 | NM_010482 | TSS22749 |
| chr9 | 81505316 | 81505459 | MACS2_peak_2874 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 27 | chr9 | unknown | gene | 80313329 | 80465289 | - | Impg1 | Impg1 | P6210 | NM_022016 | TSS11109 |
| chr9 | 81505316 | 81505459 | MACS2_peak_2874 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 27 | chr9 | unknown | gene | 81631391 | 81632552 | - | Htr1b | Htr1b | P21366 | NM_010482 | TSS22749 |
| chr9 | 81712471 | 81712562 | MACS2_peak_2875 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 44 | chr9 | unknown | gene | 81631929 | 81645156 | + | D430036J16Rik | D430036J16Rik | | NR_040393 | TSS18954 |
| chr9 | 81712471 | 81712562 | MACS2_peak_2875 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 44 | chr9 | unknown | gene | 81863743 | 82025788 | + | Mei4 | Mei4 | P15132 | NM_175213 | TSS21216 |
| chr9 | 81762528 | 81762619 | MACS2_peak_2876 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 43 | chr9 | unknown | gene | 81631929 | 81645156 | + | D430036J16Rik | D430036J16Rik | | NR_040393 | TSS18954 |
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| chr9 | 83080673 | 83080764 | MACS2_peak_2877 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 46 | chr9 | unknown | gene | 82866158 | 82975291 | - | Phip | Phip | P19829 | NM_001081216 | TSS27096 |
| chr9 | 83080673 | 83080764 | MACS2_peak_2877 | 34 | + | 5.94442 | 8.42815 | 3.44877 | 46 | chr9 | unknown | gene | 83109941 | 83146445 | - | Hmgn3 | Hmgn3 | P11531 | NM_026122 | TSS23644 |
| chr9 | 84071121 | 84071254 | MACS2_peak_2878 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 66 | chr9 | unknown | gene | 83834688 | 83872068 | + | Ttk | Ttk | P26190 | NM_009445 | TSS18877 |
| chr9 | 84071121 | 84071254 | MACS2_peak_2878 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 66 | chr9 | unknown | gene | 84774397 | 84784351 | + | 4930554C24Rik | 4930554C24Rik | | NR_040739 | TSS22802 |
| chr9 | 84513261 | 84513370 | MACS2_peak_2879 | 24 | + | 5.39702 | 7.32466 | 2.43395 | 55 | chr9 | unknown | gene | 83925136 | 84124240 | + | Bckdhb | Bckdhb | P3075 | NM_001305935 | TSS25219 |
| chr9 | 84513261 | 84513370 | MACS2_peak_2879 | 24 | + | 5.39702 | 7.32466 | 2.43395 | 55 | chr9 | unknown | gene | 84774397 | 84784351 | + | 4930554C24Rik | 4930554C24Rik | | NR_040739 | TSS22802 |
| chr9 | 84533072 | 84533163 | MACS2_peak_2880 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 5 | chr9 | unknown | gene | 83925136 | 84124240 | + | Bckdhb | Bckdhb | P3075 | NM_001305935 | TSS25219 |
| chr9 | 84533072 | 84533163 | MACS2_peak_2880 | 10 | + | 4.07277 | 4.98245 | 1.08567 | 5 | chr9 | unknown | gene | 84774397 | 84784351 | + | 4930554C24Rik | 4930554C24Rik | | NR_040739 | TSS22802 |
| chr9 | 84904646 | 84904737 | MACS2_peak_2881 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 61 | chr9 | unknown | gene | 84774397 | 84784351 | + | 4930554C24Rik | 4930554C24Rik | | NR_040739 | TSS22802 |
| chr9 | 84904646 | 84904737 | MACS2_peak_2881 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 61 | chr9 | unknown | gene | 85320438 | 85327150 | - | Fam46a | Fam46a | P6298 | NM_001160378 | TSS17355 |
| chr9 | 85332338 | 85332452 | MACS2_peak_2882 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 66 | chr9 | unknown | gene | 85320438 | 85327150 | - | Fam46a | Fam46a | P6298 | NM_001160378 | TSS17355 |
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| chr9 | 85804164 | 85804255 | MACS2_peak_2883 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 54 | chr9 | unknown | gene | 85687359 | 85749334 | - | Ibtk | Ibtk | P9349 | NM_001081282 | TSS9945 |
| chr9 | 85804164 | 85804255 | MACS2_peak_2883 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 54 | chr9 | unknown | gene | 85842379 | 85845260 | + | Tpbg | Tpbg | P23214 | NM_011627 | TSS21133 |
| chr9 | 86796514 | 86796605 | MACS2_peak_2884 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 71 | chr9 | unknown | gene | 86743632 | 86756408 | + | Prss35 | Prss35 | P23811 | NM_178738 | TSS22000 |
| chr9 | 86796514 | 86796605 | MACS2_peak_2884 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 71 | chr9 | unknown | gene | 87015536 | 87019809 | + | Ripply2 | Ripply2 | P13275 | NM_001037907 | TSS3042 |
| chr9 | 86847804 | 86847895 | MACS2_peak_2885 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 66 | chr9 | unknown | gene | 86743632 | 86756408 | + | Prss35 | Prss35 | P23811 | NM_178738 | TSS22000 |
| chr9 | 86847804 | 86847895 | MACS2_peak_2885 | 13 | + | 4.42837 | 5.68838 | 1.3392 | 66 | chr9 | unknown | gene | 87015536 | 87019809 | + | Ripply2 | Ripply2 | P13275 | NM_001037907 | TSS3042 |
| chr9 | 87241159 | 87241250 | MACS2_peak_2886 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 13 | chr9 | unknown | gene | 87144305 | 87182831 | + | Mrap2 | Mrap2 | P14198 | NM_001101482 | TSS7364 |
| chr9 | 87241159 | 87241250 | MACS2_peak_2886 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 13 | chr9 | unknown | gene | 87702799 | 87730844 | - | Tbx18 | Tbx18 | P9012 | NM_023814 | TSS12342 |
| chr9 | 87732123 | 87732214 | MACS2_peak_2887 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 27 | chr9 | unknown | gene | 87702799 | 87730844 | - | Tbx18 | Tbx18 | P9012 | NM_023814 | TSS12342 |
| chr9 | 87732123 | 87732214 | MACS2_peak_2887 | 7 | + | 3.5246 | 4.12091 | 0.75855 | 27 | chr9 | unknown | gene | 88327608 | 88370317 | + | Nt5e | Nt5e | P13339 | NM_011851 | TSS16334 |
| chr9 | 87902730 | 87902821 | MACS2_peak_2888 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 11 | chr9 | unknown | gene | 87702799 | 87730844 | - | Tbx18 | Tbx18 | P9012 | NM_023814 | TSS12342 |
| chr9 | 87902730 | 87902821 | MACS2_peak_2888 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 11 | chr9 | unknown | gene | 88327608 | 88370317 | + | Nt5e | Nt5e | P13339 | NM_011851 | TSS16334 |
| chr9 | 88553209 | 88553300 | MACS2_peak_2889 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 64 | chr9 | unknown | gene | 88521052 | 88522897 | - | Snhg5 | Snhg5 | | NR_040721 | TSS25245 |
| chr9 | 88553209 | 88553300 | MACS2_peak_2889 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 64 | chr9 | unknown | gene | 88581035 | 88588480 | + | Trim43a | Trim43a | P8554 | NM_001034906 | TSS11371 |
| chr9 | 89428732 | 89428823 | MACS2_peak_2890 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 42 | chr9 | unknown | gene | 89211189 | 89240074 | + | Mthfs | Mthfs | P17709 | NM_026829 | TSS9584 |
| chr9 | 89428732 | 89428823 | MACS2_peak_2890 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 42 | chr9 | unknown | gene | 89590034 | 89622986 | - | AF529169 | AF529169 | P6624 | NM_153509 | TSS13696 |
| chr9 | 89542304 | 89542407 | MACS2_peak_2891 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 45 | chr9 | unknown | gene | 89211189 | 89240074 | + | Mthfs | Mthfs | P17709 | NM_026829 | TSS9584 |
| chr9 | 89542304 | 89542407 | MACS2_peak_2891 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 45 | chr9 | unknown | gene | 89590034 | 89622986 | - | AF529169 | AF529169 | P6624 | NM_153509 | TSS13696 |
| chr9 | 91045893 | 91045984 | MACS2_peak_2892 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 53 | chr9 | unknown | gene | 90202048 | 90270711 | - | Tbc1d2b | Tbc1d2b | P17461 | NM_194334 | TSS21605 |
| chr9 | 91045893 | 91045984 | MACS2_peak_2892 | 16 | + | 4.78109 | 6.21193 | 1.62927 | 53 | chr9 | unknown | gene | 91360344 | 91365017 | - | Zic1 | Zic1 | P15496 | NM_009573 | TSS5903 |
| chr9 | 91305813 | 91305904 | MACS2_peak_2893 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 41 | chr9 | unknown | gene | 90202048 | 90270711 | - | Tbc1d2b | Tbc1d2b | P17461 | NM_194334 | TSS21605 |
| chr9 | 91305813 | 91305904 | MACS2_peak_2893 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 41 | chr9 | unknown | gene | 91360344 | 91365017 | - | Zic1 | Zic1 | P15496 | NM_009573 | TSS5903 |
| chr9 | 91450837 | 91450993 | MACS2_peak_2894 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 16 | chr9 | unknown | gene | 91368971 | 91386535 | + | Zic4 | Zic4 | P4515 | NM_009576 | TSS4686 |
| chr9 | 91450837 | 91450993 | MACS2_peak_2894 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 16 | chr9 | unknown | gene | 92192935 | 92209698 | + | Plscr5 | Plscr5 | P426 | NM_001195693 | TSS8595 |
| chr9 | 92167701 | 92167797 | MACS2_peak_2895 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 25 | chr9 | unknown | gene | 91368971 | 91386535 | + | Zic4 | Zic4 | P4515 | NM_009576 | TSS4686 |
| chr9 | 92167701 | 92167797 | MACS2_peak_2895 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 25 | chr9 | unknown | gene | 92192935 | 92209698 | + | Plscr5 | Plscr5 | P426 | NM_001195693 | TSS8595 |
| chr9 | 92356629 | 92356813 | MACS2_peak_2896 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 69 | chr9 | unknown | gene | 92275601 | 92297201 | + | Plscr2 | Plscr2 | P10483 | NM_008880 | TSS23656 |
| chr9 | 92356629 | 92356813 | MACS2_peak_2896 | 9 | + | 3.99867 | 4.84636 | 0.96877 | 69 | chr9 | unknown | gene | 92457377 | 92490807 | + | Plscr4 | Plscr4 | P11090 | NM_178711 | TSS22178 |
| chr9 | 92457163 | 92457292 | MACS2_peak_2897 | 27 | + | 5.56793 | 7.65146 | 2.73702 | 39 | chr9 | unknown | gene | 92309376 | 92357755 | + | 1700057G04Rik | 1700057G04Rik | P21721 | NM_001033184 | TSS2364 |
| chr9 | 92457163 | 92457292 | MACS2_peak_2897 | 27 | + | 5.56793 | 7.65146 | 2.73702 | 39 | chr9 | unknown | gene | 92457377 | 92490807 | + | Plscr4 | Plscr4 | P11090 | NM_178711 | TSS22178 |
| chr9 | 92483049 | 92483140 | MACS2_peak_2898 | 35 | + | 5.98489 | 8.51731 | 3.53253 | 30 | chr9 | unknown | gene | 92309376 | 92357755 | + | 1700057G04Rik | 1700057G04Rik | P21721 | NM_001033184 | TSS2364 |
| chr9 | 92483049 | 92483140 | MACS2_peak_2898 | 35 | + | 5.98489 | 8.51731 | 3.53253 | 30 | chr9 | unknown | gene | 92538800 | 92542869 | - | B430319G15Rik | B430319G15Rik | | NR_029474 | TSS17948 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr9 | 92639059 | 92639189 | MACS2_peak_2899 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 71 | chr9 | unknown | gene | 92542222 | 92607230 | + | Plod2 | Plod2 | P588 | NM_011961 | TSS26207 |
| chr9 | 92639059 | 92639189 | MACS2_peak_2899 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 71 | chr9 | unknown | gene | 92718715 | 92795711 | + | 4933400C23Rik | 4933400C23Rik | | NR_040770 | TSS19608 |
| chr9 | 92776537 | 92776628 | MACS2_peak_2900 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 40 | chr9 | unknown | gene | 92542222 | 92607230 | + | Plod2 | Plod2 | P588 | NM_011961 | TSS26207 |
| chr9 | 92776537 | 92776628 | MACS2_peak_2900 | 19 | + | 4.99857 | 6.6367 | 1.97891 | 40 | chr9 | unknown | gene | 92979915 | 93005733 | - | 1700034K08Rik | 1700034K08Rik | | NR_040756 | TSS20407 |
| chr9 | 94556898 | 94556989 | MACS2_peak_2901 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 20 | chr9 | unknown | gene | 94517863 | 94537875 | - | 1190002N15Rik | 1190002N15Rik | P6722 | NM_001033145 | TSS13313 |
| chr9 | 94556898 | 94556989 | MACS2_peak_2901 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 20 | chr9 | unknown | gene | 94669891 | 95229065 | + | Slc9a9 | Slc9a9 | P20972 | NM_177909 | TSS9174 |
| chr9 | 96718220 | 96718311 | MACS2_peak_2902 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 35 | chr9 | unknown | gene | 96539299 | 96631493 | - | Rasa2 | Rasa2 | P20158 | NM_053268 | TSS13891 |
| chr9 | 96718220 | 96718311 | MACS2_peak_2902 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 35 | chr9 | unknown | gene | 96731574 | 96752831 | - | E030011O05Rik | E030011O05Rik | | NR_015511 | TSS9312 |
| chr9 | 97162981 | 97163072 | MACS2_peak_2903 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 65 | chr9 | unknown | gene | 97077010 | 97110951 | - | Slc25a36 | Slc25a36 | P4275 | NM_138756 | TSS17074 |
| chr9 | 97162981 | 97163072 | MACS2_peak_2903 | 13 | + | 4.39883 | 5.62577 | 1.3392 | 65 | chr9 | unknown | gene | 97349561 | 97369844 | - | Trim42 | Trim42 | P19438 | NM_030219 | TSS9951 |
| chr9 | 97344957 | 97345048 | MACS2_peak_2904 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 52 | chr9 | unknown | gene | 97077010 | 97110951 | - | Slc25a36 | Slc25a36 | P4275 | NM_138756 | TSS17074 |
| chr9 | 97344957 | 97345048 | MACS2_peak_2904 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 52 | chr9 | unknown | gene | 97349561 | 97369844 | - | Trim42 | Trim42 | P19438 | NM_030219 | TSS9951 |
| chr9 | 97926045 | 97926136 | MACS2_peak_2905 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 47 | chr9 | unknown | gene | 97349561 | 97369844 | - | Trim42 | Trim42 | P19438 | NM_030219 | TSS9951 |
| chr9 | 97926045 | 97926136 | MACS2_peak_2905 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 47 | chr9 | unknown | gene | 98003419 | 98012175 | + | 4921534H16Rik | 4921534H16Rik | | NR_110443 | TSS12016 |
| chr9 | 98892134 | 98892355 | MACS2_peak_2906 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 65 | chr9 | unknown | gene | 98864766 | 98865759 | + | Prr23a3 | Prr23a3 | P3333 | NM_028033 | TSS15400 |
| chr9 | 98892134 | 98892355 | MACS2_peak_2906 | 7 | + | 3.37314 | 3.83612 | 0.75855 | 65 | chr9 | unknown | gene | 98903118 | 98903844 | + | 7420426K07Rik | 7420426K07Rik | P9320 | NM_001033983 | TSS25292 |
| chr9 | 98905559 | 98905650 | MACS2_peak_2907 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 34 | chr9 | unknown | gene | 98903118 | 98903844 | + | 7420426K07Rik | 7420426K07Rik | P9320 | NM_001033983 | TSS25292 |
| chr9 | 98905559 | 98905650 | MACS2_peak_2907 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 34 | chr9 | unknown | gene | 98949154 | 98955310 | - | Foxl2os | Foxl2os | | NR_003248 | TSS5682 |
| chr9 | 99263241 | 99263332 | MACS2_peak_2908 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 53 | chr9 | unknown | gene | 99229375 | 99237239 | - | Faiml | Faiml | P20818 | NM_001244762 | TSS14716 |
| chr9 | 99263241 | 99263332 | MACS2_peak_2908 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 53 | chr9 | unknown | gene | 99309966 | 99358389 | - | Esyt3 | Esyt3 | P5701 | NM_177775 | TSS2624 |
| chr9 | 99527671 | 99527762 | MACS2_peak_2909 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 18 | chr9 | unknown | gene | 99456242 | 99479899 | + | Nme9 | Nme9 | P26826 | NM_001165957 | TSS14012 |
| chr9 | 99527671 | 99527762 | MACS2_peak_2909 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 18 | chr9 | unknown | gene | 99575798 | 99584023 | + | Dbr1 | Dbr1 | P21960 | NM_031403 | TSS11546 |
| chr9 | 100972654 | 100972752 | MACS2_peak_2910 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 50 | chr9 | unknown | gene | 100643622 | 100956558 | + | Stag1 | Stag1 | P21933 | NM_009282 | TSS316 |
| chr9 | 100972654 | 100972752 | MACS2_peak_2910 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 50 | chr9 | unknown | gene | 100982037 | 101034857 | - | Pccb | Pccb | P8072 | NM_025835 | TSS18805 |
| chr9 | 101265683 | 101265796 | MACS2_peak_2911 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 41 | chr9 | unknown | gene | 101104988 | 101251832 | - | Ppp2r3a | Ppp2r3a | P22302 | NM_001161362 | TSS4103 |
| chr9 | 101265683 | 101265796 | MACS2_peak_2911 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 41 | chr9 | unknown | gene | 101342193 | 101348017 | + | Gm28979 | Gm28979 | | NR_110509 | TSS20311 |
| chr9 | 103348534 | 103348625 | MACS2_peak_2912 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 24 | chr9 | unknown | gene | 103250529 | 103288223 | - | 1300017J02Rik | 1300017J02Rik | P24692 | NM_027918 | TSS26385 |
| chr9 | 103348534 | 103348625 | MACS2_peak_2912 | 13 | + | 4.34091 | 5.50537 | 1.3392 | 24 | chr9 | unknown | gene | 103353101 | 103365368 | - | Cdv3 | Cdv3 | P4403 | NM_175833 | TSS18938 |
| chr9 | 109325741 | 109325832 | MACS2_peak_2913 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 18 | chr9 | unknown | gene | 109271124 | 109287639 | - | Fbxw14 | Fbxw14 | P388 | NM_015793 | TSS5501 |
| chr9 | 109325741 | 109325832 | MACS2_peak_2913 | 7 | + | 3.71526 | 4.50968 | 0.75855 | 18 | chr9 | unknown | gene | 109378408 | 109404263 | - | Fbxw22 | Fbxw22 | P19251 | NM_001014395 | TSS6586 |
| chr9 | 110451792 | 110451912 | MACS2_peak_2914 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 55 | chr9 | unknown | gene | 110419807 | 110422409 | + | Ngp | Ngp | P8711 | NM_008694 | TSS24204 |
| chr9 | 110451792 | 110451912 | MACS2_peak_2914 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 55 | chr9 | unknown | gene | 110476957 | 110524934 | + | Kif9 | Kif9 | P8121 | NM_010628 | TSS11988 |
| chr9 | 113929022 | 113929113 | MACS2_peak_2915 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 30 | chr9 | unknown | gene | 113741472 | 113918081 | + | Clasp2 | Clasp2 | P14694 | NM_001286599 | TSS13375 |
| chr9 | 113929022 | 113929113 | MACS2_peak_2915 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 30 | chr9 | unknown | gene | 113930933 | 113975383 | + | Ubp1 | Ubp1 | P23503 | NM_013699 | TSS13655 |
| chr9 | 115330865 | 115331054 | MACS2_peak_2916 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 182 | chr9 | unknown | gene | 115242581 | 115310056 | - | Stt3b | Stt3b | P18236 | NM_024222 | TSS23778 |
| chr9 | 115330865 | 115331054 | MACS2_peak_2916 | 14 | + | 4.69358 | 6.04847 | 1.48693 | 182 | chr9 | unknown | gene | 115336160 | 115341924 | + | 4930428G15Rik | 4930428G15Rik | | NR_040730 | TSS5252 |
| chr9 | 115351193 | 115351284 | MACS2_peak_2917 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 14 | chr9 | unknown | gene | 115336160 | 115341924 | + | 4930428G15Rik | 4930428G15Rik | | NR_040730 | TSS5252 |
| chr9 | 115351193 | 115351284 | MACS2_peak_2917 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 14 | chr9 | unknown | gene | 115381818 | 115381939 | + | Mir467h | Mir467h | | NR_130329 | TSS18844 |
| chr9 | 115629486 | 115629594 | MACS2_peak_2918 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 25 | chr9 | unknown | gene | 115381818 | 115381939 | + | Mir467h | Mir467h | | NR_130329 | TSS18844 |
| chr9 | 115629486 | 115629594 | MACS2_peak_2918 | 20 | + | 5.06439 | 6.77124 | 2.08291 | 25 | chr9 | unknown | gene | 115909454 | 116074113 | + | Gadl1 | Gadl1 | P13745 | NM_028638 | TSS10416 |
| chr9 | 116772886 | 116772977 | MACS2_peak_2919 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 9 | chr9 | unknown | gene | 116087694 | 116175037 | - | Tgfbr2 | Tgfbr2 | P21782 | NM_029575 | TSS21038 |
| chr9 | 116772886 | 116772977 | MACS2_peak_2919 | 7 | + | 3.66569 | 4.40483 | 0.75855 | 9 | chr9 | unknown | gene | 118040521 | 118069104 | + | Azi2 | Azi2 | P14374 | NM_001286508 | TSS17231 |
| chr9 | 116997647 | 116997738 | MACS2_peak_2920 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 57 | chr9 | unknown | gene | 116087694 | 116175037 | - | Tgfbr2 | Tgfbr2 | P21782 | NM_029575 | TSS21038 |
| chr9 | 116997647 | 116997738 | MACS2_peak_2920 | 15 | + | 4.72239 | 6.10186 | 1.53456 | 57 | chr9 | unknown | gene | 118040521 | 118069104 | + | Azi2 | Azi2 | P14374 | NM_001286508 | TSS17231 |
| chr9 | 117393625 | 117393716 | MACS2_peak_2921 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 44 | chr9 | unknown | gene | 116087694 | 116175037 | - | Tgfbr2 | Tgfbr2 | P21782 | NM_029575 | TSS21038 |
| chr9 | 117393625 | 117393716 | MACS2_peak_2921 | 21 | + | 5.09795 | 6.84106 | 2.13796 | 44 | chr9 | unknown | gene | 118040521 | 118069104 | + | Azi2 | Azi2 | P14374 | NM_001286508 | TSS17231 |
| chr9 | 121331250 | 121331341 | MACS2_peak_2922 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 0 | chr9 | unknown | gene | 120964453 | 121277172 | - | Ulk4 | Ulk4 | P20464 | NM_177589 | TSS17138 |
| chr9 | 121331250 | 121331341 | MACS2_peak_2922 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 0 | chr9 | unknown | gene | 121366957 | 121472999 | + | Trak1 | Trak1 | P3924 | NM_175114 | TSS17907 |
| chr9 | 123217567 | 123217658 | MACS2_peak_2923 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 48 | chr9 | unknown | gene | 123172284 | 123215909 | - | Cdcp1 | Cdcp1 | P6056 | NM_133974 | TSS7480 |
| chr9 | 123217567 | 123217658 | MACS2_peak_2923 | 22 | + | 5.16643 | 6.98622 | 2.25118 | 48 | chr9 | unknown | gene | 123259056 | 123260545 | - | Tmem158 | Tmem158 | P5438 | NM_001002267 | TSS3516 |
| chr9 | 123872963 | 123873074 | MACS2_peak_2924 | 49 | + | 6.77503 | 10.04021 | 4.94691 | 64 | chr9 | unknown | gene | 123852314 | 123861957 | - | Xcr1 | Xcr1 | P3003 | NM_011798 | TSS4977 |
| chr9 | 123872963 | 123873074 | MACS2_peak_2924 | 49 | + | 6.77503 | 10.04021 | 4.94691 | 64 | chr9 | unknown | gene | 123962125 | 123968692 | - | Ccr1 | Ccr1 | P7227 | NM_009912 | TSS15808 |
| chr9 | 123924491 | 123924601 | MACS2_peak_2925 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 46 | chr9 | unknown | gene | 123852314 | 123861957 | - | Xcr1 | Xcr1 | P3003 | NM_011798 | TSS4977 |
| chr9 | 123924491 | 123924601 | MACS2_peak_2925 | 23 | + | 5.23678 | 7.13937 | 2.32792 | 46 | chr9 | unknown | gene | 123962125 | 123968692 | - | Ccr1 | Ccr1 | P7227 | NM_009912 | TSS15808 |
| chr9 | 124130130 | 124130221 | MACS2_peak_2926 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 81 | chr9 | unknown | gene | 124121542 | 124125426 | + | Ccr5 | Ccr5 | P389 | NM_009917 | TSS22364 |
| chr9 | 124130130 | 124130221 | MACS2_peak_2926 | 19 | + | 4.9663 | 6.57181 | 1.9281 | 81 | chr9 | unknown | gene | 124291803 | 124312562 | - | 2010315B03Rik | 2010315B03Rik | P1671 | NM_001243117 | TSS8718 |
| chr9 | 124256353 | 124256610 | MACS2_peak_2927 | 100 | + | 8.15941 | 15.28786 | 10.00078 | 48 | chr9 | unknown | gene | 124121542 | 124125426 | + | Ccr5 | Ccr5 | P389 | NM_009917 | TSS22364 |
| chr9 | 124256353 | 124256610 | MACS2_peak_2927 | 100 | + | 8.15941 | 15.28786 | 10.00078 | 48 | chr9 | unknown | gene | 124291803 | 124312562 | - | 2010315B03Rik | 2010315B03Rik | P1671 | NM_001243117 | TSS8718 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chr9 | 124256692 | 124256848 | MACS2_peak_2928 | 46 | + | 5.96557 | 9.67447 | 4.60799 | 44 | chr9 | unknown | gene | 124121542 | 124125426 | + | Ccr5 | Ccr5 | P389 | NM_009917 | TSS22364 |
| chr9 | 124256692 | 124256848 | MACS2_peak_2928 | 46 | + | 5.96557 | 9.67447 | 4.60799 | 44 | chr9 | unknown | gene | 124291803 | 124312562 | - | 2010315B03Rik | 2010315B03Rik | P1671 | NM_001243117 | TSS8718 |
| chr9 | 124257308 | 124257835 | MACS2_peak_2929 | 86 | + | 7.61099 | 13.93451 | 8.69458 | 460 | chr9 | unknown | gene | 124121542 | 124125426 | + | Ccr5 | Ccr5 | P389 | NM_009917 | TSS22364 |
| chr9 | 124257308 | 124257835 | MACS2_peak_2929 | 86 | + | 7.61099 | 13.93451 | 8.69458 | 460 | chr9 | unknown | gene | 124291803 | 124312562 | - | 2010315B03Rik | 2010315B03Rik | P1671 | NM_001243117 | TSS8718 |
| chrUn_JH584304 | 68547 | 68674 | MACS2_peak_2967 | 501 | + | 8.09175 | 56.26402 | 50.18539 | 72 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 69124 | 69234 | MACS2_peak_2968 | 243 | + | 5.53506 | 30.03604 | 24.36035 | 44 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 69572 | 69726 | MACS2_peak_2969 | 102 | + | 3.83724 | 15.578 | 10.28129 | 101 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 70297 | 70430 | MACS2_peak_2970 | 464 | + | 7.11518 | 52.48341 | 46.44745 | 71 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 70988 | 71103 | MACS2_peak_2971 | 186 | + | 4.4937 | 24.21843 | 18.67113 | 64 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 72172 | 72297 | MACS2_peak_2972 | 432 | + | 6.22277 | 49.21744 | 43.22583 | 55 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 73115 | 73231 | MACS2_peak_2973 | 224 | + | 4.36847 | 28.12172 | 22.488 | 64 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 73352 | 73451 | MACS2_peak_2974 | 185 | + | 3.99807 | 24.1205 | 18.57628 | 56 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 74143 | 74240 | MACS2_peak_2975 | 136 | + | 3.55485 | 19.0491 | 13.63917 | 42 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 74976 | 75092 | MACS2_peak_2976 | 381 | + | 5.38753 | 44.09101 | 38.18373 | 53 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 76508 | 76622 | MACS2_peak_2977 | 306 | + | 4.90109 | 36.47771 | 30.67989 | 67 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 77987 | 78190 | MACS2_peak_2978 | 105 | + | 3.21503 | 15.88414 | 10.57879 | 68 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 78581 | 78713 | MACS2_peak_2979 | 397 | + | 5.50228 | 45.72553 | 39.79296 | 69 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 81411 | 81656 | MACS2_peak_2980 | 441 | + | 5.52673 | 50.1791 | 44.17626 | 189 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 83879 | 84043 | MACS2_peak_2981 | 276 | + | 4.56895 | 33.34233 | 27.60182 | 59 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 85030 | 85146 | MACS2_peak_2982 | 214 | + | 4.18081 | 27.11063 | 21.49985 | 44 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 85502 | 85593 | MACS2_peak_2983 | 123 | + | 3.3882 | 17.69964 | 12.33476 | 46 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 85738 | 85853 | MACS2_peak_2984 | 292 | + | 4.6198 | 35.02794 | 29.25109 | 61 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 86945 | 87090 | MACS2_peak_2985 | 100 | + | 3.16631 | 15.35261 | 10.06181 | 55 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 87616 | 87810 | MACS2_peak_2986 | 120 | + | 3.34191 | 17.38638 | 12.03257 | 149 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chrUn_JH584304 | 90525 | 90778 | MACS2_peak_2987 | 433 | + | 5.62211 | 49.38551 | 43.39249 | 191 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 92994 | 93183 | MACS2_peak_2988 | 275 | + | 4.65193 | 33.30706 | 27.56769 | 58 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 94154 | 94251 | MACS2_peak_2989 | 148 | + | 3.58882 | 20.25015 | 14.80971 | 54 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 94860 | 94977 | MACS2_peak_2990 | 282 | + | 4.70195 | 34.00277 | 28.24666 | 57 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 96097 | 96214 | MACS2_peak_2991 | 132 | + | 3.4935 | 18.63915 | 13.24188 | 69 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 97807 | 97926 | MACS2_peak_2992 | 9 | + | 2.01274 | 4.81314 | 0.9403 | 30 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 98356 | 98468 | MACS2_peak_2993 | 270 | + | 4.66442 | 32.73954 | 27.00959 | 60 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 99160 | 99252 | MACS2_peak_2994 | 117 | + | 3.3272 | 17.06562 | 11.72327 | 44 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 99991 | 100107 | MACS2_peak_2995 | 337 | + | 5.079 | 39.55639 | 33.71387 | 60 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 100679 | 100781 | MACS2_peak_2996 | 130 | + | 3.46206 | 18.42743 | 13.03835 | 31 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 101756 | 101868 | MACS2_peak_2997 | 276 | + | 4.62407 | 33.42968 | 27.68636 | 53 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 103236 | 103441 | MACS2_peak_2998 | 110 | + | 3.29088 | 16.38597 | 11.064 | 49 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 103829 | 103965 | MACS2_peak_2999 | 408 | + | 5.54428 | 46.82134 | 40.86883 | 61 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 106653 | 106902 | MACS2_peak_3000 | 131 | + | 3.37783 | 18.53082 | 13.13869 | 39 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 109127 | 109296 | MACS2_peak_3001 | 252 | + | 4.41523 | 30.92746 | 25.23406 | 52 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 110278 | 110394 | MACS2_peak_3002 | 177 | + | 3.99525 | 23.26707 | 17.75097 | 49 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 110987 | 111103 | MACS2_peak_3003 | 250 | + | 4.71224 | 30.75009 | 25.06013 | 59 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 112188 | 112353 | MACS2_peak_3004 | 283 | + | 5.30935 | 34.14595 | 28.38784 | 88 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 112852 | 113072 | MACS2_peak_3005 | 159 | + | 4.32339 | 21.4279 | 15.95606 | 169 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 113293 | 113394 | MACS2_peak_3006 | 45 | + | 2.98201 | 9.58135 | 4.51945 | 40 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrUn_JH584304 | 114033 | 114222 | MACS2_peak_3007 | 35 | + | 3.00507 | 8.5349 | 3.54971 | 154 | chrUn_JH584304 | unknown | gene | 52673 | 59689 | - | Pisd-ps3 | Pisd-ps3 | | NR_003518 | TSS3421 |
| chrX | 11666000 | 11666111 | MACS2_peak_3008 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 48 | chrX | unknown | gene | 11327821 | 11328151 | + | Gm4906 | Gm4906 | P4312 | NM_001114529 | TSS16891 |
| chrX | 11666000 | 11666111 | MACS2_peak_3008 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 48 | chrX | unknown | gene | 12036737 | 12160355 | - | Bcor | Bcor | P12389 | NM_001168321 | TSS6796 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chrX | 13348942 | 13349099 | MACS2_peak_3009 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 56 | chrX | unknown | gene | 13281021 | 13291492 | + | Ddx3x | Ddx3x | P24035 | NM_010028 | TSS19615 |
| chrX | 13348942 | 13349099 | MACS2_peak_3009 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 56 | chrX | unknown | gene | 13467671 | 13487339 | + | Nyx | Nyx | P18415 | NM_173415 | TSS19989 |
| chrX | 16337707 | 16337798 | MACS2_peak_3010 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 63 | chrX | unknown | gene | 15110585 | 15111489 | - | Ppp1r2-ps9 | Ppp1r2-ps9 | | NR_033171 | TSS3714 |
| chrX | 16337707 | 16337798 | MACS2_peak_3010 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 63 | chrX | unknown | gene | 16522871 | 16523559 | + | Cypt1 | Cypt1 | P17337 | NM_025738 | TSS9226 |
| chrX | 19498126 | 19498247 | MACS2_peak_3011 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 55 | chrX | unknown | gene | 19146892 | 19146971 | - | Mir222 | Mir222 | | NR_029807 | TSS14568 |
| chrX | 19498126 | 19498247 | MACS2_peak_3011 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 55 | chrX | unknown | gene | 20059569 | 20097520 | + | Chst7 | Chst7 | P659 | NM_021715 | TSS3034 |
| chrX | 20705717 | 20705808 | MACS2_peak_3012 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 9 | chrX | unknown | gene | 20688492 | 20698646 | + | Cdk16 | Cdk16 | P24641 | NM_011049 | TSS937 |
| chrX | 20705717 | 20705808 | MACS2_peak_3012 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 9 | chrX | unknown | gene | 20848542 | 20860113 | + | Araf | Araf | P7981 | NM_009703 | TSS11628 |
| chrX | 41212771 | 41212862 | MACS2_peak_3013 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 20 | chrX | unknown | gene | 39862918 | 39863583 | - | Cypt14 | Cypt14 | P12382 | NM_001191032 | TSS21507 |
| chrX | 41212771 | 41212862 | MACS2_peak_3013 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 20 | chrX | unknown | gene | 41401300 | 41678601 | + | Gria3 | Gria3 | P14052 | NM_016886 | TSS2775 |
| chrX | 46736584 | 46736675 | MACS2_peak_3014 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 14 | chrX | unknown | gene | 46329006 | 46330240 | + | Actrt1 | Actrt1 | P249 | NM_028514 | TSS25662 |
| chrX | 46736584 | 46736675 | MACS2_peak_3014 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 14 | chrX | unknown | gene | 47809369 | 47892396 | - | Smarca1 | Smarca1 | P18162 | NM_053123 | TSS3430 |
| chrX | 49088666 | 49088757 | MACS2_peak_3015 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 53 | chrX | unknown | gene | 48841465 | 48877615 | - | Gm595 | Gm595 | P16447 | NM_001085499 | TSS20223 |
| chrX | 49088666 | 49088757 | MACS2_peak_3015 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 53 | chrX | unknown | gene | 49470449 | 49499141 | + | Arhgap36 | Arhgap36 | P2850 | NM_001081123 | TSS22343 |
| chrX | 50219397 | 50219510 | MACS2_peak_3016 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 41 | chrX | unknown | gene | 50009305 | 50010235 | - | Olfr1323 | Olfr1323 | P16605 | NM_146390 | TSS1012 |
| chrX | 50219397 | 50219510 | MACS2_peak_3016 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 41 | chrX | unknown | gene | 50425495 | 50426494 | - | Olfr1324 | Olfr1324 | P22502 | NM_146292 | TSS18907 |
| chrX | 51812039 | 51812130 | MACS2_peak_3017 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 16 | chrX | unknown | gene | 51753958 | 51801233 | - | Usp26 | Usp26 | P14939 | NM_031388 | TSS26609 |
| chrX | 51812039 | 51812130 | MACS2_peak_3017 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 16 | chrX | unknown | gene | 51968694 | 51972772 | - | 1700080O16Rik | 1700080O16Rik | P14611 | NM_028851 | TSS12346 |
| chrX | 53052122 | 53052274 | MACS2_peak_3018 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 21 | chrX | unknown | gene | 53049402 | 53049487 | - | Mir542 | Mir542 | | NR_030264 | TSS9503 |
| chrX | 53052122 | 53052274 | MACS2_peak_3018 | 11 | + | 4.12371 | 5.07793 | 1.16524 | 21 | chrX | unknown | gene | 53053111 | 53057190 | - | C430049B03Rik | C430049B03Rik | | NR_038184 | TSS3668 |
| chrX | 74355720 | 74355811 | MACS2_peak_3019 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 6 | chrX | unknown | gene | 74352161 | 74353527 | - | Lage3 | Lage3 | P25473 | NM_025410 | TSS12977 |
| chrX | 74355720 | 74355811 | MACS2_peak_3019 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 6 | chrX | unknown | gene | 74365717 | 74368463 | - | Ubl4a | Ubl4a | P4517 | NM_145405 | TSS4059 |
| chrX | 76598603 | 76599150 | MACS2_peak_3020 | 320 | + | 16.39502 | 37.87159 | 32.05362 | 421 | chrX | unknown | gene | 76393349 | 76397774 | + | Cldn34b4 | Cldn34b4 | P668 | NM_001033799 | TSS19494 |
| chrX | 76598603 | 76599150 | MACS2_peak_3020 | 320 | + | 16.39502 | 37.87159 | 32.05362 | 421 | chrX | unknown | gene | 77164402 | 77475936 | - | Mir669m-2 | Mir669m-2 | | NR_035475 | TSS26017 |
| chrX | 76696399 | 76696490 | MACS2_peak_3021 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 43 | chrX | unknown | gene | 76582609 | 76602924 | - | Cldn34d | Cldn34d | P25109 | NM_001201395 | TSS5901 |
| chrX | 76696399 | 76696490 | MACS2_peak_3021 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 43 | chrX | unknown | gene | 77164402 | 77475936 | - | Mir669m-2 | Mir669m-2 | | NR_035475 | TSS26017 |
| chrX | 84508018 | 84508109 | MACS2_peak_3022 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 4 | chrX | unknown | gene | 83486675 | 83487678 | - | Tsga8 | Tsga8 | P13491 | NM_021898 | TSS26357 |
| chrX | 84508018 | 84508109 | MACS2_peak_3022 | 13 | + | 4.45831 | 5.7527 | 1.3392 | 4 | chrX | unknown | gene | 85249676 | 85270161 | + | 1600014K23Rik | 1600014K23Rik | P23630 | NM_028046 | TSS24447 |
| chrX | 84581965 | 84582056 | MACS2_peak_3023 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 58 | chrX | unknown | gene | 83486675 | 83487678 | - | Tsga8 | Tsga8 | P13491 | NM_021898 | TSS26357 |
| chrX | 84581965 | 84582056 | MACS2_peak_3023 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 58 | chrX | unknown | gene | 85249676 | 85270161 | + | 1600014K23Rik | 1600014K23Rik | P23630 | NM_028046 | TSS24447 |
| chrX | 85413568 | 85413659 | MACS2_peak_3024 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 15 | chrX | unknown | gene | 85249676 | 85270161 | + | 1600014K23Rik | 1600014K23Rik | P23630 | NM_028046 | TSS24447 |
| chrX | 85413568 | 85413659 | MACS2_peak_3024 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 15 | chrX | unknown | gene | 85574021 | 85630554 | + | Tab3 | Tab3 | P20384 | NM_025729 | TSS8303 |
| chrX | 95190941 | 95191032 | MACS2_peak_3025 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 19 | chrX | unknown | gene | 95048934 | 95166539 | - | Arhgef9 | Arhgef9 | P11195 | NM_001290385 | TSS25826 |
| chrX | 95190941 | 95191032 | MACS2_peak_3025 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 19 | chrX | unknown | gene | 95420313 | 95444840 | - | Amer1 | Amer1 | P15043 | NM_175179 | TSS6761 |
| chrX | 104228341 | 104228432 | MACS2_peak_3026 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 60 | chrX | unknown | gene | 104077434 | 104201117 | - | C77370 | C77370 | P24936 | NM_001077354 | TSS10865 |
| chrX | 104228341 | 104228432 | MACS2_peak_3026 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 60 | chrX | unknown | gene | 104280564 | 104413824 | - | Abcb7 | Abcb7 | P25266 | NM_009592 | TSS4735 |
| chrX | 104385710 | 104385801 | MACS2_peak_3027 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 55 | chrX | unknown | gene | 104077434 | 104201117 | - | C77370 | C77370 | P24936 | NM_001077354 | TSS10865 |
| chrX | 104385710 | 104385801 | MACS2_peak_3027 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 55 | chrX | unknown | gene | 104482781 | 104506262 | + | Uprt | Uprt | P19828 | NM_001081189 | TSS7587 |
| chrX | 110325513 | 110325640 | MACS2_peak_3028 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 44 | chrX | unknown | gene | 109196755 | 109198726 | + | Gm6377 | Gm6377 | P8078 | NM_001037917 | TSS20747 |
| chrX | 110325513 | 110325640 | MACS2_peak_3028 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 44 | chrX | unknown | gene | 110372752 | 110375156 | + | Gm7134 | Gm7134 | | NR_033597 | TSS21982 |
| chrX | 118592455 | 118592546 | MACS2_peak_3029 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 6 | chrX | unknown | gene | 118427234 | 118480622 | + | Tgif2lx1 | Tgif2lx1 | P15638 | NM_153109 | TSS26447 |
| chrX | 118592455 | 118592546 | MACS2_peak_3029 | 7 | + | 3.7639 | 4.6155 | 0.75855 | 6 | chrX | unknown | gene | 119927195 | 119929135 | + | Pabpc5 | Pabpc5 | P20706 | NM_053114 | TSS11067 |
| chrX | 121639649 | 121639741 | MACS2_peak_3030 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 77 | chrX | unknown | gene | 120290326 | 120906344 | + | Pcdh11x | Pcdh11x | | NR_073451 | TSS10467 |
| chrX | 121639649 | 121639741 | MACS2_peak_3030 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 77 | chrX | unknown | gene | 122394560 | 122397019 | - | Nap1l3 | Nap1l3 | P7997 | NM_138742 | TSS11859 |
| chrX | 126694057 | 126694148 | MACS2_peak_3031 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 34 | chrX | unknown | gene | 124127338 | 124135831 | - | Vmn2r121 | Vmn2r121 | P23993 | NM_001100616 | TSS604 |
| chrX | 126694057 | 126694148 | MACS2_peak_3031 | 31 | + | 5.78787 | 8.09442 | 3.14251 | 34 | chrX | unknown | gene | 126812461 | 126834004 | - | 4932411N23Rik | 4932411N23Rik | P15348 | NM_177705 | TSS2901 |
| chrX | 126777819 | 126777997 | MACS2_peak_3032 | 65 | + | 7.6559 | 11.73169 | 6.56768 | 100 | chrX | unknown | gene | 124127338 | 124135831 | - | Vmn2r121 | Vmn2r121 | P23993 | NM_001100616 | TSS604 |
| chrX | 126777819 | 126777997 | MACS2_peak_3032 | 65 | + | 7.6559 | 11.73169 | 6.56768 | 100 | chrX | unknown | gene | 126812461 | 126834004 | - | 4932411N23Rik | 4932411N23Rik | P15348 | NM_177705 | TSS2901 |
| chrX | 128750280 | 128750371 | MACS2_peak_3033 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 31 | chrX | unknown | gene | 127721175 | 127736554 | - | Cldn34c4 | Cldn34c4 | P14944 | NM_001281537 | TSS27269 |
| chrX | 128750280 | 128750371 | MACS2_peak_3033 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 31 | chrX | unknown | gene | 129051523 | 129067146 | + | 4930558G05Rik | 4930558G05Rik | | NR_045441 | TSS6401 |
| chrX | 131869699 | 131869790 | MACS2_peak_3034 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 59 | chrX | unknown | gene | 129749741 | 130460935 | + | Diap2 | Diap2 | P11591 | NM_172493 | TSS21911 |
| chrX | 131869699 | 131869790 | MACS2_peak_3034 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 59 | chrX | unknown | gene | 133582860 | 133687264 | - | Pcdh19 | Pcdh19 | P2056 | NM_001105245 | TSS11689 |
| chrX | 136577067 | 136577158 | MACS2_peak_3035 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 80 | chrX | unknown | gene | 136517998 | 136534013 | + | Kir3dl1 | Kir3dl1 | P7714 | NM_177749 | TSS12375 |
| chrX | 136577067 | 136577158 | MACS2_peak_3035 | 13 | + | 4.48867 | 5.81883 | 1.3392 | 80 | chrX | unknown | gene | 136666374 | 136668139 | + | Tceal3 | Tceal3 | P23132 | NM_001029978 | TSS14428 |
| chrX | 137370331 | 137370422 | MACS2_peak_3036 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 49 | chrX | unknown | gene | 137115396 | 137120028 | - | Esx1 | Esx1 | P24039 | NM_007957 | TSS12486 |
| chrX | 137370331 | 137370422 | MACS2_peak_3036 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 49 | chrX | unknown | gene | 137571548 | 138846624 | + | Il1rapl2 | Il1rapl2 | P25297 | NM_030688 | TSS13564 |
| chrX | 140030572 | 140030663 | MACS2_peak_3037 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 43 | chrX | unknown | gene | 139889510 | 139998507 | - | Rbm41 | Rbm41 | P19116 | NM_001172148 | TSS3446 |
| chrX | 140030572 | 140030663 | MACS2_peak_3037 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 43 | chrX | unknown | gene | 140062878 | 140106030 | + | Pih1h3b | Pih1h3b | P9034 | NM_177921 | TSS15299 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| chrX | 143482985 | 143483152 | MACS2_peak_3038 | 1454 | + | 46.5853 | 152.5218 | 145.49593 | 85 | chrX | unknown | gene | 143285673 | 143394262 | - | Chrdl1 | Chrdl1 | P16851 | NM_001114385 | TSS8622 |
| chrX | 143482985 | 143483152 | MACS2_peak_3038 | 1454 | + | 46.5853 | 152.5218 | 145.49593 | 85 | chrX | unknown | gene | 143518590 | 143791324 | + | Pak3 | Pak3 | P5465 | NM_001195048 | TSS26437 |
| chrX | 145169538 | 145169629 | MACS2_peak_3039 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 70 | chrX | unknown | gene | 144688906 | 145120498 | + | Zcchc16 | Zcchc16 | P9676 | NM_001033795 | TSS22439 |
| chrX | 145169538 | 145169629 | MACS2_peak_3039 | 23 | + | 5.26947 | 7.21205 | 2.32792 | 70 | chrX | unknown | gene | 145290358 | 145348894 | - | Lhfpl1 | Lhfpl1 | P17177 | NM_178358 | TSS17279 |
| chrX | 145386050 | 145386141 | MACS2_peak_3040 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 8 | chrX | unknown | gene | 145290358 | 145348894 | - | Lhfpl1 | Lhfpl1 | P17177 | NM_178358 | TSS17279 |
| chrX | 145386050 | 145386141 | MACS2_peak_3040 | 13 | + | 4.36967 | 5.5648 | 1.3392 | 8 | chrX | unknown | gene | 145446423 | 145487639 | - | Amot | Amot | P8404 | NM_153319 | TSS17964 |
| chrX | 148768569 | 148768660 | MACS2_peak_3041 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 12 | chrX | unknown | gene | 148488948 | 148520844 | + | Gm15114 | Gm15114 | P8134 | NM_001082966 | TSS5283 |
| chrX | 148768569 | 148768660 | MACS2_peak_3041 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 12 | chrX | unknown | gene | 148882575 | 148923540 | + | Luzp4 | Luzp4 | P11036 | NM_001114383 | TSS818 |
| chrX | 152745792 | 152745883 | MACS2_peak_3042 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 78 | chrX | unknown | gene | 152563333 | 152563969 | + | Cldn34a | Cldn34a | P24088 | NM_001199311 | TSS11935 |
| chrX | 152745792 | 152745883 | MACS2_peak_3042 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 78 | chrX | unknown | gene | 152781920 | 152808335 | + | Gpr143 | Gpr143 | P8874 | NM_010951 | TSS3943 |
| chrX | 156514047 | 156514138 | MACS2_peak_3043 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 16 | chrX | unknown | gene | 155569735 | 155623310 | - | Ptchd1 | Ptchd1 | P21122 | NM_001093750 | TSS22557 |
| chrX | 156514047 | 156514138 | MACS2_peak_3043 | 13 | + | 4.51669 | 5.88074 | 1.3392 | 16 | chrX | unknown | gene | 156539482 | 156540117 | + | 4930503H13Rik | 4930503H13Rik | | NR_033598 | TSS3623 |
| chrX | 169178935 | 169179026 | MACS2_peak_3044 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 10 | chrX | unknown | gene | 168653098 | 168673735 | - | Msl3 | Msl3 | P6442 | NM_010832 | TSS12752 |
| chrX | 169178935 | 169179026 | MACS2_peak_3044 | 12 | + | 4.20256 | 5.22909 | 1.28062 | 10 | chrX | unknown | gene | 169311530 | 169320343 | - | Hccs | Hccs | P2908 | NM_008222 | TSS22819 |
| chrX | 169989379 | 169989516 | MACS2_peak_3045 | 22 | + | 4.9975 | 6.94907 | 2.23207 | 73 | chrX | unknown | gene | 169685198 | 169989211 | + | Mid1 | Mid1 | P9587 | NM_001290512 | TSS18763 |
| chrX | 169989379 | 169989516 | MACS2_peak_3045 | 22 | + | 4.9975 | 6.94907 | 2.23207 | 73 | chrX | unknown | gene | 170672643 | 170678050 | + | Asmt | Asmt | | NR_037594 | TSS24513 |
| chrX | 169994714 | 169994884 | MACS2_peak_3046 | 25 | + | 5.12438 | 7.40233 | 2.50844 | 119 | chrX | unknown | gene | 169685198 | 169989211 | + | Mid1 | Mid1 | P9587 | NM_001290512 | TSS18763 |
| chrX | 169994714 | 169994884 | MACS2_peak_3046 | 25 | + | 5.12438 | 7.40233 | 2.50844 | 119 | chrX | unknown | gene | 170672643 | 170678050 | + | Asmt | Asmt | | NR_037594 | TSS24513 |
| chrX | 170020048 | 170020180 | MACS2_peak_3047 | 53 | + | 6.87206 | 10.50459 | 5.39374 | 60 | chrX | unknown | gene | 169685198 | 169989211 | + | Mid1 | Mid1 | P9587 | NM_001290512 | TSS18763 |
| chrX | 170020048 | 170020180 | MACS2_peak_3047 | 53 | + | 6.87206 | 10.50459 | 5.39374 | 60 | chrX | unknown | gene | 170672643 | 170678050 | + | Asmt | Asmt | | NR_037594 | TSS24513 |
| chrX | 170673290 | 170673381 | MACS2_peak_3048 | 35 | + | 6.02225 | 8.60076 | 3.58294 | 44 | chrX | unknown | gene | 169685198 | 169989211 | + | Mid1 | Mid1 | P9587 | NM_001290512 | TSS18763 |
| chrY | 4150151 | 4150288 | MACS2_peak_3049 | 124 | + | 10.53893 | 17.84365 | 12.47196 | 72 | chrY | unknown | gene | 3771672 | 3782910 | + | Gm3376 | Gm3376 | P14663 | NM_001270512 | TSS24543 |
| chrY | 4150151 | 4150288 | MACS2_peak_3049 | 124 | + | 10.53893 | 17.84365 | 12.47196 | 72 | chrY | unknown | gene | 7167019 | 7636973 | - | Gm20826 | Gm20826 | P6500 | NM_001101623 | TSS6740 |
| chrY | 90717592 | 90717683 | MACS2_peak_3050 | 13 | + | 4.35899 | 5.72876 | 1.3392 | 49 | chrY | unknown | gene | 83789753 | 85529343 | - | Gm20854 | Gm20854 | P22036 | NM_001160131 | TSS7548 |
| chrY | 90717592 | 90717683 | MACS2_peak_3050 | 13 | + | 4.35899 | 5.72876 | 1.3392 | 49 | chrY | unknown | gene | 90785441 | 90816447 | + | Erdr1 | Erdr1 | P5758 | NM_133362 | TSS9629 |
| chrY | 90717792 | 90717919 | MACS2_peak_3051 | 35 | + | 5.68667 | 8.57917 | 3.58294 | 81 | chrY | unknown | gene | 83789753 | 85529343 | - | Gm20854 | Gm20854 | P22036 | NM_001160131 | TSS7548 |
| chrY | 90717792 | 90717919 | MACS2_peak_3051 | 35 | + | 5.68667 | 8.57917 | 3.58294 | 81 | chrY | unknown | gene | 90785441 | 90816447 | + | Erdr1 | Erdr1 | P5758 | NM_133362 | TSS9629 |
| chrY | 90721978 | 90722187 | MACS2_peak_3052 | 74 | + | 6.37247 | 12.66628 | 7.47215 | 158 | chrY | unknown | gene | 83789753 | 85529343 | - | Gm20854 | Gm20854 | P22036 | NM_001160131 | TSS7548 |
| chrY | 90721978 | 90722187 | MACS2_peak_3052 | 74 | + | 6.37247 | 12.66628 | 7.47215 | 158 | chrY | unknown | gene | 90785441 | 90816447 | + | Erdr1 | Erdr1 | P5758 | NM_133362 | TSS9629 |
| chrY | 90722519 | 90722633 | MACS2_peak_3053 | 23 | + | 4.44783 | 7.15937 | 2.32792 | 69 | chrY | unknown | gene | 83789753 | 85529343 | - | Gm20854 | Gm20854 | P22036 | NM_001160131 | TSS7548 |
| chrY | 90722519 | 90722633 | MACS2_peak_3053 | 23 | + | 4.44783 | 7.15937 | 2.32792 | 69 | chrY | unknown | gene | 90785441 | 90816447 | + | Erdr1 | Erdr1 | P5758 | NM_133362 | TSS9629 |
| chrY | 90722970 | 90723230 | MACS2_peak_3054 | 11 | + | 3.66422 | 5.0765 | 1.16524 | 65 | chrY | unknown | gene | 83789753 | 85529343 | - | Gm20854 | Gm20854 | P22036 | NM_001160131 | TSS7548 |
| chrY | 90722970 | 90723230 | MACS2_peak_3054 | 11 | + | 3.66422 | 5.0765 | 1.16524 | 65 | chrY | unknown | gene | 90785441 | 90816447 | + | Erdr1 | Erdr1 | P5758 | NM_133362 | TSS9629 |
| chrY | 90723309 | 90723461 | MACS2_peak_3055 | 50 | + | 5.59505 | 10.12658 | 5.02793 | 84 | chrY | unknown | gene | 83789753 | 85529343 | - | Gm20854 | Gm20854 | P22036 | NM_001160131 | TSS7548 |
| chrY | 90723309 | 90723461 | MACS2_peak_3055 | 50 | + | 5.59505 | 10.12658 | 5.02793 | 84 | chrY | unknown | gene | 90785441 | 90816447 | + | Erdr1 | Erdr1 | P5758 | NM_133362 | TSS9629 |
| chrY | 90724928 | 90725022 | MACS2_peak_3056 | 51 | + | 5.68011 | 10.27471 | 5.17095 | 28 | chrY | unknown | gene | 83789753 | 85529343 | - | Gm20854 | Gm20854 | P22036 | NM_001160131 | TSS7548 |
| chrY | 90724928 | 90725022 | MACS2_peak_3056 | 51 | + | 5.68011 | 10.27471 | 5.17095 | 28 | chrY | unknown | gene | 90785441 | 90816447 | + | Erdr1 | Erdr1 | P5758 | NM_133362 | TSS9629 |
| chrY | 90739824 | 90739915 | MACS2_peak_3057 | 27 | + | 5.55967 | 7.67698 | 2.76031 | 31 | chrY | unknown | gene | 83789753 | 85529343 | - | Gm20854 | Gm20854 | P22036 | NM_001160131 | TSS7548 |
| chrY | 90739824 | 90739915 | MACS2_peak_3057 | 27 | + | 5.55967 | 7.67698 | 2.76031 | 31 | chrY | unknown | gene | 90785441 | 90816447 | + | Erdr1 | Erdr1 | P5758 | NM_133362 | TSS9629 |
| chrY | 90763640 | 90763736 | MACS2_peak_3058 | 69 | + | 7.00802 | 12.11177 | 6.93713 | 26 | chrY | unknown | gene | 83789753 | 85529343 | - | Gm20854 | Gm20854 | P22036 | NM_001160131 | TSS7548 |
| chrY | 90763640 | 90763736 | MACS2_peak_3058 | 69 | + | 7.00802 | 12.11177 | 6.93713 | 26 | chrY | unknown | gene | 90785441 | 90816447 | + | Erdr1 | Erdr1 | P5758 | NM_133362 | TSS9629 |
| chrY | 90767899 | 90767991 | MACS2_peak_3059 | 49 | + | 6.18129 | 10.02293 | 4.93816 | 41 | chrY | unknown | gene | 83789753 | 85529343 | - | Gm20854 | Gm20854 | P22036 | NM_001160131 | TSS7548 |
| chrY | 90767899 | 90767991 | MACS2_peak_3059 | 49 | + | 6.18129 | 10.02293 | 4.93816 | 41 | chrY | unknown | gene | 90785441 | 90816447 | + | Erdr1 | Erdr1 | P5758 | NM_133362 | TSS9629 |
| chrY | 90797939 | 90798087 | MACS2_peak_3060 | 149 | + | 8.78106 | 20.34636 | 14.90385 | 70 | chrY | unknown | gene | 83789753 | 85529343 | - | Gm20854 | Gm20854 | P22036 | NM_001160131 | TSS7548 |
| chrY | 90808262 | 90808356 | MACS2_peak_3061 | 48 | + | 5.27627 | 9.91397 | 4.83684 | 76 | chrY | unknown | gene | 83789753 | 85529343 | - | Gm20854 | Gm20854 | P22036 | NM_001160131 | TSS7548 |
| chrY | 90808723 | 90809074 | MACS2_peak_3062 | 195 | + | 9.88081 | 25.16269 | 19.596 | 264 | chrY | unknown | gene | 83789753 | 85529343 | - | Gm20854 | Gm20854 | P22036 | NM_001160131 | TSS7548 |

**Table S2. Functional annotation of enriched TBX2 ChIP-seq peaks.**

Shown are gene enrichments determined by GREAT and associated with TBX2 ChIP peaks in clusters with annotated biological processes sorted by –log10 binomial p-value.

## GO - Biological Processes

| # Term Name | Binom Rank | Binom Raw P-Value | Binom FDR Q-Val | Binom Fold Enrichment | Binom Observed Region Hits | Binom Region Set Coverage | Hyper Rank | Hyper FDR Q-Val | Hyper Fold Enrichment | Hyper Observed Gene Hits | Hyper Total Genes | Hyper Gene Set Coverage |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| spleen development | 60 | 7.39167e-6 | 1.61262e-3 | 2.1829 | 40 | 1.32% | 401 | 1.55456e-3 | 2.6365 | 18 | 45 | 0.55% |
| positive regulation of Ras protein signal transduction | 69 | 8.95426e-6 | 1.69871e-3 | 2.0973 | 43 | 1.42% | 510 | 6.02107e-3 | 2.3728 | 18 | 50 | 0.55% |
| positive regulation of DNA replication | 79 | 1.31358e-5 | 2.17655e-3 | 2.1762 | 38 | 1.26% | 364 | 6.84036e-4 | 2.5632 | 21 | 54 | 0.65% |
| cellular response to vitamin D | 95 | 2.44237e-5 | 3.36533e-3 | 2.6612 | 24 | 0.79% | 619 | 1.51980e-2 | 3.8449 | 7 | 12 | 0.22% |
| cellular response to vitamin | 97 | 2.81310e-5 | 3.79623e-3 | 2.4706 | 27 | 0.89% | 647 | 1.84477e-2 | 3.1221 | 9 | 19 | 0.28% |
| negative regulation of stress fiber assembly | 187 | 2.52657e-4 | 1.76860e-2 | 2.4957 | 20 | 0.66% | 712 | 2.96011e-2 | 2.7463 | 10 | 24 | 0.31% |
| specification of animal organ identity | 201 | 3.18392e-4 | 2.07351e-2 | 2.1570 | 26 | 0.86% | 489 | 4.66036e-3 | 3.7075 | 9 | 16 | 0.28% |
| nephric duct morphogenesis | 218 | 4.07560e-4 | 2.44723e-2 | 2.1980 | 24 | 0.79% | 619 | 1.51980e-2 | 3.8449 | 7 | 12 | 0.22% |
| cardiac right ventricle morphogenesis | 223 | 4.67781e-4 | 2.74586e-2 | 2.0676 | 27 | 0.89% | 647 | 1.84477e-2 | 3.1221 | 9 | 19 | 0.28% |
| Roundabout signaling pathway | 258 | 7.43845e-4 | 3.77400e-2 | 2.4092 | 18 | 0.60% | 677 | 2.48674e-2 | 4.7080 | 5 | 7 | 0.15% |
| atrioventricular canal development | 273 | 8.55612e-4 | 4.10255e-2 | 2.8657 | 13 | 0.43% | 813 | 4.83056e-2 | 4.1195 | 5 | 8 | 0.15% |
| regulation of epithelial cell proliferation involved in lung morphogenesis | 302 | 1.11352e-3 | 4.82647e-2 | 2.3227 | 18 | 0.60% | 611 | 1.44242e-2 | 4.3941 | 6 | 9 | 0.18% |

The test set of 3,025 genomic regions picked 3,246 genes (15%) of all 21,395 genes.

*GO Biological Process* has 13,090 terms covering 17,925 (84%) of all 21,395 genes.

13,090 ontology terms were tested (100%) using an annotation count range of [1, 1000].

GREAT version 4.0.4

Species assembly: mm10

Association rule: Basal+extension: 5000 bp upstream, 1000 bp downstream, 1000000 bp max extension, curated regulatory domains included

**Table S3. Functional annotation of enriched TBX2 ChIP-seq peaks.**

Shown are gene enrichments determined by GREAT and associated with TBX2 ChIP peaks in clusters with annotated mouse phenotypes sorted by –log10 binomial p-value.

## GO - Mouse Phenotype

| # Term Name | Binom Rank | Binom Raw P-Value | Binom FDR Q-Val | Binom Fold Enrichment | Binom Observed Region Hits | Binom Region Set Coverage | Hyper Rank | Hyper FDR Q-Val | Hyper Fold Enrichment | Hyper Observed Gene Hits | Hyper Total Genes | Hyper Gene Set Coverage |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| abnormal pulmonary trunk morphology | 18 | 3.67439e-7 | 1.95457e-4 | 2.9352 | 30 | 0.99% | 334 | 3.11254e-4 | 4.0279 | 11 | 18 | 0.34% |
| dilated respiratory conducting tubes | 20 | 5.35948e-7 | 2.56585e-4 | 2.4738 | 39 | 1.29% | 264 | 5.22476e-5 | 3.8449 | 14 | 24 | 0.43% |
| abnormal primordial germ cell proliferation | 23 | 7.19912e-7 | 2.99703e-4 | 4.1642 | 18 | 0.60% | 668 | 1.03015e-2 | 3.8449 | 7 | 12 | 0.22% |
| interdigital webbing | 25 | 1.14190e-6 | 4.37349e-4 | 2.4285 | 38 | 1.26% | 249 | 2.73371e-5 | 3.6365 | 16 | 29 | 0.49% |
| abnormal digit development | 33 | 3.08635e-6 | 8.95510e-4 | 2.1282 | 46 | 1.52% | 195 | 4.04855e-6 | 3.4690 | 20 | 38 | 0.62% |
| abnormal epaxial muscle morphology | 40 | 4.93022e-6 | 1.18017e-3 | 3.3376 | 20 | 0.66% | 655 | 9.84215e-3 | 4.3941 | 6 | 9 | 0.18% |
| dilated esophagus | 91 | 3.50163e-5 | 3.68441e-3 | 2.9019 | 20 | 0.66% | 896 | 3.00625e-2 | 3.5952 | 6 | 11 | 0.18% |
| abnormal esophagus development | 94 | 3.93148e-5 | 4.00468e-3 | 2.8773 | 20 | 0.66% | 655 | 9.84215e-3 | 4.3941 | 6 | 9 | 0.18% |
| abnormal otic vesicle development | 99 | 4.57307e-5 | 4.42295e-3 | 2.2772 | 30 | 0.99% | 785 | 1.96389e-2 | 2.7463 | 10 | 24 | 0.31% |
| abnormal tympanic membrane morphology | 111 | 8.06820e-5 | 6.95973e-3 | 2.6493 | 21 | 0.69% | 772 | 1.81914e-2 | 3.9547 | 6 | 10 | 0.18% |
| decreased cochlear coiling | 146 | 1.65556e-4 | 1.08575e-2 | 2.0556 | 32 | 1.06% | 403 | 1.01289e-3 | 3.6252 | 11 | 20 | 0.34% |
| abnormal myometrium morphology | 150 | 2.00801e-4 | 1.28178e-2 | 2.2248 | 26 | 0.86% | 729 | 1.55424e-2 | 2.6853 | 11 | 27 | 0.34% |
| polycythemia | 153 | 2.20664e-4 | 1.38095e-2 | 2.3981 | 22 | 0.73% | 806 | 2.21641e-2 | 3.1017 | 8 | 17 | 0.25% |
| increased CD4-positive, alpha-beta memory T cell number | 154 | 2.31732e-4 | 1.44080e-2 | 2.2442 | 25 | 0.83% | 1019 | 4.22013e-2 | 2.4412 | 10 | 27 | 0.31% |
| failure of palatal shelf elevation | 160 | 2.49748e-4 | 1.49459e-2 | 2.0069 | 32 | 1.06% | 392 | 8.32411e-4 | 2.9960 | 15 | 33 | 0.46% |
| variable body spotting | 171 | 3.22280e-4 | 1.80458e-2 | 2.3311 | 22 | 0.73% | 649 | 9.68185e-3 | 3.5153 | 8 | 15 | 0.25% |
| abnormal clitoris size | 181 | 3.51310e-4 | 1.85845e-2 | 2.8707 | 15 | 0.50% | 584 | 6.89131e-3 | 5.4927 | 5 | 6 | 0.15% |
| increased B-1 B cell number | 185 | 3.74932e-4 | 1.94053e-2 | 2.0666 | 28 | 0.93% | 821 | 2.37176e-2 | 2.2506 | 14 | 41 | 0.43% |
| abnormal diaphragm development | 200 | 4.51463e-4 | 2.16138e-2 | 2.9266 | 14 | 0.46% | 1038 | 4.52703e-2 | 3.2956 | 6 | 12 | 0.18% |
| abnormal germ cell physiology | 246 | 7.24391e-4 | 2.81953e-2 | 2.1467 | 23 | 0.76% | 476 | 2.68178e-3 | 3.2956 | 11 | 22 | 0.34% |
| prolonged diestrus | 250 | 7.77264e-4 | 2.97692e-2 | 2.0961 | 24 | 0.79% | 785 | 1.96389e-2 | 2.7463 | 10 | 24 | 0.31% |
| absent submandibular gland | 256 | 8.07759e-4 | 3.02121e-2 | 2.7533 | 14 | 0.46% | 742 | 1.65964e-2 | 4.7080 | 5 | 7 | 0.15% |
| absent ureteric bud | 263 | 8.54282e-4 | 3.11017e-2 | 2.4513 | 17 | 0.56% | 753 | 1.72096e-2 | 3.5491 | 7 | 13 | 0.22% |
| absent eyelids | 264 | 8.78638e-4 | 3.18673e-2 | 2.1568 | 22 | 0.73% | 452 | 1.82277e-3 | 3.6618 | 10 | 18 | 0.31% |
| absent alisphenoid bone | 284 | 1.05736e-3 | 3.56486e-2 | 2.5706 | 15 | 0.50% | 909 | 3.16026e-2 | 4.1195 | 5 | 8 | 0.15% |
| abnormal clitoris morphology | 287 | 1.07365e-3 | 3.58197e-2 | 2.3304 | 18 | 0.60% | 339 | 3.60713e-4 | 5.7673 | 7 | 8 | 0.22% |
| abnormal spinal cord lateral column morphology | 299 | 1.19261e-3 | 3.81916e-2 | 2.3751 | 17 | 0.56% | 852 | 2.61216e-2 | 5.2730 | 4 | 5 | 0.12% |
| abnormal hindlimb bud morphology | 305 | 1.25552e-3 | 3.94151e-2 | 2.1858 | 20 | 0.66% | 649 | 9.68185e-3 | 3.5153 | 8 | 15 | 0.25% |
| increased macrophage nitric oxide production | 328 | 1.49365e-3 | 4.36028e-2 | 6.1657 | 5 | 0.17% | 949 | 3.52079e-2 | 6.5912 | 3 | 3 | 0.09% |
| abnormal auditory tube | 340 | 1.66319e-3 | 4.68384e-2 | 2.9483 | 11 | 0.36% | 742 | 1.65964e-2 | 4.7080 | 5 | 7 | 0.15% |
| abnormal olfactory tract morphology | 341 | 1.67549e-3 | 4.70463e-2 | 2.0100 | 23 | 0.76% | 753 | 1.72096e-2 | 3.5491 | 7 | 13 | 0.22% |

The test set of 3,025 genomic regions picked 3,246 genes (15%) of all 21,395 genes.

*Mouse Phenotype* has 9,575 terms covering 9,654 (45%) of all 21,395 genes.

9,575 ontology terms were tested (100%) using an annotation count range of [1, 1000].

GREAT version 4.0.4

Species assembly: mm10

Association rule: Basal+extension: 5000 bp upstream, 1000 bp downstream, 1000000 bp max extension, curated regulatory domains included

**Table S4. Functional annotation of enriched TBX2 ChIP-seq peaks.**

Shown are gene enrichments determined by GREAT and associated with TBX2 ChIP peaks in clusters with annotated human phenotypes sorted by –log10 binomial p-value.

## GO - Human Phenotype

| # Term Name | Binom Rank | Binom Raw P-Value | Binom FDR Q-Val | Binom Fold Enrichment | Binom Observed Region Hits | Binom Region Set Coverage | Hyper Rank | Hyper FDR Q-Val | Hyper Fold Enrichment | Hyper Observed Gene Hits | Hyper Total Genes | Hyper Gene Set Coverage |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Myelomeningocele | 10 | 3.54575e-4 | 2.33984e-1 | 3.3458 | 12 | 0.40% | 166 | 5.83061e-2 | 3.9547 | 6 | 10 | 0.18% |
| Meningocele | 11 | 3.84161e-4 | 2.30462e-1 | 3.1297 | 13 | 0.43% | 201 | 7.72708e-2 | 3.2956 | 7 | 14 | 0.22% |
| Ulnar deviation of the hand or of fingers of the hand | 12 | 4.56351e-4 | 2.50955e-1 | 2.1801 | 24 | 0.79% | 178 | 6.24414e-2 | 2.5894 | 11 | 28 | 0.34% |
| Short 2nd finger | 34 | 2.03631e-3 | 3.95223e-1 | 2.3997 | 15 | 0.50% | 155 | 5.47553e-2 | 4.7080 | 5 | 7 | 0.15% |
| White forelock | 49 | 2.99439e-3 | 4.03265e-1 | 2.4781 | 13 | 0.43% | 223 | 8.87813e-2 | 4.1195 | 5 | 8 | 0.15% |
| Oligodactyly | 62 | 4.47491e-3 | 4.76289e-1 | 2.2741 | 14 | 0.46% | 159 | 5.61705e-2 | 3.5491 | 7 | 13 | 0.22% |
| Synostosis involving bones of the feet | 67 | 4.99086e-3 | 4.91563e-1 | 2.0104 | 18 | 0.60% | 120 | 3.60878e-2 | 3.5153 | 8 | 15 | 0.25% |
| Partial albinism | 80 | 5.60529e-3 | 4.62367e-1 | 2.5028 | 11 | 0.36% | 195 | 7.86582e-2 | 5.2730 | 4 | 5 | 0.12% |
| Lacrimal duct aplasia | 125 | 9.61403e-3 | 5.07544e-1 | 2.5810 | 9 | 0.30% | 195 | 7.86582e-2 | 5.2730 | 4 | 5 | 0.12% |

The test set of 3,025 genomic regions picked 3,246 genes (15%) of all 21,395 genes.
*Human Phenotype* has 6,599 terms covering 3,215 (15%) of all 21,395 genes.
GREAT version 4.0.4
Species assembly: mm10
Association rule: Basal+extension: 5000 bp upstream, 1000 bp downstream, 1000000 bp max extension, curated regulatory domains included

**Table S5. Genes with decreased expression in the microarrays of E14.5 control vs *Tbx2*-deficient lungs.**
Shown are the individual intensities, the individiual fold changes (FC) and the average FC over the four individual microarrays performed.

| | **Intensities** | | | | | | | | **Fold change (FC)** | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Gene Name** | **control 1** | **mutant 1** | **control 2** | **mutant 2** | **control 3** | **mutant 3** | **control 4** | **mutant 4** | **FC1** | **FC2** | **FC3** | **FC4** | **avgFC** |
| ***Ndp*** | 425 | 130 | 287 | 92 | 524 | 58 | 323 | 90 | -3.3 | -3.1 | -9.1 | -3.6 | -4.8 |
| ***Asz1*** | 295 | 151 | 292 | 56 | 328 | 54 | 427 | 106 | -1.9 | -5.2 | -6.1 | -4.0 | -4.3 |
| ***AW549542*** | 2284 | 646 | 1282 | 434 | 1728 | 466 | 1335 | 461 | -3.5 | -3.0 | -3.7 | -2.9 | -3.3 |
| ***Dgkk*** | 127 | 79 | 234 | 66 | 177 | 39 | 162 | 59 | -1.6 | -3.5 | -4.6 | -2.8 | -3.1 |
| ***Tmem27*** | 163 | 95 | 171 | 49 | 191 | 43 | 219 | 78 | -1.7 | -3.5 | -4.5 | -2.8 | -3.1 |
| ***Dcx*** | 433 | 241 | 463 | 177 | 630 | 110 | 513 | 224 | -1.8 | -2.6 | -5.7 | -2.3 | -3.1 |
| ***Tbx2*** | 9826 | 2499 | 5276 | 2059 | 8400 | 3200 | 5246 | 1758 | -3.9 | -2.6 | -2.6 | -3.0 | -3.0 |
| ***Rspo2*** | 1459 | 948 | 1341 | 629 | 2245 | 354 | 1605 | 869 | -1.5 | -2.1 | -6.3 | -1.8 | -3.0 |
| ***9230102K24Rik*** | 737 | 413 | 578 | 246 | 890 | 180 | 762 | 374 | -1.8 | -2.3 | -4.9 | -2.0 | -2.8 |
| ***A_55_P2023176*** | 274 | 169 | 231 | 114 | 311 | 66 | 262 | 121 | -1.6 | -2.0 | -4.7 | -2.2 | -2.6 |
| ***ENSMUST00000169692*** | 891 | 452 | 982 | 321 | 1491 | 604 | 952 | 402 | -2.0 | -3.1 | -2.5 | -2.4 | -2.5 |
| ***Cpa3*** | 372 | 121 | 458 | 206 | 375 | 218 | 384 | 170 | -3.1 | -2.2 | -1.7 | -2.3 | -2.3 |
| ***Dcpp1*** | 158 | 98 | 158 | 72 | 170 | 56 | 196 | 82 | -1.6 | -2.2 | -3.0 | -2.4 | -2.3 |
| ***Rhox5*** | 2554 | 1365 | 1979 | 1071 | 2825 | 711 | 2540 | 1680 | -1.9 | -1.8 | -4.0 | -1.5 | -2.3 |
| ***Asic4*** | 196 | 113 | 190 | 103 | 280 | 74 | 175 | 106 | -1.7 | -1.8 | -3.8 | -1.7 | -2.3 |
| ***Plcb1*** | 232 | 140 | 316 | 91 | 255 | 168 | 216 | 96 | -1.7 | -3.5 | -1.5 | -2.2 | -2.2 |
| ***Hist1h1b*** | 3500 | 2057 | 4094 | 1398 | 5939 | 2843 | 3890 | 1817 | -1.7 | -2.9 | -2.1 | -2.1 | -2.2 |
| ***Colec10*** | 772 | 488 | 882 | 400 | 1127 | 477 | 1129 | 492 | -1.6 | -2.2 | -2.4 | -2.3 | -2.1 |
| ***Adamdec1*** | 1551 | 870 | 984 | 609 | 1994 | 653 | 1428 | 734 | -1.8 | -1.6 | -3.1 | -1.9 | -2.1 |
| ***Dcpp3*** | 190 | 122 | 222 | 106 | 221 | 91 | 260 | 117 | -1.6 | -2.1 | -2.4 | -2.2 | -2.1 |
| ***Adh6a*** | 222 | 139 | 181 | 115 | 199 | 59 | 204 | 120 | -1.6 | -1.6 | -3.4 | -1.7 | -2.1 |
| ***Lect1*** | 157 | 102 | 183 | 96 | 195 | 69 | 212 | 116 | -1.5 | -1.9 | -2.8 | -1.8 | -2.0 |
| ***Arhgap20*** | 268 | 173 | 381 | 166 | 553 | 245 | 399 | 216 | -1.6 | -2.3 | -2.3 | -1.8 | -2.0 |
| ***Meox1*** | 1819 | 792 | 1638 | 998 | 2041 | 835 | 1283 | 851 | -2.3 | -1.6 | -2.4 | -1.5 | -2.0 |
| ***Snrpd3*** | 23872 | 15802 | 34613 | 14293 | 27304 | 14004 | 24132 | 12020 | -1.5 | -2.4 | -1.9 | -2.0 | -2.0 |
| ***Fam162b*** | 5343 | 2850 | 5086 | 2347 | 4724 | 2854 | 5284 | 2760 | -1.9 | -2.2 | -1.7 | -1.9 | -1.9 |
| ***Shisa9*** | 148 | 89 | 125 | 69 | 196 | 83 | 147 | 83 | -1.7 | -1.8 | -2.4 | -1.8 | -1.9 |
| ***Sct*** | 609 | 387 | 492 | 283 | 706 | 281 | 605 | 377 | -1.6 | -1.7 | -2.5 | -1.6 | -1.9 |
| ***Prpf38b*** | 476 | 314 | 669 | 253 | 661 | 389 | 513 | 334 | -1.5 | -2.6 | -1.7 | -1.5 | -1.8 |
| ***Ptpn5*** | 1229 | 538 | 737 | 477 | 809 | 490 | 762 | 399 | -2.3 | -1.5 | -1.7 | -1.9 | -1.8 |
| ***Fzd10*** | 607 | 328 | 565 | 324 | 592 | 320 | 466 | 294 | -1.9 | -1.7 | -1.9 | -1.6 | -1.8 |
| ***Lhx6*** | 362 | 199 | 279 | 156 | 280 | 172 | 252 | 143 | -1.8 | -1.8 | -1.6 | -1.8 | -1.8 |
| ***Nebl*** | 134 | 83 | 123 | 75 | 141 | 83 | 136 | 68 | -1.6 | -1.6 | -1.7 | -2.0 | -1.7 |
| ***Parva*** | 149 | 95 | 186 | 106 | 210 | 115 | 132 | 85 | -1.6 | -1.7 | -1.8 | -1.5 | -1.7 |
| ***Hpca*** | 753 | 382 | 439 | 289 | 639 | 391 | 447 | 289 | -2.0 | -1.5 | -1.6 | -1.5 | -1.7 |
| ***Apln*** | 2389 | 1486 | 2231 | 1418 | 2320 | 1395 | 2134 | 1323 | -1.6 | -1.6 | -1.7 | -1.6 | -1.6 |

**Table S6. Genes with increased expression in the microarrays of E14.5 control vs *Tbx2*-deficient lungs.**
Shown are the individual intensities, the individidual fold changes (FC) and the average FC over the four individual microarrays performed.

| | Intensities | | | | | | | | Fold change (FC) | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Gene Name** | **control 1** | **mutant 1** | **control 2** | **mutant 2** | **control 3** | **mutant 3** | **control 4** | **mutant 4** | **FC1** | **FC2** | **FC3** | **FC4** | **avgFC** |
| ***Ifi44*** | 24 | 143 | 43 | 359 | 16 | 264 | 43 | 213 | 6.0 | 8.3 | 16.8 | 5.0 | 9.0 |
| ***Ttn*** | 155 | 460 | 64 | 1168 | 101 | 300 | 49 | 199 | 3.0 | 18.2 | 3.0 | 4.0 | 7.0 |
| ***1700007K13Rik*** | 29 | 101 | 47 | 165 | 15 | 207 | 37 | 123 | 3.5 | 3.5 | 13.8 | 3.3 | 6.0 |
| ***Ptprv*** | 17 | 137 | 67 | 269 | 15 | 104 | 47 | 198 | 7.8 | 4.0 | 7.0 | 4.2 | 5.8 |
| ***Sln*** | 411 | 640 | 175 | 2523 | 481 | 1089 | 106 | 346 | 1.6 | 14.4 | 2.3 | 3.3 | 5.4 |
| ***Chrdl1*** | 23 | 121 | 47 | 117 | 16 | 155 | 37 | 100 | 5.3 | 2.5 | 9.9 | 2.7 | 5.1 |
| ***Cdkn1a*** | 156 | 736 | 423 | 1377 | 105 | 967 | 337 | 959 | 4.7 | 3.3 | 9.2 | 2.9 | 5.0 |
| ***Frzb*** | 44 | 279 | 64 | 242 | 34 | 241 | 81 | 227 | 6.3 | 3.8 | 7.0 | 2.8 | 5.0 |
| ***Ifi203*** | 70 | 147 | 80 | 406 | 73 | 682 | 102 | 230 | 2.1 | 5.1 | 9.3 | 2.3 | 4.7 |
| ***Rtp4*** | 478 | 2211 | 951 | 4290 | 529 | 2730 | 946 | 3537 | 4.6 | 4.5 | 5.2 | 3.7 | 4.5 |
| ***Oasl2*** | 114 | 382 | 201 | 849 | 115 | 669 | 144 | 583 | 3.3 | 4.2 | 5.8 | 4.1 | 4.4 |
| ***Asic2*** | 95 | 376 | 124 | 426 | 110 | 773 | 135 | 362 | 4.0 | 3.4 | 7.1 | 2.7 | 4.3 |
| ***Nell1*** | 303 | 479 | 235 | 554 | 201 | 1975 | 210 | 419 | 1.6 | 2.4 | 9.8 | 2.0 | 3.9 |
| ***Pmaip1*** | 210 | 941 | 402 | 1452 | 175 | 498 | 389 | 1139 | 4.5 | 3.6 | 2.8 | 2.9 | 3.5 |
| ***Usp18*** | 139 | 320 | 184 | 710 | 133 | 552 | 163 | 543 | 2.3 | 3.9 | 4.1 | 3.3 | 3.4 |
| ***Oasl1*** | 140 | 521 | 336 | 1164 | 123 | 452 | 307 | 730 | 3.7 | 3.5 | 3.7 | 2.4 | 3.3 |
| ***Gm9706*** | 134 | 398 | 351 | 1109 | 142 | 589 | 240 | 671 | 3.0 | 3.2 | 4.1 | 2.8 | 3.3 |
| ***Fabp4*** | 503 | 1038 | 512 | 1672 | 786 | 4383 | 490 | 923 | 2.1 | 3.3 | 5.6 | 1.9 | 3.2 |
| ***Isg15*** | 483 | 1484 | 1198 | 3467 | 498 | 1972 | 850 | 2249 | 3.1 | 2.9 | 4.0 | 2.6 | 3.1 |
| ***Trp53inp1*** | 2643 | 7008 | 5005 | 10575 | 2376 | 12179 | 4514 | 11530 | 2.7 | 2.1 | 5.1 | 2.6 | 3.1 |
| ***Mx2*** | 71 | 167 | 117 | 360 | 57 | 263 | 88 | 200 | 2.3 | 3.1 | 4.6 | 2.3 | 3.1 |
| ***Oas1a*** | 275 | 755 | 504 | 2037 | 383 | 1092 | 552 | 1458 | 2.7 | 4.0 | 2.9 | 2.6 | 3.1 |
| ***Il33*** | 658 | 3130 | 1207 | 2178 | 627 | 2498 | 1530 | 2499 | 4.8 | 1.8 | 4.0 | 1.6 | 3.0 |
| ***Shisa3*** | 167 | 825 | 305 | 709 | 151 | 324 | 333 | 781 | 4.9 | 2.3 | 2.2 | 2.3 | 2.9 |
| ***Cd55*** | 950 | 2330 | 1012 | 2675 | 730 | 3010 | 1010 | 2280 | 2.5 | 2.6 | 4.1 | 2.3 | 2.9 |
| ***Parp14*** | 265 | 472 | 327 | 834 | 209 | 1082 | 332 | 588 | 1.8 | 2.5 | 5.2 | 1.8 | 2.8 |
| ***Ephx1*** | 456 | 845 | 554 | 1390 | 434 | 2159 | 557 | 1037 | 1.9 | 2.5 | 5.0 | 1.9 | 2.8 |
| ***Wisp1*** | 2542 | 6877 | 2826 | 8859 | 2163 | 6441 | 3072 | 6816 | 2.7 | 3.1 | 3.0 | 2.2 | 2.8 |
| ***Itga11*** | 227 | 848 | 344 | 1105 | 196 | 352 | 338 | 759 | 3.7 | 3.2 | 1.8 | 2.2 | 2.7 |
| ***Oas1f*** | 209 | 476 | 332 | 1161 | 281 | 685 | 364 | 905 | 2.3 | 3.5 | 2.4 | 2.5 | 2.7 |
| ***Ifih1*** | 222 | 358 | 243 | 706 | 156 | 635 | 221 | 407 | 1.6 | 2.9 | 4.1 | 1.8 | 2.6 |
| ***Mndal*** | 165 | 254 | 212 | 607 | 173 | 670 | 213 | 342 | 1.5 | 2.9 | 3.9 | 1.6 | 2.5 |
| ***P2ry14*** | 1196 | 1951 | 1200 | 2126 | 1001 | 4850 | 1251 | 2004 | 1.6 | 1.8 | 4.8 | 1.6 | 2.5 |
| ***Tgtp2*** | 134 | 262 | 202 | 555 | 145 | 462 | 171 | 336 | 2.0 | 2.7 | 3.2 | 2.0 | 2.5 |
| ***Xaf1*** | 72 | 143 | 119 | 263 | 59 | 226 | 122 | 204 | 2.0 | 2.2 | 3.8 | 1.7 | 2.4 |
| ***Gdnf*** | 76 | 188 | 69 | 192 | 51 | 129 | 76 | 132 | 2.5 | 2.8 | 2.5 | 1.7 | 2.4 |
| ***Pqlc3*** | 212 | 509 | 319 | 646 | 204 | 651 | 311 | 580 | 2.4 | 2.0 | 3.2 | 1.9 | 2.4 |
| ***Smoc2*** | 7026 | 14096 | 6969 | 20878 | 5702 | 9074 | 6322 | 17627 | 2.0 | 3.0 | 1.6 | 2.8 | 2.3 |
| ***Gpr17*** | 59 | 166 | 94 | 219 | 59 | 125 | 69 | 144 | 2.8 | 2.3 | 2.1 | 2.1 | 2.3 |
| ***Celf5*** | 283 | 536 | 338 | 848 | 224 | 620 | 268 | 547 | 1.9 | 2.5 | 2.8 | 2.0 | 2.3 |
| ***Pid1*** | 179 | 311 | 176 | 412 | 168 | 518 | 194 | 353 | 1.7 | 2.3 | 3.1 | 1.8 | 2.2 |
| ***Dner*** | 89 | 223 | 86 | 258 | 77 | 140 | 99 | 151 | 2.5 | 3.0 | 1.8 | 1.5 | 2.2 |
| ***Gdf15*** | 59 | 144 | 111 | 219 | 45 | 123 | 92 | 150 | 2.4 | 2.0 | 2.7 | 1.6 | 2.2 |
| ***Ccng1*** | 1628 | 4269 | 2666 | 5112 | 1583 | 3426 | 2358 | 4849 | 2.6 | 1.9 | 2.2 | 2.1 | 2.2 |
| ***Slc19a2*** | 1038 | 2448 | 1541 | 3053 | 876 | 2173 | 1357 | 2624 | 2.4 | 2.0 | 2.5 | 1.9 | 2.2 |
| ***Gbp3*** | 165 | 351 | 246 | 578 | 176 | 463 | 296 | 486 | 2.1 | 2.3 | 2.6 | 1.6 | 2.2 |
| ***Zmat3*** | 639 | 1316 | 944 | 2145 | 528 | 1415 | 715 | 1214 | 2.1 | 2.3 | 2.7 | 1.7 | 2.2 |
| ***Slc6a2*** | 106 | 239 | 87 | 205 | 136 | 347 | 110 | 165 | 2.2 | 2.4 | 2.5 | 1.5 | 2.2 |
| ***Sulf2*** | 1076 | 2778 | 1648 | 3437 | 976 | 2165 | 1326 | 2219 | 2.6 | 2.1 | 2.2 | 1.7 | 2.1 |
| ***P4ha2*** | 1750 | 4222 | 2114 | 3270 | 1530 | 4088 | 2003 | 3856 | 2.4 | 1.5 | 2.7 | 1.9 | 2.1 |
| ***2610507I01Rik*** | 443 | 1202 | 619 | 985 | 362 | 801 | 649 | 1295 | 2.7 | 1.6 | 2.2 | 2.0 | 2.1 |
| ***3110040M04Rik*** | 71 | 121 | 74 | 185 | 160 | 425 | 97 | 156 | 1.7 | 2.5 | 2.7 | 1.6 | 2.1 |
| ***Fap*** | 949 | 2558 | 1412 | 2669 | 1162 | 2508 | 1565 | 2616 | 2.7 | 1.9 | 2.2 | 1.7 | 2.1 |
| ***Ffar4*** | 82 | 157 | 117 | 230 | 72 | 169 | 93 | 189 | 1.9 | 2.0 | 2.3 | 2.0 | 2.1 |
| ***Lgals3bp*** | 148 | 302 | 258 | 485 | 201 | 508 | 227 | 398 | 2.0 | 1.9 | 2.5 | 1.8 | 2.0 |
| ***Edn1*** | 115 | 208 | 113 | 211 | 78 | 226 | 128 | 204 | 1.8 | 1.9 | 2.9 | 1.6 | 2.0 |
| ***Crispld2*** | 766 | 1244 | 677 | 1628 | 656 | 1242 | 652 | 1352 | 1.6 | 2.4 | 1.9 | 2.1 | 2.0 |
| ***Gpr20*** | 52 | 105 | 69 | 156 | 56 | 102 | 62 | 118 | 2.0 | 2.3 | 1.8 | 1.9 | 2.0 |
| ***Oas2*** | 109 | 177 | 148 | 387 | 115 | 233 | 140 | 243 | 1.6 | 2.6 | 2.0 | 1.7 | 2.0 |
| ***Cckar*** | 922 | 1543 | 1061 | 2106 | 767 | 1814 | 937 | 1559 | 1.7 | 2.0 | 2.4 | 1.7 | 1.9 |
| ***Eppk1*** | 583 | 885 | 677 | 1357 | 429 | 1052 | 464 | 719 | 1.5 | 2.0 | 2.5 | 1.5 | 1.9 |
| ***ENSMUST00000099050*** | 55653 | 141344 | 84314 | 133382 | 82215 | 124548 | 81061 | 152736 | 2.5 | 1.6 | 1.5 | 1.9 | 1.9 |
| ***Lmcd1*** | 1240 | 2094 | 1135 | 2154 | 760 | 1489 | 1084 | 2128 | 1.7 | 1.9 | 2.0 | 2.0 | 1.9 |
| ***Lgals9*** | 108 | 162 | 122 | 273 | 119 | 228 | 132 | 243 | 1.5 | 2.2 | 1.9 | 1.8 | 1.9 |
| ***Ms4a7*** | 653 | 1161 | 1023 | 2070 | 715 | 1227 | 992 | 1828 | 1.8 | 2.0 | 1.7 | 1.8 | 1.8 |
| ***Syn2*** | 80 | 139 | 111 | 222 | 147 | 297 | 83 | 130 | 1.7 | 2.0 | 2.0 | 1.6 | 1.8 |
| ***Sntg2*** | 552 | 847 | 444 | 675 | 381 | 799 | 465 | 795 | 1.5 | 1.5 | 2.1 | 1.7 | 1.7 |
| ***Rnf213*** | 3103 | 5389 | 3651 | 5878 | 2506 | 4870 | 3651 | 5609 | 1.7 | 1.6 | 1.9 | 1.5 | 1.7 |
| ***Igf1*** | 2904 | 4867 | 3373 | 5101 | 2830 | 5767 | 3319 | 5145 | 1.7 | 1.5 | 2.0 | 1.5 | 1.7 |
| ***Gria3*** | 445 | 737 | 520 | 835 | 454 | 843 | 547 | 832 | 1.7 | 1.6 | 1.9 | 1.5 | 1.7 |

## Table S7. GO-Term analysis of upregulated genes in microarray analysis.

Shown are GO-terms of upregulated genes in the microarray determined by MouseMine sorted by raw p-value.

| Category | Term | Count | % | PValue | Genes | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini | FDR |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| GOTERM_BP_DIRECT | GO:0051607~defense response to virus | 10 | 1.45E+16 | 3.89E+06 | IFIH1, ISG15, OASL2, OASL1, PMAIP1, OAS1A, OAS2, IL33, OAS1F, MX2 | 61 | 167 | 18082 | 1.78E+15 | 2.36E+10 | 2.36E+10 | 5.75E+08 |
| INTERPRO | IPR006117:2-5-oligoadenylate synthetase, conserved site | 5 | 7.25E+15 | 5.51E+06 | OASL2, OASL1, OAS1A, OAS2, OAS1F | 64 | 8 | 20594 | 2.01E+10 | 1.00E+10 | 1.00E+10 | 6.80E+09 |
| INTERPRO | IPR026774:2-5-oligoadenylate synthase | 5 | 7.25E+15 | 3.86E+07 | OASL2, OASL1, OAS1A, OAS2, OAS1F | 64 | 12 | 20594 | 1.34E+16 | 7.03E+10 | 3.52E+09 | 4.77E+10 |
| INTERPRO | IPR018952:2-5-oligoadenylate synthetase 1, domain 2/C-terminal | 5 | 7.25E+15 | 3.86E+07 | OASL2, OASL1, OAS1A, OAS2, OAS1F | 64 | 12 | 20594 | 1.34E+16 | 7.03E+10 | 3.52E+09 | 4.77E+10 |
| INTERPRO | IPR006116:2-5-oligoadenylate synthetase, N-terminal | 5 | 7.25E+15 | 7.78E+06 | OASL2, OASL1, OAS1A, OAS2, OAS1F | 64 | 14 | 20594 | 1.15E+08 | 1.42E+11 | 4.72E+09 | 9.60E+10 |
| GOTERM_BP_DIRECT | GO:0009615~response to virus | 7 | 1.01E+16 | 3.44E+09 | IFIH1, OASL2, OASL1, TGTP2, OAS1A, OAS2, MX2 | 61 | 84 | 18082 | 2.47E+15 | 2.08E+12 | 1.04E+12 | 5.08E+11 |
| UP_KEYWORDS | Antiviral defense | 7 | 1.01E+16 | 4.23E+09 | IFIH1, ISG15, OASL2, OASL1, OAS1A, OAS2, MX2 | 66 | 100 | 22680 | 2.41E+15 | 5.41E+10 | 5.41E+10 | 4.91E+11 |
| GOTERM_MF_DIRECT | GO:0003725~double-stranded RNA binding | 6 | 8.70E+15 | 3.81E+10 | IFIH1, OASL2, OASL1, OAS1A, OAS2, OAS1F | 60 | 70 | 17446 | 2.49E+16 | 5.67E+11 | 5.67E+11 | 4.54E-03 |
| UP_KEYWORDS | Innate immunity | 8 | 1.16E+16 | 5.78E+10 | IFIH1, CD55, OASL2, OASL1, TGTP2, OAS1A, OAS2, MX2 | 66 | 241 | 22680 | 1.14E+16 | 7.39E+11 | 3.70E+11 | 6.71E-03 |
| GOTERM_MF_DIRECT | GO:0001730~2-5-oligoadenylate synthetase activity | 4 | 5.80E+15 | 5.95E+09 | OASL2, OASL1, OAS1A, OAS2 | 60 | 11 | 17446 | 1.06E+16 | 8.86E+11 | 4.43E+11 | 7.09E-03 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| UP_KEYWORDS | Immunity | 9 | 1.30E+16 | 1.86E+11 | IFIH1, CD55, OASL2, OASL1, TGTP2, OAS1A, OAS2, MX2, LGALS9 | 66 | 401 | 22680 | 7.71E+15 | 2.38E-03 | 7.95E+11 | 2.16E-02 |
| KEGG_PATHWAY | mmu04115:p53 signaling pathway | 5 | 7.25E+15 | 4.11E+10 | CDKN1A, ZMAT3, IGF1, PMAIP1, CCNG1 | 24 | 67 | 7691 | 2.39E+16 | 2.79E-03 | 2.79E-03 | 4.23E-02 |
| UP_KEYWORDS | Glycoprotein | 25 | 3.62E+16 | 7.91E+10 | CCKAR, FFAR4, SLC6A2, NELL1, ITGA11, OAS2, GDNF, SMOC2, LGALS3BP, WISP1, P4HA2, CRISPLD2, DNER, FAP, GPR20, ASIC2, GRIA3, FRZB, CD55, CHRDL1, SULF2, PTPRV, P2RY14, GPR17, GDF15 | 66 | 3815 | 22680 | 2.25E+16 | 1.01E-02 | 2.53E-03 | 9.18E-02 |
| UP_KEYWORDS | Disulfide bond | 22 | 3.19E+15 | 1.05E+12 | CCKAR, SLC6A2, NELL1, EDN1, ASIC2, ITGA11, IGF1, GRIA3, FRZB, TTN, GDNF, SMOC2, CD55, LGALS3BP, WISP1, ISG15, CRISPLD2, DNER, FAP, P2RY14, GPR17, GDF15 | 66 | 3124 | 22680 | 2.42E+16 | 1.34E-02 | 2.69E-03 | 1.22E-01 |
| UP_KEYWORDS | Secreted | 15 | 2.17E+15 | 2.46E+12 | NELL1, EDN1, IGF1, IL33, FRZB, GDNF, LGALS9, SMOC2, LGALS3BP, CHRDL1, WISP1, ISG15, CRISPLD2, FAP, GDF15 | 66 | 1685 | 22680 | 3.06E+15 | 3.11E-02 | 5.25E-03 | 2.86E-01 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| UP_SEQ_FEATURE | glycosylation site:N-linked (GlcNAc...) | 24 | 3.48E+15 | 2.84E+12 | CCKAR, FFAR4, SLC6A2, NELL1, ITGA11, ASIC2, GRIA3, FRZB, GDNF, SMOC2, CD55, LGALS3BP, CHRDL1, WISP1, SULF2, P4HA2, CRISPLD2, PTPRV, DNER, FAP, P2RY14, GPR17, GDF15, GPR20 | 58 | 3563 | 18012 | 2.09E+16 | 1.81E-01 | 1.81E-01 | 4.28E-01 |
| UP_SEQ_FEATURE | disulfide bond | 19 | 2.75E+16 | 5.04E+10 | CCKAR, NELL1, EDN1, ASIC2, ITGA11, IGF1, FRZB, TTN, GDNF, SMOC2, CD55, LGALS3BP, WISP1, CRISPLD2, DNER, P2RY14, FAP, GPR17, GDF15 | 58 | 2510 | 18012 | 2.35E+16 | 2.99E-01 | 1.63E-01 | 7.59E-01 |
| GOTERM_BP_DIRECT | GO:0061051~positive regulation of cell growth involved in cardiac muscle cell development | 3 | 4.35E+16 | 7.00E+11 | WISP1, EDN1, IGF1 | 61 | 12 | 18082 | 7.41E+15 | 3.46E-01 | 1.32E-01 | 1.03E+15 |
| GOTERM_CC_DIRECT | GO:0005576~extracellular region | 15 | 2.17E+15 | 7.80E+11 | NELL1, EDN1, IGF1, IL33, FRZB, GDNF, LGALS9, SMOC2, LGALS3BP, CHRDL1, WISP1, ISG15, CRISPLD2, FAP, GDF15 | 62 | 1753 | 19662 | 2.71E+15 | 7.51E-02 | 7.51E-02 | 8.62E-01 |
| INTERPRO | IPR002934:Nucleotidyl transferase domain | 3 | 4.35E+16 | 8.19E+11 | OASL2, OAS1A, OAS2 | 64 | 14 | 20594 | 6.90E+07 | 1.38E-01 | 3.66E-02 | 1.01E+16 |
| GOTERM_CC_DIRECT | GO:0045178~basal part of cell | 3 | 4.35E+16 | 1.25E-03 | EPPK1, FAP, EDN1 | 62 | 17 | 19662 | 5.60E+16 | 1.18E-01 | 6.06E-02 | 1.38E+15 |
| KEGG_PATHWAY | mmu05164:Influenza A | 5 | 7.25E+15 | 1.50E-03 | IFIH1, OAS1A, OAS2, IL33, MX2 | 24 | 171 | 7691 | 9.37E+15 | 9.71E-02 | 4.98E-02 | 1.53E+16 |
| GOTERM_BP_DIRECT | GO:0002376~immune system process | 7 | 1.01E+16 | 1.66E-03 | IFIH1, CD55, OASL2, OASL1, OAS2, MX2, LGALS9 | 61 | 383 | 18082 | 5.42E+15 | 6.34E-01 | 2.22E-01 | 2.42E+16 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| GOTERM_BP_DIRECT | GO:0006164~purine nucleotide biosynthetic process | 3 | 4.35E+16 | 1.98E-03 | OASL2, OAS1A, OAS2 | 61 | 20 | 18082 | 4.45E+15 | 6.99E-01 | 2.14E-01 | 2.89E+16 |
| GOTERM_BP_DIRECT | GO:0045087~innate immune response | 7 | 1.01E+16 | 2.06E-03 | IFIH1, CD55, OASL2, OASL1, OAS1A, OAS2, MX2 | 61 | 400 | 18082 | 5.19E+15 | 7.14E-01 | 1.88E-01 | 3.01E+16 |
| GOTERM_BP_DIRECT | GO:0006955~immune response | 6 | 8.70E+15 | 2.06E-03 | P2RY14, OASL2, OASL1, TGTP2, OAS2, OAS1F | 61 | 272 | 18082 | 6.54E+15 | 7.14E-01 | 1.64E-01 | 3.01E+16 |
| UP_SEQ_FEATURE | signal peptide | 20 | 2.90E+16 | 2.55E-03 | NELL1, EDN1, ITGA11, IGF1, GRIA3, FRZB, GDNF, SMOC2, CD55, LGALS3BP, CHRDL1, WISP1, SULF2, P4HA2, SHISA3, PTPRV, CRISPLD2, DNER, GDF15, PQLC3 | 58 | 3124 | 18012 | 1.99E+16 | 8.35E-01 | 4.51E-01 | 3.78E+15 |
| GOTERM_BP_DIRECT | GO:0072332~intrinsic apoptotic signaling pathway by p53 class mediator | 3 | 4.35E+16 | 4.73E-03 | PTPRV, ZMAT3, PMAIP1 | 61 | 31 | 18082 | 2.87E+16 | 9.44E-01 | 3.02E-01 | 6.78E+15 |
| GOTERM_BP_DIRECT | GO:0051482~positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G-protein coupled signaling pathway | 3 | 4.35E+16 | 4.73E-03 | EDN1, GPR17, GPR20 | 61 | 31 | 18082 | 2.87E+16 | 9.44E-01 | 3.02E-01 | 6.78E+15 |
| GOTERM_BP_DIRECT | GO:0045071~negative regulation of viral genome replication | 3 | 4.35E+16 | 5.04E-03 | ISG15, OASL1, MX2 | 61 | 32 | 18082 | 2.78E+16 | 9.53E-01 | 2.88E-01 | 7.20E+15 |
| UP_SEQ_FEATURE | domain:Ubiquitin-like 1 | 2 | 2.90E+15 | 6.32E-03 | ISG15, GM9706 | 58 | 2 | 18012 | 3.11E+16 | 9.88E-01 | 6.72E-01 | 9.12E+15 |
| UP_SEQ_FEATURE | domain:Ubiquitin-like 2 | 2 | 2.90E+15 | 6.32E-03 | ISG15, GM9706 | 58 | 2 | 18012 | 3.11E+16 | 9.88E-01 | 6.72E-01 | 9.12E+15 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| UP_SEQ_FEATURE | region of interest:Involved in the ligation of specific target proteins | 2 | 2.90E+15 | 6.32E-03 | ISG15, GM9706 | 58 | 2 | 18012 | 3.11E+16 | 9.88E-01 | 6.72E-01 | 9.12E+15 |
| UP_SEQ_FEATURE | chain:Ubiquitin cross-reactive protein | 2 | 2.90E+15 | 6.32E-03 | ISG15, GM9706 | 58 | 2 | 18012 | 3.11E+16 | 9.88E-01 | 6.72E-01 | 9.12E+15 |
| SMART | SM00214:VWC | 3 | 4.35E+16 | 6.42E-03 | CHRDL1, WISP1, NELL1 | 37 | 35 | 10425 | 2.42E+15 | 2.94E-01 | 2.94E-01 | 6.12E+15 |
| GOTERM_BP_DIRECT | GO:0051924~regulation of calcium ion transport | 3 | 4.35E+16 | 6.69E-03 | CCKAR, SLN, IGF1 | 61 | 37 | 18082 | 2.40E+16 | 9.83E-01 | 3.34E-01 | 9.45E+15 |
| INTERPRO | IPR001007:von Willebrand factor, type C | 3 | 4.35E+16 | 6.99E-03 | CHRDL1, WISP1, NELL1 | 64 | 41 | 20594 | 2.35E+15 | 7.21E-01 | 2.25E-01 | 8.30E+15 |
| KEGG_PATHWAY | mmu05162:Measles | 4 | 5.80E+15 | 7.39E-03 | IFIH1, OAS1A, OAS2, MX2 | 24 | 136 | 7691 | 9.43E+15 | 3.96E-01 | 1.55E-01 | 7.35E+15 |
| GOTERM_BP_DIRECT | GO:0035458~cellular response to interferon-beta | 3 | 4.35E+16 | 8.17E-03 | TGTP2, IFI203, GBP3 | 61 | 41 | 18082 | 2.17E+16 | 9.93E-01 | 3.64E-01 | 1.14E+16 |
| GOTERM_BP_DIRECT | GO:0030308~negative regulation of cell growth | 4 | 5.80E+15 | 8.29E-03 | CDKN1A, ZMAT3, MNDAL, FRZB | 61 | 125 | 18082 | 9.49E+15 | 9.94E-01 | 3.43E-01 | 1.16E+16 |
| UP_KEYWORDS | Cytoplasm | 22 | 3.19E+15 | 9.38E-03 | PID1, IFIH1, EPPK1, NELL1, LMCD1, IFI44, OAS2, TTN, RNF213, LGALS9, CDKN1A, ISG15, PARP14, OASL1, FABP4, TRP53INP1, TGTP2, XAF1, OAS1A, MX2, GBP3, SNTG2 | 66 | 4404 | 22680 | 1.72E+16 | 7.01E-01 | 1.58E-01 | 1.04E+16 |
| SMART | SM00213:UBQ | 3 | 4.35E+16 | 1.38E-02 | ISG15, OASL2, OASL1 | 37 | 52 | 10425 | 1.63E+16 | 5.28E-01 | 3.13E-01 | 1.27E+16 |
| GOTERM_MF_DIRECT | GO:0008201~heparin binding | 4 | 5.80E+15 | 1.45E-02 | SMOC2, WISP1, CRISPLD2, NELL1 | 60 | 151 | 17446 | 7.70E+14 | 8.87E-01 | 5.16E-01 | 1.60E+16 |
| GOTERM_BP_DIRECT | GO:0009408~response to heat | 3 | 4.35E+16 | 1.54E-02 | CCKAR, TRP53INP1, IGF1 | 61 | 57 | 18082 | 1.56E+16 | 1.00E+00 | 5.14E-01 | 2.05E+16 |
| GOTERM_BP_DIRECT | GO:0050974~detection of mechanical stimulus involved in sensory perception | 2 | 2.90E+15 | 1.65E-02 | ASIC2, IGF1 | 61 | 5 | 18082 | 1.19E+16 | 1.00E+00 | 5.13E-01 | 2.18E+15 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| GOTERM_CC_DIRECT | GO:0005615~extracellular space | 11 | 1.59E+16 | 1.67E-02 | LGALS3BP, SULF2, NELL1, FAP, EDN1, LMCD1, IGF1, IL33, FRZB, GDF15, GDNF | 62 | 1504 | 19662 | 2.32E+15 | 8.14E-01 | 4.29E-01 | 1.70E+15 |
| INTERPRO | IPR000626:Ubiquitin | 3 | 4.35E+16 | 1.74E-02 | ISG15, OASL2, OASL1 | 64 | 66 | 20594 | 1.46E+16 | 9.59E-01 | 4.13E-01 | 1.95E+15 |
| UP_KEYWORDS | Nucleotidyltransferase | 3 | 4.35E+16 | 2.01E-02 | OASL2, OAS1A, OAS2 | 66 | 76 | 22680 | 1.36E+16 | 9.26E-01 | 2.78E-01 | 2.10E+16 |
| KEGG_PATHWAY | mmu05410:Hypertrophic cardiomyopathy (HCM) | 3 | 4.35E+16 | 2.29E-02 | ITGA11, IGF1, TTN | 24 | 79 | 7691 | 1.22E+16 | 7.93E-01 | 3.26E-01 | 2.12E+16 |
| GOTERM_BP_DIRECT | GO:0034340~response to type I interferon | 2 | 2.90E+15 | 2.30E-02 | ISG15, MX2 | 61 | 7 | 18082 | 8.47E+15 | 1.00E+00 | 6.09E-01 | 2.91E+15 |
| UP_KEYWORDS | Endoplasmic reticulum | 8 | 1.16E+16 | 2.36E-02 | SLN, SULF2, P4HA2, SHISA3, EPHX1, TGTP2, OAS1A, OAS2 | 66 | 997 | 22680 | 2.76E+15 | 9.53E-01 | 2.88E-01 | 2.43E+16 |
| UP_SEQ_FEATURE | region of interest:A | 2 | 2.90E+15 | 2.50E-02 | SYN2, IGF1 | 58 | 8 | 18012 | 7.76E+15 | 1.00E+00 | 9.72E-01 | 3.18E+15 |
| GOTERM_BP_DIRECT | GO:0043065~positive regulation of apoptotic process | 5 | 7.25E+15 | 2.51E-02 | NELL1, ZMAT3, TRP53INP1, PMAIP1, FRZB | 61 | 335 | 18082 | 4.42E+15 | 1.00E+00 | 6.17E-01 | 3.13E+16 |
| KEGG_PATHWAY | mmu05414:Dilated cardiomyopathy | 3 | 4.35E+16 | 2.51E-02 | ITGA11, IGF1, TTN | 24 | 83 | 7691 | 1.16E+16 | 8.23E-01 | 2.93E-01 | 2.30E+16 |
| GOTERM_BP_DIRECT | GO:0034392~negative regulation of smooth muscle cell apoptotic process | 2 | 2.90E+15 | 2.62E-02 | EDN1, IGF1 | 61 | 8 | 18082 | 7.41E+15 | 1.00E+00 | 6.12E-01 | 3.25E+15 |
| UP_KEYWORDS | RNA-binding | 6 | 8.70E+15 | 2.89E-02 | IFIH1, OASL2, ZMAT3, OASL1, OAS1A, OAS2 | 66 | 601 | 22680 | 3.43E+16 | 9.76E-01 | 3.13E-01 | 2.88E+16 |
| GOTERM_BP_DIRECT | GO:0048661~positive regulation of smooth muscle cell proliferation | 3 | 4.35E+16 | 2.90E-02 | WISP1, EDN1, IGF1 | 61 | 80 | 18082 | 1.11E+16 | 1.00E+00 | 6.29E-01 | 3.53E+15 |
| GOTERM_BP_DIRECT | GO:0006977~DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest | 2 | 2.90E+15 | 2.95E-02 | CDKN1A, PTPRV | 61 | 9 | 18082 | 6.59E+15 | 1.00E+00 | 6.15E-01 | 3.58E+16 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| INTERPRO | IPR004021:HIN-200/IF120x | 2 | 2.90E+15 | 3.02E-02 | MNDAL, IFI203 | 64 | 10 | 20594 | 6.44E+06 | 9.96E-01 | 5.49E-01 | 3.15E+16 |
| INTERPRO | IPR011029:Death-like domain | 3 | 4.35E+16 | 3.04E-02 | IFIH1, MNDAL, IFI203 | 64 | 89 | 20594 | 1.08E+16 | 9.96E-01 | 5.05E-01 | 3.17E+16 |
| GOTERM_BP_DIRECT | GO:0070886~positive regulation of calcineurin-NFAT signaling cascade | 2 | 2.90E+15 | 3.27E-02 | LMCD1, IGF1 | 61 | 10 | 18082 | 5.93E+15 | 1.00E+00 | 6.35E-01 | 3.88E+16 |
| UP_SEQ_FEATURE | domain:Fibronectin type-III 10 | 2 | 2.90E+15 | 3.43E-02 | PTPRV, TTN | 58 | 11 | 18012 | 5.65E+15 | 1.00E+00 | 9.83E-01 | 4.09E+15 |
| UP_KEYWORDS | Cleavage on pair of basic residues | 4 | 5.80E+15 | 3.44E-02 | FAP, EDN1, GDF15, GDNF | 66 | 248 | 22680 | 5.54E+15 | 9.89E-01 | 3.34E-01 | 3.34E+15 |
| KEGG_PATHWAY | mmu04066:HIF-1 signaling pathway | 3 | 4.35E+16 | 3.68E-02 | CDKN1A, EDN1, IGF1 | 24 | 102 | 7691 | 9.43E+15 | 9.22E-01 | 3.46E-01 | 3.20E+14 |
| GOTERM_BP_DIRECT | GO:0008285~negative regulation of cell proliferation | 5 | 7.25E+15 | 3.85E-02 | CDKN1A, PTPRV, TRP53INP1, IGF1, FRZB | 61 | 384 | 18082 | 3.86E+16 | 1.00E+00 | 6.78E-01 | 4.41E+16 |
| UP_SEQ_FEATURE | compositionally biased region:Poly-Ser | 5 | 7.25E+15 | 3.97E-02 | CCKAR, SHISA3, SYN2, IFI203, TTN | 58 | 407 | 18012 | 3.82E+16 | 1.00E+00 | 9.83E-01 | 4.58E+15 |
| UP_SEQ_FEATURE | domain:VWFC 3 | 2 | 2.90E+15 | 4.04E-02 | CHRDL1, NELL1 | 58 | 13 | 18012 | 4.78E+16 | 1.00E+00 | 9.73E-01 | 4.63E+15 |
| GOTERM_MF_DIRECT | GO:0005178~integrin binding | 3 | 4.35E+16 | 4.51E-02 | WISP1, FAP, IGF1 | 60 | 100 | 17446 | 8.72E+03 | 9.99E-01 | 8.20E-01 | 4.23E+16 |
| GOTERM_BP_DIRECT | GO:0071850~mitotic cell cycle arrest | 2 | 2.90E+15 | 4.55E-02 | CDKN1A, FAP | 61 | 14 | 18082 | 4.23E+15 | 1.00E+00 | 7.23E-01 | 4.98E+15 |
| GOTERM_CC_DIRECT | GO:0005730~nucleolus | 7 | 1.01E+16 | 4.58E-02 | CDKN1A, ZMAT3, MNDAL, OASL1, TRP53INP1, IFI203, RNF213 | 62 | 842 | 19662 | 2.64E+15 | 9.91E-01 | 6.90E-01 | 4.06E+15 |
| UP_SEQ_FEATURE | topological domain:Extracellular | 13 | 1.88E+15 | 4.73E-02 | CCKAR, FFAR4, SLC6A2, ASIC2, ITGA11, GRIA3, SHISA3, PTPRV, P2RY14, FAP, DNER, GPR17, GPR20 | 58 | 2256 | 18012 | 1.79E+16 | 1.00E+00 | 9.77E-01 | 5.19E+16 |
| GOTERM_CC_DIRECT | GO:0043195~terminal bouton | 3 | 4.35E+16 | 4.81E-02 | CCKAR, SYN2, GRIA3 | 62 | 113 | 19662 | 8.42E+15 | 9.93E-01 | 6.27E-01 | 4.21E+15 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| UP_KEYWORDS | Signal | 20 | 2.90E+16 | 4.91E-02 | NELL1, EDN1, ITGA11, IGF1, GRIA3, FRZB, GDNF, SMOC2, CD55, LGALS3BP, CHRDL1, WISP1, SULF2, P4HA2, SHISA3, PTPRV, CRISPLD2, DNER, GDF15, PQLC3 | 66 | 4543 | 22680 | 1.51E+16 | 9.98E-01 | 4.15E-01 | 4.42E+15 |
| UP_SEQ_FEATURE | domain:Fibronectin type-III 9 | 2 | 2.90E+15 | 4.95E-02 | PTPRV, TTN | 58 | 16 | 18012 | 3.88E+15 | 1.00E+00 | 9.72E-01 | 5.35E+14 |
| GOTERM_MF_DIRECT | GO:0043539~protein serine/threonine kinase activator activity | 2 | 2.90E+15 | 4.96E-02 | IGF1, LGALS9 | 60 | 15 | 17446 | 3.88E+15 | 9.99E-01 | 7.80E-01 | 4.55E+15 |
| GOTERM_CC_DIRECT | GO:0005614~interstitial matrix | 2 | 2.90E+15 | 5.15E-02 | SMOC2, IGF1 | 62 | 17 | 19662 | 3.73E+16 | 9.95E-01 | 5.86E-01 | 4.44E+15 |
| UP_KEYWORDS | Growth factor | 3 | 4.35E+16 | 5.15E-02 | IGF1, GDF15, GDNF | 66 | 127 | 22680 | 8.12E+15 | 9.99E-01 | 4.06E-01 | 4.59E+15 |
| UP_KEYWORDS | Apoptosis | 5 | 7.25E+15 | 5.17E-02 | FAP, ZMAT3, TRP53INP1, PMAIP1, XAF1 | 66 | 489 | 22680 | 3.51E+15 | 9.99E-01 | 3.84E-01 | 4.60E+15 |
| GOTERM_BP_DIRECT | GO:0071356~cellular response to tumor necrosis factor | 3 | 4.35E+16 | 5.17E-02 | PID1, EDN1, FABP4 | 61 | 110 | 18082 | 8.08E+14 | 1.00E+00 | 7.53E-01 | 5.44E+15 |
| GOTERM_BP_DIRECT | GO:2000679~positive regulation of transcription regulatory region DNA binding | 2 | 2.90E+15 | 5.18E-02 | IGF1, LGALS9 | 61 | 16 | 18082 | 3.71E+15 | 1.00E+00 | 7.39E-01 | 5.45E+15 |
| UP_SEQ_FEATURE | domain:VWFC 1 | 2 | 2.90E+15 | 5.25E-02 | CHRDL1, NELL1 | 58 | 17 | 18012 | 3.65E+15 | 1.00E+00 | 9.68E-01 | 5.57E+15 |
| UP_SEQ_FEATURE | domain:VWFC 2 | 2 | 2.90E+15 | 5.25E-02 | CHRDL1, NELL1 | 58 | 17 | 18012 | 3.65E+15 | 1.00E+00 | 9.68E-01 | 5.57E+15 |
| UP_KEYWORDS | Microsome | 3 | 4.35E+16 | 5.51E-02 | EPHX1, OAS1A, OAS2 | 66 | 132 | 22680 | 7.81E+15 | 9.99E-01 | 3.84E-01 | 4.82E+16 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| GOTERM_CC_DIRECT | GO:0005737~cytoplasm | 28 | 4.06E+15 | 5.60E-02 | CCKAR, IFIH1, RTP4, NELL1, EDN1, OAS2, RNF213, WISP1, P4HA2, ISG15, OASL1, TRP53INP1, XAF1, MX2, PID1, EPPK1, MNDAL, LMCD1, IGF1, IFI44, LGALS9, CDKN1A, PARP14, FABP4, IFI203, GDF15, GBP3, SNTG2 | 62 | 6631 | 19662 | 1.34E+16 | 9.97E-01 | 5.61E-01 | 4.72E+16 |
| GOTERM_BP_DIRECT | GO:0010629~negative regulation of gene expression | 4 | 5.80E+15 | 5.79E-02 | CDKN1A, TRP53INP1, IGF1, LGALS9 | 61 | 265 | 18082 | 4.47E+15 | 1.00E+00 | 7.64E-01 | 5.86E+15 |
| GOTERM_BP_DIRECT | GO:0010613~positive regulation of cardiac muscle hypertrophy | 2 | 2.90E+15 | 5.81E-02 | EDN1, IGF1 | 61 | 18 | 18082 | 3.29E+15 | 1.00E+00 | 7.52E-01 | 5.87E+16 |
| GOTERM_BP_DIRECT | GO:0043032~positive regulation of macrophage activation | 2 | 2.90E+15 | 5.81E-02 | IL33, LGALS9 | 61 | 18 | 18082 | 3.29E+15 | 1.00E+00 | 7.52E-01 | 5.87E+16 |
| INTERPRO | IPR009030:Insulin-like growth factor binding protein, N-terminal | 3 | 4.35E+16 | 6.02E-02 | WISP1, NELL1, DNER | 64 | 130 | 20594 | 7.43E+15 | 1.00E+00 | 7.15E-01 | 5.35E+16 |
| KEGG_PATHWAY | mmu05160:Hepatitis C | 3 | 4.35E+16 | 6.17E-02 | CDKN1A, OAS1A, OAS2 | 24 | 136 | 7691 | 7.07E+15 | 9.87E-01 | 4.61E-01 | 4.80E+15 |
| UP_KEYWORDS | Magnesium | 5 | 7.25E+15 | 6.23E-02 | OASL2, ITGA11, OAS1A, OAS2, TTN | 66 | 521 | 22680 | 3.30E+15 | 1.00E+00 | 4.02E-01 | 5.26E+16 |
| GOTERM_BP_DIRECT | GO:0019229~regulation of vasoconstriction | 2 | 2.90E+15 | 6.43E-02 | EDN1, ASIC2 | 61 | 20 | 18082 | 2.96E+15 | 1.00E+00 | 7.75E-01 | 6.26E+14 |
| GOTERM_BP_DIRECT | GO:0010165~response to X-ray | 2 | 2.90E+15 | 6.75E-02 | CDKN1A, PMAIP1 | 61 | 21 | 18082 | 2.82E+15 | 1.00E+00 | 7.79E-01 | 6.44E+15 |
| GOTERM_BP_DIRECT | GO:0010001~glial cell differentiation | 2 | 2.90E+15 | 6.75E-02 | DNER, IGF1 | 61 | 21 | 18082 | 2.82E+15 | 1.00E+00 | 7.79E-01 | 6.44E+15 |
| GOTERM_BP_DIRECT | GO:0071398~cellular response to fatty acid | 2 | 2.90E+15 | 6.75E-02 | PID1, EDN1 | 61 | 21 | 18082 | 2.82E+15 | 1.00E+00 | 7.79E-01 | 6.44E+15 |
| GOTERM_MF_DIRECT | GO:0005539~glycosaminoglycan binding | 2 | 2.90E+15 | 6.87E-02 | SMOC2, CRISPLD2 | 60 | 21 | 17446 | 2.77E+16 | 1.00E+00 | 8.29E-01 | 5.72E+16 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| UP_SEQ_FEATURE | domain:Fibronectin type-III 8 | 2 | 2.90E+15 | 7.33E-02 | PTPRV, TTN | 58 | 24 | 18012 | 2.59E+16 | 1.00E+00 | 9.89E-01 | 6.83E+15 |
| GOTERM_CC_DIRECT | GO:0005578~proteinaceous extracellular matrix | 4 | 5.80E+15 | 7.49E-02 | SMOC2, LGALS3BP, WISP1, CRISPLD2 | 62 | 316 | 19662 | 4.01E+15 | 1.00E+00 | 6.22E-01 | 5.79E+14 |
| UP_SEQ_FEATURE | domain:Fibronectin type-III 7 | 2 | 2.90E+15 | 7.62E-02 | PTPRV, TTN | 58 | 25 | 18012 | 2.48E+16 | 1.00E+00 | 9.86E-01 | 6.98E+15 |
| UP_SEQ_FEATURE | binding site:Activating enzyme | 2 | 2.90E+15 | 7.92E-02 | ISG15, GM9706 | 58 | 26 | 18012 | 2.39E+16 | 1.00E+00 | 9.84E-01 | 7.12E+15 |
| INTERPRO | IPR004020:DAPIN domain | 2 | 2.90E+15 | 7.94E-02 | MNDAL, IFI203 | 64 | 27 | 20594 | 2.38E+15 | 1.00E+00 | 7.78E-01 | 6.40E+15 |
| GOTERM_BP_DIRECT | GO:0014065~phosphatidylinositol 3-kinase signaling | 2 | 2.90E+15 | 7.98E-02 | EDN1, IGF1 | 61 | 25 | 18082 | 2.37E+15 | 1.00E+00 | 8.24E-01 | 7.08E+15 |
| GOTERM_BP_DIRECT | GO:0010468~regulation of gene expression | 4 | 5.80E+15 | 8.25E-02 | NELL1, ASIC2, IGF1, GDNF | 61 | 308 | 18082 | 3.85E+16 | 1.00E+00 | 8.24E-01 | 7.20E+15 |
| GOTERM_CC_DIRECT | GO:0043025~neuronal cell body | 5 | 7.25E+15 | 8.38E-02 | DNER, ASIC2, IGF1, GRIA3, CCNG1 | 62 | 534 | 19662 | 2.97E+16 | 1.00E+00 | 6.22E-01 | 6.22E+15 |
| GOTERM_MF_DIRECT | GO:0005504~fatty acid binding | 2 | 2.90E+15 | 8.44E-02 | FFAR4, FABP4 | 60 | 26 | 17446 | 2.24E+16 | 1.00E+00 | 8.47E-01 | 6.51E+14 |
| UP_KEYWORDS | Nucleus | 19 | 2.75E+16 | 8.45E-02 | IFIH1, ZMAT3, NELL1, MNDAL, LMCD1, IL33, OAS2, TTN, CCNG1, LGALS9, CDKN1A, PARP14, OASL1, FABP4, TRP53INP1, XAF1, OAS1A, IFI203, GBP3 | 66 | 4534 | 22680 | 1.44E+16 | 1.00E+00 | 4.85E-01 | 6.41E+15 |
| UP_SEQ_FEATURE | compositionally biased region:Ser/Thr-rich | 2 | 2.90E+15 | 8.50E-02 | CD55, FRZB | 58 | 28 | 18012 | 2.22E+16 | 1.00E+00 | 9.85E-01 | 7.38E+15 |
| GOTERM_BP_DIRECT | GO:0032689~negative regulation of interferon-gamma production | 2 | 2.90E+15 | 8.59E-02 | IL33, LGALS9 | 61 | 27 | 18082 | 2.20E+16 | 1.00E+00 | 8.27E-01 | 7.35E+15 |
| GOTERM_BP_DIRECT | GO:0035025~positive regulation of Rho protein signal transduction | 2 | 2.90E+15 | 8.59E-02 | GPR17, GPR20 | 61 | 27 | 18082 | 2.20E+16 | 1.00E+00 | 8.27E-01 | 7.35E+15 |
| KEGG_PATHWAY | mmu05202:Transcriptional misregulation in cancer | 3 | 4.35E+16 | 8.63E-02 | CDKN1A, IGF1, GRIA3 | 24 | 165 | 7691 | 5.83E+15 | 9.98E-01 | 5.36E-01 | 6.05E+15 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| GOTERM_MF_DIRECT | GO:0008083~growth factor activity | 3 | 4.35E+16 | 8.64E-02 | IGF1, GDF15, GDNF | 60 | 145 | 17446 | 6.02E+15 | 1.00E+00 | 8.14E-01 | 6.60E+15 |
| UP_SEQ_FEATURE | domain:Fibronectin type-III 6 | 2 | 2.90E+15 | 8.79E-02 | PTPRV, TTN | 58 | 29 | 18012 | 2.14E+16 | 1.00E+00 | 9.83E-01 | 7.51E+15 |
| UP_KEYWORDS | Calcium | 6 | 8.70E+15 | 8.81E-02 | SMOC2, SULF2, NELL1, DNER, ITGA11, TTN | 66 | 827 | 22680 | 2.49E+16 | 1.00E+00 | 4.81E-01 | 6.57E+14 |
| SMART | SM01289:SM01289 | 2 | 2.90E+15 | 8.93E-02 | MNDAL, IFI203 | 37 | 27 | 10425 | 2.09E+15 | 9.94E-01 | 8.14E-01 | 6.00E+15 |
| GOTERM_BP_DIRECT | GO:0045840~positive regulation of mitotic nuclear division | 2 | 2.90E+15 | 9.20E-02 | EDN1, IGF1 | 61 | 29 | 18082 | 2.04E+16 | 1.00E+00 | 8.39E-01 | 7.60E+15 |
| UP_KEYWORDS | Hydrolase | 9 | 1.30E+16 | 9.73E-02 | IFIH1, USP18, SULF2, PTPRV, FAP, EPHX1, TGTP2, RNF213, GBP3 | 66 | 1646 | 22680 | 1.88E+16 | 1.00E+00 | 4.98E-01 | 6.95E+15 |
| GOTERM_BP_DIRECT | GO:2000379~positive regulation of reactive oxygen species metabolic process | 2 | 2.90E+15 | 9.80E-02 | PID1, CDKN1A | 61 | 31 | 18082 | 1.91E+16 | 1.00E+00 | 8.49E-01 | 7.82E+15 |
| GOTERM_BP_DIRECT | GO:0042771~intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator | 2 | 2.90E+15 | 9.80E-02 | CDKN1A, PMAIP1 | 61 | 31 | 18082 | 1.91E+16 | 1.00E+00 | 8.49E-01 | 7.82E+15 |
| UP_KEYWORDS | Metal-binding | 15 | 2.17E+15 | 9.85E-02 | IFIH1, SLC6A2, ZMAT3, LMCD1, ITGA11, OAS2, TTN, RNF213, SMOC2, CDKN1A, SULF2, P4HA2, OASL2, OAS1A, XAF1 | 66 | 3395 | 22680 | 1.52E+16 | 1.00E+00 | 4.85E-01 | 7.00E+15 |

**Table S8. Functional annotation analysis of upregulated genes in microarray analysis.**

Shown are functional clusters of upregulated genes in the microarray determined by DAVID functional annotation tool sorted by enrichment score.

**Annotation Cluster 1** **Enrichment Score: 3.4238609883227045**

| Category | Term | Count | % | PValue | Genes | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini | FDR |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| GOTERM_BP_DIRECT | GO:0051607~defense response to virus | 10 | 1.45E+16 | 3.89E+06 | IFIH1, ISG15, OASL2, OASL1, PMAIP1, OAS1A, OAS2, IL33, OAS1F, MX2 | 61 | 167 | 18082 | 1.78E+15 | 2.36E+10 | 2.36E+10 | 5.75E+08 |
| INTERPRO | IPR006117:2-5-oligoadenylate synthetase, conserved site | 5 | 7.25E+15 | 5.51E+06 | OASL2, OASL1, OAS1A, OAS2, OAS1F | 64 | 8 | 20594 | 2.01E+10 | 1.00E+10 | 1.00E+10 | 6.80E+09 |
| INTERPRO | IPR026774:2'-5'-oligoadenylate synthase | 5 | 7.25E+15 | 3.86E+07 | OASL2, OASL1, OAS1A, OAS2, OAS1F | 64 | 12 | 20594 | 1.34E+16 | 7.03E+10 | 3.52E+09 | 4.77E+10 |
| INTERPRO | IPR018952:2'-5'-oligoadenylate synthetase 1, domain 2/C-terminal | 5 | 7.25E+15 | 3.86E+07 | OASL2, OASL1, OAS1A, OAS2, OAS1F | 64 | 12 | 20594 | 1.34E+16 | 7.03E+10 | 3.52E+09 | 4.77E+10 |
| INTERPRO | IPR006116:2-5-oligoadenylate synthetase, N-terminal | 5 | 7.25E+15 | 7.78E+06 | OASL2, OASL1, OAS1A, OAS2, OAS1F | 64 | 14 | 20594 | 1.15E+08 | 1.42E+11 | 4.72E+09 | 9.60E+10 |
| GOTERM_BP_DIRECT | GO:0009615~response to virus | 7 | 1.01E+16 | 3.44E+09 | IFIH1, OASL2, OASL1, TGTP2, OAS1A, OAS2, MX2 | 61 | 84 | 18082 | 2.47E+15 | 2.08E+12 | 1.04E+12 | 5.08E+11 |
| UP_KEYWORDS | Antiviral defense | 7 | 1.01E+16 | 4.23E+09 | IFIH1, ISG15, OASL2, OASL1, OAS1A, OAS2, MX2 | 66 | 100 | 22680 | 2.41E+15 | 5.41E+10 | 5.41E+10 | 4.91E+11 |
| GOTERM_MF_DIRECT | GO:0003725~double-stranded RNA binding | 6 | 8.70E+15 | 3.81E+10 | IFIH1, OASL2, OASL1, OAS1A, OAS2, OAS1F | 60 | 70 | 17446 | 2.49E+16 | 5.67E+11 | 5.67E+11 | 4.54E-03 |
| UP_KEYWORDS | Innate immunity | 8 | 1.16E+16 | 5.78E+10 | IFIH1, CD55, OASL2, OASL1, TGTP2, OAS1A, OAS2, MX2 | 66 | 241 | 22680 | 1.14E+16 | 7.39E+11 | 3.70E+11 | 6.71E-03 |
| GOTERM_MF_DIRECT | GO:0001730~2'-5'-oligoadenylate synthetase activity | 4 | 5.80E+15 | 5.95E+09 | OASL2, OASL1, OAS1A, OAS2 | 60 | 11 | 17446 | 1.06E+16 | 8.86E+11 | 4.43E+11 | 7.09E-03 |
| UP_KEYWORDS | Immunity | 9 | 1.30E+16 | 1.86E+11 | IFIH1, CD55, OASL2, OASL1, TGTP2, OAS1A, OAS2, MX2, LGALS9 | 66 | 401 | 22680 | 7.71E+15 | 2.38E-03 | 7.95E+11 | 2.16E-02 |
| INTERPRO | IPR002934:Nucleotidyl transferase domain | 3 | 4.35E+16 | 8.19E+11 | OASL2, OAS1A, OAS2 | 64 | 14 | 20594 | 6.90E+07 | 1.38E-01 | 3.66E-02 | 1.01E+16 |
| KEGG_PATHWAY | mmu05164:Influenza A | 5 | 7.25E+15 | 1.50E-03 | IFIH1, OAS1A, OAS2, IL33, MX2 | 24 | 171 | 7691 | 9.37E+15 | 9.71E-02 | 4.98E-02 | 1.53E+16 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| GOTERM_BP_DIRECT | GO:0002376~immune system process | 7 | 1.01E+16 | 1.66E-03 | IFIH1, CD55, OASL2, OASL1, OAS2, MX2, LGALS9 | 61 | 383 | 18082 | 5.42E+15 | 6.34E-01 | 2.22E-01 | 2.42E+16 |
| GOTERM_BP_DIRECT | GO:0006164~purine nucleotide biosynthetic process | 3 | 4.35E+16 | 1.98E-03 | OASL2, OAS1A, OAS2 | 61 | 20 | 18082 | 4.45E+15 | 6.99E-01 | 2.14E-01 | 2.89E+16 |
| GOTERM_BP_DIRECT | GO:0045087~innate immune response | 7 | 1.01E+16 | 2.06E-03 | IFIH1, CD55, OASL2, OASL1, OAS1A, OAS2, MX2 | 61 | 400 | 18082 | 5.19E+15 | 7.14E-01 | 1.88E-01 | 3.01E+16 |
| GOTERM_BP_DIRECT | GO:0006955~immune response | 6 | 8.70E+15 | 2.06E-03 | P2RY14, OASL2, OASL1, TGTP2, OAS2, OAS1F | 61 | 272 | 18082 | 6.54E+15 | 7.14E-01 | 1.64E-01 | 3.01E+16 |
| KEGG_PATHWAY | mmu05162:Measles | 4 | 5.80E+15 | 7.39E-03 | IFIH1, OAS1A, OAS2, MX2 | 24 | 136 | 7691 | 9.43E+15 | 3.96E-01 | 1.55E-01 | 7.35E+15 |
| UP_KEYWORDS | Nucleotidyltransferase | 3 | 4.35E+16 | 2.01E-02 | OASL2, OAS1A, OAS2 | 66 | 76 | 22680 | 1.36E+16 | 9.26E-01 | 2.78E-01 | 2.10E+16 |
| UP_KEYWORDS | RNA-binding | 6 | 8.70E+15 | 2.89E-02 | IFIH1, OASL2, ZMAT3, OASL1, OAS1A, OAS2 | 66 | 601 | 22680 | 3.43E+16 | 9.76E-01 | 3.13E-01 | 2.88E+16 |
| UP_KEYWORDS | Magnesium | 5 | 7.25E+15 | 6.23E-02 | OASL2, ITGA11, OAS1A, OAS2, TTN | 66 | 521 | 22680 | 3.30E+15 | 1.00E+00 | 4.02E-01 | 5.26E+16 |
| GOTERM_MF_DIRECT | GO:0003723~RNA binding | 6 | 8.70E+15 | 1.23E-01 | IFIH1, OASL2, ZMAT3, OASL1, OAS2, OAS1F | 60 | 780 | 17446 | 2.24E+15 | 1.00E+00 | 9.62E-01 | 7.91E+15 |
| KEGG_PATHWAY | mmu05168:Herpes simplex infection | 3 | 4.35E+16 | 1.27E-01 | IFIH1, OAS1A, OAS2 | 24 | 208 | 7691 | 4.62E+16 | 1.00E+00 | 6.42E-01 | 7.53E+15 |
| UP_KEYWORDS | Nucleotide-binding | 8 | 1.16E+16 | 2.36E-01 | IFIH1, OASL2, TGTP2, OAS1A, OAS2, TTN, GBP3, MX2 | 66 | 1754 | 22680 | 1.57E+16 | 1.00E+00 | 7.76E-01 | 9.56E+14 |
| GOTERM_MF_DIRECT | GO:0005524~ATP binding | 8 | 1.16E+16 | 2.45E-01 | IFIH1, OASL2, SYN2, OASL1, OAS1A, OAS2, OAS1F, TTN | 60 | 1507 | 17446 | 1.54E+16 | 1.00E+00 | 9.70E-01 | 9.65E+15 |
| UP_KEYWORDS | Transferase | 6 | 8.70E+15 | 5.18E-01 | CDKN1A, OASL2, PARP14, OAS1A, OAS2, TTN | 66 | 1654 | 22680 | 1.25E+16 | 1.00E+00 | 9.69E-01 | 1.00E+16 |
| UP_KEYWORDS | ATP-binding | 5 | 7.25E+15 | 5.54E-01 | IFIH1, OASL2, OAS1A, OAS2, TTN | 66 | 1363 | 22680 | 1.26E+16 | 1.00E+00 | 9.64E-01 | 1.00E+16 |
| GOTERM_MF_DIRECT | GO:0000166~nucleotide binding | 7 | 1.01E+16 | 6.51E-01 | IFIH1, CELF5, OASL2, PARP14, OAS2, GBP3, MX2 | 60 | 1936 | 17446 | 1.05E+16 | 1.00E+00 | 1.00E+00 | 1.00E+16 |
| GOTERM_MF_DIRECT | GO:0016740~transferase activity | 5 | 7.25E+15 | 7.45E-01 | OASL2, PARP14, OASL1, OAS2, OAS1F | 60 | 1472 | 17446 | 9.88E-01 | 1.00E+00 | 1.00E+00 | 1.00E+16 |

**Annotation Cluster 2** **Enrichment Score: 3.3310651707009664**

| **Category** | **Term** | **Count** | **%** | **PValue** | **Genes** | **List Total** | **Pop Hits** | **Pop Total** | **Fold Enrichment** | **Bonferroni** | **Benjamini** | **FDR** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| UP_KEYWORDS | Antiviral defense | 7 | 1.01E+16 | 4.23E+09 | IFIH1, ISG15, OASL2, OASL1, OAS1A, OAS2, MX2 | 66 | 100 | 22680 | 2.41E+15 | 5.41E+10 | 5.41E+10 | 4.91E+11 |
| SMART | SM00213:UBQ | 3 | 4.35E+16 | 1.38E-02 | ISG15, OASL2, OASL1 | 37 | 52 | 10425 | 1.63E+16 | 5.28E-01 | 3.13E-01 | 1.27E+16 |
| INTERPRO | IPR000626:Ubiquitin | 3 | 4.35E+16 | 1.74E-02 | ISG15, OASL2, OASL1 | 64 | 66 | 20594 | 1.46E+16 | 9.59E-01 | 4.13E-01 | 1.95E+15 |

**Annotation Cluster 3** **Enrichment Score: 3.035633030628498**

| **Category** | **Term** | **Count** | **%** | **PValue** | **Genes** | **List Total** | **Pop Hits** | **Pop Total** | **Fold Enrichment** | **Bonferroni** | **Benjamini** | **FDR** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| UP_KEYWORDS | Glycoprotein | 25 | 3.62E+16 | 7.91E+10 | CCKAR, FFAR4, SLC6A2, NELL1, ITGA11, OAS2, GDNF, SMOC2, LGALS3BP, WISP1, P4HA2, CRISPLD2, DNER, FAP, GPR20, ASIC2, GRIA3, FRZB, CD55, CHRDL1, SULF2, PTPRV, P2RY14, GPR17, GDF15 | 66 | 3815 | 22680 | 2.25E+16 | 1.01E-02 | 2.53E-03 | 9.18E-02 |
| UP_KEYWORDS | Disulfide bond | 22 | 3.19E+15 | 1.05E+12 | CCKAR, SLC6A2, NELL1, EDN1, ASIC2, ITGA11, IGF1, GRIA3, FRZB, TTN, GDNF, SMOC2, CD55, LGALS3BP, WISP1, ISG15, CRISPLD2, DNER, FAP, P2RY14, GPR17, GDF15 | 66 | 3124 | 22680 | 2.42E+16 | 1.34E-02 | 2.69E-03 | 1.22E-01 |
| UP_KEYWORDS | Secreted | 15 | 2.17E+15 | 2.46E+12 | NELL1, EDN1, IGF1, IL33, FRZB, GDNF, LGALS9, SMOC2, LGALS3BP, CHRDL1, WISP1, ISG15, CRISPLD2, FAP, GDF15 | 66 | 1685 | 22680 | 3.06E+15 | 3.11E-02 | 5.25E-03 | 2.86E-01 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| UP_SEQ_FEATURE | glycosylation site:N-linked (GlcNAc...) | 24 | 3.48E+15 | 2.84E+12 | CCKAR, FFAR4, SLC6A2, NELL1, ITGA11, ASIC2, GRIA3, FRZB, GDNF, SMOC2, CD55, LGALS3BP, CHRDL1, WISP1, SULF2, P4HA2, CRISPLD2, PTPRV, DNER, FAP, P2RY14, GPR17, GDF15, GPR20 | 58 | 3563 | 18012 | 2.09E+16 | 1.81E-01 | 1.81E-01 | 4.28E-01 |
| UP_SEQ_FEATURE | disulfide bond | 19 | 2.75E+16 | 5.04E+10 | CCKAR, NELL1, EDN1, ASIC2, ITGA11, IGF1, FRZB, TTN, GDNF, SMOC2, CD55, LGALS3BP, WISP1, CRISPLD2, DNER, P2RY14, FAP, GPR17, GDF15 | 58 | 2510 | 18012 | 2.35E+16 | 2.99E-01 | 1.63E-01 | 7.59E-01 |
| GOTERM_CC_DIRECT | GO:0005576~extracellular region | 15 | 2.17E+15 | 7.80E+11 | NELL1, EDN1, IGF1, IL33, FRZB, GDNF, LGALS9, SMOC2, LGALS3BP, CHRDL1, WISP1, ISG15, CRISPLD2, FAP, GDF15 | 62 | 1753 | 19662 | 2.71E+15 | 7.51E-02 | 7.51E-02 | 8.62E-01 |
| UP_SEQ_FEATURE | signal peptide | 20 | 2.90E+16 | 2.55E-03 | NELL1, EDN1, ITGA11, IGF1, GRIA3, FRZB, GDNF, SMOC2, CD55, LGALS3BP, CHRDL1, WISP1, SULF2, P4HA2, SHISA3, PTPRV, CRISPLD2, DNER, GDF15, PQLC3 | 58 | 3124 | 18012 | 1.99E+16 | 8.35E-01 | 4.51E-01 | 3.78E+15 |
| GOTERM_CC_DIRECT | GO:0005615~extracellular space | 11 | 1.59E+16 | 1.67E-02 | LGALS3BP, SULF2, NELL1, FAP, EDN1, LMCD1, IGF1, IL33, FRZB, GDF15, GDNF | 62 | 1504 | 19662 | 2.32E+15 | 8.14E-01 | 4.29E-01 | 1.70E+15 |
| UP_KEYWORDS | Signal | 20 | 2.90E+16 | 4.91E-02 | NELL1, EDN1, ITGA11, IGF1, GRIA3, FRZB, GDNF, SMOC2, CD55, LGALS3BP, CHRDL1, WISP1, SULF2, P4HA2, SHISA3, PTPRV, CRISPLD2, DNER, GDF15, PQLC3 | 66 | 4543 | 22680 | 1.51E+16 | 9.98E-01 | 4.15E-01 | 4.42E+15 |

**Annotation Cluster 4** **Enrichment Score: 1.269065734222906**

| Category | Term | Count | % | PValue | Genes | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini | FDR |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| GOTERM_BP_DIRECT | GO:0043065~positive regulation of apoptotic process | 5 | 7.25E+15 | 2.51E-02 | NELL1, ZMAT3, TRP53INP1, PMAIP1, FRZB | 61 | 335 | 18082 | 4.42E+15 | 1.00E+00 | 6.67E-01 | 3.13E+16 |
| UP_KEYWORDS | Apoptosis | 5 | 7.25E+15 | 5.17E-02 | FAP, ZMAT3, TRP53INP1, PMAIP1, XAF1 | 66 | 489 | 22680 | 3.51E+15 | 9.99E-01 | 3.84E-01 | 4.60E+15 |
| GOTERM_BP_DIRECT | GO:0006915~apoptotic process | 5 | 7.25E+15 | 1.20E-01 | FAP, ZMAT3, TRP53INP1, PMAIP1, XAF1 | 61 | 570 | 18082 | 2.60E+15 | 1.00E+00 | 9.75E-01 | 8.50E+15 |

**Annotation Cluster 5** **Enrichment Score: 0.9983796718279031**

| Category | Term | Count | % | PValue | Genes | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini | FDR |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| UP_KEYWORDS | Endoplasmic reticulum | 8 | 1.16E+16 | 2.36E-02 | SLN, SULF2, P4HA2, SHISA3, EPHX1, TGTP2, OAS1A, OAS2 | 66 | 997 | 22680 | 2.76E+15 | 9.53E-01 | 2.88E-01 | 2.43E+16 |
| UP_KEYWORDS | Microsome | 3 | 4.35E+16 | 5.51E-02 | EPHX1, OAS1A, OAS2 | 66 | 132 | 22680 | 7.81E+15 | 9.99E-01 | 3.84E-01 | 4.82E+16 |
| GOTERM_CC_DIRECT | GO:0005783~endoplasmic reticulum | 8 | 1.16E+16 | 1.14E-01 | CCKAR, SLN, SULF2, P4HA2, SHISA3, EPHX1, OAS1A, OAS2 | 62 | 1323 | 19662 | 1.92E+15 | 1.00E+00 | 7.03E-01 | 7.40E+15 |
| GOTERM_CC_DIRECT | GO:0043231~intracellular membrane-bounded organelle | 3 | 4.35E+16 | 6.82E-01 | P4HA2, EPHX1, OAS2 | 62 | 751 | 19662 | 1.27E+16 | 1.00E+00 | 9.95E-01 | 1.00E+16 |

**Annotation Cluster 6** **Enrichment Score: 0.6615117943565963**

| Category | Term | Count | % | PValue | Genes | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini | FDR |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| INTERPRO | IPR027417:P-loop containing nucleoside triphosphate hydrolase | 6 | 8.70E+15 | 1.45E-01 | IFIH1, IFI44, TGTP2, RNF213, GBP3, MX2 | 64 | 909 | 20594 | 2.12E+15 | 1.00E+00 | 9.58E-01 | 8.55E+15 |
| GOTERM_MF_DIRECT | GO:0003924~GTPase activity | 3 | 4.35E+16 | 1.57E-01 | TGTP2, GBP3, MX2 | 60 | 209 | 17446 | 4.17E+15 | 1.00E+00 | 9.74E-01 | 8.70E+15 |
| UP_KEYWORDS | Nucleotide-binding | 8 | 1.16E+16 | 2.36E-01 | IFIH1, OASL2, TGTP2, OAS1A, OAS2, TTN, GBP3, MX2 | 66 | 1754 | 22680 | 1.57E+16 | 1.00E+00 | 7.76E-01 | 9.56E+14 |
| UP_KEYWORDS | GTP-binding | 3 | 4.35E+16 | 2.46E-01 | TGTP2, GBP3, MX2 | 66 | 332 | 22680 | 3.11E+15 | 1.00E+00 | 7.79E-01 | 9.62E+15 |
| GOTERM_MF_DIRECT | GO:0005525~GTP binding | 3 | 4.35E+16 | 3.73E-01 | TGTP2, GBP3, MX2 | 60 | 383 | 17446 | 2.28E+16 | 1.00E+00 | 9.90E-01 | 9.96E+15 |

**Annotation Cluster 7** **Enrichment Score: 0.5368923254839906**

| Category | Term | Count | % | PValue | Genes | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini | FDR |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| UP_KEYWORDS | Metal-binding | 15 | 2.17E+15 | 9.85E-02 | IFIH1, SLC6A2, ZMAT3, LMCD1, ITGA11, OAS2, TTN, RNF213, SMOC2, CDKN1A, SULF2, P4HA2, OASL2, OAS1A, XAF1 | 66 | 3395 | 22680 | 1.52E+16 | 1.00E+00 | 4.85E-01 | 7.00E+15 |
| GOTERM_MF_DIRECT | GO:0046872~metal ion binding | 14 | 2.03E+15 | 3.41E-01 | IFIH1, SLC6A2, ZMAT3, ITGA11, LMCD1, OAS2, RNF213, SMOC2, CDKN1A, SULF2, P4HA2, OASL2, XAF1, OAS1A | 60 | 3355 | 17446 | 1.21E+16 | 1.00E+00 | 9.88E-01 | 9.93E+15 |
| UP_KEYWORDS | Zinc | 6 | 8.70E+15 | 7.30E-01 | CDKN1A, IFIH1, ZMAT3, LMCD1, XAF1, RNF213 | 66 | 2099 | 22680 | 9.82E-01 | 1.00E+00 | 9.88E-01 | 1.00E+16 |
| **Annotation Cluster 8** | **Enrichment Score: 0.5102827409297518** | | | | | | | | | | | |
| **Category** | **Term** | **Count** | **%** | **PValue** | **Genes** | **List Total** | **Pop Hits** | **Pop Total** | **Fold Enrichment** | **Bonferroni** | **Benjamini** | **FDR** |
| UP_SEQ_FEATURE | topological domain:Extracellular | 13 | 1.88E+15 | 4.73E-02 | CCKAR, FFAR4, SLC6A2, ASIC2, ITGA11, GRIA3, SHISA3, PTPRV, P2RY14, FAP, DNER, GPR17, GPR20 | 58 | 2256 | 18012 | 1.79E+16 | 1.00E+00 | 9.99E-01 | 5.19E+16 |
| GOTERM_CC_DIRECT | GO:0016020~membrane | 28 | 4.06E+15 | 1.01E-01 | CCKAR, RTP4, FFAR4, SLC6A2, ITGA11, OAS2, RNF213, LGALS3BP, SLN, SHISA3, FAP, DNER, OASL1, GPR20, PQLC3, MNDAL, ASIC2, EPHX1, GRIA3, CD55, PTPRV, PARP14, P2RY14, TGTP2, GPR17, IFI203, GBP3, SNTG2 | 62 | 6998 | 19662 | 1.27E+16 | 1.00E+00 | 6.94E-01 | 6.93E+15 |
| UP_SEQ_FEATURE | topological domain:Cytoplasmic | 14 | 2.03E+15 | 1.13E-01 | CCKAR, RTP4, FFAR4, SLC6A2, ASIC2, ITGA11, GRIA3, SHISA3, PTPRV, P2RY14, FAP, DNER, GPR17, GPR20 | 58 | 2880 | 18012 | 1.51E+16 | 1.00E+00 | 1.00E+00 | 8.36E+15 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| UP_SEQ_FEATURE | transmembrane region | 17 | 2.46E+16 | 2.76E-01 | CCKAR, RTP4, FFAR4, SLC6A2, ASIC2, ITGA11, EPHX1, GRIA3, SLN, SHISA3, PTPRV, DNER, P2RY14, FAP, GPR17, GPR20, PQLC3 | 58 | 4312 | 18012 | 1.22E+16 | 1.00E+00 | 1.00E+00 | 9.92E+15 |
| GOTERM_CC_DIRECT | GO:0005886~plasma membrane | 17 | 2.46E+16 | 4.46E-01 | CCKAR, FFAR4, SLC6A2, ASIC2, IGF1, EPHX1, GRIA3, SLC19A2, CD55, SULF2, DNER, P2RY14, FAP, SYN2, GPR17, GPR20, SNTG2 | 62 | 4874 | 19662 | 1.11E+15 | 1.00E+00 | 9.80E-01 | 9.99E+15 |
| UP_KEYWORDS | Cell membrane | 12 | 1.74E+16 | 5.21E-01 | CCKAR, CD55, FFAR4, SLC6A2, P2RY14, DNER, FAP, ASIC2, GRIA3, GPR17, GPR20, SNTG2 | 66 | 3759 | 22680 | 1.10E+16 | 1.00E+00 | 9.66E-01 | 1.00E+16 |
| UP_KEYWORDS | Transmembrane helix | 20 | 2.90E+16 | 6.40E-01 | CCKAR, MS4A7, RTP4, FFAR4, SLC6A2, ASIC2, ITGA11, EPHX1, GRIA3, SLC19A2, SLN, P4HA2, SHISA3, PTPRV, DNER, FAP, P2RY14, GPR17, GPR20, PQLC3 | 66 | 6938 | 22680 | 9.91E-01 | 1.00E+00 | 9.76E-01 | 1.00E+15 |
| UP_KEYWORDS | Transmembrane | 20 | 2.90E+16 | 6.45E-01 | CCKAR, MS4A7, RTP4, FFAR4, SLC6A2, ASIC2, ITGA11, EPHX1, GRIA3, SLC19A2, SLN, P4HA2, SHISA3, PTPRV, DNER, FAP, P2RY14, GPR17, GPR20, PQLC3 | 66 | 6955 | 22680 | 9.88E-01 | 1.00E+00 | 9.72E-01 | 1.00E+16 |
| GOTERM_CC_DIRECT | GO:0016021~integral component of membrane | 21 | 3.04E+16 | 6.86E-01 | CCKAR, MS4A7, RTP4, FFAR4, SLC6A2, ASIC2, ITGA11, EPHX1, GRIA3, FRZB, SLC19A2, SLN, P4HA2, SHISA3, PTPRV, DNER, FAP, P2RY14, GPR17, GPR20, PQLC3 | 62 | 6878 | 19662 | 9.68E-01 | 1.00E+00 | 9.93E-01 | 1.00E+16 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| UP_KEYWORDS | Membrane | 23 | 3.33E+15 | 8.06E-01 | CCKAR, MS4A7, RTP4, FFAR4, SLC6A2, ITGA11, ASIC2, EPHX1, GRIA3, SLC19A2, CD55, SLN, P4HA2, SHISA3, PTPRV, DNER, FAP, P2RY14, GPR17, GPR20, GBP3, PQLC3, SNTG2 | 66 | 8683 | 22680 | 9.10E-01 | 1.00E+00 | 9.92E-01 | 1.00E+16 |

**Annotation Cluster 9** **Enrichment Score: 0.44982354245222245**

| Category | Term | Count | % | PValue | Genes | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini | FDR |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| UP_SEQ_FEATURE | topological domain:Extracellular | 13 | 1.88E+15 | 4.73E-02 | CCKAR, FFAR4, SLC6A2, ASIC2, ITGA11, GRIA3, SHISA3, PTPRV, P2RY14, FAP, DNER, GPR17, GPR20 | 58 | 2256 | 18012 | 1.79E+16 | 1.00E+00 | 9.99E-01 | 5.19E+16 |
| UP_SEQ_FEATURE | topological domain:Cytoplasmic | 14 | 2.03E+15 | 1.13E-01 | CCKAR, RTP4, FFAR4, SLC6A2, ASIC2, ITGA11, GRIA3, SHISA3, PTPRV, P2RY14, FAP, DNER, GPR17, GPR20 | 58 | 2880 | 18012 | 1.51E+16 | 1.00E+00 | 1.00E+00 | 8.36E+15 |
| GOTERM_CC_DIRECT | GO:0005887~integral component of plasma membrane | 7 | 1.01E+16 | 1.35E-01 | FFAR4, SLC6A2, P2RY14, ASIC2, GPR17, GPR20, SLC19A2 | 62 | 1126 | 19662 | 1.97E+16 | 1.00E+00 | 7.33E-01 | 8.01E+15 |
| GOTERM_MF_DIRECT | GO:0004871~signal transducer activity | 5 | 7.25E+15 | 1.76E-01 | CCKAR, FFAR4, P2RY14, GPR17, GPR20 | 60 | 648 | 17446 | 2.24E+16 | 1.00E+00 | 9.59E-01 | 9.00E+14 |
| GOTERM_BP_DIRECT | GO:0007165~signal transduction | 7 | 1.01E+16 | 2.36E-01 | SMOC2, CCKAR, WISP1, FFAR4, P2RY14, GPR17, GPR20 | 61 | 1255 | 18082 | 1.65E+15 | 1.00E+00 | 9.99E-01 | 9.81E+15 |
| UP_KEYWORDS | Cell membrane | 12 | 1.74E+16 | 5.21E-01 | CCKAR, CD55, FFAR4, SLC6A2, P2RY14, DNER, FAP, ASIC2, GRIA3, GPR17, GPR20, SNTG2 | 66 | 3759 | 22680 | 1.10E+16 | 1.00E+00 | 9.66E-01 | 1.00E+16 |
| UP_KEYWORDS | Receptor | 8 | 1.16E+16 | 6.33E-01 | CCKAR, FFAR4, P2RY14, DNER, ITGA11, GRIA3, GPR17, GPR20 | 66 | 2613 | 22680 | 1.05E+16 | 1.00E+00 | 9.77E-01 | 1.00E+16 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| INTERPRO | IPR000276:G protein-coupled receptor, rhodopsin-like | 5 | 7.25E+15 | 6.61E-01 | CCKAR, FFAR4, P2RY14, GPR17, GPR20 | 64 | 1458 | 20594 | 1.10E+16 | 1.00E+00 | 1.00E+00 | 1.00E+16 |
| GOTERM_BP_DIRECT | GO:0007186~G-protein coupled receptor signaling pathway | 6 | 8.70E+15 | 6.80E-01 | CCKAR, FFAR4, P2RY14, EDN1, GPR17, GPR20 | 61 | 1706 | 18082 | 1.04E+15 | 1.00E+00 | 1.00E+00 | 1.00E+16 |
| GOTERM_MF_DIRECT | GO:0004930~G-protein coupled receptor activity | 6 | 8.70E+15 | 7.18E-01 | CCKAR, FFAR4, P2RY14, GPR17, FRZB, GPR20 | 60 | 1749 | 17446 | 9.97E-01 | 1.00E+00 | 1.00E+00 | 1.00E+15 |
| UP_KEYWORDS | G-protein coupled receptor | 5 | 7.25E+15 | 7.45E-01 | CCKAR, FFAR4, P2RY14, GPR17, GPR20 | 66 | 1741 | 22680 | 9.87E-01 | 1.00E+00 | 9.89E-01 | 1.00E+16 |
| UP_KEYWORDS | Transducer | 5 | 7.25E+15 | 7.69E-01 | CCKAR, FFAR4, P2RY14, GPR17, GPR20 | 66 | 1801 | 22680 | 9.54E-01 | 1.00E+00 | 9.90E-01 | 1.00E+16 |
| INTERPRO | IPR017452:GPCR, rhodopsin-like, 7TM | 5 | 7.25E+15 | 7.78E-01 | CCKAR, FFAR4, P2RY14, GPR17, GPR20 | 64 | 1708 | 20594 | 9.42E-01 | 1.00E+00 | 1.00E+00 | 1.00E+16 |

**Annotation Cluster 10** **Enrichment Score: 0.3277560757196918**

| **Category** | **Term** | **Count** | **%** | **PValue** | **Genes** | **List Total** | **Pop Hits** | **Pop Total** | **Fold Enrichment** | **Bonferroni** | **Benjamini** | **FDR** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| UP_KEYWORDS | Differentiation | 4 | 5.80E+15 | 2.83E-01 | CHRDL1, NELL1, DNER, FRZB | 66 | 646 | 22680 | 2.13E+16 | 1.00E+00 | 8.17E-01 | 9.79E+15 |
| GOTERM_BP_DIRECT | GO:0030154~cell differentiation | 4 | 5.80E+15 | 4.82E-01 | CHRDL1, NELL1, DNER, FRZB | 61 | 780 | 18082 | 1.52E+15 | 1.00E+00 | 1.00E+00 | 1.00E+16 |
| UP_KEYWORDS | Developmental protein | 4 | 5.80E+15 | 5.34E-01 | CHRDL1, SHISA3, DNER, FRZB | 66 | 976 | 22680 | 1.41E+16 | 1.00E+00 | 9.66E-01 | 1.00E+15 |
| GOTERM_BP_DIRECT | GO:0007275~multicellular organism development | 4 | 5.80E+15 | 6.71E-01 | CHRDL1, SHISA3, DNER, FRZB | 61 | 1029 | 18082 | 1.15E+16 | 1.00E+00 | 1.00E+00 | 1.00E+15 |

**Annotation Cluster 11** **Enrichment Score: 0.01866930672055855**

| **Category** | **Term** | **Count** | **%** | **PValue** | **Genes** | **List Total** | **Pop Hits** | **Pop Total** | **Fold Enrichment** | **Bonferroni** | **Benjamini** | **FDR** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| UP_KEYWORDS | Transcription | 4 | 5.80E+15 | 9.10E-01 | PARP14, LMCD1, TRP53INP1, IL33 | 66 | 1859 | 22680 | 7.39E-01 | 1.00E+00 | 9.99E-01 | 1.00E+16 |
| GOTERM_BP_DIRECT | GO:0006351~transcription, DNA-templated | 4 | 5.80E+15 | 9.57E-01 | PARP14, LMCD1, TRP53INP1, IL33 | 61 | 1885 | 18082 | 6.29E-01 | 1.00E+00 | 1.00E+00 | 1.00E+02 |
| UP_KEYWORDS | Transcription regulation | 3 | 4.35E+16 | 9.70E-01 | PARP14, LMCD1, TRP53INP1 | 66 | 1799 | 22680 | 5.73E-01 | 1.00E+00 | 1.00E+00 | 1.00E+02 |
| GOTERM_BP_DIRECT | GO:0006355~regulation of transcription, DNA-templated | 3 | 4.35E+16 | 9.97E-01 | PARP14, LMCD1, TRP53INP1 | 61 | 2279 | 18082 | 3.90E-01 | 1.00E+00 | 1.00E+00 | 1.00E+02 |

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **Table S9. Mass Spectrometry.** | | | | | | | | | | | | | | | | | | |
| 2 | Shown is the complete list of detected proteins in mass spectrometry analysis. | | | | | | | | | | | | | | | | | | |
| 3 | | | | | | | | | | | | | | | | | | | |
| 4 | 700 | not enriched | | | | | | | | | | | | | | | | | |
| 5 | 35 | mitochondrial, proteasomal, hemoglobins, immunoglobin, ribosomal | | | | | | | | | | | | | | | | | |
| 6 | 42 | not nuclear | | | | | | | | | | | | | | | | | |
| 7 | 119 | potential candidates | | | | | | | | | | | | | | | | | |
| 8 | 919 | total | | | | | | | | | | | | | | | | | |
| 9 | **Intensity 1-TbX2_x-y_Mean_** | **Intensity 2-TbX2_x-y_Mean_** | **Intensity 3-TbX2_x-y_Mean_** | **Intensity 1-IgG_x-y_Mean** | **Intensity 2-IgG_x-y_Mean** | **Intensity 3-IgG_x-y_Mean** | **Intensity 1-IgG** | **Intensity 2-IgG** | **Intensity 3-IgG** | **Intensity 1-TbX2** | **Intensity 2-TbX2** | **Intensity 3-TbX2** | **Intensity 2-IgG-Input** | **Intensity 3-IgG-Input** | **Intensity 2-TbX2-Input** | **Intensity 3-TbX2-input** | **C: Student's T-test Signifi-cant ERM-TbX2_ERM-IgG** | **N: Pepti-des** | **N: Razor + unique peptides** |
| 10 | 14.527 | 11.944 | 11.983 | -0.133 | 0.558 | -0.220 | 17.237 | 17.928 | 17.150 | 31.049 | 28.466 | 28.505 | 18.413 | 16.327 | 17.640 | 15.405 | + | 1 | 1 |
| 11 | 14.891 | 14.526 | 14.668 | 6.146 | 2.245 | 1.073 | 22.707 | 18.806 | 17.634 | 34.180 | 33.816 | 33.958 | 18.947 | 14.175 | 23.859 | 14.721 | + | 1 | 1 |
| 12 | 9.416 | 8.748 | 7.338 | -2.110 | -1.711 | -0.390 | 17.286 | 17.685 | 19.006 | 25.170 | 24.502 | 23.092 | 20.011 | 18.779 | 16.866 | 14.642 | + | 11 | 11 |
| 13 | 14.100 | 14.393 | 14.676 | 6.040 | 1.470 | 7.622 | 22.179 | 17.609 | 23.761 | 30.966 | 31.259 | 31.542 | 16.280 | 15.997 | 18.121 | 15.611 | + | 10 | 10 |
| 14 | 0.000 | -1.776 | 3.912 | -10.189 | -8.166 | -4.010 | 16.850 | 18.873 | 23.030 | 20.261 | 18.485 | 24.173 | 29.710 | 24.369 | 17.099 | 23.424 | + | 8 | 2 |
| 15 | 12.061 | 11.729 | 11.625 | 5.765 | 1.022 | 5.738 | 23.219 | 18.476 | 23.191 | 33.038 | 32.705 | 32.602 | 18.658 | 16.249 | 24.727 | 17.227 | + | 10 | 10 |
| 16 | 6.761 | 6.800 | 7.208 | -0.194 | 0.412 | -1.584 | 16.629 | 17.236 | 15.239 | 23.336 | 23.375 | 23.783 | 17.433 | 16.214 | 18.521 | 14.630 | + | 2 | 2 |
| 17 | 3.742 | 3.401 | 3.029 | -1.007 | -5.188 | -5.362 | 21.366 | 17.185 | 17.011 | 22.508 | 22.167 | 21.795 | 24.558 | 20.188 | 21.317 | 16.214 | + | 4 | 4 |
| 18 | -1.609 | -0.964 | 2.728 | -7.043 | -6.998 | -6.346 | 17.726 | 17.772 | 18.424 | 16.924 | 17.569 | 21.261 | 22.578 | 26.961 | 22.159 | 14.908 | + | 3 | 3 |
| 19 | 8.969 | 7.610 | 7.748 | -0.162 | 4.135 | 0.147 | 16.543 | 20.841 | 16.852 | 25.733 | 24.373 | 24.512 | 17.432 | 15.978 | 17.732 | 15.795 | + | 8 | 8 |
| 20 | -4.879 | 1.912 | 1.031 | -7.588 | -7.810 | -6.736 | 16.355 | 16.133 | 17.207 | 17.041 | 23.833 | 22.952 | 26.126 | 21.761 | 24.265 | 19.576 | + | 6 | 6 |
| 21 | 3.615 | 3.796 | 1.986 | -8.508 | -0.950 | -1.031 | 15.291 | 22.848 | 22.768 | 23.612 | 23.793 | 21.982 | 26.044 | 21.554 | 24.577 | 15.416 | | 11 | 11 |
| 22 | 5.383 | 1.690 | 5.115 | -3.304 | -1.277 | -2.932 | 16.630 | 18.657 | 17.002 | 21.406 | 17.713 | 21.138 | 22.370 | 17.497 | 16.609 | 15.437 | + | 4 | 4 |
| 23 | -2.306 | 3.062 | 2.264 | -5.541 | -4.153 | -6.955 | 17.460 | 18.848 | 16.046 | 17.041 | 22.409 | 21.611 | 26.102 | 19.899 | 23.513 | 15.182 | + | 3 | 3 |
| 24 | -0.840 | 0.162 | 8.921 | -3.407 | -4.010 | -3.497 | 17.433 | 16.830 | 17.343 | 16.696 | 17.697 | 26.457 | 24.030 | 17.650 | 20.774 | 14.297 | | 6 | 6 |
| 25 | 6.942 | 8.347 | 8.093 | -0.748 | 0.397 | 4.880 | 16.760 | 17.905 | 22.387 | 23.337 | 24.743 | 24.488 | 18.717 | 16.299 | 18.435 | 14.356 | + | 3 | 3 |
| 26 | 2.787 | 5.254 | 2.811 | -1.419 | -3.614 | -2.967 | 18.804 | 16.609 | 17.256 | 21.759 | 24.226 | 21.783 | 18.481 | 21.965 | 23.037 | 14.907 | + | 8 | 8 |
| 27 | 5.193 | 4.916 | 6.071 | -1.107 | -1.256 | 0.041 | 16.961 | 16.812 | 18.108 | 20.421 | 20.143 | 21.299 | 21.045 | 15.090 | 15.727 | 14.728 | + | 4 | 4 |
| 28 | 4.891 | 6.813 | 4.026 | -1.276 | -0.465 | -1.022 | 16.020 | 16.830 | 16.274 | 22.049 | 23.971 | 21.184 | 18.335 | 16.257 | 18.202 | 16.113 | + | 4 | 4 |
| 29 | 1.388 | 8.595 | 6.469 | -1.050 | -0.363 | 0.114 | 16.452 | 17.139 | 17.616 | 17.573 | 24.780 | 22.654 | 19.456 | 15.548 | 17.137 | 15.233 | | 4 | 4 |
| 30 | 8.702 | 7.755 | -0.003 | -0.156 | -0.595 | -0.036 | 17.307 | 16.868 | 17.428 | 24.428 | 23.481 | 15.723 | 17.748 | 17.178 | 16.351 | 15.101 | | 2 | 2 |
| 31 | 0.058 | 4.747 | 2.561 | -3.246 | -3.561 | -2.792 | 17.153 | 16.838 | 17.607 | 16.257 | 20.946 | 18.760 | 23.263 | 17.534 | 17.458 | 14.940 | + | 1 | 1 |

| | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | | | | | | | | | | | | | |
| 2 | | | | | | | | | | | | | |
| 3 | | | | | | | | | | | | | |
| 4 | | | | | | | | | | | | | |
| 5 | | | | | | | | | | | | | |
| 6 | | | | | | | | | | | | | |
| 7 | | | | | | | | | | | | | |
| 8 | | | | | | | | | | | | | |
| 9 | **N: Unique peptides** | **N: Sequence coverage [%]** | **N: Mol. weight [kDa]** | **N: Score** | **N: Mean** | **N: Mean_** | **N: -Log Student's T-test p-value ERM-TbX2_ERM-IgG** | **N: Student's T-test Difference ERM-TbX2_ERM-IgG** | **T: Protein IDs** | **T: Majority protein IDs** | **T: Protein names** | **T: Gene names** | **T: id** |
| 10 | 1 | 13.1 | 11.277 | 15.246 | 17.370 | 16.523 | **3.862** | **12.750** | A0A0A0MQC1 | A0A0A0MQC1 | Immunoglobulin heavy variable 3-5 | **Ighv3-5** | 28 |
| 11 | 1 | 7.8 | 13.067 | 6.7196 | 16.561 | 19.290 | **2.774** | **11.540** | F7CGC9;A2A4A1;Q91ZF0 | F7CGC9;A2A4A1;Q91ZF0 | DnaJ homolog subfamily C member 24 | **Dnajc24** | 122 |
| 12 | 11 | 15.8 | 90.244 | 84.777 | 19.395 | 15.754 | **3.605** | **9.904** | Q8BX02;Q8BX02-2 | Q8BX02;Q8BX02-2 | KN motif and ankyrin repeat domain-containing protein 2 | **Kank2** | 1189 |
| 13 | 2 | 18.1 | 44.259 | 264.93 | 16.138 | 16.866 | **2.140** | **9.345** | P01867;P01867-2;A0A0A6YVP0 | P01867;P01867-2 | Ig gamma-2B chain C region | **Igh-3** | 552 |
| 14 | 2 | 26.8 | 32.904 | 24.318 | 27.039 | 20.261 | **1.523** | **8.167** | P48962;Q3V132 | P48962 | ADP/ATP translocase 1 | **Slc25a4** | 733 |
| 15 | 9 | 43 | 11.778 | 323.31 | 17.454 | 20.977 | **2.070** | **7.630** | A0A075B5P2;P01837 | A0A075B5P2;P01837 | Ig kappa chain C region | **Igkc** | 7 |
| 16 | 2 | 1.8 | 63.105 | 11.069 | 16.823 | 16.575 | **3.577** | **7.378** | A0A0N4SV35 | A0A0N4SV35 | membrane associated ring-CH-type finger 8 | **March8** | 67 |
| 17 | 4 | 16.5 | 29.295 | 25.206 | 22.373 | 18.766 | **2.136** | **7.243** | A2AMW0;P47757-2;P47757;P47757-4;F7CAZ6;A0A0A0MQI9;F6YHZ8 | A2AMW0;P47757-2;P47757;P47757-4;F7CAZ6 | F-actin-capping protein subunit beta | **Capzb** | 159 |
| 18 | 3 | 26.7 | 15.556 | 23.523 | 24.770 | 18.534 | **2.125** | **6.847** | A0A0A6YY29;Q9CXW3 | A0A0A6YY29;Q9CXW3 | Calcyclin-binding protein | **Cacybp** | 37 |
| 19 | 8 | 22.5 | 51.891 | 55.196 | 16.705 | 16.764 | **2.014** | **6.736** | Q3T9T1;Q3TZY4;Q80W04 | Q3T9T1;Q3TZY4;Q80W04 | Transmembrane and coiled-coil domains protein 2 | **Tmcc2** | 947 |
| 20 | 6 | 42.9 | 23.609 | 90.822 | 23.943 | 21.921 | **1.450** | **6.733** | P19157;P46425 | P19157;P46425 | Glutathione S-transferase P 1;Glutathione S-transferase P 2 | **Gstp1;Gstp2** | 634 |
| 21 | 10 | 18.6 | 85.47 | 81.719 | 23.799 | 19.997 | **1.212** | **6.629** | Q02248;E9Q6A9;D3YUH4;F7CRC6;F6QZ47;F7BAC9;D3Z5Q1;E9PW26 | Q02248;E9Q6A9 | Catenin beta-1 | **Ctnnb1** | 924 |
| 22 | 4 | 8.1 | 65.994 | 23.846 | 19.934 | 16.023 | **2.092** | **6.567** | D3Z7P3-2;D3Z7P4;D3Z7P3;F6U529 | D3Z7P3-2;D3Z7P4;D3Z7P3 | Glutaminase kidney isoform, mitochondrial | **Gls** | 316 |
| 23 | 3 | 53.1 | 5.8765 | 20.791 | 23.000 | 19.348 | **1.615** | **6.556** | A0A0N4SVQ1;Q62425 | A0A0N4SVQ1;Q62425 | Cytochrome c oxidase subunit NDUFA4 | **Ndufa4** | 71 |
| 24 | 6 | 2.8 | 293.02 | 37.436 | 20.840 | 17.536 | **0.963** | **6.386** | E9PVA8 | E9PVA8 | eIF-2-alpha kinase activator GCN1 | **Gcn1l1** | 334 |
| 25 | 3 | 11.7 | 35.633 | 23.604 | 17.508 | 16.395 | **1.623** | **6.285** | A0A075B5P4;A0A0A6YWR2;P01868;P01869 | A0A075B5P4;A0A0A6YWR2;P01868;P01869 | Ig gamma-1 chain C region secreted form;Ig gamma-1 chain C region, membrane-bound form | **Ighg1** | 9 |
| 26 | 8 | 5.5 | 216.37 | 48.365 | 20.223 | 18.972 | **2.413** | **6.284** | E9QAS4;E9QAS5;Q6PDQ2;E9PYU4;E9PYL1;A2A8L1;F6WR45 | E9QAS4;E9QAS5;Q6PDQ2 | Chromodomain-helicase-DNA-binding protein 4 | **Chd4** | 403 |
| 27 | 4 | 5.1 | 77.8 | 24.338 | 18.067 | 15.228 | **3.482** | **6.167** | Q8CIB5;A6X941 | Q8CIB5;A6X941 | Fermitin family homolog 2 | **Fermt2** | 1213 |
| 28 | 4 | 13.2 | 34.69 | 24.057 | 17.296 | 17.158 | **2.702** | **6.164** | Q8BQ10;A0A0R4J008;P70288;D3YYI8;O09106;Q3UM33;O88895 | Q8BQ10;A0A0R4J008;P70288;D3YYI8;O09106 | Histone deacetylase 2;Histone deacetylase;Histone deacetylase 1 | **Hdac2;Gm10093;Hdac1** | 76 |
| 29 | 4 | 7.4 | 73.697 | 26.668 | 17.502 | 16.185 | **1.282** | **5.917** | E9Q5C9 | E9Q5C9 | Nucleolar and coiled-body phosphoprotein 1 | **Nolc1** | 385 |
| 30 | 2 | 2.8 | 75.08 | 40.122 | 17.463 | 15.726 | **0.975** | **5.747** | Q60707 | Q60707 | T-box transcription factor TBX2 | **Tbx2** | 1022 |
| 31 | 1 | 4 | 19.774 | 6.3971 | 20.399 | 16.199 | **1.835** | **5.655** | G3UWN9;G3UXY0;G3X9K9;G3UXZ5;P97371 | G3UWN9;G3UXY0;G3X9K9;G3UXZ5;P97371 | Proteasome activator complex subunit 1 | **Psme1** | 450 |

|  | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 32 | 2.438 | 6.504 | 4.625 | -2.211 | 1.758 | -2.808 | 17.220 | 21.188 | 16.623 | 21.428 | 25.493 | 23.614 | 18.262 | 20.600 | 23.520 | 14.458 | + | 9 | 9 |
| 33 | -0.648 | 6.104 | 1.879 | -2.578 | -3.905 | -2.775 | 16.999 | 15.673 | 16.802 | 16.435 | 23.187 | 18.961 | 18.871 | 20.284 | 20.001 | 14.165 |  | 5 | 5 |
| 34 | 4.555 | 4.456 | 3.120 | -3.827 | 0.646 | -1.191 | 16.950 | 21.423 | 19.586 | 22.561 | 22.461 | 21.126 | 25.087 | 16.467 | 21.582 | 14.430 | + | 9 | 9 |
| 35 | 3.795 | 4.429 | -0.711 | -5.178 | -3.420 | -0.291 | 16.592 | 18.350 | 21.479 | 22.061 | 22.695 | 17.555 | 23.549 | 19.990 | 22.481 | 14.052 |  | 4 | 4 |
| 36 | 5.041 | 4.425 | 3.684 | -0.346 | -1.464 | -1.428 | 17.999 | 16.880 | 16.916 | 21.358 | 20.742 | 20.000 | 19.250 | 17.439 | 17.366 | 15.266 | + | 1 | 1 |
| 37 | -0.311 | 4.961 | 5.542 | -3.265 | 1.522 | -4.441 | 17.103 | 21.889 | 15.927 | 15.796 | 21.068 | 21.648 | 23.669 | 17.065 | 18.257 | 13.956 |  | 3 | 3 |
| 38 | 5.977 | 3.670 | 5.556 | -0.978 | 0.210 | -0.174 | 16.204 | 17.392 | 17.009 | 24.630 | 22.324 | 24.210 | 17.358 | 17.007 | 21.455 | 15.853 | + | 25 | 1 |
| 39 | 1.625 | 4.218 | 3.314 | -2.732 | -2.274 | -1.926 | 16.764 | 17.222 | 17.570 | 20.087 | 22.680 | 21.775 | 19.103 | 19.889 | 22.853 | 14.071 | + | 3 | 3 |
| 40 | -1.092 | -3.448 | -4.601 | -10.222 | -4.779 | -10.181 | 15.500 | 20.943 | 15.541 | 20.834 | 18.478 | 17.324 | 27.685 | 23.759 | 25.410 | 18.440 |  | 12 | 12 |
| 41 | 0.537 | 9.235 | 6.444 | -0.271 | 0.914 | -0.467 | 16.199 | 17.384 | 16.003 | 16.145 | 24.843 | 22.052 | 18.398 | 14.541 | 15.724 | 15.492 |  | 5 | 5 |
| 42 | 7.460 | 5.900 | 5.991 | -0.609 | -1.023 | 4.967 | 16.859 | 16.445 | 22.434 | 23.739 | 22.179 | 22.269 | 19.326 | 15.610 | 17.684 | 14.873 |  | 1 | 1 |
| 43 | 0.136 | 10.943 | 7.324 | 0.153 | 1.048 | 1.331 | 17.448 | 18.343 | 18.627 | 16.273 | 27.080 | 23.461 | 17.986 | 16.605 | 17.363 | 14.911 |  | 15 | 15 |
| 44 | 3.683 | 5.397 | 2.376 | -1.353 | -1.174 | -1.848 | 16.811 | 16.990 | 16.316 | 20.403 | 22.116 | 19.095 | 19.368 | 16.960 | 18.090 | 15.349 | + | 2 | 2 |
| 45 | 2.573 | 8.080 | 5.616 | -0.027 | -0.376 | 0.957 | 25.607 | 25.258 | 26.591 | 24.641 | 30.149 | 27.684 | 24.083 | 27.184 | 26.030 | 18.107 | + | 27 | 27 |
| 46 | -2.321 | 5.513 | 3.363 | -4.677 | -0.193 | -4.261 | 16.839 | 21.323 | 17.256 | 15.777 | 23.612 | 21.462 | 19.838 | 23.195 | 20.393 | 15.804 |  | 4 | 4 |
| 47 | -0.488 | 3.179 | 0.615 | -5.055 | -4.408 | -2.293 | 17.182 | 17.829 | 19.944 | 20.084 | 23.751 | 21.187 | 24.423 | 20.051 | 21.949 | 19.194 | + | 5 | 3 |
| 48 | 1.629 | 8.585 | 6.017 | -0.107 | -0.026 | 1.453 | 17.752 | 17.833 | 19.312 | 17.090 | 24.046 | 21.478 | 18.770 | 16.948 | 17.285 | 13.637 |  | 5 | 5 |
| 49 | 9.904 | 6.267 | 7.408 | 5.211 | 1.689 | 1.774 | 29.390 | 25.868 | 25.953 | 28.021 | 24.384 | 25.525 | 25.189 | 23.169 | 16.955 | 19.278 | + | 3 | 3 |
| 50 | 5.502 | 4.543 | 3.141 | -0.114 | -0.162 | -1.239 | 22.564 | 22.515 | 21.439 | 27.715 | 26.755 | 25.354 | 24.387 | 20.968 | 22.438 | 21.988 | + | 38 | 38 |
| 51 | -2.312 | 3.763 | -2.901 | -2.209 | -5.677 | -8.255 | 21.202 | 17.734 | 15.156 | 16.909 | 22.984 | 16.321 | 24.767 | 22.055 | 18.860 | 19.583 |  | 4 | 4 |
| 52 | 3.402 | 4.926 | 5.975 | -2.249 | 1.028 | 0.933 | 22.009 | 25.287 | 25.192 | 22.483 | 24.007 | 25.055 | 25.322 | 23.194 | 24.518 | 13.643 | + | 5 | 5 |
| 53 | 2.606 | -0.252 | -0.788 | -6.087 | -6.357 | -0.562 | 16.412 | 16.142 | 21.937 | 21.045 | 18.187 | 17.651 | 24.868 | 20.129 | 22.150 | 14.728 |  | 3 | 3 |
| 54 | -0.661 | 5.866 | 3.999 | -1.711 | -0.938 | -2.636 | 16.441 | 17.214 | 15.516 | 16.005 | 22.531 | 20.665 | 20.170 | 16.133 | 18.562 | 14.769 |  | 2 | 2 |
| 55 | 0.055 | 2.566 | 0.220 | -3.983 | -4.206 | -3.320 | 17.496 | 17.273 | 18.159 | 20.426 | 22.937 | 20.590 | 23.645 | 19.313 | 22.223 | 18.518 | + | 3 | 3 |
| 56 | 1.143 | -1.161 | -0.500 | -5.269 | -4.977 | -4.544 | 16.827 | 17.119 | 17.552 | 20.029 | 17.726 | 18.387 | 23.512 | 20.679 | 17.419 | 20.354 | + | 4 | 4 |
| 57 | -3.796 | 2.376 | 1.580 | -4.683 | -3.551 | -5.563 | 17.442 | 18.574 | 16.562 | 15.372 | 21.544 | 20.748 | 24.642 | 19.608 | 23.315 | 15.021 |  | 5 | 5 |
| 58 | 4.105 | 6.283 | 1.744 | -0.908 | -0.301 | -0.506 | 16.221 | 16.827 | 16.623 | 20.072 | 22.250 | 17.712 | 18.973 | 15.284 | 17.081 | 14.854 | + | 2 | 2 |
| 59 | -0.690 | 5.259 | 4.131 | -1.828 | -1.486 | -1.578 | 16.657 | 16.998 | 16.907 | 16.495 | 22.444 | 21.316 | 21.820 | 15.149 | 20.376 | 13.994 |  | 2 | 2 |
| 60 | 0.880 | -3.690 | -0.439 | -6.473 | -2.782 | -7.499 | 18.565 | 22.255 | 17.538 | 22.309 | 17.738 | 20.990 | 26.720 | 23.355 | 24.334 | 18.524 |  | 11 | 10 |

|  | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 32 | 9 | 4.8 | 285.15 | 82.628 | 19.431 | 18.989 | **1.410** | **5.610** | Q8BTI8-3;Q8BTI8-2;Q8BTI8;A0A087WPS9;A0A087WRX8 | Q8BTI8-3;Q8BTI8-2;Q8BTI8 | Serine/arginine repetitive matrix protein 2 | **Srrm2** | 1182 |
| 33 | 5 | 3 | 273.99 | 35.996 | 19.577 | 17.083 | **1.289** | **5.531** | F6ZDS4;Q7M739;F6RX08 | F6ZDS4;Q7M739;F6RX08 | Nucleoprotein TPR | **Tpr** | 426 |
| 34 | 9 | 11.4 | 104.92 | 56.13 | 20.777 | 18.006 | **1.789** | **5.501** | P30999;E9Q8Z4;E9Q8Z6;G3X9V2;E9Q904;E9Q901;D3Z2H2;E9Q8Z9;E9Q8Z8;E9Q905;E9Q907;E9Q903;E9Q986;D3Z7H6;P30999-2;E9Q8Z5;P30999-3;E9Q906;D3Z2H7 | P30999;E9Q8Z4;E9Q8Z6;G3X9V2;E9Q904;E9Q901;D3Z2H2;E9Q8Z9;E9Q8Z8;E9Q905;E9Q907;E9Q903;E9Q986;D3Z7H6;P30999-2;E9Q8Z5;P30999-3;E9Q906;D3Z2H7 | Catenin delta-1 | **Ctnnd1** | 301 |
| 35 | 4 | 8.4 | 51.373 | 24.412 | 21.770 | 18.266 | **1.190** | **5.467** | O55222;D3YZA5;F6Q5Z1 | O55222 | Integrin-linked protein kinase | **Ilk** | 529 |
| 36 | 1 | 28.1 | 3.7112 | 6.5528 | 18.344 | 16.316 | **3.278** | **5.463** | A0A0N4SVL7;A0A0N4SWF7;Q923D5 | A0A0N4SVL7;A0A0N4SWF7;Q923D5 | WW domain-binding protein 11 | **Wbp11** | 70 |
| 37 | 3 | 6.3 | 50.113 | 18.832 | 20.367 | 16.107 | **0.982** | **5.458** | Q9Z2I9 | Q9Z2I9 | Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial | **Sucla2** | 1573 |
| 38 | 1 | 57.2 | 50.135 | 9.814 | 17.182 | 18.654 | **2.613** | **5.382** | P68369;P05214 | P68369;P05214 | Tubulin alpha-1A chain;Tubulin alpha-3 chain | **Tuba1a;Tuba3a** | 873 |
| 39 | 3 | 22.3 | 19.79 | 18.626 | 19.496 | 18.462 | **2.599** | **5.363** | Q62376-2;Q62376 | Q62376-2;Q62376 | U1 small nuclear ribonucleoprotein 70 kDa | **Snrnp70** | 1069 |
| 40 | 12 | 21.5 | 82.669 | 119.23 | 25.722 | 21.925 | **1.207** | **5.347** | Q8BMS1 | Q8BMS1 | Trifunctional enzyme subunit alpha, mitochondrial;Long-chain enoyl-CoA hydratase;Long chain 3-hydroxyacyl-CoA dehydrogenase | **Hadha** | 1176 |
| 41 | 5 | 14.6 | 50.063 | 33.381 | 16.470 | 15.608 | **0.963** | **5.346** | A0A0A0MQ76;Q6DFW4;A0A087WQ46;A0A087WP00;A0A087WSU5;A0A087WSL8 | A0A0A0MQ76;Q6DFW4;A0A087WQ46;A0A087WP00 | Nucleolar protein 58 | **Nop58** | 25 |
| 42 | 1 | 10.8 | 13.214 | 15.077 | 17.468 | 16.279 | **1.255** | **5.339** | A0A140T8M9;A0A140T8M0;A0A0B4J1I0;A0A075B5N0;A0A075B5K8;F6XWB2;A0A140T8N1;A0A0G2JDE5;P01631 | A0A140T8M9;A0A140T8M0;A0A0B4J1I0;A0A075B5N0;A0A075B5K8;F6XWB2;A0A140T8N1;A0A0G2JDE5;P01631 | Ig kappa chain V-II region 26-10 | **Igkv1-110;Igkv1-35;Igkv1-99;Igkv1-115** | 2 |
| 43 | 15 | 22.8 | 93.55 | 116.5 | 17.295 | 16.137 | **0.761** | **5.290** | Q9JIK5 | Q9JIK5 | Nucleolar RNA helicase 2 | **Ddx21** | 1494 |
| 44 | 2 | 4.9 | 52.572 | 12.607 | 18.164 | 16.719 | **2.378** | **5.277** | Q9CT10 | Q9CT10 | Ran-binding protein 3 | **Ranbp3** | 1370 |
| 45 | 27 | 36.9 | 76.722 | 323.31 | 25.634 | 22.068 | **1.479** | **5.238** | P09405 | P09405 | Nucleolin | **Ncl** | 582 |
| 46 | 4 | 32.4 | 22.135 | 33.416 | 21.516 | 18.099 | **0.889** | **5.229** | Q3TFP0;Q9R0U0-3;Q9R0U0-2;Q9R0U0;A3KG57 | Q3TFP0;Q9R0U0-3;Q9R0U0-2;Q9R0U0 | Serine/arginine-rich splicing factor 10 | **Srsf10** | 949 |
| 47 | 3 | 17.3 | 37.54 | 19.66 | 22.237 | 20.572 | **1.669** | **5.021** | P62137 | P62137 | Serine/threonine-protein phosphatase PP1-alpha catalytic subunit | **Ppp1ca** | 808 |
| 48 | 5 | 14.6 | 50.421 | 53.118 | 17.859 | 15.461 | **1.117** | **4.971** | Q8BVY0 | Q8BVY0 | Ribosomal L1 domain-containing protein 1 | **Rsl1d1** | 1186 |
| 49 | 3 | 34.8 | 10.275 | 119.42 | 24.179 | 18.117 | **1.459** | **4.969** | P61514 | P61514 | 60S ribosomal protein L37a | **Rpl37a** | 798 |
| 50 | 38 | 28.8 | 188.85 | 317.06 | 22.677 | 22.213 | **2.489** | **4.900** | B9EHJ3;P39447;A0A0U1RPW2;A0A0U1RPB2 | B9EHJ3;P39447;A0A0U1RPW2 | Tight junction protein ZO-1 | **Tjp1** | 220 |
| 51 | 4 | 17.1 | 36.511 | 30.901 | 23.411 | 19.222 | **0.823** | **4.897** | P14152 | P14152 | Malate dehydrogenase, cytoplasmic | **Mdh1** | 611 |
| 52 | 5 | 37.3 | 12.554 | 32.625 | 24.258 | 19.080 | **1.685** | **4.864** | O55142 | O55142 | 60S ribosomal protein L35a | **Rpl35a** | 527 |
| 53 | 3 | 26 | 10.99 | 21.197 | 22.499 | 18.439 | **1.056** | **4.858** | P62627;A2AVR9 | P62627;A2AVR9 | Dynein light chain roadblock-type 1 | **Dynlrb1** | 825 |
| 54 | 2 | 6.1 | 40.068 | 14.573 | 18.152 | 16.666 | **1.135** | **4.829** | P54923 | P54923 | [Protein ADP-ribosylarginine] hydrolase | **Adprh** | 761 |
| 55 | 3 | 34.7 | 11.225 | 18.513 | 21.479 | 20.371 | **2.303** | **4.783** | Q8CFZ0;G3UYP0;P63280 | Q8CFZ0;G3UYP0;P63280 | SUMO-conjugating enzyme UBC9 | **Ube2i** | 460 |
| 56 | 4 | 9.3 | 73.417 | 25.416 | 22.096 | 18.887 | **2.573** | **4.757** | A0A0R4J0G0;Q8BH04 | A0A0R4J0G0;Q8BH04 | Phosphoenolpyruvate carboxykinase [GTP], mitochondrial | **Pck2** | 82 |
| 57 | 5 | 10.1 | 95.832 | 32.072 | 22.125 | 19.168 | **1.081** | **4.652** | P56399;Q3U4W8;D3YYA5 | P56399;Q3U4W8 | Ubiquitin carboxyl-terminal hydrolase 5;Ubiquitin carboxyl-terminal hydrolase | **Usp5** | 768 |
| 58 | 2 | 1.5 | 123.55 | 11.881 | 17.128 | 15.968 | **1.600** | **4.615** | B7ZC27;Q99PV0 | B7ZC27;Q99PV0 | Pre-mRNA-processing-splicing factor 8 | **Prpf8** | 216 |
| 59 | 2 | 17.8 | 14.866 | 15.591 | 18.485 | 17.185 | **1.166** | **4.531** | P16045 | P16045 | Galectin-1 | **Lgals1** | 619 |
| 60 | 9 | 31.1 | 50.648 | 70.48 | 25.037 | 21.429 | **1.072** | **4.502** | E9Q1G8;E9Q9F5;O55131 | E9Q1G8;E9Q9F5;O55131 | Septin-7 | **Sept7** | 368 |

|  | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 61 | -0.324 | -0.525 | -0.455 | -6.179 | -1.544 | -7.067 | 17.023 | 21.659 | 16.136 | 17.708 | 17.507 | 17.577 | 24.251 | 22.155 | 21.811 | 14.253 |  | 3 | 3 |
| 62 | 0.845 | 5.395 | 5.406 | -2.200 | 0.218 | 0.142 | 15.129 | 17.547 | 17.472 | 16.612 | 21.163 | 21.174 | 18.433 | 16.225 | 16.997 | 14.538 |  | 2 | 2 |
| 63 | 5.086 | 3.842 | 3.630 | -0.990 | -0.577 | 0.749 | 16.089 | 16.502 | 17.828 | 21.310 | 20.066 | 19.854 | 17.807 | 16.351 | 17.255 | 15.193 | + | 1 | 1 |
| 64 | 2.904 | -2.194 | -3.022 | -1.918 | -7.006 | -6.754 | 23.027 | 17.939 | 18.190 | 22.842 | 17.743 | 16.916 | 27.214 | 22.675 | 24.428 | 15.447 |  | 5 | 5 |
| 65 | -2.333 | 2.740 | 2.452 | -3.607 | -2.046 | -4.806 | 17.938 | 19.499 | 16.739 | 16.526 | 21.598 | 21.311 | 22.822 | 20.268 | 22.229 | 15.488 |  | 1 | 1 |
| 66 | -0.633 | 4.488 | 3.195 | -1.601 | -1.939 | -2.666 | 17.641 | 17.303 | 16.576 | 19.417 | 24.539 | 23.246 | 18.796 | 19.687 | 24.964 | 15.137 | + | 11 | 11 |
| 67 | 5.335 | 11.185 | 8.667 | 2.847 | 3.953 | 5.142 | 20.188 | 21.295 | 22.483 | 20.951 | 26.800 | 24.282 | 18.818 | 15.864 | 16.507 | 14.723 |  | 18 | 18 |
| 68 | -1.598 | -1.573 | -0.248 | -6.819 | -8.749 | -1.084 | 18.131 | 16.200 | 23.865 | 22.277 | 22.302 | 23.627 | 29.373 | 20.526 | 23.597 | 24.153 |  | 10 | 10 |
| 69 | 1.862 | -1.130 | 2.858 | -6.917 | -1.521 | -1.187 | 15.687 | 21.083 | 21.417 | 20.463 | 17.471 | 21.459 | 23.912 | 21.296 | 22.761 | 14.441 |  | 5 | 5 |
| 70 | -1.974 | 2.839 | 2.770 | -3.995 | -3.459 | -2.001 | 15.503 | 16.039 | 17.497 | 16.979 | 21.792 | 21.723 | 19.034 | 19.962 | 23.390 | 14.516 |  | 4 | 4 |
| 71 | -0.158 | 5.100 | 4.336 | -1.882 | -2.038 | 0.132 | 17.036 | 16.879 | 19.049 | 15.774 | 21.032 | 20.268 | 23.076 | 14.759 | 16.856 | 15.008 |  | 2 | 2 |
| 72 | -4.048 | 2.002 | -3.069 | -6.203 | -5.250 | -6.700 | 17.471 | 18.424 | 16.974 | 16.205 | 22.255 | 17.184 | 23.113 | 24.235 | 24.514 | 15.992 |  | 8 | 7 |
| 73 | 0.088 | 4.931 | 5.361 | -1.151 | -0.795 | -0.703 | 17.079 | 17.434 | 17.527 | 15.773 | 20.616 | 21.046 | 21.349 | 15.110 | 16.941 | 14.429 |  | 3 | 3 |
| 74 | -0.541 | 1.255 | 0.531 | -2.360 | -3.998 | -5.386 | 18.922 | 17.284 | 15.896 | 20.694 | 22.491 | 21.767 | 22.907 | 19.657 | 23.179 | 19.292 | + | 5 | 5 |
| 75 | -3.526 | -8.602 | -3.341 | -8.865 | -9.321 | -10.209 | 18.160 | 17.704 | 16.815 | 22.461 | 17.385 | 22.646 | 29.542 | 24.508 | 26.543 | 25.431 |  | 2 | 2 |
| 76 | -2.389 | 5.418 | 2.925 | -4.427 | -4.164 | 1.730 | 16.791 | 17.053 | 22.947 | 16.687 | 24.494 | 22.000 | 18.740 | 23.695 | 24.729 | 13.422 |  | 8 | 8 |
| 77 | 4.044 | 4.474 | 2.503 | -1.153 | -1.018 | 0.434 | 16.543 | 16.678 | 18.130 | 22.437 | 22.866 | 20.896 | 19.439 | 15.953 | 18.261 | 18.525 | + | 3 | 3 |
| 78 | 3.253 | 6.421 | 4.710 | -3.069 | 2.192 | 2.518 | 16.798 | 22.059 | 22.385 | 21.601 | 24.769 | 23.058 | 18.053 | 21.681 | 22.418 | 14.278 |  | 6 | 6 |
| 79 | 6.816 | 6.262 | 5.473 | 4.531 | 2.104 | -0.711 | 28.142 | 25.715 | 22.900 | 27.258 | 26.704 | 25.916 | 21.902 | 25.320 | 24.623 | 16.262 |  | 7 | 5 |
| 80 | -2.829 | 3.952 | 1.335 | -2.134 | -1.189 | -6.761 | 21.003 | 21.949 | 16.376 | 17.590 | 24.371 | 21.755 | 24.730 | 21.545 | 25.176 | 15.663 |  | 6 | 6 |
| 81 | -2.749 | 3.247 | 3.740 | -5.090 | -3.274 | 0.084 | 17.241 | 19.057 | 22.415 | 16.459 | 22.455 | 22.948 | 24.821 | 19.841 | 23.118 | 15.299 |  | 1 | 1 |
| 82 | -4.936 | 1.262 | 1.751 | -6.022 | -3.453 | -4.870 | 19.340 | 21.909 | 20.492 | 15.301 | 21.499 | 21.987 | 25.767 | 24.956 | 25.159 | 15.314 |  | 12 | 12 |
| 83 | -2.269 | 2.513 | 1.749 | -2.827 | -3.478 | -4.067 | 18.237 | 17.586 | 16.997 | 17.103 | 21.885 | 21.121 | 25.353 | 16.775 | 18.314 | 20.430 |  | 5 | 2 |
| 84 | -2.755 | 5.320 | 2.020 | -5.414 | -1.396 | -0.951 | 16.957 | 20.975 | 21.419 | 16.244 | 24.320 | 21.020 | 19.125 | 25.615 | 23.351 | 14.647 |  | 9 | 9 |
| 85 | 6.572 | 5.900 | 1.509 | 2.537 | -0.925 | 0.144 | 19.206 | 15.744 | 16.813 | 22.967 | 22.295 | 17.904 | 17.752 | 15.587 | 17.733 | 15.057 |  | 2 | 2 |
| 86 | 13.176 | 11.360 | 10.139 | 10.040 | 9.647 | 2.785 | 29.665 | 29.272 | 22.410 | 29.353 | 27.537 | 26.316 | 19.812 | 19.439 | 18.807 | 13.546 |  | 5 | 5 |
| 87 | 1.109 | 6.756 | 7.886 | 0.391 | -0.037 | 3.218 | 17.734 | 17.306 | 20.561 | 16.525 | 22.173 | 23.303 | 18.008 | 16.678 | 16.756 | 14.078 |  | 3 | 3 |
| 88 | -0.103 | 8.432 | 5.296 | 0.479 | 0.971 | 0.035 | 17.311 | 17.802 | 16.867 | 15.762 | 24.297 | 21.161 | 18.356 | 15.308 | 17.574 | 14.155 |  | 3 | 3 |
| 89 | -1.315 | 3.962 | 3.101 | -3.307 | -2.361 | -0.649 | 16.152 | 17.098 | 18.810 | 17.973 | 23.250 | 22.389 | 18.343 | 20.575 | 23.457 | 15.119 |  | 11 | 2 |

|  | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 61 | 3 | 22.3 | 17.253 | 17.354 | 23.203 | 18.032 | **1.232** | **4.495** | G3UZJ4;H3BJQ7;P99029-2;P99029 | G3UZJ4;H3BJQ7;P99029-2;P99029 | Peroxiredoxin-5, mitochondrial | **Prdx5** | 462 |
| 62 | 2 | 5.8 | 58.841 | 12.432 | 17.329 | 15.768 | **1.232** | **4.495** | Q9D554 | Q9D554 | Splicing factor 3A subunit 3 | **Sf3a3** | 1436 |
| 63 | 1 | 0.4 | 230.99 | 6.279 | 17.079 | 16.224 | **2.521** | **4.459** | K3W4L0;B2RRE2;E9QAX2;Q9JMH9-4;Q9JMH9-1;Q9JMH9;Q9JMH9-6 | K3W4L0;B2RRE2;E9QAX2;Q9JMH9-4;Q9JMH9-1;Q9JMH9;Q9JMH9-6 | Unconventional myosin-XVIIIa | **Myo18a** | 208 |
| 64 | 5 | 10 | 67.277 | 34.547 | 24.944 | 19.938 | **0.831** | **4.455** | P35564 | P35564 | Calnexin | **Canx** | 694 |
| 65 | 1 | 12.8 | 10.102 | 6.3729 | 21.545 | 18.858 | **1.142** | **4.439** | G5E919;F7CDT0;F6WMC0;P61082 | G5E919;F7CDT0;F6WMC0;P61082 | NEDD8-conjugating enzyme Ubc12 | **Ube2m** | 423 |
| 66 | 8 | 7.7 | 172.79 | 72.374 | 19.242 | 20.051 | **1.318** | **4.419** | Q01320 | Q01320 | DNA topoisomerase 2-alpha | **Top2a** | 920 |
| 67 | 18 | 15.1 | 152.04 | 214.91 | 17.341 | 15.615 | **1.141** | **4.415** | Q7TPV4 | Q7TPV4 | Myb-binding protein 1A | **Mybbp1a** | 1122 |
| 68 | 5 | 69.4 | 15.748 | 285.38 | 24.950 | 23.875 | **0.876** | **4.411** | A8DUK4;E9Q223;CON__P02070 | A8DUK4;E9Q223 | Beta-globin | **Hbbt1;Hbb-bs** | 190 |
| 69 | 5 | 10.9 | 67.314 | 31.284 | 22.604 | 18.601 | **0.932** | **4.405** | P61222 | P61222 | ATP-binding cassette sub-family E member 1 | **Abce1** | 795 |
| 70 | 4 | 14.1 | 43.062 | 24.608 | 19.498 | 18.953 | **1.206** | **4.363** | Q9CXY6 | Q9CXY6 | Interleukin enhancer-binding factor 2 | **Ilf2** | 1383 |
| 71 | 2 | 10 | 28.463 | 12.467 | 18.917 | 15.932 | **1.149** | **4.355** | O88456;A0A0R4IZW8;A0A0R4J1C2 | O88456;A0A0R4IZW8;A0A0R4J1C2 | Calpain small subunit 1 | **Capns1** | 75 |
| 72 | 7 | 16 | 61.447 | 43.267 | 23.674 | 20.253 | **1.062** | **4.346** | A2AJ72;Q3TIX6;A0A0A6YVV5;F7AM43;A2AJ71;A0A0A6YY39 | A2AJ72;Q3TIX6;A0A0A6YVV5 | Far upstream element (FUSE)-binding protein 3 | **Fubp3** | 153 |
| 73 | 3 | 17 | 15.137 | 18.748 | 18.230 | 15.685 | **1.203** | **4.343** | Q05816 | Q05816 | Fatty acid-binding protein, epidermal | **Fabp5** | 934 |
| 74 | 3 | 16.5 | 37.186 | 38.734 | 21.282 | 21.235 | **1.881** | **4.330** | P62141;A0A0J9YUU8;A0A0J9YUG2 | P62141;A0A0J9YUU8 | Serine/threonine-protein phosphatase PP1-beta catalytic subunit | **Ppp1cb** | 809 |
| 75 | 2 | 28.9 | 11.433 | 16.596 | 27.025 | 25.987 | **1.146** | **4.309** | E9Q3T0;P47955 | E9Q3T0;P47955 | 60S acidic ribosomal protein P1 | **Gm10073;Rplp1** | 377 |
| 76 | 8 | 9.9 | 122.78 | 58.529 | 21.217 | 19.076 | **0.629** | **4.271** | Q3UNN4;P97496-2;P97496;Q3UID0;Q6PDG5-2;Q6PDG5;Q3UZD0 | Q3UNN4;P97496-2;P97496;Q3UID0;Q6PDG5-2;Q6PDG5 | SWI/SNF complex subunit SMARCC1;SWI/SNF complex subunit SMARCC2 | **Smarcc1;Smarcc2** | 908 |
| 77 | 3 | 12.2 | 41.81 | 19.123 | 17.696 | 18.393 | **2.250** | **4.253** | Q925F2;D3Z5Y0 | Q925F2 | Endothelial cell-selective adhesion molecule | **Esam** | 1288 |
| 78 | 5 | 17.4 | 39.025 | 47.396 | 19.867 | 18.348 | **0.981** | **4.247** | Q3TWW8;A0A0A6YXX6 | Q3TWW8 | Serine/arginine-rich splicing factor 6 | **Srsf6** | 958 |
| 79 | 5 | 56.2 | 13.509 | 72.166 | 23.611 | 20.443 | **1.263** | **4.209** | Q3THW5;P0C0S6;Q8R029;Q3UA95;G3UWL7 | Q3THW5;P0C0S6;Q8R029;Q3UA95 | Histone H2A.V;Histone H2A.Z;Histone H2A | **H2afv;H2afz** | 584 |
| 80 | 6 | 5.7 | 136.33 | 71.316 | 23.138 | 20.419 | **0.731** | **4.181** | Q6ZQ38;D3YWC5 | Q6ZQ38 | Cullin-associated NEDD8-dissociated protein 1 | **Cand1** | 1106 |
| 81 | 1 | 4.3 | 31.2 | 7.1701 | 22.331 | 19.208 | **0.743** | **4.172** | D3Z0U5;D6RGM7;D3Z4J2;A0A0G2JFY0;A0A0A0MQ80;Q9D3R6-3;Q9D3R6;Q3UMC0 | D3Z0U5;D6RGM7;D3Z4J2;A0A0G2JFY0;A0A0A0MQ80;Q9D3R6-3;Q9D3R6;Q3UMC0 | Katanin p60 ATPase-containing subunit A-like 2;Spermatogenesis-associated protein 5 | **Katnal2;Spata5** | 27 |
| 82 | 12 | 10.9 | 161.93 | 78.691 | 25.361 | 20.236 | **0.844** | **4.141** | P23116 | P23116 | Eukaryotic translation initiation factor 3 subunit A | **Eif3a** | 647 |
| 83 | 2 | 46.3 | 15.878 | 17.375 | 21.064 | 19.372 | **1.268** | **4.122** | P02089 | P02089 | Hemoglobin subunit beta-2 | **Hbb-b2** | 555 |
| 84 | 6 | 14.9 | 70.887 | 117.32 | 22.370 | 18.999 | **0.683** | **4.115** | Q8VHM5;F7B5B5;A2AW41 | Q8VHM5;F7B5B5;A2AW41 | Heterogeneous nuclear ribonucleoprotein R | **Hnrnpr** | 429 |
| 85 | 2 | 2.5 | 84.185 | 12.638 | 16.669 | 16.395 | **1.012** | **4.075** | Q9Z1P7;G3UXN4;Q6P8V1 | Q9Z1P7;G3UXN4;Q6P8V1 | KN motif and ankyrin repeat domain-containing protein 3 | **Kank3** | 456 |
| 86 | 5 | 24.6 | 13.916 | 42.384 | 19.625 | 16.177 | **0.742** | **4.068** | P62320 | P62320 | Small nuclear ribonucleoprotein Sm D3 | **Snrpd3** | 823 |
| 87 | 2 | 27.6 | 12.678 | 30.082 | 17.343 | 15.417 | **0.805** | **4.060** | A0A140T8Q1;P01635;A0A140T8P6 | A0A140T8Q1;P01635 | Ig kappa chain V-V region K2 | **Igkv12-41** | 117 |
| 88 | 3 | 12.2 | 33.828 | 24.254 | 16.832 | 15.865 | **0.740** | **4.047** | F7AA45;E9Q8F0;Q8VH51-3;Q8VH51-2;Q8VH51;B7ZD63;B7ZD61 | F7AA45;E9Q8F0;Q8VH51-3;Q8VH51-2;Q8VH51 | RNA-binding protein 39 | **Rbm39** | 398 |
| 89 | 2 | 20.6 | 49.067 | 14.684 | 19.459 | 19.288 | **1.044** | **4.022** | Q8VDW0;D6RHT5;G3UXI6;Q8VDW0-2 | Q8VDW0 | ATP-dependent RNA helicase DDX39A | **Ddx39a** | 1255 |

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 90 | 1.052 | 3.100 | 2.145 | -2.380 | -1.338 | -2.028 | 17.036 | 18.078 | 17.388 | 19.581 | 21.629 | 20.673 | 18.500 | 20.332 | 21.401 | 15.656 | + | 2 | 2 |
| 91 | -0.826 | -4.244 | -1.400 | -6.517 | -5.555 | -6.163 | 17.004 | 17.966 | 17.358 | 20.952 | 17.535 | 20.378 | 25.360 | 21.681 | 23.823 | 19.735 | + | 9 | 9 |
| 92 | -1.044 | 0.320 | 0.340 | -3.436 | -7.041 | -1.433 | 20.041 | 16.435 | 22.044 | 21.471 | 22.835 | 22.854 | 25.054 | 21.899 | 23.456 | 21.574 | | 9 | 7 |
| 93 | 3.583 | 2.917 | -0.869 | -1.171 | -3.242 | -1.430 | 16.242 | 14.171 | 15.983 | 20.351 | 19.685 | 15.899 | 17.956 | 16.870 | 17.524 | 16.013 | | 2 | 2 |
| 94 | -2.644 | 1.727 | 1.912 | -4.389 | -5.872 | -0.192 | 18.425 | 16.943 | 22.623 | 16.962 | 21.334 | 21.519 | 25.801 | 19.828 | 22.780 | 16.433 | | 5 | 5 |
| 95 | -0.898 | -0.631 | -2.027 | -8.868 | -4.175 | -1.947 | 17.058 | 21.751 | 23.979 | 23.213 | 23.480 | 22.084 | 28.202 | 23.651 | 26.397 | 21.825 | | 9 | 9 |
| 96 | 0.794 | 5.349 | 2.666 | -3.794 | -0.424 | 1.697 | 17.576 | 20.947 | 23.067 | 21.563 | 26.118 | 23.435 | 18.190 | 24.551 | 25.527 | 16.011 | | 7 | 7 |
| 97 | 2.168 | 6.354 | 5.025 | 0.702 | 0.334 | 1.240 | 23.916 | 23.548 | 24.454 | 22.203 | 26.389 | 25.060 | 20.469 | 25.958 | 25.673 | 14.396 | + | 17 | 17 |
| 98 | 4.175 | 4.491 | 3.443 | 0.959 | 0.651 | -0.756 | 18.021 | 17.712 | 16.305 | 20.737 | 21.052 | 20.004 | 18.616 | 15.508 | 18.352 | 14.770 | + | 1 | 1 |
| 99 | -2.587 | 2.650 | 2.371 | -5.833 | -4.405 | 1.458 | 15.104 | 16.532 | 22.395 | 16.807 | 22.044 | 21.766 | 23.356 | 18.517 | 20.437 | 18.352 | | 3 | 1 |
| 100 | -2.964 | 4.908 | 4.064 | -3.356 | -4.043 | 2.206 | 17.523 | 16.836 | 23.085 | 16.869 | 24.742 | 23.897 | 25.329 | 16.429 | 24.411 | 15.256 | | 8 | 8 |
| 101 | 2.075 | 4.819 | 2.811 | 0.789 | -3.663 | 1.384 | 22.122 | 17.671 | 22.718 | 21.616 | 24.360 | 22.352 | 18.864 | 23.803 | 23.096 | 15.986 | | 12 | 12 |
| 102 | 1.462 | 5.184 | 3.722 | -0.648 | -0.583 | 0.447 | 16.662 | 16.728 | 17.757 | 17.994 | 21.716 | 20.254 | 17.929 | 16.692 | 17.181 | 15.883 | + | 1 | 1 |
| 103 | -4.206 | 5.710 | 2.728 | 0.738 | -3.353 | -4.165 | 22.064 | 17.973 | 17.161 | 14.756 | 24.672 | 21.690 | 24.487 | 18.165 | 22.506 | 15.418 | | 6 | 6 |
| 104 | -7.743 | -0.929 | -1.280 | -8.464 | -5.173 | -7.264 | 15.507 | 18.798 | 16.707 | 16.313 | 23.128 | 22.777 | 27.021 | 20.920 | 26.174 | 21.939 | | 6 | 6 |
| 105 | 4.917 | 5.089 | 2.493 | 0.571 | 3.252 | -2.238 | 18.872 | 21.553 | 16.063 | 24.237 | 24.409 | 21.814 | 21.207 | 15.395 | 19.164 | 19.478 | | 11 | 11 |
| 106 | 4.038 | 7.760 | 6.305 | 2.534 | 2.300 | 2.392 | 24.323 | 24.089 | 24.181 | 22.950 | 26.672 | 25.217 | 22.234 | 21.344 | 23.905 | 13.919 | + | 9 | 9 |
| 107 | -0.289 | -0.397 | -0.769 | -3.761 | -3.259 | -5.306 | 16.928 | 17.429 | 15.383 | 20.771 | 20.663 | 20.291 | 21.346 | 20.030 | 21.234 | 20.888 | + | 3 | 3 |
| 108 | 1.531 | 2.031 | 1.972 | 0.373 | -3.731 | -1.952 | 22.218 | 18.114 | 19.893 | 22.038 | 22.538 | 22.479 | 24.169 | 19.521 | 22.578 | 18.437 | + | 5 | 5 |
| 109 | -5.231 | 1.033 | 0.481 | -5.935 | -5.521 | -3.102 | 17.774 | 18.188 | 20.608 | 16.696 | 22.961 | 22.409 | 26.715 | 20.703 | 25.135 | 18.720 | | 11 | 11 |
| 110 | -1.218 | -0.315 | 0.460 | -3.512 | -4.378 | -3.932 | 18.185 | 17.319 | 17.766 | 17.687 | 18.591 | 19.365 | 24.253 | 19.142 | 17.780 | 20.031 | + | 5 | 5 |
| 111 | -2.359 | 0.233 | -1.284 | -5.918 | -6.743 | -1.452 | 17.271 | 16.446 | 21.738 | 20.144 | 22.735 | 21.219 | 24.591 | 21.788 | 23.980 | 21.025 | | 4 | 4 |
| 112 | 3.501 | 2.879 | 2.870 | 0.377 | -0.976 | -0.841 | 17.507 | 16.154 | 16.288 | 20.377 | 19.754 | 19.745 | 18.048 | 16.211 | 18.752 | 15.000 | + | 1 | 1 |
| 113 | -3.513 | 0.931 | 2.176 | -6.149 | -3.026 | -1.901 | 16.941 | 20.064 | 21.189 | 15.776 | 20.220 | 21.465 | 23.452 | 22.729 | 24.783 | 13.794 | | 6 | 6 |
| 114 | -1.216 | -5.822 | -0.541 | -3.232 | -5.726 | -9.274 | 23.551 | 21.058 | 17.510 | 22.604 | 17.998 | 23.278 | 26.437 | 27.130 | 26.255 | 21.384 | | 5 | 5 |
| 115 | 6.342 | 8.537 | 6.627 | 5.426 | 4.776 | 0.677 | 22.205 | 21.555 | 17.456 | 22.208 | 24.403 | 22.493 | 17.319 | 16.238 | 17.154 | 14.578 | | 2 | 2 |

|  | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 90 | 2 | 11 | 32.646 | 14.824 | 19.416 | 18.528 | **2.418** | **4.014** | E9Q715;Q05CX5;Q7TNC4-2;Q7TNC4-3;Q7TNC4-4;Q7TNC4 | E9Q715;Q05CX5;Q7TNC4-2;Q7TNC4-3;Q7TNC4-4;Q7TNC4 | Putative RNA-binding protein Luc7-like 2 | **Luc7l2** | 390 |
| 91 | 9 | 24 | 57.147 | 58.539 | 23.521 | 21.779 | **1.638** | **3.921** | Q922B2;Q8BJY7 | Q922B2 | Aspartate--tRNA ligase, cytoplasmic | **Dars** | 1282 |
| 92 | 5 | 40.7 | 28.086 | 75.46 | 23.476 | 22.515 | **1.060** | **3.842** | Q9CQV8;Q9CQV8-2;A2A5N1;O70456 | Q9CQV8;Q9CQV8-2;A2A5N1 | 14-3-3 protein beta/alpha;14-3-3 protein beta/alpha, N-terminally processed | **Ywhab** | 1357 |
| 93 | 2 | 2.6 | 108.85 | 12.312 | 17.413 | 16.768 | **1.174** | **3.825** | V9GWT6;V9GXH3;V9GXF0;V9GXP8;F8VPM7;Q99MI1-4;Q99MI1-2;Q99MI1 | V9GWT6;V9GXH3;V9GXF0;V9GXP8;F8VPM7;Q99MI1-4;Q99MI1-2;Q99MI1 | ELKS/Rab6-interacting/CAST family member 1 | **Erc1** | 433 |
| 94 | 5 | 28.9 | 16.924 | 30.636 | 22.815 | 19.607 | **0.778** | **3.816** | G3UY29;E9Q3P9;F8WGS1;P62492;P46638;G3UZD3;G3UZL4 | G3UY29;E9Q3P9;F8WGS1;P62492;P46638 | Ras-related protein Rab-11A;Ras-related protein Rab-11B | **Rab11b;Rab11a** | 376 |
| 95 | 3 | 23.8 | 32.931 | 65.133 | 25.926 | 24.111 | **0.850** | **3.811** | P51881 | P51881 | ADP/ATP translocase 2;ADP/ATP translocase 2, N-terminally processed | **Slc25a5** | 746 |
| 96 | 6 | 33.9 | 20.811 | 58.39 | 21.370 | 20.769 | **0.845** | **3.777** | Q9DCC5;P23198;D3Z1A9;D3Z313 | Q9DCC5;P23198;D3Z1A9;D3Z313 | Chromobox protein homolog 3 | **Cbx3** | 648 |
| 97 | 14 | 29.9 | 67.443 | 125.55 | 23.214 | 20.035 | **1.388** | **3.757** | Q3TUE1;A0A0G2JGW9;A0A0G2JFY5;Q3UUU2;Q91WJ8;Q91WJ8-2;A0A0G2JG00;A0A0G2JFK2;A0A0G2JGV9;A0A0G2JG96 | Q3TUE1;A0A0G2JGW9;A0A0G2JFY5;Q3UUU2;Q91WJ8;Q91WJ8-2;A0A0G2JG00;A0A0G2JFK2 | Far upstream element-binding protein 1 | **Fubp1** | 50 |
| 98 | 1 | 8.1 | 14.098 | 6.703 | 17.062 | 16.561 | **2.444** | **3.752** | Q9D937 | Q9D937 | Uncharacterized protein C11orf98 homolog |  | 1454 |
| 99 | 1 | 22.8 | 20.396 | 9.0413 | 20.937 | 19.395 | **0.596** | **3.738** | P61750;E9Q798;F6UFB9 | P61750;E9Q798 | ADP-ribosylation factor 4 | **Arf4** | 799 |
| 100 | 8 | 25.1 | 24.923 | 51.534 | 20.879 | 19.833 | **0.514** | **3.734** | A2BE93;Q9EQU5-2;Q9EQU5;A2BE92;Q9EQU5-3 | A2BE93;Q9EQU5-2;Q9EQU5;A2BE92 | Protein SET | **Set** | 180 |
| 101 | 12 | 12.3 | 135.55 | 80.654 | 21.334 | 19.541 | **0.976** | **3.732** | Q921M3;Q921M3-2 | Q921M3;Q921M3-2 | Splicing factor 3B subunit 3 | **Sf3b3** | 1280 |
| 102 | 1 | 18.2 | 7.9577 | 6.3556 | 17.311 | 16.532 | **1.509** | **3.717** | Q4FK66-2;Q4FK66 | Q4FK66-2;Q4FK66 | Pre-mRNA-splicing factor 38A | **Prpf38a** | 996 |
| 103 | 6 | 30.3 | 28.785 | 37.604 | 21.326 | 18.962 | **0.483** | **3.671** | P17918;A0A140T8V5 | P17918;A0A140T8V5 | Proliferating cell nuclear antigen | **Pcna** | 630 |
| 104 | 6 | 12.6 | 47.436 | 52.727 | 23.971 | 24.057 | **0.688** | **3.649** | Q8BG32;G3UXL5;G3UWW7;G3UYH2;G3UZ28;G3UYI4;G3UZ33;G3UYL3 | Q8BG32;G3UXL5;G3UWW7;G3UYH2 | 26S proteasome non-ATPase regulatory subunit 11 | **Psmd11** | 1142 |
| 105 | 11 | 10.1 | 131.28 | 66.913 | 18.301 | 19.321 | **0.950** | **3.638** | Q9Z0U1;Q921G9;Q9QXY1 | Q9Z0U1 | Tight junction protein ZO-2 | **Tjp2** | 1555 |
| 106 | 8 | 29.1 | 32.754 | 64.793 | 21.789 | 18.912 | **1.541** | **3.626** | Q60668-3;Q60668;F6ZV59;G5E8G0;G3X9W0;Q60668-4;Q60668-2;E9Q5B6;A0A0G2JFL4;F6SHF3;Q9D3U4 | Q60668-3;Q60668;F6ZV59;G5E8G0;G3X9W0;Q60668-4;Q60668-2;E9Q5B6 | Heterogeneous nuclear ribonucleoprotein D0 | **Hnrnpd** | 1020 |
| 107 | 3 | 16.4 | 39.834 | 18.854 | 20.688 | 21.061 | **2.337** | **3.623** | Q8BFW7-5;Q8BFW7-4;Q8BFW7 | Q8BFW7-5;Q8BFW7-4;Q8BFW7 | Lipoma-preferred partner homolog | **Lpp** | 1138 |
| 108 | 5 | 18 | 23.432 | 31.516 | 21.845 | 20.507 | **1.405** | **3.615** | Q3TLP8;P63001;Q05144;A2AC13;P60764 | Q3TLP8;P63001;Q05144 | Ras-related C3 botulinum toxin substrate 1;Ras-related C3 botulinum toxin substrate 2 | **Rac1;Rac2** | 853 |
| 109 | 11 | 18.9 | 94.208 | 98.543 | 23.709 | 21.928 | **0.759** | **3.614** | Q3U2G2;Q61316 | Q3U2G2;Q61316 | Heat shock 70 kDa protein 4 | **Hspa4** | 966 |
| 110 | 5 | 24.3 | 26.468 | 30.381 | 21.697 | 18.906 | **2.556** | **3.583** | Q9WTP6;Q9WTP6-2;F7BP55 | Q9WTP6;Q9WTP6-2 | Adenylate kinase 2, mitochondrial;Adenylate kinase 2, mitochondrial, N-terminally processed | **Ak2** | 1537 |
| 111 | 4 | 19.3 | 27.763 | 38.311 | 23.190 | 22.502 | **0.922** | **3.568** | H3BK43;H3BLJ9;H3BJL6;Q9R0P3;H3BJC6;H3BJP2;H3BKH6;H3BL99 | H3BK43;H3BLJ9;H3BJL6;Q9R0P3;H3BJC6;H3BJP2;H3BKH6 | S-formylglutathione hydrolase | **Esd** | 480 |
| 112 | 1 | 2.6 | 46.795 | 6.7267 | 17.130 | 16.876 | **2.760** | **3.563** | Q5ND52 | Q5ND52 | rRNA methyltransferase 3, mitochondrial | **Rnmtl1** | 1002 |
| 113 | 6 | 16.4 | 52.866 | 40.36 | 23.090 | 19.289 | **0.763** | **3.557** | Q8BVQ9;P46471 | Q8BVQ9;P46471 | 26S protease regulatory subunit 7 | **Psmc2** | 718 |
| 114 | 5 | 13.2 | 40.742 | 41.076 | 26.784 | 23.820 | **0.667** | **3.551** | Q9CR16 | Q9CR16 | Peptidyl-prolyl cis-trans isomerase D | **Ppid** | 1362 |
| 115 | 2 | 11.7 | 20.151 | 16.241 | 16.778 | 15.866 | **1.015** | **3.542** | Q80ZM5 | Q80ZM5 | H1 histone family, member X (H1.10 linker histone) | **H1fx** | 1136 |

|  | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 116 | 1.770 | 6.110 | 2.996 | -0.982 | 2.061 | -0.756 | 16.994 | 20.038 | 17.221 | 20.938 | 25.278 | 22.164 | 18.246 | 17.707 | 22.404 | 15.932 |  | 10 | 10 |
| 117 | -7.020 | -3.290 | -1.619 | -8.693 | -5.050 | -8.734 | 15.961 | 19.604 | 15.920 | 16.587 | 20.317 | 21.988 | 27.280 | 22.028 | 24.661 | 22.553 |  | 9 | 9 |
| 118 | -1.744 | 3.592 | 3.010 | -2.882 | -3.922 | 1.165 | 17.128 | 16.088 | 21.175 | 16.245 | 21.581 | 20.999 | 25.343 | 14.677 | 18.314 | 17.665 |  | 4 | 4 |
| 119 | -5.060 | -0.560 | -0.565 | -7.185 | -2.787 | -6.702 | 17.089 | 21.487 | 17.571 | 17.297 | 21.797 | 21.792 | 25.353 | 23.195 | 23.653 | 21.061 |  | 6 | 6 |
| 120 | 2.027 | 4.568 | 4.203 | 1.607 | 3.469 | -4.743 | 21.320 | 23.183 | 14.970 | 20.749 | 23.291 | 22.926 | 24.028 | 15.399 | 22.968 | 14.477 |  | 4 | 4 |
| 121 | 1.345 | 1.286 | -3.633 | -1.527 | -2.251 | -7.667 | 23.478 | 22.754 | 17.337 | 22.138 | 22.078 | 17.159 | 26.154 | 23.855 | 25.143 | 16.443 |  | 4 | 4 |
| 122 | -4.632 | -0.495 | -2.359 | -7.667 | -8.469 | -1.616 | 17.597 | 16.795 | 23.648 | 19.732 | 23.869 | 22.006 | 27.220 | 23.307 | 25.165 | 23.563 |  | 3 | 3 |
| 123 | -0.213 | 7.769 | 4.223 | 0.572 | 0.313 | 0.685 | 16.968 | 16.710 | 17.082 | 15.925 | 23.907 | 20.361 | 17.129 | 15.664 | 17.007 | 15.268 |  | 4 | 4 |
| 124 | -0.109 | 7.007 | 5.979 | 0.259 | 1.764 | 0.651 | 17.224 | 18.729 | 17.616 | 16.118 | 23.234 | 22.206 | 17.733 | 16.197 | 17.059 | 15.396 |  | 4 | 2 |
| 125 | 1.096 | 1.023 | -3.391 | -3.545 | -3.186 | -4.689 | 17.081 | 17.440 | 15.937 | 20.474 | 20.402 | 15.987 | 19.199 | 22.052 | 21.163 | 17.593 |  | 3 | 3 |
| 126 | 0.529 | 6.207 | 4.120 | -0.597 | 2.903 | -1.552 | 16.227 | 19.728 | 15.273 | 16.902 | 22.580 | 20.493 | 18.676 | 14.973 | 17.865 | 14.881 |  | 3 | 3 |
| 127 | -2.519 | 2.789 | -2.721 | -3.194 | -4.933 | -4.408 | 18.366 | 16.627 | 17.152 | 15.845 | 21.153 | 15.643 | 23.307 | 19.813 | 22.489 | 14.239 |  | 2 | 2 |
| 128 | 0.953 | 11.255 | 9.212 | 4.743 | 0.740 | 5.884 | 21.400 | 17.397 | 22.541 | 15.516 | 25.818 | 23.776 | 19.089 | 14.226 | 16.737 | 12.390 |  | 10 | 10 |
| 129 | 6.036 | 7.233 | 6.240 | 4.236 | 1.795 | 3.453 | 21.561 | 19.119 | 20.777 | 23.830 | 25.027 | 24.034 | 19.371 | 15.278 | 20.604 | 14.983 | + | 9 | 9 |
| 130 | 3.791 | 6.003 | 4.801 | 1.998 | 1.121 | 1.500 | 23.802 | 22.925 | 23.304 | 23.096 | 25.308 | 24.106 | 24.266 | 19.342 | 24.619 | 13.991 | + | 13 | 13 |
| 131 | 3.017 | 4.902 | 2.969 | -0.659 | 3.663 | -1.988 | 18.012 | 22.334 | 16.683 | 22.216 | 24.101 | 22.167 | 22.181 | 15.161 | 23.519 | 14.878 |  | 9 | 9 |
| 132 | 14.147 | 13.302 | 12.958 | 9.852 | 10.753 | 9.944 | 33.962 | 34.864 | 34.055 | 33.984 | 33.139 | 32.794 | 24.988 | 23.234 | 18.277 | 21.397 | + | 1 | 1 |
| 133 | 4.356 | 3.588 | 3.341 | -0.755 | 0.872 | 1.341 | 16.127 | 17.753 | 18.222 | 21.002 | 20.234 | 19.987 | 17.873 | 15.889 | 18.077 | 15.216 | + | 4 | 4 |
| 134 | 1.588 | 0.915 | -0.249 | -3.742 | -1.803 | -2.022 | 23.255 | 25.194 | 24.975 | 27.150 | 26.476 | 25.313 | 28.254 | 25.740 | 27.264 | 23.858 | + | 49 | 49 |
| 135 | -4.857 | 0.757 | -0.166 | -2.336 | -5.708 | -6.041 | 20.659 | 17.287 | 16.954 | 17.027 | 22.640 | 21.717 | 24.758 | 21.231 | 23.530 | 20.236 |  | 5 | 5 |
| 136 | 2.227 | 6.053 | 4.256 | -3.318 | 3.379 | 2.681 | 16.067 | 22.764 | 22.066 | 21.397 | 25.222 | 23.425 | 17.812 | 20.957 | 22.839 | 15.500 |  | 9 | 9 |
| 137 | 2.604 | 4.253 | 2.906 | -0.634 | 0.003 | 0.618 | 17.091 | 17.728 | 18.343 | 20.025 | 21.675 | 20.328 | 19.397 | 16.052 | 20.759 | 14.084 | + | 1 | 1 |

| | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 116 | 10 | 19.2 | 68.578 | 62.1 | 17.977 | 19.168 | **1.019** | **3.518** | A0A0G2JG10;Q497W9;O35286;A0A0G2JGQ5;Q05BH3;G3X8X0;A2A4N9;A2A4P0 | A0A0G2JG10;Q497W9;O35286 | Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 | **Dhx15** | 51 |
| 117 | 9 | 43.5 | 27.623 | 122.24 | 24.654 | 23.607 | **0.809** | **3.516** | Q9DCW4;A0A0U1RQB4;A0A0U1RNK9;A0A0N4SVE0;A0A0U1RNR3;A0A0U1RNP5;A0A0N4SWE9 | Q9DCW4;A0A0U1RQB4;A0A0U1RNK9;A0A0N4SVE0 | Electron transfer flavoprotein subunit beta | **Etfb** | 1479 |
| 118 | 4 | 34.1 | 15.846 | 27.629 | 20.010 | 17.989 | **0.695** | **3.499** | Q00915 | Q00915 | Retinol-binding protein 1 | **Rbp1** | 918 |
| 119 | 6 | 9.3 | 63.53 | 39.919 | 24.274 | 22.357 | **0.789** | **3.496** | P46061 | P46061 | Ran GTPase-activating protein 1 | **Rangap1** | 716 |
| 120 | 4 | 3.4 | 182.29 | 31.073 | 19.714 | 18.723 | **0.598** | **3.488** | E9QPX1;P39061-2;P39061-1;P39061 | E9QPX1;P39061-2;P39061-1;P39061 | Collagen alpha-1(XVIII) chain;Endostatin | **Col18a1** | 413 |
| 121 | 4 | 38.1 | 11.675 | 53.999 | 25.005 | 20.793 | **0.614** | **3.481** | P10639 | P10639 | Thioredoxin | **Txn1** | 590 |
| 122 | 3 | 68.2 | 5.0256 | 34.496 | 25.264 | 24.364 | **0.623** | **3.422** | Q6ZWY8;A0A0N4SVF0 | Q6ZWY8;A0A0N4SVF0 | Thymosin beta-10 | **Tmsb10** | 1113 |
| 123 | 4 | 3.8 | 138.55 | 25.719 | 16.396 | 16.138 | **0.668** | **3.403** | H3BL37;O08784;Q05CS0;H3BIX0 | H3BL37;O08784;Q05CS0;H3BIX0 | Treacle protein | **Tcof1** | 484 |
| 124 | 2 | 12.1 | 36.983 | 15.72 | 16.965 | 16.227 | **0.682** | **3.401** | P63087;P63087-2;A0A0G2JFF1;A0A0G2JGC1 | P63087;P63087-2;A0A0G2JFF1;A0A0G2JGC1 | Serine/threonine-protein phosphatase PP1-gamma catalytic subunit | **Ppp1cc** | 860 |
| 125 | 3 | 15.8 | 25.352 | 17.467 | 20.626 | 19.378 | **1.024** | **3.382** | Q8C266;P35278;A2A5F6;A2A5F5;Q9CQD1;P61021 | Q8C266;P35278 | Ras-related protein Rab-5C | **Rab5c** | 689 |
| 126 | 3 | 11.2 | 37.048 | 20.103 | 16.825 | 16.373 | **0.719** | **3.367** | D9J2V6;P41778-2;P41778;G3UXL9;Q3UR63;V9GXB8;O35317-2;O35984;O35317 | D9J2V6;P41778-2;P41778 | Pre-B-cell leukemia transcription factor 1 | **Pbx1** | 320 |
| 127 | 2 | 5.9 | 56.55 | 16.903 | 21.560 | 18.364 | **0.831** | **3.361** | P62814 | P62814 | V-type proton ATPase subunit B, brain isoform | **Atp6v1b2** | 831 |
| 128 | 10 | 13.4 | 112.72 | 60.847 | 16.657 | 14.563 | **0.404** | **3.351** | Q921K2;P11103-2;P11103 | Q921K2;P11103-2;P11103 | Poly [ADP-ribose] polymerase 1 | **Parp1** | 1279 |
| 129 | 9 | 19.4 | 55.249 | 57.431 | 17.324 | 17.794 | **1.839** | **3.342** | Q99LF4 | Q99LF4 | tRNA-splicing ligase RtcB homolog | **Rtcb** | 1309 |
| 130 | 13 | 26.9 | 47.688 | 85.957 | 21.804 | 19.305 | **2.073** | **3.325** | P50247;A2ALT5 | P50247 | Adenosylhomocysteinase | **Ahcy** | 738 |
| 131 | 8 | 34.3 | 34.106 | 58.916 | 18.671 | 19.199 | **0.839** | **3.291** | P11440;D3Z2T9;P97377-2;Q80YP0;P97377;Q04735-2;E9PVC7;E3W997;Q3V3A1;Q14AX6;Q14AX6-3;Q69ZA1-2;Q14AX6-2;Q8K0D0;Q04735;O35495;Q3V3A1-3;Q04899;A0A0G2JDL3;Q99J95-3;Q8K0D0-2;O35495-2;Q99J95;O35495-3;Q64261;Q99J95-2;P49615;Q69ZA1 | P11440;D3Z2T9 | Cyclin-dependent kinase 1 | **Cdk1** | 597 |
| 132 | 1 | 0.6 | 135.87 | 7.9036 | 24.111 | 19.837 | **2.711** | **3.286** | A0A087WS76;A0A140LHL6;E9Q3S4 | A0A087WS76;A0A140LHL6;E9Q3S4 | Mitogen-activated protein kinase kinase kinase 19 | **Map3k19** | 24 |
| 133 | 2 | 27.1 | 20.697 | 27.438 | 16.881 | 16.646 | **2.015** | **3.276** | P84078;P61205;Q8BSL7;P84084;D3YV25;E9Q2C2;A2A6T9 | P84078;P61205;Q8BSL7;P84084 | ADP-ribosylation factor 1;ADP-ribosylation factor 3;ADP-ribosylation factor 2;ADP-ribosylation factor 5 | **Arf1;Arf3;Arf2;Arf5** | 794 |
| 134 | 49 | 25.2 | 269.82 | 323.31 | 26.997 | 25.561 | **1.799** | **3.274** | P26039;A2AIM2;E9PUM4;Q71LX4;F6S1V7;F6SX70 | P26039 | Talin-1 | **Tln1** | 657 |
| 135 | 5 | 20.4 | 33.081 | 35.76 | 22.995 | 21.883 | **0.711** | **3.273** | D3YU12;Q8K2T1;G5E8S7;Q8K2T1-2;Q8K2T1-3 | D3YU12;Q8K2T1;G5E8S7;Q8K2T1-2;Q8K2T1-3 | NmrA-like family domain-containing protein 1 | **Nmral1** | 276 |
| 136 | 9 | 16.7 | 69.448 | 60.966 | 19.385 | 19.169 | **0.612** | **3.265** | Q8C2Q3;E9QL13;Q8C2Q3-2 | Q8C2Q3;E9QL13;Q8C2Q3-2 | RNA-binding protein 14 | **Rbm14** | 1193 |
| 137 | 1 | 3.2 | 46.638 | 8.0052 | 17.725 | 17.421 | **2.196** | **3.259** | O54941 | O54941 | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 | **Smarce1** | 524 |

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 138 | -1.607 | 1.341 | 0.044 | -5.382 | -3.726 | -0.724 | 17.585 | 19.241 | 22.243 | 19.830 | 22.778 | 21.481 | 25.274 | 20.660 | 24.269 | 18.605 | | 9 | 9 |
| 139 | -4.135 | -2.536 | 0.964 | -6.392 | -2.203 | -6.690 | 16.952 | 21.140 | 16.654 | 16.402 | 18.000 | 21.501 | 24.324 | 22.363 | 25.328 | 15.745 | | 6 | 6 |
| 140 | 5.762 | 5.105 | 5.542 | 1.817 | 3.349 | 1.774 | 26.147 | 27.680 | 26.105 | 25.668 | 25.011 | 25.448 | 25.508 | 23.154 | 25.454 | 14.357 | + | 7 | 7 |
| 141 | -4.548 | 5.514 | 2.344 | -3.538 | -3.447 | 0.907 | 16.711 | 16.802 | 21.156 | 15.505 | 25.566 | 22.397 | 18.640 | 21.857 | 23.552 | 16.553 | | 10 | 10 |
| 142 | 2.935 | 6.518 | 5.955 | 2.650 | 1.496 | 1.884 | 23.974 | 22.820 | 23.208 | 22.877 | 26.461 | 25.898 | 17.391 | 25.258 | 26.952 | 12.934 | | 9 | 9 |
| 143 | 0.068 | 6.452 | 4.138 | -3.109 | 2.477 | 1.969 | 17.188 | 22.775 | 22.267 | 19.410 | 25.794 | 23.480 | 18.643 | 21.952 | 24.466 | 14.218 | | 12 | 12 |
| 144 | -1.738 | 5.185 | 4.747 | 0.645 | -0.538 | -1.210 | 18.836 | 17.653 | 16.981 | 15.371 | 22.294 | 21.857 | 20.113 | 16.269 | 18.227 | 15.992 | | 2 | 2 |
| 145 | -0.559 | 4.400 | 3.525 | -1.318 | 1.162 | -1.745 | 17.049 | 19.529 | 16.623 | 15.676 | 20.635 | 19.760 | 22.349 | 14.387 | 17.833 | 14.637 | | 3 | 3 |
| 146 | 1.758 | 4.886 | 3.318 | -6.322 | 5.135 | 1.927 | 15.878 | 27.334 | 24.127 | 23.603 | 26.730 | 25.162 | 17.682 | 26.717 | 26.757 | 16.932 | | 18 | 18 |
| 147 | -1.522 | 5.324 | 4.050 | -0.857 | -0.265 | -0.217 | 16.334 | 16.926 | 16.974 | 16.397 | 23.243 | 21.969 | 19.242 | 15.140 | 20.611 | 15.227 | | 1 | 1 |
| 148 | -1.452 | -2.115 | -1.768 | -7.030 | -2.544 | -4.908 | 17.787 | 22.273 | 19.908 | 22.337 | 21.674 | 22.021 | 25.905 | 23.728 | 24.483 | 23.096 | | 11 | 11 |
| 149 | -0.917 | -0.480 | 0.570 | -3.923 | -3.080 | -2.824 | 24.294 | 25.137 | 25.393 | 23.879 | 24.316 | 25.365 | 29.149 | 27.286 | 27.972 | 21.619 | + | 21 | 21 |
| 150 | 0.387 | -2.806 | -3.669 | -4.839 | -5.327 | -4.920 | 17.258 | 16.770 | 17.178 | 20.371 | 17.179 | 16.316 | 24.116 | 20.079 | 19.395 | 20.575 | | 4 | 4 |
| 151 | -1.347 | 1.109 | 2.305 | -1.682 | -1.300 | -3.948 | 19.960 | 20.342 | 17.694 | 17.412 | 19.868 | 21.064 | 24.873 | 18.410 | 22.746 | 14.771 | | 7 | 7 |
| 152 | -0.697 | 0.942 | 0.656 | -7.045 | -0.494 | -0.503 | 17.964 | 24.515 | 24.506 | 22.794 | 24.434 | 24.148 | 27.073 | 22.944 | 26.085 | 20.898 | | 5 | 4 |
| 153 | 1.988 | 2.807 | 2.048 | -1.026 | -2.448 | 1.439 | 19.005 | 17.583 | 21.470 | 20.775 | 21.594 | 20.835 | 24.207 | 15.856 | 23.076 | 14.499 | | 2 | 2 |
| 154 | -2.348 | -3.178 | -3.551 | -3.253 | -7.109 | -7.438 | 21.417 | 17.561 | 17.232 | 21.649 | 20.819 | 20.446 | 25.751 | 23.589 | 23.882 | 24.112 | | 9 | 9 |
| 155 | -2.841 | 2.335 | 1.374 | 0.529 | -4.606 | -3.723 | 21.623 | 16.488 | 17.370 | 17.194 | 22.370 | 21.409 | 21.181 | 21.006 | 22.365 | 17.705 | | 2 | 2 |
| 156 | -1.317 | 4.705 | 1.697 | -4.492 | -0.012 | 0.942 | 17.541 | 22.021 | 22.975 | 17.878 | 23.900 | 20.893 | 22.533 | 21.533 | 23.551 | 14.840 | | 8 | 8 |
| 157 | 4.348 | 7.048 | -0.492 | 4.058 | -0.081 | -1.674 | 21.421 | 17.282 | 15.689 | 21.346 | 24.046 | 16.507 | 18.589 | 16.137 | 16.792 | 17.205 | | 2 | 2 |
| 158 | 6.002 | 4.198 | 0.319 | 0.425 | 1.472 | 0.027 | 16.732 | 17.780 | 16.334 | 22.463 | 20.659 | 16.780 | 16.827 | 15.788 | 18.130 | 14.792 | | 1 | 1 |
| 159 | 8.402 | 5.603 | 5.444 | 3.903 | 3.307 | 3.721 | 24.089 | 23.494 | 23.907 | 24.644 | 21.845 | 21.686 | 22.482 | 17.891 | 16.715 | 15.769 | + | 5 | 5 |
| 160 | 0.325 | 8.951 | 4.235 | -1.153 | 4.709 | 1.454 | 16.128 | 21.990 | 18.736 | 16.677 | 25.303 | 20.587 | 18.805 | 15.758 | 17.500 | 15.203 | | 13 | 13 |
| 161 | 2.212 | 0.168 | 3.001 | -1.532 | -0.608 | -0.885 | 23.785 | 24.709 | 24.432 | 25.458 | 23.414 | 26.247 | 27.676 | 22.958 | 27.161 | 19.331 | + | 5 | 5 |
| 162 | 8.535 | 5.888 | 7.080 | 5.606 | 4.509 | 3.016 | 29.778 | 28.681 | 27.188 | 29.678 | 27.031 | 28.223 | 26.998 | 21.347 | 26.125 | 16.162 | | 12 | 12 |
| 163 | -0.458 | 4.209 | 3.156 | -0.971 | -0.723 | 0.243 | 16.090 | 16.337 | 17.303 | 17.325 | 21.992 | 20.939 | 18.817 | 15.303 | 20.746 | 14.821 | | 2 | 2 |
| 164 | 2.623 | 2.899 | 3.096 | -1.770 | 1.572 | 0.519 | 19.893 | 23.235 | 22.182 | 23.321 | 23.597 | 23.794 | 18.005 | 25.321 | 27.392 | 14.003 | + | 8 | 8 |
| 165 | -1.320 | -2.726 | -4.022 | -4.129 | -8.798 | -3.434 | 21.862 | 17.193 | 22.556 | 23.587 | 22.181 | 20.885 | 27.480 | 24.501 | 24.995 | 24.820 | | 12 | 12 |
| 166 | -1.082 | 7.104 | 3.955 | -0.032 | -0.782 | 2.510 | 17.089 | 16.339 | 19.630 | 16.818 | 25.004 | 21.855 | 19.405 | 14.836 | 21.222 | 14.578 | | 5 | 5 |
| 167 | 2.212 | 3.786 | 3.382 | 1.887 | -2.176 | 1.446 | 21.779 | 17.717 | 21.339 | 21.316 | 22.890 | 22.485 | 24.356 | 15.429 | 22.620 | 15.588 | | 3 | 3 |
| 168 | -4.450 | 4.845 | 2.343 | -4.049 | -0.037 | -1.389 | 18.180 | 22.192 | 20.840 | 16.717 | 26.013 | 23.511 | 20.746 | 23.712 | 23.722 | 18.614 | | 10 | 10 |
| 169 | -3.030 | 2.272 | -1.710 | -0.679 | -4.975 | -4.920 | 21.126 | 16.831 | 16.886 | 15.799 | 21.101 | 17.119 | 24.351 | 19.260 | 23.119 | 14.539 | | 4 | 4 |
| 170 | -7.308 | -2.727 | -5.584 | -8.241 | -7.375 | -8.091 | 16.915 | 17.782 | 17.066 | 16.276 | 20.856 | 18.000 | 26.354 | 23.959 | 24.528 | 22.639 | | 10 | 10 |

|  | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 138 | 9 | 5 | 213.61 | 57.488 | 22.967 | 21.437 | **0.931** | **3.203** | B1B1A8;Q6PDN3-3;Q6PDN3;Q6PDN3-2;Q6PDN3-4 | B1B1A8;Q6PDN3-3;Q6PDN3;Q6PDN3-2 | Myosin light chain kinase, smooth muscle;Myosin light chain kinase, smooth muscle, deglutamylated form | **Mylk** | 203 |
| 139 | 6 | 12.7 | 47.408 | 36.245 | 23.343 | 20.537 | **0.696** | **3.193** | P54775;A0A140LIZ5 | P54775;A0A140LIZ5 | 26S protease regulatory subunit 6B | **Psmc4** | 759 |
| 140 | 7 | 30.1 | 20.732 | 54.993 | 24.331 | 19.906 | **2.332** | **3.156** | P62717;F6YJW4 | P62717 | 60S ribosomal protein L18a | **Rpl18a** | 827 |
| 141 | 10 | 15.5 | 89.783 | 77.529 | 20.249 | 20.053 | **0.400** | **3.129** | Q3ULG5;P97311 | Q3ULG5;P97311 | DNA helicase;DNA replication licensing factor MCM6 | **Mcm6** | 898 |
| 142 | 9 | 27.7 | 36.21 | 99.045 | 21.324 | 19.943 | **1.261** | **3.126** | Q20BD0;Q80XR6;Q99020 | Q20BD0;Q80XR6;Q99020 | Heterogeneous nuclear ribonucleoprotein A/B | **Hnrnpab** | 946 |
| 143 | 12 | 21 | 81.21 | 83.791 | 20.298 | 19.342 | **0.530** | **3.107** | Q61881;D3Z6N3 | Q61881 | DNA replication licensing factor MCM7 | **Mcm7** | 1054 |
| 144 | 2 | 8 | 28.721 | 12.62 | 18.191 | 17.109 | **0.603** | **3.099** | Q9DCC4 | Q9DCC4 | Pyrroline-5-carboxylate reductase 3 | **Pycrl** | 1471 |
| 145 | 3 | 1 | 333.73 | 18.456 | 18.368 | 16.235 | **0.804** | **3.089** | E9PX70;Q60847-2;Q60847-5;Q60847;Q60847-4;Q60847-3 | E9PX70;Q60847-2;Q60847-5;Q60847;Q60847-4;Q60847-3 | Collagen alpha-1(XII) chain | **Col12a1** | 348 |
| 146 | 14 | 25.7 | 69.265 | 178.59 | 22.200 | 21.844 | **0.364** | **3.074** | Q8BTS0;Q61656;S4R1I6;B1ARC0;B1ARB9;S4R1E3 | Q8BTS0;Q61656;S4R1I6 | Probable ATP-dependent RNA helicase DDX5 | **Ddx5** | 1045 |
| 147 | 1 | 2.2 | 45.854 | 7.3207 | 17.191 | 17.919 | **0.656** | **3.063** | D3Z5N6;Q61103 | D3Z5N6;Q61103 | Zinc finger protein ubi-d4 | **Dpf2** | 310 |
| 148 | 11 | 20.7 | 63.772 | 77.587 | 24.816 | 23.789 | **1.094** | **3.049** | A2A6U3;Q80UG5-3;Q80UG5;Q80UG5-2;A2A6U5 | A2A6U3;Q80UG5-3;Q80UG5;Q80UG5-2;A2A6U5 | Septin-9 | **Sept9** | 128 |
| 149 | 21 | 45.4 | 58.004 | 240.8 | 28.217 | 24.795 | **2.255** | **3.000** | P80317;Q61390;B1AT05 | P80317 | T-complex protein 1 subunit zeta | **Cct6a** | 889 |
| 150 | 4 | 15.3 | 57.086 | 26.739 | 22.097 | 19.985 | **1.135** | **2.999** | Q921L6;Q60598 | Q921L6;Q60598 | Src substrate cortactin | **Cttn** | 1018 |
| 151 | 7 | 10.8 | 80.208 | 45.874 | 21.642 | 18.759 | **1.039** | **2.999** | Q9CQN1 | Q9CQN1 | Heat shock protein 75 kDa, mitochondrial | **Trap1** | 1347 |
| 152 | 4 | 17.9 | 31.052 | 29.597 | 25.009 | 23.492 | **0.595** | **2.981** | O08807;B1AZS9 | O08807;B1AZS9 | Peroxiredoxin-4 | **Prdx4** | 504 |
| 153 | 2 | 5.7 | 49.03 | 13.825 | 20.031 | 18.787 | **1.193** | **2.959** | Q8BWY3 | Q8BWY3 | Eukaryotic peptide chain release factor subunit 1 | **Etf1** | 1188 |
| 154 | 9 | 20.3 | 72.544 | 71.86 | 24.670 | 23.997 | **0.981** | **2.908** | A0A0R4J1E3;Q9QXS6-3;Q9QXS6;Q9QXS6-2;F7CPL2 | A0A0R4J1E3;Q9QXS6-3;Q9QXS6;Q9QXS6-2 | Drebrin | **Dbn1** | 93 |
| 155 | 2 | 7.3 | 25.835 | 12.116 | 21.094 | 20.035 | **0.573** | **2.889** | A2ALF0;A2ALF3;F6TQL3;Q6NZB0;F7CXJ2 | A2ALF0;A2ALF3;F6TQL3;Q6NZB0;F7CXJ2 | DnaJ homolog subfamily C member 8 | **Dnajc8** | 157 |
| 156 | 3 | 17.8 | 46.908 | 62.581 | 22.033 | 19.196 | **0.525** | **2.882** | A2AFJ1;Q60973;A2AFI9;F6U539 | A2AFJ1;Q60973;A2AFI9 | Histone-binding protein RBBP7 | **Rbbp7** | 143 |
| 157 | 2 | 18.9 | 14.427 | 18.674 | 17.363 | 16.998 | **0.441** | **2.867** | P11031 | P11031 | Activated RNA polymerase II transcriptional coactivator p15 | **Sub1** | 595 |
| 158 | 1 | 6.9 | 18.376 | 6.7252 | 16.307 | 16.461 | **0.761** | **2.865** | Q9D735 | Q9D735 | Uncharacterized protein C19orf43 homolog |  | 1442 |
| 159 | 3 | 32.9 | 9.2327 | 41.243 | 20.186 | 16.242 | **1.358** | **2.839** | A0A0G2JDW7;A0A0G2JG29;Q6ZWU9 | A0A0G2JDW7;A0A0G2JG29;Q6ZWU9 | 40S ribosomal protein S27 | **Rps27** | 42 |
| 160 | 13 | 3.8 | 404.05 | 82.948 | 17.282 | 16.352 | **0.397** | **2.834** | Q61001 | Q61001 | Laminin subunit alpha-5 | **Lama5** | 1029 |
| 161 | 5 | 36.2 | 15.069 | 33.561 | 25.317 | 23.246 | **1.465** | **2.801** | P62849-2;P62849-3;P62849 | P62849-2;P62849-3;P62849 | 40S ribosomal protein S24 | **Rps24** | 836 |
| 162 | 12 | 50.7 | 14.865 | 116.75 | 24.173 | 21.143 | **1.223** | **2.791** | P62830;A2A6F8 | P62830 | 60S ribosomal protein L23 | **Rpl23** | 834 |
| 163 | 2 | 2.6 | 63.413 | 13.889 | 17.060 | 17.783 | **0.889** | **2.786** | H3BJW3;H3BJ30;Q6NVF9 | H3BJW3;H3BJ30;Q6NVF9 | Cleavage and polyadenylation specificity factor subunit 6 | **Cpsf6** | 477 |
| 164 | 8 | 28.5 | 30.53 | 57.882 | 21.663 | 20.698 | **1.301** | **2.766** | Q9CX86 | Q9CX86 | Heterogeneous nuclear ribonucleoprotein A0 | **Hnrnpa0** | 1380 |
| 165 | 12 | 35.4 | 38.676 | 102.14 | 25.991 | 24.907 | **0.676** | **2.764** | P07356;B0V2N7;B0V2N8;B0V2N5 | P07356;B0V2N7;B0V2N8;B0V2N5 | Annexin A2;Annexin | **Anxa2** | 569 |
| 166 | 4 | 21.2 | 40.092 | 35.297 | 17.121 | 17.900 | **0.461** | **2.760** | Q8CCK0 | Q8CCK0 | Core histone macro-H2A.2 | **H2afy2** | 1198 |
| 167 | 3 | 19.6 | 19.667 | 19.442 | 19.893 | 19.104 | **0.935** | **2.741** | P59999;Q3TX55;E9PWA7 | P59999 | Actin-related protein 2/3 complex subunit 4 | **Arpc4** | 778 |
| 168 | 10 | 23.7 | 55.983 | 66.896 | 22.229 | 21.168 | **0.381** | **2.737** | Q8BK67;A2AWQ2 | Q8BK67 | Protein RCC2 | **Rcc2** | 1168 |
| 169 | 4 | 16 | 38.442 | 25.155 | 21.805 | 18.829 | **0.561** | **2.702** | Q9Z1Z2 | Q9Z1Z2 | Serine-threonine kinase receptor-associated protein | **Strap** | 1568 |
| 170 | 10 | 29.4 | 43.688 | 66.95 | 25.157 | 23.584 | **0.925** | **2.696** | Q3THS6;A0A0U1RNT6;A0A0U1RNK6;A0A0U1RQ95;Q91X83;A0A0U1RQB0;A0A0U1RPH4 | Q3THS6;A0A0U1RNT6;A0A0U1RNK6 | S-adenosylmethionine synthase isoform type-2 | **Mat2a** | 952 |

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 171 | 2.932 | -2.241 | 3.382 | -0.458 | -2.037 | -1.418 | 17.754 | 16.175 | 16.794 | 21.608 | 16.435 | 22.058 | 20.428 | 15.996 | 21.983 | 15.368 | | 2 | 2 |
| 172 | -5.369 | -3.068 | -6.377 | -8.062 | -7.187 | -7.498 | 17.165 | 18.040 | 17.729 | 17.978 | 20.278 | 16.969 | 27.024 | 23.430 | 24.302 | 22.391 | | 5 | 5 |
| 173 | 0.828 | 5.156 | 4.138 | 0.777 | 1.285 | 0.169 | 16.741 | 17.250 | 16.134 | 16.648 | 20.976 | 19.958 | 17.434 | 14.496 | 17.832 | 13.807 | | 1 | 1 |
| 174 | -3.650 | -1.388 | -1.464 | -5.604 | -4.544 | -4.237 | 21.158 | 22.218 | 22.525 | 21.092 | 23.353 | 23.277 | 27.292 | 26.232 | 26.910 | 22.573 | + | 27 | 27 |
| 175 | -5.751 | -1.991 | 0.413 | -4.973 | -4.941 | -5.232 | 17.099 | 17.132 | 16.841 | 15.221 | 18.981 | 21.385 | 24.173 | 19.972 | 24.546 | 17.399 | | 5 | 5 |
| 176 | -0.084 | 5.276 | 4.717 | -1.116 | -0.281 | 3.496 | 17.077 | 17.912 | 21.688 | 17.652 | 23.013 | 22.454 | 20.235 | 16.150 | 21.134 | 14.339 | | 1 | 1 |
| 177 | -2.689 | -3.339 | -1.237 | -9.591 | -4.653 | -0.787 | 18.350 | 23.288 | 27.154 | 24.143 | 23.493 | 25.596 | 31.689 | 24.193 | 26.787 | 26.878 | | 10 | 10 |
| 178 | -5.642 | -2.016 | -1.753 | -5.766 | -8.296 | -3.081 | 17.830 | 15.300 | 20.515 | 16.838 | 20.465 | 20.727 | 26.482 | 20.710 | 24.472 | 20.488 | | 13 | 13 |
| 179 | 0.349 | 4.708 | 3.084 | 0.503 | -0.036 | 0.006 | 17.784 | 17.245 | 17.288 | 17.405 | 21.764 | 20.140 | 18.001 | 16.561 | 18.614 | 15.498 | | 1 | 1 |
| 180 | -5.171 | 0.247 | 0.061 | -5.888 | -0.486 | -6.136 | 16.868 | 22.270 | 16.620 | 16.486 | 21.905 | 21.719 | 24.679 | 20.833 | 24.938 | 18.377 | | 8 | 8 |
| 181 | 4.007 | 9.795 | 7.151 | 5.113 | 1.893 | 6.342 | 23.765 | 20.545 | 24.994 | 22.958 | 28.746 | 26.102 | 19.503 | 17.802 | 18.750 | 19.152 | | 10 | 10 |
| 182 | 3.252 | 4.698 | -2.014 | -2.093 | 1.573 | -1.085 | 16.825 | 20.491 | 17.834 | 20.913 | 22.360 | 15.648 | 21.444 | 16.393 | 20.681 | 14.642 | | 6 | 6 |
| 183 | -3.128 | -1.444 | 1.257 | -0.860 | -5.623 | -4.363 | 21.077 | 16.314 | 17.575 | 15.745 | 17.428 | 20.130 | 23.329 | 20.546 | 22.862 | 14.883 | | 7 | 7 |
| 184 | -1.336 | 0.660 | -0.267 | -6.647 | -0.424 | -1.370 | 16.970 | 23.193 | 22.247 | 21.607 | 23.603 | 22.676 | 28.018 | 19.215 | 25.743 | 20.142 | | 12 | 12 |
| 185 | -2.329 | 0.854 | -0.546 | 0.405 | -5.187 | -4.669 | 22.003 | 16.410 | 16.929 | 15.685 | 18.867 | 17.468 | 23.140 | 20.055 | 20.864 | 15.163 | | 2 | 2 |
| 186 | 7.276 | 9.480 | 7.865 | 4.831 | 6.681 | 5.689 | 24.675 | 26.525 | 25.533 | 24.254 | 26.459 | 24.844 | 19.945 | 19.743 | 17.567 | 16.390 | + | 1 | 1 |
| 187 | 1.048 | 1.132 | 1.462 | 0.566 | -4.153 | -0.126 | 21.577 | 16.857 | 20.885 | 20.516 | 20.600 | 20.930 | 26.262 | 15.759 | 24.502 | 14.434 | | 13 | 13 |
| 188 | 2.987 | 7.555 | 5.810 | 1.986 | 2.453 | 4.584 | 22.221 | 22.688 | 24.820 | 21.586 | 26.154 | 24.409 | 18.095 | 22.375 | 23.424 | 13.772 | | 8 | 6 |
| 189 | -0.946 | 4.346 | 3.167 | -0.888 | -0.190 | 0.317 | 16.308 | 17.006 | 17.513 | 15.427 | 20.718 | 19.539 | 18.019 | 16.373 | 18.373 | 14.372 | | 1 | 1 |
| 190 | -2.336 | 3.558 | 1.898 | 1.225 | -2.587 | -2.832 | 20.786 | 16.974 | 16.729 | 16.193 | 22.087 | 20.427 | 17.333 | 21.790 | 21.659 | 15.398 | | 5 | 5 |
| 191 | 9.469 | 9.089 | 9.106 | 6.138 | 7.890 | 6.383 | 23.707 | 25.459 | 23.952 | 24.938 | 24.557 | 24.575 | 19.615 | 15.524 | 16.403 | 14.534 | + | 2 | 1 |
| 192 | -6.844 | -2.751 | -3.049 | -5.862 | -6.331 | -7.699 | 18.647 | 18.178 | 16.810 | 16.659 | 20.753 | 20.455 | 25.543 | 23.475 | 25.169 | 21.839 | | 3 | 3 |
| 193 | 0.861 | 0.416 | 1.547 | -0.032 | -2.526 | -1.862 | 24.396 | 21.902 | 22.567 | 24.383 | 23.938 | 25.068 | 26.394 | 22.463 | 26.270 | 20.773 | + | 10 | 10 |
| 194 | -4.931 | -0.380 | 0.164 | -6.006 | -0.753 | -5.624 | 16.504 | 21.757 | 16.885 | 17.329 | 21.881 | 22.425 | 25.121 | 19.899 | 24.478 | 20.044 | | 13 | 6 |
| 195 | -0.632 | 3.000 | 2.572 | -1.285 | -1.374 | 0.373 | 16.118 | 16.029 | 17.777 | 16.810 | 20.442 | 20.014 | 18.906 | 15.901 | 20.251 | 14.632 | | 2 | 2 |

|  | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 171 | 2 | 5.4 | 43.231 | 12.315 | 18.212 | 18.676 | **0.646** | **2.662** | P35486 | P35486 | Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial | **Pdha1** | 692 |
| 172 | 5 | 20.2 | 17.6 | 53.852 | 25.227 | 23.346 | **1.227** | **2.644** | Q9D3D9 | Q9D3D9 | ATP synthase subunit delta, mitochondrial | **Atp5d** | 1434 |
| 173 | 1 | 1.2 | 124.31 | 6.5481 | 15.965 | 15.820 | **0.913** | **2.631** | Q9Z103 | Q9Z103 | Activity-dependent neuroprotector homeobox protein | **Adnp** | 1556 |
| 174 | 27 | 38 | 102.09 | 209.87 | 26.762 | 24.741 | **1.438** | **2.627** | Q78PY7;Q3TJ56;E9Q3E9 | Q78PY7;Q3TJ56 | Staphylococcal nuclease domain-containing protein 1 | **Snd1** | 1117 |
| 175 | 5 | 4.8 | 144.27 | 33.692 | 22.072 | 20.972 | **0.657** | **2.606** | Q8BU30 | Q8BU30 | Isoleucine--tRNA ligase, cytoplasmic | **Iars** | 1184 |
| 176 | 1 | 13.1 | 12.078 | 6.6209 | 18.193 | 17.737 | **0.516** | **2.603** | E9Q5H2;E9PZF5;P97822-2;P97822 | E9Q5H2;E9PZF5;P97822-2;P97822 | Acidic leucine-rich nuclear phosphoprotein 32 family member E | **Anp32e** | 360 |
| 177 | 8 | 57.7 | 15.112 | 178.43 | 27.941 | 26.832 | **0.421** | **2.588** | Q91VB8;P01942 | Q91VB8;P01942 | Hemoglobin subunit alpha | **haemaglobin alpha 2;Hba** | 553 |
| 178 | 13 | 18.1 | 117.81 | 108.76 | 23.596 | 22.480 | **0.587** | **2.577** | Q02053;P31254 | Q02053 | Ubiquitin-like modifier-activating enzyme 1 | **Uba1** | 922 |
| 179 | 1 | 1.1 | 70.367 | 6.3904 | 17.281 | 17.056 | **0.931** | **2.556** | Q6P9R1 | Q6P9R1 | ATP-dependent RNA helicase DDX51 | **Ddx51** | 1097 |
| 180 | 8 | 10.4 | 119.73 | 58.403 | 22.756 | 21.658 | **0.425** | **2.549** | Q91V92;Q3V117;Q3TS02 | Q91V92;Q3V117;Q3TS02 | ATP-citrate synthase | **Acly** | 994 |
| 181 | 10 | 43.8 | 32.56 | 156.47 | 18.652 | 18.951 | **0.522** | **2.535** | Q61937;Q5SQB0;Q9DAY9;Q5SQB5;E9Q5T3 | Q61937;Q5SQB0;Q9DAY9;Q5SQB5;E9Q5T3 | Nucleophosmin | **Npm1;Gm5611** | 1055 |
| 182 | 6 | 4.1 | 188.9 | 38.419 | 18.918 | 17.661 | **0.471** | **2.514** | E9PYX7;E9Q852;E9Q9C3;Q9QZQ1-2;Q9QZQ1 | E9PYX7;E9Q852;E9Q9C3;Q9QZQ1-2;Q9QZQ1 | Afadin | **Mllt4** | 356 |
| 183 | 7 | 10.1 | 87.676 | 42.183 | 21.937 | 18.873 | **0.585** | **2.510** | Q8BML9;D3Z158;Q8R1V9;A0A140LID3;A0A140LHJ3;A0A140LHZ5;A0A140LIS6;A0A140LHB3;A0A140LIN2;A0A140LII8;A0A0A6YY08;A0A140LJH2;A0A140LIR0;A0A140LJH1;A0A140LJK5;A0A140LIZ4;A0A140LHC3 | Q8BML9;D3Z158;Q8R1V9 | Glutamine-tRNA ligase | **Qars** | 298 |
| 184 | 12 | 31.5 | 50.537 | 93.982 | 23.617 | 22.942 | **0.547** | **2.500** | Q61598;Q61598-2;P50396 | Q61598;Q61598-2 | Rab GDP dissociation inhibitor beta | **Gdi2** | 1043 |
| 185 | 2 | 6.6 | 42.613 | 11.163 | 21.598 | 18.014 | **0.545** | **2.477** | P61164;Q8R5C5 | P61164;Q8R5C5 | Alpha-centractin;Beta-centractin | **Actr1a;Actr1b** | 793 |
| 186 | 1 | 4.6 | 22.59 | 6.2102 | 19.844 | 16.979 | **1.362** | **2.473** | Q6PKN7-2;Q6PKN7 | Q6PKN7-2;Q6PKN7 | Protein INCA1 | **Inca1** | 1104 |
| 187 | 13 | 7.9 | 282.89 | 84.72 | 21.011 | 19.468 | **0.764** | **2.451** | A3KGU5;A3KGU7;E9Q447;A3KGU9;P16546-2;P16546;A3KGU4 | A3KGU5;A3KGU7;E9Q447;A3KGU9;P16546-2;P16546 | Spectrin alpha chain, non-erythrocytic 1 | **Sptan1** | 187 |
| 188 | 6 | 29.5 | 24.162 | 58.982 | 20.235 | 18.598 | **0.720** | **2.443** | P30681 | P30681 | High mobility group protein B2 | **Hmgb2** | 679 |
| 189 | 1 | 1.5 | 95.493 | 6.3892 | 17.196 | 16.372 | **0.676** | **2.443** | D3Z0M9 | D3Z0M9 | DEAD box protein 23 | **Ddx23** | 294 |
| 190 | 5 | 8.3 | 88.544 | 31.782 | 19.561 | 18.529 | **0.484** | **2.438** | Q8K4Z5 | Q8K4Z5 | Splicing factor 3A subunit 1 | **Sf3a1** | 1227 |
| 191 | 1 | 17.6 | 11 | 6.7042 | 17.569 | 15.469 | **1.900** | **2.418** | A0A075B5N3;A0A0G2JE47 | A0A075B5N3;A0A0G2JE47 | Immunoglobulin kappa variable 8-28 | **Igkv8-28** | 5 |
| 192 | 3 | 20.1 | 16.46 | 78.071 | 24.509 | 23.504 | **0.780** | **2.416** | Q8BMJ3;Q60872;J3QPQ5;Q8BX20;Q3UTA4;Q3UT53;Q3TQZ4;J3QQ02;J3QPI8;J3QP87;J3QNT6;J3QMW5;D3Z367;M0QWL1 | Q8BMJ3;Q60872;J3QPQ5;Q8BX20;Q3UTA4;Q3UT53;Q3TQZ4;J3QQ02;J3QPI8;J3QP87;J3QNT6;J3QMW5;D3Z367 | Eukaryotic translation initiation factor 1A, X-chromosomal;Eukaryotic translation initiation factor 1A | **Eif1ax;Eif1a;Gm10264;Gm5662;Gm8300;Gm4027;Gm2016;Gm2056;Gm6803;Gm2035;Gm5039;Gm2075;Gm2046** | 1026 |
| 193 | 10 | 26.5 | 35.076 | 215.62 | 24.428 | 23.521 | **1.383** | **2.415** | P68040 | P68040 | Guanine nucleotide-binding protein subunit beta-2-like 1;Guanine nucleotide-binding protein subunit beta-2-like 1, N-terminally processed | **Gnb2l1** | 871 |
| 194 | 6 | 17 | 104.98 | 47.73 | 22.510 | 22.261 | **0.443** | **2.412** | P57780;E9Q2W9;D3Z761;D3Z0L8;Q91ZE6;E9PX29 | P57780;E9Q2W9 | Alpha-actinin-4 | **Actn4** | 771 |
| 195 | 2 | 3 | 106.72 | 12.782 | 17.404 | 17.441 | **0.877** | **2.409** | Q8BH74;E9Q4V9 | Q8BH74;E9Q4V9 | Nuclear pore complex protein Nup107 | **Nup107** | 1151 |

|  | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 196 | -1.982 | 3.432 | 0.992 | 1.637 | -3.072 | -3.345 | 21.540 | 16.831 | 16.559 | 16.839 | 22.253 | 19.813 | 19.156 | 20.651 | 21.949 | 15.692 |  | 5 | 5 |
| 197 | -2.222 | 1.627 | 2.527 | -2.022 | -1.943 | -1.300 | 17.484 | 17.563 | 18.206 | 17.028 | 20.877 | 21.777 | 22.608 | 16.404 | 23.471 | 15.029 |  | 3 | 3 |
| 198 | 5.474 | 8.723 | 6.792 | 4.944 | 4.717 | 4.134 | 27.138 | 26.911 | 26.328 | 25.629 | 28.878 | 26.947 | 20.249 | 24.139 | 26.107 | 14.203 |  | 41 | 41 |
| 199 | -2.484 | -3.322 | -4.453 | -9.204 | -3.570 | -4.643 | 16.750 | 22.383 | 21.310 | 22.159 | 21.321 | 20.190 | 26.497 | 25.410 | 26.899 | 22.388 |  | 9 | 9 |
| 200 | 0.240 | -2.286 | -3.107 | -3.879 | -5.240 | -3.089 | 17.247 | 15.886 | 18.037 | 20.025 | 17.500 | 16.678 | 23.617 | 18.634 | 22.586 | 16.984 |  | 3 | 3 |
| 201 | -0.095 | -2.924 | -3.436 | -3.026 | -4.730 | -5.735 | 19.327 | 17.622 | 16.617 | 21.109 | 18.280 | 17.768 | 25.667 | 19.037 | 23.653 | 18.755 |  | 5 | 5 |
| 202 | 2.052 | 4.889 | 3.811 | 0.432 | 1.682 | 1.641 | 21.984 | 23.234 | 23.193 | 21.561 | 24.398 | 23.320 | 22.660 | 20.444 | 23.985 | 15.033 |  | 7 | 2 |
| 203 | 11.028 | 9.139 | 8.870 | 8.209 | 8.288 | 5.611 | 27.829 | 27.909 | 25.232 | 29.071 | 27.182 | 26.913 | 24.295 | 14.946 | 22.422 | 13.664 |  | 9 | 9 |
| 204 | -2.192 | 4.097 | 2.001 | -2.024 | -3.303 | 2.321 | 16.890 | 15.611 | 21.235 | 17.375 | 23.664 | 21.568 | 18.834 | 18.994 | 24.022 | 15.112 |  | 7 | 5 |
| 205 | 2.217 | 4.047 | 3.380 | 1.541 | 2.771 | -1.567 | 20.969 | 22.199 | 17.861 | 20.405 | 22.235 | 21.568 | 23.244 | 15.612 | 21.256 | 15.120 |  | 3 | 3 |
| 206 | -0.412 | 7.069 | 3.566 | -0.757 | 0.376 | 3.739 | 16.742 | 17.875 | 21.238 | 17.701 | 25.183 | 21.680 | 18.692 | 16.306 | 21.813 | 14.414 |  | 8 | 8 |
| 207 | -2.591 | 3.562 | 2.213 | -3.404 | 1.688 | -1.860 | 16.108 | 21.200 | 17.651 | 16.961 | 23.114 | 21.765 | 23.811 | 15.213 | 23.331 | 15.773 |  | 3 | 1 |
| 208 | 0.817 | 9.111 | 2.148 | 3.251 | -0.202 | 2.397 | 20.775 | 17.321 | 19.920 | 16.982 | 25.275 | 18.312 | 17.690 | 17.357 | 16.915 | 15.414 |  | 14 | 14 |
| 209 | -0.950 | 0.535 | 0.222 | -0.024 | -4.630 | -2.066 | 21.767 | 17.162 | 19.726 | 20.030 | 21.515 | 21.202 | 24.686 | 18.897 | 23.618 | 18.341 |  | 5 | 5 |
| 210 | 7.625 | 2.819 | 2.629 | 6.526 | 0.001 | 0.032 | 23.899 | 17.374 | 17.405 | 22.753 | 17.948 | 17.757 | 18.746 | 16.000 | 16.835 | 13.422 |  | 3 | 3 |
| 211 | -1.215 | -0.012 | -0.592 | -2.813 | -2.658 | -2.846 | 26.077 | 26.232 | 26.044 | 25.877 | 27.080 | 26.500 | 30.610 | 27.170 | 28.650 | 25.534 | + | 10 | 10 |
| 212 | 3.106 | 3.134 | 2.288 | 0.133 | 1.662 | 0.238 | 23.688 | 25.217 | 23.793 | 26.232 | 26.260 | 25.414 | 24.864 | 22.246 | 25.096 | 21.156 | + | 21 | 21 |
| 213 | -1.588 | -5.078 | -5.122 | -1.590 | -9.184 | -7.501 | 26.152 | 18.558 | 20.241 | 24.433 | 20.943 | 20.899 | 29.386 | 26.098 | 26.534 | 25.508 |  | 7 | 7 |
| 214 | -0.345 | 3.274 | 2.384 | -0.774 | 0.612 | -0.905 | 15.973 | 17.360 | 15.843 | 16.734 | 20.353 | 19.463 | 17.608 | 15.887 | 18.913 | 15.244 |  | 1 | 1 |
| 215 | -1.340 | 5.414 | 5.242 | -0.812 | 3.487 | 0.263 | 16.650 | 20.950 | 17.726 | 15.691 | 22.446 | 22.274 | 19.503 | 15.422 | 19.791 | 14.272 |  | 2 | 2 |
| 216 | -1.647 | -1.940 | -2.577 | -4.917 | -4.537 | -3.085 | 18.521 | 18.901 | 20.353 | 17.439 | 17.146 | 16.509 | 24.680 | 22.196 | 22.980 | 15.192 | + | 4 | 4 |
| 217 | 1.118 | -0.589 | -0.935 | -1.948 | 0.749 | -5.539 | 19.800 | 22.497 | 16.209 | 19.228 | 17.522 | 17.175 | 23.753 | 19.743 | 22.033 | 14.188 |  | 19 | 4 |
| 218 | 7.957 | 8.914 | 7.207 | 4.488 | 6.734 | 6.584 | 28.243 | 30.489 | 30.339 | 27.949 | 28.905 | 27.199 | 26.914 | 20.596 | 25.511 | 14.473 |  | 11 | 11 |
| 219 | -0.880 | 6.310 | 4.348 | 1.895 | 0.144 | 1.478 | 18.385 | 16.635 | 17.969 | 15.894 | 23.084 | 21.123 | 17.409 | 15.573 | 17.183 | 16.365 |  | 2 | 2 |
| 220 | -2.758 | -0.778 | -0.398 | -3.013 | -3.531 | -3.572 | 24.398 | 23.880 | 23.840 | 22.438 | 24.418 | 24.799 | 28.740 | 26.082 | 27.172 | 23.221 |  | 18 | 18 |
| 221 | -5.516 | 0.298 | -0.321 | -5.312 | -2.179 | -4.228 | 17.321 | 20.454 | 18.405 | 15.878 | 21.691 | 21.072 | 23.791 | 21.475 | 23.044 | 19.742 |  | 3 | 3 |
| 222 | -1.116 | 7.530 | 5.345 | 0.647 | 1.586 | 3.360 | 17.542 | 18.481 | 20.255 | 14.320 | 22.966 | 20.781 | 16.943 | 16.847 | 15.934 | 14.938 |  | 2 | 2 |
| 223 | 0.906 | 2.266 | 2.649 | 0.533 | -1.516 | 0.658 | 23.857 | 21.809 | 23.983 | 22.614 | 23.973 | 24.357 | 25.335 | 21.314 | 23.900 | 19.515 |  | 13 | 13 |
| 224 | -1.882 | -0.017 | -1.138 | -1.311 | -6.847 | -1.021 | 22.076 | 16.540 | 22.367 | 20.981 | 22.846 | 21.724 | 24.761 | 22.014 | 23.814 | 21.912 |  | 4 | 4 |
| 225 | 5.613 | 2.775 | 5.127 | 2.756 | 2.461 | 2.180 | 25.344 | 25.050 | 24.769 | 25.053 | 22.215 | 24.568 | 25.042 | 20.136 | 22.813 | 16.069 |  | 3 | 3 |
| 226 | 12.759 | 7.481 | 9.011 | 12.282 | 5.970 | 4.917 | 32.214 | 25.903 | 24.850 | 31.223 | 25.945 | 27.476 | 22.861 | 17.005 | 21.400 | 15.528 |  | 3 | 3 |
| 227 | 0.406 | 1.447 | 1.842 | 0.009 | -0.160 | -2.205 | 23.964 | 23.795 | 21.749 | 22.542 | 23.583 | 23.978 | 26.343 | 21.566 | 24.113 | 20.159 |  | 31 | 23 |
| 228 | -7.527 | -6.764 | -2.981 | -7.214 | -7.124 | -8.981 | 18.142 | 18.232 | 16.375 | 16.417 | 17.180 | 20.964 | 27.364 | 23.348 | 24.967 | 22.922 |  | 11 | 11 |
| 229 | 1.426 | 5.009 | 1.563 | 3.277 | 2.591 | -3.862 | 22.786 | 22.100 | 15.647 | 21.371 | 24.954 | 21.508 | 17.843 | 21.176 | 24.692 | 15.198 |  | 7 | 7 |

| | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 196 | 5 | 5.4 | 145.81 | 31.481 | 19.903 | 18.821 | **0.462** | **2.408** | Q99NB9;G5E866;A0A087WNS2 | Q99NB9;G5E866 | Splicing factor 3B subunit 1 | **Sf3b1** | 470 |
| 197 | 3 | 9.5 | 49.184 | 26.31 | 19.506 | 19.250 | **0.747** | **2.399** | P62192 | P62192 | 26S protease regulatory subunit 4 | **Psmc1** | 810 |
| 198 | 36 | 54.3 | 66.785 | 323.31 | 22.194 | 20.155 | **1.158** | **2.398** | P14733 | P14733 | Lamin-B1 | **Lmnb1** | 614 |
| 199 | 9 | 27.4 | 36.46 | 62.98 | 25.953 | 24.643 | **0.585** | **2.386** | Q9QZD9;A2AE03 | Q9QZD9 | Eukaryotic translation initiation factor 3 subunit I | **Eif3i** | 1522 |
| 200 | 3 | 22.7 | 16.534 | 19.09 | 21.125 | 19.785 | **0.926** | **2.352** | O70591;F8WJ30 | O70591;F8WJ30 | Prefoldin subunit 2 | **Pfdn2** | 539 |
| 201 | 5 | 50.9 | 12.496 | 31.959 | 22.352 | 21.204 | **0.833** | **2.345** | P97450;E9QAD6 | P97450;E9QAD6 | ATP synthase-coupling factor 6, mitochondrial | **Atp5j** | 906 |
| 202 | 2 | 17.6 | 47.655 | 23.213 | 21.552 | 19.509 | **1.188** | **2.332** | Q60972;F6ZLC6 | Q60972 | Histone-binding protein RBBP4 | **Rbbp4** | 1028 |
| 203 | 9 | 13.6 | 87.265 | 59.342 | 19.621 | 18.043 | **0.974** | **2.310** | Q9Z110;Q9Z110-2;D3Z0B4 | Q9Z110;Q9Z110-2 | Delta-1-pyrroline-5-carboxylate synthase;Glutamate 5-kinase;Gamma-glutamyl phosphate reductase | **Aldh18a1** | 1557 |
| 204 | 5 | 8.3 | 108.34 | 32.245 | 18.914 | 19.567 | **0.386** | **2.304** | G3UZ34;A2AH85;O08810 | G3UZ34;A2AH85;O08810 | 116 kDa U5 small nuclear ribonucleoprotein component | **Eftud2** | 150 |
| 205 | 3 | 13 | 25.378 | 19.485 | 19.428 | 18.188 | **0.757** | **2.300** | Q60692 | Q60692 | Proteasome subunit beta type-6 | **Psmb6** | 1021 |
| 206 | 8 | 5.6 | 183.19 | 54.685 | 17.499 | 18.114 | **0.377** | **2.288** | P13864;J3QNW0;P13864-2 | P13864;J3QNW0;P13864-2 | DNA (cytosine-5)-methyltransferase 1;DNA (cytosine-5)-methyltransferase | **Dnmt1** | 606 |
| 207 | 1 | 18 | 19.854 | 7.337 | 19.512 | 19.552 | **0.397** | **2.253** | Q9CQ19 | Q9CQ19 | Myosin regulatory light polypeptide 9 | **Myl9** | 1330 |
| 208 | 14 | 4.8 | 350.86 | 102.57 | 17.523 | 16.165 | **0.328** | **2.210** | E9PVX6 | E9PVX6 | Proliferation marker protein Ki-67 | **Mki67** | 338 |
| 209 | 5 | 13.7 | 34.357 | 39.18 | 21.792 | 20.980 | **0.706** | **2.176** | Q9CVB6;D3YXG6 | Q9CVB6;D3YXG6 | Actin-related protein 2/3 complex subunit 2 | **Arpc2** | 1372 |
| 210 | 3 | 29.9 | 11.163 | 17.743 | 17.373 | 15.128 | **0.329** | **2.171** | G3UW58;Q0VG62;A0A087WNR7;A0A087WNL9 | G3UW58;Q0VG62;A0A087WNR7 | Uncharacterized protein C8orf59 homolog | **1810022K09Rik** | 449 |
| 211 | 8 | 62.7 | 18.559 | 250.44 | 28.890 | 27.092 | **2.451** | **2.166** | P18760;F8WGL3 | P18760;F8WGL3 | Cofilin-1 | **Cfl1** | 632 |
| 212 | 20 | 10.8 | 236.25 | 142.29 | 23.555 | 23.126 | **1.729** | **2.165** | E9QAI5;B2RQC6;G3UWN2;B2RQC6-2;E9QAT6;F6S3Z3 | E9QAI5;B2RQC6;G3UWN2;B2RQC6-2 | CAD protein;Glutamine-dependent carbamoyl-phosphate synthase;Aspartate carbamoyltransferase;Dihydroorotase | **Cad** | 206 |
| 213 | 7 | 35.2 | 20.413 | 163.4 | 27.742 | 26.021 | **0.347** | **2.162** | D3YYM6;Q91V55;P97461 | D3YYM6;Q91V55;P97461 | 40S ribosomal protein S5;40S ribosomal protein S5, N-terminally processed | **Rps5** | 288 |
| 214 | 1 | 1 | 141.55 | 6.3769 | 16.748 | 17.079 | **0.827** | **2.127** | Q9CW03 | Q9CW03 | Structural maintenance of chromosomes protein 3 | **Smc3** | 1373 |
| 215 | 2 | 6.9 | 35.226 | 11.518 | 17.463 | 17.032 | **0.342** | **2.126** | Q9QYS9-8;Q9QYS9-4;Q9QYS9-3;Q9QYS9-6;Q9QYS9-2;Q9QYS9;Q9QYS9-7;Q9QYS9-5 | Q9QYS9-8;Q9QYS9-4;Q9QYS9-3;Q9QYS9-6;Q9QYS9-2;Q9QYS9;Q9QYS9-7;Q9QYS9-5 | Protein quaking | **Qk** | 1519 |
| 216 | 4 | 14.8 | 44.669 | 26.595 | 23.438 | 19.086 | **1.570** | **2.125** | A2AGN7;O88685;B7ZCF1 | A2AGN7;O88685;B7ZCF1 | 26S protease regulatory subunit 6A | **Psmc3** | 148 |
| 217 | 4 | 70.2 | 28.696 | 25.419 | 21.748 | 18.110 | **0.475** | **2.110** | G5E8R2;G5E8R1;G5E8R0;E9Q453;E9Q456;E9Q455;S4R261 | G5E8R2;G5E8R1;G5E8R0;E9Q453;E9Q456;E9Q455 | Tropomyosin 1 | **Tpm1** | 472 |
| 218 | 11 | 71 | 7.8409 | 174.1 | 23.755 | 19.992 | **1.121** | **2.091** | P62858;G3UYV7;J3QNN8 | P62858;G3UYV7 | 40S ribosomal protein S28 | **Rps28** | 839 |
| 219 | 2 | 3.1 | 92.188 | 11.709 | 16.491 | 16.774 | **0.400** | **2.087** | Q6A068 | Q6A068 | Cell division cycle 5-like protein | **Cdc5l** | 1085 |
| 220 | 18 | 32.3 | 59.623 | 167.77 | 27.411 | 25.196 | **1.283** | **2.061** | P80316;E0CZA1 | P80316;E0CZA1 | T-complex protein 1 subunit epsilon | **Cct5** | 888 |
| 221 | 3 | 11.2 | 41.275 | 20.976 | 22.633 | 21.393 | **0.427** | **2.060** | P63085 | P63085 | Mitogen-activated protein kinase 1 | **Mapk1** | 859 |
| 222 | 2 | 3.1 | 68.23 | 13.922 | 16.895 | 15.436 | **0.309** | **2.055** | Q5SQ20;Q9EQ61 | Q5SQ20;Q9EQ61 | Pescadillo homolog | **Pes1** | 1004 |
| 223 | 13 | 25.6 | 62.581 | 81.97 | 23.324 | 21.708 | **1.093** | **2.048** | Q60864 | Q60864 | Stress-induced-phosphoprotein 1 | **Stip1** | 1024 |
| 224 | 4 | 15.9 | 32.237 | 27.995 | 23.388 | 22.863 | **0.446** | **2.047** | Q8CDN6 | Q8CDN6 | Thioredoxin-like protein 1 | **Txnl1** | 1200 |
| 225 | 3 | 17.4 | 12.784 | 47.548 | 22.589 | 19.441 | **1.075** | **2.039** | P62889 | P62889 | 60S ribosomal protein L30 | **Rpl30** | 843 |
| 226 | 3 | 23.5 | 6.4066 | 34.892 | 19.933 | 18.464 | **0.295** | **2.028** | P62892 | P62892 | 60S ribosomal protein L39 | **Rpl39** | 844 |
| 227 | 21 | 15.7 | 233.45 | 158.75 | 23.954 | 22.136 | **1.142** | **2.017** | Q3UH59;Q61879;Q5SV64;Q8BXF2 | Q3UH59;Q61879;Q5SV64 | Myosin-10 | **Myh10** | 977 |
| 228 | 11 | 33.9 | 48.354 | 106.39 | 25.356 | 23.945 | **0.588** | **2.016** | P29758 | P29758 | Ornithine aminotransferase, mitochondrial | **Oat** | 676 |
| 229 | 7 | 37 | 23.12 | 47.114 | 19.509 | 19.945 | **0.320** | **1.998** | A2AU61;A2AU62;Q64012-2;Q64012;A2AU60 | A2AU61;A2AU62;Q64012-2;Q64012;A2AU60 | RNA-binding protein Raly | **Raly** | 172 |

|  | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 230 | 0.216 | 0.790 | 1.518 | 0.212 | -1.222 | -2.439 | 25.332 | 23.898 | 22.680 | 23.212 | 23.786 | 24.514 | 27.657 | 22.582 | 26.823 | 19.168 |  | 34 | 34 |
| 231 | 0.929 | 4.812 | 3.291 | 1.768 | -0.079 | 1.385 | 25.432 | 23.585 | 25.049 | 23.789 | 27.671 | 26.151 | 22.808 | 24.520 | 26.521 | 19.199 |  | 12 | 12 |
| 232 | -0.613 | 2.066 | 2.234 | -4.004 | 0.180 | 1.570 | 15.964 | 20.147 | 21.538 | 17.887 | 20.567 | 20.734 | 24.853 | 15.082 | 22.764 | 14.237 |  | 5 | 5 |
| 233 | -2.859 | 3.213 | 2.056 | 1.134 | -1.994 | -2.640 | 20.376 | 17.249 | 16.602 | 14.949 | 21.021 | 19.864 | 24.025 | 14.460 | 21.047 | 14.569 |  | 4 | 4 |
| 234 | -2.495 | -0.081 | -2.237 | -5.797 | -0.157 | -4.753 | 15.432 | 21.072 | 16.476 | 16.246 | 18.659 | 16.504 | 21.993 | 20.465 | 23.225 | 14.256 |  | 2 | 2 |
| 235 | 12.472 | 10.777 | 11.931 | 9.261 | 9.966 | 10.100 | 28.627 | 29.332 | 29.466 | 28.445 | 26.750 | 27.904 | 23.609 | 15.123 | 17.119 | 14.828 | + | 6 | 6 |
| 236 | -0.548 | -0.770 | -0.222 | -1.415 | -3.592 | -2.343 | 26.185 | 24.008 | 25.258 | 25.822 | 25.600 | 26.148 | 28.896 | 26.305 | 28.403 | 24.337 | + | 7 | 7 |
| 237 | -1.639 | -1.166 | -1.662 | 0.419 | -6.488 | -4.190 | 24.203 | 17.296 | 19.594 | 23.543 | 24.017 | 23.521 | 27.569 | 19.999 | 27.631 | 22.735 |  | 3 | 3 |
| 238 | -3.278 | -7.200 | -8.146 | -5.543 | -9.563 | -9.310 | 22.008 | 17.987 | 18.241 | 22.196 | 18.275 | 17.328 | 29.041 | 26.060 | 28.097 | 22.852 |  | 13 | 13 |
| 239 | -6.645 | -0.452 | -5.058 | -6.003 | -6.651 | -5.269 | 17.170 | 16.522 | 17.903 | 15.579 | 21.772 | 17.166 | 25.819 | 20.526 | 24.766 | 19.683 |  | 17 | 17 |
| 240 | -0.240 | 8.323 | 4.686 | 0.777 | 0.236 | 5.991 | 17.793 | 17.252 | 23.008 | 16.385 | 24.948 | 21.310 | 18.283 | 15.749 | 17.864 | 15.386 |  | 7 | 7 |
| 241 | -1.598 | 1.747 | 0.316 | -4.253 | 0.929 | -1.947 | 16.034 | 21.216 | 18.340 | 15.015 | 18.360 | 16.929 | 21.026 | 19.547 | 17.442 | 15.784 |  | 1 | 1 |
| 242 | -6.507 | 5.523 | 4.950 | 0.508 | -1.878 | -0.312 | 29.552 | 27.166 | 28.733 | 15.874 | 27.904 | 27.331 | 29.423 | 28.667 | 30.935 | 13.827 |  | 2 | 2 |
| 243 | -0.466 | 0.560 | -0.492 | -1.787 | -1.708 | -2.547 | 24.885 | 24.964 | 24.125 | 24.824 | 25.850 | 24.798 | 28.591 | 24.752 | 27.653 | 22.927 | + | 9 | 9 |
| 244 | -5.636 | -3.308 | 0.015 | -5.955 | -6.644 | -1.926 | 17.629 | 16.941 | 21.658 | 15.775 | 18.104 | 21.427 | 28.437 | 18.732 | 19.983 | 22.840 |  | 9 | 9 |
| 245 | -0.186 | 1.082 | -1.819 | -1.917 | -2.804 | -1.745 | 24.709 | 23.822 | 24.880 | 23.944 | 25.212 | 22.312 | 27.519 | 25.732 | 25.386 | 22.875 |  | 12 | 12 |
| 246 | 1.964 | -3.180 | -5.053 | -4.201 | -4.075 | -3.454 | 16.886 | 17.012 | 17.633 | 23.945 | 18.801 | 16.927 | 25.319 | 16.855 | 22.671 | 21.290 |  | 2 | 2 |
| 247 | 1.811 | 7.347 | 4.228 | 1.278 | 2.441 | 4.224 | 17.742 | 18.904 | 20.687 | 17.917 | 23.453 | 20.334 | 18.571 | 14.355 | 16.061 | 16.152 |  | 3 | 3 |
| 248 | 2.391 | 1.751 | 1.969 | 1.937 | -2.419 | 1.170 | 21.495 | 17.138 | 20.728 | 20.769 | 20.130 | 20.347 | 23.271 | 15.845 | 22.367 | 14.390 |  | 4 | 4 |
| 249 | -1.354 | -1.079 | -1.283 | -2.009 | -4.246 | -2.802 | 27.547 | 25.310 | 26.754 | 26.566 | 26.841 | 26.637 | 31.035 | 28.076 | 28.932 | 26.908 |  | 36 | 12 |
| 250 | -3.514 | 3.731 | 0.741 | 0.507 | -2.224 | -2.663 | 21.045 | 18.314 | 17.875 | 17.345 | 24.591 | 21.600 | 17.841 | 23.234 | 24.144 | 17.575 |  | 8 | 8 |
| 251 | 3.761 | 0.108 | 4.065 | 4.835 | 2.558 | -4.781 | 24.958 | 22.682 | 15.342 | 21.261 | 17.608 | 21.565 | 19.632 | 20.615 | 18.968 | 16.032 |  | 4 | 4 |
| 252 | -0.074 | 0.405 | 0.178 | -2.335 | -1.406 | -1.056 | 27.535 | 28.464 | 28.814 | 28.553 | 29.032 | 28.804 | 32.153 | 27.586 | 30.097 | 27.156 | + | 35 | 35 |

| | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 230 | 34 | 16.9 | 272.43 | 263.66 | 25.119 | 22.996 | **1.097** | **1.991** | P19096;A0A0U1RNJ1;A0A0U1RPP5 | P19096;A0A0U1RNJ1 | Fatty acid synthase;[Acyl-carrier-protein] S-acetyltransferase;[Acyl-carrier-protein] S-malonyltransferase;3-oxoacyl-[acyl-carrier-protein] synthase;3-oxoacyl-[acyl-carrier-protein] reductase;3-hydroxyacyl-[acyl-carrier-protein] dehydratase;Enoyl-[acyl-carrier-protein] reductase;Oleoyl-[acyl-carrier-protein] hydrolase | **Fasn** | 633 |
| 231 | 12 | 27.8 | 56.891 | 101.09 | 23.664 | 22.860 | **0.720** | **1.986** | Q8BGJ5;Q922I7;Q8CB58;P17225;E9QMW9;E9Q279;F7DCW4;F7AXP1;G8JL74;G3UXA6;Q8BHD7-2;Q8BHD7;E9Q0W3;F7C521;G3UY95;G3UZ01 | Q8BGJ5;Q922I7;Q8CB58;P17225;E9QMW9 | Polypyrimidine tract-binding protein 1 | **Ptbp1** | 1145 |
| 232 | 5 | 16.2 | 36.154 | 31.582 | 19.968 | 18.501 | **0.445** | **1.980** | Q9WUM5 | Q9WUM5 | Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial | **Suclg1** | 1544 |
| 233 | 4 | 17.8 | 27.013 | 24.543 | 19.242 | 17.808 | **0.376** | **1.970** | Q9Z1Q5 | Q9Z1Q5 | Chloride intracellular channel protein 1 | **Clic1** | 1563 |
| 234 | 2 | 11.5 | 39.547 | 15.101 | 21.229 | 18.741 | **0.446** | **1.965** | P28474 | P28474 | Alcohol dehydrogenase class-3 | **Adh5** | 671 |
| 235 | 6 | 43 | 10.071 | 98.032 | 19.366 | 15.973 | **1.589** | **1.951** | P56391;A0A140LIU3 | P56391 | Cytochrome c oxidase subunit 6B1 | **Cox6b1** | 767 |
| 236 | 7 | 29 | 23.564 | 97.506 | 27.600 | 26.370 | **1.389** | **1.937** | Q9CR57 | Q9CR57 | 60S ribosomal protein L14 | **Rpl14** | 1365 |
| 237 | 3 | 13.4 | 16.302 | 31.776 | 23.784 | 25.183 | **0.401** | **1.931** | A0A0A0MQM0;Q8BGY2;P63242 | A0A0A0MQM0;Q8BGY2;P63242 | Eukaryotic translation initiation factor 5A;Eukaryotic translation initiation factor 5A-2;Eukaryotic translation initiation factor 5A-1 | **Eif5a;Eif5a2** | 29 |
| 238 | 4 | 44.5 | 34.216 | 152.03 | 27.551 | 25.475 | **0.415** | **1.930** | P14869;S4R1N1 | P14869;S4R1N1 | 60S acidic ribosomal protein P0 | **Rplp0** | 615 |
| 239 | 10 | 20.2 | 102.72 | 120.4 | 23.173 | 22.224 | **0.433** | **1.922** | A1BN54;Q7TPR4;Q9JI91;O88990;D3YY95 | A1BN54;Q7TPR4 | Alpha-actinin-1 | **Actn1** | 120 |
| 240 | 7 | 12 | 86.906 | 42.098 | 17.016 | 16.625 | **0.246** | **1.922** | E9QN31;Q922K7 | E9QN31;Q922K7 | Probable 28S rRNA (cytosine-C(5))-methyltransferase | **Nop2** | 409 |
| 241 | 1 | 21.6 | 5.6521 | 7.6632 | 20.287 | 16.613 | **0.463** | **1.912** | E9PW90;Q91YT7 | E9PW90;Q91YT7 | YTH domain-containing family protein 2 | **Ythdf2** | 342 |
| 242 | 2 | 1.4 | 238.09 | 11.915 | 29.045 | 22.381 | **0.180** | **1.883** | A0A0U1RNK7;E9PX48;A2A9M5;A2A9M4;Q8R1A4-2;Q8R1A4;A0A0U1RP53;A2AW79;F6ZJ55;A0A0U1RNY4 | A0A0U1RNK7;E9PX48;A2A9M5;A2A9M4;Q8R1A4-2;Q8R1A4;A0A0U1RP53;A2AW79;F6ZJ55;A0A0U1RNY4 | Dedicator of cytokinesis protein 7 | **Dock7** | 101 |
| 243 | 9 | 68.6 | 14.957 | 96.811 | 26.672 | 25.290 | **1.897** | **1.881** | P62962;Q5SX49;CON__P02584;J3QMC2 | P62962;Q5SX49 | Profilin-1;Profilin | **Pfn1** | 851 |
| 244 | 1 | 51.7 | 16.145 | 197.55 | 23.584 | 21.411 | **0.352** | **1.865** | Q9CR49 | Q9CR49 | Hemoglobin subunit epsilon-Y2 | **Hbb-y** | 1364 |
| 245 | 10 | 58.4 | 27.771 | 200.07 | 26.626 | 24.131 | **0.960** | **1.848** | P63101;D3YXN6;D3YXF4;D3YW45 | P63101;D3YXN6 | 14-3-3 protein zeta/delta | **Ywhaz** | 861 |
| 246 | 2 | 5.5 | 53.12 | 13.119 | 21.087 | 21.980 | **0.359** | **1.820** | Q9WUM4 | Q9WUM4 | Coronin-1C | **Coro1c** | 1543 |
| 247 | 3 | 9 | 33.88 | 18.113 | 16.463 | 16.106 | **0.426** | **1.814** | P10711;E9PYD5;P10711-2 | P10711;E9PYD5;P10711-2 | Transcription elongation factor A protein 1 | **Tcea1** | 591 |
| 248 | 4 | 5.8 | 109.55 | 27.02 | 19.558 | 18.379 | **0.596** | **1.808** | Q61768;E9QAK5;P28738;P33175 | Q61768;E9QAK5;P28738;P33175 | Kinesin-1 heavy chain;Kinesin-like protein;Kinesin heavy chain isoform 5C;Kinesin heavy chain isoform 5A | **Kif5b;Kif5c;Kif5a** | 1051 |
| 249 | 12 | 66.3 | 42.019 | 137.14 | 29.556 | 27.920 | **1.266** | **1.780** | P68033;P63268;P68134;P62737;D3YZY0;A0A0U1RQ96;D3Z2K3 | P68033;P63268;P68134;P62737;D3YZY0 | Actin, alpha cardiac muscle 1;Actin, gamma-enteric smooth muscle;Actin, alpha skeletal muscle;Actin, aortic smooth muscle | **Actc1;Actg2;Acta1;Acta2** | 870 |
| 250 | 8 | 34 | 21.935 | 52.703 | 20.537 | 20.859 | **0.313** | **1.779** | F8WJG3;P62996 | F8WJG3;P62996 | Transformer-2 protein homolog beta | **Tra2b** | 446 |
| 251 | 4 | 20.3 | 25.991 | 30.49 | 20.123 | 17.500 | **0.218** | **1.774** | Q02105 | Q02105 | Complement C1q subcomponent subunit C | **C1qc** | 923 |
| 252 | 35 | 57 | 59.752 | 323.31 | 29.870 | 28.626 | **1.918** | **1.769** | Q03265;D3Z6F5;D6RJ16 | Q03265;D3Z6F5 | ATP synthase subunit alpha, mitochondrial;ATP synthase subunit alpha | **Atp5a1** | 928 |

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 253 | 0.717 | 2.367 | 1.592 | -0.616 | 0.049 | -0.058 | 22.049 | 22.714 | 22.607 | 21.861 | 23.511 | 22.736 | 24.870 | 20.459 | 23.706 | 18.581 | + | 2 | 1 |
| 254 | -3.061 | -0.385 | -1.897 | -0.682 | -5.039 | -4.822 | 21.514 | 17.158 | 17.374 | 15.281 | 17.958 | 16.446 | 23.671 | 20.721 | 21.679 | 15.005 | | 1 | 1 |
| 255 | -3.356 | -1.729 | -3.219 | -5.675 | -1.710 | -6.100 | 17.032 | 20.996 | 16.606 | 15.731 | 17.357 | 15.868 | 23.669 | 21.744 | 23.156 | 15.018 | | 1 | 1 |
| 256 | 3.707 | 4.519 | 0.479 | -1.103 | -1.090 | 5.742 | 15.892 | 15.904 | 22.736 | 20.301 | 21.113 | 17.073 | 17.893 | 16.096 | 18.184 | 15.003 | | 2 | 2 |
| 257 | -8.081 | 2.074 | 0.118 | -2.173 | -6.601 | -2.268 | 22.337 | 17.910 | 22.242 | 15.200 | 25.355 | 23.399 | 23.349 | 25.672 | 25.116 | 21.446 | | 15 | 15 |
| 258 | -3.319 | -2.079 | -2.482 | -3.295 | -5.343 | -4.374 | 25.321 | 23.273 | 24.242 | 23.930 | 25.170 | 24.767 | 29.603 | 27.629 | 28.494 | 26.004 | | 26 | 26 |
| 259 | -0.958 | 8.541 | 6.887 | 2.461 | 5.764 | 1.132 | 18.305 | 21.608 | 16.976 | 16.669 | 26.168 | 24.514 | 16.094 | 15.594 | 20.765 | 14.489 | | 13 | 13 |
| 260 | 1.285 | 3.437 | 2.842 | 1.549 | 3.292 | -2.366 | 20.449 | 22.192 | 16.534 | 20.329 | 22.481 | 21.886 | 21.399 | 16.401 | 23.233 | 14.855 | | 2 | 2 |
| 261 | 5.069 | -0.306 | -1.110 | 3.147 | -2.205 | -2.342 | 23.605 | 18.253 | 18.116 | 22.515 | 17.141 | 16.336 | 21.302 | 19.614 | 20.976 | 13.916 | | 3 | 3 |
| 262 | -2.297 | 4.971 | 4.634 | 1.387 | 3.238 | -2.340 | 18.711 | 20.561 | 14.983 | 15.583 | 22.851 | 22.514 | 18.147 | 16.501 | 21.210 | 14.550 | | 3 | 3 |
| 263 | 3.518 | 4.810 | 2.546 | 1.172 | 1.949 | 2.780 | 23.279 | 24.056 | 24.887 | 23.777 | 25.070 | 22.806 | 21.820 | 22.394 | 24.750 | 15.769 | | 4 | 4 |
| 264 | 1.619 | 1.643 | 1.182 | 0.349 | -0.436 | -0.410 | 26.827 | 26.042 | 26.068 | 26.048 | 26.072 | 25.611 | 28.189 | 24.767 | 27.229 | 21.629 | + | 11 | 11 |
| 265 | -0.367 | 1.792 | 3.889 | 0.826 | -1.820 | 1.394 | 20.388 | 17.742 | 20.956 | 16.051 | 18.211 | 20.308 | 22.745 | 16.379 | 17.499 | 15.337 | | 4 | 4 |
| 266 | -2.687 | -2.703 | -1.955 | -3.806 | -4.185 | -4.234 | 27.197 | 26.819 | 26.770 | 27.008 | 26.993 | 27.740 | 32.803 | 29.204 | 30.785 | 28.606 | + | 33 | 33 |
| 267 | 1.240 | 4.384 | 2.528 | 1.484 | 1.187 | 0.629 | 24.364 | 24.067 | 23.509 | 23.542 | 26.685 | 24.829 | 19.966 | 25.794 | 26.106 | 18.496 | | 16 | 16 |
| 268 | 2.622 | 6.136 | 5.291 | 3.162 | 3.735 | 2.381 | 24.217 | 24.790 | 23.436 | 22.278 | 25.792 | 24.947 | 18.303 | 23.807 | 24.816 | 14.495 | | 11 | 11 |
| 269 | 0.269 | 0.798 | 1.032 | -2.090 | -0.589 | 0.018 | 22.488 | 23.990 | 24.597 | 23.672 | 24.201 | 24.435 | 26.780 | 22.378 | 25.724 | 21.082 | | 9 | 9 |
| 270 | 0.935 | 1.903 | 1.304 | 0.642 | -0.533 | -0.698 | 21.776 | 20.600 | 20.436 | 20.798 | 21.766 | 21.168 | 22.044 | 20.223 | 21.133 | 18.594 | + | 2 | 2 |
| 271 | 1.595 | 1.009 | 0.695 | 1.585 | -1.397 | -1.602 | 20.704 | 17.722 | 17.516 | 19.379 | 18.793 | 18.479 | 21.336 | 16.901 | 18.946 | 16.622 | | 2 | 2 |
| 272 | 8.480 | 1.938 | 5.416 | 7.006 | 4.397 | -0.267 | 24.210 | 21.601 | 16.938 | 24.581 | 18.040 | 21.517 | 18.835 | 15.575 | 17.430 | 14.773 | | 3 | 3 |
| 273 | 5.019 | -1.014 | -0.245 | 2.825 | -2.059 | -1.695 | 22.745 | 17.861 | 18.225 | 22.857 | 16.824 | 17.593 | 22.818 | 17.022 | 21.567 | 14.108 | | 3 | 3 |
| 274 | -4.837 | -2.539 | -5.967 | -7.119 | -3.196 | -7.705 | 17.174 | 21.097 | 16.587 | 16.902 | 19.201 | 15.773 | 26.186 | 22.399 | 21.891 | 21.588 | | 7 | 6 |
| 275 | -0.362 | 6.702 | 3.490 | 2.830 | 0.981 | 1.378 | 19.366 | 17.518 | 17.914 | 16.009 | 23.073 | 19.860 | 16.865 | 16.208 | 18.242 | 14.499 | | 4 | 4 |
| 276 | 5.145 | 5.914 | 3.388 | 5.515 | 6.695 | -2.398 | 24.158 | 25.338 | 16.246 | 24.154 | 24.924 | 22.398 | 16.521 | 20.767 | 22.610 | 15.409 | | 11 | 11 |
| 277 | -1.967 | 2.581 | -0.966 | -3.941 | -0.112 | -0.931 | 16.807 | 20.636 | 19.818 | 16.149 | 20.697 | 17.150 | 22.670 | 18.828 | 21.817 | 14.415 | | 4 | 4 |
| 278 | -7.254 | -2.534 | -2.318 | -7.423 | -1.599 | -7.716 | 16.455 | 22.278 | 16.162 | 15.862 | 20.583 | 20.799 | 26.054 | 21.702 | 24.573 | 21.661 | | 6 | 6 |
| 279 | -1.495 | -0.431 | -0.457 | -2.617 | -2.544 | -1.834 | 27.493 | 27.566 | 28.276 | 26.751 | 27.815 | 27.789 | 31.138 | 29.083 | 29.800 | 26.692 | + | 40 | 40 |
| 280 | 9.405 | 10.899 | 8.109 | 8.231 | 8.301 | 7.277 | 25.142 | 25.211 | 24.188 | 25.135 | 26.629 | 23.840 | 17.471 | 16.350 | 17.192 | 14.268 | | 8 | 8 |
| 281 | -2.809 | -0.541 | -0.694 | -3.813 | -0.493 | -4.272 | 17.053 | 20.373 | 16.594 | 15.643 | 17.911 | 17.758 | 22.196 | 19.536 | 21.608 | 15.296 | | 3 | 3 |
| 282 | 2.030 | 5.420 | 3.809 | 1.662 | 2.379 | 2.698 | 25.967 | 26.684 | 27.003 | 25.305 | 28.695 | 27.084 | 23.149 | 25.460 | 27.707 | 18.843 | | 28 | 28 |

| | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 253 | 1 | 13.3 | 18.521 | 8.2166 | 22.665 | 21.144 | **1.566** | **1.767** | Q9R0P5 | Q9R0P5 | Destrin | **Dstn** | 1532 |
| 254 | 1 | 2.1 | 48.063 | 6.7453 | 22.196 | 18.342 | **0.464** | **1.733** | Q91VK1 | Q91VK1 | Basic leucine zipper and W2 domain-containing protein 2 | **Bzw2** | 1264 |
| 255 | 1 | 6.7 | 21.701 | 6.6422 | 22.707 | 19.087 | **0.507** | **1.727** | Q9D0R8 | Q9D0R8 | Protein LSM12 homolog | **Lsm12** | 1416 |
| 256 | 2 | 19.1 | 13.815 | 12.221 | 16.994 | 16.593 | **0.265** | **1.719** | Q9CWW6 | Q9CWW6 | Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 | **Pin4** | 1379 |
| 257 | 6 | 40.9 | 49.035 | 138.85 | 24.510 | 23.281 | **0.191** | **1.718** | Q9Z1N5 | Q9Z1N5 | Spliceosome RNA helicase Ddx39b | **Ddx39b** | 1561 |
| 258 | 26 | 65.2 | 57.477 | 231.75 | 28.616 | 27.249 | **1.157** | **1.711** | P80314 | P80314 | T-complex protein 1 subunit beta | **Cct2** | 886 |
| 259 | 4 | 42.7 | 46.049 | 122.34 | 15.844 | 17.627 | **0.203** | **1.704** | Q61029-3;Q61029;Q61029-2;Q61029-4;Q61033-2 | Q61029-3;Q61029;Q61029-2;Q61029-4;Q61033-2 | Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/gamma;Lamina-associated polypeptide 2, isoforms alpha/zeta | **Tmpo** | 1030 |
| 260 | 2 | 18.8 | 11.557 | 12.042 | 18.900 | 19.044 | **0.401** | **1.697** | P63166;A0A087WRQ4 | P63166;A0A087WRQ4 | Small ubiquitin-related modifier 1 | **Sumo1** | 862 |
| 261 | 3 | 14.7 | 31.616 | 18.854 | 20.458 | 17.446 | **0.252** | **1.684** | Q8JZZ5;P53811 | Q8JZZ5;P53811 | Phosphatidylinositol transfer protein beta isoform | **Pitpnb** | 754 |
| 262 | 3 | 5.8 | 56.784 | 18.24 | 17.324 | 17.880 | **0.227** | **1.675** | O35841 | O35841 | Apoptosis inhibitor 5 | **Api5** | 518 |
| 263 | 4 | 12.9 | 34.003 | 43.819 | 22.107 | 20.260 | **0.967** | **1.658** | G3UY42;Q8CCS6-2;Q8CCS6;D3YUB9;D3Z055;G3UWS5;D3Z5F7;G3UX74 | G3UY42;Q8CCS6-2;Q8CCS6;D3YUB9;D3Z055;G3UWS5;D3Z5F7 | Polyadenylate-binding protein 2 | **Pabpn1;Gm20521** | 458 |
| 264 | 11 | 65.4 | 14.839 | 96.589 | 26.478 | 24.429 | **2.281** | **1.647** | P62245;F8WJ41;D3YVB4;D3Z712 | P62245;F8WJ41;D3YVB4;D3Z712 | 40S ribosomal protein S15a | **Rps15a** | 814 |
| 265 | 4 | 4.9 | 87.428 | 23.771 | 19.562 | 16.418 | **0.446** | **1.638** | E9PV24;E9PV24-2;CON__P02672 | E9PV24;E9PV24-2 | Fibrinogen alpha chain;Fibrinopeptide A;Fibrinogen alpha chain | **Fga** | 331 |
| 266 | 33 | 73 | 56.3 | 323.31 | 31.003 | 29.695 | **2.353** | **1.626** | P56480 | P56480 | ATP synthase subunit beta, mitochondrial | **Atp5b** | 769 |
| 267 | 16 | 20.1 | 88.846 | 139.06 | 22.880 | 22.301 | **0.789** | **1.617** | Q62318;Q62318-2 | Q62318;Q62318-2 | Transcription intermediary factor 1-beta | **Trim28** | 1067 |
| 268 | 11 | 28.9 | 66.821 | 99.149 | 21.055 | 19.656 | **0.635** | **1.591** | G5E924;Q8R081;G3UY38;G3UYY3;G3UY56 | G5E924;Q8R081;G3UY38 | Heterogeneous nuclear ribonucleoprotein L | **Hnrnpl** | 475 |
| 269 | 9 | 30.2 | 54.507 | 89.479 | 24.579 | 23.403 | **1.120** | **1.587** | Q61553;A0A0G2JDU7;F7BDR1 | Q61553;A0A0G2JDU7 | Fascin | **Fscn1** | 1039 |
| 270 | 2 | 21.1 | 14.237 | 23.815 | 21.134 | 19.864 | **1.444** | **1.577** | Q8BGB5 | Q8BGB5 | LIM domain-containing protein 2 | **Limd2** | 1143 |
| 271 | 2 | 4.3 | 64.279 | 11.303 | 19.118 | 17.784 | **0.670** | **1.571** | Q8BP47 | Q8BP47 | Asparagine--tRNA ligase, cytoplasmic | **Nars** | 1177 |
| 272 | 3 | 21.9 | 15.076 | 17.952 | 17.205 | 16.102 | **0.214** | **1.566** | Q9QXA5;Q9CY46;D3YTP8 | Q9QXA5;Q9CY46;D3YTP8 | U6 snRNA-associated Sm-like protein LSm4 | **Lsm4** | 1384 |
| 273 | 3 | 38.1 | 11.234 | 20.676 | 19.920 | 17.837 | **0.252** | **1.563** | A2AUM6;P16254 | A2AUM6;P16254 | Signal recognition particle 14 kDa protein;Signal recognition particle 14 kDa protein, N-terminally processed | **Srp14** | 175 |
| 274 | 6 | 7.6 | 105.73 | 39.156 | 24.293 | 21.740 | **0.376** | **1.559** | Q3V3R1 | Q3V3R1 | Monofunctional C1-tetrahydrofolate synthase, mitochondrial | **Mthfd1l** | 995 |
| 275 | 4 | 3 | 181.85 | 36.45 | 16.536 | 16.371 | **0.296** | **1.547** | A0A0R4J170;Q3TKT4;Q3TKT4-2;G3UX35;E9QAB8;F2Z4A9;H3BLH0;Q6DIC0 | A0A0R4J170;Q3TKT4;Q3TKT4-2;G3UX35 | Transcription activator BRG1 | **Smarca4** | 92 |
| 276 | 11 | 6.4 | 235.63 | 89.072 | 18.644 | 19.010 | **0.202** | **1.545** | E9Q7G0;F6ZQA3 | E9Q7G0;F6ZQA3 | Nuclear mitotic apparatus protein 1 | **Numa1** | 393 |
| 277 | 4 | 9.6 | 57.927 | 25.533 | 20.749 | 18.116 | **0.356** | **1.544** | P52293;F2Z431;A2A602;A2A600;A2A601;A6PW68 | P52293;F2Z431;A2A602;A2A600;A2A601 | Importin subunit alpha-1 | **Kpna2** | 747 |
| 278 | 6 | 13.9 | 51.564 | 48.194 | 23.878 | 23.117 | **0.237** | **1.544** | P40124;B1ARS0 | P40124;B1ARS0 | Adenylyl cyclase-associated protein 1;Adenylyl cyclase-associated protein | **Cap1** | 702 |
| 279 | 38 | 43.6 | 95.313 | 323.31 | 30.110 | 28.246 | **1.632** | **1.537** | P58252;G3UXK8 | P58252 | Elongation factor 2 | **Eef2** | 774 |
| 280 | 8 | 32.7 | 34.306 | 61.505 | 16.911 | 15.730 | **0.816** | **1.535** | P35550;A0A140LIR6;Q80WS3 | P35550 | rRNA 2-O-methyltransferase fibrillarin | **Fbl** | 693 |
| 281 | 3 | 8.7 | 43.066 | 18.69 | 20.866 | 18.452 | **0.468** | **1.511** | Q63844;D3Z6D8;D3Z3G6;A0A0U1RPZ0;A0A0U1RPX4 | Q63844;D3Z6D8;D3Z3G6 | Mitogen-activated protein kinase 3;Mitogen-activated protein kinase | **Mapk3** | 1075 |
| 282 | 28 | 48.1 | 73.74 | 254.3 | 24.305 | 23.275 | **0.666** | **1.506** | Q9D0E1-2;Q9D0E1;B8JK33;B8JK32;F6W322;F7C9U3;G3X924;Q91VC4 | Q9D0E1-2;Q9D0E1;B8JK33;B8JK32 | Heterogeneous nuclear ribonucleoprotein M | **Hnrnpm** | 1407 |

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 283 | -0.949 | 7.550 | 4.964 | 1.573 | 4.571 | 0.904 | 18.617 | 21.615 | 17.948 | 15.672 | 24.172 | 21.586 | 17.699 | 16.390 | 18.078 | 15.165 | | 13 | 8 |
| 284 | -0.831 | -3.841 | -3.902 | -3.814 | -3.285 | -5.993 | 18.125 | 18.654 | 15.946 | 20.165 | 17.156 | 17.095 | 23.386 | 20.492 | 23.121 | 18.872 | | 2 | 2 |
| 285 | -3.359 | -0.610 | -1.475 | -6.812 | -1.595 | -1.433 | 16.203 | 21.419 | 21.582 | 15.031 | 17.780 | 16.916 | 22.370 | 23.660 | 23.041 | 13.740 | | 2 | 2 |
| 286 | -7.555 | -2.386 | -2.694 | -6.266 | -6.993 | -3.723 | 17.823 | 17.097 | 20.367 | 15.980 | 21.150 | 20.841 | 24.663 | 23.516 | 25.854 | 21.216 | | 8 | 8 |
| 287 | 0.699 | 2.785 | 1.361 | -1.586 | 1.707 | 0.396 | 22.849 | 26.142 | 24.831 | 23.974 | 26.061 | 24.637 | 27.116 | 21.754 | 24.167 | 22.385 | | 23 | 23 |
| 288 | -0.016 | -0.527 | -0.479 | -2.081 | -1.536 | -1.696 | 23.957 | 24.502 | 24.342 | 24.808 | 24.297 | 24.345 | 27.680 | 24.396 | 26.495 | 23.153 | + | 12 | 11 |
| 289 | 5.710 | 1.232 | 3.038 | 4.236 | 0.649 | 0.803 | 30.823 | 27.235 | 27.390 | 30.892 | 26.415 | 28.220 | 28.669 | 24.505 | 27.484 | 22.881 | | 22 | 22 |
| 290 | 0.802 | 1.826 | 1.683 | 0.249 | -0.153 | -0.072 | 23.084 | 22.683 | 22.763 | 21.109 | 22.133 | 21.990 | 26.304 | 19.367 | 22.870 | 17.744 | + | 5 | 5 |
| 291 | 6.661 | 4.461 | 5.493 | 5.801 | 3.484 | 3.099 | 24.987 | 22.669 | 22.284 | 24.223 | 22.024 | 23.055 | 22.762 | 15.608 | 20.211 | 14.915 | | 2 | 2 |
| 292 | -2.464 | 4.594 | 0.998 | 0.076 | 0.126 | -1.294 | 17.897 | 17.947 | 16.527 | 15.398 | 22.457 | 18.861 | 19.095 | 16.547 | 20.884 | 14.842 | | 5 | 5 |
| 293 | -2.679 | -5.508 | -2.314 | -2.507 | -5.528 | -6.682 | 21.643 | 18.622 | 17.469 | 20.588 | 17.759 | 20.953 | 25.247 | 23.054 | 24.280 | 22.254 | | 8 | 8 |
| 294 | -0.449 | -0.820 | -1.024 | -6.288 | -1.011 | 0.883 | 16.942 | 22.219 | 24.112 | 22.022 | 21.651 | 21.447 | 25.600 | 20.858 | 23.976 | 20.967 | | 6 | 6 |
| 295 | 2.546 | 1.622 | 2.238 | 0.936 | 0.835 | 0.546 | 26.456 | 26.355 | 26.066 | 25.782 | 24.858 | 25.474 | 27.259 | 23.781 | 26.068 | 20.404 | + | 10 | 10 |
| 296 | 2.083 | 6.130 | 4.682 | 1.694 | 3.705 | 3.414 | 22.790 | 24.801 | 24.510 | 22.363 | 26.410 | 24.962 | 20.537 | 21.655 | 25.238 | 15.322 | | 6 | 6 |
| 297 | 6.895 | 4.631 | 6.010 | 5.924 | 2.865 | 4.748 | 23.222 | 20.163 | 22.046 | 22.680 | 20.415 | 21.794 | 17.888 | 16.707 | 16.590 | 14.979 | | 4 | 4 |
| 298 | 6.207 | 5.773 | 6.250 | 5.462 | 4.827 | 3.945 | 25.928 | 25.293 | 24.411 | 25.277 | 24.844 | 25.320 | 20.310 | 20.622 | 24.569 | 13.571 | + | 7 | 7 |
| 299 | -6.973 | -5.307 | -0.268 | -6.190 | -3.405 | -6.941 | 17.614 | 20.399 | 16.863 | 15.338 | 17.005 | 22.043 | 24.520 | 23.088 | 22.389 | 22.234 | | 4 | 4 |
| 300 | -0.513 | 4.504 | 1.809 | -2.724 | 1.874 | 2.682 | 18.311 | 22.909 | 23.717 | 21.325 | 26.341 | 23.646 | 19.210 | 22.860 | 25.881 | 17.794 | | 17 | 17 |
| 301 | 0.978 | -1.578 | -0.560 | 0.085 | -2.852 | -2.322 | 29.069 | 26.132 | 26.662 | 28.703 | 26.148 | 27.166 | 29.696 | 28.271 | 29.577 | 25.873 | | 17 | 17 |
| 302 | -2.947 | 4.395 | 3.040 | -0.772 | 0.271 | 1.068 | 16.081 | 17.123 | 17.921 | 15.608 | 22.949 | 21.595 | 17.415 | 16.290 | 21.036 | 16.073 | | 6 | 2 |
| 303 | -4.276 | 0.284 | -2.800 | -4.732 | -4.691 | -1.285 | 16.989 | 17.030 | 20.436 | 16.242 | 20.803 | 17.718 | 23.002 | 20.440 | 23.017 | 18.020 | | 3 | 3 |
| 304 | 5.022 | 0.665 | 0.875 | 3.045 | 2.171 | -2.537 | 22.649 | 21.775 | 17.067 | 21.515 | 17.159 | 17.368 | 22.102 | 17.106 | 17.892 | 15.095 | | 1 | 1 |
| 305 | 2.816 | 5.850 | 4.597 | 2.350 | 2.755 | 4.321 | 23.108 | 23.513 | 25.080 | 23.638 | 26.672 | 25.419 | 17.924 | 23.592 | 24.981 | 16.663 | | 16 | 14 |
| 306 | -0.273 | 9.527 | 4.727 | 3.014 | 2.147 | 4.997 | 19.461 | 18.594 | 21.444 | 15.926 | 25.726 | 20.926 | 17.411 | 15.483 | 17.728 | 14.670 | | 9 | 9 |

|  | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 283 | 8 | 23.6 | 69.084 | 53.625 | 17.045 | 16.622 | **0.212** | **1.506** | A0A0R4J0Q5;P21619;P21619-2 | A0A0R4J0Q5;P21619;P21619-2 | Lamin-B2 | **Lmnb2** | 87 |
| 284 | 2 | 23.5 | 8.9723 | 20.333 | 21.939 | 20.997 | **0.503** | **1.506** | P29595 | P29595 | NEDD8 | **Nedd8** | 675 |
| 285 | 2 | 3.6 | 68.692 | 13.327 | 23.015 | 18.390 | **0.307** | **1.465** | P07724 | P07724 | Serum albumin | **Alb** | 570 |
| 286 | 8 | 28.3 | 44.172 | 66.869 | 24.090 | 23.535 | **0.303** | **1.449** | P62334 | P62334 | 26S protease regulatory subunit 10B | **Psmc6** | 824 |
| 287 | 23 | 14.5 | 249.55 | 168.64 | 24.435 | 23.276 | **0.563** | **1.443** | A0A087WS56;Q3UHL6;A0A087WR50;P11276;B7ZNJ1;B9EHT6;A0A087WSN6;A0A087WS99;Q4KL80 | A0A087WS56;Q3UHL6;A0A087WR50;P11276;B7ZNJ1;B9EHT6;A0A087WSN6 | Fibronectin;Anastellin | **Fn1** | 20 |
| 288 | 11 | 40 | 29.174 | 112.77 | 26.038 | 24.824 | **2.471** | **1.431** | P62259;D6REF3;F6WA09 | P62259;D6REF3 | 14-3-3 protein epsilon | **Ywhae** | 815 |
| 289 | 22 | 70.4 | 17.671 | 230.05 | 26.587 | 25.183 | **0.338** | **1.430** | F6YVP7;P62270;A0A140T8T3;S4R1N6 | F6YVP7;P62270;A0A140T8T3;S4R1N6 | 40S ribosomal protein S18 | **Gm10260;Rps18** | 424 |
| 290 | 5 | 13.1 | 51.386 | 37.792 | 22.836 | 20.307 | **1.852** | **1.429** | Q99JY0;D3YXU1 | Q99JY0;D3YXU1 | Trifunctional enzyme subunit beta, mitochondrial;3-ketoacyl-CoA thiolase | **Hadhb** | 1294 |
| 291 | 2 | 30.8 | 5.8378 | 12.694 | 19.185 | 17.563 | **0.597** | **1.410** | P56382 | P56382 | ATP synthase subunit epsilon, mitochondrial | **Atp5e** | 766 |
| 292 | 3 | 16.9 | 37.006 | 28.604 | 17.821 | 17.863 | **0.269** | **1.406** | A0A0J9YUM4;A0A0J9YU62;O88712-2;O88712;A0A0J9YUR5;O88712-3;A0A0J9YU66;A0A0J9YVI3;A0A0J9YTW3;A0A0J9YVC3 | A0A0J9YUM4;A0A0J9YU62;O88712-2;O88712;A0A0J9YUR5;O88712-3 | C-terminal-binding protein 1 | **Ctbp1** | 60 |
| 293 | 8 | 9.9 | 140.21 | 68.001 | 24.151 | 23.267 | **0.367** | **1.405** | Q9Z1Q9;G3UY93;G3UYW2;G3UZ22 | Q9Z1Q9;G3UY93 | Valine--tRNA ligase | **Vars** | 1564 |
| 294 | 6 | 38.4 | 23.596 | 40.918 | 23.229 | 22.471 | **0.253** | **1.374** | P34022;H7BX22 | P34022;H7BX22 | Ran-specific GTPase-activating protein | **Ranbp1** | 687 |
| 295 | 10 | 36.9 | 24.604 | 79.705 | 25.520 | 23.236 | **2.003** | **1.363** | Q6ZWV3;I7HLV2;P86048;B7FAU6 | Q6ZWV3;I7HLV2;P86048 | 60S ribosomal protein L10;60S ribosomal protein L10-like | **Rpl10;Rpl10l** | 1110 |
| 296 | 6 | 21 | 44.547 | 150.79 | 21.096 | 20.280 | **0.435** | **1.361** | Q921F2;A0A087WR97;Q6VYI4;Q6VYI5;Q8BLD4;Q8R0B4;A0A087WRZ5;A0A087WQA5;A0A087WSE4;A0A087WSH7;H3BJV1;A0A087WRP4;A0A087WQX8;A0A087WS74;A0A087WSC6;A0A087WNY6;A0A087WP57 | Q921F2;A0A087WR97;Q6VYI4;Q6VYI5;Q8BLD4;Q8R0B4;A0A087WRZ5;A0A087WQA5;A0A087WSE4 | TAR DNA-binding protein 43 | **Tardbp** | 21 |
| 297 | 4 | 10.3 | 23.934 | 26.594 | 17.298 | 15.784 | **0.530** | **1.333** | Q8BJF9;B1AVH5;Q8C0P5 | Q8BJF9 | Charged multivesicular body protein 2b | **Chmp2b** | 1164 |
| 298 | 7 | 38.6 | 23.532 | 103.08 | 20.466 | 19.070 | **1.339** | **1.332** | Q9D1J3 | Q9D1J3 | SAP domain-containing ribonucleoprotein | **Sarnp** | 1425 |
| 299 | 4 | 6.4 | 57.788 | 24.37 | 23.804 | 22.311 | **0.228** | **1.329** | Q9D0F3;D3Z5B9 | Q9D0F3 | Protein ERGIC-53 | **Lman1** | 1408 |
| 300 | 17 | 14.2 | 149.62 | 108.39 | 21.035 | 21.838 | **0.234** | **1.323** | A0A087WPL5;E9QNN1;O70133;O70133-2;O70133-3;Q3UR42;A0A0R4J2C3;A0A087WRT3 | A0A087WPL5;E9QNN1;O70133;O70133-2;O70133-3;Q3UR42 | ATP-dependent RNA helicase A | **Dhx9** | 19 |
| 301 | 17 | 72.7 | 22.127 | 205.97 | 28.983 | 27.725 | **0.487** | **1.310** | P62082;F6SVV1 | P62082;F6SVV1 | 40S ribosomal protein S7 | **Rps7;Gm9493** | 807 |
| 302 | 2 | 19.8 | 49.279 | 12.673 | 16.853 | 18.555 | **0.220** | **1.307** | P70333 | P70333 | Heterogeneous nuclear ribonucleoprotein H2 | **Hnrnph2** | 879 |
| 303 | 3 | 23 | 14.255 | 18.251 | 21.721 | 20.518 | **0.301** | **1.305** | Q9CQF7;Q9CWM4 | Q9CQF7;Q9CWM4 | Prefoldin subunit 1 | **Pfdn1** | 1343 |
| 304 | 1 | 15.5 | 7.6566 | 6.7174 | 19.604 | 16.494 | **0.226** | **1.294** | E9Q4B9;E9Q827;P56212-2;P56212;P60840-2;P60840 | E9Q4B9;E9Q827;P56212-2;P56212;P60840-2;P60840 | cAMP-regulated phosphoprotein 19;Alpha-endosulfine | **Arpp19;Ensa** | 380 |
| 305 | 14 | 38.7 | 54.54 | 111.41 | 20.758 | 20.822 | **0.528** | **1.279** | Q99K48;Q99K48-2 | Q99K48;Q99K48-2 | Non-POU domain-containing octamer-binding protein | **Nono** | 1298 |
| 306 | 9 | 18.1 | 64.464 | 76.712 | 16.447 | 16.199 | **0.162** | **1.274** | Q9D6Z1;F7CHQ7;F7CHP9;E0CXZ0;A2APD7;F6U250;F6V095;F6USW7 | Q9D6Z1;F7CHQ7 | Nucleolar protein 56 | **Nop56** | 1441 |

|  | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 307 | -2.595 | -0.365 | -0.196 | -1.643 | -3.618 | -1.675 | 23.955 | 21.980 | 23.923 | 22.116 | 24.346 | 24.515 | 27.306 | 23.889 | 26.598 | 22.823 |  | 29 | 17 |
| 308 | -1.323 | -1.292 | -0.126 | -2.361 | -1.994 | -2.166 | 21.536 | 21.903 | 21.731 | 20.886 | 20.917 | 22.084 | 27.152 | 20.642 | 24.619 | 19.801 | + | 13 | 13 |
| 309 | -0.820 | 0.467 | -0.003 | -1.247 | -2.033 | -0.837 | 25.926 | 25.141 | 26.336 | 25.731 | 27.019 | 26.548 | 28.883 | 25.463 | 28.374 | 24.728 |  | 21 | 21 |
| 310 | -2.521 | -4.460 | -2.112 | -7.352 | -2.636 | -2.846 | 17.620 | 22.337 | 22.126 | 19.585 | 17.646 | 19.994 | 27.712 | 22.232 | 25.033 | 19.179 |  | 5 | 5 |
| 311 | 3.095 | 5.072 | 3.034 | 1.744 | 2.667 | 3.052 | 24.861 | 25.785 | 26.169 | 22.998 | 24.975 | 22.936 | 26.440 | 19.795 | 24.930 | 14.874 |  | 1 | 1 |
| 312 | 0.835 | 1.486 | -2.990 | -2.369 | -2.945 | 0.906 | 17.704 | 17.129 | 20.980 | 20.503 | 21.154 | 16.679 | 24.652 | 15.495 | 23.257 | 16.080 |  | 2 | 2 |
| 313 | -11.042 | -1.570 | -1.592 | -6.489 | -6.920 | -4.533 | 21.430 | 20.999 | 23.386 | 15.338 | 24.810 | 24.789 | 29.576 | 26.261 | 27.190 | 25.571 |  | 39 | 39 |
| 314 | 1.444 | 3.413 | 1.584 | 0.266 | -0.304 | 2.789 | 21.397 | 20.827 | 23.920 | 21.659 | 23.628 | 21.798 | 25.070 | 17.192 | 22.901 | 17.528 |  | 7 | 7 |
| 315 | 0.217 | -0.547 | -1.717 | -3.430 | -3.464 | 1.175 | 17.840 | 17.805 | 22.445 | 23.385 | 22.621 | 21.451 | 26.756 | 15.784 | 24.132 | 22.204 |  | 6 | 6 |
| 316 | -0.019 | -3.915 | 0.552 | -1.628 | -0.709 | -4.679 | 23.130 | 24.049 | 20.079 | 23.139 | 19.242 | 23.710 | 26.694 | 22.822 | 25.229 | 21.086 |  | 13 | 13 |
| 317 | 7.801 | 4.899 | 6.201 | 6.638 | 4.909 | 3.739 | 24.984 | 23.256 | 22.086 | 24.047 | 21.145 | 22.447 | 19.913 | 16.780 | 17.342 | 15.148 |  | 2 | 2 |
| 318 | -10.020 | -7.212 | -3.449 | -8.052 | -7.223 | -9.010 | 17.324 | 18.153 | 16.367 | 14.249 | 17.057 | 20.819 | 27.797 | 22.956 | 25.593 | 22.944 |  | 7 | 7 |
| 319 | -4.139 | -3.320 | -3.831 | -6.969 | -1.075 | -6.841 | 16.824 | 22.718 | 16.952 | 17.730 | 18.548 | 18.038 | 25.915 | 21.671 | 23.880 | 19.857 |  | 5 | 5 |
| 320 | -2.944 | 4.902 | 3.793 | 0.420 | 3.251 | -1.475 | 18.654 | 21.485 | 16.759 | 15.442 | 23.287 | 22.179 | 20.294 | 16.173 | 22.052 | 14.718 |  | 7 | 7 |
| 321 | -0.646 | 0.620 | -0.051 | -1.651 | -1.206 | -0.763 | 28.759 | 29.204 | 29.647 | 28.028 | 29.293 | 28.622 | 31.421 | 29.398 | 30.433 | 26.915 |  | 12 | 12 |
| 322 | -1.272 | 5.414 | 3.127 | 1.439 | 0.638 | 1.670 | 17.796 | 16.994 | 18.027 | 17.165 | 23.851 | 21.564 | 18.248 | 14.465 | 21.689 | 15.185 |  | 9 | 6 |
| 323 | 4.250 | 1.201 | 2.055 | 3.448 | 0.539 | -0.003 | 28.706 | 25.796 | 25.255 | 27.680 | 24.631 | 25.486 | 27.583 | 22.931 | 25.703 | 21.158 |  | 11 | 11 |
| 324 | -1.252 | 0.764 | -0.139 | -1.578 | -1.548 | -1.012 | 24.369 | 24.398 | 24.935 | 23.978 | 25.993 | 25.091 | 27.763 | 24.131 | 27.484 | 22.975 |  | 15 | 15 |
| 325 | 0.698 | 1.495 | 0.381 | -0.990 | 0.410 | -0.357 | 22.506 | 23.906 | 23.139 | 23.069 | 23.865 | 22.751 | 25.926 | 21.066 | 24.046 | 20.695 |  | 12 | 12 |
| 326 | 3.520 | 2.660 | 2.421 | 2.016 | 1.705 | 1.397 | 27.490 | 27.178 | 26.870 | 27.645 | 26.785 | 26.546 | 27.051 | 23.895 | 26.415 | 21.835 | + | 3 | 3 |
| 327 | 8.006 | 5.325 | 6.628 | 5.994 | 4.743 | 5.759 | 23.111 | 21.859 | 22.875 | 24.340 | 21.659 | 22.962 | 18.266 | 15.968 | 18.503 | 14.164 |  | 2 | 2 |
| 328 | -1.548 | 5.907 | 3.325 | 6.116 | -0.755 | -1.131 | 23.135 | 16.264 | 15.888 | 16.932 | 24.387 | 21.804 | 17.628 | 16.408 | 22.127 | 14.832 |  | 12 | 12 |
| 329 | 4.975 | 2.729 | 4.204 | -0.658 | 3.283 | 5.842 | 16.907 | 20.849 | 23.407 | 21.300 | 19.054 | 20.529 | 19.530 | 15.601 | 17.438 | 15.212 |  | 1 | 1 |
| 330 | -6.755 | -2.610 | -7.121 | -7.728 | -8.589 | -3.567 | 17.239 | 16.378 | 21.401 | 16.135 | 20.280 | 15.769 | 27.965 | 21.970 | 22.752 | 23.028 |  | 11 | 11 |
| 331 | -6.938 | -2.760 | -0.843 | -5.572 | -0.954 | -7.369 | 18.969 | 23.587 | 17.172 | 16.608 | 20.786 | 22.704 | 25.481 | 23.601 | 25.826 | 21.267 |  | 8 | 8 |
| 332 | 0.657 | 3.242 | 1.452 | 0.207 | 0.200 | 1.592 | 23.977 | 23.970 | 25.362 | 24.320 | 26.905 | 25.116 | 24.437 | 23.103 | 25.914 | 21.412 |  | 14 | 14 |
| 333 | -0.507 | -0.782 | -5.013 | 0.690 | -5.653 | -4.682 | 24.299 | 17.956 | 18.927 | 22.471 | 22.196 | 17.966 | 26.801 | 20.417 | 25.062 | 20.894 |  | 18 | 18 |
| 334 | -0.428 | 1.060 | -4.772 | -3.120 | -2.157 | -2.185 | 21.062 | 22.025 | 21.997 | 20.979 | 22.466 | 16.634 | 26.039 | 22.324 | 24.234 | 18.578 |  | 10 | 10 |
| 335 | -4.044 | -3.982 | -4.226 | -7.389 | -6.051 | -2.066 | 15.281 | 16.620 | 20.604 | 17.328 | 17.390 | 17.146 | 24.375 | 20.965 | 21.197 | 21.548 |  | 4 | 4 |
| 336 | 3.698 | 2.745 | 8.454 | 3.663 | 2.912 | 5.077 | 23.746 | 22.995 | 25.159 | 19.645 | 18.692 | 24.402 | 20.053 | 20.112 | 17.629 | 14.265 |  | 9 | 9 |
| 337 | -3.738 | 3.919 | -3.178 | -3.149 | -0.957 | -2.071 | 22.090 | 24.282 | 23.167 | 21.157 | 28.813 | 21.716 | 26.160 | 24.318 | 26.750 | 23.038 |  | 25 | 25 |
| 338 | -0.912 | 0.370 | 0.393 | -1.824 | -1.103 | -0.391 | 25.063 | 25.784 | 26.497 | 24.647 | 25.929 | 25.951 | 28.318 | 25.456 | 27.617 | 23.501 |  | 10 | 10 |

|  | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 307 | 17 | 34.7 | 84.787 | 207.97 | 25.598 | 24.711 | **0.551** | **1.260** | P07901;B7ZC50;A2A6A2;B7ZC49 | P07901 | Heat shock protein HSP 90-alpha | **Hsp90aa1** | 572 |
| 308 | 13 | 33.3 | 47.411 | 114.65 | 23.897 | 22.210 | **1.435** | **1.260** | P05202 | P05202 | Aspartate aminotransferase, mitochondrial | **Got2** | 562 |
| 309 | 19 | 52.7 | 46.153 | 266.74 | 27.173 | 26.551 | **1.146** | **1.254** | P60843;Q8BTU6;P10630;P10630-2;E9Q561;D6RJ60;D6RJ11 | P60843 | Eukaryotic initiation factor 4A-I | **Eif4a1** | 788 |
| 310 | 5 | 34.2 | 16.101 | 38.79 | 24.972 | 22.106 | **0.298** | **1.247** | P12787 | P12787 | Cytochrome c oxidase subunit 5A, mitochondrial | **Cox5a** | 603 |
| 311 | 1 | 0.8 | 130.34 | 6.491 | 23.117 | 19.902 | **0.739** | **1.246** | A2A934;A2A930;A2A931;A2A933;A2A935-2;A2A935;A2A935-3 | A2A934;A2A930;A2A931;A2A933;A2A935-2;A2A935;A2A935-3 | PR domain zinc finger protein 16 | **Prdm16** | 134 |
| 312 | 2 | 5.1 | 57.428 | 14.797 | 20.074 | 19.668 | **0.271** | **1.246** | Q925I1-2;Q925I1 | Q925I1-2;Q925I1 | ATPase family AAA domain-containing protein 3 | **Atad3** | 1289 |
| 313 | 39 | 46.3 | 89.321 | 323.31 | 27.919 | 26.380 | **0.143** | **1.246** | Q01853 | Q01853 | Transitional endoplasmic reticulum ATPase | **Vcp** | 921 |
| 314 | 7 | 41.7 | 22.395 | 48.908 | 21.131 | 20.214 | **0.466** | **1.230** | Q9WVA4;A0A0A6YXG6;Q9R1Q8 | Q9WVA4 | Transgelin-2 | **Tagln2** | 1549 |
| 315 | 6 | 10.8 | 88.231 | 43.829 | 21.270 | 23.168 | **0.304** | **1.224** | P09055;P09055-2 | P09055;P09055-2 | Integrin beta-1 | **Itgb1** | 580 |
| 316 | 12 | 19.5 | 102.71 | 85.643 | 24.758 | 23.158 | **0.261** | **1.211** | P46935;Q3V335;V9GWV8;V9GXK3;G3X9H8;Q8CFI0-2 | P46935 | E3 ubiquitin-protein ligase NEDD4 | **Nedd4** | 720 |
| 317 | 2 | 25.3 | 10.561 | 22.089 | 18.347 | 16.245 | **0.434** | **1.206** | P58059;D3YVZ9 | P58059;D3YVZ9 | 28S ribosomal protein S21, mitochondrial | **Mrps21** | 773 |
| 318 | 7 | 47.9 | 19.53 | 56.125 | 25.377 | 24.269 | **0.240** | **1.201** | P19783;M0QWX7 | P19783 | Cytochrome c oxidase subunit 4 isoform 1, mitochondrial | **Cox4i1** | 638 |
| 319 | 5 | 5 | 132.35 | 35.344 | 23.793 | 21.869 | **0.241** | **1.198** | F8WHM5;Q61543;E9PWD8;F6RSH1 | F8WHM5;Q61543 | Golgi apparatus protein 1 | **Glg1** | 441 |
| 320 | 7 | 3.5 | 244.54 | 42.735 | 18.234 | 18.385 | **0.158** | **1.185** | Q6P4T2 | Q6P4T2 | U5 small nuclear ribonucleoprotein 200 kDa helicase | **Snrnp200** | 1090 |
| 321 | 12 | 54.3 | 17.971 | 285.47 | 30.410 | 28.674 | **1.241** | **1.180** | P17742;F8VPN3;V9GXC1;V9GX31 | P17742;F8VPN3 | Peptidyl-prolyl cis-trans isomerase A;Peptidyl-prolyl cis-trans isomerase A, N-terminally processed;Peptidyl-prolyl cis-trans isomerase | **Ppia;Gm5160** | 627 |
| 322 | 6 | 5.5 | 181.91 | 39.574 | 16.356 | 18.437 | **0.232** | **1.174** | Q64511 | Q64511 | DNA topoisomerase 2-beta | **Top2b** | 1080 |
| 323 | 11 | 50.7 | 23.363 | 137.17 | 25.257 | 23.430 | **0.346** | **1.174** | Q9DB20;F6XVM5;F7D3P8 | Q9DB20 | ATP synthase subunit O, mitochondrial | **Atp5o** | 1458 |
| 324 | 15 | 41.2 | 44.55 | 156.28 | 25.947 | 25.229 | **0.893** | **1.170** | P09411;S4R2M7;P09041 | P09411;S4R2M7 | Phosphoglycerate kinase 1;Phosphoglycerate kinase | **Pgk1** | 583 |
| 325 | 12 | 16.6 | 100.11 | 107.53 | 23.496 | 22.370 | **1.051** | **1.170** | P26231;E0CXB9;Q65CL1;Q61301-2;Q61301-3;Q61301 | P26231 | Catenin alpha-1 | **Ctnna1** | 661 |
| 326 | 3 | 20.9 | 13.015 | 29.23 | 25.473 | 24.125 | **1.427** | **1.161** | P62855 | P62855 | 40S ribosomal protein S26 | **Rps26** | 838 |
| 327 | 2 | 16.1 | 13.608 | 87.137 | 17.117 | 16.334 | **0.598** | **1.155** | Q9CQA6 | Q9CQA6 | Coiled-coil-helix-coiled-coil-helix domain-containing protein 1 | **Chchd1** | 1338 |
| 328 | 3 | 34.5 | 42.161 | 96.954 | 17.018 | 18.479 | **0.132** | **1.151** | Q91VM5;S4R1F6 | Q91VM5 | RNA binding motif protein, X-linked-like-1 | **Rbmxl1** | 1265 |
| 329 | 1 | 11.7 | 8.0515 | 6.7807 | 17.565 | 16.325 | **0.224** | **1.147** | A0A0J9YTR7;Q9Z126 | A0A0J9YTR7;Q9Z126 | Platelet factor 4 | **Pf4** | 56 |
| 330 | 11 | 15.8 | 117.53 | 95.087 | 24.967 | 22.890 | **0.207** | **1.133** | Q8BKG3 | Q8BKG3 | Inactive tyrosine-protein kinase 7 | **Ptk7** | 1170 |
| 331 | 7 | 17.2 | 63.45 | 54.484 | 24.541 | 23.547 | **0.160** | **1.118** | O88477 | O88477 | Insulin-like growth factor 2 mRNA-binding protein 1 | **Igf2bp1** | 543 |
| 332 | 12 | 37.9 | 24.233 | 109.65 | 23.770 | 23.663 | **0.554** | **1.117** | A0A0J9YUZ4;P63158;A0A0J9YUD8;D3YVC6;D3YZ18 | A0A0J9YUZ4;P63158;A0A0J9YUD8;D3YVC6;D3YZ18 | High mobility group protein B1 | **Hmgb1** | 63 |
| 333 | 18 | 16.7 | 604.25 | 109.94 | 23.609 | 22.978 | **0.172** | **1.114** | E9Q616 | E9Q616 | AHNAK nucleoprotein | **Ahnak** | 387 |
| 334 | 10 | 12.3 | 110.33 | 65.623 | 24.182 | 21.406 | **0.246** | **1.107** | Q02788;D3Z7D5 | Q02788;D3Z7D5 | Collagen alpha-2(VI) chain | **Col6a2** | 926 |
| 335 | 4 | 32.1 | 23.897 | 39.95 | 22.670 | 21.372 | **0.272** | **1.085** | Q91V41;A2AL34 | Q91V41;A2AL34 | Ras-related protein Rab-14 | **Rab14** | 1259 |
| 336 | 9 | 3.2 | 332.91 | 59.721 | 20.083 | 15.947 | **0.225** | **1.082** | E9Q557;E9PZW0 | E9Q557;E9PZW0 | Desmoplakin | **Dsp** | 382 |
| 337 | 25 | 6.3 | 532.04 | 160.14 | 25.239 | 24.894 | **0.156** | **1.060** | Q9JHU4;F6ZX84 | Q9JHU4 | Cytoplasmic dynein 1 heavy chain 1 | **Dync1h1** | 1493 |
| 338 | 10 | 31.3 | 28.68 | 119.95 | 26.887 | 25.559 | **0.819** | **1.056** | P62754 | P62754 | 40S ribosomal protein S6 | **Rps6** | 828 |

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 339 | 2.163 | 1.653 | -0.119 | 2.264 | -0.095 | -1.622 | 25.726 | 23.366 | 21.839 | 25.709 | 25.199 | 23.427 | 24.998 | 21.925 | 24.650 | 22.442 | | 6 | 6 |
| 340 | -6.695 | 0.866 | -0.279 | -3.903 | -6.432 | 1.101 | 18.635 | 16.106 | 23.640 | 14.648 | 22.209 | 21.064 | 23.724 | 21.353 | 23.467 | 19.218 | | 4 | 4 |
| 341 | 1.570 | 1.736 | 0.609 | 0.470 | 0.829 | -0.495 | 25.487 | 25.846 | 24.522 | 25.011 | 25.177 | 24.049 | 26.628 | 23.406 | 27.034 | 19.848 | | 46 | 46 |
| 342 | 6.209 | 7.681 | 7.602 | 4.620 | 6.759 | 7.027 | 23.190 | 25.330 | 25.597 | 22.655 | 24.128 | 24.048 | 18.407 | 18.733 | 17.793 | 15.100 | | 6 | 6 |
| 343 | -2.845 | 8.936 | 7.162 | 1.020 | 2.558 | 6.616 | 16.698 | 18.236 | 22.294 | 13.608 | 25.389 | 23.615 | 16.060 | 15.296 | 19.447 | 13.461 | | 4 | 4 |
| 344 | -10.034 | -3.618 | -4.490 | -6.719 | -10.673 | -3.783 | 20.919 | 16.965 | 23.855 | 16.459 | 22.875 | 22.003 | 29.580 | 25.696 | 27.297 | 25.689 | | 24 | 24 |
| 345 | -2.595 | 7.234 | 4.902 | -0.308 | 2.264 | 4.580 | 15.995 | 18.567 | 20.882 | 15.697 | 25.526 | 23.194 | 16.822 | 15.783 | 21.825 | 14.759 | | 7 | 7 |
| 346 | 3.913 | 6.991 | 4.963 | 4.706 | 3.515 | 4.645 | 22.784 | 21.593 | 22.722 | 22.980 | 26.058 | 24.029 | 16.874 | 19.281 | 22.752 | 15.381 | | 9 | 9 |
| 347 | -2.010 | -1.282 | -1.626 | -2.728 | -2.769 | -2.421 | 27.401 | 27.359 | 27.708 | 26.893 | 27.621 | 27.277 | 31.203 | 29.054 | 30.319 | 27.487 | + | 37 | 37 |
| 348 | -4.432 | 2.313 | 1.120 | -1.206 | -1.863 | -0.887 | 17.235 | 16.578 | 17.555 | 14.783 | 21.528 | 20.335 | 21.422 | 15.461 | 17.465 | 20.965 | | 2 | 2 |
| 349 | 4.310 | 3.139 | 3.872 | 2.713 | 2.826 | 2.851 | 28.411 | 28.524 | 28.549 | 28.820 | 27.648 | 28.381 | 27.319 | 24.078 | 26.581 | 22.438 | + | 23 | 23 |
| 350 | 0.116 | 0.878 | 1.306 | -1.263 | 0.837 | -0.191 | 21.387 | 23.487 | 22.459 | 21.215 | 21.977 | 22.405 | 24.811 | 20.489 | 22.858 | 19.340 | | 4 | 4 |
| 351 | -3.264 | -3.397 | -3.167 | -8.239 | -3.694 | -0.776 | 17.180 | 21.725 | 24.642 | 21.600 | 21.467 | 21.697 | 28.692 | 22.145 | 26.841 | 22.887 | | 19 | 19 |
| 352 | -1.313 | -0.249 | 0.247 | -0.155 | -0.831 | -3.175 | 26.319 | 25.643 | 23.299 | 24.216 | 25.280 | 25.777 | 28.093 | 24.855 | 28.034 | 23.026 | | 12 | 12 |
| 353 | -0.660 | 0.786 | -0.093 | -1.128 | -1.006 | -0.677 | 28.897 | 29.019 | 29.348 | 28.222 | 29.668 | 28.789 | 31.250 | 28.800 | 29.895 | 27.869 | | 20 | 20 |
| 354 | 10.318 | 7.513 | 8.865 | 9.107 | 7.940 | 6.826 | 31.132 | 29.964 | 28.851 | 29.655 | 26.851 | 28.202 | 24.439 | 19.610 | 20.450 | 18.225 | | 4 | 4 |
| 355 | 3.210 | 6.468 | 4.612 | 3.405 | 4.350 | 3.742 | 25.480 | 26.425 | 25.817 | 23.821 | 27.079 | 25.223 | 19.448 | 24.702 | 26.761 | 14.462 | | 18 | 18 |
| 356 | -4.854 | -0.642 | -5.101 | -7.478 | -3.497 | -2.369 | 17.037 | 21.018 | 22.146 | 17.518 | 21.729 | 17.271 | 26.714 | 22.315 | 22.085 | 22.659 | | 4 | 4 |
| 357 | -1.999 | 4.783 | 3.788 | 0.298 | 1.744 | 1.790 | 16.486 | 17.932 | 17.978 | 15.044 | 21.826 | 20.832 | 17.109 | 15.267 | 17.552 | 16.535 | | 2 | 2 |
| 358 | -1.712 | -0.545 | -2.203 | -2.238 | -2.526 | -2.417 | 24.700 | 24.413 | 24.521 | 23.809 | 24.977 | 23.318 | 28.347 | 25.530 | 27.416 | 23.627 | | 21 | 21 |
| 359 | -8.019 | -0.978 | -1.623 | -9.994 | -1.611 | -1.710 | 14.993 | 23.376 | 23.277 | 15.689 | 22.730 | 22.085 | 27.307 | 22.667 | 25.508 | 21.908 | | 7 | 7 |
| 360 | -4.089 | 3.361 | -3.112 | -6.297 | -0.666 | 0.453 | 15.821 | 21.452 | 22.571 | 17.264 | 24.714 | 18.241 | 23.527 | 20.709 | 23.587 | 19.118 | | 1 | 1 |
| 361 | -3.516 | 2.617 | 0.751 | -0.915 | -0.764 | -1.131 | 22.490 | 22.642 | 22.274 | 19.964 | 26.096 | 24.231 | 22.931 | 23.880 | 25.299 | 21.660 | | 10 | 8 |
| 362 | -1.509 | 0.259 | 0.076 | -1.874 | -0.992 | -0.875 | 27.774 | 28.655 | 28.772 | 27.122 | 28.890 | 28.706 | 31.183 | 28.111 | 30.461 | 26.801 | | 39 | 37 |
| 363 | -1.918 | -0.044 | 0.457 | -1.876 | -1.581 | -0.609 | 27.006 | 27.301 | 28.273 | 25.508 | 27.382 | 27.883 | 30.636 | 27.128 | 29.299 | 25.553 | | 47 | 47 |
| 364 | 5.377 | 7.210 | 5.418 | 4.130 | 5.555 | 5.815 | 22.912 | 24.337 | 24.597 | 24.661 | 26.494 | 24.701 | 17.389 | 20.175 | 25.169 | 13.399 | | 6 | 6 |

|  | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 339 | 6 | 39.1 | 17.951 | 88.268 | 23.462 | 23.546 | **0.326** | **1.050** | P62983;A0A0A6YW67;E9Q9J0;E9Q4P0;E9Q5F6;E9QNP0;Q5SX22;P62984;P0CG49;P0CG50;J3QK04;D3YYZ2 | P62983;A0A0A6YW67;E9Q9J0;E9Q4P0;E9Q5F6;E9QNP0;Q5SX22;P62984;P0CG49;P0CG50;J3QK04 | Ubiquitin-40S ribosomal protein S27a;Ubiquitin;40S ribosomal protein S27a;Ubiquitin-60S ribosomal protein L40;Ubiquitin;60S ribosomal protein L40;Polyubiquitin-B;Ubiquitin;Polyubiquitin-C;Ubiquitin;Ubiquitin-related 1;Ubiquitin-related 2 | **Rps27a;Gm8797;Uba52;Kxd1;Ubc;Ubb;Gm7808** | 852 |
| 340 | 4 | 6.5 | 74.406 | 28.686 | 22.538 | 21.343 | **0.117** | **1.042** | F6ZEW4;E9Q1T9;Q9ERK4;E9QAX7 | F6ZEW4;E9Q1T9;Q9ERK4;E9QAX7 | Exportin-2 | **Cse1l** | 370 |
| 341 | 37 | 24.8 | 226.37 | 301.77 | 25.017 | 23.441 | **0.915** | **1.037** | Q8VDD5;F2Z494 | Q8VDD5 | Myosin-9 | **Myh9** | 1249 |
| 342 | 6 | 35.6 | 20.139 | 44.245 | 18.570 | 16.446 | **0.500** | **1.028** | Q80X32 | Q80X32 | UPF0461 protein C5orf24 homolog |  | 1131 |
| 343 | 4 | 11.3 | 47.756 | 25.43 | 15.678 | 16.454 | **0.090** | **1.019** | P32067;A2AR07;D6RI87;F6SXM5 | P32067;A2AR07;D6RI87 | Lupus La protein homolog | **Ssb** | 683 |
| 344 | 24 | 41.8 | 57.058 | 314.89 | 27.638 | 26.493 | **0.131** | **1.011** | P09103;E9Q8G8 | P09103 | Protein disulfide-isomerase | **P4hb** | 581 |
| 345 | 7 | 10.2 | 96.735 | 43.174 | 16.302 | 18.292 | **0.110** | **1.001** | P49717;Q9CWV1-2;Q9CWV1 | P49717 | DNA replication licensing factor MCM4 | **Mcm4** | 735 |
| 346 | 8 | 39.1 | 28.329 | 63.04 | 18.078 | 19.067 | **0.436** | **1.001** | H7BX95;Q6PDM2;Q6PDM2-3;Q6PDM2-2;F7AI47 | H7BX95;Q6PDM2;Q6PDM2-3;Q6PDM2-2 | Serine/arginine-rich splicing factor 1 | **Srsf1** | 486 |
| 347 | 37 | 58.2 | 57.844 | 323.31 | 30.128 | 28.903 | **1.868** | **1.000** | P52480;P52480-2;E9Q509;G3X925;P53657 | P52480;P52480-2 | Pyruvate kinase PKM | **Pkm** | 748 |
| 348 | 2 | 3.1 | 117.82 | 12.66 | 18.441 | 19.215 | **0.179** | **0.986** | P11087-2;P11087 | P11087-2;P11087 | Collagen alpha-1(I) chain | **Col1a1** | 596 |
| 349 | 23 | 56.7 | 22.591 | 166.18 | 25.698 | 24.510 | **1.328** | **0.977** | Q6ZWN5;F7CJS8;D3YWH9;Q9CXW7;D3Z673;D3YUV6 | Q6ZWN5;F7CJS8;D3YWH9;Q9CXW7 | 40S ribosomal protein S9 | **Rps9** | 1109 |
| 350 | 4 | 17.9 | 22.23 | 28.944 | 22.650 | 21.099 | **0.626** | **0.972** | Q9D2G2-2;Q9D2G2 | Q9D2G2-2;Q9D2G2 | Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial | **Dlst** | 1431 |
| 351 | 19 | 32.2 | 75.288 | 141.91 | 25.419 | 24.864 | **0.167** | **0.960** | F8WIT2;P14824 | F8WIT2;P14824 | Annexin;Annexin A6 | **Anxa6** | 444 |
| 352 | 12 | 41.9 | 23.464 | 96.631 | 26.474 | 25.530 | **0.391** | **0.949** | P19253;A0A140T8K2 | P19253 | 60S ribosomal protein L13a | **Rpl13a** | 635 |
| 353 | 20 | 53.5 | 35.81 | 323.31 | 30.025 | 28.882 | **1.007** | **0.948** | P16858;S4R1W1;A0A0A0MQF6;S4R257;D3YYI5;S4R1W8;S4R1N5;V9GX06;V9GXA7;A0A0R4J0X7;S4R2G5;Q64467 | P16858;S4R1W1;A0A0A0MQF6;S4R257;D3YYI5 | Glyceraldehyde-3-phosphate dehydrogenase | **Gapdh;Gm3839;Gm7293** | 623 |
| 354 | 4 | 53.6 | 6.6767 | 205.85 | 22.025 | 19.338 | **0.379** | **0.941** | P62274;D3YYL7 | P62274 | 40S ribosomal protein S29 | **Rps29** | 818 |
| 355 | 16 | 26.9 | 75.441 | 144.4 | 22.075 | 20.611 | **0.401** | **0.931** | Q8VIJ6 | Q8VIJ6 | Splicing factor, proline- and glutamine-rich | **Sfpq** | 1258 |
| 356 | 4 | 43.2 | 13.426 | 30.935 | 24.515 | 22.372 | **0.162** | **0.915** | A0A0G2JDL9;Q99JI6;P62835;A0A0G2JED9;A0A0G2JE52 | A0A0G2JDL9;Q99JI6;P62835;A0A0G2JED9;A0A0G2JE52 | Ras-related protein Rap-1b;Ras-related protein Rap-1A | **Rap1b;Rap1a** | 40 |
| 357 | 2 | 9.1 | 28.659 | 13.359 | 16.188 | 17.044 | **0.158** | **0.913** | A0A0U1RNM2;A1L3S7;Q8VHR5;Q8VHR5-2 | A0A0U1RNM2;A1L3S7;Q8VHR5;Q8VHR5-2 | Transcriptional repressor p66-beta | **Gatad2b** | 102 |
| 358 | 21 | 41.7 | 60.448 | 164.23 | 26.939 | 25.521 | **0.844** | **0.907** | P11983;P11983-2;F2Z483 | P11983;P11983-2 | T-complex protein 1 subunit alpha | **Tcp1** | 601 |
| 359 | 7 | 23.6 | 49.027 | 68.382 | 24.987 | 23.708 | **0.089** | **0.898** | O54734 | O54734 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit | **Ddost** | 523 |
| 360 | 1 | 25.5 | 5.2631 | 14.867 | 22.118 | 21.353 | **0.102** | **0.890** | G3UZX6;H7BWX9;D3Z794;G3UZ60;G3UWI9;G3UWX9;G3UZA7;P61957;Q9Z172-2;Q9Z172 | G3UZX6;H7BWX9;D3Z794;G3UZ60;G3UWI9;G3UWX9;G3UZA7;P61957;Q9Z172-2;Q9Z172 | Small ubiquitin-related modifier;Small ubiquitin-related modifier 2;Small ubiquitin-related modifier 3 | **Sumo3;Sumo2** | 314 |
| 361 | 8 | 30.1 | 45.729 | 70.83 | 23.406 | 23.480 | **0.186** | **0.887** | Q9Z2X1;Q9Z2X1-2;J3QM80;J3QMT0;J3QNH2;J3QMV8;J3QP45 | Q9Z2X1;Q9Z2X1-2;J3QM80;J3QMT0 | Heterogeneous nuclear ribonucleoprotein F;Heterogeneous nuclear ribonucleoprotein F, N-terminally processed | **Hnrnpf** | 1575 |
| 362 | 33 | 51.7 | 70.87 | 323.31 | 29.647 | 28.631 | **0.594** | **0.856** | P63017;Q504P4;D3Z5E2;D3YW43;P17156 | P63017;Q504P4 | Heat shock cognate 71 kDa protein | **Hspa8** | 855 |
| 363 | 33 | 47.2 | 83.28 | 323.31 | 28.882 | 27.426 | **0.449** | **0.853** | P11499;E9Q3D6;E9Q0C3;E9PX27;D3Z1R1 | P11499 | Heat shock protein HSP 90-beta | **Hsp90ab1** | 598 |
| 364 | 6 | 36.9 | 17.89 | 46.372 | 18.782 | 19.284 | **0.449** | **0.835** | Q8BL97-3;Q8BL97-4;Q8BL97-2;Q8BL97 | Q8BL97-3;Q8BL97-4;Q8BL97-2;Q8BL97 | Serine/arginine-rich splicing factor 7 | **Srsf7** | 1171 |

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 365 | 0.141 | 2.770 | 1.519 | 0.259 | 1.053 | 0.629 | 27.511 | 28.305 | 27.882 | 26.580 | 29.210 | 27.958 | 26.008 | 28.497 | 29.418 | 23.460 | | 24 | 24 |
| 366 | -2.293 | -2.158 | -1.413 | -3.090 | -2.766 | -2.496 | 26.062 | 26.387 | 26.656 | 25.303 | 25.438 | 26.183 | 30.573 | 27.732 | 29.352 | 25.841 | | 12 | 12 |
| 367 | -5.207 | -3.321 | -2.466 | -5.015 | -4.322 | -4.134 | 24.669 | 25.363 | 25.550 | 23.151 | 25.036 | 25.892 | 31.048 | 28.320 | 29.198 | 27.517 | | 42 | 42 |
| 368 | 3.675 | 2.056 | 2.396 | 2.654 | 1.555 | 1.452 | 27.674 | 26.576 | 26.472 | 27.525 | 25.905 | 26.245 | 26.574 | 23.467 | 25.231 | 22.468 | | 8 | 8 |
| 369 | 0.108 | -0.891 | -2.038 | -5.181 | 0.174 | -0.215 | 15.415 | 20.769 | 20.381 | 18.200 | 17.202 | 16.055 | 24.439 | 16.753 | 22.459 | 13.726 | | 2 | 2 |
| 370 | -5.714 | 1.445 | -4.320 | -0.799 | -5.921 | -4.265 | 21.375 | 16.252 | 17.909 | 15.368 | 22.528 | 16.762 | 23.453 | 20.894 | 23.783 | 18.382 | | 2 | 2 |
| 371 | -7.470 | -1.160 | -7.382 | -6.897 | -6.205 | -5.297 | 17.954 | 18.645 | 19.553 | 16.501 | 22.811 | 16.589 | 26.297 | 23.404 | 25.123 | 22.820 | | 3 | 2 |
| 372 | -2.629 | -1.044 | -1.555 | -3.405 | -1.751 | -2.449 | 25.720 | 27.375 | 26.676 | 25.025 | 26.610 | 26.099 | 30.449 | 27.802 | 28.865 | 26.444 | | 26 | 26 |
| 373 | -1.404 | -0.349 | -0.163 | -0.974 | -1.141 | -2.158 | 25.852 | 25.685 | 24.668 | 24.154 | 25.209 | 25.395 | 27.542 | 26.110 | 27.012 | 24.104 | | 6 | 6 |
| 374 | 12.849 | 10.191 | 11.391 | 10.093 | 10.067 | 11.913 | 28.218 | 28.192 | 30.038 | 29.577 | 26.920 | 28.120 | 20.597 | 15.653 | 19.019 | 14.439 | | 12 | 12 |
| 375 | -0.648 | 1.376 | 0.348 | -0.783 | -0.224 | -0.227 | 25.392 | 25.951 | 25.949 | 24.771 | 26.795 | 25.767 | 27.716 | 24.635 | 26.781 | 24.057 | | 11 | 11 |
| 376 | -6.378 | -4.249 | -4.641 | -2.547 | -6.562 | -8.458 | 23.570 | 19.555 | 17.659 | 15.993 | 18.122 | 17.730 | 27.284 | 24.950 | 20.386 | 24.356 | | 11 | 11 |
| 377 | -4.006 | -2.282 | 0.333 | -2.107 | -3.468 | -2.634 | 17.871 | 16.510 | 17.344 | 16.561 | 18.285 | 20.899 | 23.909 | 16.046 | 21.682 | 19.451 | | 4 | 4 |
| 378 | -1.977 | -0.511 | -1.684 | -2.617 | -1.903 | -1.905 | 24.101 | 24.815 | 24.813 | 23.748 | 25.214 | 24.041 | 29.245 | 24.192 | 27.619 | 23.831 | | 8 | 8 |
| 379 | -4.309 | -1.767 | -1.570 | -4.905 | -3.223 | -1.756 | 22.854 | 24.536 | 26.003 | 22.278 | 24.819 | 25.016 | 30.070 | 25.448 | 27.769 | 25.405 | | 35 | 33 |
| 380 | -2.834 | -2.188 | -0.616 | -2.387 | -2.378 | -3.108 | 24.358 | 24.367 | 23.636 | 21.832 | 22.478 | 24.050 | 29.272 | 24.217 | 27.177 | 22.155 | | 15 | 15 |
| 381 | -1.246 | -0.740 | -1.382 | -3.232 | -2.029 | -0.339 | 17.097 | 18.300 | 19.989 | 17.353 | 17.859 | 17.217 | 25.317 | 15.341 | 19.662 | 17.535 | | 3 | 3 |
| 382 | 6.941 | 6.206 | 5.156 | 4.766 | 5.670 | 5.650 | 30.860 | 31.765 | 31.744 | 31.242 | 30.507 | 29.456 | 28.485 | 23.704 | 27.475 | 21.127 | | 15 | 15 |
| 383 | 1.178 | 2.558 | 2.122 | -0.051 | 1.735 | 1.963 | 24.268 | 26.054 | 26.282 | 24.112 | 25.492 | 25.056 | 25.888 | 22.750 | 25.261 | 20.606 | | 1 | 1 |
| 384 | -0.340 | -1.099 | -1.099 | -0.642 | -2.079 | -2.025 | 27.252 | 25.814 | 25.868 | 26.300 | 25.541 | 25.541 | 28.946 | 26.842 | 28.470 | 24.811 | | 18 | 18 |
| 385 | -0.826 | 0.570 | 0.771 | -0.626 | 0.004 | -1.066 | 24.038 | 24.667 | 23.597 | 23.754 | 25.151 | 25.352 | 28.211 | 21.116 | 26.965 | 22.196 | | 13 | 13 |
| 386 | 1.998 | 1.179 | 1.044 | 0.574 | 0.988 | 0.461 | 26.471 | 26.886 | 26.358 | 26.608 | 25.789 | 25.654 | 27.431 | 24.364 | 26.363 | 22.857 | | 11 | 11 |
| 387 | -7.674 | -1.325 | -7.263 | -7.377 | -6.692 | -4.363 | 17.861 | 18.546 | 20.875 | 16.709 | 23.059 | 17.120 | 27.865 | 22.611 | 26.244 | 22.523 | | 12 | 12 |
| 388 | -2.038 | -1.683 | -0.811 | -2.832 | -2.294 | -1.553 | 22.200 | 22.738 | 23.479 | 21.756 | 22.111 | 22.983 | 27.800 | 22.264 | 24.733 | 22.854 | | 16 | 16 |
| 389 | -3.782 | -7.093 | -1.600 | -4.015 | -6.589 | -4.009 | 23.067 | 20.493 | 23.073 | 21.073 | 17.763 | 23.255 | 28.593 | 25.570 | 25.390 | 24.321 | | 7 | 7 |
| 390 | 13.579 | 6.394 | 8.950 | 12.526 | 7.942 | 6.331 | 30.000 | 25.417 | 23.805 | 29.161 | 21.977 | 24.532 | 18.542 | 16.407 | 16.844 | 14.320 | | 6 | 6 |
| 391 | -0.348 | 4.220 | 2.304 | -0.527 | 2.879 | 1.702 | 20.367 | 23.772 | 22.595 | 20.401 | 24.968 | 23.053 | 25.681 | 16.106 | 22.272 | 19.225 | | 12 | 12 |
| 392 | 3.544 | 2.516 | 2.164 | 3.093 | 0.707 | 2.313 | 28.257 | 25.871 | 27.477 | 27.792 | 26.764 | 26.412 | 26.724 | 23.604 | 26.455 | 22.040 | | 9 | 9 |

| | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 365 | 24 | 56.3 | 48.51 | 282.39 | 27.252 | 26.439 | **0.450** | **0.829** | P61979-3;P61979;B2M1R6;P61979-2;H3BLL4;H3BKD0;H3BK96;H3BKI8;H3BLP7;Q8BT23;H3BJ43;H3BJS9 | P61979-3;P61979;B2M1R6;P61979-2;H3BLL4;H3BKD0;H3BK96 | Heterogeneous nuclear ribonucleoprotein K | **Hnrnpk** | 803 |
| 366 | 11 | 54.7 | 18.927 | 191.07 | 29.153 | 27.597 | **1.206** | **0.829** | B1AXW5;B1AXW6;P35700;B1AXW4 | B1AXW5;B1AXW6;P35700;B1AXW4 | Peroxiredoxin-1 | **Prdx1** | 201 |
| 367 | 40 | 58 | 72.421 | 323.31 | 29.684 | 28.358 | **0.411** | **0.826** | P20029 | P20029 | 78 kDa glucose-regulated protein | **Hspa5** | 639 |
| 368 | 8 | 38.5 | 15.807 | 57.497 | 25.020 | 23.849 | **0.587** | **0.822** | P62267 | P62267 | 40S ribosomal protein S23 | **Rps23** | 817 |
| 369 | 2 | 8.9 | 28.127 | 14.028 | 20.596 | 18.092 | **0.165** | **0.801** | P20108 | P20108 | Thioredoxin-dependent peroxide reductase, mitochondrial | **Prdx3** | 641 |
| 370 | 2 | 2.5 | 91.736 | 16.741 | 22.174 | 21.083 | **0.108** | **0.799** | Q3TKD0;Q99LG2;Q8BFY9-2;Q8BFY9;J3QMX2;E9PV58 | Q3TKD0;Q99LG2;Q8BFY9-2;Q8BFY9;J3QMX2;E9PV58 | Transportin-2;Transportin-1 | **Tnpo1;Tnpo2** | 955 |
| 371 | 2 | 17 | 22.541 | 21.74 | 24.850 | 23.971 | **0.137** | **0.796** | P61027 | P61027 | Ras-related protein Rab-10 | **Rab10** | 790 |
| 372 | 26 | 71.9 | 47.14 | 323.31 | 29.125 | 27.654 | **0.520** | **0.792** | P17182;Q6PHC1;B1ARR7;B0QZL1;B1ARR6;A0A0N4SUI6;A0A0N4SUX5;D3Z6E4;D3Z2S4;D3YVD3;P17183;P21550;J3QPZ9;Q5SX59;Q5SX60;Q5SX61;A0A0N4SUW8 | P17182;Q6PHC1 | Alpha-enolase | **Eno1** | 626 |
| 373 | 6 | 17.9 | 13.293 | 52.191 | 26.826 | 25.558 | **0.666** | **0.786** | Q9D1R9;A0A0G2JGY8;A0A0G2JEY6;D3YWC0 | Q9D1R9 | 60S ribosomal protein L34 | **Rpl34** | 1429 |
| 374 | 12 | 33.9 | 36.198 | 142.28 | 18.125 | 16.729 | **0.329** | **0.786** | A0A075B5P5;P03987-2;P03987 | A0A075B5P5;P03987-2;P03987 | Ig gamma-3 chain C region | **Ighg3** | 10 |
| 375 | 11 | 44.4 | 24.423 | 107.23 | 26.175 | 25.419 | **0.557** | **0.770** | P62827;Q14AA6;Q61820 | P62827;Q14AA6 | GTP-binding nuclear protein Ran | **Ran;1700009N14Rik** | 833 |
| 376 | 11 | 20.3 | 72.585 | 115.32 | 26.117 | 22.371 | **0.154** | **0.766** | Q8K2B3 | Q8K2B3 | Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial | **Sdha** | 1224 |
| 377 | 4 | 12.4 | 37.063 | 22.797 | 19.978 | 20.567 | **0.222** | **0.751** | O35887;G3UY49;G3UWR0;G3UWV3;Q6XLQ8;G3V004;G3UXA8 | O35887;G3UY49;G3UWR0;G3UWV3;Q6XLQ8 | Calumenin | **Calu** | 520 |
| 378 | 8 | 37.4 | 21.778 | 131.77 | 26.718 | 25.725 | **0.672** | **0.751** | Q61171;D3Z4A4 | Q61171;D3Z4A4 | Peroxiredoxin-2 | **Prdx2** | 1036 |
| 379 | 33 | 40.8 | 92.475 | 323.31 | 27.759 | 26.587 | **0.231** | **0.746** | P08113;F7C312 | P08113;F7C312 | Endoplasmin | **Hsp90b1** | 574 |
| 380 | 15 | 48.5 | 35.611 | 229.94 | 26.745 | 24.666 | **0.458** | **0.745** | P08249;A0A0G2JF23;A0A0G2JGY4 | P08249 | Malate dehydrogenase, mitochondrial | **Mdh2** | 577 |
| 381 | 3 | 7.2 | 68.721 | 20.855 | 20.329 | 18.598 | **0.360** | **0.744** | Q8JZN5;A0A0G2JDY4;A0A0G2JF25 | Q8JZN5;A0A0G2JDY4 | Acyl-CoA dehydrogenase family member 9, mitochondrial | **Acad9** | 1217 |
| 382 | 15 | 59.6 | 16.445 | 195.26 | 26.094 | 24.301 | **0.547** | **0.739** | P14131 | P14131 | 40S ribosomal protein S16 | **Rps16** | 609 |
| 383 | 1 | 9.6 | 12.504 | 26.321 | 24.319 | 22.934 | **0.415** | **0.737** | P34884 | P34884 | Macrophage migration inhibitory factor | **Mif** | 688 |
| 384 | 18 | 41.9 | 46.109 | 194.79 | 27.894 | 26.641 | **0.619** | **0.736** | P27659;A0A087WQK0;A0A087WNS0 | P27659 | 60S ribosomal protein L3 | **Rpl3** | 667 |
| 385 | 13 | 16.6 | 97.183 | 92.498 | 24.664 | 24.581 | **0.551** | **0.735** | P70168 | P70168 | Importin subunit beta-1 | **Kpnb1** | 877 |
| 386 | 11 | 48 | 24.146 | 81.081 | 25.897 | 24.610 | **1.016** | **0.733** | Q9CZM2;E9QAZ2;B8JKK2 | Q9CZM2;E9QAZ2 | 60S ribosomal protein L15;Ribosomal protein L15 | **Rpl15;Gm10020** | 404 |
| 387 | 12 | 24.4 | 65.322 | 90.331 | 25.238 | 24.384 | **0.117** | **0.723** | Q76MZ3;G3UXQ1;H3BJ83;H3BIV7;H3BLQ0;Q3TTF6;H3BKU1;G3UWS4;Q7TNP2;G3UWL2 | Q76MZ3 | Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform | **Ppp2r1a** | 1115 |
| 388 | 16 | 26 | 85.462 | 137.3 | 25.032 | 23.794 | **0.618** | **0.715** | Q99KI0 | Q99KI0 | Aconitate hydratase, mitochondrial | **Aco2** | 1300 |
| 389 | 7 | 29.2 | 30.255 | 67.916 | 27.082 | 24.855 | **0.146** | **0.713** | Q8C2Q8;Q91VR2;A2AKV1;A2AKV2;A2AKV3;A2AKU9;A2AKV0 | Q8C2Q8;Q91VR2;A2AKV1;A2AKV2;A2AKV3;A2AKU9 | ATP synthase subunit gamma;ATP synthase subunit gamma, mitochondrial | **Atp5c1** | 1194 |
| 390 | 6 | 29.3 | 10.531 | 74.964 | 17.474 | 15.582 | **0.090** | **0.708** | Q99N91 | Q99N91 | 39S ribosomal protein L34, mitochondrial | **Mrpl34** | 1316 |
| 391 | 12 | 7.1 | 192.75 | 77.727 | 20.894 | 20.749 | **0.160** | **0.708** | B7ZNH7;K3W4R4;Q80X19-2;Q80X19 | B7ZNH7;K3W4R4;Q80X19-2;Q80X19 | Collagen alpha-1(XIV) chain | **Col14a1** | 217 |
| 392 | 9 | 54.4 | 15.798 | 87.452 | 25.164 | 24.248 | **0.360** | **0.704** | P61358;A2A4Q0 | P61358;A2A4Q0 | 60S ribosomal protein L27 | **Rpl27** | 797 |

|  | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 393 | -3.094 | 7.190 | 5.260 | -0.546 | 3.717 | 4.076 | 18.375 | 22.637 | 22.997 | 14.908 | 25.192 | 23.261 | 18.272 | 19.569 | 20.220 | 15.783 |  | 9 | 9 |
| 394 | 4.343 | 2.028 | 1.787 | 3.717 | 0.916 | 1.416 | 28.196 | 25.394 | 25.894 | 28.660 | 26.344 | 26.103 | 25.751 | 23.206 | 25.877 | 22.756 |  | 7 | 7 |
| 395 | -4.354 | -1.256 | -2.400 | -5.136 | -0.054 | -4.893 | 17.197 | 22.280 | 17.440 | 14.729 | 17.827 | 16.683 | 23.853 | 20.814 | 22.895 | 15.271 |  | 5 | 5 |
| 396 | -1.354 | 1.865 | 0.051 | -2.063 | -1.041 | 1.597 | 20.699 | 21.721 | 24.359 | 21.314 | 24.534 | 22.720 | 23.620 | 21.905 | 24.539 | 20.798 |  | 6 | 6 |
| 397 | -3.386 | 6.434 | 3.466 | 0.620 | 0.489 | 3.399 | 17.170 | 17.040 | 19.950 | 15.258 | 25.078 | 22.110 | 18.063 | 15.038 | 22.809 | 14.479 |  | 11 | 11 |
| 398 | -4.261 | 4.084 | -1.239 | -1.210 | -1.852 | -0.342 | 16.941 | 16.299 | 17.808 | 15.124 | 23.469 | 18.146 | 18.506 | 17.795 | 21.050 | 17.720 |  | 4 | 4 |
| 399 | -0.646 | 5.944 | 3.212 | -0.813 | 1.378 | 5.976 | 16.008 | 18.199 | 22.796 | 16.807 | 23.397 | 20.665 | 18.655 | 14.986 | 20.177 | 14.730 |  | 4 | 4 |
| 400 | -6.966 | -1.378 | -1.967 | -7.927 | -2.820 | -1.534 | 16.084 | 21.191 | 22.477 | 15.851 | 21.439 | 20.849 | 25.366 | 22.656 | 24.605 | 21.029 |  | 9 | 9 |
| 401 | -2.325 | -2.706 | -1.140 | -3.590 | -2.552 | -1.944 | 20.880 | 21.918 | 22.526 | 22.103 | 21.722 | 23.288 | 24.556 | 24.384 | 25.064 | 23.792 |  | 16 | 16 |
| 402 | -0.482 | -2.428 | -5.884 | -1.263 | -7.153 | -2.292 | 23.080 | 17.190 | 22.051 | 22.297 | 20.352 | 16.895 | 27.654 | 21.032 | 25.069 | 20.490 |  | 7 | 7 |
| 403 | -1.751 | 5.501 | 3.864 | 1.713 | 2.816 | 1.173 | 17.363 | 18.466 | 16.823 | 15.063 | 22.315 | 20.677 | 16.983 | 14.317 | 17.730 | 15.897 |  | 2 | 2 |
| 404 | -4.878 | -2.330 | 2.240 | -3.287 | -1.397 | -2.131 | 19.131 | 21.021 | 20.287 | 15.874 | 18.423 | 22.992 | 24.623 | 20.214 | 22.738 | 18.767 |  | 4 | 4 |
| 405 | 0.909 | 5.538 | 3.855 | 4.861 | 2.324 | 1.271 | 21.712 | 19.175 | 18.122 | 17.476 | 22.105 | 20.422 | 18.647 | 15.054 | 17.546 | 15.588 |  | 2 | 2 |
| 406 | 1.365 | 6.199 | 4.752 | 2.299 | 4.798 | 3.387 | 22.924 | 25.423 | 24.012 | 21.819 | 26.652 | 25.205 | 17.966 | 23.284 | 26.268 | 14.638 |  | 17 | 14 |
| 407 | -1.251 | 1.023 | 0.051 | -1.098 | -0.610 | -0.265 | 22.254 | 22.741 | 23.086 | 19.886 | 22.161 | 21.188 | 26.733 | 19.969 | 22.354 | 19.921 |  | 8 | 8 |
| 408 | -3.499 | 4.171 | -2.814 | 2.591 | -3.301 | -3.216 | 22.222 | 16.330 | 16.415 | 16.824 | 24.494 | 17.509 | 20.372 | 18.890 | 20.352 | 20.294 |  | 4 | 4 |
| 409 | -0.989 | 2.265 | 0.660 | 0.587 | 0.805 | -1.239 | 23.629 | 23.847 | 21.803 | 23.791 | 27.044 | 25.439 | 21.257 | 24.826 | 26.569 | 22.990 |  | 12 | 12 |
| 410 | -0.674 | 0.534 | 0.066 | -2.360 | 0.558 | 0.000 | 21.831 | 24.749 | 24.191 | 23.146 | 24.353 | 23.885 | 25.824 | 22.558 | 25.737 | 21.901 |  | 10 | 10 |
| 411 | 0.392 | 0.712 | -4.448 | -2.167 | -1.691 | -1.192 | 22.001 | 22.477 | 22.976 | 22.456 | 22.776 | 17.615 | 27.095 | 21.242 | 23.868 | 20.260 |  | 27 | 27 |
| 412 | 0.339 | 4.233 | 2.351 | 1.161 | 2.574 | 1.522 | 23.172 | 24.586 | 23.533 | 21.887 | 25.781 | 23.899 | 18.976 | 25.047 | 25.326 | 17.770 |  | 16 | 12 |
| 413 | -0.459 | -0.115 | 0.759 | -0.851 | -0.332 | -0.297 | 26.655 | 27.174 | 27.210 | 25.902 | 26.245 | 27.119 | 28.866 | 26.147 | 28.444 | 24.277 |  | 15 | 15 |
| 414 | -1.967 | -0.197 | -0.241 | -2.752 | -0.113 | -1.192 | 22.594 | 25.233 | 24.154 | 22.485 | 24.255 | 24.212 | 27.156 | 23.536 | 26.232 | 22.673 |  | 12 | 11 |
| 415 | -1.414 | -1.142 | -1.244 | -2.127 | -1.509 | -1.807 | 24.906 | 25.524 | 25.227 | 24.500 | 24.772 | 24.670 | 28.458 | 25.609 | 27.616 | 24.212 | + | 19 | 19 |
| 416 | -1.123 | -0.346 | -0.175 | -1.610 | -0.780 | -0.881 | 29.096 | 29.926 | 29.825 | 28.357 | 29.134 | 29.305 | 32.416 | 28.996 | 31.177 | 27.783 |  | 30 | 30 |
| 417 | -7.322 | -1.987 | -8.109 | -7.013 | -4.533 | -7.491 | 18.080 | 20.560 | 17.603 | 17.113 | 22.447 | 16.325 | 27.147 | 23.039 | 24.913 | 23.957 |  | 9 | 9 |
| 418 | -6.316 | -0.205 | -1.327 | -4.094 | -2.515 | -2.829 | 21.097 | 22.676 | 22.362 | 17.777 | 23.888 | 22.766 | 27.364 | 23.018 | 26.051 | 22.135 |  | 15 | 15 |

| | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 393 | 8 | 13.8 | 90.875 | 58.006 | 18.921 | 18.001 | **0.071** | **0.703** | Q04750 | Q04750 | DNA topoisomerase 1 | **Top1** | 930 |
| 394 | 7 | 35.8 | 14.552 | 257.04 | 24.479 | 24.316 | **0.232** | **0.703** | Q6ZWV7;G3UWD7;F6XS56 | Q6ZWV7;G3UWD7 | 60S ribosomal protein L35 | **Rpl35;Gm10269** | 1111 |
| 395 | 5 | 17.3 | 39.502 | 31.221 | 22.333 | 19.083 | **0.135** | **0.691** | Q9JHJ0 | Q9JHJ0 | Tropomodulin-3 | **Tmod3** | 1492 |
| 396 | 6 | 33.8 | 25.186 | 50.171 | 22.762 | 22.668 | **0.183** | **0.690** | Q9WUK2-2;Q9WUK2 | Q9WUK2-2;Q9WUK2 | Eukaryotic translation initiation factor 4H | **Eif4h** | 1542 |
| 397 | 11 | 10.8 | 121.63 | 67.838 | 16.550 | 18.644 | **0.077** | **0.668** | Q91ZW3;Q6PGB8;Q6PGB8-2;F6Z6F4;Q8BS67 | Q91ZW3 | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 | **Smarca5** | 1277 |
| 398 | 4 | 4.6 | 96.02 | 23.635 | 18.151 | 19.385 | **0.096** | **0.663** | Q9Z1X4;Q9Z1X4-3;Q45VK5;Q9Z1X4-2;Q91WM1-2;Q91WM1 | Q9Z1X4;Q9Z1X4-3;Q45VK5;Q9Z1X4-2 | Interleukin enhancer-binding factor 3 | **Ilf3** | 1566 |
| 399 | 4 | 7.8 | 60.85 | 25.054 | 16.821 | 17.453 | **0.084** | **0.657** | Z4YKB8;Q3TEA8-2;Q3TEA8;A2AM65;Z4YKA3;Q3TEA8-3;A2AM69;A2AM70;A2AM63 | Z4YKB8;Q3TEA8-2;Q3TEA8;A2AM65;Z4YKA3;Q3TEA8-3 | Heterochromatin protein 1-binding protein 3 | **Hp1bp3** | 948 |
| 400 | 9 | 11.3 | 106.91 | 60.427 | 24.011 | 22.817 | **0.088** | **0.656** | Q8BGQ7 | Q8BGQ7 | Alanine--tRNA ligase, cytoplasmic | **Aars** | 1146 |
| 401 | 16 | 14.5 | 158.39 | 113.33 | 24.470 | 24.428 | **0.402** | **0.639** | A2AVJ7;Q99PL5;Q99PL5-8;Q99PL5-7;Q99PL5-6;Q99PL5-5;Q99PL5-4;Q99PL5-3;Q99PL5-2;Q99PL5-12;Q99PL5-11;Q99PL5-10;Q99PL5-9 | A2AVJ7;Q99PL5 | Ribosome-binding protein 1 | **Rrbp1** | 177 |
| 402 | 7 | 53.4 | 10.344 | 46.354 | 24.343 | 22.779 | **0.095** | **0.638** | P56135;F8WHP8 | P56135;F8WHP8 | ATP synthase subunit f, mitochondrial | **Atp5j2** | 765 |
| 403 | 2 | 4.3 | 71.439 | 16.548 | 15.650 | 16.813 | **0.102** | **0.637** | Q3U9G9 | Q3U9G9 | Lamin-B receptor | **Lbr** | 970 |
| 404 | 4 | 12.6 | 43.185 | 29.4 | 22.418 | 20.753 | **0.103** | **0.616** | Q9DBC7;A2AI69 | Q9DBC7 | cAMP-dependent protein kinase type I-alpha regulatory subunit;cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed | **Prkar1a** | 1461 |
| 405 | 2 | 7.9 | 21.139 | 11.099 | 16.850 | 16.567 | **0.131** | **0.615** | Q9CPT5;D3Z7M5;D6RDE0 | Q9CPT5;D3Z7M5;D6RDE0 | Nucleolar protein 16 | **Nop16** | 315 |
| 406 | 14 | 31.8 | 76.775 | 129.39 | 20.625 | 20.453 | **0.141** | **0.610** | Q3U0V1;A0A0G2JE55;A0A0G2JGT1 | Q3U0V1 | Far upstream element-binding protein 2 | **Khsrp** | 963 |
| 407 | 8 | 10.5 | 108.49 | 73.718 | 23.351 | 21.137 | **0.355** | **0.599** | Q04857 | Q04857 | Collagen alpha-1(VI) chain | **Col6a1** | 931 |
| 408 | 4 | 8.8 | 71.527 | 28.071 | 19.631 | 20.323 | **0.066** | **0.595** | A2AW05;Q08943;Q08943-2 | A2AW05;Q08943;Q08943-2 | FACT complex subunit SSRP1 | **Ssrp1** | 178 |
| 409 | 7 | 37.3 | 51.217 | 192.33 | 23.041 | 24.779 | **0.201** | **0.594** | Q8C2Q7;O35737 | Q8C2Q7;O35737 | Heterogeneous nuclear ribonucleoprotein H;Heterogeneous nuclear ribonucleoprotein H, N-terminally processed | **Hnrnph1** | 517 |
| 410 | 9 | 38.4 | 31.395 | 88.274 | 24.191 | 23.819 | **0.236** | **0.576** | A0A0G2JDV8;Q9DAW9;A0A0G2JFI6;A0A0G2JFC8;A0A0G2JFG3 | A0A0G2JDV8;Q9DAW9;A0A0G2JFI6 | Calponin-3 | **Cnn3** | 41 |
| 411 | 27 | 10 | 353.93 | 179.36 | 24.168 | 22.064 | **0.123** | **0.568** | E9PWQ3;J3QQ16;A0A087WS16;D3YWD1 | E9PWQ3;J3QQ16;A0A087WS16;D3YWD1 | | **Col6a3** | 346 |
| 412 | 12 | 24.5 | 72.584 | 105.25 | 22.011 | 21.548 | **0.175** | **0.555** | Q3U741;Q501J6;Q501J6-2 | Q3U741;Q501J6;Q501J6-2 | Probable ATP-dependent RNA helicase DDX17 | **Ddx17** | 969 |
| 413 | 15 | 38.9 | 33.509 | 142.21 | 27.506 | 26.360 | **0.617** | **0.555** | P47911;E9PUX4;A0A0J9YU32 | P47911;E9PUX4 | 60S ribosomal protein L6 | **Rpl6;Gm5428** | 725 |
| 414 | 11 | 39.5 | 28.467 | 109.49 | 25.346 | 24.452 | **0.223** | **0.551** | Q6IRU2 | Q6IRU2 | Tropomyosin alpha-4 chain | **Tpm4** | 1087 |
| 415 | 16 | 44.1 | 62.277 | 256.9 | 27.034 | 25.914 | **1.313** | **0.548** | O08553 | O08553 | Dihydropyrimidinase-related protein 2 | **Dpysl2** | 498 |
| 416 | 30 | 41.8 | 50.113 | 323.31 | 30.706 | 29.480 | **0.622** | **0.542** | P10126;D3Z3I8;D3YZ68;P62631 | P10126;D3Z3I8;D3YZ68 | Elongation factor 1-alpha 1 | **Eef1a1** | 588 |
| 417 | 9 | 57.4 | 23.407 | 96.23 | 25.093 | 24.435 | **0.090** | **0.539** | Q99PT1 | Q99PT1 | Rho GDP-dissociation inhibitor 1 | **Arhgdia** | 1319 |
| 418 | 15 | 32.3 | 64.217 | 106.66 | 25.191 | 24.093 | **0.098** | **0.530** | Q9CWJ9 | Q9CWJ9 | Bifunctional purine biosynthesis protein PURH;Phosphoribosylaminoimidazolecarboxamide formyltransferase;IMP cyclohydrolase | **Atic** | 1376 |

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 419 | 6.650 | 3.232 | 3.789 | 5.863 | 2.642 | 3.577 | 28.023 | 24.802 | 25.737 | 27.945 | 24.527 | 25.083 | 23.300 | 21.020 | 23.047 | 19.543 | | 5 | 5 |
| 420 | 8.261 | 8.587 | 8.506 | 10.072 | 9.602 | 4.101 | 27.981 | 27.510 | 22.009 | 25.845 | 26.171 | 26.090 | 20.190 | 15.626 | 19.615 | 15.554 | | 6 | 6 |
| 421 | -2.775 | -1.861 | -2.359 | -7.542 | -0.952 | -0.078 | 16.928 | 23.518 | 24.392 | 21.503 | 22.417 | 21.919 | 25.875 | 23.064 | 25.561 | 22.995 | | 12 | 12 |
| 422 | -2.678 | -0.704 | -1.478 | -1.773 | -3.585 | -1.042 | 26.608 | 24.796 | 27.339 | 24.079 | 26.053 | 25.279 | 30.546 | 26.216 | 28.653 | 24.861 | | 19 | 19 |
| 423 | 4.337 | 2.063 | 2.025 | 3.957 | 2.014 | 0.931 | 29.945 | 28.001 | 26.918 | 29.283 | 27.009 | 26.971 | 27.688 | 24.286 | 26.901 | 22.991 | | 5 | 5 |
| 424 | -4.105 | 2.625 | 1.938 | -0.283 | -2.036 | 1.256 | 17.906 | 16.153 | 19.445 | 14.821 | 21.550 | 20.864 | 19.093 | 17.286 | 23.440 | 14.411 | | 2 | 2 |
| 425 | 1.093 | -0.734 | 0.078 | 0.379 | -0.475 | -0.949 | 28.515 | 27.661 | 27.187 | 28.153 | 26.326 | 27.138 | 28.897 | 27.375 | 28.394 | 25.725 | | 15 | 15 |
| 426 | -3.969 | -0.990 | -0.799 | -2.195 | -3.597 | -1.413 | 24.329 | 22.927 | 25.111 | 21.313 | 24.292 | 24.483 | 28.297 | 24.751 | 27.114 | 23.449 | | 16 | 16 |
| 427 | 0.702 | 0.366 | 1.420 | 1.488 | -1.038 | 0.597 | 20.602 | 18.077 | 19.711 | 16.821 | 16.486 | 17.539 | 22.572 | 15.656 | 17.712 | 14.527 | | 3 | 3 |
| 428 | -0.590 | -1.116 | 0.603 | -2.401 | 0.642 | -0.748 | 20.603 | 23.645 | 22.255 | 21.236 | 20.710 | 22.429 | 23.758 | 22.249 | 21.396 | 22.256 | | 4 | 4 |
| 429 | 0.434 | 5.661 | 3.396 | 1.019 | 3.437 | 3.644 | 17.687 | 20.105 | 20.313 | 17.348 | 22.575 | 20.310 | 16.614 | 16.723 | 19.375 | 14.453 | | 2 | 2 |
| 430 | -4.721 | 3.603 | 1.237 | -2.548 | -1.202 | 2.506 | 16.517 | 17.863 | 21.571 | 15.541 | 23.865 | 21.499 | 17.246 | 20.883 | 23.329 | 17.194 | | 9 | 9 |
| 431 | -8.316 | -0.587 | -1.256 | -4.740 | -2.911 | -3.799 | 20.531 | 22.359 | 21.472 | 15.156 | 22.884 | 22.215 | 25.779 | 24.763 | 24.605 | 22.337 | | 3 | 3 |
| 432 | 1.207 | 2.873 | -1.896 | -0.608 | 2.089 | -0.584 | 20.020 | 22.717 | 20.044 | 19.939 | 21.604 | 16.835 | 24.214 | 17.042 | 23.614 | 13.849 | | 6 | 6 |
| 433 | 9.965 | 7.840 | 7.968 | 7.463 | 8.154 | 8.878 | 26.114 | 26.805 | 27.530 | 26.855 | 24.730 | 24.858 | 21.103 | 16.200 | 19.697 | 14.083 | | 9 | 9 |
| 434 | -2.137 | -1.296 | -1.502 | -2.492 | -2.448 | -1.256 | 21.646 | 21.689 | 22.881 | 21.002 | 21.844 | 21.637 | 25.675 | 22.600 | 25.420 | 20.860 | | 7 | 7 |
| 435 | 0.484 | 3.139 | 1.729 | 1.587 | 0.615 | 1.899 | 23.872 | 22.899 | 24.183 | 22.429 | 25.083 | 23.673 | 22.997 | 21.571 | 24.958 | 18.931 | | 6 | 6 |
| 436 | 2.632 | 1.090 | -1.459 | 0.044 | -0.460 | 1.434 | 24.337 | 23.833 | 25.727 | 25.745 | 24.203 | 21.654 | 25.502 | 23.084 | 24.930 | 21.295 | | 10 | 10 |
| 437 | 0.179 | 5.415 | -0.050 | -0.615 | 2.982 | 1.975 | 16.834 | 20.430 | 19.423 | 16.556 | 21.792 | 16.326 | 18.386 | 16.512 | 17.413 | 15.341 | | 2 | 2 |
| 438 | -2.686 | -2.391 | -3.065 | -5.337 | -4.368 | 0.378 | 15.871 | 16.840 | 21.586 | 17.577 | 17.873 | 17.199 | 22.492 | 19.925 | 20.790 | 19.737 | | 1 | 1 |
| 439 | -4.800 | 5.357 | 2.706 | 3.627 | -2.919 | 1.374 | 22.748 | 16.202 | 20.496 | 14.849 | 25.007 | 22.356 | 17.170 | 21.073 | 24.217 | 15.082 | | 6 | 6 |
| 440 | -5.764 | 1.933 | -0.208 | -0.981 | -3.653 | -0.586 | 22.273 | 19.602 | 22.668 | 16.064 | 23.761 | 21.620 | 25.848 | 20.661 | 23.132 | 20.523 | | 9 | 9 |
| 441 | -1.082 | -0.636 | -0.830 | -1.070 | -1.364 | -1.295 | 28.905 | 28.610 | 28.680 | 28.127 | 28.573 | 28.380 | 31.854 | 28.096 | 30.384 | 28.035 | | 38 | 38 |
| 442 | -3.370 | -1.836 | -1.048 | -2.462 | -2.551 | -2.402 | 23.974 | 23.886 | 24.035 | 22.238 | 23.771 | 24.559 | 28.367 | 24.507 | 27.669 | 23.546 | | 17 | 17 |
| 443 | -5.611 | -4.573 | -4.914 | -7.188 | -6.431 | -2.622 | 16.694 | 17.450 | 21.259 | 16.043 | 17.081 | 16.740 | 26.176 | 21.588 | 23.575 | 19.733 | | 11 | 11 |
| 444 | 2.248 | 2.902 | 3.204 | 0.708 | 3.963 | 2.559 | 19.721 | 22.976 | 21.572 | 20.683 | 21.336 | 21.638 | 22.440 | 15.585 | 21.812 | 15.057 | | 1 | 1 |
| 445 | -2.169 | -0.441 | -0.309 | -1.856 | -1.232 | -0.915 | 24.660 | 25.284 | 25.601 | 23.411 | 25.139 | 25.271 | 28.314 | 24.718 | 27.669 | 23.490 | | 11 | 11 |
| 446 | -0.330 | 0.492 | 1.009 | -0.268 | 0.002 | 0.389 | 26.230 | 26.499 | 26.887 | 25.725 | 26.547 | 27.064 | 27.912 | 25.084 | 27.717 | 24.392 | | 22 | 22 |

|  | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 419 | 5 | 30.5 | 12.254 | 55.927 | 22.160 | 21.295 | **0.137** | **0.530** | Q6ZWZ4;A0A140T8K6;P47964;D3YX71 | Q6ZWZ4;A0A140T8K6;P47964 | 60S ribosomal protein L36 | **Rpl36** | 112 |
| 420 | 6 | 28.3 | 12.441 | 39.435 | 17.908 | 17.584 | **0.098** | **0.526** | P83882;A0A0A6YW33 | P83882;A0A0A6YW33 | 60S ribosomal protein L36a | **Rpl36a;Gm6525** | 893 |
| 421 | 12 | 39.1 | 51.572 | 83.265 | 24.470 | 24.278 | **0.078** | **0.525** | P30416;F6S2D5;F7CAT1 | P30416 | Peptidyl-prolyl cis-trans isomerase FKBP4;Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed | **Fkbp4** | 678 |
| 422 | 19 | 49.4 | 46.533 | 268.44 | 28.381 | 26.757 | **0.210** | **0.513** | P19324;A0A140LHR4;A0A140LHK0 | P19324 | Serpin H1 | **Serpinh1** | 636 |
| 423 | 5 | 22.3 | 17.779 | 60.647 | 25.987 | 24.946 | **0.163** | **0.508** | Q8BP67;F6RSK3 | Q8BP67 | 60S ribosomal protein L24 | **Rpl24** | 1179 |
| 424 | 2 | 27 | 19.889 | 13.662 | 18.189 | 18.926 | **0.076** | **0.507** | A0A023T672;Q9CWZ3-2;Q9CWZ3;A0A0G2JEA9;A0A0G2JFX7;A0A0N4SUH6 | A0A023T672;Q9CWZ3-2;Q9CWZ3;A0A0G2JEA9;A0A0G2JFX7;A0A0N4SUH6 | RNA-binding protein 8A | **RBM8;Rbm8a** | 0 |
| 425 | 15 | 41.8 | 24.205 | 232.79 | 28.136 | 27.060 | **0.307** | **0.494** | P62242 | P62242 | 40S ribosomal protein S8 | **Rps8** | 813 |
| 426 | 16 | 34.7 | 34.4 | 155.06 | 26.524 | 25.282 | **0.149** | **0.482** | P47962;D3YYV8 | P47962;D3YYV8 | 60S ribosomal protein L5 | **Rpl5** | 727 |
| 427 | 3 | 6.4 | 59.262 | 18.949 | 19.114 | 16.119 | **0.235** | **0.480** | Q00612;A3KG36 | Q00612;A3KG36 | Glucose-6-phosphate 1-dehydrogenase X;Glucose-6-phosphate 1-dehydrogenase | **G6pdx** | 916 |
| 428 | 4 | 10.9 | 57.026 | 26.268 | 23.003 | 21.826 | **0.175** | **0.468** | Q7TQE2;Q62523;A0A0N4SVD2;A0A0N4SUX7;A0A0N4SVP4 | Q7TQE2;Q62523 | Zyxin | **Zyx** | 1073 |
| 429 | 2 | 3 | 82.504 | 11.259 | 16.668 | 16.914 | **0.096** | **0.464** | Q3TUQ5;O35691 | Q3TUQ5;O35691 | Pinin | **Pnn** | 515 |
| 430 | 9 | 13.7 | 98.197 | 54.883 | 19.065 | 20.261 | **0.054** | **0.454** | Q3UJB0 | Q3UJB0 | SAP domain-containing protein | **Sf3b2** | 981 |
| 431 | 3 | 16.3 | 27.372 | 25.024 | 25.271 | 23.471 | **0.059** | **0.430** | Q9QUM9;E0CXB1 | Q9QUM9;E0CXB1 | Proteasome subunit alpha type-6 | **Psma6** | 1509 |
| 432 | 6 | 23.8 | 20.605 | 39.725 | 20.628 | 18.732 | **0.092** | **0.429** | Q3UHX2 | Q3UHX2 | 28 kDa heat- and acid-stable phosphoprotein | **Pdap1** | 979 |
| 433 | 9 | 40.6 | 19.803 | 66.598 | 18.652 | 16.890 | **0.206** | **0.426** | E9QPX3;Q9CXZ1 | E9QPX3;Q9CXZ1 | NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial | **Ndufs4** | 414 |
| 434 | 7 | 15.1 | 53.247 | 49.517 | 24.138 | 23.140 | **0.368** | **0.420** | Q9DCD0 | Q9DCD0 | 6-phosphogluconate dehydrogenase, decarboxylating | **Pgd** | 1472 |
| 435 | 6 | 23.9 | 36.169 | 42.749 | 22.284 | 21.945 | **0.185** | **0.417** | P70372 | P70372 | ELAV-like protein 1 | **Elavl1** | 881 |
| 436 | 10 | 42.2 | 15.86 | 68.21 | 24.293 | 23.112 | **0.114** | **0.415** | P62911;P17932 | P62911 | 60S ribosomal protein L32 | **Rpl32** | 848 |
| 437 | 2 | 0.5 | 442.36 | 11.002 | 17.449 | 16.377 | **0.067** | **0.401** | Q80T14 | Q80T14 | Extracellular matrix protein FRAS1 | **Fras1** | 1126 |
| 438 | 1 | 1.8 | 80.085 | 7.0991 | 21.208 | 20.264 | **0.078** | **0.395** | Q8CHW4 | Q8CHW4 | Translation initiation factor eIF-2B subunit epsilon | **Eif2b5** | 1210 |
| 439 | 6 | 17.4 | 43.158 | 54.7 | 19.122 | 19.650 | **0.037** | **0.394** | Q7TNV0;E9Q8Y1;D3YVJ6 | Q7TNV0;E9Q8Y1;D3YVJ6 | Protein DEK | **Dek** | 1121 |
| 440 | 9 | 14.9 | 83.953 | 59.281 | 23.254 | 21.828 | **0.055** | **0.394** | Q99MD9;B1AU75;B1AU76;Q99MD9-2 | Q99MD9;B1AU75;B1AU76 | Nuclear autoantigenic sperm protein | **Nasp** | 1313 |
| 441 | 13 | 69.1 | 41.792 | 323.31 | 29.975 | 29.210 | **1.180** | **0.394** | P63260;P60710;E9Q5F4;E9Q1F2;G3UZ07;E9Q606;B1ATY1;G3UYG0;F8WGM8;E9Q2D1;F6WX90;V9GXQ2 | P63260;P60710;E9Q5F4;E9Q1F2;G3UZ07 | Actin, cytoplasmic 2;Actin, cytoplasmic 2, N-terminally processed;Actin, cytoplasmic 1;Actin, cytoplasmic 1, N-terminally processed | **Actg1;Actb** | 785 |
| 442 | 17 | 43.4 | 58.066 | 181.72 | 26.437 | 25.607 | **0.221** | **0.387** | P80315;G5E839;G3UYW5;G3UXF3;G3UXG2 | P80315;G5E839 | T-complex protein 1 subunit delta | **Cct4** | 887 |
| 443 | 8 | 12.9 | 116.03 | 66.205 | 23.882 | 21.654 | **0.094** | **0.381** | Z4YJV4;Q60597-2;Q60597;Q60597-4;Q60597-3;Q5SVY0;Q5SVY1 | Z4YJV4;Q60597-2;Q60597;Q60597-4;Q60597-3 | 2-oxoglutarate dehydrogenase, mitochondrial | **Ogdh** | 1017 |
| 444 | 1 | 4.6 | 24.824 | 12.371 | 19.013 | 18.435 | **0.141** | **0.375** | A2ABZ2;Q922W5;Q922Q4 | A2ABZ2;Q922W5;Q922Q4 | Pyrroline-5-carboxylate reductase 1, mitochondrial;Pyrroline-5-carboxylate reductase 2 | **Pycr1;Pycr2** | 137 |
| 445 | 11 | 24.3 | 50.06 | 130.47 | 26.516 | 25.580 | **0.212** | **0.361** | Q9D8N0 | Q9D8N0 | Elongation factor 1-gamma | **Eef1g** | 1450 |
| 446 | 22 | 51.1 | 31.419 | 181.22 | 26.498 | 26.055 | **0.332** | **0.350** | P14148;F6XI62 | P14148;F6XI62 | 60S ribosomal protein L7 | **Rpl7** | 610 |

|  | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 447 | -1.610 | -0.631 | -1.029 | -2.144 | -1.251 | -0.899 | 23.014 | 23.908 | 24.260 | 22.409 | 23.388 | 22.990 | 26.960 | 23.357 | 25.739 | 22.299 |  | 6 | 6 |
| 448 | -5.788 | -0.900 | -0.092 | -2.847 | -1.040 | -3.917 | 17.821 | 19.628 | 16.751 | 15.642 | 20.530 | 21.338 | 22.915 | 18.422 | 23.596 | 19.264 |  | 5 | 5 |
| 449 | 4.625 | 2.891 | 2.779 | 3.632 | 2.969 | 2.679 | 29.589 | 28.926 | 28.636 | 29.314 | 27.580 | 27.468 | 27.380 | 24.535 | 26.790 | 22.588 |  | 17 | 17 |
| 450 | -5.817 | -4.472 | -6.143 | -8.282 | -2.331 | -6.828 | 16.240 | 22.190 | 17.694 | 17.145 | 18.490 | 16.819 | 26.795 | 22.248 | 23.313 | 22.610 |  | 5 | 5 |
| 451 | -1.349 | -0.063 | -0.971 | -1.646 | -0.684 | -0.992 | 26.127 | 27.089 | 26.781 | 25.775 | 27.060 | 26.153 | 29.341 | 26.205 | 28.436 | 25.811 |  | 53 | 53 |
| 452 | 6.073 | 4.626 | 3.229 | 6.595 | 0.523 | 5.875 | 23.105 | 17.034 | 22.386 | 23.427 | 21.981 | 20.584 | 17.556 | 15.466 | 19.005 | 15.704 |  | 3 | 3 |
| 453 | -2.354 | -0.709 | -0.644 | -2.012 | -1.568 | -1.062 | 22.041 | 22.485 | 22.991 | 21.539 | 23.184 | 23.249 | 26.082 | 22.024 | 24.654 | 23.132 |  | 5 | 3 |
| 454 | -0.802 | -0.866 | -0.817 | -0.403 | -1.792 | -1.198 | 26.858 | 25.470 | 26.064 | 25.599 | 25.535 | 25.584 | 28.556 | 25.967 | 28.033 | 24.768 |  | 11 | 11 |
| 455 | -2.736 | -4.345 | -6.618 | -5.698 | -6.191 | -2.709 | 17.384 | 16.891 | 20.374 | 20.028 | 18.419 | 16.146 | 27.033 | 19.132 | 23.647 | 21.881 |  | 10 | 10 |
| 456 | -4.386 | 6.429 | 4.511 | -0.256 | 2.094 | 3.826 | 16.824 | 19.174 | 20.906 | 15.083 | 25.898 | 23.980 | 17.730 | 16.430 | 23.902 | 15.037 |  | 15 | 15 |
| 457 | 1.632 | -0.308 | 0.795 | 1.108 | 0.157 | -0.024 | 29.021 | 28.070 | 27.890 | 28.822 | 26.882 | 27.986 | 28.903 | 26.924 | 28.993 | 25.388 |  | 22 | 22 |
| 458 | -2.475 | -0.554 | -2.507 | 0.083 | -2.721 | -3.723 | 21.006 | 18.202 | 17.200 | 16.830 | 18.751 | 16.798 | 22.343 | 19.504 | 18.808 | 19.801 |  | 2 | 2 |
| 459 | -2.032 | -0.343 | -0.653 | -2.682 | -0.682 | -0.459 | 24.612 | 26.613 | 26.836 | 23.884 | 25.573 | 25.264 | 28.733 | 25.856 | 27.621 | 24.211 |  | 33 | 33 |
| 460 | -1.275 | -1.768 | -0.608 | -0.424 | -2.155 | -1.861 | 27.917 | 26.185 | 26.480 | 26.236 | 25.743 | 26.904 | 29.618 | 27.063 | 29.076 | 25.946 |  | 18 | 18 |
| 461 | -3.497 | 2.894 | -2.009 | -0.790 | -1.130 | -1.443 | 16.972 | 16.632 | 16.320 | 15.437 | 21.828 | 16.925 | 19.002 | 16.523 | 22.459 | 15.409 |  | 2 | 2 |
| 462 | -1.274 | 1.067 | -0.212 | 0.362 | -1.240 | -0.284 | 23.421 | 21.820 | 22.776 | 20.720 | 23.061 | 21.782 | 25.382 | 20.737 | 23.993 | 19.994 |  | 7 | 7 |
| 463 | 8.067 | 6.876 | 4.971 | 6.207 | 7.276 | 5.702 | 27.501 | 28.570 | 26.997 | 28.102 | 26.910 | 25.005 | 19.386 | 23.202 | 25.112 | 14.956 |  | 11 | 11 |
| 464 | -2.738 | 4.836 | 3.284 | 0.448 | 2.492 | 1.722 | 20.778 | 22.822 | 22.052 | 17.021 | 24.596 | 23.043 | 19.505 | 21.155 | 23.748 | 15.772 |  | 8 | 8 |
| 465 | 4.271 | 1.968 | 2.502 | 4.858 | 1.834 | 1.399 | 30.274 | 27.250 | 26.815 | 29.093 | 26.790 | 27.324 | 26.604 | 24.229 | 26.338 | 23.306 |  | 18 | 18 |
| 466 | 0.407 | 1.022 | 0.375 | -0.360 | 0.750 | 0.776 | 22.795 | 23.904 | 23.931 | 23.052 | 23.668 | 23.021 | 24.708 | 21.601 | 24.484 | 20.808 |  | 3 | 3 |
| 467 | -9.465 | -2.243 | -2.736 | -8.337 | -4.309 | -2.408 | 17.010 | 21.037 | 22.939 | 14.510 | 21.732 | 21.239 | 26.555 | 24.139 | 25.237 | 22.712 |  | 9 | 9 |
| 468 | -3.899 | -4.540 | -3.944 | -5.303 | -6.305 | -1.382 | 17.353 | 16.351 | 21.274 | 16.600 | 15.959 | 16.555 | 26.047 | 19.264 | 21.287 | 19.711 |  | 4 | 4 |
| 469 | -2.227 | -2.197 | -1.473 | -1.681 | -2.638 | -2.156 | 26.250 | 25.293 | 25.776 | 24.597 | 24.627 | 25.351 | 30.026 | 25.837 | 28.488 | 25.160 |  | 15 | 15 |
| 470 | 2.004 | 0.623 | 0.830 | 1.560 | 0.828 | 0.502 | 27.962 | 27.230 | 26.904 | 27.676 | 26.294 | 26.501 | 28.330 | 24.474 | 28.120 | 23.223 |  | 20 | 20 |
| 471 | -2.598 | -2.006 | -5.149 | -6.516 | -1.289 | -2.509 | 16.418 | 21.645 | 20.425 | 19.139 | 19.731 | 16.588 | 25.045 | 20.822 | 23.623 | 19.850 |  | 8 | 8 |
| 472 | -0.218 | 6.465 | 5.549 | 3.375 | 3.809 | 4.074 | 24.645 | 25.080 | 25.345 | 20.337 | 27.020 | 26.105 | 19.418 | 23.124 | 26.722 | 14.389 |  | 6 | 6 |
| 473 | -8.104 | -5.066 | -4.708 | -7.870 | -4.666 | -5.879 | 16.932 | 20.137 | 18.923 | 14.987 | 18.025 | 18.383 | 26.201 | 23.403 | 23.018 | 23.164 |  | 4 | 4 |

| | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 447 | 6 | 19.3 | 48.978 | 51.902 | 25.159 | 24.019 | **0.297** | **0.342** | A0A0J9YTY0;A0A0J9YUL3;Q8C1B7-3;Q8C1B7-2;Q8C1B7;A0A0J9YVA6;A0A0J9YUV6;B7ZC46;B1AQY9;B1AQZ0;Q9R1T4-2;Q9R1T4-3;Q8CHH9;Q8CHH9-2;Q9R1T4 | A0A0J9YTY0;A0A0J9YUL3;Q8C1B7-3;Q8C1B7-2;Q8C1B7;A0A0J9YVA6 | Septin-11 | **Sept11** | 58 |
| 448 | 5 | 17 | 54.191 | 30.903 | 20.668 | 21.430 | **0.060** | **0.341** | P54823 | P54823 | Probable ATP-dependent RNA helicase DDX6 | **Ddx6** | 760 |
| 449 | 17 | 56.6 | 17.258 | 174.01 | 25.958 | 24.689 | **0.197** | **0.339** | P61255;B1ARA3;B1ARA5 | P61255;B1ARA3;B1ARA5 | 60S ribosomal protein L26 | **Rpl26** | 796 |
| 450 | 5 | 29.4 | 26.476 | 66.857 | 24.522 | 22.962 | **0.063** | **0.336** | Q8BHC4;B0QZX9 | Q8BHC4;B0QZX9 | Dephospho-CoA kinase domain-containing protein | **Dcakd** | 1156 |
| 451 | 49 | 25.4 | 274.63 | 323.31 | 27.773 | 27.124 | **0.263** | **0.313** | B7FAV1;B7FAU9;Q8BTM8;F6XC15;J3JS91;Q8BTM8-2;F6Z2C0 | B7FAV1;B7FAU9;Q8BTM8 | Filamin-A | **Flna** | 214 |
| 452 | 3 | 22 | 13.527 | 19.929 | 16.511 | 17.355 | **0.051** | **0.312** | P62317;D3Z5N9 | P62317;D3Z5N9 | Small nuclear ribonucleoprotein Sm D2 | **Snrpd2;Gm5449** | 822 |
| 453 | 3 | 16.5 | 27.7 | 62.428 | 24.053 | 23.893 | **0.192** | **0.312** | P68254-2;P68254;F6YY69;F6VW30 | P68254-2;P68254;F6YY69;F6VW30 | 14-3-3 protein theta | **Ywhaq** | 872 |
| 454 | 11 | 38.2 | 24.916 | 176.52 | 27.261 | 26.401 | **0.306** | **0.303** | P53026;Q5XJF6;D6RE43 | P53026;Q5XJF6 | 60S ribosomal protein L10a;Ribosomal protein | **Rpl10a** | 752 |
| 455 | 10 | 33.9 | 54.356 | 88.094 | 23.082 | 22.764 | **0.067** | **0.300** | P97807;P97807-2;H3BKG7 | P97807;P97807-2 | Fumarate hydratase, mitochondrial | **Fh** | 909 |
| 456 | 15 | 20.1 | 102.08 | 115.25 | 17.080 | 19.469 | **0.028** | **0.296** | P97310;A0A0N4SVY2 | P97310 | DNA replication licensing factor MCM2 | **Mcm2** | 897 |
| 457 | 22 | 51.9 | 29.885 | 323.31 | 27.914 | 27.190 | **0.167** | **0.293** | P97351 | P97351 | 40S ribosomal protein S3a | **Rps3a** | 903 |
| 458 | 2 | 21.7 | 15.893 | 13.517 | 20.923 | 19.305 | **0.074** | **0.275** | D3Z2X5;Q61205;Q8CA83;D3Z7E6 | D3Z2X5;Q61205;Q8CA83;D3Z7E6 | Platelet-activating factor acetylhydrolase IB subunit gamma | **Pafah1b3** | 303 |
| 459 | 22 | 78.2 | 29.02 | 323.31 | 27.295 | 25.916 | **0.109** | **0.265** | P21107-2;D3Z2H9;D3Z6I8;E9Q7Q3;E9Q5J9;A0A0R4J1P2;P21107;D3YVR0 | P21107-2;D3Z2H9;D3Z6I8;E9Q7Q3;E9Q5J9;A0A0R4J1P2;P21107 | Tropomyosin alpha-3 chain | **Tpm3;Tpm3-rs7** | 644 |
| 460 | 18 | 64.2 | 26.674 | 218.41 | 28.340 | 27.511 | **0.156** | **0.263** | P62908;D3YV43;A0A140LI77 | P62908;D3YV43;A0A140LI77 | 40S ribosomal protein S3 | **Rps3** | 847 |
| 461 | 2 | 3 | 87.555 | 11.484 | 17.762 | 18.934 | **0.044** | **0.250** | Q8VDF2-2;Q8VDF2 | Q8VDF2-2;Q8VDF2 | E3 ubiquitin-protein ligase UHRF1 | **Uhrf1** | 1250 |
| 462 | 7 | 24.1 | 36.108 | 56.338 | 23.059 | 21.994 | **0.109** | **0.247** | Q6ZWX6 | Q6ZWX6 | Eukaryotic translation initiation factor 2 subunit 1 | **Eif2s1** | 1112 |
| 463 | 11 | 20.7 | 52.601 | 116.86 | 21.294 | 20.034 | **0.085** | **0.243** | Q8CFQ9;P56959;G3UXT7;G3UZD2;Q91VQ2;F6QCI0;Q8BQ46 | Q8CFQ9;P56959;G3UXT7 | RNA-binding protein FUS | **Fus** | 770 |
| 464 | 8 | 12.1 | 94.629 | 51.673 | 20.330 | 19.760 | **0.034** | **0.240** | Q8K310;A0A087WSU2;A0A087WQD6;A0A087WSP7;A0A087WQZ1;A0A087WQP4;A0A087WNP3;A0A087WPU5;A0A087WPQ5;A0A087WSF8;A0A087WQ54;A0A087WNW7 | Q8K310;A0A087WSU2 | Matrin-3 | **Matr3** | 1225 |
| 465 | 4 | 60.2 | 24.305 | 323.31 | 25.416 | 24.822 | **0.058** | **0.217** | P47963 | P47963 | 60S ribosomal protein L13 | **Rpl13** | 728 |
| 466 | 3 | 35.7 | 13.777 | 25.19 | 23.155 | 22.646 | **0.189** | **0.212** | P70349;B0R1E3 | P70349;B0R1E3 | Histidine triad nucleotide-binding protein 1 | **Hint1** | 880 |
| 467 | 9 | 21.3 | 66.406 | 63.102 | 25.347 | 23.975 | **0.023** | **0.203** | O88342;A0A0J9YU05 | O88342 | WD repeat-containing protein 1 | **Wdr1** | 542 |
| 468 | 4 | 13.4 | 39.736 | 26.689 | 22.656 | 20.499 | **0.046** | **0.202** | G5E902;Q8VEM8 | G5E902;Q8VEM8 | Phosphate carrier protein, mitochondrial | **Slc25a3** | 474 |
| 469 | 15 | 49.2 | 32.838 | 272.69 | 27.931 | 26.824 | **0.200** | **0.193** | P14206 | P14206 | 40S ribosomal protein SA | **Rpsa** | 612 |
| 470 | 20 | 58.6 | 29.597 | 161.29 | 26.402 | 25.671 | **0.131** | **0.189** | P62702;V9GWY0 | P62702;V9GWY0 | 40S ribosomal protein S4, X isoform;40S ribosomal protein S4 | **Rps4x;Gm15013** | 826 |
| 471 | 8 | 33.1 | 31.474 | 55.043 | 22.934 | 21.737 | **0.034** | **0.187** | Q8BH95;F6T930 | Q8BH95;F6T930 | Enoyl-CoA hydratase, mitochondrial | **Echs1** | 1154 |
| 472 | 6 | 38.4 | 19.329 | 61.132 | 21.271 | 20.555 | **0.029** | **0.179** | P84104;P84104-2;A2A4X6 | P84104;P84104-2;A2A4X6 | Serine/arginine-rich splicing factor 3 | **Srsf3;Gm12355** | 896 |
| 473 | 4 | 7.7 | 64.697 | 27.297 | 24.802 | 23.091 | **0.043** | **0.179** | Q61576;A2A4H9;F6W360 | Q61576;A2A4H9 | Peptidyl-prolyl cis-trans isomerase FKBP10 | **Fkbp10** | 1042 |

|  | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 474 | 2.919 | 5.738 | 3.738 | 4.611 | 4.205 | 3.048 | 22.087 | 21.682 | 20.525 | 19.697 | 22.516 | 20.516 | 18.647 | 16.307 | 17.424 | 16.132 |  | 2 | 2 |
| 475 | 4.054 | 6.418 | 5.143 | 3.438 | 6.109 | 5.540 | 20.635 | 23.306 | 22.737 | 22.730 | 25.094 | 23.819 | 18.763 | 15.631 | 22.293 | 15.059 |  | 8 | 6 |
| 476 | -0.612 | 0.305 | 0.267 | -0.319 | -0.277 | 0.041 | 24.815 | 24.858 | 25.176 | 24.021 | 24.938 | 24.899 | 26.684 | 23.585 | 26.958 | 22.306 |  | 22 | 22 |
| 477 | 0.192 | 1.089 | 1.364 | 0.021 | 0.987 | 1.151 | 22.937 | 23.903 | 24.067 | 21.716 | 22.614 | 22.888 | 24.828 | 21.004 | 22.079 | 20.969 |  | 7 | 7 |
| 478 | 0.190 | -0.425 | 0.385 | -0.584 | -0.273 | 0.541 | 25.838 | 26.149 | 26.963 | 26.088 | 25.474 | 26.283 | 28.102 | 24.741 | 27.619 | 24.178 |  | 12 | 12 |
| 479 | 8.855 | 9.437 | 8.670 | 6.741 | 9.849 | 9.948 | 23.929 | 27.037 | 27.136 | 24.455 | 25.038 | 24.271 | 18.466 | 15.910 | 17.152 | 14.050 |  | 8 | 8 |
| 480 | 2.969 | -1.325 | -0.376 | 3.050 | -0.893 | -1.310 | 30.856 | 26.912 | 26.496 | 29.688 | 25.394 | 26.344 | 29.731 | 25.881 | 28.055 | 25.383 |  | 12 | 12 |
| 481 | -5.153 | 0.292 | 0.214 | -4.844 | 0.098 | -0.320 | 17.680 | 22.622 | 22.204 | 15.648 | 21.093 | 21.015 | 24.893 | 20.154 | 23.157 | 18.446 |  | 4 | 4 |
| 482 | -4.506 | -0.615 | -1.232 | -5.189 | -0.488 | -1.078 | 17.147 | 21.847 | 21.257 | 17.027 | 20.918 | 20.302 | 24.470 | 20.200 | 23.725 | 19.342 |  | 6 | 6 |
| 483 | 2.183 | 2.505 | 1.738 | 1.748 | 1.899 | 2.390 | 29.273 | 29.424 | 29.915 | 28.451 | 28.772 | 28.006 | 28.460 | 26.590 | 27.998 | 24.537 |  | 14 | 14 |
| 484 | -2.066 | -2.161 | -3.333 | -3.673 | -1.655 | -2.611 | 22.762 | 24.779 | 23.824 | 23.902 | 23.806 | 22.634 | 29.174 | 23.696 | 27.372 | 24.562 |  | 16 | 16 |
| 485 | -4.878 | -1.462 | -1.399 | -2.361 | -2.612 | -3.134 | 24.037 | 23.787 | 23.265 | 20.467 | 23.884 | 23.947 | 28.010 | 24.787 | 27.111 | 23.580 |  | 14 | 14 |
| 486 | 0.843 | 0.300 | 0.579 | 1.276 | -0.375 | 0.470 | 27.504 | 25.854 | 26.699 | 26.270 | 25.727 | 26.006 | 27.609 | 24.849 | 26.984 | 23.869 |  | 25 | 25 |
| 487 | 10.204 | 7.082 | 6.717 | 10.016 | 7.770 | 5.879 | 27.254 | 25.008 | 23.118 | 26.783 | 23.661 | 23.296 | 19.072 | 15.405 | 18.732 | 14.426 |  | 3 | 3 |
| 488 | -1.394 | -0.841 | -0.234 | -1.537 | -0.607 | -0.660 | 25.703 | 26.633 | 26.581 | 24.798 | 25.351 | 25.958 | 28.412 | 26.069 | 27.863 | 24.521 |  | 25 | 25 |
| 489 | -1.158 | -0.363 | -0.001 | -1.496 | -0.122 | -0.230 | 23.544 | 24.918 | 24.810 | 22.995 | 23.790 | 24.152 | 26.854 | 23.226 | 25.686 | 22.619 |  | 26 | 6 |
| 490 | 7.832 | 8.018 | 8.223 | 8.183 | 8.625 | 6.995 | 25.243 | 25.685 | 24.055 | 23.748 | 23.934 | 24.139 | 18.728 | 15.392 | 16.576 | 15.256 |  | 2 | 2 |
| 491 | -1.631 | 3.283 | 3.110 | 2.505 | 1.492 | 0.500 | 18.973 | 17.960 | 16.969 | 15.181 | 20.095 | 19.922 | 16.616 | 16.320 | 18.643 | 14.980 |  | 1 | 1 |
| 492 | 5.340 | 1.997 | 3.131 | 5.694 | 3.521 | 1.003 | 31.371 | 29.198 | 26.680 | 29.831 | 26.488 | 27.622 | 26.584 | 24.770 | 27.111 | 21.871 |  | 8 | 8 |
| 493 | 2.100 | 0.358 | 0.872 | 2.120 | 1.564 | -0.583 | 30.680 | 30.124 | 27.976 | 29.168 | 27.425 | 27.940 | 29.820 | 27.299 | 29.288 | 24.847 |  | 5 | 5 |
| 494 | -8.668 | 1.275 | -0.497 | -3.840 | -2.053 | -2.217 | 23.005 | 24.792 | 24.628 | 16.468 | 26.412 | 24.640 | 28.203 | 25.487 | 26.446 | 23.828 |  | 24 | 24 |
| 495 | -2.788 | -1.545 | -5.778 | -6.608 | -2.150 | -1.501 | 17.496 | 21.954 | 22.603 | 20.425 | 21.668 | 17.434 | 27.497 | 20.712 | 25.522 | 20.903 |  | 7 | 7 |
| 496 | 6.820 | 4.036 | 4.391 | 6.212 | 5.289 | 3.610 | 30.766 | 29.842 | 28.163 | 30.515 | 27.732 | 28.086 | 26.110 | 22.996 | 26.199 | 21.192 |  | 15 | 15 |
| 497 | 3.877 | 1.111 | 0.492 | 3.918 | -0.651 | 2.118 | 20.642 | 16.073 | 18.842 | 20.366 | 17.600 | 16.981 | 17.491 | 15.957 | 18.043 | 14.936 |  | 1 | 1 |
| 498 | -2.844 | -1.819 | -2.694 | -2.765 | -3.437 | -1.218 | 18.143 | 17.470 | 19.690 | 17.541 | 18.565 | 17.691 | 26.200 | 15.614 | 23.153 | 17.616 |  | 10 | 10 |
| 499 | 0.887 | -0.585 | -1.088 | 0.260 | -0.124 | -0.977 | 28.359 | 27.975 | 27.123 | 28.296 | 26.825 | 26.321 | 29.281 | 26.917 | 28.073 | 26.745 |  | 11 | 11 |
| 500 | -9.450 | -0.651 | -2.320 | -9.377 | -0.720 | -2.339 | 16.151 | 24.808 | 23.189 | 15.137 | 23.936 | 22.267 | 26.465 | 24.591 | 24.996 | 24.177 |  | 12 | 12 |

|  | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 474 | 2 | 3.4 | 52.244 | 15.198 | 17.477 | 16.778 | **0.064** | **0.177** | P0CG14 | P0CG14 | Chromosome transmission fidelity protein 8 homolog isoform 2 | **Chtf8** | 585 |
| 475 | 6 | 21.2 | 46.839 | 38.933 | 17.197 | 18.676 | **0.057** | **0.175** | Q91VC3;E9PV04;A0A0N4SVP8;A2AFK7;A0A0N4SVM5 | Q91VC3;E9PV04;A0A0N4SVP8;A2AFK7 | Eukaryotic initiation factor 4A-III;Eukaryotic initiation factor 4A-III, N-terminally processed | **Eif4a3;Gm8994** | 1262 |
| 476 | 19 | 35.5 | 70.67 | 226.92 | 25.134 | 24.632 | **0.207** | **0.172** | P29341;Q9D4E6;Q62029;F6ZAX1;Q8C7D3;A2A5N3 | P29341 | Polyadenylate-binding protein 1 | **Pabpc1** | 674 |
| 477 | 3 | 33.7 | 20.252 | 121.19 | 22.916 | 21.524 | **0.118** | **0.162** | Q9CXW4;E9PYL9;A2BH06 | Q9CXW4;E9PYL9 | 60S ribosomal protein L11 | **Rpl11;Gm10036** | 355 |
| 478 | 12 | 34.5 | 31.231 | 89.79 | 26.422 | 25.899 | **0.138** | **0.155** | P25444;A0A140T8L5;D3YVC1;J3QMG5;D3YWJ3;F6YTZ4;E9Q1N8;D3Z536 | P25444;A0A140T8L5;D3YVC1;J3QMG5;D3YWJ3;F6YTZ4;E9Q1N8 | 40S ribosomal protein S2 | **Rps2;Gm5786;Gm6576;Gm18025** | 656 |
| 479 | 8 | 64.7 | 12.974 | 68.335 | 17.188 | 15.601 | **0.045** | **0.141** | Q3UQA7;A0A087WPM0;A0A087WNU1 | Q3UQA7;A0A087WPM0 | Selenoprotein H | **Selh;2700094K13Rik** | 988 |
| 480 | 12 | 57.2 | 16.085 | 296.99 | 27.806 | 26.719 | **0.025** | **0.141** | Q9CZX8;D3YUT3;D3Z722;D3YUG3;D3Z5R8;S4R223 | Q9CZX8;D3YUT3;D3Z722;D3YUG3;D3Z5R8;S4R223 | 40S ribosomal protein S19 | **Rps19** | 1401 |
| 481 | 4 | 7.4 | 73.163 | 23.377 | 22.524 | 20.801 | **0.019** | **0.139** | F8WHZ9;F8WGR0;Q9QYC0-2;Q9QYC0;E9Q1K3;F6V4G5;D3Z0T1;F6RDR0 | F8WHZ9;F8WGR0;Q9QYC0-2;Q9QYC0;E9Q1K3 | Alpha-adducin | **Add1** | 437 |
| 482 | 6 | 7.5 | 122.66 | 37.184 | 22.335 | 21.533 | **0.023** | **0.134** | Q9EPU0-2;Q9EPU0 | Q9EPU0-2;Q9EPU0 | Regulator of nonsense transcripts 1 | **Upf1** | 1483 |
| 483 | 14 | 45.7 | 21.644 | 244.47 | 27.525 | 26.267 | **0.166** | **0.130** | P35980 | P35980 | 60S ribosomal protein L18 | **Rpl18** | 697 |
| 484 | 16 | 99 | 10.963 | 156.83 | 26.435 | 25.967 | **0.062** | **0.126** | Q64433 | Q64433 | 10 kDa heat shock protein, mitochondrial | **Hspe1** | 1079 |
| 485 | 14 | 46.4 | 39.355 | 161.28 | 26.398 | 25.345 | **0.035** | **0.122** | P05064;A6ZI44;A0A0U1RPN8;D3YWI1;D3Z510;D3YV98;A0A0U1RPT5;Q9CPQ9;A6ZI46;A6ZI47 | P05064;A6ZI44;A0A0U1RPN8;D3YWI1;D3Z510;D3YV98;A0A0U1RPT5;Q9CPQ9;A6ZI46 | Fructose-bisphosphate aldolase A;Fructose-bisphosphate aldolase | **Aldoa;Aldoart1** | 561 |
| 486 | 25 | 42.5 | 47.153 | 246.73 | 26.229 | 25.427 | **0.083** | **0.117** | Q9D8E6 | Q9D8E6 | 60S ribosomal protein L4 | **Rpl4** | 1449 |
| 487 | 3 | 13.7 | 13.819 | 27.744 | 17.239 | 16.579 | **0.023** | **0.113** | A0A0U1RP30;Q8K2F8 | A0A0U1RP30;Q8K2F8 | Protein LSM14 homolog A | **Lsm14a** | 103 |
| 488 | 25 | 44.2 | 59.555 | 212.31 | 27.240 | 26.192 | **0.088** | **0.112** | P42932;H3BL49;H3BJB6;H3BLL1;H3BKG2;H3BKR8 | P42932;H3BL49;H3BJB6 | T-complex protein 1 subunit theta | **Cct8** | 708 |
| 489 | 2 | 56 | 49.83 | 110.47 | 25.040 | 24.153 | **0.068** | **0.109** | P68372 | P68372 | Tubulin beta-4B chain | **Tubb4b** | 874 |
| 490 | 2 | 15.2 | 13.874 | 14.55 | 17.060 | 15.916 | **0.062** | **0.090** | E9PUY1;O35680 | E9PUY1;O35680 | 28S ribosomal protein S12, mitochondrial | **Mrps12** | 328 |
| 491 | 1 | 17.6 | 12.274 | 7.1162 | 16.468 | 16.812 | **0.017** | **0.088** | P62878 | P62878 | E3 ubiquitin-protein ligase RBX1;E3 ubiquitin-protein ligase RBX1, N-terminally processed | **Rbx1** | 842 |
| 492 | 8 | 57.1 | 8.2038 | 119.79 | 25.677 | 24.491 | **0.017** | **0.084** | Q9JJI8 | Q9JJI8 | 60S ribosomal protein L38 | **Rpl38** | 1497 |
| 493 | 5 | 31.5 | 17.804 | 252.07 | 28.560 | 27.068 | **0.026** | **0.076** | P35979;F8VQK7 | P35979 | 60S ribosomal protein L12 | **Rpl12** | 696 |
| 494 | 24 | 48 | 67.63 | 194.2 | 26.845 | 25.137 | **0.008** | **0.073** | P40142;E0CY51 | P40142 | Transketolase | **Tkt** | 703 |
| 495 | 7 | 33.6 | 30.446 | 64.015 | 24.104 | 23.213 | **0.008** | **0.050** | G3UX26;Q60930;D3YZT5;D3YUN8 | G3UX26;Q60930 | Voltage-dependent anion-selective channel protein 2 | **Vdac2** | 452 |
| 496 | 15 | 68.8 | 14.463 | 148.03 | 24.553 | 23.696 | **0.013** | **0.045** | P62900;A0A0A6YX26;A0A0A6YXL3 | P62900;A0A0A6YX26;A0A0A6YXL3 | 60S ribosomal protein L31 | **Rpl31** | 846 |
| 497 | 1 | 2.8 | 67.928 | 6.4461 | 16.724 | 16.490 | **0.006** | **0.031** | E9Q740;F8VQC1 | E9Q740;F8VQC1 | Signal recognition particle subunit SRP72 | **Srp72** | 391 |
| 498 | 10 | 18.4 | 79.776 | 75.652 | 20.907 | 20.384 | **0.010** | **0.021** | Q91VD9;A0A087WQR0;A0A087WQ77;A0A087WR47;A0A087WP77 | Q91VD9 | NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial | **Ndufs1** | 1263 |
| 499 | 11 | 46.8 | 17.695 | 217.47 | 28.099 | 27.409 | **0.009** | **0.019** | P62751;A0A140T8M7;D3YTY6 | P62751;A0A140T8M7 | 60S ribosomal protein L23a | **Rpl23a** | 114 |
| 500 | 12 | 27 | 60.452 | 90.323 | 25.528 | 24.587 | **0.000** | **0.005** | Q8VCQ8;E9QA16;S4R1T7;E9Q0M9;D3Z6I7;E9QA15;E9Q9F3;F6QLP8;F6RGN9;F6ZAW1;F6T2Z7;REV__B2RXW8;REV__Q8BSS9;REV__B8QI34;REV__B2RXQ2 | Q8VCQ8;E9QA16;S4R1T7;E9Q0M9;D3Z6I7;E9QA15 |  | **Cald1** | 401 |

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 501 | -1.958 | -2.093 | 3.427 | 1.637 | -0.267 | -1.999 | 21.103 | 19.199 | 17.467 | 16.927 | 16.792 | 22.312 | 23.462 | 15.471 | 23.408 | 14.362 | | 8 | 8 |
| 502 | -3.925 | -2.166 | -3.086 | -3.055 | -3.300 | -3.474 | 17.235 | 16.990 | 16.816 | 15.873 | 17.632 | 16.711 | 20.390 | 20.191 | 19.181 | 20.413 | | 1 | 1 |
| 503 | -2.650 | -3.884 | -4.062 | -4.713 | -4.304 | -4.351 | 17.041 | 17.450 | 17.403 | 18.320 | 17.087 | 16.908 | 23.251 | 20.257 | 22.012 | 19.929 | | 4 | 4 |
| 504 | -5.120 | -3.790 | -2.384 | -5.330 | -3.480 | -5.683 | 16.974 | 18.824 | 16.621 | 15.343 | 16.673 | 18.079 | 23.896 | 20.712 | 21.470 | 19.454 | | 1 | 1 |
| 505 | -6.641 | -5.132 | -4.494 | -3.547 | -3.623 | -3.647 | 16.859 | 16.783 | 16.759 | 15.184 | 16.694 | 17.331 | 18.008 | 22.804 | 22.698 | 20.952 | | 1 | 1 |
| 506 | -5.096 | -2.835 | -3.038 | -2.486 | -2.912 | -2.472 | 17.346 | 16.920 | 17.360 | 15.963 | 18.224 | 18.021 | 24.314 | 15.350 | 23.137 | 18.980 | | 2 | 2 |
| 507 | -5.224 | -4.716 | -5.102 | -5.336 | -5.193 | -7.186 | 17.519 | 17.662 | 15.669 | 16.500 | 17.009 | 16.622 | 24.406 | 21.304 | 23.361 | 20.087 | | 1 | 1 |
| 508 | -4.381 | -0.872 | -3.673 | -2.856 | -2.519 | -2.634 | 17.197 | 17.534 | 17.419 | 15.709 | 19.217 | 16.417 | 23.762 | 16.344 | 20.370 | 19.809 | | 2 | 2 |
| 509 | -7.034 | -3.978 | -6.297 | -8.115 | -9.354 | -6.897 | 17.315 | 16.076 | 18.532 | 14.936 | 17.992 | 15.674 | 26.406 | 24.453 | 19.249 | 24.691 | | 3 | 3 |
| 510 | -3.304 | -0.713 | -2.115 | -4.599 | -3.625 | -3.563 | 16.341 | 17.315 | 17.377 | 15.400 | 17.991 | 16.589 | 22.015 | 19.865 | 18.218 | 19.190 | | 16 | 1 |
| 511 | -5.624 | -4.466 | -3.697 | -6.387 | -7.219 | -5.760 | 16.635 | 15.803 | 17.262 | 16.304 | 17.461 | 18.231 | 24.413 | 21.631 | 23.175 | 20.680 | | 1 | 1 |
| 512 | -0.199 | 1.501 | 0.168 | -2.935 | -3.787 | -3.369 | 17.803 | 16.951 | 17.369 | 17.105 | 18.804 | 17.472 | 22.335 | 19.141 | 20.270 | 14.338 | | 1 | 1 |
| 513 | -7.586 | -4.651 | -6.921 | -6.881 | -8.009 | -9.179 | 18.674 | 17.545 | 16.376 | 15.942 | 18.877 | 16.607 | 26.092 | 25.018 | 23.023 | 24.032 | | 6 | 6 |
| 514 | -0.965 | -0.038 | -1.159 | -4.965 | -5.037 | -6.360 | 17.938 | 17.865 | 16.543 | 17.168 | 18.095 | 16.974 | 25.039 | 20.766 | 20.905 | 15.361 | | 2 | 2 |
| 515 | -1.617 | -1.103 | 0.999 | -3.735 | -3.810 | -4.174 | 17.908 | 17.832 | 17.468 | 16.065 | 16.580 | 18.681 | 22.650 | 20.634 | 18.896 | 16.469 | | 2 | 2 |
| 516 | -3.313 | -1.989 | -3.990 | -4.264 | -5.551 | -4.230 | 17.100 | 15.813 | 17.134 | 16.773 | 18.096 | 16.095 | 21.846 | 20.883 | 20.463 | 19.708 | | 2 | 2 |
| 517 | -4.052 | -2.189 | -3.677 | -4.290 | -2.006 | -2.368 | 16.023 | 18.308 | 17.945 | 16.058 | 17.921 | 16.433 | 23.711 | 16.915 | 21.253 | 18.967 | | 3 | 3 |
| 518 | -1.316 | -0.368 | -0.039 | -3.419 | -3.618 | -4.383 | 17.510 | 17.311 | 16.546 | 16.127 | 17.075 | 17.404 | 23.367 | 18.491 | 16.073 | 18.813 | | 4 | 4 |
| 519 | -3.662 | -1.058 | -4.099 | -2.410 | -3.692 | -3.470 | 17.399 | 16.116 | 16.339 | 15.779 | 18.384 | 15.342 | 23.597 | 16.020 | 21.142 | 17.742 | | 2 | 2 |
| 520 | -3.176 | -1.954 | -1.873 | -1.482 | -0.131 | -0.951 | 16.952 | 18.303 | 17.483 | 16.349 | 17.571 | 17.651 | 20.766 | 16.102 | 20.441 | 18.607 | | 3 | 2 |
| 521 | -5.620 | -3.787 | -5.210 | -6.302 | -5.920 | -5.208 | 16.192 | 16.574 | 17.286 | 15.878 | 17.711 | 16.289 | 23.441 | 21.547 | 20.920 | 22.077 | | 5 | 4 |
| 522 | -7.176 | -7.014 | -6.680 | -9.435 | -8.597 | -9.903 | 16.838 | 17.676 | 16.370 | 17.323 | 17.486 | 17.819 | 27.982 | 24.564 | 26.003 | 22.996 | | 11 | 2 |
| 523 | -5.337 | -2.440 | -2.957 | -2.814 | -3.776 | -4.138 | 17.133 | 16.172 | 15.810 | 15.439 | 18.335 | 17.818 | 25.142 | 14.753 | 22.608 | 18.942 | | 4 | 4 |
| 524 | -3.638 | -2.791 | -4.404 | -2.121 | -2.304 | -1.988 | 17.160 | 16.977 | 17.293 | 16.573 | 17.420 | 15.807 | 22.399 | 16.162 | 20.905 | 19.518 | | 1 | 1 |
| 525 | -2.110 | 0.124 | -0.935 | -6.665 | -7.697 | -7.419 | 17.084 | 16.053 | 16.330 | 16.122 | 18.357 | 17.298 | 24.629 | 22.869 | 20.867 | 15.599 | | 3 | 3 |
| 526 | -0.764 | 2.017 | 1.206 | -7.068 | -6.627 | -8.042 | 17.927 | 18.369 | 16.954 | 15.379 | 18.160 | 17.349 | 24.835 | 25.156 | 16.794 | 15.492 | | 2 | 2 |
| 527 | -5.140 | -2.760 | -3.180 | -4.157 | -4.097 | -3.833 | 17.028 | 17.088 | 17.352 | 15.253 | 17.633 | 17.213 | 21.996 | 20.374 | 21.594 | 19.192 | | 2 | 2 |
| 528 | -1.082 | -1.619 | -1.547 | -1.733 | -0.987 | -3.873 | 17.375 | 18.121 | 15.236 | 17.358 | 16.821 | 16.893 | 22.551 | 15.666 | 19.229 | 17.652 | | 2 | 2 |

|  | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 501 | 8 | 16.9 | 52.22 | 48.014 | 19.466 | 18.885 | **0.000** | **0.002** | P60229 | P60229 | Eukaryotic translation initiation factor 3 subunit E | **Eif3e** | 781 |
| 502 | 1 | 4.4 | 53.974 | 8.6081 | 20.290 | 19.797 | **NaN** | **0.000** | A0A087WNV1;A0A087WSR7;A0A087WR52;Q8K2K6-3;Q8K2K6-2;Q8K2K6-1;Q8K2K6 | A0A087WNV1;A0A087WSR7;A0A087WR52;Q8K2K6-3;Q8K2K6-2;Q8K2K6-1;Q8K2K6 | Arf-GAP domain and FG repeat-containing protein 1 | **Agfg1** | 15 |
| 503 | 4 | 2.9 | 218.71 | 24.286 | 21.754 | 20.970 | **NaN** | **0.000** | Z4YL78;A0A0R4J0K2;K3W4R5;A2AGT5-2;A2AGT5-3;A2AGT5 | Z4YL78;A0A0R4J0K2;K3W4R5;A2AGT5-2;A2AGT5-3;A2AGT5 | Cytoskeleton-associated protein 5 | **Ckap5** | 86 |
| 504 | 1 | 15.4 | 16.678 | 23.115 | 22.304 | 20.462 | **NaN** | **0.000** | D3Z0F3;A0A0R4J1N9;P40630-2;P40630 | D3Z0F3;A0A0R4J1N9;P40630-2;P40630 | Transcription factor A, mitochondrial | **Tfam** | 95 |
| 505 | 1 | 26.3 | 4.1719 | 8.1108 | 20.406 | 21.825 | **NaN** | **0.000** | A0A140LHG0;P17427;P17426-2;P17426 | A0A140LHG0;P17427;P17426-2;P17426 | AP-2 complex subunit alpha-2;AP-2 complex subunit alpha-1 | **Ap2a2;Ap2a1** | 108 |
| 506 | 2 | 41.5 | 6.088 | 13.085 | 19.832 | 21.059 | **NaN** | **0.000** | A0A140LJ59;Q9DBZ5;Q3TY56;Q9DBZ5-2 | A0A140LJ59;Q9DBZ5;Q3TY56;Q9DBZ5-2 | Eukaryotic translation initiation factor 3 subunit K | **Eif3k** | 111 |
| 507 | 1 | 12.6 | 16.518 | 12.083 | 22.855 | 21.724 | **NaN** | **0.000** | A2A701;A2A702;Q99JX4 | A2A701;A2A702;Q99JX4 | Eukaryotic translation initiation factor 3 subunit M | **Eif3m** | 129 |
| 508 | 2 | 10.4 | 27.763 | 24.697 | 20.053 | 20.090 | **NaN** | **0.000** | F7BUB8;F6S4K9;A2A839;A2A838;A2A842;A2A841;P48193-2;P48193;F7CR30 | F7BUB8;F6S4K9;A2A839;A2A838;A2A842;A2A841;P48193-2;P48193;F7CR30 | Protein 4.1 | **Epb4.1;Epb41** | 132 |
| 509 | 3 | 8.6 | 48.455 | 20.324 | 25.430 | 21.970 | **NaN** | **0.000** | A2AIW9;Q9DC61 | A2AIW9;Q9DC61 | Mitochondrial-processing peptidase subunit alpha | **Pmpca** | 152 |
| 510 | 1 | 4.9 | 469.02 | 7.7749 | 20.940 | 18.704 | **NaN** | **0.000** | B1B0C7;E9PZ16 | B1B0C7;E9PZ16 | Basement membrane-specific heparan sulfate proteoglycan core protein | **Hspg2** | 202 |
| 511 | 1 | 7.1 | 19.569 | 8.5427 | 23.022 | 21.927 | **NaN** | **0.000** | D3YWT0;D3Z569;D3YTS1;Q9R0P6 | D3YWT0;D3Z569;D3YTS1;Q9R0P6 | Signal peptidase complex catalytic subunit SEC11;Signal peptidase complex catalytic subunit SEC11A | **Sec11a** | 275 |
| 512 | 1 | 8 | 17.222 | 6.6662 | 20.738 | 17.304 | **NaN** | **0.000** | D6RFA7;D3YUP1;Q9WVG6-2;Q9WVG6 | D6RFA7;D3YUP1;Q9WVG6-2;Q9WVG6 | Histone-arginine methyltransferase CARM1 | **Carm1** | 278 |
| 513 | 6 | 18.5 | 49.573 | 49.835 | 25.555 | 23.528 | **NaN** | **0.000** | D3YXT0;Q91WD5;A0A0A6YXD3;A0A0A6YW30 | D3YXT0;Q91WD5 | NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial | **Ndufs2** | 286 |
| 514 | 2 | 31.9 | 14.038 | 17.223 | 22.903 | 18.133 | **NaN** | **0.000** | D3Z568;Q9CQH3;F6Y6V5;D3YX99;D3Z6W9 | D3Z568;Q9CQH3;F6Y6V5;D3YX99;D3Z6W9 | NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial | **Ndufb5** | 308 |
| 515 | 2 | 40.3 | 12.455 | 13.669 | 21.642 | 17.682 | **NaN** | **0.000** | E0CYA9;Q9CQ36 | E0CYA9;Q9CQ36 | DNA polymerase epsilon subunit 4 | **Pole4** | 321 |
| 516 | 2 | 23.5 | 14.729 | 14.362 | 21.364 | 20.085 | **NaN** | **0.000** | E0CYQ2;Q9CQ48 | E0CYQ2;Q9CQ48 | NudC domain-containing protein 2 | **Nudcd2** | 323 |
| 517 | 3 | 27 | 8.7887 | 19.938 | 20.313 | 20.110 | **NaN** | **0.000** | E9PV44;O35143 | E9PV44;O35143 | ATPase inhibitor, mitochondrial | **Atpif1** | 333 |
| 518 | 4 | 5.7 | 144.77 | 23.174 | 20.929 | 17.443 | **NaN** | **0.000** | E9Q175;E9PVU0;E9Q3L1;E9Q174;V9GXM4;V9GX76;Q64331 | E9Q175;E9PVU0;E9Q3L1;E9Q174;V9GXM4;V9GX76 |  | **Myo6** | 337 |
| 519 | 2 | 15.7 | 14.913 | 12.912 | 19.809 | 19.442 | **NaN** | **0.000** | E9PZS8;Q61387 | E9PZS8;Q61387 | Cytochrome c oxidase subunit 7A-related protein, mitochondrial | **Cox7a2l** | 362 |
| 520 | 2 | 15.8 | 28.021 | 11.836 | 18.434 | 19.524 | **NaN** | **0.000** | E9Q9E4;E9PZX7;P30285;D6RHS5;D3YWB0 | E9Q9E4;E9PZX7;P30285;D6RHS5;D3YWB0 | Cyclin-dependent kinase 4 | **Cdk4** | 363 |
| 521 | 4 | 5.1 | 107.8 | 27.76 | 22.494 | 21.498 | **NaN** | **0.000** | E9Q035;Q921I1;P47758 | E9Q035;Q921I1 | Serotransferrin | **Gm20425;Tf** | 364 |
| 522 | 2 | 39.4 | 34.216 | 43.489 | 26.273 | 24.499 | **NaN** | **0.000** | E9Q070;D3YVM5 | E9Q070;D3YVM5 | 60S acidic ribosomal protein P0 | **Gm8730;Rplp0** | 365 |
| 523 | 4 | 7.5 | 91.677 | 27.017 | 19.948 | 20.775 | **NaN** | **0.000** | E9Q0U7;Q61699-2;Q61699;D3Z3I9 | E9Q0U7;Q61699-2;Q61699 | Heat shock protein 105 kDa | **Hsph1** | 367 |
| 524 | 1 | 4.7 | 53.13 | 8.3125 | 19.281 | 20.211 | **NaN** | **0.000** | E9Q242;P54822 | E9Q242;P54822 | Adenylosuccinate lyase | **Adsl** | 372 |
| 525 | 3 | 21.1 | 18.922 | 22.272 | 23.749 | 18.233 | **NaN** | **0.000** | E9Q6R3;O08547;D6RES2;A0A0G2JF08 | E9Q6R3;O08547 | Vesicle-trafficking protein SEC22b | **Sec22b** | 388 |
| 526 | 2 | 5.1 | 115.95 | 16.049 | 24.996 | 16.143 | **NaN** | **0.000** | E9QKZ2;Q91YE6;E0CY46;F6TLX3;E0CXB2 | E9QKZ2;Q91YE6;E0CY46;F6TLX3;E0CXB2 | Importin-9 | **Ipo9** | 406 |
| 527 | 2 | 7.9 | 40.271 | 11.847 | 21.185 | 20.393 | **NaN** | **0.000** | F6QHD1;Q80WJ7;E9PUX0;F6ZQL0;F6ZSG0;F6QFT1 | F6QHD1;Q80WJ7;E9PUX0;F6ZQL0;F6ZSG0;F6QFT1 | Protein LYRIC | **Mtdh** | 416 |
| 528 | 2 | 9.9 | 32.545 | 13.029 | 19.108 | 18.440 | **NaN** | **0.000** | F6SQH7;Q91VA6 | F6SQH7;Q91VA6 | Polymerase delta-interacting protein 2 | **Poldip2** | 419 |

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 529 | -6.740 | -4.755 | -3.118 | -6.224 | -6.394 | -4.579 | 16.321 | 16.150 | 17.965 | 14.778 | 16.764 | 18.401 | 22.754 | 22.334 | 23.541 | 19.496 | | 1 | 1 |
| 530 | -0.889 | 0.336 | -1.839 | -3.027 | -3.181 | -4.164 | 17.875 | 17.721 | 16.738 | 17.450 | 18.675 | 16.500 | 22.137 | 19.667 | 16.658 | 20.020 | | 2 | 2 |
| 531 | -4.548 | -3.388 | -3.360 | -4.967 | -3.523 | -4.580 | 16.565 | 18.008 | 16.952 | 16.210 | 17.370 | 17.398 | 20.736 | 22.326 | 21.653 | 19.863 | | 2 | 2 |
| 532 | -6.322 | -4.742 | -5.993 | -8.281 | -9.353 | -8.145 | 17.285 | 16.213 | 17.420 | 16.293 | 17.873 | 16.622 | 27.981 | 23.150 | 24.536 | 20.695 | | 7 | 7 |
| 533 | -5.430 | -2.768 | -2.623 | -4.321 | -3.794 | -3.397 | 16.481 | 17.008 | 17.405 | 15.024 | 17.685 | 17.831 | 21.715 | 19.890 | 21.719 | 19.188 | | 4 | 4 |
| 534 | -3.797 | -2.610 | -4.008 | -2.248 | -2.032 | -2.118 | 16.665 | 16.882 | 16.796 | 16.410 | 17.597 | 16.199 | 22.285 | 15.543 | 21.423 | 18.991 | | 1 | 1 |
| 535 | -6.087 | -3.427 | -4.990 | -1.031 | -0.503 | -1.970 | 17.147 | 17.674 | 16.208 | 15.564 | 18.225 | 16.662 | 21.257 | 15.098 | 22.406 | 20.897 | | 3 | 3 |
| 536 | -2.608 | -2.246 | -3.488 | -2.888 | -3.650 | -4.307 | 17.848 | 17.086 | 16.429 | 17.221 | 17.583 | 16.342 | 22.266 | 19.205 | 22.463 | 17.195 | | 4 | 2 |
| 537 | -4.123 | -2.489 | -3.905 | -6.820 | -7.174 | -7.139 | 17.645 | 17.291 | 17.325 | 17.179 | 18.813 | 17.397 | 28.269 | 20.661 | 22.036 | 20.568 | | 4 | 4 |
| 538 | -4.486 | -3.146 | -3.892 | -5.166 | -3.673 | -4.116 | 16.377 | 17.869 | 17.426 | 16.688 | 18.028 | 17.281 | 25.613 | 17.473 | 21.060 | 21.288 | | 7 | 2 |
| 539 | -4.062 | -2.658 | -4.820 | -3.675 | -3.122 | -5.349 | 18.375 | 18.928 | 16.702 | 17.036 | 18.440 | 16.278 | 24.686 | 19.415 | 22.290 | 19.906 | | 3 | 3 |
| 540 | -7.062 | -4.494 | -5.128 | -6.150 | -4.603 | -5.372 | 16.873 | 18.421 | 17.651 | 14.905 | 17.473 | 16.839 | 25.280 | 20.767 | 24.215 | 19.719 | | 3 | 3 |
| 541 | -1.635 | -0.573 | -2.040 | -2.729 | -1.524 | -0.565 | 15.972 | 17.177 | 18.136 | 17.877 | 18.939 | 17.472 | 20.335 | 17.065 | 22.287 | 16.738 | | 4 | 4 |
| 542 | -3.977 | -2.640 | -4.576 | -4.170 | -1.536 | -3.014 | 16.201 | 18.836 | 17.358 | 16.690 | 18.027 | 16.092 | 25.426 | 15.316 | 21.742 | 19.593 | | 2 | 2 |
| 543 | -1.404 | -1.291 | -1.287 | -5.209 | -6.394 | -3.851 | 16.504 | 15.320 | 17.863 | 17.266 | 17.380 | 17.384 | 23.356 | 20.071 | 22.105 | 15.236 | | 3 | 3 |
| 544 | -4.351 | -2.588 | -3.167 | -6.850 | -6.024 | -6.121 | 16.305 | 17.131 | 17.034 | 15.628 | 17.391 | 16.812 | 24.589 | 21.722 | 21.015 | 18.943 | | 4 | 2 |
| 545 | -2.814 | 0.035 | -0.722 | -5.386 | -3.967 | -5.236 | 16.651 | 18.070 | 16.801 | 15.623 | 18.472 | 17.715 | 23.008 | 21.066 | 18.523 | 18.350 | | 3 | 3 |
| 546 | -3.412 | -2.297 | -4.881 | -3.114 | -3.410 | -0.610 | 16.478 | 16.183 | 18.983 | 17.528 | 18.642 | 16.058 | 23.970 | 15.216 | 23.893 | 17.986 | | 2 | 2 |
| 547 | -1.626 | 0.703 | 0.642 | -0.864 | -2.754 | -0.502 | 18.455 | 16.565 | 18.817 | 16.464 | 18.792 | 18.731 | 21.517 | 17.121 | 20.438 | 15.741 | | 2 | 2 |
| 548 | -2.617 | -0.758 | -0.097 | -5.239 | -5.190 | -4.696 | 16.073 | 16.122 | 16.616 | 15.987 | 17.846 | 18.507 | 23.366 | 19.259 | 22.325 | 14.882 | | 2 | 2 |
| 549 | -6.047 | -5.622 | -5.144 | -5.726 | -6.687 | -6.244 | 17.522 | 16.561 | 17.004 | 16.871 | 17.296 | 17.773 | 22.640 | 23.856 | 23.510 | 22.325 | | 2 | 2 |
| 550 | -5.776 | -4.847 | -4.946 | -3.057 | -3.803 | -2.182 | 16.835 | 16.089 | 17.710 | 16.585 | 17.513 | 17.415 | 18.051 | 21.734 | 24.756 | 19.965 | | 1 | 1 |
| 551 | -5.145 | -4.258 | -2.204 | -2.820 | -2.630 | -4.080 | 17.595 | 17.786 | 16.336 | 15.259 | 16.147 | 18.200 | 24.300 | 16.530 | 22.373 | 18.436 | | 1 | 1 |
| 552 | -7.542 | -6.382 | -4.637 | -8.092 | -6.503 | -6.446 | 15.946 | 17.535 | 17.592 | 16.071 | 17.232 | 18.976 | 24.619 | 23.457 | 25.167 | 22.060 | | 3 | 3 |
| 553 | -3.499 | 0.437 | -1.512 | -3.419 | -3.270 | -3.733 | 17.291 | 17.439 | 16.977 | 14.916 | 18.853 | 16.903 | 22.737 | 18.683 | 21.674 | 15.157 | | 1 | 1 |
| 554 | -5.271 | -4.902 | -6.247 | -8.330 | -8.913 | -8.767 | 16.987 | 16.404 | 16.550 | 16.760 | 17.129 | 15.783 | 26.599 | 24.035 | 21.348 | 22.713 | | 2 | 2 |
| 555 | -4.063 | -4.090 | -4.184 | -6.790 | -5.453 | -5.769 | 15.994 | 17.330 | 17.014 | 17.300 | 17.274 | 17.179 | 25.548 | 20.019 | 22.018 | 20.708 | | 6 | 6 |
| 556 | -6.987 | -6.114 | -6.596 | -5.353 | -5.893 | -4.909 | 16.430 | 15.889 | 16.873 | 16.411 | 17.284 | 16.802 | 19.795 | 23.771 | 23.911 | 22.886 | | 2 | 2 |

| | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 529 | 1 | 9.2 | 16.809 | 6.3965 | 22.544 | 21.519 | **NaN** | **0.000** | F6VF36;Q9DBG7 | F6VF36;Q9DBG7 | Signal recognition particle receptor subunit alpha | **Srpr** | 422 |
| 530 | 1 | 20.6 | 21.316 | 22.84 | 20.902 | 18.339 | **NaN** | **0.000** | F7AI87;O35226-2;O35226-3 | F7AI87;O35226-2;O35226-3 | 26S proteasome non-ATPase regulatory subunit 4 | **Psmd4** | 428 |
| 531 | 2 | 6.8 | 48.334 | 12.1 | 21.531 | 20.758 | **NaN** | **0.000** | G3UZ26;G3UYY1;P50431;G3UZZ9 | G3UZ26;G3UYY1;P50431;G3UZZ9 | Serine hydroxymethyltransferase;Serine hydroxymethyltransferase, cytosolic | **Shmt1** | 461 |
| 532 | 7 | 54 | 18.749 | 69.401 | 25.566 | 22.615 | **NaN** | **0.000** | Q9DCX2;G3X9L6;B1ASE2 | Q9DCX2;G3X9L6;B1ASE2 | ATP synthase subunit d, mitochondrial | **Atp5h;Gm10250** | 467 |
| 533 | 4 | 5.2 | 111.97 | 24.459 | 20.803 | 20.454 | **NaN** | **0.000** | Q60875;Q60875-5;Q60875-4;H3BJ45;H3BJU7;H3BJ40;H3BJX8;H3BKH9;Q60875-2;Q60875-3;H3BLF9;H3BLJ1;H3BIX8;H3BJM4;H3BJ59;H3BL15;H3BJ48 | Q60875;Q60875-5;Q60875-4;H3BJ45;H3BJU7;H3BJ40;H3BJX8;H3BKH9;Q60875-2;Q60875-3 | Rho guanine nucleotide exchange factor 2 | **Arhgef2** | 478 |
| 534 | 1 | 3.8 | 52.763 | 8.5768 | 18.914 | 20.207 | **NaN** | **0.000** | Q6P1B9;O08539-2;O08539 | Q6P1B9;O08539-2;O08539 | Myc box-dependent-interacting protein 1 | **Bin1** | 497 |
| 535 | 3 | 15.6 | 50.526 | 20.337 | 18.177 | 21.652 | **NaN** | **0.000** | Q3TMN1;Q3UI33;O08663;M0QWX0;M0QW48 | Q3TMN1;Q3UI33;O08663 | Methionine aminopeptidase 2 | **Metap2** | 500 |
| 536 | 2 | 5.2 | 101.19 | 14.654 | 20.736 | 19.829 | **NaN** | **0.000** | Q5SVG5;Q5SVG4;O35643 | Q5SVG5;Q5SVG4;O35643 | AP-1 complex subunit beta-1 | **Ap1b1** | 512 |
| 537 | 4 | 23.9 | 35.774 | 26.265 | 24.465 | 21.302 | **NaN** | **0.000** | O70400;S4R1V0 | O70400;S4R1V0 | PDZ and LIM domain protein 1 | **Pdlim1** | 535 |
| 538 | 1 | 57.8 | 15.84 | 66.284 | 21.543 | 21.174 | **NaN** | **0.000** | P02088 | P02088 | Hemoglobin subunit beta-1 | **Hbb-b1** | 554 |
| 539 | 3 | 9.6 | 36.572 | 19.91 | 22.050 | 21.098 | **NaN** | **0.000** | P16125;A0A0N4SVV8;D3Z7F0 | P16125;A0A0N4SVV8;D3Z7F0 | L-lactate dehydrogenase B chain;L-lactate dehydrogenase | **Ldhb** | 620 |
| 540 | 3 | 15 | 36.539 | 21.683 | 23.024 | 21.967 | **NaN** | **0.000** | P26516 | P26516 | 26S proteasome non-ATPase regulatory subunit 7 | **Psmd7** | 663 |
| 541 | 4 | 10.1 | 53.706 | 25.853 | 18.700 | 19.512 | **NaN** | **0.000** | P28658 | P28658 | Ataxin-10 | **Atxn10** | 672 |
| 542 | 2 | 12.7 | 22.794 | 12.618 | 20.371 | 20.667 | **NaN** | **0.000** | P30412 | P30412 | Peptidyl-prolyl cis-trans isomerase C | **Ppic** | 677 |
| 543 | 3 | 16 | 23.035 | 19.485 | 21.714 | 18.671 | **NaN** | **0.000** | P35293 | P35293 | Ras-related protein Rab-18 | **Rab18** | 691 |
| 544 | 2 | 28.9 | 18.709 | 12.617 | 23.155 | 19.979 | **NaN** | **0.000** | P45591 | P45591 | Cofilin-2 | **Cfl2** | 714 |
| 545 | 3 | 10.9 | 46.481 | 19.907 | 22.037 | 18.437 | **NaN** | **0.000** | P45952 | P45952 | Medium-chain specific acyl-CoA dehydrogenase, mitochondrial | **Acadm** | 715 |
| 546 | 2 | 4.8 | 76.722 | 14.85 | 19.593 | 20.939 | **NaN** | **0.000** | P47856-2;P47856;Q9Z2Z9 | P47856-2;P47856;Q9Z2Z9 | Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1;Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 2 | **Gfpt1;Gfpt2** | 724 |
| 547 | 2 | 9.7 | 26.157 | 12.098 | 19.319 | 18.089 | **NaN** | **0.000** | P50518;A0A0N4SW34 | P50518;A0A0N4SW34 | V-type proton ATPase subunit E 1 | **Atp6v1e1** | 740 |
| 548 | 2 | 13.2 | 23.547 | 14.545 | 21.312 | 18.604 | **NaN** | **0.000** | P53994;Q3TEG7;P59279 | P53994;Q3TEG7;P59279 | Ras-related protein Rab-2A;Ras-related protein Rab-2B | **Rab2a;Rab2b** | 755 |
| 549 | 2 | 29.4 | 7.7412 | 13.848 | 23.248 | 22.917 | **NaN** | **0.000** | P60060 | P60060 | Protein transport protein Sec61 subunit gamma | **Sec61g** | 779 |
| 550 | 1 | 8.5 | 20.198 | 9.1185 | 19.892 | 22.361 | **NaN** | **0.000** | P61924 | P61924 | Coatomer subunit zeta-1 | **Copz1** | 801 |
| 551 | 1 | 14.7 | 10.458 | 15.835 | 20.415 | 20.404 | **NaN** | **0.000** | P62075 | P62075 | Mitochondrial import inner membrane translocase subunit Tim13 | **Timm13** | 805 |
| 552 | 3 | 19.5 | 13.17 | 19.129 | 24.038 | 23.614 | **NaN** | **0.000** | P62869;A6PWE0 | P62869 | Transcription elongation factor B polypeptide 2 | **Tceb2** | 841 |
| 553 | 1 | 3.7 | 46.67 | 8.5209 | 20.710 | 18.415 | **NaN** | **0.000** | P63005 | P63005 | Platelet-activating factor acetylhydrolase IB subunit alpha | **Pafah1b1** | 854 |
| 554 | 2 | 11 | 19.462 | 32.964 | 25.317 | 22.031 | **NaN** | **0.000** | P63028 | P63028 | Translationally-controlled tumor protein | **Tpt1** | 856 |
| 555 | 6 | 16.3 | 48.328 | 39.033 | 22.783 | 21.363 | **NaN** | **0.000** | Q3TRH2;Q9D8W5;B1AT36 | Q3TRH2;Q9D8W5;B1AT36 | 26S proteasome non-ATPase regulatory subunit 12 | **Psmd12** | 956 |
| 556 | 2 | 10.7 | 34.425 | 23.195 | 21.783 | 23.398 | **NaN** | **0.000** | Q3UFY7;A0A0R4J146;Q3UFY7-3;Q3UFY7-2;Q3UFY7-4 | Q3UFY7;A0A0R4J146;Q3UFY7-3;Q3UFY7-2;Q3UFY7-4 | 7-methylguanosine phosphate-specific 5-nucleotidase | **Nt5c3b** | 975 |

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 557 | -5.689 | -3.520 | -3.549 | -8.251 | -7.899 | -7.732 | 16.939 | 17.291 | 17.458 | 15.701 | 17.869 | 17.840 | 26.994 | 23.387 | 24.810 | 17.969 | | 7 | 7 |
| 558 | -3.790 | -2.570 | -2.554 | -1.364 | -2.278 | -1.915 | 18.272 | 17.358 | 17.722 | 15.208 | 16.428 | 16.444 | 21.273 | 18.000 | 17.940 | 20.055 | | 1 | 1 |
| 559 | -3.845 | -1.545 | -2.743 | -3.664 | -3.920 | -5.087 | 16.795 | 16.539 | 15.372 | 16.341 | 18.641 | 17.443 | 20.861 | 20.056 | 20.542 | 19.830 | | 2 | 2 |
| 560 | -2.335 | -1.118 | -1.206 | -6.616 | -5.902 | -6.151 | 15.939 | 16.653 | 16.404 | 16.267 | 17.485 | 17.397 | 24.349 | 20.760 | 23.039 | 14.166 | | 3 | 3 |
| 561 | -6.350 | -4.804 | -4.962 | -6.760 | -6.162 | -6.906 | 16.350 | 16.948 | 16.204 | 15.999 | 17.545 | 17.387 | 25.399 | 20.821 | 22.709 | 21.989 | | 6 | 6 |
| 562 | -4.951 | -3.256 | -3.450 | -4.904 | -5.266 | -4.757 | 17.641 | 17.278 | 17.787 | 15.894 | 17.588 | 17.395 | 24.347 | 20.742 | 23.209 | 18.480 | | 6 | 6 |
| 563 | -6.055 | -3.881 | -3.852 | -3.688 | -4.327 | -3.740 | 16.855 | 16.216 | 16.803 | 14.981 | 17.155 | 17.184 | 19.567 | 21.519 | 22.669 | 19.402 | | 2 | 2 |
| 564 | -5.407 | -3.042 | -3.805 | -3.252 | -2.489 | -1.130 | 16.377 | 17.139 | 18.499 | 15.414 | 17.779 | 17.016 | 24.117 | 15.140 | 22.491 | 19.150 | | 1 | 1 |
| 565 | -1.964 | -1.282 | -1.294 | -1.679 | -0.983 | -1.990 | 17.059 | 17.755 | 16.748 | 16.267 | 16.950 | 16.938 | 20.552 | 16.925 | 22.133 | 14.330 | | 4 | 4 |
| 566 | -0.911 | -0.395 | 0.345 | -4.531 | -3.107 | -4.586 | 17.371 | 18.795 | 17.316 | 16.834 | 17.350 | 18.090 | 24.304 | 19.500 | 20.074 | 15.416 | | 3 | 3 |
| 567 | -5.967 | -2.303 | -3.868 | -3.244 | -3.664 | -2.427 | 16.271 | 15.850 | 17.087 | 14.215 | 17.879 | 16.314 | 23.710 | 15.319 | 21.684 | 18.680 | | 3 | 3 |
| 568 | -5.119 | -3.944 | -3.926 | -4.627 | -1.797 | -1.477 | 15.581 | 18.411 | 18.730 | 15.999 | 17.173 | 17.192 | 19.102 | 21.313 | 20.884 | 21.352 | | 1 | 1 |
| 569 | -2.672 | -3.713 | -2.903 | -2.507 | -1.456 | -1.904 | 16.663 | 17.714 | 17.267 | 17.528 | 16.487 | 17.298 | 18.669 | 19.672 | 20.564 | 19.836 | | 2 | 2 |
| 570 | -5.360 | -3.634 | -3.660 | -7.476 | -6.552 | -6.837 | 16.421 | 17.344 | 17.060 | 15.500 | 17.225 | 17.199 | 21.918 | 25.874 | 22.150 | 19.568 | | 2 | 2 |
| 571 | -5.235 | -4.143 | -5.344 | -7.356 | -7.006 | -5.985 | 16.747 | 17.097 | 18.117 | 17.267 | 18.359 | 17.158 | 26.398 | 21.807 | 23.482 | 21.522 | | 9 | 9 |
| 572 | -6.381 | -2.519 | -2.925 | -4.786 | -3.224 | -2.671 | 15.847 | 17.409 | 17.962 | 14.031 | 17.892 | 17.486 | 20.526 | 20.741 | 21.286 | 19.537 | | 2 | 2 |
| 573 | -0.798 | -0.263 | -0.673 | -4.820 | -3.439 | -4.633 | 16.591 | 17.972 | 16.778 | 16.415 | 16.950 | 16.540 | 23.238 | 19.584 | 19.530 | 14.896 | | 3 | 3 |
| 574 | -6.539 | -3.869 | -4.729 | -3.566 | -4.106 | -4.572 | 17.594 | 17.054 | 16.589 | 14.806 | 17.476 | 16.616 | 22.075 | 20.246 | 22.342 | 20.349 | | 3 | 3 |
| 575 | -5.134 | -4.856 | -5.953 | -4.314 | -4.679 | -3.561 | 16.984 | 16.619 | 17.737 | 17.130 | 17.407 | 16.311 | 22.273 | 20.322 | 23.996 | 20.530 | | 3 | 3 |
| 576 | -0.733 | -0.222 | -0.130 | -5.150 | -6.069 | -3.639 | 16.947 | 16.028 | 18.458 | 17.836 | 18.347 | 18.439 | 23.254 | 20.940 | 22.579 | 14.559 | | 3 | 3 |
| 577 | -3.376 | -2.244 | -1.842 | -0.628 | -1.446 | -1.788 | 18.298 | 17.480 | 17.138 | 15.510 | 16.642 | 17.044 | 23.379 | 14.473 | 22.118 | 15.654 | | 4 | 4 |
| 578 | -3.526 | -2.384 | -3.105 | -1.387 | -0.634 | 1.262 | 16.072 | 16.824 | 18.720 | 16.994 | 18.136 | 17.415 | 20.389 | 14.527 | 22.429 | 18.611 | | 3 | 3 |
| 579 | -4.094 | -2.678 | -3.465 | -3.118 | -4.437 | -2.754 | 17.808 | 16.490 | 18.172 | 16.505 | 17.922 | 17.134 | 22.597 | 19.256 | 19.561 | 21.638 | | 6 | 6 |
| 580 | -5.009 | -4.531 | -3.760 | -6.653 | -4.814 | -4.606 | 15.112 | 16.950 | 17.158 | 16.786 | 17.264 | 18.035 | 22.211 | 21.318 | 21.744 | 21.846 | | 2 | 2 |
| 581 | -4.153 | -2.513 | -3.832 | -0.964 | -1.342 | -1.858 | 19.279 | 18.901 | 18.385 | 16.301 | 17.942 | 16.623 | 20.890 | 19.598 | 20.944 | 19.965 | | 1 | 1 |
| 582 | -4.656 | -3.075 | -3.801 | -4.328 | -1.416 | -2.689 | 15.817 | 18.729 | 17.456 | 16.326 | 17.906 | 17.181 | 21.668 | 18.622 | 21.663 | 20.301 | | 4 | 4 |
| 583 | -2.981 | -1.965 | -3.674 | -1.546 | 0.411 | -1.611 | 16.825 | 18.782 | 16.760 | 17.226 | 18.242 | 16.532 | 21.445 | 15.297 | 21.605 | 18.807 | | 2 | 2 |
| 584 | -4.419 | -1.986 | -3.746 | -6.285 | -6.423 | -5.211 | 16.409 | 16.271 | 17.483 | 16.121 | 18.553 | 16.794 | 25.529 | 19.859 | 22.392 | 18.688 | | 3 | 3 |
| 585 | -5.835 | -3.751 | -4.234 | -4.860 | -6.170 | -3.698 | 17.276 | 15.965 | 18.438 | 15.366 | 17.450 | 16.967 | 23.543 | 20.727 | 19.629 | 22.773 | | 4 | 4 |
| 586 | -4.896 | -3.231 | -3.788 | -5.181 | -5.390 | -6.759 | 17.656 | 17.448 | 16.079 | 16.223 | 17.889 | 17.331 | 24.740 | 20.935 | 22.853 | 19.386 | | 15 | 4 |

|  | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 557 | 7 | 25.9 | 52.278 | 59.457 | 25.190 | 21.390 | **NaN** | **0.000** | Q3UJQ9;Q9D0K2 | Q3UJQ9;Q9D0K2 | Succinyl-CoA:3-ketoacid-coenzyme A transferase;Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial | **Oxct1** | 982 |
| 558 | 1 | 13.1 | 19.628 | 6.9301 | 19.636 | 18.998 | **NaN** | **0.000** | Q59J78 | Q59J78 | Mimitin, mitochondrial | **Ndufaf2** | 1001 |
| 559 | 2 | 9.3 | 67.73 | 12.653 | 20.458 | 20.186 | **NaN** | **0.000** | Q5SUH7;Q5SUH6;Q99KN9-2;Q99KN9 | Q5SUH7;Q5SUH6;Q99KN9-2;Q99KN9 | Clathrin interactor 1 | **Clint1** | 1009 |
| 560 | 3 | 8.9 | 62.258 | 23.54 | 22.555 | 18.603 | **NaN** | **0.000** | Q5SUW3;Q60760-3;Q60760-2;Q60760 | Q5SUW3;Q60760-3;Q60760-2;Q60760 | Growth factor receptor-bound protein 10 | **Grb10** | 1011 |
| 561 | 6 | 23.7 | 44.593 | 57.176 | 23.110 | 22.349 | **NaN** | **0.000** | Q61081 | Q61081 | Hsp90 co-chaperone Cdc37;Hsp90 co-chaperone Cdc37, N-terminally processed | **Cdc37** | 1033 |
| 562 | 6 | 24.6 | 30.016 | 36.249 | 22.545 | 20.845 | **NaN** | **0.000** | Q61166 | Q61166 | Microtubule-associated protein RP/EB family member 1 | **Mapre1** | 1035 |
| 563 | 2 | 13.9 | 19.007 | 13.67 | 20.543 | 21.035 | **NaN** | **0.000** | Q9D8L3;Q62186 | Q9D8L3;Q62186 | Translocon-associated protein subunit delta | **Ssr4** | 1064 |
| 564 | 1 | 5.3 | 26.201 | 7.1185 | 19.629 | 20.821 | **NaN** | **0.000** | Q62348 | Q62348 | Translin | **Tsn** | 1068 |
| 565 | 4 | 6.7 | 94.944 | 24.875 | 18.738 | 18.232 | **NaN** | **0.000** | Q6P542 | Q6P542 | ATP-binding cassette sub-family F member 1 | **Abcf1** | 1091 |
| 566 | 3 | 12.7 | 32.342 | 19.705 | 21.902 | 17.745 | **NaN** | **0.000** | Q6ZQI3 | Q6ZQI3 | Malectin | **Mlec** | 1108 |
| 567 | 3 | 44.8 | 6.3814 | 19.131 | 19.514 | 20.182 | **NaN** | **0.000** | Q78IK2 | Q78IK2 | Up-regulated during skeletal muscle growth protein 5 | **Usmg5** | 1116 |
| 568 | 1 | 3.9 | 64.647 | 8.1521 | 20.207 | 21.118 | **NaN** | **0.000** | Q7M6Y3-2;Q7M6Y3-3;Q7M6Y3-4;Q7M6Y3-6;Q7M6Y3-5;Q7M6Y3 | Q7M6Y3-2;Q7M6Y3-3;Q7M6Y3-4;Q7M6Y3-6;Q7M6Y3-5;Q7M6Y3 | Phosphatidylinositol-binding clathrin assembly protein | **Picalm** | 1119 |
| 569 | 2 | 3.7 | 158.42 | 13.35 | 19.171 | 20.200 | **NaN** | **0.000** | Q80TM9-2;Q80TM9;Q80TM9-7;Q80TM9-5;Q80TM9-4;Q80TM9-6;Q80TM9-3 | Q80TM9-2;Q80TM9;Q80TM9-7;Q80TM9-5;Q80TM9-4;Q80TM9-6;Q80TM9-3 | Nischarin | **Nisch** | 1127 |
| 570 | 2 | 11.1 | 31.253 | 12.187 | 23.896 | 20.859 | **NaN** | **0.000** | Q8BH58 | Q8BH58 | TIP41-like protein | **Tiprl** | 1148 |
| 571 | 9 | 12.9 | 109.4 | 67.665 | 24.102 | 22.502 | **NaN** | **0.000** | Q8BHN3-2;Q8BHN3;Q8BHN3-3 | Q8BHN3-2;Q8BHN3 | Neutral alpha-glucosidase AB | **Ganab** | 1158 |
| 572 | 2 | 3.5 | 136.35 | 11.802 | 20.633 | 20.412 | **NaN** | **0.000** | Q8BI84-2;Q8BI84 | Q8BI84-2;Q8BI84 | Melanoma inhibitory activity protein 3 | **Mia3** | 1160 |
| 573 | 3 | 3.7 | 112.8 | 19.707 | 21.411 | 17.213 | **NaN** | **0.000** | Q8BIJ6;E9PWN3;E9PWN2 | Q8BIJ6;E9PWN3;E9PWN2 | Isoleucine--tRNA ligase, mitochondrial | **Iars2** | 1161 |
| 574 | 3 | 9.6 | 64.403 | 18.969 | 21.161 | 21.345 | **NaN** | **0.000** | Q8BJW6;Q8BJW6-2;D6RFN2;D6RGA6;D3YZZ6 | Q8BJW6;Q8BJW6-2 | Eukaryotic translation initiation factor 2A;Eukaryotic translation initiation factor 2A, N-terminally processed | **Eif2a** | 1165 |
| 575 | 3 | 4 | 134.19 | 18.876 | 21.298 | 22.263 | **NaN** | **0.000** | Q8BMJ2 | Q8BMJ2 | Leucine--tRNA ligase, cytoplasmic | **Lars** | 1174 |
| 576 | 3 | 11.1 | 43.221 | 18.685 | 22.097 | 18.569 | **NaN** | **0.000** | Q8BP48;A0A0G2JFL1 | Q8BP48 | Methionine aminopeptidase 1 | **Metap1** | 1178 |
| 577 | 4 | 10.5 | 49.523 | 25.53 | 18.926 | 18.886 | **NaN** | **0.000** | Q8CI12;Q5F247 | Q8CI12;Q5F247 | Smoothelin-like protein 2 | **Smtnl2** | 1211 |
| 578 | 3 | 6.6 | 57.402 | 16.985 | 17.458 | 20.520 | **NaN** | **0.000** | Q8CIH9 | Q8CIH9 | Amidophosphoribosyltransferase | **Ppat** | 1214 |
| 579 | 6 | 19.3 | 57.93 | 38.21 | 20.926 | 20.599 | **NaN** | **0.000** | Q8CIN4;A3KGC3;A3KGC4;A3KGC5;Q61036-2;Q61036 | Q8CIN4 | Serine/threonine-protein kinase PAK 2;PAK-2p27;PAK-2p34 | **Pak2** | 1215 |
| 580 | 2 | 5.4 | 91.369 | 15.349 | 21.764 | 21.795 | **NaN** | **0.000** | Q8JZQ9 | Q8JZQ9 | Eukaryotic translation initiation factor 3 subunit B | **Eif3b** | 1218 |
| 581 | 1 | 7.8 | 35.377 | 6.9782 | 20.244 | 20.455 | **NaN** | **0.000** | Q8R010 | Q8R010 | Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 | **Aimp2** | 1231 |
| 582 | 4 | 6.7 | 56.614 | 22.952 | 20.145 | 20.982 | **NaN** | **0.000** | Q8R1Q8 | Q8R1Q8 | Cytoplasmic dynein 1 light intermediate chain 1 | **Dync1li1** | 1237 |
| 583 | 2 | 7.3 | 40.88 | 12.982 | 18.371 | 20.206 | **NaN** | **0.000** | Q8R574;B1AT82;Q9D0M1 | Q8R574;B1AT82;Q9D0M1 | Phosphoribosyl pyrophosphate synthase-associated protein 2;Phosphoribosyl pyrophosphate synthase-associated protein 1 | **Prpsap2;Prpsap1** | 1243 |
| 584 | 3 | 19 | 31.025 | 68.455 | 22.694 | 20.540 | **NaN** | **0.000** | Q8R5L1;O35658 | Q8R5L1;O35658 | Complement component 1 Q subcomponent-binding protein, mitochondrial | **C1qbp** | 1245 |
| 585 | 4 | 45.6 | 22.086 | 40.709 | 22.135 | 21.201 | **NaN** | **0.000** | Q91XV3 | Q91XV3 | Brain acid soluble protein 1 | **Basp1** | 1272 |
| 586 | 4 | 31.8 | 50.09 | 25.888 | 22.838 | 21.120 | **NaN** | **0.000** | Q922F4 | Q922F4 | Tubulin beta-6 chain | **Tubb6** | 1284 |

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 587 | -5.539 | -2.425 | -4.005 | -5.293 | -5.580 | -5.574 | 17.019 | 16.732 | 16.738 | 15.800 | 18.914 | 17.334 | 25.123 | 19.502 | 22.419 | 20.259 | | 6 | 6 |
| 588 | -5.253 | -3.575 | -5.437 | -0.808 | -0.962 | -2.501 | 18.510 | 18.355 | 16.816 | 16.356 | 18.035 | 16.173 | 24.069 | 14.566 | 22.126 | 21.093 | | 3 | 3 |
| 589 | -5.452 | -4.480 | -4.269 | -6.355 | -6.032 | -5.575 | 16.553 | 16.876 | 17.333 | 16.983 | 17.955 | 18.166 | 24.191 | 21.625 | 23.845 | 21.025 | | 25 | 7 |
| 590 | -4.445 | -2.964 | -4.548 | -3.342 | -4.826 | -4.878 | 18.082 | 16.598 | 16.547 | 16.488 | 17.968 | 16.384 | 22.954 | 19.895 | 23.526 | 18.339 | | 1 | 1 |
| 591 | -5.626 | -4.253 | -4.923 | -6.652 | -6.967 | -6.710 | 17.885 | 17.570 | 17.827 | 16.009 | 17.382 | 16.712 | 25.160 | 23.915 | 21.373 | 21.898 | | 2 | 2 |
| 592 | -3.924 | -2.504 | -2.023 | -3.747 | -2.215 | -3.373 | 16.706 | 18.238 | 17.080 | 15.269 | 16.690 | 17.170 | 21.296 | 19.610 | 19.928 | 18.458 | | 1 | 1 |
| 593 | -6.035 | -4.999 | -5.993 | -3.322 | -4.782 | -3.352 | 17.370 | 15.911 | 17.340 | 16.381 | 17.418 | 16.424 | 25.207 | 16.177 | 23.509 | 21.324 | | 1 | 1 |
| 594 | -6.049 | -5.148 | -6.503 | -6.409 | -7.300 | -5.946 | 16.840 | 15.950 | 17.303 | 16.525 | 17.426 | 16.071 | 25.365 | 21.134 | 24.213 | 20.934 | | 5 | 5 |
| 595 | -1.029 | -0.062 | -0.612 | -3.018 | -2.831 | -4.176 | 17.886 | 18.072 | 16.727 | 16.577 | 17.544 | 16.994 | 22.195 | 19.611 | 20.464 | 14.747 | | 2 | 2 |
| 596 | -5.071 | -4.187 | -5.717 | -6.580 | -7.675 | -8.516 | 18.616 | 17.520 | 16.679 | 17.794 | 18.678 | 17.148 | 26.693 | 23.699 | 24.260 | 21.470 | | 4 | 4 |
| 597 | -1.809 | -1.684 | -2.219 | -3.035 | -1.165 | -4.402 | 16.515 | 18.385 | 15.148 | 16.623 | 16.748 | 16.212 | 19.720 | 19.379 | 18.453 | 18.410 | | 2 | 2 |
| 598 | -3.351 | -2.733 | -1.803 | -5.444 | -5.908 | -6.740 | 17.341 | 16.876 | 16.044 | 16.207 | 16.825 | 17.756 | 25.603 | 19.966 | 23.303 | 15.814 | | 5 | 5 |
| 599 | -3.283 | -1.676 | -5.021 | -2.911 | -2.971 | -1.137 | 17.792 | 17.732 | 19.566 | 17.196 | 18.803 | 15.458 | 25.161 | 16.246 | 23.124 | 17.834 | | 4 | 4 |
| 600 | -5.350 | -4.227 | -2.286 | -2.948 | -3.089 | -3.731 | 17.401 | 17.260 | 16.618 | 15.340 | 16.463 | 18.404 | 23.268 | 17.430 | 22.351 | 19.029 | | 5 | 5 |
| 601 | -5.867 | -3.097 | -4.808 | -4.913 | -5.420 | -4.651 | 17.198 | 16.691 | 17.460 | 15.215 | 17.984 | 16.274 | 23.891 | 20.332 | 22.712 | 19.452 | | 3 | 3 |
| 602 | -3.786 | -0.912 | -0.346 | -3.200 | -3.658 | -5.014 | 18.684 | 18.225 | 16.870 | 14.415 | 17.289 | 17.856 | 22.968 | 20.799 | 22.622 | 13.781 | | 2 | 2 |
| 603 | -8.250 | -4.875 | -5.598 | -6.960 | -6.009 | -5.929 | 16.536 | 17.487 | 17.567 | 14.946 | 18.321 | 17.599 | 24.059 | 22.934 | 22.683 | 23.709 | | 4 | 4 |
| 604 | -4.055 | -1.203 | -4.417 | -2.235 | -3.554 | -2.910 | 17.950 | 16.631 | 17.275 | 16.352 | 19.204 | 15.990 | 18.911 | 21.458 | 23.044 | 17.770 | | 2 | 2 |
| 605 | -1.155 | 0.036 | -0.344 | -5.249 | -6.516 | -5.618 | 17.051 | 15.785 | 16.682 | 17.460 | 18.651 | 18.271 | 24.083 | 20.518 | 22.335 | 14.895 | | 2 | 2 |
| 606 | -3.140 | -4.209 | -4.472 | -1.867 | -2.094 | -1.576 | 17.609 | 17.382 | 17.901 | 17.908 | 16.839 | 16.576 | 22.444 | 16.508 | 22.791 | 19.305 | | 5 | 5 |
| 607 | -5.130 | -4.047 | -4.105 | -7.600 | -6.943 | -6.180 | 16.285 | 16.942 | 17.705 | 15.675 | 16.757 | 16.700 | 25.850 | 21.920 | 23.324 | 18.285 | | 10 | 10 |
| 608 | -9.141 | -6.164 | -6.873 | -7.461 | -7.704 | -7.956 | 17.468 | 17.225 | 16.972 | 14.960 | 17.937 | 17.228 | 25.372 | 24.486 | 25.343 | 22.859 | | 3 | 3 |
| 609 | -4.912 | -1.177 | -3.145 | -3.958 | -3.041 | -3.054 | 16.276 | 17.193 | 17.180 | 15.183 | 18.917 | 16.950 | 24.846 | 15.621 | 20.899 | 19.290 | | 2 | 2 |
| 610 | -2.690 | -1.844 | -1.794 | -2.414 | -2.875 | -0.632 | 16.324 | 15.863 | 18.107 | 16.679 | 17.525 | 17.575 | 20.166 | 17.310 | 19.354 | 19.383 | | 3 | 3 |
| 611 | -6.001 | -5.597 | -4.898 | -4.939 | -5.478 | -5.827 | 17.530 | 16.991 | 16.642 | 16.055 | 16.459 | 17.158 | 22.882 | 22.055 | 22.403 | 21.709 | | 2 | 2 |
| 612 | -3.010 | 1.942 | -1.193 | -4.640 | -3.189 | -4.319 | 17.054 | 18.505 | 17.374 | 15.256 | 20.207 | 17.073 | 24.144 | 19.243 | 22.331 | 14.200 | | 3 | 3 |
| 613 | -2.417 | 1.411 | 0.892 | -0.246 | 0.507 | -0.368 | 22.394 | 23.147 | 22.272 | 20.501 | 24.329 | 23.810 | 23.494 | 21.786 | 25.236 | 20.599 | | 10 | 10 |
| 614 | 2.333 | -0.422 | -1.048 | 0.800 | 0.491 | -0.414 | 28.147 | 27.838 | 26.933 | 28.320 | 25.565 | 24.939 | 28.521 | 26.173 | 26.476 | 25.498 | | 9 | 9 |
| 615 | 6.700 | 5.039 | 4.639 | 9.109 | 8.083 | -0.761 | 25.878 | 24.852 | 16.008 | 25.678 | 24.016 | 23.616 | 18.148 | 15.390 | 23.452 | 14.503 | | 9 | 3 |
| 616 | -9.924 | -6.224 | -7.277 | -3.134 | -9.133 | -11.093 | 23.588 | 17.588 | 15.629 | 14.775 | 18.475 | 17.422 | 28.930 | 24.513 | 26.679 | 22.719 | | 4 | 4 |
| 617 | 11.089 | 9.867 | 9.528 | 10.030 | 10.604 | 9.970 | 26.849 | 27.423 | 26.789 | 26.971 | 25.750 | 25.411 | 17.991 | 15.647 | 16.802 | 14.964 | | 5 | 5 |
| 618 | -3.533 | -3.070 | -1.280 | -4.050 | -2.181 | -1.491 | 23.758 | 25.627 | 26.317 | 22.755 | 23.218 | 25.008 | 29.730 | 25.887 | 27.971 | 24.605 | | 25 | 25 |
| 619 | -3.226 | -2.537 | -2.093 | -2.609 | -2.351 | -2.731 | 21.916 | 22.175 | 21.795 | 20.507 | 21.196 | 21.641 | 26.397 | 22.655 | 24.923 | 22.544 | | 21 | 21 |
| 620 | -5.839 | -4.636 | -5.992 | -7.567 | -4.676 | -4.055 | 16.520 | 19.412 | 20.033 | 16.196 | 17.398 | 16.043 | 27.082 | 21.093 | 24.713 | 19.356 | | 7 | 7 |
| 621 | 2.313 | 7.635 | 6.576 | 3.761 | 6.369 | 6.634 | 21.509 | 24.117 | 24.382 | 18.294 | 23.616 | 22.557 | 19.140 | 16.356 | 17.705 | 14.258 | | 1 | 1 |
| 622 | -4.970 | -3.036 | -2.819 | -2.997 | -3.568 | -4.005 | 18.431 | 17.860 | 17.423 | 16.107 | 18.040 | 18.257 | 23.043 | 19.813 | 21.509 | 20.644 | | 1 | 1 |

| | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 587 | 6 | 19.8 | 38.384 | 51.327 | 22.313 | 21.339 | **NaN** | **0.000** | Q99JB2;A2AG41;A2AG39;F6WI02 | Q99JB2 | Stomatin-like protein 2, mitochondrial | **Stoml2** | 1291 |
| 588 | 3 | 46.6 | 11.424 | 25.875 | 19.317 | 21.610 | **NaN** | **0.000** | Q9CPQ8;J3QNM7 | Q9CPQ8 | ATP synthase subunit g, mitochondrial | **Atp5l** | 1324 |
| 589 | 2 | 55.5 | 49.953 | 82.342 | 22.908 | 22.435 | **NaN** | **0.000** | Q9CWF2 | Q9CWF2 | Tubulin beta-2B chain | **Tubb2b** | 1375 |
| 590 | 1 | 2.8 | 32.065 | 6.3145 | 21.425 | 20.933 | **NaN** | **0.000** | Q9CY50 | Q9CY50 | Translocon-associated protein subunit alpha | **Ssr1** | 1385 |
| 591 | 2 | 6.1 | 44.729 | 13.109 | 24.538 | 21.635 | **NaN** | **0.000** | Q9CZ30;B1AYJ9;Q9CZ30-2 | Q9CZ30;B1AYJ9;Q9CZ30-2 | Obg-like ATPase 1 | **Ola1** | 1391 |
| 592 | 1 | 2.3 | 76.118 | 7.7988 | 20.453 | 19.193 | **NaN** | **0.000** | Q9CZJ2 | Q9CZJ2 | Heat shock 70 kDa protein 12B | **Hspa12b** | 1394 |
| 593 | 1 | 5.1 | 22.223 | 7.553 | 20.692 | 22.416 | **NaN** | **0.000** | Q9D0B6 | Q9D0B6 | Protein PBDC1 | **Pbdc1** | 1406 |
| 594 | 5 | 22.6 | 29.497 | 37.429 | 23.249 | 22.574 | **NaN** | **0.000** | Q9D0M3-2;Q9D0M3 | Q9D0M3-2;Q9D0M3 | Cytochrome c1, heme protein, mitochondrial | **Cyc1** | 1413 |
| 595 | 2 | 4.8 | 52.767 | 11.877 | 20.903 | 17.606 | **NaN** | **0.000** | Q9D1A2 | Q9D1A2 | Cytosolic non-specific dipeptidase | **Cndp2** | 1419 |
| 596 | 4 | 23.3 | 24.911 | 27.003 | 25.196 | 22.865 | **NaN** | **0.000** | Q9D1D4;Q9D1D4-2 | Q9D1D4;Q9D1D4-2 | Transmembrane emp24 domain-containing protein 10 | **Tmed10** | 1421 |
| 597 | 2 | 10.7 | 27.385 | 11.541 | 19.549 | 18.432 | **NaN** | **0.000** | Q9D1E6 | Q9D1E6 | Tubulin-folding cofactor B | **Tbcb** | 1422 |
| 598 | 5 | 13.9 | 39.638 | 35.315 | 22.784 | 19.558 | **NaN** | **0.000** | Q9D6R2;Q9D6R2-2 | Q9D6R2;Q9D6R2-2 | Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial | **Idh3a** | 1440 |
| 599 | 4 | 22.8 | 32.667 | 38.762 | 20.703 | 20.479 | **NaN** | **0.000** | Q9D819 | Q9D819 | Inorganic pyrophosphatase | **Ppa1** | 1445 |
| 600 | 5 | 21.4 | 21.708 | 31.77 | 20.349 | 20.690 | **NaN** | **0.000** | Q9DB15 | Q9DB15 | 39S ribosomal protein L12, mitochondrial | **Mrpl12** | 1457 |
| 601 | 3 | 10.3 | 47.262 | 18.703 | 22.111 | 21.082 | **NaN** | **0.000** | Q9DBG5 | Q9DBG5 | Perilipin-3 | **Plin3** | 1464 |
| 602 | 2 | 14.3 | 24.683 | 31.743 | 21.883 | 18.201 | **NaN** | **0.000** | Q9DC70 | Q9DC70 | NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial | **Ndufs7** | 1469 |
| 603 | 4 | 16.4 | 65.4 | 88.46 | 23.496 | 23.196 | **NaN** | **0.000** | Q9ER67;A2AG48;A2AG46;A2AG49;A2AG47 | Q9ER67;A2AG48;A2AG46;A2AG49 | Melanoma-associated antigen D2 | **Maged2** | 1486 |
| 604 | 2 | 0.4 | 341.12 | 12.646 | 20.185 | 20.407 | **NaN** | **0.000** | Q9ERU9 | Q9ERU9 | E3 SUMO-protein ligase RanBP2 | **Ranbp2** | 1489 |
| 605 | 2 | 25.7 | 11.528 | 11.537 | 22.301 | 18.615 | **NaN** | **0.000** | Q9JIX0 | Q9JIX0 | Transcription and mRNA export factor ENY2 | **Eny2** | 1496 |
| 606 | 5 | 16.8 | 42.722 | 28.916 | 19.476 | 21.048 | **NaN** | **0.000** | Q9JK81;F8WGG3;F7A3N3 | Q9JK81;F8WGG3 | UPF0160 protein MYG1, mitochondrial | **Myg1** | 1500 |
| 607 | 10 | 8.6 | 188.74 | 64.653 | 23.885 | 20.805 | **NaN** | **0.000** | Q9JKF1;A0A0U1RNG5 | Q9JKF1 | Ras GTPase-activating-like protein IQGAP1 | **Iqgap1** | 1502 |
| 608 | 3 | 5.9 | 80.751 | 24.091 | 24.929 | 24.101 | **NaN** | **0.000** | Q9QUR6 | Q9QUR6 | Prolyl endopeptidase | **Prep** | 1510 |
| 609 | 2 | 15.4 | 20.767 | 13.76 | 20.234 | 20.094 | **NaN** | **0.000** | Q9QXT0 | Q9QXT0 | Protein canopy homolog 2 | **Cnpy2** | 1512 |
| 610 | 3 | 4.5 | 96.023 | 16.974 | 18.738 | 19.369 | **NaN** | **0.000** | Q9WU78;Q9WU78-3 | Q9WU78;Q9WU78-3 | Programmed cell death 6-interacting protein | **Pdcd6ip** | 1540 |
| 611 | 2 | 13.1 | 35.638 | 16.795 | 22.469 | 22.056 | **NaN** | **0.000** | Q9Z1D1 | Q9Z1D1 | Eukaryotic translation initiation factor 3 subunit G | **Eif3g** | 1559 |
| 612 | 3 | 5.3 | 62.995 | 18.4 | 21.694 | 18.266 | **NaN** | **0.000** | Q9Z247 | Q9Z247 | Peptidyl-prolyl cis-trans isomerase FKBP9 | **Fkbp9** | 1570 |
| 613 | 10 | 26.6 | 51.112 | 95.461 | 22.640 | 22.918 | **0.001** | **-0.002** | Q9WTM5 | Q9WTM5 | RuvB-like 2 | **Ruvbl2** | 1536 |
| 614 | 9 | 56.4 | 18.916 | 311.83 | 27.347 | 25.987 | **0.001** | **-0.004** | P63325;Q3UW83 | P63325;Q3UW83 | 40S ribosomal protein S10 | **Rps10** | 867 |
| 615 | 2 | 64.8 | 13.607 | 58.461 | 16.769 | 18.977 | **0.002** | **-0.018** | F8WIX8;Q64523;Q6GSS7 | F8WIX8;Q64523;Q6GSS7 | Histone H2A;Histone H2A type 2-C;Histone H2A type 2-A | **Hist1h2al;Hist2h2ac;Hist2h2aa1** | 445 |
| 616 | 4 | 16.3 | 25.976 | 35.081 | 26.721 | 24.699 | **0.003** | **-0.022** | P00405 | P00405 | Cytochrome c oxidase subunit 2 | **Mtco2** | 551 |
| 617 | 5 | 23 | 21.733 | 74.106 | 16.819 | 15.883 | **0.026** | **-0.040** | Q9DCI9 | Q9DCI9 | 39S ribosomal protein L32, mitochondrial | **Mrpl32** | 1474 |
| 618 | 25 | 43.9 | 73.46 | 298.13 | 27.808 | 26.288 | **0.017** | **-0.053** | P38647 | P38647 | Stress-70 protein, mitochondrial | **Hspa9** | 700 |
| 619 | 21 | 11.3 | 274.22 | 136.93 | 24.526 | 23.733 | **0.055** | **-0.055** | Q62261;A0A0A0MQG2;Q62261-2 | Q62261;A0A0A0MQG2;Q62261-2 | Spectrin beta chain, non-erythrocytic 1 | **Sptbn1** | 1065 |
| 620 | 7 | 55.3 | 8.4689 | 46.131 | 24.088 | 22.035 | **0.016** | **-0.056** | Q9CPQ1;A0A0G2JDA6;D3Z6E1 | Q9CPQ1 | Cytochrome c oxidase subunit 6C | **Cox6c** | 1322 |
| 621 | 1 | 14.9 | 9.3114 | 7.7637 | 17.748 | 15.982 | **0.014** | **-0.080** | E9Q2Z4;J3QM43;A3KGL9;B7ZCQ3;F6W687;P09602 | E9Q2Z4;J3QM43;A3KGL9;B7ZCQ3;F6W687;P09602 | Non-histone chromosomal protein HMG-17 | **Gm16494;Gm6594;Hmgn2** | 186 |
| 622 | 1 | 21 | 8.6402 | 13.204 | 21.428 | 21.076 | **0.039** | **-0.085** | A0A0N4SW94;O35682 | A0A0N4SW94;O35682 | Myeloid-associated differentiation marker | **Myadm** | 73 |

|  | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 623 | -0.042 | 1.966 | 0.875 | 1.247 | 0.830 | 0.983 | 24.907 | 24.490 | 24.643 | 23.658 | 25.666 | 24.575 | 26.241 | 21.079 | 25.533 | 21.867 |  | 9 | 5 |
| 624 | -5.537 | 2.170 | -6.618 | -2.065 | -6.047 | -1.586 | 21.365 | 17.383 | 21.844 | 17.077 | 24.784 | 15.996 | 25.947 | 20.913 | 24.109 | 21.120 |  | 6 | 6 |
| 625 | -0.405 | 10.356 | 11.596 | 4.662 | 7.333 | 9.857 | 21.439 | 24.110 | 26.634 | 15.220 | 25.982 | 27.221 | 18.582 | 14.972 | 16.480 | 14.771 |  | 2 | 1 |
| 626 | 2.508 | 1.197 | -0.556 | 1.155 | 1.810 | 0.495 | 27.041 | 27.696 | 26.381 | 27.067 | 25.757 | 24.003 | 26.944 | 24.829 | 26.366 | 22.753 |  | 12 | 12 |
| 627 | -0.803 | -4.595 | -0.650 | -4.075 | -1.395 | -0.258 | 18.055 | 20.735 | 21.872 | 20.733 | 16.940 | 20.885 | 23.598 | 20.662 | 22.502 | 20.568 |  | 2 | 2 |
| 628 | -1.628 | 6.661 | 5.112 | 2.964 | 2.932 | 4.574 | 22.797 | 22.765 | 24.407 | 16.940 | 25.228 | 23.679 | 17.956 | 21.710 | 22.699 | 14.436 |  | 17 | 17 |
| 629 | -5.413 | -3.377 | -2.852 | -4.223 | -1.933 | -5.152 | 17.856 | 20.146 | 16.926 | 15.650 | 17.687 | 18.212 | 23.547 | 20.610 | 22.932 | 19.195 |  | 3 | 3 |
| 630 | -6.842 | -5.480 | -7.040 | -4.262 | -6.496 | -8.248 | 20.150 | 17.916 | 16.164 | 16.294 | 17.655 | 16.095 | 24.761 | 24.063 | 24.160 | 22.111 |  | 7 | 7 |
| 631 | 2.091 | 0.645 | 0.019 | 1.913 | 0.787 | 0.535 | 27.839 | 26.714 | 26.462 | 27.492 | 26.047 | 25.420 | 26.842 | 25.012 | 26.911 | 23.893 |  | 14 | 14 |
| 632 | 2.782 | 3.034 | 3.651 | 2.783 | 3.564 | 3.625 | 22.773 | 23.554 | 23.615 | 22.160 | 22.413 | 23.030 | 24.435 | 15.545 | 23.224 | 15.533 |  | 7 | 7 |
| 633 | -8.485 | -4.694 | -3.443 | -7.929 | -2.418 | -5.765 | 16.906 | 22.418 | 19.070 | 15.258 | 19.049 | 20.300 | 25.451 | 24.219 | 24.910 | 22.576 |  | 10 | 10 |
| 634 | -2.599 | -0.837 | -0.359 | -1.296 | -1.257 | -0.667 | 25.217 | 25.255 | 25.846 | 23.000 | 24.762 | 25.240 | 28.760 | 24.265 | 28.029 | 23.169 |  | 19 | 19 |
| 635 | -1.593 | 0.148 | -2.962 | -1.866 | -0.452 | -1.492 | 25.080 | 26.494 | 25.454 | 24.224 | 25.965 | 22.854 | 28.820 | 25.072 | 27.284 | 24.348 |  | 7 | 7 |
| 636 | -0.864 | -4.779 | -1.961 | -4.043 | -1.678 | -1.280 | 18.116 | 20.481 | 20.879 | 22.060 | 18.145 | 20.962 | 24.162 | 20.156 | 24.493 | 21.354 |  | 4 | 4 |
| 637 | -0.760 | -1.244 | -1.235 | 0.649 | -1.962 | -1.280 | 27.124 | 24.514 | 25.196 | 24.890 | 24.406 | 24.414 | 28.045 | 24.906 | 27.355 | 23.943 |  | 10 | 10 |
| 638 | 3.025 | -2.047 | 0.309 | 2.509 | -2.311 | 1.766 | 28.723 | 23.903 | 27.979 | 28.279 | 23.208 | 25.563 | 28.001 | 24.427 | 27.612 | 22.896 |  | 12 | 12 |
| 639 | -3.566 | 6.488 | 2.531 | 1.152 | 1.951 | 3.047 | 20.619 | 21.418 | 22.514 | 15.339 | 25.393 | 21.436 | 19.597 | 19.338 | 22.513 | 15.297 |  | 3 | 3 |
| 640 | 0.400 | -4.641 | -5.484 | -1.194 | -6.854 | -0.916 | 21.163 | 15.502 | 21.441 | 22.305 | 17.263 | 16.421 | 24.285 | 20.428 | 23.270 | 20.539 |  | 6 | 3 |
| 641 | -1.365 | -0.311 | -0.665 | -1.351 | -0.834 | 0.652 | 23.194 | 23.711 | 25.198 | 22.619 | 23.674 | 23.319 | 26.150 | 22.941 | 25.847 | 22.121 |  | 13 | 13 |
| 642 | -3.222 | 4.083 | 3.036 | 0.632 | 2.617 | 1.455 | 16.989 | 18.974 | 17.812 | 16.053 | 23.358 | 22.311 | 17.661 | 15.053 | 23.135 | 15.415 |  | 4 | 4 |
| 643 | 9.837 | 9.468 | 7.789 | 8.420 | 9.953 | 9.548 | 25.615 | 27.148 | 26.743 | 26.269 | 25.900 | 24.221 | 17.932 | 16.458 | 18.097 | 14.767 |  | 8 | 8 |
| 644 | 2.235 | 2.807 | 2.215 | 0.894 | 3.771 | 3.427 | 25.575 | 28.452 | 28.107 | 25.369 | 25.941 | 25.349 | 26.139 | 23.222 | 26.884 | 19.385 |  | 10 | 10 |
| 645 | -1.336 | -5.892 | -1.529 | -6.181 | -0.755 | -0.983 | 18.093 | 23.519 | 23.290 | 22.913 | 18.356 | 22.719 | 26.283 | 22.263 | 25.786 | 22.711 |  | 13 | 13 |
| 646 | -7.733 | -3.968 | -2.210 | -3.347 | -7.615 | -2.073 | 20.927 | 16.660 | 22.201 | 16.027 | 19.791 | 21.549 | 26.809 | 21.740 | 24.790 | 22.728 |  | 8 | 8 |

| | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 623 | 5 | 37.8 | 34.917 | 37.222 | 23.660 | 23.700 | **0.050** | **-0.087** | Q61990-2;Q61990-3;Q61990;E9Q7D8;P57722-2;P57722 | Q61990-2;Q61990-3;Q61990;E9Q7D8;P57722-2;P57722 | Poly(rC)-binding protein 2;Poly(rC)-binding protein 3 | **Pcbp2;Pcbp3** | 1057 |
| 624 | 6 | 23.9 | 42.713 | 39.631 | 23.430 | 22.615 | **0.010** | **-0.096** | Q04447 | Q04447 | Creatine kinase B-type | **Ckb** | 929 |
| 625 | 1 | 3.5 | 50.346 | 8.2301 | 16.777 | 15.625 | **0.008** | **-0.102** | A6BLY7 | A6BLY7 | Keratin, type I cytoskeletal 28 | **Krt28** | 188 |
| 626 | 11 | 34.8 | 51.828 | 134.71 | 25.886 | 24.559 | **0.036** | **-0.103** | P97855;A0A0J9YUY8;A0A0J9YTQ8 | P97855 | Ras GTPase-activating protein-binding protein 1 | **G3bp1** | 910 |
| 627 | 2 | 19.7 | 17.138 | 14.971 | 22.130 | 21.535 | **0.021** | **-0.106** | P61089 | P61089 | Ubiquitin-conjugating enzyme E2 N | **Ube2n** | 791 |
| 628 | 2 | 37 | 36.609 | 323.31 | 19.833 | 18.568 | **0.014** | **-0.108** | B2RXM2;J3QNY1;Q8BG05-2 | B2RXM2;J3QNY1;Q8BG05-2 | Heterogeneous nuclear ribonucleoprotein A3 | **Gm6793;Gm9242;Hnrnpa3** | 211 |
| 629 | 3 | 46.4 | 9.4173 | 21.014 | 22.079 | 21.064 | **0.030** | **-0.112** | S4R238;Q9D9P1;D3Z0L4;Q9CRB9 | S4R238;Q9D9P1;D3Z0L4;Q9CRB9 | MICOS complex subunit Mic19 | **Chchd3** | 293 |
| 630 | 7 | 12.8 | 68.526 | 44.732 | 24.412 | 23.135 | **0.032** | **-0.119** | Q8R050-2;Q8R050;Q149F3;F7CE88 | Q8R050-2;Q8R050;Q149F3 | Eukaryotic peptide chain release factor GTP-binding subunit ERF3A;Eukaryotic peptide chain release factor GTP-binding subunit ERF3B | **Gspt1;Gspt2** | 1232 |
| 631 | 14 | 52.7 | 21.397 | 128.8 | 25.927 | 25.402 | **0.075** | **-0.160** | Q6ZWZ7;Q9CPR4;B2RY53 | Q6ZWZ7;Q9CPR4 | 60S ribosomal protein L17 | **Rpl17** | 1114 |
| 632 | 7 | 29.7 | 29.994 | 50.238 | 19.990 | 19.378 | **0.170** | **-0.168** | Q61792;A2A6G9;A2A6H0;A2A6G7;A2A6G8;A2A6G6;A2A6H1;A2A6G5;E9Q0N6;A2A6G0;A2A6G4 | Q61792;A2A6G9;A2A6H0;A2A6G7;A2A6G8;A2A6G6 | LIM and SH3 domain protein 1 | **Lasp1** | 1052 |
| 633 | 10 | 16.6 | 85.652 | 63.435 | 24.835 | 23.743 | **0.026** | **-0.170** | Q8JZN2;Q91W50;A0A0G2JF72;A0A0G2JDJ7;A0A0G2JE62 | Q8JZN2;Q91W50;A0A0G2JF72 | Cold shock domain-containing protein E1 | **Csde1** | 1216 |
| 634 | 19 | 42.4 | 60.629 | 187.97 | 26.512 | 25.599 | **0.097** | **-0.192** | P80318;E9Q133;Q3U0I3;F6Q609;F6ZVG8 | P80318;E9Q133;Q3U0I3 | T-complex protein 1 subunit gamma | **Cct3** | 890 |
| 635 | 7 | 52.3 | 16.93 | 93.088 | 26.946 | 25.816 | **0.070** | **-0.199** | Q60605;Q60605-2;Q8CI43 | Q60605;Q60605-2 | Myosin light polypeptide 6 | **Myl6** | 1019 |
| 636 | 4 | 6.3 | 100.16 | 27.371 | 22.159 | 22.924 | **0.047** | **-0.201** | J3KMQ2;Q8VDM4 | J3KMQ2;Q8VDM4 | 26S proteasome non-ATPase regulatory subunit 2 | **Gm5422;Psmd2** | 489 |
| 637 | 10 | 44.8 | 21.853 | 116.12 | 26.476 | 25.649 | **0.097** | **-0.215** | A0A140T8T4;P51410;A0A0G2JES3;D3Z629;D3YZT0;A0A0G2JFQ3;S4R1R7 | A0A140T8T4;P51410;A0A0G2JES3;D3Z629;D3YZT0 | 60S ribosomal protein L9 | **Rpl9** | 118 |
| 638 | 12 | 55 | 17.222 | 139.15 | 26.214 | 25.254 | **0.037** | **-0.226** | P62301;Q921R2;A0A0U1RQ71 | P62301;Q921R2 | 40S ribosomal protein S13 | **Rps13** | 820 |
| 639 | 3 | 16.8 | 22.186 | 20.702 | 19.467 | 18.905 | **0.026** | **-0.232** | Q61686;D3Z0U2 | Q61686 | Chromobox protein homolog 5 | **Cbx5** | 1046 |
| 640 | 3 | 23.5 | 28.302 | 25.737 | 22.357 | 21.904 | **0.032** | **-0.253** | P61982 | P61982 | 14-3-3 protein gamma;14-3-3 protein gamma, N-terminally processed | **Ywhag** | 804 |
| 641 | 13 | 27.8 | 59.652 | 112.3 | 24.545 | 23.984 | **0.148** | **-0.269** | P80313;A0A0N4SV00;A0A0N4SV22 | P80313;A0A0N4SV00 | T-complex protein 1 subunit eta | **Cct7** | 66 |
| 642 | 4 | 25.1 | 27.372 | 29.643 | 16.357 | 19.275 | **0.039** | **-0.269** | D3Z0S6;Q62189;D6RI83;A2CES4;F8VQ88;Q9CQI7 | D3Z0S6;Q62189 | U1 small nuclear ribonucleoprotein A | **Snrpa** | 295 |
| 643 | 8 | 47.7 | 18.607 | 129.44 | 17.195 | 16.432 | **0.130** | **-0.276** | P60824;K4DI65;D3YU80 | P60824;K4DI65;D3YU80 | Cold-inducible RNA-binding protein | **Cirbp** | 787 |
| 644 | 10 | 81.9 | 9.1413 | 261.79 | 24.680 | 23.134 | **0.109** | **-0.279** | Q9CQR2 | Q9CQR2 | 40S ribosomal protein S21 | **Rps21** | 1352 |
| 645 | 13 | 35.3 | 43.698 | 88.349 | 24.273 | 24.249 | **0.041** | **-0.280** | P50580;P50580-2;D3YVH7 | P50580;P50580-2;D3YVH7 | Proliferation-associated protein 2G4 | **Pa2g4** | 742 |
| 646 | 8 | 21 | 48.234 | 89.673 | 24.274 | 23.759 | **0.043** | **-0.292** | Q9DB77;A0A140LI98 | Q9DB77 | Cytochrome b-c1 complex subunit 2, mitochondrial | **Uqcrc2** | 1460 |

|  | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 647 | -6.193 | 0.668 | 0.689 | -1.452 | -0.560 | -1.949 | 21.797 | 22.690 | 21.300 | 14.914 | 21.775 | 21.796 | 24.923 | 21.576 | 24.065 | 18.150 |  | 5 | 5 |
| 648 | 1.040 | 6.302 | 3.919 | -0.385 | 7.573 | 4.988 | 16.242 | 24.201 | 21.616 | 15.993 | 21.255 | 18.872 | 18.266 | 14.989 | 16.765 | 13.141 |  | 4 | 4 |
| 649 | -1.036 | 0.146 | -0.440 | -0.872 | 0.207 | 0.255 | 22.164 | 23.242 | 23.291 | 21.751 | 22.932 | 22.347 | 25.235 | 20.837 | 24.736 | 20.837 |  | 4 | 4 |
| 650 | -3.421 | -2.131 | -1.393 | -3.188 | -1.605 | -1.227 | 21.922 | 23.505 | 23.883 | 20.898 | 22.188 | 22.926 | 26.529 | 23.691 | 26.470 | 22.168 |  | 16 | 16 |
| 651 | 0.784 | 1.731 | -6.275 | -0.784 | -1.653 | -0.391 | 21.159 | 20.290 | 21.552 | 22.144 | 23.090 | 15.085 | 23.582 | 20.305 | 24.338 | 18.381 |  | 4 | 4 |
| 652 | 1.092 | 2.633 | 0.857 | 2.870 | 2.325 | 0.326 | 30.790 | 30.245 | 28.246 | 27.996 | 29.537 | 27.761 | 28.783 | 27.058 | 28.742 | 25.066 |  | 44 | 44 |
| 653 | 3.108 | 0.837 | 1.060 | 3.299 | 1.764 | 0.908 | 30.817 | 29.281 | 28.425 | 29.928 | 27.656 | 27.879 | 28.095 | 26.939 | 28.371 | 25.268 |  | 16 | 16 |
| 654 | -2.143 | -1.025 | -1.505 | -1.657 | -1.278 | -0.749 | 27.575 | 27.954 | 28.483 | 26.453 | 27.571 | 27.091 | 30.323 | 28.141 | 30.132 | 27.060 |  | 29 | 29 |
| 655 | 2.049 | 2.238 | 1.664 | 2.897 | 2.254 | 1.867 | 27.880 | 27.236 | 26.850 | 27.946 | 28.136 | 27.562 | 21.769 | 28.195 | 28.489 | 23.306 |  | 11 | 11 |
| 656 | -1.724 | -5.433 | -5.055 | -1.380 | -7.348 | -2.388 | 23.062 | 17.094 | 22.054 | 21.433 | 17.723 | 18.102 | 24.611 | 24.273 | 25.193 | 21.120 |  | 5 | 5 |
| 657 | 9.267 | 7.571 | 7.192 | 9.009 | 8.569 | 7.577 | 34.095 | 33.655 | 32.663 | 33.738 | 32.041 | 31.662 | 26.268 | 23.904 | 26.490 | 22.450 |  | 4 | 4 |
| 658 | 4.248 | 1.592 | 1.676 | 4.014 | 2.234 | 2.417 | 28.302 | 26.522 | 26.706 | 27.650 | 24.993 | 25.078 | 27.210 | 21.366 | 26.561 | 20.243 |  | 13 | 13 |
| 659 | -7.578 | -1.985 | -1.409 | -3.236 | -2.169 | -4.412 | 20.807 | 21.874 | 19.632 | 15.473 | 21.065 | 21.642 | 25.440 | 22.647 | 24.671 | 21.431 |  | 7 | 7 |
| 660 | 3.752 | 1.505 | 0.212 | 3.620 | 2.707 | 0.364 | 29.717 | 28.804 | 26.461 | 30.114 | 27.867 | 26.574 | 25.867 | 26.326 | 28.511 | 24.213 |  | 13 | 13 |
| 661 | -1.218 | -0.425 | -0.248 | 0.624 | 2.317 | -3.609 | 20.493 | 22.186 | 16.260 | 16.622 | 17.415 | 17.592 | 23.161 | 16.576 | 21.115 | 14.565 |  | 4 | 4 |
| 662 | -5.329 | -3.851 | -4.538 | -5.170 | -0.933 | -6.341 | 18.091 | 22.329 | 16.921 | 16.693 | 18.170 | 17.484 | 26.249 | 20.274 | 24.324 | 19.719 |  | 6 | 6 |
| 663 | -6.121 | -2.485 | -2.598 | -6.191 | -1.119 | -2.619 | 17.148 | 22.220 | 20.720 | 16.899 | 20.535 | 20.422 | 24.642 | 22.036 | 23.984 | 22.057 |  | 5 | 5 |
| 664 | 6.545 | 1.523 | 1.058 | 7.113 | -0.164 | 3.462 | 24.653 | 17.376 | 21.002 | 23.187 | 18.165 | 17.700 | 19.416 | 15.664 | 17.526 | 15.758 |  | 3 | 3 |
| 665 | -7.254 | -4.756 | -6.374 | -3.352 | -6.878 | -6.839 | 20.284 | 16.758 | 16.797 | 16.271 | 18.770 | 17.151 | 23.690 | 23.582 | 24.688 | 22.363 |  | 3 | 3 |

|  | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 647 | 5 | 8.9 | 76.221 | 33.419 | 23.249 | 21.107 | **0.043** | **-0.292** | Q61584;Q61584-2;A0A0G2JEP0;Q61584-5;Q61584-6;Q61584-4;Q61584-7;Q61584-3;A0A0H2UH27;Q6P5B5;A0A0G2JGL6;E9QAS9;E9QAT0;D3Z6U8;E9QNF5;A0A0G2JGH0;Q6AXB7;E9QAS8;P35922-7;P35922;P35922-2;P35922-3;P35922-8;P35922-9;Q9WVR4 | Q61584;Q61584-2;A0A0G2JEP0;Q61584-5;Q61584-6;Q61584-4;Q61584-7;Q61584-3;A0A0H2UH27 | Fragile X mental retardation syndrome-related protein 1 | **Fxr1** | 47 |
| 648 | 4 | 8 | 59.698 | 25.268 | 16.627 | 14.953 | **0.037** | **-0.305** | E9Q4Q2;D3YZC9;D3YZD0;Q64213-2;Q64213-3;Q64213;F8WHF9;F6Z9W2;D3YVH4 | E9Q4Q2;D3YZC9;D3YZD0;Q64213-2;Q64213-3;Q64213;F8WHF9 | Splicing factor 1 | **Sf1** | 381 |
| 649 | 4 | 30.5 | 20.83 | 30.678 | 23.036 | 22.786 | **0.241** | **-0.306** | P70296;D3Z1V4;D6RHS6 | P70296;D3Z1V4;D6RHS6 | Phosphatidylethanolamine-binding protein 1;Hippocampal cholinergic neurostimulating peptide | **Pebp1** | 878 |
| 650 | 16 | 38.1 | 63.691 | 123.8 | 25.110 | 24.319 | **0.135** | **-0.308** | Q8BMK4 | Q8BMK4 | Cytoskeleton-associated protein 4 | **Ckap4** | 1175 |
| 651 | 4 | 14 | 42.295 | 26.542 | 21.943 | 21.359 | **0.041** | **-0.311** | Q9R0N0 | Q9R0N0 | Galactokinase | **Galk1** | 1530 |
| 652 | 39 | 74 | 53.687 | 323.31 | 27.920 | 26.904 | **0.120** | **-0.313** | P20152;A0A0A6YWC8;A2AKJ2;G5E846;G3X981;P15331-3;P15331;P15331-2 | P20152;A0A0A6YWC8 | Vimentin | **Vim** | 642 |
| 653 | 16 | 34.6 | 28.024 | 242.93 | 27.517 | 26.819 | **0.116** | **-0.322** | P62918 | P62918 | 60S ribosomal protein L8 | **Rpl8** | 849 |
| 654 | 8 | 56.1 | 49.67 | 323.31 | 29.232 | 28.596 | **0.324** | **-0.329** | P99024;CON__ENSEMBL:ENSBTAP00000025008;A2AQ07;G3UZR1 | P99024 | Tubulin beta-5 chain | **Tubb5** | 913 |
| 655 | 5 | 74.2 | 13.95 | 287.53 | 24.982 | 25.898 | **0.443** | **-0.356** | Q8CGP6;Q8CGP7;Q8CGP5;Q8BFU2;P22752;A0A0N4SV66;Q8R1M2;Q8CGP4;P27661 | Q8CGP6;Q8CGP7;Q8CGP5;Q8BFU2;P22752;A0A0N4SV66;Q8R1M2;Q8CGP4;P27661 | Histone H2A type 1-H;Histone H2A type 1-K;Histone H2A type 1-F;Histone H2A type 3;Histone H2A type 1;Histone H2A.J;Histone H2A;Histone H2AX | **Hist1h2ah;Hist1h2ak;Hist1h2af;Hist3h2a;Hist1h2ab;H2afj;Hist1h2aa;H2afx** | 646 |
| 656 | 5 | 34 | 23.384 | 50.468 | 24.442 | 23.156 | **0.058** | **-0.365** | Q60817;P70670 | Q60817;P70670 | Nascent polypeptide-associated complex subunit alpha;Nascent polypeptide-associated complex subunit alpha, muscle-specific form | **Naca** | 884 |
| 657 | 4 | 9 | 14.416 | 58.071 | 25.086 | 24.470 | **0.187** | **-0.375** | Q642K5;P62862 | Q642K5;P62862 | 40S ribosomal protein S30 | **Fau** | 840 |
| 658 | 13 | 52.5 | 18.562 | 126.54 | 24.288 | 23.402 | **0.136** | **-0.383** | O09167;Q9CQM8;A0A140T8K5 | O09167;Q9CQM8 | 60S ribosomal protein L21 | **Rpl21** | 507 |
| 659 | 7 | 17.3 | 67.839 | 92.603 | 24.043 | 23.051 | **0.065** | **-0.385** | Q99MN1;Q8R2P8 | Q99MN1;Q8R2P8 | Lysine--tRNA ligase | **Kars** | 1315 |
| 660 | 13 | 70.9 | 11.367 | 222.93 | 26.097 | 26.362 | **0.103** | **-0.407** | P62806 | P62806 | Histone H4 | **Hist1h4a** | 830 |
| 661 | 4 | 11.1 | 29.884 | 24.091 | 19.868 | 17.840 | **0.081** | **-0.408** | Q99LB2 | Q99LB2 | Dehydrogenase/reductase SDR family member 4 | **Dhrs4** | 1306 |
| 662 | 6 | 19.9 | 31.814 | 39.982 | 23.262 | 22.022 | **0.089** | **-0.425** | Q9CQA3 | Q9CQA3 | Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial | **Sdhb** | 1337 |
| 663 | 5 | 9.8 | 97.512 | 34.921 | 23.339 | 23.020 | **0.078** | **-0.425** | Q9QZE5;Q7TNQ1 | Q9QZE5 | Coatomer subunit gamma-1 | **Copg1** | 1523 |
| 664 | 3 | 33.6 | 12.575 | 25.241 | 17.540 | 16.642 | **0.054** | **-0.429** | Q9Z1P6 | Q9Z1P6 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7 | **Ndufa7** | 1562 |
| 665 | 3 | 9.5 | 55.674 | 25.283 | 23.636 | 23.525 | **0.116** | **-0.439** | Q8BZY3;Q8R3C7;Q61655 | Q8BZY3;Q8R3C7;Q61655 | ATP-dependent RNA helicase DDX19A | **Ddx19b;Ddx19a** | 1044 |

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 666 | 3.152 | 2.567 | -0.703 | 2.628 | 2.674 | 1.034 | 24.316 | 24.363 | 22.722 | 24.500 | 23.914 | 20.644 | 22.669 | 20.708 | 24.233 | 18.462 | | 8 | 5 |
| 667 | -2.191 | -0.574 | -0.270 | -1.133 | 0.292 | -0.869 | 24.057 | 25.482 | 24.321 | 21.915 | 23.531 | 23.835 | 26.677 | 23.703 | 26.434 | 21.776 | | 14 | 14 |
| 668 | 3.491 | 0.009 | 1.132 | 4.417 | 0.613 | 0.962 | 28.513 | 24.710 | 25.059 | 27.587 | 24.105 | 25.228 | 25.768 | 22.425 | 26.125 | 22.067 | | 9 | 9 |
| 669 | 0.905 | 6.346 | 5.694 | 1.146 | 6.343 | 6.851 | 19.005 | 24.202 | 24.710 | 16.473 | 21.913 | 21.261 | 19.403 | 16.315 | 16.841 | 14.294 | | 1 | 1 |
| 670 | 5.236 | 5.312 | 2.934 | 5.142 | 6.071 | 3.674 | 29.278 | 30.207 | 27.810 | 29.379 | 29.455 | 27.077 | 23.625 | 24.648 | 27.336 | 20.949 | | 11 | 11 |
| 671 | -3.212 | -1.153 | -2.430 | -3.143 | 2.165 | -4.393 | 17.878 | 23.186 | 16.628 | 15.959 | 18.017 | 16.741 | 22.657 | 19.384 | 23.853 | 14.488 | | 2 | 2 |
| 672 | 6.528 | 2.362 | 0.707 | 5.485 | 0.631 | 4.913 | 22.786 | 17.932 | 22.214 | 22.571 | 18.405 | 16.750 | 18.225 | 16.377 | 17.083 | 15.004 | | 2 | 2 |
| 673 | -3.702 | -2.350 | -2.165 | -1.581 | -2.475 | -2.709 | 23.855 | 22.961 | 22.726 | 20.778 | 22.130 | 22.315 | 26.617 | 24.254 | 26.982 | 21.979 | | 23 | 23 |
| 674 | -5.752 | -5.540 | 0.503 | -5.372 | -5.065 | 1.126 | 16.502 | 16.809 | 23.000 | 16.666 | 16.879 | 22.922 | 28.296 | 15.452 | 21.620 | 23.217 | | 6 | 5 |
| 675 | 2.325 | 5.370 | 4.086 | 4.358 | 4.453 | 4.457 | 24.551 | 24.646 | 24.650 | 23.251 | 26.296 | 25.012 | 18.213 | 22.174 | 24.438 | 17.414 | | 6 | 6 |
| 676 | -3.382 | -2.746 | -1.856 | -2.587 | -1.899 | -2.005 | 23.123 | 23.811 | 23.706 | 22.038 | 22.674 | 23.563 | 27.538 | 23.883 | 26.256 | 24.583 | | 9 | 9 |
| 677 | -3.536 | -2.340 | -3.510 | -5.213 | -0.875 | -1.794 | 17.420 | 21.758 | 20.838 | 16.786 | 17.983 | 16.812 | 25.530 | 19.734 | 22.400 | 18.244 | | 4 | 4 |
| 678 | 0.192 | 5.540 | 1.178 | 4.189 | 0.539 | 3.700 | 22.464 | 18.813 | 21.974 | 15.955 | 21.303 | 16.941 | 19.056 | 17.492 | 17.222 | 14.303 | | 1 | 1 |
| 679 | -7.962 | -5.876 | -3.664 | -3.542 | -3.162 | -9.243 | 21.988 | 22.368 | 16.288 | 15.995 | 18.082 | 20.293 | 25.824 | 25.237 | 25.312 | 22.603 | | 16 | 16 |
| 680 | -1.731 | 5.166 | 2.400 | 3.907 | 0.182 | 3.304 | 20.785 | 17.060 | 20.182 | 16.049 | 22.945 | 20.179 | 19.578 | 14.178 | 21.802 | 13.756 | | 4 | 4 |
| 681 | -1.425 | -1.725 | -0.126 | -0.840 | -0.554 | -0.313 | 23.607 | 23.893 | 24.134 | 22.674 | 22.374 | 23.973 | 27.939 | 20.955 | 25.960 | 22.238 | | 15 | 15 |
| 682 | 0.835 | 0.385 | -0.471 | 0.930 | 0.817 | 0.576 | 26.578 | 26.465 | 26.224 | 25.798 | 25.348 | 24.492 | 26.614 | 24.682 | 26.515 | 23.412 | | 14 | 14 |
| 683 | -6.321 | -4.483 | -4.549 | -6.487 | -0.571 | -6.695 | 16.890 | 22.807 | 16.683 | 15.116 | 16.954 | 16.888 | 25.477 | 21.277 | 24.750 | 18.125 | | 7 | 7 |
| 684 | 7.888 | 3.286 | 2.364 | 6.748 | 2.280 | 6.109 | 22.280 | 17.812 | 21.641 | 23.366 | 18.763 | 17.841 | 17.180 | 13.884 | 16.086 | 14.870 | | 2 | 2 |
| 685 | 2.844 | 2.033 | 1.973 | 3.171 | 2.466 | 2.829 | 29.132 | 28.427 | 28.790 | 27.968 | 27.157 | 27.098 | 27.406 | 24.516 | 27.183 | 23.066 | | 8 | 8 |
| 686 | 8.834 | 9.714 | 8.305 | 7.993 | 10.933 | 9.548 | 25.037 | 27.977 | 26.592 | 24.943 | 25.823 | 24.415 | 18.571 | 15.517 | 17.554 | 14.665 | | 4 | 4 |
| 687 | -5.376 | -6.377 | -6.258 | -7.451 | -1.609 | -7.298 | 17.137 | 22.979 | 17.289 | 18.651 | 17.650 | 17.769 | 25.222 | 23.953 | 24.817 | 23.237 | | 5 | 5 |
| 688 | 2.567 | 1.028 | 1.386 | 3.182 | 2.002 | 1.471 | 29.088 | 27.908 | 27.376 | 28.343 | 26.804 | 27.162 | 27.657 | 24.154 | 27.735 | 23.817 | | 16 | 16 |
| 689 | -3.921 | -2.622 | -3.522 | -4.234 | -3.175 | -0.952 | 16.297 | 17.356 | 19.579 | 16.942 | 18.241 | 17.341 | 24.002 | 17.060 | 22.996 | 18.730 | | 1 | 1 |
| 690 | -3.719 | 0.272 | -1.253 | -0.617 | -1.025 | -1.353 | 24.424 | 24.015 | 23.687 | 20.790 | 24.781 | 23.256 | 25.084 | 24.996 | 26.041 | 22.977 | | 11 | 11 |
| 691 | -3.494 | -1.482 | -1.565 | -2.247 | 0.108 | -2.645 | 23.668 | 26.022 | 23.270 | 21.438 | 23.450 | 23.367 | 28.402 | 23.427 | 26.809 | 23.055 | | 6 | 6 |
| 692 | 1.513 | 5.750 | 3.030 | 4.756 | 3.196 | 4.235 | 22.457 | 20.896 | 21.935 | 20.892 | 25.130 | 22.410 | 19.172 | 16.228 | 23.768 | 14.991 | | 8 | 8 |
| 693 | 5.059 | 1.017 | 0.535 | 5.211 | -2.446 | 5.751 | 23.136 | 15.479 | 23.677 | 22.019 | 17.977 | 17.495 | 20.887 | 14.964 | 18.038 | 15.882 | | 1 | 1 |
| 694 | 3.456 | 3.391 | 3.406 | -0.580 | 6.976 | 5.764 | 15.839 | 23.396 | 22.184 | 22.194 | 22.129 | 22.144 | 18.401 | 14.439 | 22.895 | 14.582 | | 1 | 1 |

| | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 666 | 5 | 18.3 | 49.704 | 33.977 | 21.688 | 21.348 | **0.122** | **-0.440** | G3UXJ6;G3UZ48;G3UZI2;A0A0R4J259;Q7TMK9-2;G3V018;Q7TMK9;G3UWM1;G3UXU5;S4R1E9;G3UY67;G3UYK7 | G3UXJ6;G3UZ48;G3UZI2;A0A0R4J259;Q7TMK9-2;G3V018;Q7TMK9 | Heterogeneous nuclear ribonucleoprotein Q | **Syncrip** | 99 |
| 667 | 14 | 20.1 | 56.585 | 110.67 | 25.190 | 24.105 | **0.235** | **-0.442** | Q61753;F6ZSB7 | Q61753;F6ZSB7 | D-3-phosphoglycerate dehydrogenase | **Phgdh** | 1050 |
| 668 | 9 | 47.2 | 13.742 | 86.447 | 24.097 | 24.096 | **0.103** | **-0.454** | P62852 | P62852 | 40S ribosomal protein S25 | **Rps25** | 837 |
| 669 | 1 | 1 | 126.13 | 6.768 | 17.859 | 15.568 | **0.065** | **-0.465** | E9Q944;E9Q238 | E9Q944;E9Q238 | KN motif and ankyrin repeat domains 1 | **Kank1** | 371 |
| 670 | 10 | 37.8 | 15.199 | 118.71 | 24.137 | 24.143 | **0.169** | **-0.468** | F8WI35;P84244;P84228;P68433;P02301;E0CZ27;E0CYR7 | F8WI35;P84244;P84228;P68433;P02301;E0CZ27 | Histone H3;Histone H3.3;Histone H3.2;Histone H3.1;Histone H3.3C | **H3f3a;Hist1h3b;Hist1h3a;H3f3c** | 443 |
| 671 | 2 | 21.8 | 18.37 | 13.843 | 21.020 | 19.171 | **0.080** | **-0.475** | Q9QUR7 | Q9QUR7 | Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 | **Pin1** | 1511 |
| 672 | 2 | 4.9 | 46.7 | 13.492 | 17.301 | 16.044 | **0.072** | **-0.478** | P28301 | P28301 | Protein-lysine 6-oxidase | **Lox** | 670 |
| 673 | 23 | 22.5 | 141.74 | 172.03 | 25.436 | 24.480 | **0.336** | **-0.484** | Q8VDJ3;A0A087WP83;A0A087WS92;A0A087WQY9;A0A087WPC5;A0A087WPH2 | Q8VDJ3;A0A087WP83 | Vigilin | **Hdlbp** | 1251 |
| 674 | 5 | 45.1 | 16.235 | 49.866 | 21.874 | 22.419 | **0.058** | **-0.493** | P06467;A7M7S6 | P06467;A7M7S6 | Hemoglobin subunit zeta | **Hbz;Hba-x** | 566 |
| 675 | 6 | 23.1 | 25.476 | 49.442 | 20.194 | 20.926 | **0.218** | **-0.495** | Q62093 | Q62093 | Serine/arginine-rich splicing factor 2 | **Srsf2** | 1059 |
| 676 | 9 | 29.2 | 36.498 | 64.829 | 25.711 | 25.420 | **0.434** | **-0.498** | P06151;G5E8N5;D3Z736;D3YZQ9;D3YVR7;D3YZE4;P00342 | P06151;G5E8N5 | L-lactate dehydrogenase A chain;L-lactate dehydrogenase | **Ldha** | 565 |
| 677 | 4 | 22.2 | 23.478 | 33.977 | 22.632 | 20.322 | **0.134** | **-0.501** | B1AWE0;Q6PFA2;B1AWE1;B1AWD8;B1AWD9;O08585 | B1AWE0;Q6PFA2;B1AWE1;B1AWD8;B1AWD9;O08585 | Clathrin light chain A | **Clta** | 199 |
| 678 | 1 | 3.3 | 44.355 | 6.8584 | 18.274 | 15.763 | **0.090** | **-0.506** | Q8QZY9 | Q8QZY9 | Splicing factor 3B subunit 4 | **Sf3b4** | 1230 |
| 679 | 15 | 17.9 | 101.2 | 98.894 | 25.531 | 23.958 | **0.079** | **-0.518** | Q922D8 | Q922D8 | C-1-tetrahydrofolate synthase, cytoplasmic;Methylenetetrahydrofolate dehydrogenase;Methenyltetrahydrofolate cyclohydrolase;Formyltetrahydrofolate synthetase;C-1-tetrahydrofolate synthase, cytoplasmic, N-terminally processed | **Mthfd1** | 1283 |
| 680 | 4 | 4.9 | 93.28 | 26.391 | 16.878 | 17.779 | **0.079** | **-0.519** | Q8BJ71;Q8BJ71-2 | Q8BJ71;Q8BJ71-2 | Nuclear pore complex protein Nup93 | **Nup93** | 1163 |
| 681 | 14 | 36.1 | 50.906 | 107.96 | 24.447 | 24.099 | **0.436** | **-0.523** | P54071;D6RIL6;A0A0U1RP68;A0A0U1RPR1 | P54071 | Isocitrate dehydrogenase [NADP], mitochondrial | **Idh2** | 756 |
| 682 | 14 | 50 | 18.431 | 118.96 | 25.648 | 24.963 | **0.591** | **-0.525** | P62281 | P62281 | 40S ribosomal protein S11 | **Rps11** | 819 |
| 683 | 6 | 13.6 | 85.359 | 48.346 | 23.377 | 21.437 | **0.091** | **-0.533** | P12382;Q8C605;Q9WUA3-2;Q9WUA3 | P12382 | ATP-dependent 6-phosphofructokinase, liver type | **Pfkl** | 602 |
| 684 | 2 | 15.7 | 15.147 | 14.352 | 15.532 | 15.478 | **0.086** | **-0.534** | Q9DB42 | Q9DB42 | Zinc finger protein 593 | **Znf593** | 1459 |
| 685 | 8 | 37.8 | 16.605 | 96.817 | 25.961 | 25.124 | **0.709** | **-0.539** | P14115 | P14115 | 60S ribosomal protein L27a | **Rpl27a** | 608 |
| 686 | 4 | 31.6 | 8.4977 | 55.921 | 17.044 | 16.109 | **0.224** | **-0.541** | Q9D115 | Q9D115 | Zinc finger protein 706 | **Znf706** | 1418 |
| 687 | 5 | 7.7 | 137.61 | 46.345 | 24.588 | 24.027 | **0.102** | **-0.551** | Q05D44 | Q05D44 | Eukaryotic translation initiation factor 5B | **Eif5b** | 935 |
| 688 | 16 | 38.7 | 29.976 | 123.54 | 25.906 | 25.776 | **0.335** | **-0.558** | P12970;A0A140T8L1;A0A140T8L3;F6VBB8;V9GX35 | P12970;A0A140T8L1;A0A140T8L3 | 60S ribosomal protein L7a | **Rpl7a** | 604 |
| 689 | 1 | 10.6 | 15.057 | 7.8013 | 20.531 | 20.863 | **0.212** | **-0.568** | A0A0G2JFB4;A0A0G2JH04;P63073 | A0A0G2JFB4;A0A0G2JH04;P63073 | Eukaryotic translation initiation factor 4E | **Eif4e** | 49 |
| 690 | 7 | 46.6 | 37.497 | 130.29 | 25.040 | 24.509 | **0.183** | **-0.568** | P60335;A0A087WR61;A0A087WSI1;A0A087WRH3;A0A0R4J044;P57724 | P60335 | Poly(rC)-binding protein 1 | **Pcbp1** | 783 |
| 691 | 6 | 70.5 | 16.837 | 116.96 | 25.914 | 24.932 | **0.210** | **-0.586** | P62204;Q3UKW2;Q9D6P8;P20801 | P62204;Q3UKW2 | Calmodulin | **Calm1** | 812 |
| 692 | 8 | 15.7 | 82.406 | 54.316 | 17.700 | 19.379 | **0.182** | **-0.631** | Q52KC3;P49718 | Q52KC3;P49718 | DNA helicase;DNA replication licensing factor MCM5 | **Mcm5** | 736 |
| 693 | 1 | 8.4 | 19.133 | 8.168 | 17.925 | 16.960 | **0.074** | **-0.635** | Q9CQ40 | Q9CQ40 | 39S ribosomal protein L49, mitochondrial | **Mrpl49** | 1331 |
| 694 | 1 | 3.5 | 23.026 | 6.4736 | 16.420 | 18.738 | **0.097** | **-0.635** | P60334 | P60334 | Cysteine dioxygenase type 1 | **Cdo1** | 782 |

|  | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 695 | 3.711 | 3.136 | 1.997 | 4.307 | 6.042 | 0.433 | 21.023 | 22.759 | 17.149 | 21.387 | 20.811 | 19.672 | 18.457 | 14.977 | 19.446 | 15.904 |  | 2 | 2 |
| 696 | 0.160 | 4.349 | 2.531 | 1.777 | 3.736 | 3.480 | 24.493 | 26.453 | 26.197 | 23.455 | 27.645 | 25.826 | 18.735 | 26.698 | 25.390 | 21.201 |  | 18 | 18 |
| 697 | -2.679 | 3.762 | 2.121 | 1.974 | 1.080 | 2.109 | 24.606 | 23.713 | 24.741 | 20.454 | 26.895 | 25.254 | 18.567 | 26.698 | 27.083 | 19.183 |  | 12 | 12 |
| 698 | -8.614 | -6.635 | -8.014 | -4.606 | -8.729 | -7.969 | 20.867 | 16.743 | 17.504 | 16.383 | 18.363 | 16.984 | 28.745 | 22.200 | 26.160 | 23.835 |  | 10 | 10 |
| 699 | -7.745 | -7.092 | -1.261 | -9.916 | -2.022 | -2.196 | 15.672 | 23.565 | 23.391 | 16.240 | 16.893 | 22.723 | 25.691 | 25.483 | 24.080 | 23.889 |  | 6 | 6 |
| 700 | -0.538 | 3.825 | 2.156 | 0.792 | 3.528 | 3.092 | 23.505 | 26.241 | 25.806 | 22.885 | 27.248 | 25.579 | 18.933 | 26.494 | 25.405 | 21.440 |  | 18 | 4 |
| 701 | -5.884 | -4.259 | -3.442 | -6.379 | -2.587 | -2.648 | 16.146 | 19.938 | 19.878 | 15.081 | 16.706 | 17.523 | 26.358 | 18.692 | 23.449 | 18.481 |  | 12 | 12 |
| 702 | -1.377 | 5.191 | 1.390 | 2.299 | 2.366 | 2.529 | 21.650 | 21.717 | 21.880 | 17.665 | 24.233 | 20.432 | 22.589 | 16.114 | 22.340 | 15.744 |  | 15 | 10 |
| 703 | -0.119 | -1.904 | -5.039 | -3.844 | -2.827 | 1.608 | 16.771 | 17.788 | 22.223 | 20.805 | 19.019 | 15.885 | 26.155 | 15.074 | 22.672 | 19.175 |  | 12 | 12 |
| 704 | -4.414 | -1.401 | -2.820 | -3.958 | -2.227 | -0.424 | 15.766 | 17.497 | 19.300 | 15.223 | 18.236 | 16.817 | 23.290 | 16.158 | 18.172 | 21.103 |  | 2 | 2 |
| 705 | 0.907 | 3.203 | 2.152 | 2.224 | 3.443 | 2.630 | 27.402 | 28.622 | 27.808 | 26.503 | 28.799 | 27.748 | 23.674 | 26.682 | 28.797 | 22.396 |  | 21 | 21 |
| 706 | -4.306 | 5.067 | 3.278 | 4.359 | 0.664 | 1.067 | 20.795 | 17.099 | 17.502 | 14.448 | 23.821 | 22.032 | 17.094 | 15.777 | 21.833 | 15.675 |  | 5 | 5 |
| 707 | 0.840 | -0.947 | 2.662 | 2.163 | 1.735 | 0.749 | 22.374 | 21.946 | 20.960 | 19.501 | 17.714 | 21.323 | 25.528 | 14.894 | 22.669 | 14.653 |  | 8 | 8 |
| 708 | -2.084 | -4.535 | -6.121 | -5.080 | -3.286 | -2.265 | 16.760 | 18.554 | 19.575 | 20.027 | 17.576 | 15.990 | 24.945 | 18.735 | 24.596 | 19.626 |  | 7 | 7 |
| 709 | -6.335 | -6.125 | -1.553 | -8.044 | -2.925 | -0.924 | 15.739 | 20.859 | 22.860 | 17.321 | 17.532 | 22.104 | 24.566 | 23.001 | 24.187 | 23.126 |  | 12 | 12 |
| 710 | 0.482 | -3.139 | -2.561 | 0.414 | -0.466 | -3.040 | 20.542 | 19.662 | 17.088 | 20.166 | 16.544 | 17.123 | 24.520 | 15.736 | 23.664 | 15.703 |  | 6 | 6 |
| 711 | -3.088 | 4.399 | 3.920 | 3.356 | 1.968 | 2.031 | 23.062 | 21.674 | 21.738 | 15.565 | 23.052 | 22.573 | 22.854 | 16.559 | 22.425 | 14.882 |  | 5 | 5 |
| 712 | -6.014 | 2.531 | 1.343 | -0.556 | 0.505 | 0.039 | 20.993 | 22.053 | 21.588 | 14.829 | 23.373 | 22.186 | 23.860 | 19.237 | 23.140 | 18.545 |  | 6 | 6 |
| 713 | 1.978 | 3.356 | -2.623 | 3.180 | 3.401 | -1.721 | 22.394 | 22.615 | 17.492 | 20.934 | 22.311 | 16.333 | 20.086 | 18.342 | 23.348 | 14.563 |  | 13 | 13 |
| 714 | -6.840 | -3.759 | -4.328 | -4.861 | -3.686 | -4.190 | 21.337 | 22.513 | 22.008 | 18.665 | 21.746 | 21.177 | 28.325 | 24.072 | 26.477 | 24.533 |  | 21 | 21 |
| 715 | -5.123 | -3.701 | -0.911 | -3.003 | -1.346 | -3.179 | 17.307 | 18.965 | 17.132 | 16.202 | 17.624 | 20.414 | 24.518 | 16.103 | 24.129 | 18.521 |  | 4 | 4 |
| 716 | 1.376 | 0.777 | 0.842 | 1.264 | 2.172 | 1.790 | 26.516 | 27.424 | 27.042 | 25.829 | 25.230 | 25.294 | 27.156 | 23.348 | 26.812 | 22.094 |  | 5 | 5 |
| 717 | -5.527 | -0.309 | -4.099 | -2.359 | -2.538 | -2.744 | 17.966 | 17.787 | 17.581 | 16.036 | 21.253 | 17.463 | 20.502 | 20.148 | 21.350 | 21.776 |  | 3 | 3 |

| | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 695 | 2 | 3.1 | 110.69 | 23.56 | 16.717 | 17.675 | **0.138** | **-0.646** | E9PV26;H3BLA4;H3BJU6 | E9PV26;H3BLA4;H3BJU6 | Proline-rich 36 | **Prr36** | 332 |
| 696 | 3 | 40.3 | 22.099 | 323.31 | 22.716 | 23.296 | **0.182** | **-0.651** | P43277;I7HFT9;Q07133 | P43277 | Histone H1.3 | **Hist1h1d** | 712 |
| 697 | 12 | 38.7 | 33.056 | 103.62 | 22.632 | 23.133 | **0.122** | **-0.653** | Q9Z204-2;Q9Z204-4;Q9Z204-3;Q9Z204;Q9Z204-5 | Q9Z204-2;Q9Z204-4;Q9Z204-3;Q9Z204;Q9Z204-5 | Heterogeneous nuclear ribonucleoproteins C1/C2 | **Hnrnpc** | 1569 |
| 698 | 10 | 85.2 | 11.651 | 133.39 | 25.473 | 24.998 | **0.178** | **-0.653** | P99027 | P99027 | 60S acidic ribosomal protein P2 | **Rplp2** | 915 |
| 699 | 6 | 16.2 | 68.839 | 49.836 | 25.587 | 23.985 | **0.069** | **-0.655** | Q8BGD9 | Q8BGD9 | Eukaryotic translation initiation factor 4B | **Eif4b** | 1144 |
| 700 | 4 | 39.6 | 21.266 | 36.242 | 22.714 | 23.423 | **0.161** | **-0.656** | P15864 | P15864 | Histone H1.2 | **Hist1h1c** | 618 |
| 701 | 12 | 13.4 | 113.84 | 82.364 | 22.525 | 20.965 | **0.172** | **-0.657** | Q61941;E9Q8F4;Q8C9V5;Q8BGK0 | Q61941;E9Q8F4;Q8C9V5;Q8BGK0 | NAD(P) transhydrogenase, mitochondrial | **Nnt** | 1056 |
| 702 | 10 | 7.7 | 223.35 | 94.573 | 19.352 | 19.042 | **0.128** | **-0.663** | E9QPE7;O08638-2;O08638 | E9QPE7;O08638-2;O08638 | Myosin-11 | **Myh11** | 412 |
| 703 | 12 | 15.9 | 112.98 | 81.138 | 20.615 | 20.924 | **0.109** | **-0.667** | Q8VDN2;D3YYN7;A0A0G2JGX4;Q8VCE0;Q6PIC6;Q6PIE5;Q91WH7;E9QNX7;Q9WV27;Q64436;Q9Z1W8 | Q8VDN2 | Sodium/potassium-transporting ATPase subunit alpha-1 | **Atp1a1** | 1253 |
| 704 | 2 | 29.5 | 20.165 | 22.682 | 19.724 | 19.637 | **0.193** | **-0.675** | P28667 | P28667 | MARCKS-related protein | **Marcksl1** | 673 |
| 705 | 21 | 66.3 | 37.402 | 323.31 | 25.178 | 25.596 | **0.377** | **-0.678** | O88569;O88569-2;O88569-3;A0A0N4SUM2 | O88569;O88569-2;O88569-3 | Heterogeneous nuclear ribonucleoproteins A2/B1 | **Hnrnpa2b1** | 545 |
| 706 | 5 | 18.8 | 36.766 | 32.156 | 16.436 | 18.754 | **0.078** | **-0.683** | A0A140LHA2;Q9WVA3;A0A140LIM5;A0A140LJ21;A0A140LI47 | A0A140LHA2;Q9WVA3 | Mitotic checkpoint protein BUB3 | **Bub3** | 106 |
| 707 | 8 | 21.7 | 38.937 | 49.238 | 20.211 | 18.661 | **0.245** | **-0.697** | Q9D051 | Q9D051 | Pyruvate dehydrogenase E1 component subunit beta, mitochondrial | **Pdhb** | 1403 |
| 708 | 7 | 22.9 | 51.065 | 60.994 | 21.840 | 22.111 | **0.187** | **-0.703** | Q9Z0N1;Q9Z0N2;A2AAW9 | Q9Z0N1;Q9Z0N2;A2AAW9 | Eukaryotic translation initiation factor 2 subunit 3, X-linked;Eukaryotic translation initiation factor 2 subunit 3, Y-linked | **Eif2s3x;Eif2s3y** | 1554 |
| 709 | 12 | 11.6 | 176.07 | 83.188 | 23.784 | 23.656 | **0.096** | **-0.706** | Q6NZJ6;E9PVC5;E9Q9E1;E9PVC6;Q6NZJ6-2;A0A0J9YUS5;A0A0J9YVC1;A0A0J9YUC1;E9Q770;A0A0N4SVL0;Q80XI3-2;A2AMI7;Q80XI3-4;A0A0R4J112;Z4YKC4;A2AMI2;Q80XI3;Q80XI3-3;D3Z439;A0A0J9YUL1 | Q6NZJ6;E9PVC5;E9Q9E1;E9PVC6;Q6NZJ6-2;A0A0J9YUS5 | Eukaryotic translation initiation factor 4 gamma 1 | **Eif4g1** | 335 |
| 710 | 6 | 16.5 | 57.598 | 39.471 | 20.128 | 19.684 | **0.176** | **-0.708** | Q8C0C7;E9PWY9;D6RIJ2 | Q8C0C7;E9PWY9 | Phenylalanine--tRNA ligase alpha subunit | **Farsa** | 347 |
| 711 | 5 | 17.7 | 35.732 | 31.686 | 19.706 | 18.653 | **0.104** | **-0.708** | P45376;D3YVJ7 | P45376;D3YVJ7 | Aldose reductase | **Akr1b1;Akr1b3** | 713 |
| 712 | 6 | 24.5 | 30.641 | 40.348 | 21.548 | 20.843 | **0.094** | **-0.709** | P48758;Q8K354 | P48758 | Carbonyl reductase [NADPH] 1 | **Cbr1** | 732 |
| 713 | 12 | 3.3 | 534.18 | 76.359 | 19.214 | 18.955 | **0.105** | **-0.716** | Q9QXS1;Q9QXS1-11;E9Q3W4;Q9QXS1-16;Q9QXS1-2;Q9QXS1-8;Q9QXS1-7;Q9QXS1-14;Q9QXS1-4;Q9QXS1-6;Q9QXS1-3;Q9QXS1-5;Q9QXS1-13;Q9QXS1-12;Q9QXS1-9;Q9QXS1-10;Q9QXS1-15;E9Q9J6;A0A0R4J223;F6R059;A0A0R4J218;A0A0R4J221;E9PW24 | Q9QXS1;Q9QXS1-11;E9Q3W4;Q9QXS1-16;Q9QXS1-2;Q9QXS1-8;Q9QXS1-7;Q9QXS1-14;Q9QXS1-4;Q9QXS1-6;Q9QXS1-3;Q9QXS1-5;Q9QXS1-13;Q9QXS1-12;Q9QXS1-9;Q9QXS1-10;Q9QXS1-15 | Plectin | **Plec** | 378 |
| 714 | 21 | 32.9 | 72.369 | 220.96 | 26.198 | 25.505 | **0.294** | **-0.730** | A0A0R4J0Z1;P08003 | A0A0R4J0Z1;P08003 | Protein disulfide-isomerase A4 | **Pdia4** | 89 |
| 715 | 4 | 7.6 | 75.673 | 32.688 | 20.311 | 21.325 | **0.208** | **-0.736** | Q9D0I9 | Q9D0I9 | Arginine--tRNA ligase, cytoplasmic | **Rars** | 1411 |
| 716 | 4 | 35.2 | 14.759 | 47.275 | 25.252 | 24.453 | **1.078** | **-0.744** | P67984 | P67984 | 60S ribosomal protein L22 | **Rpl22** | 869 |
| 717 | 3 | 5.1 | 101.43 | 21.113 | 20.325 | 21.563 | **0.187** | **-0.765** | Q68FL6;E9QB02;F6W0G8 | Q68FL6;E9QB02;F6W0G8 | Methionine--tRNA ligase, cytoplasmic | **Mars** | 405 |

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 718 | 2.153 | 0.656 | 0.635 | 2.678 | 2.039 | 1.029 | 27.031 | 26.392 | 25.382 | 26.216 | 24.718 | 24.698 | 26.046 | 22.659 | 25.535 | 22.590 | | 12 | 12 |
| 719 | -2.034 | 4.110 | 3.435 | 1.680 | 3.119 | 3.030 | 21.747 | 23.186 | 23.098 | 15.980 | 22.123 | 21.449 | 23.856 | 16.279 | 20.297 | 15.729 | | 5 | 3 |
| 720 | -7.427 | -5.451 | -4.495 | -5.851 | -3.302 | -5.898 | 17.317 | 19.865 | 17.270 | 15.974 | 17.950 | 18.906 | 24.433 | 21.901 | 24.023 | 22.779 | | 6 | 6 |
| 721 | -1.457 | -3.592 | -1.055 | -5.094 | 0.696 | 0.637 | 16.225 | 22.015 | 21.956 | 20.099 | 17.964 | 20.501 | 23.285 | 19.353 | 22.620 | 20.492 | | 4 | 4 |
| 722 | 10.369 | 2.664 | 0.726 | 9.167 | -0.447 | 7.394 | 26.088 | 16.474 | 24.315 | 26.402 | 18.696 | 16.759 | 18.570 | 15.271 | 16.667 | 15.398 | | 1 | 1 |
| 723 | -4.412 | -5.101 | -4.099 | -6.733 | -2.452 | -2.022 | 16.712 | 20.993 | 21.423 | 17.312 | 16.623 | 17.624 | 26.229 | 20.661 | 24.221 | 19.227 | | 6 | 6 |
| 724 | -3.895 | -3.733 | -3.635 | -3.545 | -4.386 | -0.913 | 21.456 | 20.615 | 24.089 | 20.057 | 20.220 | 20.318 | 26.752 | 23.251 | 24.621 | 23.284 | | 18 | 18 |
| 725 | -2.667 | -4.294 | -5.340 | -5.368 | -3.813 | -0.648 | 16.123 | 17.678 | 20.843 | 18.979 | 17.353 | 16.307 | 21.947 | 21.034 | 21.955 | 21.339 | | 3 | 3 |
| 726 | 0.737 | -3.686 | -3.415 | -1.202 | -1.656 | -0.999 | 21.847 | 21.394 | 22.051 | 22.381 | 17.958 | 18.229 | 25.338 | 20.761 | 24.770 | 18.518 | | 4 | 4 |
| 727 | -6.619 | -4.366 | -3.437 | -4.313 | -3.842 | -3.682 | 26.556 | 27.027 | 27.187 | 22.837 | 25.090 | 26.019 | 32.151 | 29.587 | 30.202 | 28.710 | | 44 | 44 |
| 728 | -2.870 | -6.147 | -3.159 | -3.482 | -2.499 | -3.607 | 22.219 | 23.203 | 22.094 | 22.765 | 19.488 | 22.476 | 26.467 | 24.936 | 26.136 | 25.133 | | 9 | 6 |
| 729 | 6.080 | 3.655 | 4.604 | 6.392 | 5.980 | 4.599 | 24.111 | 23.699 | 22.317 | 23.496 | 21.071 | 22.020 | 17.658 | 17.779 | 19.367 | 15.466 | | 7 | 7 |
| 730 | -2.626 | -5.229 | -4.794 | -3.879 | -1.104 | -5.032 | 21.009 | 23.784 | 19.856 | 21.717 | 19.114 | 19.550 | 27.174 | 22.602 | 26.609 | 22.078 | | 14 | 14 |
| 731 | -3.849 | 3.367 | 2.414 | -1.007 | 4.980 | 0.626 | 16.099 | 22.086 | 17.731 | 14.886 | 22.102 | 21.149 | 18.172 | 16.038 | 21.722 | 15.748 | | 2 | 2 |
| 732 | 1.564 | 0.866 | 0.907 | 1.593 | 2.323 | 2.145 | 28.249 | 28.980 | 28.802 | 27.601 | 26.903 | 26.944 | 27.759 | 25.554 | 27.246 | 24.827 | + | 9 | 9 |
| 733 | -3.791 | 4.466 | -0.815 | 3.613 | -1.333 | 0.313 | 22.692 | 17.746 | 19.392 | 15.266 | 23.523 | 18.242 | 17.246 | 20.912 | 23.570 | 14.544 | | 6 | 6 |
| 734 | 6.888 | 5.790 | 5.994 | 8.308 | 6.619 | 6.508 | 25.098 | 23.409 | 23.298 | 23.438 | 22.339 | 22.543 | 18.166 | 15.414 | 18.592 | 14.507 | | 5 | 5 |
| 735 | -4.493 | -0.283 | 0.318 | -1.742 | -1.472 | 1.526 | 17.961 | 18.232 | 21.230 | 16.313 | 20.523 | 21.124 | 19.822 | 19.585 | 22.152 | 19.459 | | 4 | 4 |
| 736 | -2.274 | -2.174 | -1.024 | -1.259 | -0.642 | -0.716 | 26.180 | 26.797 | 26.723 | 23.999 | 24.099 | 25.249 | 28.625 | 26.254 | 28.079 | 24.467 | | 31 | 31 |
| 737 | -1.398 | -6.094 | -6.005 | -1.525 | -6.911 | -2.195 | 21.713 | 16.327 | 21.043 | 20.936 | 16.240 | 16.329 | 26.388 | 20.088 | 23.150 | 21.518 | | 9 | 9 |
| 738 | -4.192 | -2.287 | 1.138 | -3.085 | -1.425 | 2.047 | 17.036 | 18.696 | 22.168 | 16.455 | 18.360 | 21.784 | 25.004 | 15.238 | 21.746 | 19.547 | | 5 | 3 |
| 739 | -2.454 | -3.675 | -7.634 | -3.793 | -4.420 | -2.631 | 21.833 | 21.206 | 22.995 | 21.317 | 20.097 | 16.137 | 27.930 | 23.322 | 25.496 | 22.046 | | 9 | 9 |
| 740 | 0.177 | -4.086 | -5.064 | -4.424 | 0.145 | -1.766 | 15.919 | 20.488 | 18.577 | 22.070 | 17.807 | 16.829 | 24.347 | 16.339 | 23.373 | 20.413 | | 4 | 4 |
| 741 | -6.033 | -3.026 | -2.855 | -5.331 | 0.271 | -3.894 | 16.382 | 21.983 | 17.819 | 14.196 | 17.204 | 17.374 | 24.392 | 19.034 | 20.958 | 19.500 | | 5 | 5 |
| 742 | -5.846 | -3.795 | -3.848 | -0.638 | -4.104 | -5.769 | 21.415 | 17.949 | 16.284 | 15.758 | 17.809 | 17.757 | 21.825 | 22.282 | 23.645 | 19.564 | | 1 | 1 |
| 743 | -4.708 | 0.177 | -0.771 | -3.487 | 1.698 | -0.527 | 17.327 | 22.512 | 20.288 | 17.667 | 22.552 | 21.604 | 26.408 | 15.221 | 22.115 | 22.634 | | 8 | 8 |
| 744 | 0.729 | 0.812 | 1.379 | 0.639 | 2.766 | 2.512 | 22.763 | 24.890 | 24.636 | 22.092 | 22.175 | 22.743 | 23.311 | 20.937 | 21.439 | 21.288 | | 4 | 4 |
| 745 | -1.773 | 2.972 | -0.276 | -1.520 | 2.916 | 2.541 | 15.904 | 20.340 | 19.965 | 16.257 | 21.003 | 17.754 | 19.844 | 15.004 | 20.373 | 15.689 | | 1 | 1 |
| 746 | 2.022 | -1.046 | 1.653 | 1.628 | 1.668 | 2.347 | 27.304 | 27.345 | 28.023 | 26.618 | 23.550 | 26.249 | 27.672 | 23.680 | 26.247 | 22.945 | | 11 | 11 |
| 747 | -2.771 | 3.481 | -2.566 | 2.480 | 0.833 | -2.121 | 22.700 | 21.053 | 18.099 | 16.685 | 22.937 | 16.890 | 23.211 | 17.229 | 22.901 | 16.011 | | 6 | 6 |
| 748 | 1.096 | 4.094 | 1.310 | 4.784 | -0.673 | 5.506 | 22.808 | 17.351 | 23.530 | 17.047 | 20.044 | 17.260 | 19.302 | 16.745 | 16.732 | 15.169 | | 3 | 3 |
| 749 | -8.090 | -5.254 | -1.314 | -1.605 | -6.228 | -3.654 | 23.614 | 18.992 | 21.565 | 16.808 | 19.644 | 23.583 | 28.741 | 21.698 | 26.726 | 23.069 | | 16 | 16 |
| 750 | 1.836 | 0.522 | 0.696 | 2.438 | 2.402 | 1.384 | 29.086 | 29.049 | 28.031 | 27.783 | 26.470 | 26.643 | 27.897 | 25.398 | 27.123 | 24.771 | | 9 | 9 |
| 751 | 6.767 | 4.168 | 6.026 | 7.276 | 7.578 | 5.310 | 24.448 | 24.749 | 22.481 | 24.406 | 21.807 | 23.665 | 19.295 | 15.049 | 18.693 | 16.584 | | 3 | 3 |

| | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 718 | 12 | 42.8 | 23.247 | 140.54 | 24.353 | 24.063 | **0.480** | **-0.768** | A2A547;P84099 | A2A547;P84099 | Ribosomal protein L19;60S ribosomal protein L19 | **Rpl19** | 125 |
| 719 | 3 | 1.1 | 312.3 | 18.887 | 20.067 | 18.013 | **0.143** | **-0.772** | Q61554 | Q61554 | Fibrillin-1 | **Fbn1** | 1040 |
| 720 | 6 | 15.7 | 70.612 | 43.796 | 23.167 | 23.401 | **0.252** | **-0.774** | Q3TPJ8;A2BFF9;O88487;A2BFF8;A2BFF5;Q3TYJ3;D3Z0M6;O88485-2;O88485 | Q3TPJ8;A2BFF9;O88487;A2BFF8;A2BFF5 | Cytoplasmic dynein 1 intermediate chain 2 | **Dync1i2** | 181 |
| 721 | 4 | 6.7 | 91.712 | 30.269 | 21.319 | 21.556 | **0.139** | **-0.781** | Q9EQH3 | Q9EQH3 | Vacuolar protein sorting-associated protein 35 | **Vps35** | 1484 |
| 722 | 1 | 4.9 | 26.422 | 7.0993 | 16.921 | 16.032 | **0.066** | **-0.785** | Q9CPN9 | Q9CPN9 | Peptidase S1 domain-containing protein | **2210010C04Rik** | 1321 |
| 723 | 6 | 11.3 | 52.75 | 40.735 | 23.445 | 21.724 | **0.202** | **-0.802** | Q9CPY7-2;Q9CPY7;A0A0G2JEM7 | Q9CPY7-2;Q9CPY7 | Cytosol aminopeptidase | **Lap3** | 1328 |
| 724 | 18 | 8.6 | 273.81 | 128.87 | 25.002 | 23.952 | **0.314** | **-0.806** | Q07113 | Q07113 | Cation-independent mannose-6-phosphate receptor | **Igf2r** | 938 |
| 725 | 3 | 29.5 | 11.031 | 21.28 | 21.491 | 21.647 | **0.199** | **-0.824** | F6THG2;Q91Z25;Q9WV32 | F6THG2;Q91Z25;Q9WV32 | Actin-related protein 2/3 complex subunit 1B | **Arpc1b** | 420 |
| 726 | 4 | 10 | 47.357 | 29.24 | 23.050 | 21.644 | **0.226** | **-0.836** | Q99JY9;Q641P0-2;Q641P0;A0A087WRA1 | Q99JY9;Q641P0-2;Q641P0 | Actin-related protein 3;Actin-related protein 3B | **Actr3;Actr3b** | 1295 |
| 727 | 44 | 74 | 60.955 | 323.31 | 30.869 | 29.456 | **0.375** | **-0.862** | P63038;P63038-2;D3Z2F2;D3Z7J9 | P63038 | 60 kDa heat shock protein, mitochondrial | **Hspd1** | 858 |
| 728 | 6 | 58.7 | 35.73 | 121.21 | 25.701 | 25.635 | **0.320** | **-0.863** | P62960;A2BGG7 | P62960 | Nuclease-sensitive element-binding protein 1 | **Ybx1** | 850 |
| 729 | 7 | 30.6 | 24.944 | 41.434 | 17.718 | 17.416 | **0.420** | **-0.878** | Q9CQ06;A0A0A6YXP0 | Q9CQ06 | 39S ribosomal protein L24, mitochondrial | **Mrpl24** | 1329 |
| 730 | 13 | 50.4 | 41.525 | 119.76 | 24.888 | 24.343 | **0.245** | **-0.878** | P42208;E9Q3V6;F6WYM0;D3YYB1;D3Z3C0;D3Z1S1;F6UKN5;D3YZU7;G3UYQ0;D3YV76 | P42208;E9Q3V6;F6WYM0;D3YYB1;D3Z3C0 | Septin-2 | **sSept2** | 706 |
| 731 | 1 | 3 | 75.029 | 13.721 | 17.105 | 18.735 | **0.112** | **-0.889** | Q9R190 | Q9R190 | Metastasis-associated protein MTA2 | **Mta2** | 1533 |
| 732 | 9 | 41.7 | 16.273 | 175.01 | 26.656 | 26.037 | **1.346** | **-0.908** | P62264;D3YVF4;D3Z7I1 | P62264;D3YVF4;D3Z7I1 | 40S ribosomal protein S14 | **Rps14** | 816 |
| 733 | 6 | 10.2 | 76.723 | 35.747 | 19.079 | 19.057 | **0.118** | **-0.911** | Q3THK7 | Q3THK7 | GMP synthase [glutamine-hydrolyzing] | **Gmps** | 951 |
| 734 | 5 | 43.6 | 11.993 | 37.969 | 16.790 | 16.549 | **0.615** | **-0.921** | Q9CQX4 | Q9CQX4 | PCNA-associated factor | **Paf** | 1358 |
| 735 | 4 | 23.2 | 33.572 | 23.316 | 19.704 | 20.806 | **0.192** | **-0.923** | Q922Y1 | Q922Y1 | UBX domain-containing protein 1 | **Ubxn1** | 1287 |
| 736 | 31 | 21.5 | 191.55 | 297.51 | 27.439 | 26.273 | **1.001** | **-0.951** | Q68FD5;Q5SXR6;F6Z1R4 | Q68FD5;Q5SXR6 | Clathrin heavy chain 1;Clathrin heavy chain | **Cltc** | 1013 |
| 737 | 9 | 35.1 | 28.374 | 62.124 | 23.238 | 22.334 | **0.156** | **-0.955** | A2AFQ2;Q99N15;O08756 | A2AFQ2;Q99N15 | 3-hydroxyacyl-CoA dehydrogenase type-2 | **Hsd17b10** | 145 |
| 738 | 3 | 23.4 | 32.967 | 20.678 | 20.121 | 20.646 | **0.166** | **-0.959** | P47754;A0A0N4SVM0;D6RCW7 | P47754;A0A0N4SVM0;D6RCW7 | F-actin-capping protein subunit alpha-2 | **Capza2** | 723 |
| 739 | 9 | 19 | 51.736 | 100.77 | 25.626 | 23.771 | **0.231** | **-0.973** | Q9CZU6;Q80X68 | Q9CZU6;Q80X68 | Citrate synthase, mitochondrial;Citrate synthase | **Cs;Csl** | 1398 |
| 740 | 4 | 17.9 | 36.213 | 25.43 | 20.343 | 21.893 | **0.178** | **-0.976** | Q9CQ62 | Q9CQ62 | 2,4-dienoyl-CoA reductase, mitochondrial | **Decr1** | 1334 |
| 741 | 5 | 53.5 | 10.916 | 39.251 | 21.713 | 20.229 | **0.192** | **-0.986** | Q9CQ75 | Q9CQ75 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 | **Ndufa2** | 1336 |
| 742 | 1 | 1.5 | 82.499 | 7.4153 | 22.054 | 21.604 | **0.236** | **-0.992** | Q91VR5 | Q91VR5 | ATP-dependent RNA helicase DDX1 | **Ddx1** | 1266 |
| 743 | 8 | 40.1 | 41.829 | 60.348 | 20.814 | 22.375 | **0.178** | **-0.995** | Q8BWT1 | Q8BWT1 | 3-ketoacyl-CoA thiolase, mitochondrial | **Acaa2** | 1187 |
| 744 | 4 | 20.5 | 29.546 | 25.465 | 22.124 | 21.363 | **0.644** | **-0.999** | Q9R1P4 | Q9R1P4 | Proteasome subunit alpha type-1 | **Psma1** | 1534 |
| 745 | 1 | 0.9 | 112.87 | 6.3909 | 17.424 | 18.031 | **0.193** | **-1.005** | E9PWG6 | E9PWG6 | Condensin-2 complex subunit G2 | **Ncapg** | 345 |
| 746 | 11 | 51.1 | 15.733 | 163.81 | 25.676 | 24.596 | **0.432** | **-1.005** | P41105;F6Z0X0 | P41105 | 60S ribosomal protein L28 | **Rpl28** | 704 |
| 747 | 6 | 4.7 | 201.77 | 38.5 | 20.220 | 19.456 | **0.155** | **-1.017** | Q6P5H2-2;Q6P5H2 | Q6P5H2-2;Q6P5H2 | Nestin | **Nes** | 1094 |
| 748 | 3 | 21.4 | 19.212 | 16.627 | 18.023 | 15.951 | **0.182** | **-1.039** | A0A0A6YVP4;Q9CPR5-2;Q9CPR5;F8WHN1 | A0A0A6YVP4;Q9CPR5-2;Q9CPR5 | 39S ribosomal protein L15, mitochondrial | **Mrpl15** | 32 |
| 749 | 16 | 38.4 | 48.1 | 176.51 | 25.220 | 24.897 | **0.168** | **-1.057** | Q922R8;Q3TML0 | Q922R8;Q3TML0 | Protein disulfide-isomerase A6 | **Pdia6** | 1286 |
| 750 | 9 | 47.9 | 13.373 | 119.47 | 26.648 | 25.947 | **0.918** | **-1.057** | P60867 | P60867 | 40S ribosomal protein S20 | **Rps20** | 789 |
| 751 | 3 | 21.6 | 11.952 | 24.257 | 17.172 | 17.639 | **0.435** | **-1.067** | Q9CQF8 | Q9CQF8 | Ribosomal protein 63, mitochondrial | **Mrpl57** | 1344 |

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 752 | 4.570 | 3.460 | -1.347 | 1.352 | 4.253 | 4.287 | 18.497 | 21.398 | 21.432 | 23.320 | 22.210 | 17.403 | 18.021 | 16.270 | 22.648 | 14.852 | | 3 | 2 |
| 753 | -0.981 | -3.187 | -1.166 | -0.686 | -1.197 | -0.222 | 24.412 | 23.901 | 24.876 | 23.497 | 21.291 | 23.311 | 28.287 | 21.910 | 25.949 | 23.006 | | 21 | 21 |
| 754 | -8.679 | -7.816 | -2.322 | -7.471 | -3.540 | -4.566 | 18.176 | 22.107 | 21.081 | 16.166 | 17.028 | 22.523 | 27.980 | 23.314 | 25.768 | 23.922 | | 12 | 12 |
| 755 | 4.168 | 4.538 | 2.755 | 5.245 | 6.088 | 3.428 | 29.036 | 29.879 | 27.219 | 28.830 | 29.200 | 27.418 | 20.443 | 27.139 | 28.454 | 20.870 | | 18 | 18 |
| 756 | 0.550 | 6.125 | 1.407 | -0.813 | 6.609 | 5.617 | 16.748 | 24.170 | 23.178 | 16.574 | 22.148 | 17.431 | 18.077 | 17.044 | 16.351 | 15.696 | | 3 | 3 |
| 757 | -0.102 | -0.317 | -1.088 | 0.409 | 1.040 | 0.380 | 25.556 | 26.187 | 25.527 | 25.342 | 25.127 | 24.356 | 25.921 | 24.373 | 26.376 | 24.512 | + | 15 | 15 |
| 758 | -2.845 | 3.693 | 1.330 | 1.766 | 1.157 | 2.617 | 17.414 | 16.805 | 18.266 | 16.268 | 22.806 | 20.443 | 16.833 | 14.463 | 22.414 | 15.812 | | 3 | 3 |
| 759 | -7.302 | -0.077 | -0.053 | -0.813 | -2.973 | -0.270 | 24.395 | 22.234 | 24.937 | 16.365 | 23.589 | 23.614 | 26.913 | 23.502 | 25.330 | 22.003 | | 4 | 4 |
| 760 | -2.837 | -2.864 | -3.360 | -1.588 | -2.506 | -1.560 | 23.420 | 22.502 | 23.448 | 21.125 | 21.097 | 20.601 | 27.454 | 22.561 | 25.667 | 22.256 | + | 13 | 13 |
| 761 | -2.289 | 4.085 | 2.850 | -1.085 | 5.444 | 3.702 | 17.437 | 23.967 | 22.224 | 15.969 | 22.342 | 21.107 | 20.971 | 16.074 | 20.267 | 16.248 | | 2 | 2 |
| 762 | -3.478 | 4.314 | 2.125 | 2.224 | 2.301 | 1.856 | 22.676 | 22.754 | 22.309 | 16.032 | 23.824 | 21.635 | 19.058 | 21.847 | 24.018 | 15.002 | | 3 | 3 |
| 763 | 1.558 | 5.559 | 3.799 | 3.889 | 5.789 | 4.697 | 25.578 | 27.478 | 26.386 | 24.626 | 28.627 | 26.867 | 17.158 | 26.221 | 25.531 | 20.604 | | 18 | 6 |
| 764 | 2.991 | -0.955 | -1.814 | 1.120 | 3.269 | -0.653 | 21.931 | 24.080 | 20.158 | 22.901 | 18.955 | 18.096 | 25.439 | 16.182 | 24.935 | 14.886 | | 6 | 6 |
| 765 | -7.550 | -6.849 | -0.886 | -3.192 | -2.310 | -6.264 | 21.485 | 22.367 | 18.413 | 15.821 | 16.522 | 22.485 | 26.193 | 23.161 | 24.135 | 22.608 | | 10 | 10 |
| 766 | -0.016 | 2.843 | -1.590 | -0.288 | 3.261 | 1.802 | 18.156 | 21.705 | 20.246 | 17.533 | 20.393 | 15.959 | 19.996 | 16.892 | 19.804 | 15.294 | | 3 | 3 |
| 767 | -3.466 | 3.871 | -2.476 | 2.338 | -3.265 | 2.394 | 22.577 | 16.975 | 22.634 | 14.926 | 22.263 | 15.916 | 23.867 | 16.612 | 21.733 | 15.052 | | 3 | 3 |
| 768 | 5.600 | 1.899 | 0.572 | 5.500 | 4.280 | 1.845 | 25.801 | 24.581 | 22.146 | 25.518 | 21.818 | 20.491 | 17.964 | 22.639 | 17.234 | 22.603 | | 11 | 11 |
| 769 | -1.281 | 7.442 | 2.915 | 2.263 | 6.476 | 3.892 | 21.509 | 25.722 | 23.138 | 16.731 | 25.454 | 20.927 | 22.306 | 16.187 | 21.306 | 14.719 | | 13 | 13 |
| 770 | -0.639 | 1.288 | 0.708 | -0.657 | 2.546 | 3.093 | 17.397 | 20.600 | 21.147 | 16.309 | 18.237 | 17.656 | 19.091 | 17.017 | 18.415 | 15.482 | | 1 | 1 |
| 771 | 5.671 | 4.447 | 4.942 | 6.552 | 5.109 | 7.060 | 23.034 | 21.591 | 23.542 | 22.724 | 21.500 | 21.995 | 16.358 | 16.606 | 18.256 | 15.850 | | 6 | 6 |
| 772 | -1.541 | -2.990 | -0.005 | -0.203 | -0.051 | -0.543 | 24.221 | 24.374 | 23.882 | 21.406 | 19.957 | 22.942 | 27.545 | 21.304 | 25.816 | 20.078 | | 4 | 3 |
| 773 | -5.674 | -4.295 | -3.344 | -1.140 | -5.130 | -3.298 | 20.595 | 16.605 | 18.437 | 15.567 | 16.946 | 17.897 | 24.560 | 18.910 | 22.820 | 19.662 | | 3 | 3 |
| 774 | -5.523 | 0.574 | 0.246 | 1.721 | -4.091 | 1.442 | 21.777 | 15.966 | 21.498 | 15.778 | 21.875 | 21.547 | 25.063 | 15.050 | 24.054 | 18.547 | | 4 | 4 |
| 775 | 9.594 | 7.712 | 8.094 | 10.238 | 10.188 | 8.768 | 27.001 | 26.950 | 25.530 | 26.250 | 24.369 | 24.750 | 18.568 | 14.956 | 17.392 | 15.921 | | 6 | 6 |
| 776 | -0.601 | 6.427 | -1.089 | 5.951 | -0.160 | 2.746 | 22.950 | 16.839 | 19.745 | 17.678 | 24.706 | 17.190 | 17.917 | 16.081 | 21.290 | 15.269 | | 6 | 6 |
| 777 | -11.433 | -3.054 | -1.916 | -5.247 | -4.122 | -3.206 | 23.711 | 24.836 | 25.752 | 16.238 | 24.617 | 25.755 | 30.906 | 27.011 | 28.820 | 26.521 | | 29 | 29 |
| 778 | -8.316 | -6.948 | -6.071 | -7.461 | -7.629 | -2.409 | 17.329 | 17.162 | 22.382 | 15.449 | 16.817 | 17.695 | 27.352 | 22.230 | 24.859 | 22.672 | | 11 | 11 |
| 779 | -0.587 | 3.079 | 1.593 | -0.433 | 5.092 | 3.269 | 17.333 | 22.858 | 21.035 | 15.270 | 18.936 | 17.450 | 19.485 | 16.048 | 16.946 | 14.768 | | 2 | 2 |
| 780 | -5.889 | 2.396 | 1.736 | 0.482 | 2.262 | -0.646 | 21.435 | 23.215 | 20.307 | 15.660 | 23.945 | 23.286 | 23.542 | 18.364 | 23.731 | 19.368 | | 7 | 7 |
| 781 | 2.642 | -0.304 | 0.191 | -3.890 | 4.770 | 5.525 | 16.394 | 25.054 | 25.809 | 20.205 | 17.258 | 17.753 | 24.345 | 16.223 | 16.579 | 18.546 | | 7 | 7 |

| | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 752 | 2 | 8.5 | 50.784 | 14.495 | 17.145 | 18.750 | **0.200** | **-1.070** | P97379-2;P97379 | P97379-2;P97379 | Ras GTPase-activating protein-binding protein 2 | **G3bp2** | 904 |
| 753 | 20 | 33.9 | 56.537 | 204.61 | 25.098 | 24.478 | **0.638** | **-1.076** | P47738;A0A0G2JEU1;A0A0G2JFQ0;A0A0G2JF60;D3YYF3;G3UWP3;Q9JHW9;Q9CZS1 | P47738;A0A0G2JEU1;A0A0G2JFQ0 | Aldehyde dehydrogenase, mitochondrial | **Aldh2** | 721 |
| 754 | 11 | 27.3 | 52.851 | 143.74 | 25.647 | 24.845 | **0.177** | **-1.080** | Q9CZ13;A0A0A6YW82;A0A0A6YWX6 | Q9CZ13 | Cytochrome b-c1 complex subunit 1, mitochondrial | **Uqcrc1** | 1390 |
| 755 | 18 | 39.1 | 38.833 | 318.09 | 23.791 | 24.662 | **0.504** | **-1.100** | Q5EBP8;P49312;P49312-2 | Q5EBP8;P49312;P49312-2 | Heterogeneous nuclear ribonucleoprotein A1;Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed | **Hnrnpa1** | 734 |
| 756 | 3 | 4 | 74.596 | 21.748 | 17.561 | 16.024 | **0.142** | **-1.111** | P82198 | P82198 | Transforming growth factor-beta-induced protein ig-h3 | **Tgfbi** | 891 |
| 757 | 15 | 27.4 | 78.168 | 156.84 | 25.147 | 25.444 | **1.405** | **-1.112** | Q60865;F6YP03;A2BH47;F6YLI0 | Q60865 | Caprin-1 | **Caprin1** | 1025 |
| 758 | 3 | 3.2 | 117 | 19.787 | 15.648 | 19.113 | **0.224** | **-1.121** | F8WHR6;Q569Z5-2;Q569Z5 | F8WHR6;Q569Z5-2;Q569Z5 | Probable ATP-dependent RNA helicase DDX46 | **Ddx46** | 442 |
| 759 | 4 | 22.7 | 24.693 | 24.979 | 25.208 | 23.666 | **0.166** | **-1.125** | O70251;A0A087WS46;M0QWK5;M0QWH8;G3UX43 | O70251;A0A087WS46 | Elongation factor 1-beta | **Eef1b;Eef1b2** | 532 |
| 760 | 13 | 34.5 | 49.538 | 100.92 | 25.007 | 23.962 | **1.486** | **-1.136** | D3YVN7;Q8BFR5;Q8BFR5-2;A0A0U1RPC4;A0A0U1RNQ6 | D3YVN7;Q8BFR5;Q8BFR5-2 | Elongation factor Tu;Elongation factor Tu, mitochondrial | **Gm9755;Tufm** | 280 |
| 761 | 2 | 1.6 | 167.32 | 13.244 | 18.522 | 18.257 | **0.154** | **-1.138** | P08122 | P08122 | Collagen alpha-2(IV) chain;Canstatin | **Col4a2** | 575 |
| 762 | 3 | 15.4 | 12.259 | 61.738 | 20.453 | 19.510 | **0.187** | **-1.140** | P84089 | P84089 | Enhancer of rudimentary homolog | **Erh** | 895 |
| 763 | 6 | 40.6 | 21.977 | 80.989 | 21.689 | 23.068 | **0.377** | **-1.153** | P43274 | P43274 | Histone H1.4 | **Hist1h1e** | 709 |
| 764 | 6 | 12.8 | 63.988 | 40.404 | 20.811 | 19.910 | **0.249** | **-1.172** | O70194 | O70194 | Eukaryotic translation initiation factor 3 subunit D | **Eif3d** | 531 |
| 765 | 10 | 19.2 | 55.758 | 68.129 | 24.677 | 23.371 | **0.184** | **-1.174** | Q9CZN7 | Q9CZN7 | Serine hydroxymethyltransferase | **Shmt2** | 1395 |
| 766 | 3 | 22.2 | 18.211 | 18.003 | 18.444 | 17.549 | **0.287** | **-1.179** | Q3THM8;B7FAU5;O08579;I7HJS1 | Q3THM8;B7FAU5;O08579;I7HJS1 | Emerin | **Emd** | 213 |
| 767 | 3 | 24 | 19.961 | 21.519 | 20.239 | 18.392 | **0.148** | **-1.180** | D3YV69;P35279-2;P35279;P61294;Q8BHD0 | D3YV69;P35279-2;P35279;P61294 | Ras-related protein Rab-6A;Ras-related protein Rab-6B | **Rab6a;Rab6b** | 279 |
| 768 | 8 | 52.4 | 30.764 | 137.99 | 20.301 | 19.919 | **0.255** | **-1.185** | Q9JKB3-2;Q9JKB3;A0A0A0MQD2;B2RUF0;Q9Z2C8-2;Q9Z2C8 | Q9JKB3-2;Q9JKB3 | Y-box-binding protein 3 | **Ybx3** | 1501 |
| 769 | 13 | 4.9 | 350.64 | 89.694 | 19.246 | 18.012 | **0.159** | **-1.185** | Q6NVD0;Q6NVD0-2 | Q6NVD0 | FRAS1-related extracellular matrix protein 2 | **Frem2** | 1088 |
| 770 | 1 | 0.4 | 321.59 | 6.4475 | 18.054 | 16.948 | **0.392** | **-1.208** | E9Q6A7;A2A655;A2A654 | E9Q6A7;A2A655;A2A654 | Bptf protein | **Bptf** | 126 |
| 771 | 6 | 47.3 | 13.215 | 37.498 | 16.482 | 17.053 | **0.827** | **-1.221** | Q9CR80 | Q9CR80 | Protein FAM32A | **Fam32a** | 1368 |
| 772 | 3 | 46.3 | 14.339 | 88.513 | 24.424 | 22.947 | **0.644** | **-1.247** | Q9D7S7-2;Q9D7S7 | Q9D7S7-2;Q9D7S7 | 60S ribosomal protein L22-like 1 | **Rpl22l1** | 1443 |
| 773 | 3 | 9.5 | 47.874 | 25.212 | 21.735 | 21.241 | **0.394** | **-1.248** | Q9DBL1;E9Q5L3 | Q9DBL1;E9Q5L3 | Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial | **Acadsb** | 1467 |
| 774 | 4 | 10 | 41.655 | 27.93 | 20.056 | 21.301 | **0.174** | **-1.258** | Q99L47;F8WJK8;E9Q1V0 | Q99L47;F8WJK8 | Hsc70-interacting protein | **St13** | 447 |
| 775 | 4 | 55.4 | 7.4158 | 68.368 | 16.762 | 16.656 | **0.778** | **-1.265** | Q9CQP0 | Q9CQP0 | 39S ribosomal protein L33, mitochondrial | **Mrpl33** | 1349 |
| 776 | 6 | 19.8 | 45.789 | 35.889 | 16.999 | 18.279 | **0.158** | **-1.267** | Q99KP6-3;Q99KP6;Q99KP6-2 | Q99KP6-3;Q99KP6;Q99KP6-2 | Pre-mRNA-processing factor 19 | **Prpf19** | 1303 |
| 777 | 29 | 52.7 | 56.678 | 323.31 | 28.959 | 27.671 | **0.156** | **-1.276** | P27773;F6Q404 | P27773 | Protein disulfide-isomerase A3 | **Pdia3** | 668 |
| 778 | 11 | 44.9 | 30.755 | 86.312 | 24.791 | 23.765 | **0.281** | **-1.279** | Q60932-2;Q60932;F2Z471 | Q60932-2;Q60932;F2Z471 | Voltage-dependent anion-selective channel protein 1 | **Vdac1** | 1027 |
| 779 | 2 | 10.6 | 25.345 | 12.057 | 17.766 | 15.857 | **0.263** | **-1.281** | Q9D8X2 | Q9D8X2 | Coiled-coil domain-containing protein 124 | **Ccdc124** | 1453 |
| 780 | 7 | 18.6 | 50.213 | 45.42 | 20.953 | 21.550 | **0.175** | **-1.285** | P60122;D3YW60;Q05CB6 | P60122 | RuvB-like 1 | **Ruvbl1** | 780 |
| 781 | 7 | 42.7 | 29.367 | 55.889 | 20.284 | 17.562 | **0.153** | **-1.292** | Q9CR68 | Q9CR68 | Cytochrome b-c1 complex subunit Rieske, mitochondrial;Cytochrome b-c1 complex subunit 11 | **Uqcrfs1** | 1367 |

|  | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 782 | 9.555 | 7.454 | 8.510 | 9.821 | 9.926 | 9.667 | 26.919 | 27.024 | 26.765 | 26.545 | 24.444 | 25.500 | 18.515 | 15.681 | 19.575 | 14.406 |  | 4 | 4 |
| 783 | 5.429 | 6.690 | 5.515 | 5.560 | 8.273 | 7.767 | 22.434 | 25.147 | 24.642 | 22.501 | 23.762 | 22.587 | 19.145 | 14.604 | 18.270 | 15.874 |  | 1 | 1 |
| 784 | -1.217 | -3.324 | -5.070 | -4.145 | -0.505 | -0.951 | 16.400 | 20.040 | 19.595 | 20.240 | 18.133 | 16.387 | 24.238 | 16.854 | 23.998 | 18.915 |  | 9 | 9 |
| 785 | -5.984 | 2.834 | 2.231 | 0.378 | 1.338 | 1.469 | 21.726 | 22.687 | 22.818 | 14.644 | 23.462 | 22.859 | 22.765 | 19.932 | 22.471 | 18.786 |  | 2 | 2 |
| 786 | -2.752 | 3.027 | 1.855 | 0.798 | 3.832 | 1.642 | 20.426 | 23.461 | 21.270 | 16.100 | 21.878 | 20.707 | 20.831 | 18.426 | 22.950 | 14.753 |  | 6 | 6 |
| 787 | 0.535 | 3.673 | 2.168 | 3.263 | 3.550 | 3.706 | 27.026 | 27.313 | 27.469 | 25.914 | 29.051 | 27.547 | 20.717 | 26.809 | 28.666 | 22.092 |  | 25 | 25 |
| 788 | -8.967 | -4.798 | -5.753 | -4.433 | -3.451 | -7.453 | 19.287 | 20.269 | 16.267 | 14.828 | 18.996 | 18.042 | 24.482 | 22.958 | 23.961 | 23.629 |  | 5 | 5 |
| 789 | -6.154 | -5.218 | -6.505 | -6.476 | -4.104 | -3.045 | 16.930 | 19.302 | 20.361 | 17.475 | 18.410 | 17.124 | 27.467 | 19.346 | 23.967 | 23.291 |  | 12 | 12 |
| 790 | 4.418 | 6.852 | 5.026 | 6.338 | 7.940 | 6.271 | 24.201 | 25.804 | 24.135 | 22.781 | 25.215 | 23.388 | 16.912 | 18.815 | 21.320 | 15.406 |  | 4 | 4 |
| 791 | -5.984 | 0.469 | -1.110 | -2.652 | 2.279 | -1.992 | 17.749 | 22.680 | 18.408 | 16.294 | 22.747 | 21.168 | 24.850 | 15.952 | 23.167 | 21.389 |  | 7 | 7 |
| 792 | -4.313 | -3.215 | -2.955 | 2.205 | -4.219 | -4.205 | 22.483 | 16.059 | 16.074 | 15.888 | 16.987 | 17.246 | 24.760 | 15.797 | 21.823 | 18.580 |  | 5 | 5 |
| 793 | -4.057 | -3.944 | -4.586 | -3.614 | 0.041 | -4.748 | 18.432 | 22.087 | 17.298 | 17.086 | 17.199 | 16.557 | 24.585 | 19.507 | 22.861 | 19.425 |  | 4 | 4 |
| 794 | -7.998 | -3.753 | -3.832 | -4.853 | -4.727 | -1.685 | 18.232 | 18.358 | 21.400 | 16.633 | 20.878 | 20.799 | 25.962 | 20.207 | 25.926 | 23.337 |  | 8 | 8 |
| 795 | -0.776 | 0.196 | -7.201 | -0.972 | -1.402 | -1.085 | 24.725 | 24.295 | 24.612 | 23.012 | 23.984 | 16.587 | 27.555 | 23.839 | 26.205 | 21.371 |  | 6 | 6 |
| 796 | 1.676 | 5.463 | 3.767 | 4.536 | 5.595 | 5.103 | 26.852 | 27.910 | 27.419 | 25.626 | 29.413 | 27.716 | 18.227 | 26.404 | 27.166 | 20.733 |  | 15 | 12 |
| 797 | -6.829 | -0.398 | -0.557 | -2.119 | -0.984 | -0.224 | 22.215 | 23.350 | 24.111 | 16.031 | 22.462 | 22.303 | 26.760 | 21.909 | 24.764 | 20.956 |  | 8 | 8 |
| 798 | -6.617 | -4.204 | -5.620 | -4.620 | -5.055 | -2.305 | 16.911 | 16.477 | 19.226 | 16.225 | 18.637 | 17.221 | 24.215 | 18.848 | 23.455 | 22.227 |  | 4 | 4 |
| 799 | 3.237 | 4.390 | 7.985 | 6.318 | 6.326 | 7.482 | 23.291 | 23.299 | 24.454 | 20.630 | 21.783 | 25.378 | 17.953 | 15.992 | 18.533 | 16.253 |  | 10 | 9 |
| 800 | -4.404 | -6.188 | -4.895 | -6.341 | -2.359 | -2.187 | 17.142 | 21.123 | 21.296 | 19.347 | 17.563 | 18.856 | 25.291 | 21.674 | 24.976 | 22.526 |  | 13 | 2 |
| 801 | -6.844 | -1.827 | -1.688 | -2.090 | -1.391 | -2.230 | 22.825 | 23.524 | 22.685 | 16.570 | 21.587 | 21.726 | 27.432 | 22.398 | 24.279 | 22.549 |  | 9 | 9 |
| 802 | -4.178 | -1.550 | -1.897 | 1.290 | -1.478 | -2.784 | 20.646 | 17.878 | 16.572 | 15.874 | 18.501 | 18.154 | 22.996 | 15.717 | 20.096 | 20.007 |  | 2 | 2 |
| 803 | -3.526 | 3.534 | 2.638 | -3.369 | 4.809 | 5.868 | 17.344 | 25.522 | 26.581 | 17.507 | 24.568 | 23.672 | 19.117 | 22.309 | 21.165 | 20.902 |  | 3 | 3 |
| 804 | -3.833 | 1.815 | 0.779 | -0.272 | 1.050 | 2.677 | 15.922 | 17.243 | 18.870 | 15.761 | 21.409 | 20.374 | 16.758 | 15.628 | 22.251 | 16.938 |  | 4 | 4 |
| 805 | -2.533 | -7.842 | -8.595 | -2.276 | -8.439 | -3.416 | 25.298 | 19.135 | 24.158 | 23.385 | 18.076 | 17.323 | 28.541 | 26.607 | 27.187 | 24.649 |  | 5 | 5 |
| 806 | 0.464 | -1.997 | -1.680 | 1.624 | -0.087 | 0.228 | 27.274 | 25.563 | 25.878 | 26.290 | 23.829 | 24.147 | 26.062 | 25.237 | 26.312 | 25.341 |  | 8 | 8 |
| 807 | 1.588 | 2.194 | 1.094 | -1.623 | 5.911 | 5.582 | 16.842 | 24.376 | 24.047 | 17.524 | 18.131 | 17.030 | 20.489 | 16.441 | 18.123 | 13.749 |  | 1 | 1 |
| 808 | -3.814 | -8.934 | -1.264 | -2.151 | -2.593 | -4.247 | 24.947 | 24.506 | 22.851 | 21.868 | 16.748 | 24.418 | 28.039 | 26.159 | 26.575 | 24.788 |  | 11 | 11 |

|  | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 782 | 4 | 33 | 12.648 | 58.416 | 17.098 | 16.990 | **0.997** | **-1.299** | Q99LY9;B1ARW4 | Q99LY9;B1ARW4 | NADH dehydrogenase [ubiquinone] iron-sulfur protein 5;NADH dehydrogenase [ubiquinone] iron-sulfur protein 5, N-terminally processed | **Ndufs5** | 1311 |
| 783 | 1 | 15.5 | 6.305 | 6.7968 | 16.874 | 17.072 | **0.644** | **-1.322** | A2AEB8;A2AEB7;A2AEB6;A2AEB5;A2AEB4;A2AEB3;Q9R0Q4 | A2AEB8;A2AEB7;A2AEB6;A2AEB5;A2AEB4;A2AEB3;Q9R0Q4 | Mortality factor 4-like protein 2 | **Morf4l2** | 141 |
| 784 | 9 | 21.1 | 57.229 | 55.119 | 20.546 | 21.456 | **0.347** | **-1.336** | Q5XJY5 | Q5XJY5 | Coatomer subunit delta | **Arcn1** | 1016 |
| 785 | 2 | 25 | 11.922 | 14.313 | 21.348 | 20.628 | **0.182** | **-1.368** | P26883;F6X9I3 | P26883;F6X9I3 | Peptidyl-prolyl cis-trans isomerase FKBP1A;Peptidyl-prolyl cis-trans isomerase | **Fkbp1a** | 665 |
| 786 | 6 | 8.4 | 116.9 | 60.986 | 19.628 | 18.852 | **0.280** | **-1.380** | Q80X50-4;Q80X50;Q80X50-5;A0A0H2UH17;A0A0G2JDV6;Q80X50-2;Q80X50-3;A0A0G2JFN7 | Q80X50-4;Q80X50;Q80X50-5;A0A0H2UH17;A0A0G2JDV6;Q80X50-2;Q80X50-3 | Ubiquitin-associated protein 2-like | **Ubap2l** | 1133 |
| 787 | 25 | 25.5 | 86.805 | 323.31 | 23.763 | 25.379 | **0.687** | **-1.381** | G3XA10;Q8VEK3 | G3XA10;Q8VEK3 | Heterogeneous nuclear ribonucleoprotein U | **Gm28062;Hnrnpu** | 468 |
| 788 | 5 | 46 | 24.196 | 57.999 | 23.720 | 23.795 | **0.329** | **-1.394** | A0A087WNP6;Q4VAA2-2;Q4VAA2;F8WGL9;A0A087WS49;A0A087WRM0 | A0A087WNP6;Q4VAA2-2;Q4VAA2 | Protein CDV3 | **Cdv3** | 13 |
| 789 | 12 | 32 | 47.994 | 113.92 | 23.406 | 23.629 | **0.583** | **-1.417** | P14211 | P14211 | Calreticulin | **Calr** | 613 |
| 790 | 4 | 11 | 64.988 | 32.827 | 17.864 | 18.363 | **0.710** | **-1.418** | Q5SUT0;Q5SUS9;Q61545;Q5SUS8 | Q5SUT0;Q5SUS9;Q61545 | RNA-binding protein EWS | **Ewsr1** | 1010 |
| 791 | 7 | 5.3 | 197.09 | 46.286 | 20.401 | 22.278 | **0.223** | **-1.420** | P02469;E9QN70;E9PYT5 | P02469;E9QN70 | Laminin subunit beta-1 | **Lamb1** | 410 |
| 792 | 5 | 15.8 | 44.889 | 34.194 | 20.278 | 20.201 | **0.260** | **-1.421** | Q07417 | Q07417 | Short-chain specific acyl-CoA dehydrogenase, mitochondrial | **Acads** | 939 |
| 793 | 4 | 21.8 | 27.254 | 27.611 | 22.046 | 21.143 | **0.415** | **-1.422** | Q9CQ60;D3Z4X1;F6X8L5;Q8CBG6 | Q9CQ60;D3Z4X1;F6X8L5;Q8CBG6 | 6-phosphogluconolactonase | **Pgls** | 1333 |
| 794 | 8 | 34.4 | 28.948 | 73.589 | 23.084 | 24.632 | **0.342** | **-1.440** | Q9CQQ7;A0A0G2JGX3 | Q9CQQ7 | ATP synthase F(0) complex subunit B1, mitochondrial | **Atp5f1** | 1351 |
| 795 | 4 | 30.2 | 19.895 | 68.923 | 25.697 | 23.788 | **0.245** | **-1.441** | Q6ZWQ9;Q3THE2;D3YV37;D3Z249 | Q6ZWQ9;Q3THE2 | Myosin regulatory light chain 12B | **Myl12a;Myl12b** | 950 |
| 796 | 12 | 38.1 | 22.576 | 265.22 | 22.315 | 23.949 | **0.563** | **-1.442** | P43276 | P43276 | Histone H1.5 | **Hist1h1b** | 711 |
| 797 | 8 | 44.4 | 23.713 | 57.224 | 24.335 | 22.860 | **0.272** | **-1.486** | P24369 | P24369 | Peptidyl-prolyl cis-trans isomerase B | **Ppib** | 651 |
| 798 | 4 | 17.1 | 43.953 | 41.301 | 21.532 | 22.841 | **0.604** | **-1.487** | O54724 | O54724 | Polymerase I and transcript release factor | **Ptrf** | 522 |
| 799 | 9 | 17.2 | 81.8 | 60.705 | 16.973 | 17.393 | **0.435** | **-1.504** | Q02257 | Q02257 | Junction plakoglobin | **Jup** | 925 |
| 800 | 2 | 33.2 | 42.004 | 21.368 | 23.483 | 23.751 | **0.453** | **-1.533** | Q8BFZ3 | Q8BFZ3 | Beta-actin-like protein 2 | **Actbl2** | 1139 |
| 801 | 9 | 27.1 | 44.816 | 152.9 | 24.915 | 23.414 | **0.379** | **-1.549** | Q8QZT1 | Q8QZT1 | Acetyl-CoA acetyltransferase, mitochondrial | **Acat1** | 1228 |
| 802 | 2 | 5.6 | 45.026 | 13.636 | 19.356 | 20.051 | **0.460** | **-1.551** | A2ATI9;Q99JX3-2;Q99JX3 | A2ATI9;Q99JX3-2;Q99JX3 | Golgi reassembly-stacking protein 2 | **Gorasp2** | 170 |
| 803 | 2 | 23.4 | 11.614 | 58.927 | 20.713 | 21.034 | **0.159** | **-1.554** | P17095 | P17095 | High mobility group protein HMG-I/HMG-Y | **Hmga1** | 624 |
| 804 | 4 | 4 | 143.23 | 26.302 | 16.193 | 19.594 | **0.334** | **-1.565** | Q9CU62 | Q9CU62 | Structural maintenance of chromosomes protein 1A | **Smc1a** | 1371 |
| 805 | 5 | 51.1 | 15.524 | 93.581 | 27.574 | 25.918 | **0.236** | **-1.614** | P63276 | P63276 | 40S ribosomal protein S17 | **Rps17** | 865 |
| 806 | 8 | 41.2 | 17.587 | 67.045 | 25.650 | 25.827 | **0.823** | **-1.659** | P47915;F6QL70;W4VSN7;D3Z1N9;F6YH22;F6VZG1 | P47915;F6QL70;W4VSN7;D3Z1N9 | 60S ribosomal protein L29 | **Rpl29;Gm17669;Gm3550;Gm10709** | 726 |
| 807 | 1 | 26.2 | 4.7704 | 10.114 | 18.465 | 15.936 | **0.269** | **-1.664** | A2ARQ2;D6RCY2;D6RIP7;A2ARQ4;P84102 | A2ARQ2;D6RCY2;D6RIP7;A2ARQ4;P84102 | Small EDRK-rich factor 2 | **Serf2** | 167 |
| 808 | 11 | 28.2 | 47.006 | 88.422 | 27.099 | 25.682 | **0.288** | **-1.673** | Q9DCL9;D3Z6P1;D6RCU8 | Q9DCL9 | Multifunctional protein ADE2;Phosphoribosylaminoimidazole-succinocarboxamide synthase;Phosphoribosylaminoimidazole carboxylase | **Paics** | 1476 |

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 809 | -3.009 | -4.825 | -2.937 | -2.127 | -0.708 | -2.834 | 22.019 | 23.438 | 21.313 | 21.241 | 19.425 | 21.313 | 24.141 | 24.153 | 25.026 | 23.474 | | 10 | 10 |
| 810 | 11.278 | 2.165 | 0.403 | 9.959 | 4.213 | 4.798 | 27.807 | 22.060 | 22.645 | 27.521 | 18.408 | 16.647 | 19.361 | 16.334 | 16.968 | 15.519 | | 6 | 6 |
| 811 | 11.822 | 9.090 | 10.862 | 12.703 | 12.538 | 11.681 | 28.977 | 28.812 | 27.955 | 28.229 | 25.497 | 27.269 | 17.701 | 14.848 | 17.345 | 15.469 | | 12 | 12 |
| 812 | -2.876 | -7.674 | -2.535 | -3.016 | -2.197 | -2.709 | 22.378 | 23.196 | 22.685 | 21.625 | 16.827 | 21.966 | 27.553 | 23.234 | 26.312 | 22.690 | | 11 | 11 |
| 813 | -4.688 | -3.999 | -3.801 | -2.844 | -3.598 | -0.819 | 17.047 | 16.293 | 19.072 | 16.609 | 17.298 | 17.495 | 24.929 | 14.852 | 23.599 | 18.994 | | 8 | 8 |
| 814 | -4.346 | -3.171 | -1.000 | -4.237 | 0.685 | 0.308 | 15.427 | 20.349 | 19.972 | 17.208 | 18.382 | 20.553 | 23.412 | 15.916 | 23.895 | 19.212 | | 6 | 4 |
| 815 | 2.242 | -2.594 | -1.643 | 4.063 | -0.927 | 0.184 | 27.889 | 22.898 | 24.010 | 27.730 | 22.894 | 23.845 | 26.515 | 21.137 | 25.879 | 25.097 | | 6 | 6 |
| 816 | -2.244 | 2.348 | -0.873 | -0.580 | 2.854 | 2.276 | 18.019 | 21.452 | 20.875 | 16.135 | 20.727 | 17.506 | 22.011 | 15.185 | 20.885 | 15.874 | | 2 | 2 |
| 817 | -7.441 | -5.887 | -1.707 | -2.500 | -6.547 | -0.625 | 21.783 | 17.736 | 23.658 | 15.351 | 16.905 | 21.085 | 26.387 | 22.179 | 24.075 | 21.508 | | 15 | 15 |
| 818 | -5.105 | -1.133 | -3.991 | -3.213 | -3.001 | 1.387 | 17.049 | 17.260 | 21.649 | 16.308 | 20.280 | 17.423 | 24.175 | 16.348 | 23.536 | 19.291 | | 4 | 4 |
| 819 | 9.337 | 8.653 | 7.029 | 10.760 | 11.044 | 8.760 | 30.946 | 31.230 | 28.945 | 30.763 | 30.079 | 28.455 | 16.783 | 23.588 | 24.558 | 18.294 | | 15 | 15 |
| 820 | 0.146 | -1.450 | 1.214 | 0.582 | 2.919 | 1.977 | 24.175 | 26.512 | 25.570 | 22.885 | 21.290 | 23.954 | 24.273 | 22.912 | 22.979 | 22.501 | | 6 | 6 |
| 821 | 7.790 | 7.071 | 6.830 | 9.074 | 9.556 | 8.638 | 26.227 | 26.709 | 25.791 | 25.970 | 25.251 | 25.010 | 18.627 | 15.679 | 21.257 | 15.103 | + | 5 | 5 |
| 822 | 5.586 | 0.096 | 0.152 | 5.776 | 1.086 | 4.583 | 22.401 | 17.711 | 21.208 | 22.281 | 16.791 | 16.847 | 17.888 | 15.362 | 16.929 | 16.462 | | 3 | 3 |
| 823 | -4.764 | -2.045 | -4.966 | -5.161 | -1.434 | 0.552 | 16.886 | 20.613 | 22.599 | 16.912 | 19.631 | 16.710 | 24.816 | 19.278 | 23.193 | 20.159 | | 10 | 10 |
| 824 | 5.322 | 6.618 | 8.332 | 8.486 | 8.456 | 9.151 | 25.910 | 25.880 | 26.575 | 24.215 | 25.511 | 27.225 | 18.712 | 16.136 | 18.473 | 19.313 | | 11 | 2 |
| 825 | 5.253 | 4.017 | 3.333 | 7.114 | 6.889 | 4.449 | 24.925 | 24.700 | 22.259 | 23.570 | 22.334 | 21.651 | 18.255 | 17.366 | 21.311 | 15.324 | | 2 | 2 |
| 826 | 5.459 | 4.843 | 4.939 | 8.742 | 6.007 | 6.365 | 25.181 | 22.446 | 22.804 | 21.660 | 21.044 | 21.140 | 18.507 | 14.371 | 17.355 | 15.047 | | 4 | 4 |
| 827 | -5.122 | -1.606 | -0.151 | -0.114 | -0.065 | -0.758 | 22.866 | 22.915 | 22.222 | 16.847 | 20.364 | 21.818 | 25.148 | 20.813 | 24.671 | 19.267 | | 9 | 9 |
| 828 | -6.243 | -1.305 | -0.736 | 2.286 | -1.495 | -3.128 | 22.282 | 18.501 | 16.868 | 15.279 | 20.217 | 20.786 | 24.075 | 15.918 | 23.568 | 19.476 | | 2 | 2 |
| 829 | -4.451 | -3.650 | -3.637 | -3.853 | 0.674 | -2.573 | 15.617 | 20.144 | 16.897 | 16.156 | 16.958 | 16.971 | 24.006 | 14.934 | 23.201 | 18.014 | | 21 | 11 |
| 830 | -10.436 | -7.030 | -3.424 | -2.607 | -8.879 | -3.418 | 23.023 | 16.751 | 22.212 | 14.101 | 17.507 | 21.113 | 26.648 | 24.612 | 25.472 | 23.602 | | 17 | 17 |
| 831 | 1.641 | 3.408 | 3.494 | 5.277 | 5.649 | 3.620 | 24.455 | 24.827 | 22.798 | 20.018 | 21.784 | 21.870 | 21.805 | 16.553 | 21.255 | 15.497 | | 5 | 5 |
| 832 | 2.570 | 6.490 | 3.474 | 2.124 | 8.851 | 7.793 | 21.058 | 27.786 | 26.727 | 22.561 | 26.481 | 23.465 | 21.090 | 16.779 | 21.680 | 18.302 | | 11 | 11 |
| 833 | -4.967 | -2.732 | -3.873 | -2.713 | -0.113 | -2.396 | 17.958 | 20.557 | 18.275 | 15.198 | 17.434 | 16.292 | 23.724 | 17.616 | 22.684 | 17.647 | | 5 | 5 |
| 834 | 7.831 | 1.679 | 0.132 | 0.676 | 7.931 | 7.464 | 16.615 | 23.871 | 23.403 | 24.761 | 18.609 | 17.062 | 16.670 | 15.208 | 17.481 | 16.378 | | 4 | 4 |

| | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 809 | 10 | 32.2 | 44.005 | 63.742 | 24.147 | 24.250 | **0.903** | **-1.701** | Q3UMP4;Q9CY58;A0A0N4SV32;Q9CY58-3;Q9CY58-2;A0A0N4SWH2;Q9CY58-4;A0A0N4SUQ1;A0A0N4SUN8;A0A0N4SV40;A0A0N4SVK5 | Q3UMP4;Q9CY58;A0A0N4SV32;Q9CY58-3;Q9CY58-2;A0A0N4SWH2;Q9CY58-4 | Plasminogen activator inhibitor 1 RNA-binding protein | **Serbp1** | 985 |
| 810 | 6 | 26.3 | 20.448 | 40.323 | 17.847 | 16.243 | **0.168** | **-1.708** | D3YZ09;Q9CY66-3;Q9CY66-2;Q9CY66;F6SL78 | D3YZ09;Q9CY66-3;Q9CY66-2;Q9CY66;F6SL78 | H/ACA ribonucleoprotein complex subunit 1 | **Gar1** | 289 |
| 811 | 12 | 59.3 | 15.874 | 165.13 | 16.274 | 16.407 | **0.932** | **-1.716** | Q9D1I6 | Q9D1I6 | 39S ribosomal protein L14, mitochondrial | **Mrpl14** | 1424 |
| 812 | 11 | 24.2 | 68.527 | 103.35 | 25.394 | 24.501 | **0.441** | **-1.721** | Q91YQ5;A0A0N4SUJ8 | Q91YQ5 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 | **Rpn1** | 1273 |
| 813 | 6 | 30.3 | 43.934 | 58.381 | 19.891 | 21.296 | **0.934** | **-1.742** | B7ZNL2;Q78ZA7;A0A140LJ37;A0A140LJB5;A0A140LI20 | B7ZNL2;Q78ZA7 | Nucleosome assembly protein 1-like 4 | **Nap1l4** | 218 |
| 814 | 4 | 13.2 | 65.583 | 26.996 | 19.664 | 21.553 | **0.400** | **-1.758** | Q5SF07;A6X8Z3;Q5SF07-2 | Q5SF07;A6X8Z3;Q5SF07-2 | Insulin-like growth factor 2 mRNA-binding protein 2 | **Igf2bp2** | 1003 |
| 815 | 6 | 58.6 | 17.04 | 101.76 | 23.826 | 25.488 | **0.347** | **-1.771** | P62843;D3YTQ9 | P62843;D3YTQ9 | 40S ribosomal protein S15 | **Rps15** | 835 |
| 816 | 2 | 4 | 56.598 | 12.159 | 18.598 | 18.379 | **0.441** | **-1.773** | Q99K28;Q99K28-2 | Q99K28;Q99K28-2 | ADP-ribosylation factor GTPase-activating protein 2 | **Arfgap2** | 1296 |
| 817 | 15 | 16.3 | 109.75 | 98.61 | 24.283 | 22.792 | **0.296** | **-1.787** | O55143-2;O55143;Q8R429;B1ATS4;B1ATS5;E9Q559;Q64518-2;Q64518-3;Q64518 | O55143-2;O55143 | Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 | **Atp2a2** | 528 |
| 818 | 4 | 8 | 39.771 | 25.48 | 20.262 | 21.413 | **0.399** | **-1.801** | P00329 | P00329 | Alcohol dehydrogenase 1 | **Adh1** | 550 |
| 819 | 15 | 52.9 | 26.94 | 323.31 | 20.185 | 21.426 | **0.866** | **-1.848** | O08583;O08583-2;Q9JJW6-2;G3X9I4;Q9JJW6 | O08583;O08583-2;Q9JJW6-2 | THO complex subunit 4;Aly/REF export factor 2 | **Alyref;Alyref 2** | 499 |
| 820 | 6 | 48.8 | 17.699 | 162.12 | 23.593 | 22.740 | **0.837** | **-1.856** | Q64152-2;Q64152 | Q64152-2;Q64152 | Transcription factor BTF3 | **Btf3** | 1077 |
| 821 | 5 | 36.5 | 22.106 | 73.511 | 17.153 | 18.180 | **2.046** | **-1.859** | E9PW20;Q9CY57-5;Q9CY57-4;Q9CY57-3;Q9CY57-2;Q9CY57;D3YZA1;D3Z7T7 | E9PW20;Q9CY57-5;Q9CY57-4;Q9CY57-3;Q9CY57-2;Q9CY57;D3YZA1;D3Z7T7 | Chromatin target of PRMT1 protein | **Chtop** | 340 |
| 822 | 3 | 9.8 | 33.34 | 24.121 | 16.625 | 16.695 | **0.335** | **-1.870** | Q9D773;B1B1D8;B1B1D7 | Q9D773;B1B1D8;B1B1D7 | 39S ribosomal protein L2, mitochondrial | **Mrpl2** | 204 |
| 823 | 10 | 17.5 | 75.6 | 61.017 | 22.047 | 21.676 | **0.424** | **-1.910** | E9Q800;Q8CAQ8-3;Q8CAQ8-2;Q8CAQ8;Q8CAQ8-5;E9QAY6;A0A0U1RP81;Q3TZK4;E9PVS5;A0A0U1RQ14;Q8CAQ8-4 | E9Q800;Q8CAQ8-3;Q8CAQ8-2;Q8CAQ8;Q8CAQ8-5;E9QAY6;A0A0U1RP81 | MICOS complex subunit Mic60 | **Immt** | 395 |
| 824 | 2 | 10.3 | 62.844 | 12.785 | 17.424 | 18.893 | **1.011** | **-1.940** | Q3UV17 | Q3UV17 | Keratin, type II cytoskeletal 2 oral | **Krt76** | 991 |
| 825 | 2 | 3.9 | 33.249 | 42.986 | 17.811 | 18.317 | **0.889** | **-1.950** | Q8BM41;Q8CGC4 | Q8BM41;Q8CGC4 | Protein LSM14 homolog B | **Lsm14b** | 1172 |
| 826 | 4 | 20.9 | 26.717 | 55.35 | 16.439 | 16.201 | **1.046** | **-1.958** | P14106 | P14106 | Complement C1q subcomponent subunit B | **C1qb** | 607 |
| 827 | 9 | 11.6 | 105.53 | 63.826 | 22.980 | 21.969 | **0.593** | **-1.980** | Q8R1B4;M0QWV3 | Q8R1B4 | Eukaryotic translation initiation factor 3 subunit C | **Eif3c** | 1233 |
| 828 | 2 | 5 | 56.888 | 13.534 | 19.996 | 21.522 | **0.346** | **-1.982** | O70310 | O70310 | Glycylpeptide N-tetradecanoyltransferase 1 | **Nmt1** | 533 |
| 829 | 2 | 58.1 | 32.848 | 79.491 | 19.470 | 20.608 | **0.657** | **-1.995** | E9Q450;P58771-2;E9Q452;Q8BSH3;Q8BP43;E9Q454;F8WID5;P58771;E9Q448;B7ZNL3;S4R2U0 | E9Q450;P58771-2;E9Q452;Q8BSH3;Q8BP43;E9Q454;F8WID5;P58771;E9Q448;B7ZNL3;S4R2U0 | Tropomyosin alpha-1 chain | **Tpm1** | 379 |
| 830 | 17 | 15.4 | 170.08 | 132.75 | 25.630 | 24.537 | **0.285** | **-1.995** | Q8CGC7 | Q8CGC7 | Bifunctional glutamate/proline--tRNA ligase;Glutamate--tRNA ligase;Proline--tRNA ligase | **Eprs** | 1204 |
| 831 | 5 | 35 | 15.236 | 40.926 | 19.179 | 18.376 | **1.084** | **-2.001** | P32020-2;P32020 | P32020-2;P32020 | Non-specific lipid-transfer protein | **Scp2** | 682 |
| 832 | 11 | 53.4 | 16.369 | 127.9 | 18.934 | 19.991 | **0.361** | **-2.078** | Q9JMG1 | Q9JMG1 | Endothelial differentiation-related factor 1 | **Edf1** | 1507 |
| 833 | 5 | 9.7 | 46.325 | 30.104 | 20.670 | 20.165 | **0.950** | **-2.117** | Q9JHI5 | Q9JHI5 | Isovaleryl-CoA dehydrogenase, mitochondrial | **Ivd** | 1491 |
| 834 | 4 | 34.8 | 15.261 | 27.396 | 15.939 | 16.930 | **0.257** | **-2.143** | Q9CQN7 | Q9CQN7 | 39S ribosomal protein L41, mitochondrial | **Mrpl41** | 1348 |

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 835 | -1.291 | 4.253 | -0.536 | -0.050 | 4.523 | 4.509 | 17.564 | 22.136 | 22.122 | 16.574 | 22.118 | 17.329 | 20.187 | 15.039 | 20.301 | 15.428 | | 1 | 1 |
| 836 | -3.655 | -7.199 | -2.472 | -2.333 | -2.375 | -1.976 | 23.356 | 23.313 | 23.713 | 21.488 | 17.944 | 22.671 | 28.273 | 23.105 | 26.671 | 23.614 | | 17 | 17 |
| 837 | 6.098 | 5.983 | -0.361 | 6.480 | 7.256 | 4.630 | 23.313 | 24.089 | 21.463 | 22.969 | 22.853 | 16.509 | 16.887 | 16.779 | 18.458 | 15.284 | | 1 | 1 |
| 838 | -6.729 | -3.509 | 0.419 | -0.585 | -1.760 | -0.824 | 24.618 | 23.443 | 24.379 | 17.452 | 20.673 | 24.601 | 28.027 | 22.378 | 26.578 | 21.785 | | 5 | 5 |
| 839 | -5.465 | -3.135 | -4.707 | -4.435 | 1.622 | -3.775 | 16.569 | 22.627 | 17.229 | 15.469 | 17.799 | 16.226 | 21.899 | 20.110 | 23.355 | 18.511 | | 4 | 4 |
| 840 | -3.675 | -0.969 | -2.480 | -0.524 | 0.269 | -0.134 | 17.505 | 18.298 | 17.895 | 16.301 | 19.007 | 17.496 | 21.040 | 15.019 | 20.340 | 19.612 | | 3 | 3 |
| 841 | -4.139 | 4.857 | 3.992 | 3.715 | 3.372 | 4.420 | 22.462 | 22.119 | 23.167 | 14.418 | 23.414 | 22.549 | 18.629 | 18.864 | 21.790 | 15.324 | | 16 | 1 |
| 842 | -2.472 | 0.204 | 0.691 | -1.021 | 2.198 | 4.053 | 16.681 | 19.899 | 21.755 | 14.467 | 17.143 | 17.630 | 19.217 | 16.187 | 17.946 | 15.932 | | 1 | 1 |
| 843 | -6.046 | -3.815 | -7.139 | -0.603 | -1.383 | -8.143 | 24.020 | 23.240 | 16.480 | 16.542 | 18.774 | 15.449 | 26.313 | 22.933 | 24.346 | 20.831 | | 9 | 9 |
| 844 | -4.158 | 4.419 | 2.488 | 3.569 | 3.785 | 2.307 | 21.774 | 21.990 | 20.511 | 14.068 | 22.645 | 20.715 | 16.984 | 19.425 | 21.907 | 14.545 | | 4 | 4 |
| 845 | -4.892 | -2.294 | -4.335 | 0.778 | -0.412 | -4.924 | 23.460 | 22.270 | 17.758 | 15.662 | 18.259 | 16.219 | 23.211 | 22.154 | 25.370 | 15.737 | | 3 | 2 |
| 846 | 0.251 | 6.178 | 2.129 | 1.878 | 6.812 | 6.904 | 19.186 | 24.120 | 24.212 | 16.271 | 22.199 | 18.149 | 18.875 | 15.741 | 16.520 | 15.521 | | 2 | 1 |
| 847 | 1.637 | 3.654 | -1.782 | 5.465 | 3.383 | 1.785 | 22.436 | 20.354 | 18.756 | 19.981 | 21.997 | 16.561 | 18.453 | 15.489 | 20.694 | 15.992 | | 4 | 4 |
| 848 | -0.011 | 0.434 | -4.611 | -1.379 | 2.609 | 1.758 | 21.036 | 25.024 | 24.173 | 22.069 | 22.515 | 17.470 | 23.311 | 21.519 | 21.144 | 23.016 | | 2 | 2 |
| 849 | -0.859 | -0.339 | -0.792 | 2.259 | 1.938 | 1.022 | 23.292 | 22.971 | 22.054 | 20.719 | 21.240 | 20.787 | 21.538 | 20.527 | 22.266 | 20.891 | + | 4 | 4 |
| 850 | -4.581 | 2.341 | -3.271 | 0.991 | 1.485 | -0.757 | 20.679 | 21.172 | 18.931 | 16.161 | 23.082 | 17.470 | 17.508 | 21.867 | 20.327 | 21.155 | | 7 | 7 |
| 851 | 6.687 | 4.211 | 4.029 | 8.311 | 7.999 | 5.879 | 25.307 | 24.996 | 22.875 | 25.220 | 22.744 | 22.562 | 17.983 | 16.009 | 18.943 | 18.123 | | 7 | 7 |
| 852 | -5.626 | 0.226 | -4.993 | 2.023 | -0.159 | -4.983 | 23.770 | 21.588 | 16.765 | 15.920 | 21.772 | 16.553 | 19.368 | 24.126 | 26.194 | 16.899 | | 1 | 1 |
| 853 | -4.346 | -0.616 | 3.139 | 2.978 | 0.414 | 2.071 | 22.584 | 20.020 | 21.677 | 14.084 | 17.814 | 21.569 | 23.745 | 15.468 | 22.211 | 14.649 | | 13 | 1 |
| 854 | -7.331 | -4.985 | -4.829 | -6.356 | -1.580 | -1.837 | 17.211 | 21.987 | 21.730 | 15.086 | 17.432 | 17.588 | 25.966 | 21.169 | 23.726 | 21.108 | | 5 | 5 |
| 855 | 4.735 | 5.042 | -2.851 | 5.714 | 5.151 | 3.488 | 26.671 | 26.108 | 24.445 | 24.319 | 24.625 | 16.732 | 19.094 | 22.821 | 23.947 | 15.221 | | 1 | 1 |
| 856 | -0.182 | -2.034 | -1.839 | -1.992 | 2.798 | 2.607 | 17.348 | 22.138 | 21.946 | 18.629 | 16.777 | 16.972 | 21.755 | 16.924 | 22.935 | 14.687 | | 2 | 2 |
| 857 | 4.352 | 7.175 | 6.028 | 6.080 | 9.456 | 9.488 | 24.987 | 28.362 | 28.395 | 24.198 | 27.022 | 25.875 | 18.259 | 19.554 | 19.906 | 19.787 | | 7 | 7 |
| 858 | -5.054 | -5.780 | -1.158 | 1.325 | 0.155 | -5.891 | 24.385 | 23.215 | 17.169 | 17.216 | 16.490 | 21.113 | 25.154 | 20.966 | 22.506 | 22.035 | | 4 | 4 |
| 859 | -8.514 | -5.628 | -7.274 | -7.220 | -2.098 | -4.509 | 17.055 | 22.177 | 19.766 | 14.933 | 17.819 | 16.173 | 26.774 | 21.775 | 24.480 | 22.415 | | 13 | 13 |
| 860 | -6.755 | -5.665 | -6.342 | -1.967 | -7.206 | -1.985 | 22.163 | 16.924 | 22.145 | 16.512 | 17.602 | 16.924 | 26.647 | 21.613 | 23.266 | 23.267 | | 2 | 2 |
| 861 | 1.236 | 2.392 | 0.824 | 4.964 | 1.659 | 5.444 | 21.328 | 18.022 | 21.808 | 17.607 | 18.764 | 17.196 | 17.085 | 15.642 | 18.140 | 14.603 | | 1 | 1 |
| 862 | -5.748 | -3.376 | -3.780 | -2.204 | -3.380 | 0.393 | 18.553 | 17.376 | 21.149 | 15.495 | 17.867 | 17.463 | 25.122 | 16.391 | 21.180 | 21.306 | | 6 | 6 |
| 863 | -3.204 | -0.719 | 2.157 | -2.014 | 3.866 | 4.127 | 16.198 | 22.077 | 22.338 | 15.504 | 17.988 | 20.865 | 16.919 | 19.504 | 22.824 | 14.592 | | 4 | 4 |
| 864 | 3.394 | 5.362 | 4.581 | 3.883 | 8.431 | 8.851 | 22.672 | 27.219 | 27.639 | 23.708 | 25.676 | 24.895 | 17.775 | 19.802 | 19.508 | 21.120 | | 4 | 4 |
| 865 | -6.723 | -1.184 | -4.234 | -4.854 | 1.999 | -1.358 | 17.462 | 24.315 | 20.958 | 14.987 | 20.526 | 17.476 | 24.346 | 20.287 | 23.238 | 20.181 | | 5 | 5 |

| | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 835 | 1 | 2.3 | 37.988 | 7.6068 | 17.613 | 17.865 | **0.401** | **-2.185** | Q8BKL1;Q8BJJ6;Q62280 | Q8BKL1;Q8BJJ6;Q62280 | Protein SSXT | **Ss18** | 1066 |
| 836 | 17 | 57.2 | 33.296 | 183.06 | 25.689 | 25.143 | **0.709** | **-2.214** | O35129;F6QPR1;F6Q8V7 | O35129;F6QPR1 | Prohibitin-2 | **Phb2** | 509 |
| 837 | 1 | 0.9 | 152.01 | 8.1781 | 16.833 | 16.871 | **0.415** | **-2.216** | E9Q3G8 | E9Q3G8 | RanBP2-type domain-containing protein | **Nup153** | 375 |
| 838 | 5 | 37.1 | 14.515 | 194.96 | 25.203 | 24.182 | **0.456** | **-2.217** | Q6ZWZ6;P63323 | Q6ZWZ6;P63323 | 40S ribosomal protein S12 | **Rps12** | 866 |
| 839 | 4 | 10.2 | 44.116 | 23.856 | 21.004 | 20.933 | **0.477** | **-2.239** | Q99KJ8 | Q99KJ8 | Dynactin subunit 2 | **Dctn2** | 1301 |
| 840 | 3 | 10.9 | 47.989 | 16.8 | 18.029 | 19.976 | **1.290** | **-2.245** | E9QAQ5;Q9WV60 | E9QAQ5;Q9WV60 | Glycogen synthase kinase-3 beta | **Gsk3b** | 402 |
| 841 | 1 | 41.8 | 34.476 | 6.8928 | 18.747 | 18.557 | **0.323** | **-2.266** | A2AL12;Q8BG05;A2AL13;V9GX38 | A2AL12;Q8BG05 | Heterogeneous nuclear ribonucleoprotein A3 | **Hnrnpa3** | 154 |
| 842 | 1 | 2.5 | 54.752 | 7.1681 | 17.702 | 16.939 | **0.567** | **-2.269** | Q8K0E8 | Q8K0E8 | Fibrinogen beta chain;Fibrinopeptide B;Fibrinogen beta chain | **Fgb** | 1220 |
| 843 | 9 | 19.1 | 55.814 | 56.167 | 24.623 | 22.589 | **0.371** | **-2.291** | P24547;A0A0A6YXS4;A0A0A6YY72 | P24547;A0A0A6YXS4 | Inosine-5-monophosphate dehydrogenase 2 | **Impdh2** | 653 |
| 844 | 4 | 7.9 | 48.37 | 23.436 | 18.204 | 18.226 | **0.365** | **-2.304** | Q60749;A0A087WSL3;A0A087WR32;Q9WU01-2;Q9WU01 | Q60749 | KH domain-containing, RNA-binding, signal transduction-associated protein 1 | **Khdrbs1** | 1023 |
| 845 | 2 | 2.4 | 112.22 | 13.95 | 22.682 | 20.554 | **0.537** | **-2.321** | E9PXB7;Q8CFI0-3;Q8CFI0 | E9PXB7;Q8CFI0-3;Q8CFI0 | E3 ubiquitin-protein ligase NEDD4-like | **Nedd4l** | 349 |
| 846 | 1 | 14.6 | 10.617 | 7.9548 | 17.308 | 16.021 | **0.414** | **-2.345** | P17095-1 | P17095-1 | High mobility group protein HMG-I/HMG-Y | **Hmga1** | 625 |
| 847 | 4 | 18.1 | 29.237 | 25.891 | 16.971 | 18.343 | **0.550** | **-2.375** | P09021;F6W0B3;P10629-2;P09024;P32043;P09023;P02830;P09092;P10629;P09025;P09632;P20615;P09633;P09079;P28357 | P09021 | Homeobox protein Hox-A5 | **Hoxa5** | 579 |
| 848 | 2 | 3.7 | 84.266 | 15.448 | 22.415 | 22.080 | **0.521** | **-2.392** | B2RPU8;D3Z5B1;Q9D1L0 | B2RPU8;D3Z5B1;Q9D1L0 | Coiled-coil-helix-coiled-coil-helix domain-containing protein 2 | **Zbed5;Chchd2** | 205 |
| 849 | 4 | 6 | 121.64 | 25.562 | 21.033 | 21.579 | **2.392** | **-2.403** | Q6A0A9 | Q6A0A9 | Constitutive coactivator of PPAR-gamma-like protein 1 | **FAM120A** | 1086 |
| 850 | 7 | 14.4 | 74.237 | 52.118 | 19.688 | 20.741 | **0.468** | **-2.410** | P48678;P48678-2;P48678-3;D3YUF7 | P48678;P48678-2;P48678-3 | Prelamin-A/C;Lamin-A/C | **Lmna** | 731 |
| 851 | 7 | 31.9 | 10.197 | 43.579 | 16.996 | 18.533 | **0.988** | **-2.421** | Q8R1F0 | Q8R1F0 | Leydig cell tumor 10 kDa protein homolog | **D8Ertd738e** | 1234 |
| 852 | 1 | 3.7 | 20.991 | 10.473 | 21.747 | 21.546 | **0.364** | **-2.425** | A0A0N4SUN5 | A0A0N4SUN5 | Nuclear receptor-interacting protein 2 | **Nrip2** | 65 |
| 853 | 1 | 20.4 | 73.427 | 7.9982 | 19.606 | 18.430 | **0.458** | **-2.429** | Q62095 | Q62095 | ATP-dependent RNA helicase DDX3Y | **Ddx3y** | 1060 |
| 854 | 3 | 30.8 | 32.939 | 35.911 | 23.567 | 22.417 | **0.633** | **-2.458** | P47753;Q5RKN9;A0A0G2JE27 | P47753;Q5RKN9;A0A0G2JE27 | F-actin-capping protein subunit alpha-1 | **Capza1** | 722 |
| 855 | 1 | 0.6 | 195.04 | 6.6934 | 20.957 | 19.584 | **0.392** | **-2.476** | A0A0N4SVZ4 | A0A0N4SVZ4 | von Willebrand factor D and EGF domain-containing protein | **Vwde** | 72 |
| 856 | 2 | 5.6 | 48.327 | 14.121 | 19.339 | 18.811 | **0.676** | **-2.490** | Q3TIV5;Q3TIV5-3;Q3TIV5-2 | Q3TIV5;Q3TIV5-3;Q3TIV5-2 | Zinc finger CCCH domain-containing protein 15 | **Zc3h15** | 953 |
| 857 | 6 | 53.1 | 7.0662 | 196.59 | 18.906 | 19.847 | **0.826** | **-2.490** | Q8K003 | Q8K003 | Translation machinery-associated protein 7 | **Tma7** | 1219 |
| 858 | 4 | 10.4 | 54.272 | 25.059 | 23.060 | 22.270 | **0.403** | **-2.527** | O08749 | O08749 | Dihydrolipoyl dehydrogenase, mitochondrial | **Dld** | 502 |
| 859 | 13 | 25.3 | 61.336 | 96.577 | 24.275 | 23.447 | **0.676** | **-2.530** | P26443;F7CFA5 | P26443 | Glutamate dehydrogenase 1, mitochondrial | **Glud1** | 662 |
| 860 | 2 | 29.3 | 6.4913 | 38.962 | 24.130 | 23.266 | **0.646** | **-2.535** | A0A087WP98;A0A087WPN6;P26350;A0A087WQN2 | A0A087WP98;A0A087WPN6;P26350;A0A087WQN2 | Prothymosin alpha;Prothymosin alpha, N-terminally processed;Thymosin alpha | **Ptma** | 17 |
| 861 | 1 | 2.7 | 44.887 | 6.7691 | 16.364 | 16.372 | **0.927** | **-2.538** | P26151 | P26151 | High affinity immunoglobulin gamma Fc receptor I | **Fcgr1** | 660 |
| 862 | 6 | 10.3 | 107.58 | 41.936 | 20.756 | 21.243 | **0.899** | **-2.571** | Q99K41 | Q99K41 | EMILIN-1 | **Emilin1** | 1297 |
| 863 | 4 | 6.2 | 108.18 | 23.544 | 18.212 | 18.708 | **0.437** | **-2.581** | Q569Z6;Q8BZN7;F6YSQ2;F6YH92 | Q569Z6;Q8BZN7 | Thyroid hormone receptor-associated protein 3 | **Thrap3** | 999 |
| 864 | 4 | 27.1 | 14.055 | 93.649 | 18.788 | 20.314 | **0.704** | **-2.609** | Q6NSP9;P52927 | Q6NSP9;P52927 | High mobility group protein HMGI-C | **Hmga2** | 751 |
| 865 | 5 | 13.3 | 52.318 | 30.91 | 22.316 | 21.710 | **0.446** | **-2.643** | E9PYI8;Q9JMA1 | E9PYI8;Q9JMA1 | Ubiquitin carboxyl-terminal hydrolase;Ubiquitin carboxyl-terminal hydrolase 14 | **Usp14** | 354 |

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 866 | -5.198 | -2.542 | -4.797 | -2.461 | -1.281 | -0.806 | 21.024 | 22.204 | 22.679 | 16.674 | 19.330 | 17.074 | 24.633 | 22.337 | 23.118 | 20.626 | | 6 | 6 |
| 867 | 0.824 | 1.257 | 1.487 | -0.741 | 5.812 | 6.524 | 17.340 | 23.893 | 24.605 | 17.519 | 17.952 | 18.182 | 20.157 | 16.005 | 16.914 | 16.476 | | 3 | 3 |
| 868 | -4.729 | -4.202 | -5.689 | -5.796 | -0.130 | -0.615 | 16.553 | 22.219 | 21.734 | 17.085 | 17.612 | 16.125 | 23.600 | 21.099 | 23.407 | 20.221 | | 25 | 2 |
| 869 | -6.460 | -5.664 | -6.990 | -6.187 | -4.208 | -0.569 | 18.317 | 20.296 | 23.935 | 16.738 | 17.534 | 16.207 | 28.254 | 20.754 | 27.054 | 19.341 | | 7 | 5 |
| 870 | -3.560 | -2.702 | -1.257 | 1.839 | -1.717 | 0.522 | 21.413 | 17.857 | 20.095 | 15.878 | 16.736 | 18.181 | 23.611 | 15.536 | 22.851 | 16.024 | | 4 | 4 |
| 871 | -6.099 | -1.540 | -6.137 | -6.304 | 1.168 | -0.479 | 16.784 | 24.255 | 22.609 | 16.707 | 21.267 | 16.670 | 25.458 | 20.717 | 25.667 | 19.946 | | 12 | 12 |
| 872 | -4.332 | -0.908 | -2.896 | -0.013 | -1.376 | 1.562 | 22.214 | 20.851 | 23.789 | 16.491 | 19.914 | 17.927 | 25.571 | 18.883 | 22.964 | 18.680 | | 20 | 20 |
| 873 | -3.012 | -2.845 | -3.613 | -1.302 | 1.239 | -1.005 | 17.943 | 20.484 | 18.240 | 17.191 | 17.357 | 16.589 | 19.020 | 19.470 | 20.863 | 19.542 | + | 2 | 2 |
| 874 | -1.872 | -0.189 | 4.099 | 4.954 | 0.836 | 4.655 | 21.844 | 17.726 | 21.546 | 15.999 | 17.682 | 21.970 | 17.008 | 16.773 | 20.128 | 15.615 | | 1 | 1 |
| 875 | -2.930 | -1.692 | -2.658 | -3.548 | 2.688 | 2.087 | 16.475 | 22.711 | 22.110 | 16.320 | 17.558 | 16.591 | 24.095 | 15.952 | 22.820 | 15.680 | | 6 | 6 |
| 876 | 0.252 | 3.998 | 2.539 | 4.296 | 5.682 | 5.384 | 26.247 | 27.633 | 27.335 | 25.162 | 28.907 | 27.449 | 16.619 | 27.283 | 27.287 | 22.532 | | 12 | 8 |
| 877 | 2.153 | -4.618 | -4.310 | 2.146 | 0.529 | -0.547 | 23.913 | 22.296 | 21.221 | 23.331 | 16.560 | 16.868 | 22.585 | 20.949 | 22.189 | 20.167 | | 4 | 2 |
| 878 | -4.413 | -3.571 | 0.418 | 3.371 | -0.408 | -1.539 | 21.093 | 17.314 | 16.183 | 16.869 | 17.711 | 21.700 | 19.284 | 16.160 | 22.724 | 19.839 | | 3 | 3 |
| 879 | 6.784 | -0.450 | 7.011 | 6.931 | 7.962 | 7.537 | 25.653 | 26.684 | 26.259 | 23.914 | 16.681 | 24.142 | 20.946 | 16.498 | 17.993 | 16.269 | | 4 | 4 |
| 880 | -7.645 | -0.472 | -5.932 | -1.617 | -1.602 | -1.591 | 22.020 | 22.035 | 22.046 | 15.019 | 22.191 | 16.732 | 23.935 | 23.339 | 24.115 | 21.212 | | 2 | 2 |
| 881 | -1.895 | -5.221 | -5.962 | 3.104 | -5.355 | -1.476 | 25.616 | 17.157 | 21.036 | 20.831 | 17.505 | 16.765 | 25.376 | 19.648 | 23.945 | 21.508 | | 10 | 10 |
| 882 | -1.004 | -4.163 | -7.099 | 0.596 | -1.458 | -1.909 | 24.529 | 22.476 | 22.025 | 21.863 | 18.704 | 15.768 | 26.051 | 21.816 | 24.218 | 21.516 | | 4 | 4 |
| 883 | -8.856 | -5.739 | -7.353 | -3.737 | -5.890 | -2.712 | 20.489 | 18.336 | 21.514 | 15.063 | 18.180 | 16.566 | 25.680 | 22.772 | 24.474 | 23.363 | | 13 | 13 |
| 884 | -8.577 | -3.719 | -3.295 | -3.240 | -1.262 | -1.465 | 23.116 | 25.094 | 24.891 | 16.110 | 20.968 | 21.392 | 28.123 | 24.589 | 26.705 | 22.668 | | 10 | 10 |
| 885 | 0.109 | -6.708 | -1.649 | 0.746 | 0.856 | -0.136 | 23.733 | 23.842 | 22.851 | 22.948 | 16.130 | 21.189 | 23.395 | 22.578 | 22.823 | 22.855 | | 9 | 9 |
| 886 | -2.644 | 3.873 | -1.336 | 7.335 | 3.789 | -1.380 | 25.271 | 21.725 | 16.555 | 15.599 | 22.117 | 16.908 | 20.247 | 15.625 | 21.207 | 15.280 | | 12 | 7 |
| 887 | 4.265 | 0.441 | -0.077 | 6.357 | 5.099 | 3.051 | 23.109 | 21.851 | 19.803 | 21.128 | 17.304 | 16.787 | 17.462 | 16.042 | 19.281 | 14.446 | | 1 | 1 |
| 888 | -5.622 | -2.445 | -2.077 | -0.350 | 0.924 | -0.572 | 22.732 | 24.006 | 22.510 | 19.465 | 22.642 | 23.010 | 26.100 | 20.065 | 25.757 | 24.417 | + | 11 | 11 |
| 889 | -4.987 | 7.280 | 5.304 | 7.162 | 4.865 | 5.762 | 23.874 | 21.577 | 22.474 | 14.073 | 26.341 | 24.364 | 17.759 | 15.665 | 22.766 | 15.354 | | 4 | 4 |
| 890 | -6.083 | -3.750 | -5.137 | -5.229 | 0.142 | 0.548 | 17.025 | 22.397 | 22.802 | 15.459 | 17.792 | 16.404 | 23.343 | 21.166 | 22.321 | 20.762 | | 3 | 1 |
| 891 | -1.665 | 1.035 | 2.351 | -0.014 | 6.553 | 5.693 | 17.481 | 24.048 | 23.188 | 16.171 | 18.872 | 20.187 | 18.164 | 16.826 | 21.933 | 13.740 | | 3 | 3 |

| | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 866 | 3 | 22.8 | 40.489 | 44.321 | 23.485 | 21.872 | **1.297** | **-2.663** | P08752;A0A0A6YWA9;P18872-2;P18872;B2RSH2;A2A610;A2AE31;A2AE32;Q66L47;P20612;Q3V3I2;P50149;Q8CGK7;D3Z2M7 | P08752;A0A0A6YWA9;P18872-2;P18872;B2RSH2 | Guanine nucleotide-binding protein G(i) subunit alpha-2;Guanine nucleotide-binding protein G(o) subunit alpha;Guanine nucleotide-binding protein G(i) subunit alpha-1 | **Gnai2;Gnao1;Gnai1** | 578 |
| 867 | 3 | 32.6 | 9.6523 | 24.35 | 18.081 | 16.695 | **0.505** | **-2.676** | P20491 | P20491 | High affinity immunoglobulin epsilon receptor subunit gamma | **Fcer1g** | 643 |
| 868 | 2 | 55.5 | 49.906 | 17.03 | 22.349 | 21.814 | **0.653** | **-2.693** | Q7TMM9 | Q7TMM9 | Tubulin beta-2A chain | **Tubb2a** | 1120 |
| 869 | 5 | 20.8 | 48.542 | 51.065 | 24.504 | 23.198 | **0.737** | **-2.717** | E9PW66;P28656 | E9PW66;P28656 | Nucleosome assembly protein 1-like 1 | **Nap1l1** | 341 |
| 870 | 4 | 13 | 34.877 | 27.166 | 19.573 | 19.438 | **1.033** | **-2.721** | Q922Q8 | Q922Q8 | Leucine-rich repeat-containing protein 59 | **Lrrc59** | 1285 |
| 871 | 12 | 12.2 | 139.41 | 82.586 | 23.087 | 22.807 | **0.425** | **-2.721** | F8WHL2;Q8CIE6 | F8WHL2;Q8CIE6 | Coatomer subunit alpha;Coatomer subunit alpha;Xenin;Proxenin | **Copa** | 440 |
| 872 | 11 | 36.6 | 67.766 | 130.4 | 22.227 | 20.822 | **0.994** | **-2.770** | P26041 | P26041 | Moesin | **Msn** | 658 |
| 873 | 2 | 3.3 | 115.26 | 11.9 | 19.245 | 20.202 | **1.545** | **-2.801** | A0A0U1RPL0;Q7TQH0-3;Q7TQH0-2;E9Q5Q0;Q3TGG2;Q7TQH0 | A0A0U1RPL0;Q7TQH0-3;Q7TQH0-2;E9Q5Q0;Q3TGG2;Q7TQH0 | Ataxin-2-like protein | **Atxn2l** | 104 |
| 874 | 1 | 5.7 | 17.922 | 6.7632 | 16.890 | 17.871 | **0.561** | **-2.802** | Q561M1;Q9D358-2;Q9D358 | Q561M1;Q9D358-2;Q9D358 | Low molecular weight phosphotyrosine protein phosphatase | **Acp1** | 998 |
| 875 | 6 | 24.1 | 25.147 | 41.569 | 20.023 | 19.250 | **0.632** | **-2.836** | Q62446 | Q62446 | Peptidyl-prolyl cis-trans isomerase FKBP3 | **Fkbp3** | 1071 |
| 876 | 8 | 43.7 | 21.785 | 256.25 | 21.951 | 24.909 | **1.150** | **-2.858** | P43275 | P43275 | Histone H1.1 | **Hist1h1a** | 710 |
| 877 | 2 | 35.1 | 8.6191 | 16.484 | 21.767 | 21.178 | **0.562** | **-2.968** | D6RH49;D3YYB0;Q6ZWY3 | D6RH49;D3YYB0;Q6ZWY3 | 40S ribosomal protein S27;40S ribosomal protein S27-like | **Rps27l** | 287 |
| 878 | 3 | 9.5 | 29.032 | 22.041 | 17.722 | 21.282 | **0.643** | **-2.997** | A0A087WPF9;A0A087WQS2;Q9CQC6 | A0A087WPF9;A0A087WQS2;Q9CQC6 | Basic leucine zipper and W2 domain-containing protein 1 | **Bzw1** | 18 |
| 879 | 4 | 26.4 | 15.944 | 28.348 | 18.722 | 17.131 | **0.542** | **-3.028** | Q99N92 | Q99N92 | 39S ribosomal protein L27, mitochondrial | **Mrpl27** | 1317 |
| 880 | 2 | 11.3 | 44.868 | 13.851 | 23.637 | 22.663 | **0.643** | **-3.080** | P63037;B1AXY1 | P63037;B1AXY1 | DnaJ homolog subfamily A member 1 | **Dnaja1** | 857 |
| 881 | 10 | 12.5 | 107.5 | 63.224 | 22.512 | 22.726 | **0.495** | **-3.117** | Q64737;D6RCG1;Q64737-2 | Q64737 | Trifunctional purine biosynthetic protein adenosine-3;Phosphoribosylamine--glycine ligase;Phosphoribosylformylglycinamidine cyclo-ligase;Phosphoribosylglycinamide formyltransferase | **Gart** | 1083 |
| 882 | 4 | 38 | 8.2355 | 52.113 | 23.934 | 22.867 | **0.757** | **-3.165** | Q06185;Q8BTB6 | Q06185 | ATP synthase subunit e, mitochondrial | **Atp5i** | 936 |
| 883 | 12 | 18.1 | 109.94 | 89.569 | 24.226 | 23.919 | **1.160** | **-3.203** | O70318 | O70318 | Band 4.1-like protein 2 | **Epb41l2** | 534 |
| 884 | 8 | 40.3 | 17.274 | 112.09 | 26.356 | 24.687 | **0.822** | **-3.208** | P54227;D3Z5N2;D3Z1Z8 | P54227;D3Z5N2;D3Z1Z8 | Stathmin | **Stmn1** | 309 |
| 885 | 9 | 13.3 | 117.34 | 58.866 | 22.987 | 22.839 | **0.716** | **-3.238** | P27546-2;P27546;A0A140T8T5;A0A0G2JFH2;P27546-3;A0A0G2JDN7;E9PZ43;P27546-4;A0A0G2JFT4;A0A0G2JG35;A0A0G2JFK3;A0A0G2JDY5;A0A0G2JE57;A0A0G2JDU1 | P27546-2;P27546;A0A140T8T5;A0A0G2JFH2;P27546-3;A0A0G2JDN7;E9PZ43;P27546-4 | Microtubule-associated protein 4;Microtubule-associated protein | **Map4** | 666 |
| 886 | 7 | 28.6 | 53.497 | 97.761 | 17.936 | 18.243 | **0.437** | **-3.283** | P31001 | P31001 | Desmin | **Des** | 680 |
| 887 | 1 | 8.5 | 19.675 | 6.8778 | 16.752 | 16.864 | **0.919** | **-3.293** | A0A140LIX7 | A0A140LIX7 | Ras-related protein Rab-34 | **Rab34** | 110 |
| 888 | 2 | 49 | 27.217 | 236.23 | 23.082 | 25.087 | **1.301** | **-3.382** | E9QN08;Q80T06;P57776;A0A0R4J1E2;P57776-3;D3YUQ9;Q91VK2;D3YZT9;D3YY68 | E9QN08;Q80T06;P57776;A0A0R4J1E2;P57776-3;D3YUQ9;Q91VK2;D3YZT9 | Elongation factor 1-delta | **Eef1d** | 408 |
| 889 | 4 | 21.1 | 20.861 | 25.809 | 16.712 | 19.060 | **0.368** | **-3.397** | P10922 | P10922 | Histone H1.0;Histone H1.0, N-terminally processed | **H1f0** | 594 |
| 890 | 1 | 11.2 | 20.828 | 7.6855 | 22.254 | 21.542 | **0.812** | **-3.477** | P55821 | P55821 | Stathmin-2 | **Stmn2** | 764 |
| 891 | 3 | 18.4 | 17.27 | 18.679 | 17.495 | 17.836 | **0.669** | **-3.504** | Q9CQH7 | Q9CQH7 | Transcription factor BTF3 homolog 4 | **Btf3l4** | 1345 |

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 892 | -2.332 | -8.153 | -2.061 | -0.256 | -0.824 | -0.895 | 24.269 | 23.700 | 23.629 | 23.290 | 17.469 | 23.560 | 28.745 | 20.304 | 27.143 | 24.100 | | 17 | 17 |
| 893 | -2.432 | 5.872 | 5.224 | 5.515 | 7.381 | 6.636 | 22.185 | 24.051 | 23.306 | 14.242 | 22.545 | 21.898 | 17.598 | 15.742 | 17.220 | 16.127 | | 15 | 14 |
| 894 | -4.179 | -2.631 | -2.669 | 3.455 | -3.983 | 2.006 | 23.259 | 15.821 | 21.810 | 15.475 | 17.022 | 16.984 | 24.051 | 15.557 | 23.613 | 15.694 | | 4 | 4 |
| 895 | -5.568 | -3.557 | -5.097 | -3.221 | -0.215 | 0.347 | 18.630 | 21.636 | 22.197 | 15.942 | 17.953 | 16.413 | 22.824 | 20.876 | 20.984 | 22.036 | + | 2 | 2 |
| 896 | -2.607 | -2.347 | -1.130 | 3.170 | 2.123 | -0.233 | 25.876 | 24.829 | 22.473 | 18.672 | 18.932 | 20.149 | 25.047 | 20.364 | 22.283 | 20.275 | + | 9 | 9 |
| 897 | -1.415 | 1.845 | 0.654 | 5.393 | 8.241 | -1.025 | 22.399 | 25.247 | 15.980 | 15.063 | 18.323 | 17.133 | 17.815 | 16.196 | 16.926 | 16.031 | | 2 | 2 |
| 898 | -0.324 | 1.532 | 1.488 | 0.621 | 5.818 | 7.995 | 17.788 | 22.984 | 25.161 | 15.697 | 17.553 | 17.509 | 18.769 | 15.564 | 17.525 | 14.517 | | 2 | 2 |
| 899 | -5.564 | -3.925 | -5.316 | -1.406 | -0.695 | -0.821 | 21.677 | 22.387 | 22.262 | 16.143 | 17.782 | 16.391 | 25.716 | 20.449 | 23.816 | 19.598 | + | 5 | 4 |
| 900 | 3.796 | -0.358 | 2.290 | 5.385 | 6.361 | 6.178 | 22.877 | 23.853 | 23.671 | 19.920 | 15.766 | 18.414 | 19.038 | 15.947 | 17.513 | 14.736 | + | 1 | 1 |
| 901 | -5.802 | -2.775 | -2.380 | 5.695 | -2.465 | -1.912 | 26.754 | 18.594 | 19.147 | 14.311 | 17.337 | 17.733 | 25.285 | 16.833 | 19.785 | 20.440 | | 8 | 8 |
| 902 | 0.978 | 4.787 | 0.359 | 9.487 | 7.295 | 2.206 | 29.367 | 27.176 | 22.086 | 21.525 | 25.333 | 20.906 | 22.953 | 16.807 | 23.924 | 17.169 | | 26 | 21 |
| 903 | -0.627 | 2.591 | 1.990 | 8.340 | 1.224 | 7.367 | 24.406 | 17.290 | 23.433 | 15.564 | 18.782 | 18.181 | 17.246 | 14.886 | 17.100 | 15.282 | | 1 | 1 |
| 904 | -0.826 | 1.152 | 1.901 | 0.862 | 7.592 | 6.772 | 17.569 | 24.299 | 23.479 | 15.632 | 17.611 | 18.360 | 17.536 | 15.878 | 18.252 | 14.665 | | 1 | 1 |
| 905 | 4.832 | -0.583 | -1.062 | 6.201 | 5.743 | 4.309 | 23.859 | 23.400 | 21.966 | 23.239 | 17.824 | 17.346 | 18.284 | 17.030 | 20.761 | 16.054 | | 2 | 2 |
| 906 | 6.868 | -0.473 | 4.834 | 8.663 | 8.321 | 7.848 | 25.276 | 24.933 | 24.460 | 25.137 | 17.796 | 23.103 | 17.224 | 16.001 | 21.148 | 15.390 | | 4 | 4 |
| 907 | -5.869 | -5.000 | -6.642 | -0.691 | -0.158 | -3.003 | 22.264 | 22.798 | 19.952 | 16.476 | 17.345 | 15.703 | 24.336 | 21.575 | 23.629 | 21.060 | + | 4 | 4 |
| 908 | -5.477 | -2.381 | -3.577 | -3.582 | 2.204 | 3.607 | 16.736 | 22.521 | 23.924 | 15.281 | 18.377 | 17.181 | 25.373 | 15.261 | 22.770 | 18.746 | | 8 | 8 |
| 909 | -2.611 | 4.747 | -0.890 | -1.098 | 8.400 | 7.678 | 16.210 | 25.708 | 24.986 | 14.858 | 22.216 | 16.580 | 18.921 | 15.696 | 17.394 | 17.545 | | 11 | 1 |
| 910 | -6.244 | -0.013 | -5.933 | 0.615 | 0.711 | 0.230 | 22.242 | 22.338 | 21.857 | 16.241 | 22.471 | 16.552 | 26.433 | 16.822 | 23.602 | 21.368 | | 4 | 4 |
| 911 | 0.167 | 5.929 | 0.524 | 5.557 | 8.063 | 6.759 | 21.811 | 24.317 | 23.013 | 16.344 | 22.106 | 16.701 | 18.091 | 14.417 | 17.537 | 14.817 | | 3 | 3 |
| 912 | -3.422 | -1.919 | -2.311 | 7.383 | 3.729 | -4.922 | 28.441 | 24.787 | 16.136 | 16.774 | 18.277 | 17.885 | 26.614 | 15.503 | 21.580 | 18.812 | | 10 | 10 |
| 913 | -7.166 | -2.249 | -3.186 | 2.891 | -5.229 | 3.864 | 25.378 | 17.258 | 26.351 | 15.946 | 20.863 | 19.926 | 24.326 | 20.648 | 24.105 | 22.118 | | 14 | 11 |
| 914 | -3.345 | -1.200 | -1.887 | 2.541 | 3.360 | 2.161 | 22.355 | 23.173 | 21.975 | 15.536 | 17.680 | 16.994 | 24.415 | 15.212 | 20.103 | 17.659 | + | 6 | 6 |
| 915 | -0.537 | -0.302 | 0.809 | 8.427 | 0.098 | 6.182 | 25.013 | 16.683 | 22.767 | 17.150 | 17.386 | 18.496 | 17.615 | 15.556 | 19.118 | 16.256 | | 1 | 1 |
| 916 | -3.081 | -3.035 | -3.016 | 2.370 | 2.611 | 1.565 | 23.137 | 23.377 | 22.331 | 18.002 | 18.049 | 18.067 | 26.779 | 14.754 | 23.817 | 18.350 | + | 8 | 8 |
| 917 | -0.972 | -3.052 | -0.141 | 5.824 | 4.735 | 1.233 | 26.842 | 25.752 | 22.250 | 19.992 | 17.913 | 20.824 | 23.592 | 18.443 | 23.881 | 18.048 | + | 13 | 13 |
| 918 | -0.829 | -2.962 | 2.659 | 4.085 | 5.428 | 5.699 | 22.602 | 23.946 | 24.217 | 18.556 | 16.423 | 22.044 | 22.550 | 14.485 | 24.006 | 14.765 | + | 6 | 6 |
| 919 | -5.227 | -2.879 | -3.324 | 4.336 | 3.461 | -2.419 | 23.395 | 22.519 | 16.639 | 15.306 | 17.654 | 17.209 | 22.756 | 15.361 | 20.924 | 20.142 | | 3 | 3 |
| 920 | -5.266 | -0.154 | -1.093 | 0.136 | 6.888 | 3.569 | 18.018 | 24.769 | 21.451 | 15.711 | 20.823 | 19.884 | 21.191 | 14.573 | 22.942 | 19.012 | | 7 | 7 |
| 921 | -4.853 | -4.054 | -4.142 | -2.218 | 3.540 | 2.752 | 18.185 | 23.944 | 23.155 | 17.427 | 18.226 | 18.138 | 25.188 | 15.618 | 24.451 | 20.109 | + | 2 | 2 |
| 922 | -1.834 | 8.239 | -0.601 | 5.956 | 8.939 | 8.298 | 22.599 | 25.582 | 24.941 | 14.789 | 24.862 | 16.022 | 17.701 | 15.585 | 17.713 | 15.534 | | 3 | 3 |
| 923 | -1.323 | -0.143 | 0.002 | 3.502 | 6.832 | 6.191 | 20.854 | 24.184 | 23.543 | 15.835 | 17.015 | 17.160 | 18.880 | 15.824 | 19.875 | 14.442 | + | 1 | 1 |
| 924 | -6.121 | -4.489 | -3.972 | 2.833 | 1.250 | -0.205 | 22.709 | 21.125 | 19.670 | 15.937 | 17.569 | 18.085 | 21.839 | 17.912 | 23.236 | 20.879 | + | 7 | 7 |
| 925 | 0.920 | 2.219 | 1.318 | 7.701 | 7.534 | 8.540 | 23.898 | 23.731 | 24.737 | 16.550 | 17.849 | 16.948 | 16.748 | 15.646 | 16.444 | 14.816 | + | 2 | 2 |

| | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 892 | 17 | 59.9 | 29.82 | 205.63 | 24.525 | 25.622 | **0.817** | **-3.523** | P67778;Q5SQG5 | P67778;Q5SQG5 | Prohibitin | **Phb** | 868 |
| 893 | 1 | 22.1 | 73.101 | 100.08 | 16.670 | 16.674 | **0.595** | **-3.622** | Q62167 | Q62167 | ATP-dependent RNA helicase DDX3X | **Ddx3x** | 1063 |
| 894 | 4 | 16 | 44.76 | 29.232 | 19.804 | 19.653 | **0.716** | **-3.653** | P61161 | P61161 | Actin-related protein 2 | **Actr2** | 792 |
| 895 | 2 | 27.1 | 9.9583 | 13.467 | 21.850 | 21.510 | **1.372** | **-3.711** | Q9CQS8;E9PW43 | Q9CQS8;E9PW43 | Protein transport protein Sec61 subunit beta | **Sec61b;Gm10320** | 1354 |
| 896 | 9 | 18.2 | 59.795 | 58.414 | 22.706 | 21.279 | **1.549** | **-3.715** | P24270;A2AL20 | P24270;A2AL20 | Catalase | **Cat** | 650 |
| 897 | 2 | 26.3 | 8.496 | 12.678 | 17.006 | 16.478 | **0.592** | **-3.842** | P62309 | P62309 | Small nuclear ribonucleoprotein G | **Snrpg** | 821 |
| 898 | 2 | 6.6 | 30.372 | 43.649 | 17.166 | 16.021 | **0.796** | **-3.913** | Q07079 | Q07079 | Insulin-like growth factor-binding protein 5 | **Igfbp5** | 937 |
| 899 | 4 | 24.8 | 28.211 | 48.367 | 23.082 | 21.707 | **2.691** | **-3.961** | P68510 | P68510 | 14-3-3 protein eta | **Ywhah** | 876 |
| 900 | 1 | 10.1 | 10.678 | 7.3103 | 17.492 | 16.124 | **1.504** | **-4.065** | Q8CF66 | Q8CF66 | Ragulator complex protein LAMTOR4;Ragulator complex protein LAMTOR4, N-terminally processed | **Lamtor4** | 1201 |
| 901 | 8 | 26.1 | 53.408 | 55.968 | 21.059 | 20.112 | **0.650** | **-4.092** | Q02819 | Q02819 | Nucleobindin-1 | **Nucb1** | 927 |
| 902 | 12 | 45.5 | 54.565 | 243.9 | 19.880 | 20.547 | **0.771** | **-4.288** | P11679 | P11679 | Keratin, type II cytoskeletal 8 | **Krt8** | 599 |
| 903 | 1 | 10.6 | 26.221 | 6.9259 | 16.066 | 16.191 | **0.822** | **-4.325** | Q792Z1 | Q792Z1 | Trypsin 10 | **Try10** | 1118 |
| 904 | 1 | 6.8 | 15.776 | 7.3386 | 16.707 | 16.459 | **0.889** | **-4.333** | P07309 | P07309 | Transthyretin | **Ttr** | 568 |
| 905 | 2 | 13.6 | 12.405 | 13.397 | 17.657 | 18.408 | **1.036** | **-4.355** | P83870 | P83870 | PHD finger-like domain-containing protein 5A | **Phf5a** | 892 |
| 906 | 4 | 28 | 21.356 | 28.579 | 16.612 | 18.269 | **0.965** | **-4.534** | A2A6T4;Q8R035;Q8R035-2 | A2A6T4;Q8R035;Q8R035-2 | Peptidyl-tRNA hydrolase ICT1, mitochondrial | **Ict1** | 127 |
| 907 | 4 | 21.9 | 35.166 | 26.579 | 22.956 | 22.345 | **1.993** | **-4.553** | Q3UZG4;P31230 | Q3UZG4;P31230 | Aminoacyl tRNA synthase complex-interacting multifunctional protein 1;Endothelial monocyte-activating polypeptide 2 | **Aimp1** | 681 |
| 908 | 8 | 21 | 46.839 | 51.675 | 20.317 | 20.758 | **0.893** | **-4.555** | Q9Z2I8;Q9Z2I8-2;A0A0N4SWD1 | Q9Z2I8;Q9Z2I8-2 | Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial | **Suclg2** | 1572 |
| 909 | 1 | 71.4 | 16.761 | 10.601 | 17.308 | 17.470 | **0.534** | **-4.578** | Q8BG13 | Q8BG13 | RNA-binding protein 3 | **Rbm3** | 1141 |
| 910 | 4 | 22.4 | 26.402 | 39.667 | 21.628 | 22.485 | **1.059** | **-4.582** | D3YX79;Q9Z2U1 | D3YX79;Q9Z2U1 | Proteasome subunit alpha type;Proteasome subunit alpha type-5 | **Gm8394;Psma5** | 284 |
| 911 | 3 | 32.9 | 16.277 | 21.476 | 16.254 | 16.177 | **1.078** | **-4.586** | A2AA85;Q6NXN1-2;Q6NXN1 | A2AA85;Q6NXN1-2;Q6NXN1 | SUZ domain-containing protein 1 | **Szrd1** | 136 |
| 912 | 10 | 8.7 | 169.74 | 78.961 | 21.058 | 20.196 | **0.556** | **-4.614** | Q9WTQ5-2;Q9WTQ5 | Q9WTQ5-2;Q9WTQ5 | A-kinase anchor protein 12 | **Akap12** | 1538 |
| 913 | 11 | 7 | 277.82 | 69.378 | 22.487 | 23.112 | **0.655** | **-4.709** | Q80X90 | Q80X90 | Filamin-B | **Flnb** | 1135 |
| 914 | 6 | 9.8 | 67.941 | 40.85 | 19.814 | 18.881 | **2.581** | **-4.831** | Q8BMF4 | Q8BMF4 | Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial | **Dlat** | 1173 |
| 915 | 1 | 13.6 | 12.965 | 6.7739 | 16.586 | 17.687 | **0.909** | **-4.912** | A0A0G2JEK4;A0A075B5K1;P01652 | A0A0G2JEK4;A0A075B5K1;P01652 | Ig kappa chain V-V region J606 | **Igkv11-125** | 1 |
| 916 | 8 | 31.1 | 32.191 | 59.254 | 20.767 | 21.083 | **4.101** | **-5.226** | P17751;H7BXC3 | P17751;H7BXC3 | Triosephosphate isomerase | **Tpi1** | 628 |
| 917 | 13 | 20.8 | 79.481 | 99.797 | 21.017 | 20.964 | **1.506** | **-5.319** | P51660 | P51660 | Peroxisomal multifunctional enzyme type 2;(3R)-hydroxyacyl-CoA dehydrogenase;Enoyl-CoA hydratase 2 | **Hsd17b4** | 744 |
| 918 | 6 | 15.5 | 45.626 | 51.265 | 18.518 | 19.385 | **1.475** | **-5.448** | P62196;Q8K1K2 | P62196 | 26S protease regulatory subunit 8 | **Psmc5** | 811 |
| 919 | 3 | 16.1 | 38.361 | 20.724 | 19.059 | 20.533 | **1.176** | **-5.603** | H3BKL5;Q921H8;H3BJZ9;Q8VCH0;H3BJC1;H3BKA1 | H3BKL5;Q921H8;H3BJZ9;Q8VCH0 | 3-ketoacyl-CoA thiolase A, peroxisomal;3-ketoacyl-CoA thiolase B, peroxisomal | **Acaa1a;Acaa1b** | 482 |
| 920 | 7 | 5.7 | 153.91 | 45.668 | 17.882 | 20.977 | **1.071** | **-5.702** | O88322 | O88322 | Nidogen-2 | **Nid2** | 541 |
| 921 | 2 | 19.2 | 20.583 | 24.253 | 20.403 | 22.280 | **1.456** | **-5.708** | P97315 | P97315 | Cysteine and glycine-rich protein 1 | **Csrp1** | 901 |
| 922 | 3 | 35.7 | 11.549 | 26.682 | 16.643 | 16.623 | **0.813** | **-5.796** | Q9DAM7 | Q9DAM7 | Transmembrane protein 263 | **Tmem263** | 1455 |
| 923 | 1 | 0.7 | 131.73 | 6.2807 | 17.352 | 17.158 | **2.255** | **-5.996** | Q3URV1-2;Q3URV1 | Q3URV1-2;Q3URV1 | Protein broad-minded | **Tbc1d32** | 989 |
| 924 | 7 | 12.5 | 74.342 | 44.36 | 19.875 | 22.058 | **2.314** | **-6.153** | A2AL50;Q8C0I1;A2AL49;H3BKN2;H3BIY5 | A2AL50;Q8C0I1;A2AL49;H3BKN2 | Alkyldihydroxyacetonephosphate synthase, peroxisomal | **Agps** | 156 |
| 925 | 1 | 12 | 12.991 | 12.581 | 16.197 | 15.630 | **3.698** | **-6.439** | P18529 | P18529 | Ig heavy chain V region 5-76 | | 631 |

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 926 | 1.248 | 0.740 | 1.199 | 8.692 | 9.312 | 6.097 | 24.242 | 24.861 | 21.647 | 23.209 | 22.702 | 23.161 | 16.926 | 14.174 | 22.857 | 21.067 | + | 5 | 5 |
| 927 | -5.182 | 1.954 | -0.843 | 6.365 | 5.850 | 5.948 | 22.567 | 22.052 | 22.149 | 16.916 | 24.052 | 21.255 | 17.056 | 15.347 | 24.681 | 19.515 | + | 7 | 7 |
| 928 | 0.176 | 0.959 | 1.550 | 8.383 | 9.459 | 9.618 | 25.723 | 26.798 | 26.957 | 16.702 | 17.485 | 18.077 | 18.156 | 16.524 | 17.550 | 15.503 | + | 1 | 1 |

|  | T | U | V | W | X | Y | Z | AA | AB | AC | AD | AE | AF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 926 | 5 | 19.9 | 35.181 | 42.802 | 15.550 | 21.962 | **2.656** | **-6.971** | D3YWT1;D3Z3N4 | D3YWT1;D3Z3N4 | Heterogeneous nuclear ribonucleoprotein H3 | **Hnrnph3** | 283 |
| 927 | 7 | 9.9 | 91.545 | 42.082 | 16.202 | 22.098 | **1.627** | **-7.411** | P25206 | P25206 | DNA replication licensing factor MCM3 | **Mcm3** | 655 |
| 928 | 1 | 0.7 | 127.71 | 6.2752 | 17.340 | 16.526 | **3.923** | **-8.258** | Q8R4D5 | Q8R4D5 | Transient receptor potential cation channel subfamily M member 8 | **Trpm8** | 1241 |

**Table S10. GO-Term analysis of interaction candidates.**

Shown are GO-terms of candidate proteins for interaction with TBX2 determined by MouseMine sorted by Gene ID.

| ID | Gene Name | Species | GOTERM_BP_DIRECT |
|---|---|---|---|
| 1810022K09Rik | RIKEN cDNA 1810022K09 gene(1810022K09Rik) | Mus musculus | GO:0002230~positive regulation of defense response to virus by host,GO:0098779~mitophagy in response to mitochondrial depolarization,GO:0098792~xenophagy, |
| Abce1 | ATP-binding cassette, sub-family E (OABP), member 1(Abce1) | Mus musculus | GO:0000054~ribosomal subunit export from nucleus,GO:0006413~translational initiation,GO:0006415~translational termination,GO:0060702~negative regulation of endoribonuclease activity, |
| Acly | ATP citrate lyase(Acly) | Mus musculus | GO:0006084~acetyl-CoA metabolic process,GO:0006085~acetyl-CoA biosynthetic process,GO:0006101~citrate metabolic process,GO:0006107~oxaloacetate metabolic process,GO:0006629~lipid metabolic process,GO:0006633~fatty acid biosynthetic process,GO:0008152~metabolic process,GO:0008610~lipid biosynthetic process, |
| Actn4 | actinin alpha 4(Actn4) | Mus musculus | GO:0001666~response to hypoxia,GO:0006810~transport,GO:0015031~protein transport,GO:0030050~vesicle transport along actin filament,GO:0030335~positive regulation of cell migration,GO:0035357~peroxisome proliferator activated receptor signaling pathway,GO:0042981~regulation of apoptotic process,GO:0048384~retinoic acid receptor signaling pathway,GO:0048549~positive regulation of pinocytosis,GO:0051017~actin filament bundle assembly,GO:0051271~negative regulation of cellular component movement,GO:0051272~positive regulation of cellular component movement,GO:0070830~bicellular tight junction assembly,GO:1900025~negative regulation of substrate adhesion-dependent cell spreading,GO:1901224~positive regulation of NIK/NF-kappaB signaling,GO:1902396~protein localization to bicellular tight junction,GO:1903506~regulation of nucleic acid-templated transcription, |
| Actr1a | ARP1 actin-related protein 1A, centractin alpha(Actr1a) | Mus musculus | |

| | E | F | G |
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| 4 | | | |
| 5 | **GOTERM_CC_DIRECT** | **GOTERM_MF_DIRECT** | **INTERPRO** |
| 6 | | | |
| 7 | GO:0005737~cytoplasm,GO:0005739~mitochondrion,GO:0005852~eukaryotic translation initiation factor 3 complex,GO:0016020~membrane, | GO:0000166~nucleotide binding,GO:0005506~iron ion binding,GO:0005524~ATP binding,GO:0016887~ATPase activity,GO:0043024~ribosomal small subunit binding,GO:0060698~endoribonuclease inhibitor activity, | IPR003439:ABC transporter-like,IPR003593:AAA+ ATPase domain,IPR007209:RNase L inhibitor RLI, possible metal-binding domain,IPR013283:ABC transporter, ABCE,IPR017871:ABC transporter, conserved site,IPR017896:4Fe-4S ferredoxin-type, iron-sulpur binding domain,IPR017900:4Fe-4S ferredoxin, iron-sulphur binding, conserved site,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |
| 8 | GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0005739~mitochondrion,GO:0005829~cytosol,GO:0005886~plasma membrane,GO:0009346~citrate lyase complex,GO:0016020~membrane,GO:0070062~extracellular exosome, | GO:0000166~nucleotide binding,GO:0003824~catalytic activity,GO:0003878~ATP citrate synthase activity,GO:0005524~ATP binding,GO:0016740~transferase activity,GO:0046872~metal ion binding,GO:0046912~transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer,GO:0048037~cofactor binding, | IPR002020:Citrate synthase-like,IPR003781:CoA-binding,IPR005810:Succinyl-CoA ligase, alpha subunit,IPR005811:ATP-citrate lyase/succinyl-CoA ligase,IPR013816:ATP-grasp fold, subdomain 2,IPR014608:ATP-citrate synthase,IPR016040:NAD(P)-binding domain,IPR016102:Succinyl-CoA synthetase-like,IPR016142:Citrate synthase-like, large alpha subdomain,IPR016143:Citrate synthase-like, small alpha subdomain,IPR017440:ATP-citrate lyase/succinyl-CoA ligase, active site,IPR017866:Succinyl-CoA synthetase, beta subunit, conserved site, |
| 9 | GO:0001725~stress fiber,GO:0005615~extracellular space,GO:0005622~intracellular,GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005903~brush border,GO:0005911~cell-cell junction,GO:0005925~focal adhesion,GO:0015629~actin cytoskeleton,GO:0030018~Z disc,GO:0030054~cell junction,GO:0030529~intracellular ribonucleoprotein complex,GO:0030863~cortical cytoskeleton,GO:0031143~pseudopodium,GO:0043005~neuron projection,GO:0043234~protein complex,GO:0048471~perinuclear region of cytoplasm,GO:0070062~extracellular exosome, | GO:0000977~RNA polymerase II regulatory region sequence-specific DNA binding,GO:0001882~nucleoside binding,GO:0003779~actin binding,GO:0005509~calcium ion binding,GO:0005515~protein binding,GO:0030374~ligand-dependent nuclear receptor transcription coactivator activity,GO:0031490~chromatin DNA binding,GO:0032403~protein complex binding,GO:0035257~nuclear hormone receptor binding,GO:0042803~protein homodimerization activity,GO:0042974~retinoic acid receptor binding,GO:0044325~ion channel binding,GO:0044822~poly(A) RNA binding,GO:0046872~metal ion binding,GO:0047485~protein N-terminus binding,GO:0051015~actin filament binding, | IPR001589:Actinin-type, actin-binding, conserved site,IPR001715:Calponin homology domain,IPR002017:Spectrin repeat,IPR002048:EF-hand domain,IPR011992:EF-hand-like domain,IPR014837:EF-hand, Ca insensitive,IPR018159:Spectrin/alpha-actinin,IPR018247:EF-Hand 1, calcium-binding site, |
| 10 | GO:0002177~manchette,GO:0005737~cytoplasm,GO:0005813~centrosome,GO:0005814~centriole,GO:0005856~cytoskeleton,GO:0005869~dynactin complex,GO:0015630~microtubule cytoskeleton,GO:0030137~COPI-coated vesicle,GO:0043209~myelin sheath,GO:0070062~extracellular exosome,GO:1990752~microtubule end, | GO:0000166~nucleotide binding,GO:0005524~ATP binding, | IPR004000:Actin-related protein,IPR004001:Actin, conserved site,IPR020902:Actin/actin-like conserved site, |

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| 5 | **KEGG Pathway** | **PIR Superfamily** | **UP_KEYWORDS** | **UP_SEQ_FEATURE** |
| 6 |  |  | Acetylation,Complete proteome,Phosphoprotein,Proteomics identification,Reference proteome, | chain:Uncharacterized protein C8orf59 homolog,modified residue, |
| 7 |  |  | ATP-binding,Chaperone,Complete proteome,Cytoplasm,Mitochondrion,Nucleotide-binding,Phosphoprotein,Reference proteome,Repeat, | chain:ATP-binding cassette sub-family E member 1,domain:4Fe-4S ferredoxin-type 1,domain:4Fe-4S ferredoxin-type 2,domain:ABC transporter 1,domain:ABC transporter 2,modified residue,nucleotide phosphate-binding region:ATP 1,nucleotide phosphate-binding region:ATP 2,sequence conflict, |
| 8 | mmu00020:Citrate cycle (TCA cycle),mmu01100:Metabolic pathways,mmu01130:Biosynthesis of antibiotics, | PIRSF036511:ATP citrate synthase, fused large and small subunits, | Acetylation,ATP-binding,Complete proteome,Cytoplasm,Lipid biosynthesis,Lipid metabolism,Magnesium,Metal-binding,Nucleotide-binding,Phosphoprotein,Proteomics identification,Reference proteome,Transferase,Ubl conjugation, | active site:Tele-phosphohistidine intermediate,chain:ATP-citrate synthase,metal ion-binding site:Magnesium,modified residue,nucleotide phosphate-binding region:ATP,region of interest:CoA-binding, |
| 9 | mmu04510:Focal adhesion,mmu04520:Adherens junction,mmu04530:Tight junction,mmu04670:Leukocyte transendothelial migration,mmu04810:Regulation of actin cytoskeleton,mmu05146:Amoebiasis,mmu05203:Viral carcinogenesis,mmu05322:Systemic lupus erythematosus, |  | Acetylation,Actin-binding,Calcium,Cell junction,Coiled coil,Complete proteome,Cytoplasm,Direct protein sequencing,Metal-binding,Nucleus,Phosphoprotein,Protein transport,Proteomics identification,Reference proteome,Repeat,Transport, | calcium-binding region:1,calcium-binding region:2,chain:Alpha-actinin-4,domain:Actin-binding,domain:CH 1,domain:CH 2,domain:EF-hand 1,domain:EF-hand 2,modified residue,region of interest:Polyphosphoinositide (PIP2)-binding,repeat:Spectrin 1,repeat:Spectrin 2,repeat:Spectrin 3,repeat:Spectrin 4, |
| 10 |  |  | Acetylation,ATP-binding,Complete proteome,Cytoplasm,Cytoskeleton,Nucleotide-binding,Reference proteome, | chain:Alpha-centractin,modified residue, |

| | A | B | C | D |
|---|---|---|---|---|
| 11 | Adnp | activity-dependent neuroprotective protein(Adnp) | Mus musculus | GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0007614~short-term memory,GO:0009743~response to carbohydrate,GO:0010035~response to inorganic substance,GO:0010629~negative regulation of gene expression,GO:0010835~regulation of protein ADP-ribosylation,GO:0010976~positive regulation of neuron projection development,GO:0030828~positive regulation of cGMP biosynthetic process,GO:0031668~cellular response to extracellular stimulus,GO:0032091~negative regulation of protein binding,GO:0032147~activation of protein kinase activity,GO:0033484~nitric oxide homeostasis,GO:0043524~negative regulation of neuron apoptotic process,GO:0044849~estrous cycle,GO:0045773~positive regulation of axon extension,GO:0050731~positive regulation of peptidyl-tyrosine phosphorylation,GO:0050805~negative regulation of synaptic transmission,GO:0051965~positive regulation of synapse assembly, |
| 12 | Adprh | ADP-ribosylarginine hydrolase(Adprh) | Mus musculus | GO:0006464~cellular protein modification process,GO:0051725~protein de-ADP-ribosylation, |
| 13 | Afdn | afadin, adherens junction formation factor(Afdn) | Mus musculus | GO:0007155~cell adhesion,GO:0007165~signal transduction,GO:0021537~telencephalon development,GO:0021987~cerebral cortex development,GO:0034334~adherens junction maintenance,GO:0043547~positive regulation of GTPase activity,GO:0048854~brain morphogenesis,GO:0048872~homeostasis of number of cells,GO:0060019~radial glial cell differentiation,GO:0060563~neuroepithelial cell differentiation,GO:0070445~regulation of oligodendrocyte progenitor proliferation,GO:0090557~establishment of endothelial intestinal barrier,GO:1902414~protein localization to cell junction, |
| 14 | Ahcy | S-adenosylhomocysteine hydrolase(Ahcy) | Mus musculus | GO:0002439~chronic inflammatory response to antigenic stimulus,GO:0006730~one-carbon metabolic process,GO:0007584~response to nutrient,GO:0019510~S-adenosylhomocysteine catabolic process,GO:0033353~S-adenosylmethionine cycle,GO:0042745~circadian sleep/wake cycle,GO:0071268~homocysteine biosynthetic process, |
| 15 | Aldh18a1 | aldehyde dehydrogenase 18 family, member A1(Aldh18a1) | Mus musculus | GO:0006536~glutamate metabolic process,GO:0006561~proline biosynthetic process,GO:0006592~ornithine biosynthetic process,GO:0008152~metabolic process,GO:0008652~cellular amino acid biosynthetic process,GO:0016310~phosphorylation,GO:0019240~citrulline biosynthetic process,GO:0055114~oxidation-reduction process,GO:0055129~L-proline biosynthetic process, |
| 16 | Anp32e | acidic (leucine-rich) nuclear phosphoprotein 32 family, member E(Anp32e) | Mus musculus | GO:0006334~nucleosome assembly,GO:0006913~nucleocytoplasmic transport,GO:0016569~covalent chromatin modification,GO:0042981~regulation of apoptotic process,GO:0043486~histone exchange, |

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| 11 | GO:0005615~extracellular space,GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0030424~axon,GO:0030425~dendrite,GO:0043025~neuronal cell body, | GO:0003677~DNA binding,GO:0003682~chromatin binding,GO:0005507~copper ion binding,GO:0005515~protein binding,GO:0042277~peptide binding,GO:0046872~metal ion binding,GO:0048487~beta-tubulin binding, | IPR001356:Homeodomain,IPR007087:Zinc finger, C2H2,IPR009057:Homeodomain-like,IPR015880:Zinc finger, C2H2-like, |
| 12 | GO:0005622~intracellular, | GO:0000287~magnesium ion binding,GO:0003875~ADP-ribosylarginine hydrolase activity,GO:0016787~hydrolase activity, | IPR005502:ADP-ribosylation/Crystallin J1,IPR012108:ADP-ribosylarginine hydrolase, |
| 13 | GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0005886~plasma membrane,GO:0005911~cell-cell junction,GO:0005912~adherens junction,GO:0005913~cell-cell adherens junction,GO:0030054~cell junction,GO:0043296~apical junction complex,GO:0045177~apical part of cell, | GO:0005515~protein binding,GO:0017016~Ras GTPase binding,GO:0030274~LIM domain binding,GO:0050839~cell adhesion molecule binding,GO:0098641~cadherin binding involved in cell-cell adhesion, | IPR000159:Ras-association,IPR000253:Forkhead-associated (FHA) domain,IPR001478:PDZ domain,IPR002710:Dilute,IPR008984:SMAD/FHA domain, |
| 14 | GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005829~cytosol,GO:0042470~melanosome,GO:0043005~neuron projection,GO:0070062~extracellular exosome, | GO:0004013~adenosylhomocysteinase activity,GO:0005507~copper ion binding,GO:0030554~adenyl nucleotide binding,GO:0042802~identical protein binding,GO:0043621~protein self-association,GO:0051287~NAD binding, | IPR000043:Adenosylhomocysteinase,IPR015878:S-adenosyl-L-homocysteine hydrolase, NAD binding domain,IPR016040:NAD(P)-binding domain,IPR020082:S-adenosyl-L-homocysteine hydrolase, conserved site, |
| 15 | GO:0005737~cytoplasm,GO:0005739~mitochondrion,GO:0005743~mitochondrial inner membrane,GO:0016020~membrane, | GO:0000166~nucleotide binding,GO:0003824~catalytic activity,GO:0004349~glutamate 5-kinase activity,GO:0004350~glutamate-5-semialdehyde dehydrogenase activity,GO:0005524~ATP binding,GO:0016301~kinase activity,GO:0016491~oxidoreductase activity,GO:0016620~oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor,GO:0016740~transferase activity,GO:0017084~delta1-pyrroline-5-carboxylate synthetase activity,GO:0042802~identical protein binding,GO:0044822~poly(A) RNA binding, | IPR000965:Gamma-glutamyl phosphate reductase GPR,IPR001048:Aspartate/glutamate/uridylate kinase,IPR001057:Glutamate/acetylglutamate kinase,IPR005715:Glutamate 5-kinase/delta-1-pyrroline-5-carboxylate synthase,IPR005766:Delta l-pyrroline-5-carboxylate synthetase,IPR015590:Aldehyde dehydrogenase domain,IPR016161:Aldehyde/histidinol dehydrogenase,IPR016162:Aldehyde dehydrogenase, N-terminal,IPR016163:Aldehyde dehydrogenase, C-terminal,IPR019797:Glutamate 5-kinase, conserved site,IPR020593:Gamma-glutamyl phosphate reductase GPR, conserved site, |
| 16 | GO:0000812~Swr1 complex,GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0016023~cytoplasmic, membrane-bounded vesicle,GO:0031410~cytoplasmic vesicle, | GO:0019212~phosphatase inhibitor activity,GO:0042393~histone binding, | IPR001611:Leucine-rich repeat, |

| | H | I | J | K |
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| 11 | | | Acetylation,Coiled coil,Complete proteome,DNA-binding,Homeobox,Isopeptide bond,Metal-binding,Methylation,Nucleus,Phosphoprotein,Reference proteome,Repeat,Transcription,Transcription regulation,Ubl conjugation,Zinc,Zinc-finger, | chain:Activity-dependent neuroprotector homeobox protein,compositionally biased region:Glu-rich,DNA-binding region:Homeobox,modified residue,region of interest:Neuroprotective peptide,zinc finger region:C2H2-type 1; atypical,zinc finger region:C2H2-type 2,zinc finger region:C2H2-type 3,zinc finger region:C2H2-type 4; atypical,zinc finger region:C2H2-type 5; atypical, |
| 12 | | PIRSF016939:ADP-ribosylarginine hydrolase, | Complete proteome,Hydrolase,Magnesium,Reference proteome, | chain:[Protein ADP-ribosylarginine] hydrolase, |
| 13 | mmu04014:Ras signaling pathway,mmu04015:Rap1 signaling pathway,mmu04024:cAMP signaling pathway,mmu04520:Adherens junction,mmu04530:Tight junction,mmu04670:Leukocyte transendothelial migration, | | 3D-structure,Acetylation,Alternative splicing,Cell adhesion,Cell junction,Coiled coil,Complete proteome,Phosphoprotein,Proteomics identification,Reference proteome,Repeat, | chain:Afadin,compositionally biased region:Glu/Lys-rich,compositionally biased region:Poly-Glu,compositionally biased region:Pro-rich,domain:Dilute,domain:FHA,domain:PDZ,domain:Ras-associating 1,domain:Ras-associating 2,helix,modified residue,sequence conflict,splice variant,strand,turn, |
| 14 | mmu00270:Cysteine and methionine metabolism,mmu01100:Metabolic pathways, | PIRSF001109:adenosylhomocysteine hydrolase, SAHH type, | 3D-structure,Acetylation,Complete proteome,Cytoplasm,Hydrolase,NAD,One-carbon metabolism,Phosphoprotein,Proteomics identification,Reference proteome, | binding site:Substrate,chain:Adenosylhomocysteinase,modified residue,region of interest:NAD binding,sequence conflict, |
| 15 | mmu00330:Arginine and proline metabolism,mmu01100:Metabolic pathways,mmu01230:Biosynthesis of amino acids, | PIRSF036429:Delta-1-pyrroline-5-carboxylate synthetase, | Alternative splicing,Amino-acid biosynthesis,ATP-binding,Complete proteome,Kinase,Membrane,Mitochondrion,Mitochondrion inner membrane,Multifunctional enzyme,NADP,Nucleotide-binding,Oxidoreductase,Proline biosynthesis,Proteomics identification,Reference proteome,Transferase, | chain:Delta-1-pyrroline-5-carboxylate synthetase,region of interest:Gamma-glutamyl phosphate reductase,region of interest:Glutamate 5-kinase,splice variant, |
| 16 | | | Acetylation,Alternative splicing,Chaperone,Chromatin regulator,Complete proteome,Cytoplasm,Leucine-rich repeat,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat, | chain:Acidic leucine-rich nuclear phosphoprotein 32 family member E,compositionally biased region:Asp/Glu-rich (highly acidic),modified residue,repeat:LRR 1,repeat:LRR 2,repeat:LRR 3,repeat:LRR 4,sequence conflict,splice variant, |

| | A | B | C | D |
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| 17 | Anxa2 | annexin A2(Anxa2) | Mus musculus | GO:0001525~angiogenesis,GO:0001765~membrane raft assembly,GO:0001934~positive regulation of protein phosphorylation,GO:0002091~negative regulation of receptor internalization,GO:0006900~membrane budding,GO:0006936~muscle contraction,GO:0007589~body fluid secretion,GO:0030199~collagen fibril organization,GO:0031340~positive regulation of vesicle fusion,GO:0032804~negative regulation of low-density lipoprotein particle receptor catabolic process,GO:0036035~osteoclast development,GO:0042730~fibrinolysis,GO:0048146~positive regulation of fibroblast proliferation,GO:0051099~positive regulation of binding,GO:0051290~protein heterotetramerization,GO:0071229~cellular response to acid chemical,GO:0072661~protein targeting to plasma membrane,GO:0097066~response to thyroid hormone,GO:1900121~negative regulation of receptor binding,GO:2000273~positive regulation of receptor activity, |
| 18 | Arf1 | ADP-ribosylation factor 1(Arf1) | Mus musculus | GO:0002090~regulation of receptor internalization,GO:0006810~transport,GO:0006878~cellular copper ion homeostasis,GO:0007015~actin filament organization,GO:0007264~small GTPase mediated signal transduction,GO:0015031~protein transport,GO:0016192~vesicle-mediated transport,GO:0034315~regulation of Arp2/3 complex-mediated actin nucleation,GO:0034379~very-low-density lipoprotein particle assembly,GO:0043085~positive regulation of catalytic activity,GO:0045807~positive regulation of endocytosis,GO:0045956~positive regulation of calcium ion-dependent exocytosis,GO:0050714~positive regulation of protein secretion,GO:0055108~Golgi to transport vesicle transport,GO:0060292~long term synaptic depression,GO:0060999~positive regulation of dendritic spine development,GO:0070142~synaptic vesicle budding,GO:0097061~dendritic spine organization,GO:0097212~lysosomal membrane organization,GO:1902307~positive regulation of sodium ion transmembrane transport,GO:1902824~positive regulation of late endosome to lysosome transport,GO:1902953~positive regulation of ER to Golgi vesicle-mediated transport,GO:1903725~regulation of phospholipid metabolic process, |
| 19 | Arf4 | ADP-ribosylation factor 4(Arf4) | Mus musculus | GO:0006471~protein ADP-ribosylation,GO:0006810~transport,GO:0006890~retrograde vesicle-mediated transport, Golgi to ER,GO:0007173~epidermal growth factor receptor signaling pathway,GO:0007264~small GTPase mediated signal transduction,GO:0007420~brain development,GO:0007612~learning,GO:0015031~protein transport,GO:0016192~vesicle-mediated transport,GO:0016477~cell migration,GO:0031584~activation of phospholipase D activity,GO:0043066~negative regulation of apoptotic process,GO:0045176~apical protein localization,GO:0045197~establishment or maintenance of epithelial cell apical/basal polarity,GO:0045944~positive regulation of transcription from RNA polymerase II promoter,GO:0048678~response to axon injury,GO:0060996~dendritic spine development,GO:0061512~protein localization to cilium,GO:2000377~regulation of reactive oxygen species metabolic process, |

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| 17 | GO:0001725~stress fiber,GO:0001726~ruffle,GO:0005576~extracellular region,GO:0005578~proteinaceous extracellular matrix,GO:0005604~basement membrane,GO:0005615~extracellular space,GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005765~lysosomal membrane,GO:0005768~endosome,GO:0005769~early endosome,GO:0005811~lipid particle,GO:0005829~cytosol,GO:0005886~plasma membrane,GO:0005911~cell-cell junction,GO:0005913~cell-cell adherens junction,GO:0005938~cell cortex,GO:0009986~cell surface,GO:0016020~membrane,GO:0016323~basolateral plasma membrane,GO:0019897~extrinsic component of plasma membrane,GO:0030054~cell junction,GO:0030496~midbody,GO:0031902~late endosome membrane,GO:0031982~vesicle,GO:0035749~myelin sheath adaxonal region,GO:0042383~sarcolemma,GO:0042470~melanosome,GO:0043220~Schmidt-Lanterman incisure,GO:0043234~protein complex,GO:0044354~macropinosome,GO:0045121~membrane raft,GO:0048471~perinuclear region of cytoplasm,GO:0070062~extracellular exosome,GO:1990667~PCSK9-AnxA2 complex, | GO:0002020~protease binding,GO:0004859~phospholipase inhibitor activity,GO:0005509~calcium ion binding,GO:0005515~protein binding,GO:0005544~calcium-dependent phospholipid binding,GO:0005546~phosphatidylinositol-4,5-bisphosphate binding,GO:0008092~cytoskeletal protein binding,GO:0017137~Rab GTPase binding,GO:0019834~phospholipase A2 inhibitor activity,GO:0030546~receptor activator activity,GO:0044548~S100 protein binding,GO:0044822~poly(A) RNA binding,GO:0048306~calcium-dependent protein binding,GO:0098641~cadherin binding involved in cell-cell adhesion, | IPR001464:Annexin,IPR002389:Annexin, type II,IPR018252:Annexin repeat, conserved site,IPR018502:Annexin repeat, |
| 18 | GO:0000139~Golgi membrane,GO:0005622~intracellular,GO:0005737~cytoplasm,GO:0005770~late endosome,GO:0005778~peroxisomal membrane,GO:0005794~Golgi apparatus,GO:0005802~trans-Golgi network,GO:0005829~cytosol,GO:0005886~plasma membrane,GO:0005925~focal adhesion,GO:0012505~endomembrane system,GO:0014069~postsynaptic density,GO:0016020~membrane,GO:0030017~sarcomere,GO:0030054~cell junction,GO:0030137~COPI-coated vesicle,GO:0031252~cell leading edge,GO:0043005~neuron projection,GO:0045202~synapse,GO:0045211~postsynaptic membrane,GO:0048471~perinuclear region of cytoplasm,GO:0070062~extracellular exosome, | GO:0000166~nucleotide binding,GO:0000287~magnesium ion binding,GO:0005515~protein binding,GO:0005525~GTP binding,GO:0019003~GDP binding,GO:0042803~protein homodimerization activity,GO:0044822~poly(A) RNA binding,GO:1990583~phospholipase D activator activity, | IPR005225:Small GTP-binding protein domain,IPR006689:Small GTPase superfamily, ARF/SAR type,IPR024156:Small GTPase superfamily, ARF type,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |
| 19 | GO:0005622~intracellular,GO:0005737~cytoplasm,GO:0005794~Golgi apparatus,GO:0005829~cytosol,GO:0005886~plasma membrane,GO:0016020~membrane,GO:0016021~integral component of membrane,GO:0031012~extracellular matrix,GO:0032587~ruffle membrane,GO:0043197~dendritic spine,GO:0070062~extracellular exosome, | GO:0000166~nucleotide binding,GO:0005154~epidermal growth factor receptor binding,GO:0005515~protein binding,GO:0005525~GTP binding, | IPR005225:Small GTP-binding protein domain,IPR006689:Small GTPase superfamily, ARF/SAR type,IPR024156:Small GTPase superfamily, ARF type,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |

| | H | I | J | K |
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| 17 | | | 3D-structure,Acetylation,Annexin,Basement membrane,Calcium,Calcium/phospholipid-binding,Complete proteome,Extracellular matrix,Isopeptide bond,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,Secreted,Ubl conjugation, | chain:Annexin A2,modified residue,region of interest:S100A10-binding site,repeat:Annexin 1,repeat:Annexin 2,repeat:Annexin 3,repeat:Annexin 4, |
| 18 | mmu04144:Endocytosis,mmu05134:Legionellosis, | | 3D-structure,Acetylation,Cell junction,Cell membrane,Complete proteome,Cytoplasm,Direct protein sequencing,ER-Golgi transport,Golgi apparatus,GTP-binding,Lipoprotein,Membrane,Myristate,Nucleotide-binding,Postsynaptic cell membrane,Protein transport,Reference proteome,Synapse,Synaptosome,Transport, | chain:ADP-ribosylation factor 1,helix,lipid moiety-binding region:N-myristoyl glycine,modified residue,nucleotide phosphate-binding region:GTP,sequence conflict,strand,turn, |
| 19 | | | Complete proteome,ER-Golgi transport,Golgi apparatus,GTP-binding,Lipoprotein,Membrane,Myristate,Nucleotide-binding,Phosphoprotein,Protein transport,Proteomics identification,Reference proteome,Transmembrane,Transmembrane helix,Transport, | chain:ADP-ribosylation factor 4,lipid moiety-binding region:N-myristoyl glycine,nucleotide phosphate-binding region:GTP,sequence conflict, |

| | A | B | C | D |
|---|---|---|---|---|
| 20 | Arpc2 | actin related protein 2/3 complex, subunit 2(Arpc2) | Mus musculus | GO:0010592~positive regulation of lamellipodium assembly,GO:0014911~positive regulation of smooth muscle cell migration,GO:0030833~regulation of actin filament polymerization,GO:0030838~positive regulation of actin filament polymerization,GO:0034314~Arp2/3 complex-mediated actin nucleation,GO:0036120~cellular response to platelet-derived growth factor stimulus,GO:0090314~positive regulation of protein targeting to membrane,GO:1900026~positive regulation of substrate adhesion-dependent cell spreading,GO:1904628~cellular response to phorbol 13-acetate 12-myristate,GO:2000251~positive regulation of actin cytoskeleton reorganization, |
| 21 | Arpc4 | actin related protein 2/3 complex, subunit 4(Arpc4) | Mus musculus | GO:0030041~actin filament polymerization,GO:0034314~Arp2/3 complex-mediated actin nucleation, |
| 22 | Atp6v1b2 | ATPase, H+ transporting, lysosomal V1 subunit B2(Atp6v1b2) | Mus musculus | GO:0006810~transport,GO:0006811~ion transport,GO:0015991~ATP hydrolysis coupled proton transport,GO:0015992~proton transport,GO:0046034~ATP metabolic process, |
| 23 | Cacybp | calcyclin binding protein(Cacybp) | Mus musculus | GO:0007568~aging,GO:0045740~positive regulation of DNA replication,GO:0055007~cardiac muscle cell differentiation,GO:0060416~response to growth hormone,GO:0060548~negative regulation of cell death,GO:0071277~cellular response to calcium ion, |

|  | E | F | G |
|---|---|---|---|
| 20 | GO:0005737~cytoplasm,GO:0005768~endosome,GO:0005794~Golgi apparatus,GO:0005856~cytoskeleton,GO:0005885~Arp2/3 protein complex,GO:0005886~plasma membrane,GO:0005925~focal adhesion,GO:0015629~actin cytoskeleton,GO:0030054~cell junction,GO:0030426~growth cone,GO:0031252~cell leading edge,GO:0036195~muscle cell projection membrane,GO:0042995~cell projection,GO:0043005~neuron projection,GO:0043197~dendritic spine,GO:0043198~dendritic shaft,GO:0043204~perikaryon,GO:0043679~axon terminus,GO:0045202~synapse,GO:0070062~extracellular exosome,GO:0097440~apical dendrite, | GO:0003779~actin binding,GO:0005200~structural constituent of cytoskeleton,GO:0005515~protein binding,GO:0032403~protein complex binding,GO:0035254~glutamate receptor binding,GO:0051015~actin filament binding,GO:0051117~ATPase binding, | IPR007188:ARP2/3 complex, 34kDa subunit (p34-Arc), |
| 21 | GO:0005737~cytoplasm,GO:0005856~cytoskeleton,GO:0005885~Arp2/3 protein complex,GO:0015629~actin cytoskeleton,GO:0042995~cell projection,GO:0070062~extracellular exosome, | GO:0003779~actin binding,GO:0005200~structural constituent of cytoskeleton,GO:0019899~enzyme binding,GO:0030674~protein binding, bridging,GO:0051015~actin filament binding, | IPR008384:ARP2/3 complex, 20kDa subunit (P20-Arc), |
| 22 | GO:0001726~ruffle,GO:0005737~cytoplasm,GO:0005765~lysosomal membrane,GO:0005829~cytosol,GO:0005886~plasma membrane,GO:0005902~microvillus,GO:0012505~endomembrane system,GO:0016020~membrane,GO:0016021~integral component of membrane,GO:0033180~proton-transporting V-type ATPase, V1 domain,GO:0042470~melanosome,GO:0043209~myelin sheath,GO:0043231~intracellular membrane-bounded organelle,GO:0070062~extracellular exosome, | GO:0005524~ATP binding,GO:0016787~hydrolase activity,GO:0016820~hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, | IPR000194:ATPase, F1/V1/A1 complex, alpha/beta subunit, nucleotide-binding domain,IPR004100:ATPase, alpha/beta subunit, N-terminal,IPR005723:ATPase, V1 complex, subunit B,IPR020003:ATPase, alpha/beta subunit, nucleotide-binding domain, active site,IPR022879:V-type ATP synthase regulatory subunit B/beta,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |
| 23 | GO:0005634~nucleus,GO:0005641~nuclear envelope lumen,GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0030877~beta-catenin destruction complex,GO:0043005~neuron projection,GO:0044297~cell body,GO:0070062~extracellular exosome, | GO:0005515~protein binding,GO:0042803~protein homodimerization activity, | IPR007052:CS-like domain,IPR007699:SGS,IPR008978:HSP20-like chaperone,IPR015120:Siah interacting protein, N-terminal, |

|  | H | I | J | K |
|---|---|---|---|---|
| 20 | mmu04144:Endocytosis,mmu04666:Fc gamma R-mediated phagocytosis,mmu04810:Regulation of actin cytoskeleton,mmu05100:Bacterial invasion of epithelial cells,mmu05132:Salmonella infection, |  | Acetylation,Actin-binding,Cell junction,Cell projection,Complete proteome,Cytoplasm,Cytoskeleton,Direct protein sequencing,Proteomics identification,Reference proteome,Synapse,Synaptosome, | chain:Actin-related protein 2/3 complex subunit 2,modified residue, |
| 21 | mmu04144:Endocytosis,mmu04666:Fc gamma R-mediated phagocytosis,mmu04810:Regulation of actin cytoskeleton,mmu05100:Bacterial invasion of epithelial cells,mmu05132:Salmonella infection, |  | Acetylation,Actin-binding,Cell projection,Complete proteome,Cytoplasm,Cytoskeleton,Direct protein sequencing,Proteomics identification,Reference proteome, | chain:Actin-related protein 2/3 complex subunit 4,modified residue, |
| 22 | mmu00190:Oxidative phosphorylation,mmu01100:Metabolic pathways,mmu04145:Phagosome,mmu04721:Synaptic vesicle cycle,mmu04966:Collecting duct acid secretion,mmu05323:Rheumatoid arthritis, |  | Complete proteome,Direct protein sequencing,Hydrogen ion transport,Hydrolase,Ion transport,Membrane,Reference proteome,Transport, | chain:V-type proton ATPase subunit B, brain isoform,modified residue,sequence conflict, |
| 23 | mmu04310:Wnt signaling pathway, |  | 3D-structure,Acetylation,Coiled coil,Complete proteome,Cytoplasm,Direct protein sequencing,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Ubl conjugation pathway, | chain:Calcyclin-binding protein,domain:CS,domain:SGS,helix,modified residue,region of interest:Interaction with S100A6,region of interest:Interaction with SIAH1,region of interest:Interaction with SKP1,turn, |

| | A | B | C | D |
|---|---|---|---|---|
| 24 | Cad | carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase(Cad) | Mus musculus | GO:0000050~urea cycle,GO:0001889~liver development,GO:0006207~'de novo' pyrimidine nucleobase biosynthetic process,GO:0006221~pyrimidine nucleotide biosynthetic process,GO:0006228~UTP biosynthetic process,GO:0006520~cellular amino acid metabolic process,GO:0006526~arginine biosynthetic process,GO:0006541~glutamine metabolic process,GO:0006807~nitrogen compound metabolic process,GO:0007507~heart development,GO:0007565~female pregnancy,GO:0007595~lactation,GO:0008152~metabolic process,GO:0014075~response to amine,GO:0017144~drug metabolic process,GO:0018107~peptidyl-threonine phosphorylation,GO:0019240~citrulline biosynthetic process,GO:0031000~response to caffeine,GO:0031100~organ regeneration,GO:0032868~response to insulin,GO:0033574~response to testosterone,GO:0035690~cellular response to drug,GO:0042594~response to starvation,GO:0044205~'de novo' UMP biosynthetic process,GO:0046777~protein autophosphorylation,GO:0051414~response to cortisol,GO:0071364~cellular response to epidermal growth factor stimulus, |
| 25 | Cand1 | cullin associated and neddylation disassociated 1(Cand1) | Mus musculus | GO:0010265~SCF complex assembly,GO:0016567~protein ubiquitination,GO:0030154~cell differentiation,GO:0043086~negative regulation of catalytic activity,GO:0045893~positive regulation of transcription, DNA-templated,GO:0045899~positive regulation of RNA polymerase II transcriptional preinitiation complex assembly, |
| 26 | Canx | calnexin(Canx) | Mus musculus | GO:0002474~antigen processing and presentation of peptide antigen via MHC class I,GO:0006457~protein folding,GO:0007568~aging,GO:0048488~synaptic vesicle endocytosis,GO:0061077~chaperone-mediated protein folding,GO:0072583~clathrin-mediated endocytosis, |

|  | E | F | G |
|---|---|---|---|
| 24 | GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0005829~cytosol,GO:0016020~membrane,GO:0016363~nuclear matrix,GO:0042995~cell projection,GO:0043025~neuronal cell body,GO:0043195~terminal bouton,GO:0043234~protein complex,GO:0070062~extracellular exosome, | GO:0000166~nucleotide binding,GO:0002134~UTP binding,GO:0003824~catalytic activity,GO:0004070~aspartate carbamoyltransferase activity,GO:0004087~carbamoyl-phosphate synthase (ammonia) activity,GO:0004088~carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity,GO:0004151~dihydroorotase activity,GO:0004672~protein kinase activity,GO:0005524~ATP binding,GO:0008270~zinc ion binding,GO:0016597~amino acid binding,GO:0016740~transferase activity,GO:0016743~carboxyl- or carbamoyltransferase activity,GO:0016787~hydrolase activity,GO:0016810~hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds,GO:0016812~hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amides,GO:0016874~ligase activity,GO:0019899~enzyme binding,GO:0042802~identical protein binding,GO:0046872~metal ion binding, | IPR002082:Aspartate carbamoyltransferase,IPR002195:Dihydroorotase, conserved site,IPR002474:Carbamoyl-phosphate synthase, small subunit N-terminal domain,IPR005479:Carbamoyl-phosphate synthetase large subunit-like, ATP-binding domain,IPR005480:Carbamoyl-phosphate synthetase, large subunit oligomerisation domain,IPR005483:Carbamoyl-phosphate synthase large subunit, CPSase domain,IPR006130:Aspartate/ornithine carbamoyltransferase,IPR006131:Aspartate/ornithine carbamoyltransferase, Asp/Orn-binding domain,IPR006132:Aspartate/ornithine carbamoyltransferase, carbamoyl-P binding,IPR006274:Carbamoyl-phosphate synthase, small subunit,IPR006275:Carbamoyl-phosphate synthase, large subunit,IPR006680:Amidohydrolase 1,IPR011059:Metal-dependent hydrolase, composite domain,IPR011607:Methylglyoxal synthase-like domain,IPR011761:ATP-grasp fold,IPR013815:ATP-grasp fold, subdomain 1,IPR013816:ATP-grasp fold, subdomain 2,IPR016185:Pre-ATP-grasp domain,IPR017926:Glutamine amidotransferase, |
| 25 | GO:0000151~ubiquitin ligase complex,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0005794~Golgi apparatus,GO:0016020~membrane,GO:0031461~cullin-RING ubiquitin ligase complex,GO:0070062~extracellular exosome, | GO:0005515~protein binding,GO:0017025~TBP-class protein binding, | IPR011989:Armadillo-like helical,IPR013932:TATA-binding protein interacting (TIP20),IPR016024:Armadillo-type fold, |
| 26 | GO:0005737~cytoplasm,GO:0005783~endoplasmic reticulum,GO:0005789~endoplasmic reticulum membrane,GO:0005790~smooth endoplasmic reticulum,GO:0005791~rough endoplasmic reticulum,GO:0005840~ribosome,GO:0016020~membrane,GO:0016021~integral component of membrane,GO:0030424~axon,GO:0031012~extracellular matrix,GO:0032839~dendrite cytoplasm,GO:0042470~melanosome,GO:0043025~neuronal cell body,GO:0043197~dendritic spine,GO:0043209~myelin sheath,GO:0043234~protein complex,GO:0044233~ER-mitochondrion membrane contact site,GO:0070062~extracellular exosome,GO:0071556~integral component of lumenal side of endoplasmic reticulum membrane, | GO:0001948~glycoprotein binding,GO:0005509~calcium ion binding,GO:0005515~protein binding,GO:0030246~carbohydrate binding,GO:0034185~apolipoprotein binding,GO:0035255~ionotropic glutamate receptor binding,GO:0044822~poly(A) RNA binding,GO:0046872~metal ion binding,GO:0051082~unfolded protein binding, | IPR001580:Calreticulin/calnexin,IPR009033:Calreticulin/calnexin, P domain,IPR013320:Concanavalin A-like lectin/glucanase, subgroup,IPR018124:Calreticulin/calnexin, conserved site, |

| | H | I | J | K |
|---|---|---|---|---|
| 24 | mmu00240:Pyrimidine metabolism,mmu00250:Alanine, aspartate and glutamate metabolism,mmu01100:Metabolic pathways, | | Acetylation,Allosteric enzyme,Alternative splicing,ATP-binding,Complete proteome,Cytoplasm,Hydrolase,Ligase,Metal-binding,Multifunctional enzyme,Nucleotide-binding,Nucleus,Phosphoprotein,Pyrimidine biosynthesis,Reference proteome,Repeat,Transferase,Zinc, | |
| 25 | | | Acetylation,Complete proteome,Cytoplasm,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,Ubl conjugation pathway, | chain:Cullin-associated NEDD8-dissociated protein 1,compositionally biased region:Asp-rich,modified residue,repeat:HEAT 1,repeat:HEAT 10,repeat:HEAT 11,repeat:HEAT 12,repeat:HEAT 13,repeat:HEAT 14,repeat:HEAT 15,repeat:HEAT 16,repeat:HEAT 17,repeat:HEAT 18,repeat:HEAT 19,repeat:HEAT 2,repeat:HEAT 20,repeat:HEAT 21,repeat:HEAT 22,repeat:HEAT 23,repeat:HEAT 24,repeat:HEAT 25,repeat:HEAT 26,repeat:HEAT 27,repeat:HEAT 3,repeat:HEAT 4,repeat:HEAT 5,repeat:HEAT 6,repeat:HEAT 7,repeat:HEAT 8,repeat:HEAT 9, |
| 26 | mmu04141:Protein processing in endoplasmic reticulum,mmu04145:Phagosome,mmu04612:Antigen processing and presentation,mmu04918:Thyroid hormone synthesis,mmu05166:HTLV-I infection, | | Acetylation,Calcium,Chaperone,Coiled coil,Complete proteome,Disulfide bond,Endoplasmic reticulum,Lectin,Lipoprotein,Membrane,Metal-binding,Palmitate,Phosphoprotein,Reference proteome,Repeat,Signal,Transmembrane,Transmembrane helix,Ubl conjugation, | binding site:Carbohydrate,chain:Calnexin,disulfide bond,metal ion-binding site:Calcium,metal ion-binding site:Calcium; via carbonyl oxygen,modified residue,region of interest:4 X approximate repeats,region of interest:P domain (Extended arm),repeat:1-1,repeat:1-2,repeat:1-3,repeat:1-4,repeat:2-1,repeat:2-2,repeat:2-3,repeat:2-4,sequence conflict,signal peptide,topological domain:Cytoplasmic,topological domain:Lumenal,transmembrane region, |

| | A | B | C | D |
|---|---|---|---|---|
| 27 | Capns1 | calpain, small subunit 1(Capns1) | Mus musculus | GO:0006508~proteolysis, |
| 28 | Capzb | capping protein (actin filament) muscle Z-line, beta(Capzb) | Mus musculus | GO:0000902~cell morphogenesis,GO:0007010~cytoskeleton organization,GO:0010591~regulation of lamellipodium assembly,GO:0022604~regulation of cell morphogenesis,GO:0030030~cell projection organization,GO:0030032~lamellipodium assembly,GO:0030036~actin cytoskeleton organization,GO:0031115~negative regulation of microtubule polymerization,GO:0031175~neuron projection development,GO:0048747~muscle fiber development,GO:0051016~barbed-end actin filament capping,GO:0051490~negative regulation of filopodium assembly,GO:0051693~actin filament capping,GO:0090036~regulation of protein kinase C signaling,GO:0098609~cell-cell adhesion, |
| 29 | Cbx3 | chromobox 3(Cbx3) | Mus musculus | GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0016569~covalent chromatin modification,GO:0045815~positive regulation of gene expression, epigenetic,GO:0045892~negative regulation of transcription, DNA-templated,GO:0048511~rhythmic process,GO:0071549~cellular response to dexamethasone stimulus, |
| 30 | Cct5 | chaperonin containing Tcp1, subunit 5 (epsilon)(Cct5) | Mus musculus | GO:0006457~protein folding,GO:0007339~binding of sperm to zona pellucida,GO:0009615~response to virus,GO:0032212~positive regulation of telomere maintenance via telomerase,GO:0050821~protein stabilization,GO:1901998~toxin transport,GO:1904851~positive regulation of establishment of protein localization to telomere,GO:1904871~positive regulation of protein localization to Cajal body,GO:1904874~positive regulation of telomerase RNA localization to Cajal body, |
| 31 | Cct6a | chaperonin containing Tcp1, subunit 6a (zeta)(Cct6a) | Mus musculus | GO:0006457~protein folding,GO:0007339~binding of sperm to zona pellucida,GO:0032212~positive regulation of telomere maintenance via telomerase,GO:0050821~protein stabilization,GO:1901998~toxin transport,GO:1904851~positive regulation of establishment of protein localization to telomere,GO:1904871~positive regulation of protein localization to Cajal body,GO:1904874~positive regulation of telomerase RNA localization to Cajal body, |
| 32 | Cdc5l | cell division cycle 5-like (S. pombe)(Cdc5l) | Mus musculus | GO:0000278~mitotic cell cycle,GO:0000398~mRNA splicing, via spliceosome,GO:0006281~DNA repair,GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0006357~regulation of transcription from RNA polymerase II promoter,GO:0006397~mRNA processing,GO:0006974~cellular response to DNA damage stimulus,GO:0007049~cell cycle,GO:0008380~RNA splicing,GO:0030154~cell differentiation,GO:0044344~cellular response to fibroblast growth factor stimulus,GO:0071352~cellular response to interleukin-2,GO:0072422~signal transduction involved in DNA damage checkpoint,GO:1904568~cellular response to wortmannin,GO:1990090~cellular response to nerve growth factor stimulus,GO:1990646~cellular response to prolactin, |

| | E | F | G |
|---|---|---|---|
| 27 | GO:0005737~cytoplasm,GO:0005829~cytosol,GO:0005886~plasma membrane,GO:0016020~membrane,GO:0070062~extracellular exosome, | GO:0004198~calcium-dependent cysteine-type endopeptidase activity,GO:0005509~calcium ion binding,GO:0046872~metal ion binding,GO:0046982~protein heterodimerization activity, | IPR002048:EF-hand domain,IPR011992:EF-hand-like domain,IPR018247:EF-Hand 1, calcium-binding site, |
| 28 | GO:0001669~acrosomal vesicle,GO:0005737~cytoplasm,GO:0005856~cytoskeleton,GO:0005884~actin filament,GO:0005903~brush border,GO:0005913~cell-cell adherens junction,GO:0008290~F-actin capping protein complex,GO:0014704~intercalated disc,GO:0016020~membrane,GO:0030018~Z disc,GO:0030027~lamellipodium,GO:0030863~cortical cytoskeleton,GO:0033150~cytoskeletal calyx,GO:0043025~neuronal cell body,GO:0043197~dendritic spine,GO:0070062~extracellular exosome,GO:0071203~WASH complex, | GO:0003779~actin binding,GO:0005515~protein binding,GO:0048487~beta-tubulin binding,GO:0051015~actin filament binding,GO:0098641~cadherin binding involved in cell-cell adhesion, | IPR001698:WASH complex, F-actin capping protein, beta subunit,IPR019771:F-actin capping protein, beta subunit, conserved site, |
| 29 | GO:0000775~chromosome, centromeric region,GO:0000779~condensed chromosome, centromeric region,GO:0000784~nuclear chromosome, telomeric region,GO:0000785~chromatin,GO:0005634~nucleus,GO:0005635~nuclear envelope,GO:0005654~nucleoplasm,GO:0005719~nuclear euchromatin,GO:0005720~nuclear heterochromatin,GO:0005819~spindle,GO:0010369~chromocenter,GO:0031618~nuclear pericentric heterochromatin,GO:0035985~senescence-associated heterochromatin focus, | GO:0000976~transcription regulatory region sequence-specific DNA binding,GO:0005515~protein binding,GO:0019899~enzyme binding,GO:0019904~protein domain specific binding,GO:0042802~identical protein binding,GO:1990226~histone methyltransferase binding, | IPR000953:Chromo domain/shadow,IPR008251:Chromo shadow domain,IPR016197:Chromo domain-like,IPR017984:Chromo domain subgroup,IPR023779:Chromo domain, conserved site,IPR023780:Chromo domain, |
| 30 | GO:0002199~zona pellucida receptor complex,GO:0005730~nucleolus,GO:0005737~cytoplasm,GO:0005813~centrosome,GO:0005832~chaperonin-containing T-complex,GO:0005856~cytoskeleton,GO:0005874~microtubule,GO:0043209~myelin sheath,GO:0044297~cell body,GO:0070062~extracellular exosome, | GO:0000166~nucleotide binding,GO:0005515~protein binding,GO:0005524~ATP binding,GO:0031681~G-protein beta-subunit binding,GO:0048487~beta-tubulin binding,GO:0051082~unfolded protein binding, | IPR002194:Chaperonin TCP-1, conserved site,IPR002423:Chaperonin Cpn60/TCP-1,IPR012718:T-complex protein 1, epsilon subunit,IPR017998:Chaperone tailless complex polypeptide 1 (TCP-1),IPR027409:GroEL-like apical domain,IPR027410:TCP-1-like chaperonin intermediate domain,IPR027413:GroEL-like equatorial domain, |
| 31 | GO:0001669~acrosomal vesicle,GO:0002199~zona pellucida receptor complex,GO:0005737~cytoplasm,GO:0005832~chaperonin-containing T-complex,GO:0005874~microtubule,GO:0031012~extracellular matrix,GO:0044297~cell body,GO:0070062~extracellular exosome, | GO:0000166~nucleotide binding,GO:0005515~protein binding,GO:0005524~ATP binding,GO:0044183~protein binding involved in protein folding,GO:0044822~poly(A) RNA binding,GO:0051082~unfolded protein binding,GO:0071987~WD40-repeat domain binding, | IPR002194:Chaperonin TCP-1, conserved site,IPR002423:Chaperonin Cpn60/TCP-1,IPR012722:T-complex protein 1, zeta subunit,IPR017998:Chaperone tailless complex polypeptide 1 (TCP-1),IPR027409:GroEL-like apical domain,IPR027410:TCP-1-like chaperonin intermediate domain,IPR027413:GroEL-like equatorial domain, |
| 32 | GO:0000974~Prp19 complex,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005662~DNA replication factor A complex,GO:0005681~spliceosomal complex,GO:0005730~nucleolus,GO:0005737~cytoplasm,GO:0016020~membrane,GO:0016607~nuclear speck,GO:0032993~protein-DNA complex,GO:0048471~perinuclear region of cytoplasm,GO:0071013~catalytic step 2 spliceosome, | GO:0000981~RNA polymerase II transcription factor activity, sequence-specific DNA binding,GO:0001135~transcription factor activity, RNA polymerase II transcription factor recruiting,GO:0001222~transcription corepressor binding,GO:0003677~DNA binding,GO:0003723~RNA binding,GO:0008157~protein phosphatase 1 binding,GO:0019901~protein kinase binding,GO:0043522~leucine zipper domain binding,GO:0043565~sequence-specific DNA binding,GO:0044212~transcription regulatory region DNA binding,GO:0044822~poly(A) RNA binding,GO:0071987~WD40-repeat domain binding, | IPR001005:SANT/Myb domain,IPR009057:Homeodomain-like,IPR017930:Myb domain,IPR021786:Domain of unknown function DUF3351, |

|  | H | I | J | K |
|---|---|---|---|---|
| 27 |  |  | Acetylation,Calcium,Cell membrane,Complete proteome,Cytoplasm,Membrane,Metal-binding,Phosphoprotein,Proteomics identification,Reference proteome,Repeat, | calcium-binding region:1,calcium-binding region:2,calcium-binding region:3,chain:Calpain small subunit 1,compositionally biased region:Gly-rich (hydrophobic),compositionally biased region:Poly-Gly,compositionally biased region:Poly-Pro,domain:EF-hand 1; atypical,domain:EF-hand 2,domain:EF-hand 3,domain:EF-hand 4,domain:EF-hand 5,modified residue,sequence conflict, |
| 28 | mmu04144:Endocytosis, |  | Acetylation,Actin capping,Actin-binding,Alternative splicing,Complete proteome,Cytoplasm,Cytoskeleton,Direct protein sequencing,Phosphoprotein,Proteomics identification,Reference proteome, | chain:F-actin-capping protein subunit beta,modified residue,splice variant, |
| 29 |  |  | Acetylation,Biological rhythms,Chromatin regulator,Complete proteome,Direct protein sequencing,Isopeptide bond,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,Repressor,Transcription,Transcription regulation,Ubl conjugation, | chain:Chromobox protein homolog 3,domain:Chromo 1,domain:Chromo 2; shadow subtype,modified residue, |
| 30 |  |  | Acetylation,ATP-binding,Chaperone,Complete proteome,Cytoplasm,Cytoskeleton,Direct protein sequencing,Nucleotide-binding,Phosphoprotein,Proteomics identification,Reference proteome, | chain:T-complex protein 1 subunit epsilon,modified residue,sequence conflict, |
| 31 |  |  | Acetylation,ATP-binding,Chaperone,Complete proteome,Cytoplasm,Direct protein sequencing,Nucleotide-binding,Phosphoprotein,Reference proteome, | chain:T-complex protein 1 subunit zeta,modified residue, |
| 32 | mmu03040:Spliceosome, |  | Activator,Cell cycle,Coiled coil,Complete proteome,Cytoplasm,Direct protein sequencing,DNA damage,DNA repair,DNA-binding,Isopeptide bond,mRNA processing,mRNA splicing,Nucleus,Phosphoprotein,Reference proteome,Repeat,RNA-binding,Spliceosome,Transcription,Transcription regulation,Ubl conjugation, | chain:Cell division cycle 5-related protein,DNA-binding region:H-T-H motif,domain:HTH myb-type 1,domain:HTH myb-type 2,modified residue,region of interest:Interaction with DAPK3,region of interest:Interaction with PLRG1,region of interest:Interaction with PPP1R8, |

|  | A | B | C | D |
|---|---|---|---|---|
| 33 | Cdk1 | cyclin-dependent kinase 1(Cdk1) | Mus musculus | GO:0006461~protein complex assembly,GO:0006468~protein phosphorylation,GO:0006915~apoptotic process,GO:0007049~cell cycle,GO:0007067~mitotic nuclear division,GO:0007095~mitotic G2 DNA damage checkpoint,GO:0007569~cell aging,GO:0008283~cell proliferation,GO:0009636~response to toxic substance,GO:0010243~response to organonitrogen compound,GO:0010628~positive regulation of gene expression,GO:0014070~response to organic cyclic compound,GO:0014075~response to amine,GO:0014823~response to activity,GO:0016310~phosphorylation,GO:0018105~peptidyl-serine phosphorylation,GO:0018107~peptidyl-threonine phosphorylation,GO:0030261~chromosome condensation,GO:0030855~epithelial cell differentiation,GO:0031100~organ regeneration,GO:0033160~positive regulation of protein import into nucleus, translocation,GO:0034501~protein localization to kinetochore,GO:0042493~response to drug,GO:0043066~negative regulation of apoptotic process,GO:0044772~mitotic cell cycle phase transition,GO:0045471~response to ethanol,GO:0045740~positive regulation of DNA replication,GO:0045931~positive regulation of mitotic cell cycle,GO:0046686~response to cadmium ion,GO:0046688~response to copper ion,GO:0048678~response to axon injury,GO:0051301~cell division,GO:0055015~ventricular cardiac muscle cell development,GO:0060045~positive regulation of cardiac muscle cell proliferation,GO:0070301~cellular response to hydrogen peroxide,GO:0090166~Golgi disassembly,GO:1900182~positive regulation of protein localization to nucleus, |
| 34 | Cfl1 | cofilin 1, non-muscle(Cfl1) | Mus musculus | GO:0000281~mitotic cytokinesis,GO:0001755~neural crest cell migration,GO:0001842~neural fold formation,GO:0002576~platelet degranulation,GO:0006468~protein phosphorylation,GO:0006606~protein import into nucleus,GO:0006928~movement of cell or subcellular component,GO:0007010~cytoskeleton organization,GO:0007015~actin filament organization,GO:0009615~response to virus,GO:0022604~regulation of cell morphogenesis,GO:0030010~establishment of cell polarity,GO:0030030~cell projection organization,GO:0030042~actin filament depolymerization,GO:0030043~actin filament fragmentation,GO:0030836~positive regulation of actin filament depolymerization,GO:0043200~response to amino acid,GO:0044794~positive regulation by host of viral process,GO:0045792~negative regulation of cell size,GO:0061001~regulation of dendritic spine morphogenesis, |
| 35 | Chd4 | chromodomain helicase DNA binding protein 4(Chd4) | Mus musculus | GO:0000122~negative regulation of transcription from RNA polymerase II promoter,GO:0006325~chromatin organization,GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0016569~covalent chromatin modification,GO:0043044~ATP-dependent chromatin remodeling,GO:0051225~spindle assembly,GO:0072553~terminal button organization, |

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| 33 | GO:0000784~nuclear chromosome, telomeric region,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0005739~mitochondrion,GO:0005813~centrosome,GO:0005856~cytoskeleton,GO:0005876~spindle microtubule,GO:0016020~membrane,GO:0030496~midbody,GO:0070062~extracellular exosome,GO:0072686~mitotic spindle, | GO:0000166~nucleotide binding,GO:0003682~chromatin binding,GO:0004672~protein kinase activity,GO:0004674~protein serine/threonine kinase activity,GO:0004693~cyclin-dependent protein serine/threonine kinase activity,GO:0005515~protein binding,GO:0005524~ATP binding,GO:0008353~RNA polymerase II carboxy-terminal domain kinase activity,GO:0016301~kinase activity,GO:0016740~transferase activity,GO:0030332~cyclin binding,GO:0030544~Hsp70 protein binding,GO:0035173~histone kinase activity, | IPR000719:Protein kinase, catalytic domain,IPR008271:Serine/threonine-protein kinase, active site,IPR011009:Protein kinase-like domain,IPR017441:Protein kinase, ATP binding site, |
| 34 | GO:0005576~extracellular region,GO:0005615~extracellular space,GO:0005622~intracellular,GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005829~cytosol,GO:0005856~cytoskeleton,GO:0005886~plasma membrane,GO:0005911~cell-cell junction,GO:0005925~focal adhesion,GO:0015629~actin cytoskeleton,GO:0016020~membrane,GO:0016363~nuclear matrix,GO:0030027~lamellipodium,GO:0030864~cortical actin cytoskeleton,GO:0031012~extracellular matrix,GO:0031252~cell leading edge,GO:0031258~lamellipodium membrane,GO:0031982~vesicle,GO:0032587~ruffle membrane,GO:0042995~cell projection,GO:0070062~extracellular exosome, | GO:0003779~actin binding,GO:0051015~actin filament binding,GO:1902936~phosphatidylinositol bisphosphate binding, | IPR002108:Actin-binding, cofilin/tropomyosin type,IPR017904:ADF/Cofilin/Destrin,IPR027234:Cofilin 1/2, |
| 35 | GO:0000790~nuclear chromatin,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0005813~centrosome,GO:0005856~cytoskeleton,GO:0016020~membrane,GO:0016581~NuRD complex,GO:0032993~protein-DNA complex,GO:0043234~protein complex, | GO:0000166~nucleotide binding,GO:0000978~RNA polymerase II core promoter proximal region sequence-specific DNA binding,GO:0000980~RNA polymerase II distal enhancer sequence-specific DNA binding,GO:0001103~RNA polymerase II repressing transcription factor binding,GO:0003676~nucleic acid binding,GO:0003677~DNA binding,GO:0004386~helicase activity,GO:0005515~protein binding,GO:0005524~ATP binding,GO:0008017~microtubule binding,GO:0008026~ATP-dependent helicase activity,GO:0008134~transcription factor binding,GO:0008270~zinc ion binding,GO:0016787~hydrolase activity,GO:0016818~hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides,GO:0031492~nucleosomal DNA binding,GO:0046872~metal ion binding, | IPR000330:SNF2-related,IPR000953:Chromo domain/shadow,IPR001650:Helicase, C-terminal,IPR001965:Zinc finger, PHD-type,IPR002464:DNA/RNA helicase, ATP-dependent, DEAH-box type, conserved site,IPR009462:Domain of unknown function DUF1086,IPR009463:Domain of unknown function DUF1087,IPR011011:Zinc finger, FYVE/PHD-type,IPR012957:CHD, C-terminal 2,IPR012958:CHD, N-terminal,IPR013083:Zinc finger, RING/FYVE/PHD-type,IPR014001:Helicase, superfamily 1/2, ATP-binding domain,IPR016197:Chromo domain-like,IPR019786:Zinc finger, PHD-type, conserved site,IPR019787:Zinc finger, PHD-finger,IPR023780:Chromo domain,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |

|  | H | I | J | K |
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| 33 | mmu04110:Cell cycle,mmu04114:Oocyte meiosis,mmu04115:p53 signaling pathway,mmu04540:Gap junction,mmu04914:Progesterone-mediated oocyte maturation,mmu05168:Herpes simplex infection,mmu05203:Viral carcinogenesis, |  | Acetylation,Apoptosis,ATP-binding,Cell cycle,Cell division,Complete proteome,Cytoplasm,Cytoskeleton,Direct protein sequencing,Isopeptide bond,Kinase,Mitochondrion,Mitosis,Nucleotide-binding,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Serine/threonine-protein kinase,Transferase,Ubl conjugation, | active site:Proton acceptor,binding site:ATP,chain:Cell division control protein 2 homolog,cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin),domain:Protein kinase,modified residue,nucleotide phosphate-binding region:ATP,sequence conflict, |
| 34 | mmu04360:Axon guidance,mmu04666:Fc gamma R-mediated phagocytosis,mmu04810:Regulation of actin cytoskeleton,mmu05133:Pertussis, |  | Acetylation,Actin-binding,Cell membrane,Cell projection,Complete proteome,Cytoplasm,Cytoskeleton,Direct protein sequencing,Membrane,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome, | chain:Cofilin-1,domain:ADF-H,modified residue,short sequence motif:Nuclear localization signal, |
| 35 | mmu05203:Viral carcinogenesis, |  | Acetylation,ATP-binding,Chromatin regulator,Complete proteome,Cytoplasm,Cytoskeleton,DNA-binding,Helicase,Hydrolase,Isopeptide bond,Metal-binding,Nucleotide-binding,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,Transcription,Transcription regulation,Ubl conjugation,Zinc,Zinc-finger, | chain:Chromodomain-helicase-DNA-binding protein 4,compositionally biased region:Glu-rich,compositionally biased region:Lys-rich,compositionally biased region:Pro-rich,domain:Chromo 1,domain:Chromo 2,domain:Helicase ATP-binding,domain:Helicase C-terminal,modified residue,nucleotide phosphate-binding region:ATP,short sequence motif:DEAH box,zinc finger region:PHD-type 1,zinc finger region:PHD-type 2, |

|  | A | B | C | D |
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| 36 | Col12a1 | collagen, type XII, alpha 1(Col12a1) | Mus musculus | GO:0005576~extracellular region,GO:0005578~proteinaceous extracellular matrix,GO:0005581~collagen trimer,GO:0005595~collagen type XII trimer,GO:0005615~extracellular space,GO:0031012~extracellular matrix,GO:0070062~extracellular exosome,GO:1903561~extracellular vesicle, |
| 37 | Col18a1 | collagen, type XVIII, alpha 1(Col18a1) | Mus musculus | GO:0001525~angiogenesis,GO:0001886~endothelial cell morphogenesis,GO:0007155~cell adhesion,GO:0007275~multicellular organism development,GO:0008284~positive regulation of cell proliferation,GO:0030198~extracellular matrix organization,GO:0030335~positive regulation of cell migration,GO:0042493~response to drug,GO:0051599~response to hydrostatic pressure,GO:2000353~positive regulation of endothelial cell apoptotic process, |
| 38 | Cpsf6 | cleavage and polyadenylation specific factor 6(Cpsf6) | Mus musculus | GO:0006378~mRNA polyadenylation,GO:0006397~mRNA processing,GO:0051262~protein tetramerization, |

|  | E | F | G |
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| 36 |  | IPR001791:Laminin G domain,IPR002035:von Willebrand factor, type A,IPR003961:Fibronectin, type III,IPR008160:Collagen triple helix repeat,IPR013320:Concanavalin A-like lectin/glucanase, subgroup,IPR013783:Immunoglobulin-like fold, | mmu04974:Protein digestion and absorption, |
| 37 | GO:0005576~extracellular region,GO:0005578~proteinaceous extracellular matrix,GO:0005581~collagen trimer,GO:0005604~basement membrane,GO:0005615~extracellular space,GO:0031012~extracellular matrix,GO:0070062~extracellular exosome, | GO:0005198~structural molecule activity,GO:0046872~metal ion binding, | IPR001791:Laminin G domain,IPR008160:Collagen triple helix repeat,IPR010363:Domain of unknown function DUF959, collagen XVIII, N-terminal,IPR010515:Collagenase NC10/endostatin,IPR013320:Concanavalin A-like lectin/glucanase, subgroup,IPR015526:Frizzled/secreted frizzled-related protein,IPR016186:C-type lectin-like,IPR016187:C-type lectin fold,IPR020067:Frizzled domain, |
| 38 | GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005849~mRNA cleavage factor complex,GO:0016020~membrane,GO:0030529~intracellular ribonucleoprotein complex,GO:0042382~paraspeckles, | GO:0000166~nucleotide binding,GO:0003676~nucleic acid binding,GO:0003723~RNA binding,GO:0003729~mRNA binding,GO:0044822~poly(A) RNA binding, | IPR000504:RNA recognition motif domain,IPR012677:Nucleotide-binding, alpha-beta plait, |

| | H | I | J | K |
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| 36 | | SM00060:FN3,SM00210:TSPN,SM00327:VWA, | Alternative splicing,Cell adhesion,Collagen,Complete proteome,Disulfide bond,Extracellular matrix,Glycoprotein,Hydroxylation,Proteomics identification,Reference proteome,Repeat,Secreted,Signal, | chain:Collagen alpha-1(XII) chain,compositionally biased region:Poly-Thr,domain:Fibronectin type-III 1,domain:Fibronectin type-III 10,domain:Fibronectin type-III 11,domain:Fibronectin type-III 12,domain:Fibronectin type-III 13,domain:Fibronectin type-III 14,domain:Fibronectin type-III 15,domain:Fibronectin type-III 16,domain:Fibronectin type-III 17,domain:Fibronectin type-III 18,domain:Fibronectin type-III 2,domain:Fibronectin type-III 3,domain:Fibronectin type-III 4,domain:Fibronectin type-III 5,domain:Fibronectin type-III 6,domain:Fibronectin type-III 7,domain:Fibronectin type-III 8,domain:Fibronectin type-III 9,domain:TSP N-terminal,domain:VWFA 1,domain:VWFA 2,domain:VWFA 3,domain:VWFA 4,glycosylation site:N-linked (GlcNAc...),glycosylation site:O-linked (Xyl...) (chondroitin sulfate),modified residue,region of interest:Nonhelical region (NC1),region of interest:Nonhelical region (NC2),region of interest:Nonhelical region (NC3),region of interest:Triple-helical region (COL1) with 2 imperfections,region of interest:Triple-helical region (COL2) with 1 imperfection,sequence conflict,short sequence motif:Cell attachment site,signal peptide,splice variant, |
| 37 | mmu04974:Protein digestion and absorption, | | 3D-structure,Alternative promoter usage,Alternative splicing,Cell adhesion,Collagen,Complete proteome,Developmental protein,Direct protein sequencing,Disulfide bond,Extracellular matrix,Glycoprotein,Hydroxylation,Metal-binding,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,Secreted,Signal,Zinc, | chain:Collagen alpha-1(XVIII) chain,chain:Endostatin,disulfide bond,domain:FZ,domain:TSP N-terminal,glycosylation site:N-linked (GlcNAc...),helix,metal ion-binding site:Zinc,metal ion-binding site:Zinc; alternate,mutagenesis site,region of interest:Nonhelical region 1 (NC1),region of interest:Nonhelical region 10 (NC10),region of interest:Nonhelical region 11 (NC11),region of interest:Nonhelical region 2 (NC2),region of interest:Nonhelical region 3 (NC3),region of interest:Nonhelical region 4 (NC4),region of interest:Nonhelical region 5 (NC5),region of interest:Nonhelical region 6 (NC6),region of interest:Nonhelical region 7 (NC7),region of interest:Nonhelical region 8 (NC8),region of interest:Nonhelical region 9 (NC9),region of interest:Triple-helical region 1 (COL1),region of interest:Triple-helical region 10 (COL10),region of interest:Triple-helical region 2 (COL2),region of interest:Triple-helical region 3 (COL3),region of interest:Triple-helical region 4 (COL4),region of interest:Triple-helical region 5 (COL5),region of interest:Triple-helical region 6 (COL6),region of interest:Triple-helical region 7 (COL7),region of interest:Triple-helical region 8 (COL8),region of interest:Triple-helical region 9 (COL9),sequence conflict,short sequence motif:Cell attachment site,signal peptide,splice variant,strand,turn, |
| 38 | mmu03015:mRNA surveillance pathway, | | Complete proteome,mRNA processing,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,RNA-binding, | chain:Cleavage and polyadenylation specificity factor subunit 6,compositionally biased region:Arg-rich,compositionally biased region:Pro-rich,domain:RRM,modified residue,region of interest:Necessary for interaction with NUDT21/CPSF5,region of interest:Sufficient for nuclear targeting,sequence conflict, |

| | A | B | C | D |
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| 39 | Ctnnb1 | catenin (cadherin associated protein), beta 1(Ctnnb1) | Mus musculus | GO:0000122~negative regulation of transcription from RNA polymerase II promoter,GO:0000578~embryonic axis specification,GO:0000904~cell morphogenesis involved in differentiation,GO:0001501~skeletal system development,GO:0001569~patterning of blood vessels,GO:0001570~vasculogenesis,GO:0001658~branching involved in ureteric bud morphogenesis,GO:0001701~in utero embryonic development,GO:0001702~gastrulation with mouth forming second,GO:0001706~endoderm formation,GO:0001708~cell fate specification,GO:0001709~cell fate determination,GO:0001711~endodermal cell fate commitment,GO:0001764~neuron migration,GO:0001822~kidney development,GO:0001840~neural plate development,GO:0001944~vasculature development,GO:0002052~positive regulation of neuroblast proliferation,GO:0002053~positive regulation of mesenchymal cell proliferation,GO:0002089~lens morphogenesis in camera-type eye,GO:0003223~ventricular compact myocardium morphogenesis,GO:0003266~regulation of secondary heart field cardioblast proliferation,GO:0003338~metanephros morphogenesis,GO:0003340~negative regulation of mesenchymal to epithelial transition involved in metanephros morphogenesis,GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0006357~regulation of transcription from RNA polymerase II promoter,GO:0007155~cell adhesion,GO:0007160~cell-matrix adhesion,GO:0007268~chemical synaptic transmission,GO:0007398~ectoderm development,GO:0007399~nervous system development,GO:0007403~glial cell fate determination,GO:0007507~heart development,GO:0008283~cell proliferation,GO:0008284~positive regulation of cell proliferation,GO:0008285~negative regulation of cell proliferation,GO:0009948~anterior/posterior axis specification,GO:0009950~dorsal/ventral axis specification,GO:0009953~dorsal/ventral pattern formation,GO:0009954~proximal/distal pattern formation,GO:0009987~cellular process,GO:0010468~regulation of gene expression,GO:0010628~positive regulation of gene expression,GO:0010629~negative regulation of gene expression,GO:0010718~positive regulation of epithelial to mesenchymal transition,GO:0010909~positive regulation of heparan sulfate proteoglycan biosynthetic process,GO:0014010~Schwann cell proliferation,GO:0016055~Wnt signaling pathway,GO:0016331~morphogenesis of embryonic epithelium,GO:0016337~single organismal cell-cell adhesion,GO:0019827~stem cell population maintenance,GO:0021819~layer formation in cerebral cortex,GO:0022009~central nervous system vasculogenesis,GO:0022405~hair cycle process,GO:0030097~hemopoiesis,GO:0030154~cell differentiation,GO:0030182~neuron differentiation,GO:0030217~T cell differentiation,GO:0030316~osteoclast differentiation,GO:0030324~lung development,GO:0030539~male genitalia development,GO:0030856~regulation of epithelial cell differentiation,GO:0030858~positive regulation of epithelial cell differentiation,GO:0030900~forebrain development,GO:0030901~midbrain development,GO:0030902~hindbrain development,GO:0030997~regulation of centriole-centriole cohesion,GO:0031016~pancreas development,GO:0031069~hair follicle morphogenesis,GO:0031641~regulation of myelination,GO:0032212~positive regulation of telomere maintenance via telomerase,GO:0032331~negative regulation of chondrocyte differentiation,GO:0032355~response to estradiol,GO:0033077~T cell differentiation in thymus,GO:0033234~negative regulation of protein sumoylation,GO:0034097~response to cytokine,GO:0034332~adherens junction organization,GO:0034333~adherens junction assembly,GO:0034394~protein localization to cell surface,GO:0034613~cellular protein localization,GO:0035050~embryonic heart tube development,GO:0035112~genitalia morphogenesis,GO:0035115~embryonic forelimb morphogenesis,GO:0035116~embryonic hindlimb morphogenesis,GO:0036023~embryonic skeletal limb joint morphogenesis,GO:0042127~regulation of cell proliferation,GO:0042129~regulation of T cell proliferation,GO:0042475~odontogenesis of dentin-containing tooth,GO:0042493~response to drug,GO:0042733~embryonic digit morphogenesis,GO:0042981~regulation of apoptotic process,GO:0043065~positive regulation of apoptotic process,GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB signaling,GO:0043410~positive regulation of MAPK cascade,GO:0043525~positive regulation of neuron apoptotic process,GO:0043588~skin development,GO:0043627~response to estrogen,GO:0044334~canonical Wnt signaling pathway involved in positive regulation of epithelial to mesenchymal transition,GO:0044336~canonical Wnt signaling pathway involved in negative regulation of apoptotic process,GO:0045453~bone resorption,GO:0045595~regulation of cell differentiation,GO:0045596~negative regulation of cell differentiation,GO:0045603~positive regulation of endothelial cell differentiation,GO:0045667~regulation of osteoblast differentiation,GO:0045669~positive regulation of osteoblast differentiation,GO:0045670~regulation of osteoclast differentiation,GO:0045671~negative regulation of osteoclast differentiation,GO:0045743~positive regulation of fibroblast growth factor receptor signaling pathway,GO:0045892~negative regulation of transcription, DNA-templated,GO:0045893~positive regulation of transcription, DNA-templated,GO:0045944~positive regulation of transcription from RNA polymerase II promoter,GO:0045976~negative regulation of mitotic cell cycle, embryonic,GO:0048096~chromatin-mediated maintenance of transcription,GO:0048469~cell maturation,GO:0048489~synaptic vesicle transport,GO:0048513~animal organ development,GO:0048538~thymus development,GO:0048599~oocyte development,GO:0048617~embryonic foregut morphogenesis,GO:0048643~positive regulation of skeletal muscle tissue development,GO:0048660~regulation of smooth muscle cell proliferation,GO:0048715~negative regulation of oligodendrocyte differentiation,GO:0050808~synapse organization,GO:0051091~positive regulation of sequence-specific DNA binding transcription factor activity,GO:0051145~smooth muscle cell differentiation,GO:0051291~protein heterooligomerization,GO:0051569~regulation of histone H3-K4 methylation,GO:0051973~positive regulation of telomerase activity,GO:0060038~cardiac muscle cell proliferation,GO:0060066~oviduct development,GO:0060070~canonical Wnt signaling pathway,GO:0060173~limb development,GO:0060439~trachea morphogenesis,GO:0060440~trachea formation,GO:0060441~epithelial tube branching involved in lung morphogenesis,GO:0060479~lung cell differentiation,GO:0060484~lung-associated mesenchyme development,GO:0060485~mesenchyme development,GO:0060492~lung induction,GO:0060742~epithelial cell differentiation involved in prostate gland development,GO:0060769~positive regulation of epithelial cell proliferation involved in prostate gland development,GO:0060789~hair follicle placode formation,GO:0060916~mesenchymal cell proliferation involved in lung development,GO:0060947~cardiac vascular smooth muscle cell differentiation,GO:0060982~coronary artery morphogenesis,GO:0060983~epicardium-derived cardiac vascular smooth muscle cell differentiation,GO:0061047~positive regulation of branching involved in lung morphogenesis,GO:0061154~endothelial tube morphogenesis,GO:0061198~fungiform papilla formation,GO:0061324~canonical Wnt signaling pathway involved in positive regulation of cardiac outflow tract cell proliferation,GO:0061549~sympathetic ganglion development,GO:0061550~cranial ganglion development,GO:0070602~regulation of centromeric sister chromatid cohesion,GO:0071260~cellular response to mechanical stimulus,GO:0071363~cellular response to growth factor stimulus,GO:0071681~cellular response to indole-3-methanol,GO:0072001~renal system development,GO:0072033~renal vesicle formation,GO:0072053~renal inner medulla development,GO:0072054~renal outer medulla development,GO:0072079~nephron tubule formation,GO:0072132~mesenchyme morphogenesis,GO:0072182~regulation of nephron tubule epithelial cell differentiation,GO:0090279~regulation of calcium ion import,GO:1901215~negative regulation of neuron death,GO:1903204~negative regulation of oxidative stress-induced neuron death,GO:1904173~regulation of histone demethylase activity (H3-K4 specific),GO:1904499~regulation of chromatin-mediated maintenance of transcription,GO:1904501~positive regulation of chromatin-mediated maintenance of transcription,GO:1904793~regulation of euchromatin binding,GO:1904796~regulation of core promoter binding,GO:1904886~beta-catenin destruction complex disassembly,GO:1904888~cranial skeletal system development,GO:1904948~midbrain dopaminergic neuron differentiation,GO:1904954~canonical Wnt signaling pathway involved in midbrain dopaminergic neuron differentiation,GO:1990314~cellular response to insulin-like growth factor stimulus,GO:1990403~embryonic brain development,GO:1990791~dorsal root ganglion development,GO:2000008~regulation of protein localization to cell surface,GO:2000017~positive regulation of determination of dorsal identity,GO:2000144~positive regulation of DNA-templated transcription, initiation,GO:2001234~negative regulation of apoptotic signaling pathway, |

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| 39 | GO:0000922~spindle pole,GO:0005634~nucleus,GO:0005667~transcription factor complex,GO:0005719~nuclear euchromatin,GO:0005737~cytoplasm,GO:0005813~centrosome,GO:0005829~cytosol,GO:0005856~cytoskeleton,GO:0005886~plasma membrane,GO:0005911~cell-cell junction,GO:0005912~adherens junction,GO:0005913~cell-cell adherens junction,GO:0005916~fascia adherens,GO:0005923~bicellular tight junction,GO:0005925~focal adhesion,GO:0005938~cell cortex,GO:0014704~intercalated disc,GO:0016020~membrane,GO:0016323~basolateral plasma membrane,GO:0016328~lateral plasma membrane,GO:0016342~catenin complex,GO:0016600~flotillin complex,GO:0030018~Z disc,GO:0030027~lamellipodium,GO:0030054~cell junction,GO:0030877~beta-catenin destruction complex,GO:0031253~cell projection membrane,GO:0031528~microvillus membrane,GO:0032993~protein-DNA complex,GO:0034750~Scrib-APC-beta-catenin complex,GO:0043005~neuron projection,GO:0043198~dendritic shaft,GO:0043234~protein complex,GO:0043296~apical junction complex,GO:0044798~nuclear transcription factor complex,GO:0045177~apical part of cell,GO:0045202~synapse,GO:0048471~perinuclear region of cytoplasm,GO:0070062~extracellular exosome,GO:0070369~beta-catenin-TCF7L2 complex,GO:0071664~catenin-TCF7L2 complex,GO:0071944~cell periphery,GO:1990907~beta-catenin-TCF complex,GO:1990909~Wnt signalosome, | GO:0001085~RNA polymerase II transcription factor binding,GO:0001102~RNA polymerase II activating transcription factor binding,GO:0003677~DNA binding,GO:0003682~chromatin binding,GO:0003690~double-stranded DNA binding,GO:0003700~transcription factor activity, sequence-specific DNA binding,GO:0003713~transcription coactivator activity,GO:0004871~signal transducer activity,GO:0005515~protein binding,GO:0008022~protein C-terminus binding,GO:0008134~transcription factor binding,GO:0019899~enzyme binding,GO:0019900~kinase binding,GO:0019901~protein kinase binding,GO:0019903~protein phosphatase binding,GO:0030331~estrogen receptor binding,GO:0032403~protein complex binding,GO:0035255~ionotropic glutamate receptor binding,GO:0035257~nuclear hormone receptor binding,GO:0044212~transcription regulatory region DNA binding,GO:0044325~ion channel binding,GO:0045294~alpha-catenin binding,GO:0045296~cadherin binding,GO:0046332~SMAD binding,GO:0046982~protein heterodimerization activity,GO:0050998~nitric-oxide synthase binding,GO:0070411~I-SMAD binding,GO:0070491~repressing transcription factor binding,GO:0098641~cadherin binding involved in cell-cell adhesion,GO:1990188~euchromatin binding,GO:1990226~histone methyltransferase binding, | IPR000225:Armadillo,IPR011989:Armadillo-like helical,IPR013284:Beta-catenin,IPR016024:Armadillo-type fold |

|  | H | I | J | K |
|---|---|---|---|---|
| 39 | mmu04015:Rap1 signaling pathway,mmu04310:Wnt signaling pathway,mmu04390:Hippo signaling pathway,mmu04510:Focal adhesion,mmu04520:Adherens junction,mmu04550:Signaling pathways regulating pluripotency of stem cells,mmu04670:Leukocyte transendothelial migration,mmu04916:Melanogenesis,mmu04919:Thyroid hormone signaling pathway,mmu05100:Bacterial invasion of epithelial cells,mmu05166:HTLV-I infection,mmu05200:Pathways in cancer,mmu05205:Proteoglycans in cancer,mmu05210:Colorectal cancer,mmu05213:Endometrial cancer,mmu05215:Prostate cancer,mmu05216:Thyroid cancer,mmu05217:Basal cell carcinoma,mmu05412:Arrhythmogenic right ventricular cardiomyopathy (ARVC), |  | 3D-structure,Acetylation,Activator,Cell adhesion,Cell junction,Cell membrane,Complete proteome,Cytoplasm,Cytoskeleton,Glycoprotein,Membrane,Neurogenesis,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,S-nitrosylation,Transcription,Transcription regulation,Ubl conjugation,Wnt signaling pathway, | chain:Catenin beta-1,helix,modified residue,region of interest:Interaction with SCRIB,repeat:ARM 1,repeat:ARM 10,repeat:ARM 11,repeat:ARM 12,repeat:ARM 2,repeat:ARM 3,repeat:ARM 4,repeat:ARM 5,repeat:ARM 6,repeat:ARM 7,repeat:ARM 8,repeat:ARM 9,sequence conflict,strand,turn, |

| | A | B | C | D |
|---|---|---|---|---|
| 40 | Ctnnd1 | catenin (cadherin associated protein), delta 1(Ctnnd1) | Mus musculus | GO:0001738~morphogenesis of a polarized epithelium,GO:0001822~kidney development,GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0007155~cell adhesion,GO:0007435~salivary gland morphogenesis,GO:0010954~positive regulation of protein processing,GO:0016055~Wnt signaling pathway,GO:0016337~single organismal cell-cell adhesion,GO:0030216~keratinocyte differentiation,GO:0060690~epithelial cell differentiation involved in salivary gland development,GO:0072102~glomerulus morphogenesis,GO:0090090~negative regulation of canonical Wnt signaling pathway,GO:1900086~positive regulation of peptidyl-tyrosine autophosphorylation, |
| 41 | Cttn | cortactin(Cttn) | Mus musculus | GO:0006886~intracellular protein transport,GO:0006897~endocytosis,GO:0006898~receptor-mediated endocytosis,GO:0006930~substrate-dependent cell migration, cell extension,GO:0030041~actin filament polymerization,GO:0030516~regulation of axon extension,GO:0030838~positive regulation of actin filament polymerization,GO:0031532~actin cytoskeleton reorganization,GO:0045987~positive regulation of smooth muscle contraction,GO:0048041~focal adhesion assembly,GO:0048812~neuron projection morphogenesis,GO:0048870~cell motility,GO:0097062~dendritic spine maintenance,GO:0097581~lamellipodium organization,GO:1903146~regulation of mitophagy,GO:2001237~negative regulation of extrinsic apoptotic signaling pathway, |
| 42 | Dars | aspartyl-tRNA synthetase(Dars) | Mus musculus | GO:0006412~translation,GO:0006418~tRNA aminoacylation for protein translation,GO:0006422~aspartyl-tRNA aminoacylation, |
| 43 | Dbn1 | drebrin 1(Dbn1) | Mus musculus | GO:0007015~actin filament organization,GO:0007275~multicellular organism development,GO:0007399~nervous system development,GO:0010643~cell communication by chemical coupling,GO:0010644~cell communication by electrical coupling,GO:0010811~positive regulation of cell-substrate adhesion,GO:0010976~positive regulation of neuron projection development,GO:0030154~cell differentiation,GO:0030833~regulation of actin filament polymerization,GO:0032232~negative regulation of actin filament bundle assembly,GO:0032507~maintenance of protein location in cell,GO:0045773~positive regulation of axon extension,GO:0048699~generation of neurons,GO:0051489~regulation of filopodium assembly,GO:0060134~prepulse inhibition,GO:0061003~positive regulation of dendritic spine morphogenesis,GO:0061351~neural precursor cell proliferation,GO:0071356~cellular response to tumor necrosis factor,GO:0071560~cellular response to transforming growth factor beta stimulus,GO:0090327~negative regulation of locomotion involved in locomotory behavior,GO:0098828~modulation of inhibitory postsynaptic potential,GO:1900026~positive regulation of substrate adhesion-dependent cell spreading,GO:1902897~regulation of postsynaptic density protein 95 clustering,GO:1904113~negative regulation of muscle filament sliding,GO:1904622~negative regulation of actin-dependent ATPase activity,GO:2000463~positive regulation of excitatory postsynaptic potential, |

| | E | F | G |
|---|---|---|---|
| 40 | GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005829~cytosol,GO:0005886~plasma membrane,GO:0005911~cell-cell junction,GO:0005913~cell-cell adherens junction,GO:0005915~zonula adherens,GO:0005923~bicellular tight junction,GO:0016020~membrane,GO:0016600~flotillin complex,GO:0030027~lamellipodium,GO:0030426~growth cone,GO:0030496~midbody,GO:0043197~dendritic spine,GO:0045202~synapse,GO:0070062~extracellular exosome, | GO:0005102~receptor binding,GO:0005515~protein binding,GO:0019901~protein kinase binding,GO:0019903~protein phosphatase binding,GO:0019904~protein domain specific binding,GO:0045296~cadherin binding,GO:0050839~cell adhesion molecule binding,GO:0098641~cadherin binding involved in cell-cell adhesion, | IPR000225:Armadillo,IPR011989:Armadillo-like helical,IPR016024:Armadillo-type fold, |
| 41 | GO:0001726~ruffle,GO:0002102~podosome,GO:0005737~cytoplasm,GO:0005794~Golgi apparatus,GO:0005829~cytosol,GO:0005856~cytoskeleton,GO:0005884~actin filament,GO:0005886~plasma membrane,GO:0005905~clathrin-coated pit,GO:0005913~cell-cell adherens junction,GO:0005925~focal adhesion,GO:0005938~cell cortex,GO:0008076~voltage-gated potassium channel complex,GO:0016020~membrane,GO:0030027~lamellipodium,GO:0030054~cell junction,GO:0030426~growth cone,GO:0030863~cortical cytoskeleton,GO:0042995~cell projection,GO:0043197~dendritic spine,GO:0043231~intracellular membrane-bounded organelle,GO:0070062~extracellular exosome,GO:1990023~mitotic spindle midzone, | GO:0005515~protein binding,GO:0005522~profilin binding,GO:0070064~proline-rich region binding,GO:0071933~Arp2/3 complex binding,GO:0098641~cadherin binding involved in cell-cell adhesion, | IPR001452:Src homology-3 domain,IPR003134:Hs1/Cortactin,IPR015503:Cortactin, |
| 42 | GO:0005737~cytoplasm,GO:0016020~membrane,GO:0070062~extracellular exosome, | GO:0000166~nucleotide binding,GO:0003676~nucleic acid binding,GO:0004812~aminoacyl-tRNA ligase activity,GO:0004815~aspartate-tRNA ligase activity,GO:0005524~ATP binding,GO:0016874~ligase activity,GO:0044822~poly(A) RNA binding, | IPR002312:Aspartyl/Asparaginyl-tRNA synthetase, class IIb,IPR004364:Aminoacyl-tRNA synthetase, class II (D/K/N),IPR004365:Nucleic acid binding, OB-fold, tRNA/helicase-type,IPR004523:Aspartyl-tRNA synthetases,IPR006195:Aminoacyl-tRNA synthetase, class II,IPR012340:Nucleic acid-binding, OB-fold,IPR018150:Aminoacyl-tRNA synthetase, class II (D/K/N)-like, |
| 43 | GO:0005622~intracellular,GO:0005737~cytoplasm,GO:0005884~actin filament,GO:0005886~plasma membrane,GO:0005911~cell-cell junction,GO:0005913~cell-cell adherens junction,GO:0005921~gap junction,GO:0005938~cell cortex,GO:0014069~postsynaptic density,GO:0015629~actin cytoskeleton,GO:0016020~membrane,GO:0030027~lamellipodium,GO:0030054~cell junction,GO:0030175~filopodium,GO:0030426~growth cone,GO:0032279~asymmetric synapse,GO:0042995~cell projection,GO:0043025~neuronal cell body,GO:0043197~dendritic spine,GO:0043198~dendritic shaft,GO:0044295~axonal growth cone,GO:0044308~axonal spine,GO:0044309~neuron spine,GO:0045211~postsynaptic membrane,GO:0048471~perinuclear region of cytoplasm,GO:0060076~excitatory synapse,GO:1902737~dendritic filopodium, | GO:0003779~actin binding,GO:0005515~protein binding,GO:0005522~profilin binding,GO:0008092~cytoskeletal protein binding,GO:0051015~actin filament binding,GO:0098641~cadherin binding involved in cell-cell adhesion, | IPR002108:Actin-binding, cofilin/tropomyosin type, |

| | H | I | J | K |
|---|---|---|---|---|
| 40 | mmu04015:Rap1 signaling pathway,mmu04520:Adherens junction,mmu04670:Leukocyte transendothelial migration, | | Acetylation,Alternative splicing,Cell adhesion,Cell membrane,Coiled coil,Complete proteome,Cytoplasm,Membrane,Nucleus,Phosphoprotein, Proteomics identification,Reference proteome,Repeat,Transcription,Transcription regulation,Wnt signaling pathway, | chain:Catenin delta-1,modified residue,mutagenesis site,repeat:ARM 1,repeat:ARM 10,repeat:ARM 2,repeat:ARM 3,repeat:ARM 4,repeat:ARM 5,repeat:ARM 6,repeat:ARM 7,repeat:ARM 8,repeat:ARM 9,sequence conflict,short sequence motif:Nuclear localization signal,splice variant, |
| 41 | mmu04530:Tight junction,mmu05100:Bacterial invasion of epithelial cells,mmu05205:Proteoglycans in cancer, | | 3D-structure,Acetylation,Cell junction,Cell membrane,Cell projection,Coated pit,Coiled coil,Complete proteome,Cytoplasm,Cytoskeleton,Direct protein sequencing,Endocytosis,Isopeptide bond,Membrane,Methylation,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,SH3 domain,Ubl conjugation, | chain:Src substrate cortactin,domain:SH3,modified residue,repeat:Cortactin 1,repeat:Cortactin 2,repeat:Cortactin 3,repeat:Cortactin 4,repeat:Cortactin 5,repeat:Cortactin 6,repeat:Cortactin 7; truncated,sequence conflict, |
| 42 | mmu00970:Aminoacyl-tRNA biosynthesis, | | Acetylation,Aminoacyl-tRNA synthetase,ATP-binding,Complete proteome,Cytoplasm,Ligase,Nucleotide-binding,Phosphoprotein,Protein biosynthesis,Proteomics identification,Reference proteome, | chain:Aspartyl-tRNA synthetase, cytoplasmic,modified residue, |
| 43 | | | Acetylation,Actin-binding,Alternative splicing,Cell junction,Cell projection,Coiled coil,Complete proteome,Cytoplasm,Developmental protein,Differentiation,Direct protein sequencing,Neurogenesis,Phosphoprotein,Proteomics identification,Reference proteome, | chain:Drebrin,domain:ADF-H,modified residue,sequence conflict,splice variant, |

| | A | B | C | D |
|---|---|---|---|---|
| 44 | Ddx21 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 21(Ddx21) | Mus musculus | GO:0001649~osteoblast differentiation,GO:0006351~transcription, DNA-templated,GO:0006364~rRNA processing,GO:0006366~transcription from RNA polymerase II promoter,GO:0009615~response to virus,GO:0010501~RNA secondary structure unwinding,GO:0043330~response to exogenous dsRNA, |
| 45 | Ddx23 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 23(Ddx23) | Mus musculus | GO:0000375~RNA splicing, via transesterification reactions,GO:0010501~RNA secondary structure unwinding, |
| 46 | Ddx39 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 39(Ddx39) | Mus musculus | GO:0000398~mRNA splicing, via spliceosome,GO:0006397~mRNA processing,GO:0006406~mRNA export from nucleus,GO:0006974~cellular response to DNA damage stimulus,GO:0008380~RNA splicing,GO:0010468~regulation of gene expression,GO:0010501~RNA secondary structure unwinding, |
| 47 | Ddx39a | afadin, adherens junction formation factor(AFDN) | Homo sapiens | GO:0007155~cell adhesion,GO:0007165~signal transduction,GO:0007267~cell-cell signaling,GO:0021987~cerebral cortex development,GO:0032880~regulation of protein localization,GO:0034332~adherens junction organization,GO:0034334~adherens junction maintenance,GO:0043547~positive regulation of GTPase activity,GO:0048854~brain morphogenesis,GO:0048872~homeostasis of number of cells,GO:0060019~radial glial cell differentiation,GO:0060563~neuroepithelial cell differentiation,GO:0070445~regulation of oligodendrocyte progenitor proliferation,GO:0090557~establishment of endothelial intestinal barrier,GO:0098609~cell-cell adhesion, |
| 48 | Ddx5 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 5(Ddx5) | Mus musculus | GO:0000122~negative regulation of transcription from RNA polymerase II promoter,GO:0000381~regulation of alternative mRNA splicing, via spliceosome,GO:0001701~in utero embryonic development,GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0006357~regulation of transcription from RNA polymerase II promoter,GO:0006397~mRNA processing,GO:0007623~circadian rhythm,GO:0008380~RNA splicing,GO:0009299~mRNA transcription,GO:0010501~RNA secondary structure unwinding,GO:0033148~positive regulation of intracellular estrogen receptor signaling pathway,GO:0043517~positive regulation of DNA damage response, signal transduction by p53 class mediator,GO:0045069~regulation of viral genome replication,GO:0045667~regulation of osteoblast differentiation,GO:0045893~positive regulation of transcription, DNA-templated,GO:0045944~positive regulation of transcription from RNA polymerase II promoter,GO:0048511~rhythmic process,GO:0060765~regulation of androgen receptor signaling pathway,GO:0072332~intrinsic apoptotic signaling pathway by p53 class mediator,GO:2001014~regulation of skeletal muscle cell differentiation, |
| 49 | Ddx51 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 51(Ddx51) | Mus musculus | GO:0006364~rRNA processing,GO:0010501~RNA secondary structure unwinding,GO:0042254~ribosome biogenesis, |

| | E | F | G |
|---|---|---|---|
| 44 | GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005730~nucleolus,GO:0016020~membrane, | GO:0000166~nucleotide binding,GO:0003676~nucleic acid binding,GO:0003723~RNA binding,GO:0003724~RNA helicase activity,GO:0003725~double-stranded RNA binding,GO:0004004~ATP-dependent RNA helicase activity,GO:0004386~helicase activity,GO:0005515~protein binding,GO:0005524~ATP binding,GO:0016787~hydrolase activity,GO:0019843~rRNA binding,GO:0030515~snoRNA binding,GO:0044822~poly(A) RNA binding,GO:0097322~7SK snRNA binding, | IPR001650:Helicase, C-terminal,IPR011545:DNA/RNA helicase, DEAD/DEAH box type, N-terminal,IPR012562:GUCT,IPR012677:Nucleotide-binding, alpha-beta plait,IPR014001:Helicase, superfamily 1/2, ATP-binding domain,IPR014014:RNA helicase, DEAD-box type, Q motif,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |
| 45 | GO:0005634~nucleus,GO:0005682~U5 snRNP,GO:0005730~nucleolus,GO:0046540~U4/U6 x U5 tri-snRNP complex,GO:0070062~extracellular exosome,GO:0071013~catalytic step 2 spliceosome, | GO:0004004~ATP-dependent RNA helicase activity,GO:0005524~ATP binding,GO:0044822~poly(A) RNA binding, | IPR000629:RNA helicase, ATP-dependent, DEAD-box, conserved site,IPR001650:Helicase, C-terminal,IPR011545:DNA/RNA helicase, DEAD/DEAH box type, N-terminal,IPR014001:Helicase, superfamily 1/2, ATP-binding domain,IPR014014:RNA helicase, DEAD-box type, Q motif,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |
| 46 | GO:0005634~nucleus,GO:0005681~spliceosomal complex,GO:0005737~cytoplasm,GO:0016020~membrane, | GO:0000166~nucleotide binding,GO:0003676~nucleic acid binding,GO:0004004~ATP-dependent RNA helicase activity,GO:0004386~helicase activity,GO:0005524~ATP binding,GO:0016787~hydrolase activity,GO:0016887~ATPase activity,GO:0044822~poly(A) RNA binding, | IPR001650:Helicase, C-terminal,IPR011545:DNA/RNA helicase, DEAD/DEAH box type, N-terminal,IPR014001:Helicase, superfamily 1/2, ATP-binding domain,IPR014014:RNA helicase, DEAD-box type, Q motif,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |
| 47 | GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0005829~cytosol,GO:0005886~plasma membrane,GO:0005911~cell-cell junction,GO:0005913~cell-cell adherens junction,GO:0030054~cell junction,GO:0045177~apical part of cell, | GO:0005515~protein binding,GO:0008022~protein C-terminus binding,GO:0017016~Ras GTPase binding,GO:0098641~cadherin binding involved in cell-cell adhesion, | IPR000159:Ras-association,IPR000253:Forkhead-associated (FHA) domain,IPR001478:PDZ domain,IPR002710:Dilute,IPR008984:SMAD/FHA domain, |
| 48 | GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005681~spliceosomal complex,GO:0005730~nucleolus,GO:0016020~membrane,GO:0030529~intracellular ribonucleoprotein complex,GO:0031012~extracellular matrix,GO:0070062~extracellular exosome,GO:0071013~catalytic step 2 spliceosome, | GO:0000166~nucleotide binding,GO:0003676~nucleic acid binding,GO:0003712~transcription cofactor activity,GO:0003713~transcription coactivator activity,GO:0003723~RNA binding,GO:0003724~RNA helicase activity,GO:0004004~ATP-dependent RNA helicase activity,GO:0004386~helicase activity,GO:0005515~protein binding,GO:0005516~calmodulin binding,GO:0005524~ATP binding,GO:0016787~hydrolase activity,GO:0019899~enzyme binding,GO:0030331~estrogen receptor binding,GO:0036002~pre-mRNA binding,GO:0044822~poly(A) RNA binding,GO:0048306~calcium-dependent protein binding,GO:0050681~androgen receptor binding, | IPR000629:RNA helicase, ATP-dependent, DEAD-box, conserved site,IPR001650:Helicase, C-terminal,IPR011545:DNA/RNA helicase, DEAD/DEAH box type, N-terminal,IPR012587:P68HR,IPR014001:Helicase, superfamily 1/2, ATP-binding domain,IPR014014:RNA helicase, DEAD-box type, Q motif,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |
| 49 | GO:0005634~nucleus,GO:0005730~nucleolus,GO:0016020~membrane, | GO:0000166~nucleotide binding,GO:0003676~nucleic acid binding,GO:0003723~RNA binding,GO:0004004~ATP-dependent RNA helicase activity,GO:0004386~helicase activity,GO:0005524~ATP binding,GO:0016787~hydrolase activity,GO:0044822~poly(A) RNA binding, | IPR000629:RNA helicase, ATP-dependent, DEAD-box, conserved site,IPR001650:Helicase, C-terminal,IPR011545:DNA/RNA helicase, DEAD/DEAH box type, N-terminal,IPR014001:Helicase, superfamily 1/2, ATP-binding domain,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |

|  | H | I | J | K |
|---|---|---|---|---|
| 44 |  |  | 3D-structure,Acetylation,ATP-binding,Complete proteome,Helicase,Hydrolase,Nucleotide-binding,Nucleus,Phosphoprotein,Reference proteome,Repeat,RNA-binding,rRNA processing,Transcription, | chain:Nucleolar RNA helicase 2,compositionally biased region:Poly-Lys,domain:Helicase ATP-binding,domain:Helicase C-terminal,modified residue,nucleotide phosphate-binding region:ATP,region of interest:3 X 37 AA tandem repeats,region of interest:3 X 5 AA repeats,repeat:1-1,repeat:1-2,repeat:1-3,repeat:2-1,repeat:2-2,repeat:2-3,sequence conflict,short sequence motif:DEVD box,short sequence motif:Q motif, |
| 45 | mmu03040:Spliceosome, |  | Coiled coil,Complete proteome,Proteomics identification,Reference proteome, |  |
| 46 |  |  | Acetylation,Alternative splicing,ATP-binding,Complete proteome,Cytoplasm,Helicase,Hydrolase,Isopeptide bond,mRNA processing,mRNA splicing,Nucleotide-binding,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Ubl conjugation, | chain:ATP-dependent RNA helicase DDX39,domain:Helicase ATP-binding,domain:Helicase C-terminal,modified residue,nucleotide phosphate-binding region:ATP,short sequence motif:DECD box,short sequence motif:Q motif,splice variant, |
| 47 | hsa04014:Ras signaling pathway,hsa04015:Rap1 signaling pathway,hsa04024:cAMP signaling pathway,hsa04520:Adherens junction,hsa04530:Tight junction,hsa04670:Leukocyte transendothelial migration, | SM00228:PDZ,SM00240:FHA,SM00314:RA,SM01132:SM01132, | 3D-structure,Acetylation,Alternative splicing,Cell adhesion,Cell junction,Chromosomal rearrangement,Coiled coil,Complete proteome,Phosphoprotein,Proteomics identification,Proto-oncogene,Reference proteome,Repeat, | chain:Afadin,compositionally biased region:Asp/Glu-rich (acidic),compositionally biased region:Glu/Lys-rich,compositionally biased region:Pro-rich,domain:Dilute,domain:FHA,domain:PDZ,domain:Ras-associating 1,domain:Ras-associating 2,helix,modified residue,sequence conflict,site:Breakpoint for translocation to form MLL- MLLT4,splice variant,strand, |
| 48 | mmu03040:Spliceosome,mmu05202:Transcriptional misregulation in cancer,mmu05205:Proteoglycans in cancer, |  | Acetylation,ATP-binding,Biological rhythms,Complete proteome,Helicase,Hydrolase,Isopeptide bond,Methylation,mRNA processing,mRNA splicing,Nucleotide-binding,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,RNA-binding,Spliceosome,Transcription,Transcription regulation,Ubl conjugation, | chain:Probable ATP-dependent RNA helicase DDX5,domain:Helicase ATP-binding,domain:Helicase C-terminal,modified residue,nucleotide phosphate-binding region:ATP,short sequence motif:DEAD box,short sequence motif:Q motif, |
| 49 |  |  | Acetylation,ATP-binding,Complete proteome,Helicase,Hydrolase,Nucleotide-binding,Nucleus,Phosphoprotein,Reference proteome,Ribosome biogenesis,RNA-binding,rRNA processing, | chain:ATP-dependent RNA helicase DDX51,compositionally biased region:Arg-rich,domain:Helicase ATP-binding,domain:Helicase C-terminal,nucleotide phosphate-binding region:ATP,sequence conflict,short sequence motif:DEAD box,short sequence motif:Q motif, |

| | A | B | C | D |
|---|---|---|---|---|
| 50 | Dhx15 | DEAH (Asp-Glu-Ala-His) box polypeptide 15(Dhx15) | Mus musculus | GO:0000398~mRNA splicing, via spliceosome,GO:0006397~mRNA processing,GO:0008380~RNA splicing,GO:0009636~response to toxic substance,GO:0043279~response to alkaloid, |
| 51 | Dnajc24 | DnaJ heat shock protein family (Hsp40) member C24(Dnajc24) | Mus musculus | GO:0006810~transport,GO:0017183~peptidyl-diphthamide biosynthetic process from peptidyl-histidine,GO:0032781~positive regulation of ATPase activity,GO:0055114~oxidation-reduction process, |
| 52 | Dnajc8 | DnaJ heat shock protein family (Hsp40) member C8(Dnajc8) | Mus musculus | |
| 53 | Dnmt1 | DNA methyltransferase (cytosine-5) 1(Dnmt1) | Mus musculus | GO:0000122~negative regulation of transcription from RNA polymerase II promoter,GO:0000183~chromatin silencing at rDNA,GO:0006306~DNA methylation,GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0007265~Ras protein signal transduction,GO:0008152~metabolic process,GO:0010216~maintenance of DNA methylation,GO:0010424~DNA methylation on cytosine within a CG sequence,GO:0010468~regulation of gene expression,GO:0010628~positive regulation of gene expression,GO:0016458~gene silencing,GO:0016569~covalent chromatin modification,GO:0032259~methylation,GO:0032776~DNA methylation on cytosine,GO:0042127~regulation of cell proliferation,GO:0042493~response to drug,GO:0043045~DNA methylation involved in embryo development,GO:0044026~DNA hypermethylation,GO:0045892~negative regulation of transcription, DNA-templated,GO:0046498~S-adenosylhomocysteine metabolic process,GO:0046499~S-adenosylmethioninamine metabolic process,GO:0046500~S-adenosylmethionine metabolic process,GO:0051571~positive regulation of histone H3-K4 methylation,GO:0051573~negative regulation of histone H3-K9 methylation,GO:0071230~cellular response to amino acid stimulus,GO:0071560~cellular response to transforming growth factor beta stimulus,GO:0090116~C-5 methylation of cytosine,GO:0090309~positive regulation of methylation-dependent chromatin silencing, |
| 54 | Dpf2 | D4, zinc and double PHD fingers family 2(Dpf2) | Mus musculus | GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0006915~apoptotic process, |
| 55 | Dynlrb1 | dynein light chain roadblock-type 1(Dynlrb1) | Mus musculus | GO:0006810~transport,GO:0007018~microtubule-based movement,GO:0007632~visual behavior, |

|  | E | F | G |
|---|---|---|---|
| 50 | GO:0005634~nucleus,GO:0005681~spliceosomal complex,GO:0005689~U12-type spliceosomal complex,GO:0005730~nucleolus,GO:0005737~cytoplasm,GO:0071008~U2-type post-mRNA release spliceosomal complex, | GO:0000166~nucleotide binding,GO:0003676~nucleic acid binding,GO:0003725~double-stranded RNA binding,GO:0004004~ATP-dependent RNA helicase activity,GO:0004386~helicase activity,GO:0005524~ATP binding,GO:0008026~ATP-dependent helicase activity,GO:0016787~hydrolase activity,GO:0044822~poly(A) RNA binding, | IPR001650:Helicase, C-terminal,IPR002464:DNA/RNA helicase, ATP-dependent, DEAH-box type, conserved site,IPR007502:Helicase-associated domain,IPR011545:DNA/RNA helicase, DEAD/DEAH box type, N-terminal,IPR011709:Domain of unknown function DUF1605,IPR014001:Helicase, superfamily 1/2, ATP-binding domain,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |
| 51 | GO:0005737~cytoplasm,GO:0005856~cytoskeleton, | GO:0001671~ATPase activator activity,GO:0008198~ferrous iron binding,GO:0008270~zinc ion binding,GO:0046872~metal ion binding, | IPR001623:DnaJ domain,IPR007872:Zinc finger, DPH-type, |
| 52 | GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0045171~intercellular bridge, |  | IPR001623:DnaJ domain, |
| 53 | GO:0000792~heterochromatin,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005657~replication fork,GO:0005721~pericentric heterochromatin,GO:0005737~cytoplasm,GO:0043025~neuronal cell body,GO:0043234~protein complex, | GO:0003677~DNA binding,GO:0003682~chromatin binding,GO:0003690~double-stranded DNA binding,GO:0003723~RNA binding,GO:0003824~catalytic activity,GO:0003886~DNA (cytosine-5-)-methyltransferase activity,GO:0005515~protein binding,GO:0008168~methyltransferase activity,GO:0008270~zinc ion binding,GO:0008327~methyl-CpG binding,GO:0009008~DNA-methyltransferase activity,GO:0016740~transferase activity,GO:0019904~protein domain specific binding,GO:0030331~estrogen receptor binding,GO:0042826~histone deacetylase binding,GO:0045322~unmethylated CpG binding,GO:0046872~metal ion binding,GO:0051718~DNA (cytosine-5-)-methyltransferase activity, acting on CpG substrates,GO:1990841~promoter-specific chromatin binding, | IPR001025:Bromo adjacent homology (BAH) domain,IPR001525:C-5 cytosine methyltransferase,IPR002857:Zinc finger, CXXC-type,IPR010506:DMAP1-binding,IPR017198:DNA (cytosine-5)-methyltransferase 1, eukaryote,IPR018117:DNA methylase, C-5 cytosine-specific, active site,IPR022702:DNA (cytosine-5)-methyltransferase 1, replication foci domain, |
| 54 | GO:0000790~nuclear chromatin,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0005813~centrosome,GO:0043231~intracellular membrane-bounded organelle,GO:0090544~BAF-type complex, | GO:0000978~RNA polymerase II core promoter proximal region sequence-specific DNA binding,GO:0003676~nucleic acid binding,GO:0008270~zinc ion binding,GO:0046872~metal ion binding, | IPR001965:Zinc finger, PHD-type,IPR007087:Zinc finger, C2H2,IPR011011:Zinc finger, FYVE/PHD-type,IPR013083:Zinc finger, RING/FYVE/PHD-type,IPR015880:Zinc finger, C2H2-like,IPR019787:Zinc finger, PHD-finger,IPR025750:Requiem/DPF N-terminal domain, |
| 55 | GO:0005737~cytoplasm,GO:0005813~centrosome,GO:0005856~cytoskeleton,GO:0005868~cytoplasmic dynein complex,GO:0005874~microtubule,GO:0016020~membrane,GO:0030286~dynein complex, | GO:0003774~motor activity,GO:0005515~protein binding,GO:0042802~identical protein binding,GO:0045505~dynein intermediate chain binding, | IPR004942:Dynein light chain-related,IPR016561:Dynein light chain, roadblock-type, |

|  | H | I | J | K |
|---|---|---|---|---|
| 50 | mmu03040:Spliceosome, |  | Acetylation,ATP-binding,Complete proteome,Helicase,Hydrolase,mRNA processing,mRNA splicing,Nucleotide-binding,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome, | chain:Putative pre-mRNA-splicing factor ATP- dependent RNA helicase DHX15,compositionally biased region:Poly-Gln,compositionally biased region:Poly-Glu,compositionally biased region:Poly-Pro,domain:Helicase ATP-binding,domain:Helicase C-terminal,modified residue,nucleotide phosphate-binding region:ATP,sequence conflict,short sequence motif:DEAH box, |
| 51 |  |  | 3D-structure,Complete proteome,Cytoplasm,Cytoskeleton,Electron transport,Iron,Metal-binding,Proteomics identification,Reference proteome,Transport,Zinc,Zinc-finger, | chain:DnaJ homolog subfamily C member 24,domain:J,helix,sequence conflict,splice variant,strand,zinc finger region:DPH-type, |
| 52 |  |  | Acetylation,Chaperone,Coiled coil,Complete proteome,Phosphoprotein,Proteomics identification,Reference proteome, | chain:DnaJ homolog subfamily C member 8,domain:J,modified residue,sequence conflict, |
| 53 | mmu00270:Cysteine and methionine metabolism,mmu01100:Metabolic pathways,mmu05206:MicroRNAs in cancer, | PIRSF037404:DNA (cytosine-5)-methyltransferase 1, DNMT1 type, | 3D-structure,Acetylation,Activator,Allosteric enzyme,Alternative splicing,Chromatin regulator,Complete proteome,Cytoplasm,Direct protein sequencing,DNA-binding,Isopeptide bond,Metal-binding,Methylation,Methyltransferase,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,Repressor,S-adenosyl-L-methionine,Transcription,Transcription regulation,Transferase,Ubl conjugation,Zinc,Zinc-finger, | chain:DNA (cytosine-5)-methyltransferase 1,domain:BAH 1,domain:BAH 2,metal ion-binding site:Zinc,modified residue,mutagenesis site,region of interest:7 X 2 AA tandem repeats of K-G,region of interest:Catalytic,region of interest:DNA replication foci-targeting sequence,region of interest:Interaction with DMAP1,region of interest:Interaction with DNMT3A,region of interest:Interaction with DNMT3B,region of interest:Interaction with HDAC1,region of interest:Interaction with PCNA,region of interest:Interaction with the PRC2/EED-EZH2 complex,repeat:1,repeat:2,repeat:3,repeat:4,repeat:5,repeat:6,repeat:7; approximate,sequence conflict,short sequence motif:Nuclear localization signal,splice variant,zinc finger region:CXXC-type, |
| 54 |  |  | Acetylation,Apoptosis,Complete proteome,Cytoplasm,Isopeptide bond,Metal-binding,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,Transcription,Transcription regulation,Ubl conjugation,Zinc,Zinc-finger, | chain:Zinc finger protein ubi-d4,modified residue,sequence conflict,zinc finger region:C2H2-type,zinc finger region:PHD-type 1,zinc finger region:PHD-type 2, |
| 55 |  | PIRSF009998:cytoplasmic dynein light chain, LC7 type, | 3D-structure,Acetylation,Complete proteome,Cytoplasm,Cytoskeleton,Dynein,Microtubule,Motor protein,Proteomics identification,Reference proteome,Transport, | chain:Dynein light chain roadblock-type 1,helix,modified residue,sequence conflict,strand,turn, |

| | A | B | C | D |
|---|---|---|---|---|
| 56 | Eftud2 | elongation factor Tu GTP binding domain containing 2(Eftud2) | Mus musculus | GO:0006397~mRNA processing,GO:0008380~RNA splicing,GO:0035690~cellular response to drug,GO:0042220~response to cocaine, |
| 57 | Eif1ax | eukaryotic translation initiation factor 1A, X-linked(Eif1ax) | Mus musculus | GO:0006412~translation,GO:0006413~translational initiation, |
| 58 | Eif3a | eukaryotic translation initiation factor 3, subunit A(Eif3a) | Mus musculus | GO:0001731~formation of translation preinitiation complex,GO:0001732~formation of cytoplasmic translation initiation complex,GO:0002188~translation reinitiation,GO:0006412~translation,GO:0006413~translational initiation,GO:0006446~regulation of translational initiation,GO:0070373~negative regulation of ERK1 and ERK2 cascade,GO:0075522~IRES-dependent viral translational initiation,GO:0075525~viral translational termination-reinitiation, |
| 59 | Eif3i | eukaryotic translation initiation factor 3, subunit I(Eif3i) | Mus musculus | GO:0001731~formation of translation preinitiation complex,GO:0006412~translation,GO:0006413~translational initiation,GO:0006446~regulation of translational initiation, |
| 60 | Erc1 | ELKS/RAB6-interacting/CAST family member 1(Erc1) | Mus musculus | GO:0006810~transport,GO:0007252~I-kappaB phosphorylation,GO:0015031~protein transport,GO:0042147~retrograde transport, endosome to Golgi,GO:0098609~cell-cell adhesion, |
| 61 | Esam | endothelial cell-specific adhesion molecule(Esam) | Mus musculus | GO:0007155~cell adhesion,GO:0007156~homophilic cell adhesion via plasma membrane adhesion molecules,GO:0016337~single organismal cell-cell adhesion,GO:0016338~calcium-independent cell-cell adhesion via plasma membrane cell-adhesion molecules, |
| 62 | Esd | esterase D/formylglutathione hydrolase(Esd) | Mus musculus | GO:0046294~formaldehyde catabolic process, |

|  | E | F | G |
|---|---|---|---|
| 56 | GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005681~spliceosomal complex,GO:0005737~cytoplasm,GO:0015030~Cajal body,GO:0016020~membrane,GO:0016607~nuclear speck,GO:0031012~extracellular matrix,GO:0071013~catalytic step 2 spliceosome, | GO:0000166~nucleotide binding,GO:0003746~translation elongation factor activity,GO:0003924~GTPase activity,GO:0005515~protein binding,GO:0005525~GTP binding,GO:0044822~poly(A) RNA binding, | IPR000640:Translation elongation factor EFG, V domain,IPR000795:Elongation factor, GTP-binding domain,IPR004161:Translation elongation factor EFTu/EF1A, domain 2,IPR005225:Small GTP-binding protein domain,IPR005517:Translation elongation factor EFG/EF2, domain IV,IPR009000:Translation elongation/initiation factor/Ribosomal, beta-barrel,IPR009022:Elongation factor G, III-V domain,IPR014721:Ribosomal protein S5 domain 2-type fold, subgroup,IPR020568:Ribosomal protein S5 domain 2-type fold,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |
| 57 |  | GO:0003723~RNA binding,GO:0003743~translation initiation factor activity,GO:0044822~poly(A) RNA binding, | IPR001253:Translation initiation factor 1A (eIF-1A),IPR006196:RNA-binding domain, S1, IF1 type,IPR012340:Nucleic acid-binding, OB-fold,IPR018104:Translation initiation factor 1A (eIF-1A), conserved site, |
| 58 | GO:0005634~nucleus,GO:0005730~nucleolus,GO:0005737~cytoplasm, GO:0005815~microtubule organizing center,GO:0005852~eukaryotic translation initiation factor 3 complex,GO:0005856~cytoskeleton,GO:0005874~microtubule,GO:0016020~membrane,GO:0016282~eukaryotic 43S preinitiation complex,GO:0033290~eukaryotic 48S preinitiation complex,GO:0043614~multi-eIF complex,GO:0071540~eukaryotic translation initiation factor 3 complex, eIF3e,GO:0071541~eukaryotic translation initiation factor 3 complex, eIF3m, | GO:0003723~RNA binding,GO:0003729~mRNA binding,GO:0003743~translation initiation factor activity,GO:0005515~protein binding,GO:0030971~receptor tyrosine kinase binding,GO:0044822~poly(A) RNA binding, | IPR000717:Proteasome component (PCI) domain,IPR027512:Eukaryotic translation initiation factor 3 subunit A, |
| 59 | GO:0005737~cytoplasm,GO:0005852~eukaryotic translation initiation factor 3 complex,GO:0016282~eukaryotic 43S preinitiation complex,GO:0033290~eukaryotic 48S preinitiation complex,GO:0070062~extracellular exosome,GO:0071541~eukaryotic translation initiation factor 3 complex, eIF3m, | GO:0003743~translation initiation factor activity,GO:0019899~enzyme binding, | IPR001680:WD40 repeat,IPR015943:WD40/YVTN repeat-like-containing domain,IPR017986:WD40-repeat-containing domain,IPR019775:WD40 repeat, conserved site,IPR027525:Eukaryotic translation initiation factor 3 subunit I, |
| 60 | GO:0000139~Golgi membrane,GO:0005737~cytoplasm,GO:0005794~Golgi apparatus,GO:0005913~cell-cell adherens junction,GO:0008385~IkappaB kinase complex,GO:0016020~membrane,GO:0045202~synapse,GO:0048786~presynaptic active zone, | GO:0005515~protein binding,GO:0017137~Rab GTPase binding,GO:0030165~PDZ domain binding,GO:0098641~cadherin binding involved in cell-cell adhesion, | IPR019018:Rab-binding domain FIP-RBD,IPR019323:CAZ complex, RIM-binding protein, |
| 61 | GO:0005886~plasma membrane,GO:0005912~adherens junction,GO:0005923~bicellular tight junction,GO:0016020~membrane,GO:0016021~integral component of membrane,GO:0030054~cell junction,GO:0070062~extracellular exosome, |  | IPR003598:Immunoglobulin subtype 2,IPR003599:Immunoglobulin subtype,IPR007110:Immunoglobulin-like domain,IPR013106:Immunoglobulin V-set,IPR013783:Immunoglobulin-like fold, |
| 62 | GO:0005737~cytoplasm,GO:0016023~cytoplasmic, membrane-bounded vesicle,GO:0031410~cytoplasmic vesicle,GO:0070062~extracellular exosome, | GO:0016787~hydrolase activity,GO:0016788~hydrolase activity, acting on ester bonds,GO:0018738~S-formylglutathione hydrolase activity,GO:0052689~carboxylic ester hydrolase activity, | IPR000801:Putative esterase,IPR014186:S-formylglutathione hydrolase, |

| | H | I | J | K |
|---|---|---|---|---|
| 56 | mmu03040:Spliceosome, | | Acetylation,Complete proteome,Elongation factor,GTP-binding,Isopeptide bond,mRNA processing,mRNA splicing,Nucleotide-binding,Nucleus,Phosphoprotein,Protein biosynthesis,Proteomics identification,Reference proteome,Spliceosome,Ubl conjugation, | chain:116 kDa U5 small nuclear ribonucleoprotein component,modified residue,nucleotide phosphate-binding region:GTP, |
| 57 | mmu03013:RNA transport, | | Complete proteome,Initiation factor,Isopeptide bond,Protein biosynthesis,Reference proteome,Ubl conjugation, | chain:Eukaryotic translation initiation factor 1A, X-chromosomal,domain:S1-like,sequence conflict, |
| 58 | mmu03013:RNA transport, | | Acetylation,Coiled coil,Complete proteome,Cytoplasm,Cytoskeleton,Initiation factor,Nucleus,Phosphoprotein,Protein biosynthesis,Reference proteome,Repeat,RNA editing,RNA-binding, | chain:Eukaryotic translation initiation factor 3 subunit A,compositionally biased region:Asp-rich,compositionally biased region:Glu-rich,domain:PCI,modified residue,region of interest:21 X 10 AA approximate tandem repeats of [DA]-[DE]-[ED]-R-[PLIGFSV]-[RPS]-[RW]- [RL]-[GNIHT]-[DGLPTAM],region of interest:Interaction with EIF3B,repeat:10,repeat:11,repeat:12,repeat:13,repeat:14,repeat:15,repeat:16,repeat:17,repeat:18,repeat:19,repeat:1; truncated,repeat:2,repeat:20,repeat:21; approximate,repeat:3; approximate,repeat:4,repeat:5,repeat:6,repeat:7,repeat:8,repeat:9,sequence conflict, |
| 59 | mmu03013:RNA transport, | | Acetylation,Complete proteome,Cytoplasm,Direct protein sequencing,Initiation factor,Isopeptide bond,Phosphoprotein,Protein biosynthesis,Proteomics identification,Reference proteome,Repeat,Ubl conjugation,WD repeat, | chain:Eukaryotic translation initiation factor 3 subunit I,cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin),modified residue,repeat:WD 1,repeat:WD 2,repeat:WD 3,repeat:WD 4,repeat:WD 5, |
| 60 | mmu04064:NF-kappa B signaling pathway, | | Acetylation,Alternative splicing,Coiled coil,Complete proteome,Cytoplasm,Golgi apparatus,Membrane,Phosphoprotein,Protein transport,Proteomics identification,Reference proteome,Transport, | chain:ELKS/RAB6-interacting/CAST family member 1,modified residue,sequence conflict,splice variant, |
| 61 | mmu04514:Cell adhesion molecules (CAMs),mmu04670:Leukocyte transendothelial migration, | | Cell adhesion,Cell junction,Cell membrane,Complete proteome,Disulfide bond,Glycoprotein,Immunoglobulin domain,Membrane,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,Signal,Tight junction,Transmembrane,Transmembrane helix, | chain:Endothelial cell-selective adhesion molecule,disulfide bond,domain:Ig-like C2-type,domain:Ig-like V-type,glycosylation site:N-linked (GlcNAc...),signal peptide,topological domain:Cytoplasmic,topological domain:Extracellular,transmembrane region, |
| 62 | mmu01200:Carbon metabolism, | | Acetylation,Complete proteome,Cytoplasm,Cytoplasmic vesicle,Hydrolase,Proteomics identification,Reference proteome,Serine esterase, | active site:Charge relay system,chain:S-formylglutathione hydrolase,modified residue,sequence conflict, |

| | A | B | C | D |
|---|---|---|---|---|
| 63 | Etf1 | eukaryotic translation termination factor 1(Etf1) | Mus musculus | GO:0000184~nuclear-transcribed mRNA catabolic process, nonsense-mediated decay,GO:0006412~translation,GO:0006415~translational termination,GO:0006479~protein methylation,GO:0016032~viral process, |
| 64 | Etfb | electron transferring flavoprotein, beta polypeptide(Etfb) | Mus musculus | GO:0006810~transport,GO:0033539~fatty acid beta-oxidation using acyl-CoA dehydrogenase,GO:0055114~oxidation-reduction process, |
| 65 | Fabp5 | fatty acid binding protein 5, epidermal(Fabp5) | Mus musculus | GO:0006006~glucose metabolic process,GO:0006629~lipid metabolic process,GO:0006656~phosphatidylcholine biosynthetic process,GO:0006810~transport,GO:0009611~response to wounding,GO:0015758~glucose transport, |
| 66 | Fermt2 | fermitin family member 2(Fermt2) | Mus musculus | GO:0007155~cell adhesion,GO:0007160~cell-matrix adhesion,GO:0007179~transforming growth factor beta receptor signaling pathway,GO:0007229~integrin-mediated signaling pathway,GO:0008360~regulation of cell shape,GO:0016055~Wnt signaling pathway,GO:0033622~integrin activation,GO:0034446~substrate adhesion-dependent cell spreading,GO:0048041~focal adhesion assembly,GO:0072657~protein localization to membrane, |
| 67 | Fubp1 | far upstream element (FUSE) binding protein 1(Fubp1) | Mus musculus | GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0006357~regulation of transcription from RNA polymerase II promoter,GO:0010628~positive regulation of gene expression,GO:0016049~cell growth,GO:0017145~stem cell division,GO:0071425~hematopoietic stem cell proliferation, |
| 68 | Fubp3 | far upstream element (FUSE) binding protein 3(Fubp3) | Mus musculus | GO:0006351~transcription, DNA-templated,GO:0010628~positive regulation of gene expression,GO:0045893~positive regulation of transcription, DNA-templated,GO:0045944~positive regulation of transcription from RNA polymerase II promoter, |
| 69 | Gcn1l1 | GCN1 general control of amino-acid synthesis 1-like 1 (yeast)(Gcn1l1) | Mus musculus | GO:0006417~regulation of translation,GO:0033554~cellular response to stress,GO:0033674~positive regulation of kinase activity,GO:0034198~cellular response to amino acid starvation,GO:0036003~positive regulation of transcription from RNA polymerase II promoter in response to stress,GO:1990253~cellular response to leucine starvation, |
| 70 | Gdi2 | guanosine diphosphate (GDP) dissociation inhibitor 2(Gdi2) | Mus musculus | GO:0007264~small GTPase mediated signal transduction,GO:0015031~protein transport,GO:0016192~vesicle-mediated transport,GO:0055114~oxidation-reduction process, |

|  | E | F | G |
|---|---|---|---|
| 63 | GO:0005737~cytoplasm, | GO:0003747~translation release factor activity,GO:0016149~translation release factor activity, codon specific,GO:0044822~poly(A) RNA binding, | IPR004403:Peptide chain release factor eRF1/aRF1,IPR005140:eRF1 domain 1/Pelota-like,IPR005141:eRF1 domain 2,IPR005142:eRF1 domain 3,IPR024049:Peptide Chain Release Factor eRF1/aRF1, N-terminal, |
| 64 | GO:0005739~mitochondrion,GO:0005759~mitochondrial matrix,GO:0017133~mitochondrial electron transfer flavoprotein complex,GO:0043231~intracellular membrane-bounded organelle,GO:0070062~extracellular exosome, | GO:0009055~electron carrier activity, | IPR000049:Electron transfer flavoprotein, beta-subunit, conserved site,IPR012255:Electron transfer flavoprotein, beta subunit,IPR014729:Rossmann-like alpha/beta/alpha sandwich fold,IPR014730:Electron transfer flavoprotein, alpha/beta-subunit, N-terminal, |
| 65 | GO:0005737~cytoplasm,GO:0070062~extracellular exosome, | GO:0005215~transporter activity,GO:0005504~fatty acid binding,GO:0008289~lipid binding, | IPR000463:Cytosolic fatty-acid binding,IPR000566:Lipocalin/cytosolic fatty-acid binding protein domain,IPR011038:Calycin-like,IPR012674:Calycin, |
| 66 | GO:0001725~stress fiber,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0005856~cytoskeleton,GO:0005886~plasma membrane,GO:0005925~focal adhesion,GO:0005938~cell cortex,GO:0009986~cell surface,GO:0016020~membrane,GO:0030054~cell junction,GO:0031234~extrinsic component of cytoplasmic side of plasma membrane,GO:0031258~lamellipodium membrane,GO:0031674~I band,GO:0031941~filamentous actin,GO:0042995~cell projection, | GO:0005547~phosphatidylinositol-3,4,5-trisphosphate binding,GO:0008289~lipid binding, | IPR001849:Pleckstrin homology domain,IPR011993:Pleckstrin homology-like domain,IPR014352:FERM/acyl-CoA-binding protein, 3-helical bundle,IPR019748:FERM central domain,IPR019749:Band 4.1 domain, |
| 67 | GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0016021~integral component of membrane, | GO:0001205~transcriptional activator activity, RNA polymerase II distal enhancer sequence-specific binding,GO:0003676~nucleic acid binding,GO:0003677~DNA binding,GO:0003723~RNA binding,GO:0005515~protein binding,GO:0044822~poly(A) RNA binding, | IPR004087:K Homology domain,IPR004088:K Homology domain, type 1,IPR015096:Domain of unknown function DUF1897, |
| 68 | GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0016020~membrane, | GO:0000978~RNA polymerase II core promoter proximal region sequence-specific DNA binding,GO:0001077~transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding,GO:0003697~single-stranded DNA binding,GO:0044822~poly(A) RNA binding, | IPR004087:K Homology domain,IPR004088:K Homology domain, type 1,IPR015096:Domain of unknown function DUF1897, |
| 69 | GO:0005737~cytoplasm,GO:0005844~polysome,GO:0005913~cell-cell adherens junction,GO:0016020~membrane, | GO:0005515~protein binding,GO:0019887~protein kinase regulator activity,GO:0019901~protein kinase binding,GO:0043022~ribosome binding,GO:0044822~poly(A) RNA binding,GO:0098641~cadherin binding involved in cell-cell adhesion, | IPR000225:Armadillo,IPR011989:Armadillo-like helical,IPR016024:Armadillo-type fold,IPR021133:HEAT, type 2,IPR026827:Proteasome component ECM29/Translational activator GCN1, |
| 70 | GO:0005622~intracellular,GO:0005737~cytoplasm,GO:0005794~Golgi apparatus,GO:0005925~focal adhesion,GO:0016020~membrane,GO:0031982~vesicle,GO:0043209~myelin sheath,GO:0070062~extracellular exosome, | GO:0005092~GDP-dissociation inhibitor activity,GO:0005093~Rab GDP-dissociation inhibitor activity,GO:0005096~GTPase activator activity,GO:0016491~oxidoreductase activity,GO:0031267~small GTPase binding,GO:0044822~poly(A) RNA binding, | IPR000806:Rab GDI protein,IPR018203:GDP dissociation inhibitor,IPR023753:Pyridine nucleotide-disulphide oxidoreductase, FAD/NAD(P)-binding domain, |

|  | H | I | J | K |
|---|---|---|---|---|
| 63 | mmu03015:mRNA surveillance pathway, |  | 3D-structure,Acetylation,Complete proteome,Cytoplasm,Host-virus interaction,Nonsense-mediated mRNA decay,Phosphoprotein,Protein biosynthesis,Reference proteome, | chain:Eukaryotic peptide chain release factor subunit 1,modified residue,sequence conflict, |
| 64 |  | PIRSF000090:electron transfer flavoprotein, beta subunit, | Acetylation,Complete proteome,Direct protein sequencing,Electron transport,FAD,Flavoprotein,Methylation,Mitochondrion,Phosphoprotein,Proteomics identification,Reference proteome,Transport, | chain:Electron transfer flavoprotein subunit beta,modified residue,sequence conflict, |
| 65 | mmu03320:PPAR signaling pathway, |  | 3D-structure,Acetylation,Complete proteome,Cytoplasm,Direct protein sequencing,Disulfide bond,Lipid-binding,Phosphoprotein,Reference proteome,Transport, | binding site:Fatty acid,chain:Fatty acid-binding protein, epidermal,disulfide bond,modified residue,region of interest:Fatty acid binding, |
| 66 |  |  | Cell adhesion,Cell junction,Cell membrane,Cell projection,Cell shape,Complete proteome,Cytoplasm,Cytoskeleton,Lipid-binding,Membrane,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Wnt signaling pathway, | chain:Fermitin family homolog 2,domain:FERM,domain:PH,modified residue,sequence conflict, |
| 67 |  |  | 3D-structure,Acetylation,Alternative splicing,Complete proteome,Direct protein sequencing,DNA-binding,Membrane,Methylation,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,Transcription,Transcription regulation,Transmembrane,Transmembrane helix,Ubl conjugation, | chain:Far upstream element-binding protein 1,compositionally biased region:Gly-rich,compositionally biased region:Poly-Gly,compositionally biased region:Pro-rich,domain:KH 1,domain:KH 2,domain:KH 3,domain:KH 4,helix,modified residue,sequence conflict,splice variant,strand,turn, |
| 68 |  |  | Complete proteome,Proteomics identification,Reference proteome, |  |
| 69 |  |  | Acetylation,Activator,Coiled coil,Complete proteome,Cytoplasm,Phosphoprotein,Reference proteome,Repeat,Stress response,Translation regulation, |  |
| 70 |  |  | Acetylation,Alternative splicing,Complete proteome,Cytoplasm,Direct protein sequencing,GTPase activation,Membrane,Phosphoprotein,Reference proteome, | chain:Rab GDP dissociation inhibitor beta,modified residue,sequence conflict,splice variant, |

|  | A | B | C | D |
|---|---|---|---|---|
| 71 | Gnb2l1 | receptor for activated C kinase 1(RACK1) | Homo sapiens | GO:0001934~positive regulation of protein phosphorylation,GO:0006915~apoptotic process,GO:0006919~activation of cysteine-type endopeptidase activity involved in apoptotic process,GO:0007049~cell cycle,GO:0007369~gastrulation,GO:0010629~negative regulation of gene expression,GO:0010803~regulation of tumor necrosis factor-mediated signaling pathway,GO:0016032~viral process,GO:0017148~negative regulation of translation,GO:0030178~negative regulation of Wnt signaling pathway,GO:0030308~negative regulation of cell growth,GO:0030335~positive regulation of cell migration,GO:0030822~positive regulation of cAMP catabolic process,GO:0032436~positive regulation of proteasomal ubiquitin-dependent protein catabolic process,GO:0032464~positive regulation of protein homooligomerization,GO:0032880~regulation of protein localization,GO:0033137~negative regulation of peptidyl-serine phosphorylation,GO:0042998~positive regulation of Golgi to plasma membrane protein transport,GO:0043065~positive regulation of apoptotic process,GO:0043547~positive regulation of GTPase activity,GO:0048511~rhythmic process,GO:0050765~negative regulation of phagocytosis,GO:0051302~regulation of cell division,GO:0051343~positive regulation of cyclic-nucleotide phosphodiesterase activity,GO:0051726~regulation of cell cycle,GO:0051898~negative regulation of protein kinase B signaling,GO:0051901~positive regulation of mitochondrial depolarization,GO:0061099~negative regulation of protein tyrosine kinase activity,GO:0071333~cellular response to glucose stimulus,GO:0071363~cellular response to growth factor stimulus,GO:0098609~cell-cell adhesion,GO:1900102~negative regulation of endoplasmic reticulum unfolded protein response,GO:1903208~negative regulation of hydrogen peroxide-induced neuron death,GO:2000114~regulation of establishment of cell polarity,GO:2000304~positive regulation of ceramide biosynthetic process,GO:2000543~positive regulation of gastrulation,GO:2001244~positive regulation of intrinsic apoptotic signaling pathway, |
| 72 | Gstp1 | glutathione S-transferase, pi 1(Gstp1) | Mus musculus | GO:0000302~response to reactive oxygen species,GO:0002674~negative regulation of acute inflammatory response,GO:0006749~glutathione metabolic process,GO:0006805~xenobiotic metabolic process,GO:0008152~metabolic process,GO:0009636~response to toxic substance,GO:0009890~negative regulation of biosynthetic process,GO:0014003~oligodendrocyte development,GO:0031100~organ regeneration,GO:0031667~response to nutrient levels,GO:0032355~response to estradiol,GO:0032691~negative regulation of interleukin-1 beta production,GO:0032720~negative regulation of tumor necrosis factor production,GO:0032869~cellular response to insulin stimulus,GO:0032872~regulation of stress-activated MAPK cascade,GO:0032873~negative regulation of stress-activated MAPK cascade,GO:0032930~positive regulation of superoxide anion generation,GO:0033591~response to L-ascorbic acid,GO:0035726~common myeloid progenitor cell proliferation,GO:0043066~negative regulation of apoptotic process,GO:0043124~negative regulation of I-kappaB kinase/NF-kappaB signaling,GO:0043200~response to amino acid,GO:0043407~negative regulation of MAP kinase activity,GO:0043508~negative regulation of JUN kinase activity,GO:0045471~response to ethanol,GO:0048147~negative regulation of fibroblast proliferation,GO:0051771~negative regulation of nitric-oxide synthase biosynthetic process,GO:0070372~regulation of ERK1 and ERK2 cascade,GO:0070373~negative regulation of ERK1 and ERK2 cascade,GO:0070664~negative regulation of leukocyte proliferation,GO:0071222~cellular response to lipopolysaccharide,GO:0071364~cellular response to epidermal growth factor stimulus,GO:0071385~cellular response to glucocorticoid stimulus,GO:0071460~cellular response to cell-matrix adhesion,GO:0071638~negative regulation of monocyte chemotactic protein-1 production,GO:2000429~negative regulation of neutrophil aggregation,GO:2000469~negative regulation of peroxidase activity,GO:2001237~negative regulation of extrinsic apoptotic signaling pathway, |
| 73 | Gstp2 | glutathione S-transferase, pi 2(Gstp2) | Mus musculus | GO:0006749~glutathione metabolic process,GO:0008152~metabolic process, |
| 74 | H1fx | H1 histone family, member X(H1fx) | Mus musculus | GO:0006334~nucleosome assembly,GO:0098609~cell-cell adhesion, |
| 75 | H2afv | H2A histone family, member V(H2afv) | Mus musculus | GO:0006342~chromatin silencing, |
| 76 | H2afy2 | H2A histone family, member Y2(H2afy2) | Mus musculus | GO:0000122~negative regulation of transcription from RNA polymerase II promoter,GO:0006334~nucleosome assembly,GO:0006342~chromatin silencing,GO:0007420~brain development,GO:0007549~dosage compensation,GO:0016569~covalent chromatin modification,GO:0045618~positive regulation of keratinocyte differentiation,GO:0045814~negative regulation of gene expression, epigenetic,GO:0071169~establishment of protein localization to chromatin,GO:1901837~negative regulation of transcription of nuclear large rRNA transcript from RNA polymerase I promoter, |

| | E | F | G |
|---|---|---|---|
| 71 | GO:0001891~phagocytic cup,GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005739~mitochondrion,GO:0005829~cytosol,GO:0005913~cell-cell adherens junction,GO:0015935~small ribosomal subunit,GO:0030425~dendrite,GO:0030496~midbody,GO:0043025~neuronal cell body,GO:0043204~perikaryon,GO:0048471~perinuclear region of cytoplasm,GO:0070062~extracellular exosome,GO:1990630~IRE1-RACK1-PP2A complex, | GO:0005080~protein kinase C binding,GO:0005102~receptor binding,GO:0005515~protein binding,GO:0008200~ion channel inhibitor activity,GO:0008656~cysteine-type endopeptidase activator activity involved in apoptotic process,GO:0019899~enzyme binding,GO:0019903~protein phosphatase binding,GO:0030292~protein tyrosine kinase inhibitor activity,GO:0030971~receptor tyrosine kinase binding,GO:0032947~protein complex scaffold,GO:0035591~signaling adaptor activity,GO:0042169~SH2 domain binding,GO:0042803~protein homodimerization activity,GO:0044822~poly(A) RNA binding,GO:0098641~cadherin binding involved in cell-cell adhesion, | IPR001680:WD40 repeat,IPR015943:WD40/YVTN repeat-like-containing domain,IPR017986:WD40-repeat-containing domain,IPR019775:WD40 repeat, conserved site,IPR020472:G-protein beta WD-40 repeat, |
| 72 | GO:0005615~extracellular space,GO:0005622~intracellular,GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005739~mitochondrion,GO:0005829~cytosol,GO:0005886~plasma membrane,GO:0031982~vesicle,GO:0043234~protein complex,GO:0070062~extracellular exosome,GO:0097057~TRAF2-GSTP1 complex, | GO:0004364~glutathione transferase activity,GO:0004602~glutathione peroxidase activity,GO:0008144~drug binding,GO:0008432~JUN kinase binding,GO:0016740~transferase activity,GO:0019207~kinase regulator activity,GO:0019901~protein kinase binding,GO:0035730~S-nitrosoglutathione binding,GO:0035731~dinitrosyl-iron complex binding,GO:0043295~glutathione binding, | IPR003082:Glutathione S-transferase, Pi class,IPR004045:Glutathione S-transferase, N-terminal,IPR004046:Glutathione S-transferase, C-terminal,IPR010987:Glutathione S-transferase, C-terminal-like,IPR012336:Thioredoxin-like fold, |
| 73 | GO:0005615~extracellular space,GO:0005622~intracellular,GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005739~mitochondrion,GO:0005829~cytosol,GO:0005886~plasma membrane,GO:0031982~vesicle,GO:0070062~extracellular exosome,GO:0097057~TRAF2-GSTP1 complex, | GO:0004364~glutathione transferase activity,GO:0004602~glutathione peroxidase activity,GO:0008144~drug binding,GO:0016740~transferase activity,GO:0019901~protein kinase binding,GO:0035730~S-nitrosoglutathione binding,GO:0035731~dinitrosyl-iron complex binding,GO:0043295~glutathione binding, | IPR003082:Glutathione S-transferase, Pi class,IPR004045:Glutathione S-transferase, N-terminal,IPR004046:Glutathione S-transferase, C-terminal,IPR010987:Glutathione S-transferase, C-terminal-like,IPR012336:Thioredoxin-like fold, |
| 74 | GO:0000786~nucleosome,GO:0005634~nucleus,GO:0005730~nucleolus,GO:0005913~cell-cell adherens junction, | GO:0003677~DNA binding,GO:0005515~protein binding,GO:0044822~poly(A) RNA binding,GO:0098641~cadherin binding involved in cell-cell adhesion, | IPR005818:Histone H1/H5,IPR005819:Histone H5,IPR011991:Winged helix-turn-helix DNA-binding domain, |
| 75 | GO:0000786~nucleosome,GO:0000790~nuclear chromatin,GO:0005634~nucleus,GO:0005694~chromosome,GO:0070062~extracellular exosome, | GO:0003677~DNA binding,GO:0046982~protein heterodimerization activity, | IPR002119:Histone H2A,IPR007125:Histone core,IPR009072:Histone-fold, |
| 76 | GO:0000784~nuclear chromosome, telomeric region,GO:0000785~chromatin,GO:0000786~nucleosome,GO:0000790~nuclear chromatin,GO:0001740~Barr body,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005694~chromosome,GO:0035098~ESC/E(Z) complex,GO:0070062~extracellular exosome, | GO:0000977~RNA polymerase II regulatory region sequence-specific DNA binding,GO:0003677~DNA binding,GO:0031490~chromatin DNA binding,GO:0044212~transcription regulatory region DNA binding,GO:0046982~protein heterodimerization activity, | IPR002119:Histone H2A,IPR002589:Appr-1-p processing,IPR007125:Histone core,IPR009072:Histone-fold,IPR021171:Core histone macro-H2A, |

| | H | I | J | K |
|---|---|---|---|---|
| 71 | hsa05162:Measles, | SM00320:WD40, | 3D-structure,Acetylation,Apoptosis,Biological rhythms,Cell cycle,Cell membrane,Cell projection,Complete proteome,Cytoplasm,Developmental protein,Direct protein sequencing,Gastrulation,Growth regulation,Host-virus interaction,Membrane,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,Translation regulation,WD repeat, | chain:Guanine nucleotide-binding protein subunit beta-2-like 1,modified residue,repeat:WD 1,repeat:WD 2,repeat:WD 3,repeat:WD 4,repeat:WD 5,repeat:WD 6,repeat:WD 7,sequence conflict, |
| 72 | mmu00480:Glutathione metabolism,mmu00980:Metabolism of xenobiotics by cytochrome P450,mmu00982:Drug metabolism - cytochrome P450,mmu05204:Chemical carcinogenesis, | | 3D-structure,Acetylation,Complete proteome,Cytoplasm,Direct protein sequencing,Mitochondrion,Nucleus,Phosphoprotein,Reference proteome,Transferase, | chain:Glutathione S-transferase P 1,chain:Glutathione S-transferase P 2,domain:GST C-terminal,domain:GST N-terminal,helix,modified residue,strand,turn, |
| 73 | mmu00480:Glutathione metabolism,mmu00980:Metabolism of xenobiotics by cytochrome P450,mmu00982:Drug metabolism - cytochrome P450,mmu05204:Chemical carcinogenesis, | | Complete proteome,Reference proteome,Transferase, | chain:Glutathione S-transferase P 1,chain:Glutathione S-transferase P 2,domain:GST C-terminal,domain:GST N-terminal,helix,modified residue,strand,turn, |
| 74 | | | Chromosome,Complete proteome,DNA-binding,Nucleus,Proteomics identification,Reference proteome, | |
| 75 | mmu05034:Alcoholism,mmu05322:Systemic lupus erythematosus, | | Acetylation,Chromosome,Complete proteome,DNA-binding,Nucleosome core,Nucleus,Reference proteome,Ubl conjugation, | chain:Histone H2A.v,cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin),modified residue,sequence conflict, |
| 76 | mmu05034:Alcoholism,mmu05322:Systemic lupus erythematosus, | PIRSF037942:core histone macro-H2A, | Chromatin regulator,Chromosome,Complete proteome,DNA-binding,Isopeptide bond,Nucleosome core,Nucleus,Reference proteome,Ubl conjugation, | chain:Core histone macro-H2A.2,domain:Histone H2A,domain:Macro,modified residue,sequence conflict, |

|  | A | B | C | D |
|---|---|---|---|---|
| 77 | H2afz | H2A histone family, member Z(H2afz) | Mus musculus | GO:0006342~chromatin silencing,GO:0007275~multicellular organism development,GO:0032869~cellular response to insulin stimulus,GO:0045944~positive regulation of transcription from RNA polymerase II promoter,GO:0071392~cellular response to estradiol stimulus, |
| 78 | Hdac1 | histone deacetylase 1(Hdac1) | Mus musculus | GO:0000122~negative regulation of transcription from RNA polymerase II promoter,GO:0000183~chromatin silencing at rDNA,GO:0001975~response to amphetamine,GO:0006325~chromatin organization,GO:0006346~methylation-dependent chromatin silencing,GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0006476~protein deacetylation,GO:0007492~endoderm development,GO:0007623~circadian rhythm,GO:0008284~positive regulation of cell proliferation,GO:0008285~negative regulation of cell proliferation,GO:0009913~epidermal cell differentiation,GO:0010629~negative regulation of gene expression,GO:0010870~positive regulation of receptor biosynthetic process,GO:0016569~covalent chromatin modification,GO:0016575~histone deacetylation,GO:0021766~hippocampus development,GO:0030182~neuron differentiation,GO:0032732~positive regulation of interleukin-1 production,GO:0032760~positive regulation of tumor necrosis factor production,GO:0032922~circadian regulation of gene expression,GO:0034599~cellular response to oxidative stress,GO:0042475~odontogenesis of dentin-containing tooth,GO:0042517~positive regulation of tyrosine phosphorylation of Stat3 protein,GO:0042733~embryonic digit morphogenesis,GO:0043044~ATP-dependent chromatin remodeling,GO:0043066~negative regulation of apoptotic process,GO:0043124~negative regulation of I-kappaB kinase/NF-kappaB signaling,GO:0043524~negative regulation of neuron apoptotic process,GO:0043922~negative regulation by host of viral transcription,GO:0045892~negative regulation of transcription, DNA-templated,GO:0045893~positive regulation of transcription, DNA-templated,GO:0045944~positive regulation of transcription from RNA polymerase II promoter,GO:0046676~negative regulation of insulin secretion,GO:0048511~rhythmic process,GO:0048714~positive regulation of oligodendrocyte differentiation,GO:0060766~negative regulation of androgen receptor signaling pathway,GO:0060789~hair follicle placode formation,GO:0061029~eyelid development in camera-type eye,GO:0061198~fungiform papilla formation,GO:0070932~histone H3 deacetylation,GO:0070933~histone H4 deacetylation,GO:0090090~negative regulation of canonical Wnt signaling pathway,GO:2000343~positive regulation of chemokine (C-X-C motif) ligand 2 production,GO:2000676~positive regulation of type B pancreatic cell apoptotic process,GO:2000757~negative regulation of peptidyl-lysine acetylation,GO:2001243~negative regulation of intrinsic apoptotic signaling pathway, |

| | E | F | G |
|---|---|---|---|
| 77 | GO:0000786~nucleosome,GO:0000790~nuclear chromatin,GO:0001740~Barr body,GO:0005634~nucleus,GO:0005694~chromosome,GO:0005719~nuclear euchromatin,GO:0005720~nuclear heterochromatin,GO:0070062~extracellular exosome, | GO:0000978~RNA polymerase II core promoter proximal region sequence-specific DNA binding,GO:0000979~RNA polymerase II core promoter sequence-specific DNA binding,GO:0000980~RNA polymerase II distal enhancer sequence-specific DNA binding,GO:0003677~DNA binding,GO:0031490~chromatin DNA binding,GO:0031492~nucleosomal DNA binding,GO:0046982~protein heterodimerization activity, | IPR002119:Histone H2A,IPR007125:Histone core,IPR009072:Histone-fold, |
| 78 | GO:0000118~histone deacetylase complex,GO:0000785~chromatin,GO:0000790~nuclear chromatin,GO:0000792~heterochromatin,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005667~transcription factor complex,GO:0005737~cytoplasm,GO:0005829~cytosol,GO:0016580~Sin3 complex,GO:0016581~NuRD complex,GO:0017053~transcriptional repressor complex,GO:0043005~neuron projection,GO:0043025~neuronal cell body,GO:0043234~protein complex,GO:0048471~perinuclear region of cytoplasm, | GO:0000976~transcription regulatory region sequence-specific DNA binding,GO:0000978~RNA polymerase II core promoter proximal region sequence-specific DNA binding,GO:0000980~RNA polymerase II distal enhancer sequence-specific DNA binding,GO:0001047~core promoter binding,GO:0001085~RNA polymerase II transcription factor binding,GO:0001103~RNA polymerase II repressing transcription factor binding,GO:0001106~RNA polymerase II transcription corepressor activity,GO:0003677~DNA binding,GO:0003682~chromatin binding,GO:0003700~transcription factor activity, sequence-specific DNA binding,GO:0003714~transcription corepressor activity,GO:0004407~histone deacetylase activity,GO:0005515~protein binding,GO:0008134~transcription factor binding,GO:0016787~hydrolase activity,GO:0019213~deacetylase activity,GO:0019899~enzyme binding,GO:0031492~nucleosomal DNA binding,GO:0032041~NAD-dependent histone deacetylase activity (H3-K14 specific),GO:0032403~protein complex binding,GO:0033558~protein deacetylase activity,GO:0033613~activating transcription factor binding,GO:0035851~Krueppel-associated box domain binding,GO:0042826~histone deacetylase binding,GO:0044212~transcription regulatory region DNA binding,GO:0047485~protein N-terminus binding,GO:0051059~NF-kappaB binding,GO:0070491~repressing transcription factor binding, | IPR000286:Histone deacetylase superfamily,IPR003084:Histone deacetylase,IPR023801:Histone deacetylase domain, |

|  | H | I | J | K |
|---|---|---|---|---|
| 77 | mmu05034:Alcoholism,mmu05322:Systemic lupus erythematosus, |  | Acetylation,Chromosome,Complete proteome,Developmental protein,DNA-binding,Isopeptide bond,Methylation,Nucleosome core,Nucleus,Proteomics identification,Reference proteome,Ubl conjugation, | chain:Histone H2A.Z,cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin),modified residue,region of interest:Required for interaction with INCENP,sequence conflict, |
| 78 | mmu04110:Cell cycle,mmu04330:Notch signaling pathway,mmu04919:Thyroid hormone signaling pathway,mmu05016:Huntington's disease,mmu05034:Alcoholism,mmu05169:Epstein-Barr virus infection,mmu05200:Pathways in cancer,mmu05202:Transcriptional misregulation in cancer,mmu05203:Viral carcinogenesis,mmu05220:Chronic myeloid leukemia, | PIRSF037913:histone deacetylase class I, eukaryotic type, | Acetylation,Biological rhythms,Chromatin regulator,Complete proteome,Hydrolase,Isopeptide bond,Methylation,Nucleus,Phosphoprotein,Reference proteome,Repressor,S-nitrosylation,Transcription,Transcription regulation,Ubl conjugation, | chain:Histone deacetylase 1,cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO),modified residue,region of interest:Histone deacetylase, |

| | A | B | C | D |
|---|---|---|---|---|
| 79 | Hdac2 | histone deacetylase 2(Hdac2) | Mus musculus | GO:0000122~negative regulation of transcription from RNA polymerase II promoter,GO:0000183~chromatin silencing at rDNA,GO:0001975~response to amphetamine,GO:0003300~cardiac muscle hypertrophy,GO:0006325~chromatin organization,GO:0006344~maintenance of chromatin silencing,GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0006476~protein deacetylation,GO:0008284~positive regulation of cell proliferation,GO:0009913~epidermal cell differentiation,GO:0010718~positive regulation of epithelial to mesenchymal transition,GO:0010870~positive regulation of receptor biosynthetic process,GO:0010977~negative regulation of neuron projection development,GO:0016358~dendrite development,GO:0016569~covalent chromatin modification,GO:0016575~histone deacetylation,GO:0021766~hippocampus development,GO:0030182~neuron differentiation,GO:0031000~response to caffeine,GO:0032496~response to lipopolysaccharide,GO:0032732~positive regulation of interleukin-1 production,GO:0032760~positive regulation of tumor necrosis factor production,GO:0032922~circadian regulation of gene expression,GO:0034605~cellular response to heat,GO:0035094~response to nicotine,GO:0035984~cellular response to trichostatin A,GO:0042220~response to cocaine,GO:0042475~odontogenesis of dentin-containing tooth,GO:0042493~response to drug,GO:0042517~positive regulation of tyrosine phosphorylation of Stat3 protein,GO:0042733~embryonic digit morphogenesis,GO:0043044~ATP-dependent chromatin remodeling,GO:0043066~negative regulation of apoptotic process,GO:0043392~negative regulation of DNA binding,GO:0043433~negative regulation of sequence-specific DNA binding transcription factor activity,GO:0045862~positive regulation of proteolysis,GO:0045892~negative regulation of transcription, DNA-templated,GO:0045944~positive regulation of transcription from RNA polymerase II promoter,GO:0048149~behavioral response to ethanol,GO:0048511~rhythmic process,GO:0048714~positive regulation of oligodendrocyte differentiation,GO:0051091~positive regulation of sequence-specific DNA binding transcription factor activity,GO:0051896~regulation of protein kinase B signaling,GO:0055013~cardiac muscle cell development,GO:0055093~response to hyperoxia,GO:0060044~negative regulation of cardiac muscle cell proliferation,GO:0060297~regulation of sarcomere organization,GO:0060789~hair follicle placode formation,GO:0061000~negative regulation of dendritic spine development,GO:0061029~eyelid development in camera-type eye,GO:0061198~fungiform papilla formation,GO:0070301~cellular response to hydrogen peroxide,GO:0070734~histone H3-K27 methylation,GO:0070932~histone H3 deacetylation,GO:0070933~histone H4 deacetylation,GO:0071300~cellular response to retinoic acid,GO:0071560~cellular response to transforming growth factor beta stimulus,GO:0090090~negative regulation of canonical Wnt signaling pathway,GO:0090311~regulation of protein deacetylation,GO:1902894~negative regulation of pri-miRNA transcription from RNA polymerase II promoter,GO:1903351~cellular response to dopamine,GO:2000757~negative regulation of peptidyl-lysine acetylation,GO:2001243~negative regulation of intrinsic apoptotic signaling pathway, |
| 80 | Hmgb2 | high mobility group box 2(Hmgb2) | Mus musculus | GO:0001938~positive regulation of endothelial cell proliferation,GO:0002376~immune system process,GO:0002437~inflammatory response to antigenic stimulus,GO:0006265~DNA topological change,GO:0006310~DNA recombination,GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0006357~regulation of transcription from RNA polymerase II promoter,GO:0006935~chemotaxis,GO:0006954~inflammatory response,GO:0007283~spermatogenesis,GO:0007289~spermatid nucleus differentiation,GO:0008584~male gonad development,GO:0010628~positive regulation of gene expression,GO:0010629~negative regulation of gene expression,GO:0032075~positive regulation of nuclease activity,GO:0032496~response to lipopolysaccharide,GO:0032728~positive regulation of interferon-beta production,GO:0042493~response to drug,GO:0043388~positive regulation of DNA binding,GO:0045087~innate immune response,GO:0045089~positive regulation of innate immune response,GO:0045595~regulation of cell differentiation,GO:0045648~positive regulation of erythrocyte differentiation,GO:0045654~positive regulation of megakaryocyte differentiation,GO:0045892~negative regulation of transcription, DNA-templated,GO:0045893~positive regulation of transcription, DNA-templated,GO:0045944~positive regulation of transcription from RNA polymerase II promoter,GO:0048545~response to steroid hormone,GO:0050767~regulation of neurogenesis,GO:0050829~defense response to Gram-negative bacterium,GO:0050830~defense response to Gram-positive bacterium,GO:0060326~cell chemotaxis,GO:0071222~cellular response to lipopolysaccharide,GO:0072091~regulation of stem cell proliferation,GO:1902042~negative regulation of extrinsic apoptotic signaling pathway via death domain receptors, |
| 81 | Hnrnpa0 | heterogeneous nuclear ribonucleoprotein A0(Hnrnpa0) | Mus musculus | GO:0006954~inflammatory response,GO:0032496~response to lipopolysaccharide,GO:0070935~3'-UTR-mediated mRNA stabilization, |
| 82 | Hnrnpab | heterogeneous nuclear ribonucleoprotein A/B(Hnrnpab) | Mus musculus | GO:0000122~negative regulation of transcription from RNA polymerase II promoter,GO:0001837~epithelial to mesenchymal transition,GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0045893~positive regulation of transcription, DNA-templated, |

| | E | F | G |
|---|---|---|---|
| 79 | GO:0000118~histone deacetylase complex,GO:0000785~chromatin,GO:0000790~nuclear chromatin,GO:0000792~heterochromatin,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005657~replication fork,GO:0005667~transcription factor complex,GO:0005737~cytoplasm,GO:0016580~Sin3 complex,GO:0016581~NuRD complex,GO:0017053~transcriptional repressor complex,GO:0035098~ESC/E(Z) complex,GO:0043234~protein complex,GO:0090571~RNA polymerase II transcription repressor complex, | GO:0000978~RNA polymerase II core promoter proximal region sequence-specific DNA binding,GO:0000979~RNA polymerase II core promoter sequence-specific DNA binding,GO:0000980~RNA polymerase II distal enhancer sequence-specific DNA binding,GO:0001047~core promoter binding,GO:0001103~RNA polymerase II repressing transcription factor binding,GO:0001226~RNA polymerase II transcription corepressor binding,GO:0003682~chromatin binding,GO:0003700~transcription factor activity, sequence-specific DNA binding,GO:0004407~histone deacetylase activity,GO:0005515~protein binding,GO:0008134~transcription factor binding,GO:0016787~hydrolase activity,GO:0019213~deacetylase activity,GO:0019899~enzyme binding,GO:0031072~heat shock protein binding,GO:0031490~chromatin DNA binding,GO:0031492~nucleosomal DNA binding,GO:0032041~NAD-dependent histone deacetylase activity (H3-K14 specific),GO:0033558~protein deacetylase activity,GO:0034739~histone deacetylase activity (H4-K16 specific),GO:0035851~Krueppel-associated box domain binding,GO:0043565~sequence-specific DNA binding,GO:0044822~poly(A) RNA binding,GO:0051059~NF-kappaB binding, | IPR000286:Histone deacetylase superfamily,IPR003084:Histone deacetylase,IPR023801:Histone deacetylase domain, |
| 80 | GO:0000790~nuclear chromatin,GO:0000793~condensed chromosome,GO:0005576~extracellular region,GO:0005615~extracellular space,GO:0005623~cell,GO:0005634~nucleus,GO:0005694~chromosome,GO:0005730~nucleolus,GO:0005737~cytoplasm,GO:0043234~protein complex,GO:0048471~perinuclear region of cytoplasm, | GO:0001158~enhancer sequence-specific DNA binding,GO:0003677~DNA binding,GO:0003684~damaged DNA binding,GO:0003690~double-stranded DNA binding,GO:0003700~transcription factor activity, sequence-specific DNA binding,GO:0008134~transcription factor binding,GO:0008144~drug binding,GO:0008301~DNA binding, bending,GO:0019904~protein domain specific binding,GO:0042056~chemoattractant activity,GO:0044212~transcription regulatory region DNA binding,GO:0044378~non-sequence-specific DNA binding, bending,GO:0044822~poly(A) RNA binding,GO:0050786~RAGE receptor binding,GO:0097100~supercoiled DNA binding, | IPR009071:High mobility group (HMG) box domain,IPR017967:HMG box A DNA-binding domain, conserved site, |
| 81 | GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0030529~intracellular ribonucleoprotein complex, | GO:0000166~nucleotide binding,GO:0003676~nucleic acid binding,GO:0003723~RNA binding,GO:0017091~AU-rich element binding,GO:0019901~protein kinase binding,GO:0044822~poly(A) RNA binding, | IPR000504:RNA recognition motif domain,IPR012677:Nucleotide-binding, alpha-beta plait, |
| 82 | GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0019013~viral nucleocapsid,GO:0030529~intracellular ribonucleoprotein complex,GO:0090575~RNA polymerase II transcription factor complex, | GO:0000166~nucleotide binding,GO:0003676~nucleic acid binding,GO:0003677~DNA binding,GO:0003700~transcription factor activity, sequence-specific DNA binding,GO:0003723~RNA binding,GO:0005515~protein binding,GO:0043565~sequence-specific DNA binding,GO:0044822~poly(A) RNA binding, | IPR000504:RNA recognition motif domain,IPR012677:Nucleotide-binding, alpha-beta plait,IPR012956:CARG-binding factor, N-terminal, |

|  | H | I | J | K |
|---|---|---|---|---|
| 79 | mmu04110:Cell cycle,mmu04330:Notch signaling pathway,mmu04919:Thyroid hormone signaling pathway,mmu05016:Huntington's disease,mmu05034:Alcoholism,mmu05169:Epstein-Barr virus infection,mmu05200:Pathways in cancer,mmu05202:Transcriptional misregulation in cancer,mmu05203:Viral carcinogenesis,mmu05220:Chronic myeloid leukemia, | PIRSF037913:histone deacetylase class I, eukaryotic type, | Acetylation,Biological rhythms,Chromatin regulator,Complete proteome,Cytoplasm,Hydrolase,Isopeptide bond,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repressor,S-nitrosylation,Transcription,Transcription regulation,Ubl conjugation, | chain:Histone deacetylase 2,compositionally biased region:Poly-Gly,modified residue,region of interest:Histone deacetylase,sequence conflict, |
| 80 |  |  | Acetylation,Chemotaxis,Chromosome,Coiled coil,Complete proteome,Cytoplasm,Disulfide bond,DNA recombination,DNA-binding,Immunity,Inflammatory response,Innate immunity,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,Secreted,Transcription,Transcription regulation, | chain:High mobility group protein B2,compositionally biased region:Asp/Glu-rich (acidic),DNA-binding region:HMG box 1,DNA-binding region:HMG box 2,modified residue,sequence conflict, |
| 81 |  |  | Acetylation,Complete proteome,Isopeptide bond,Methylation,Nucleus,Phosphoprotein,Reference proteome,Repeat,Ribonucleoprotein,RNA-binding,Ubl conjugation, |  |
| 82 |  |  | Acetylation,Complete proteome,Cytoplasm,Direct protein sequencing,DNA-binding,Methylation,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,Repressor,Ribonucleoprotein,RNA-binding,Transcription,Transcription regulation,Viral nucleoprotein,Virion, | chain:Heterogeneous nuclear ribonucleoprotein A/B,compositionally biased region:Gly-rich,compositionally biased region:Poly-Ala,domain:RRM 1,domain:RRM 2,modified residue,sequence conflict, |

|  | A | B | C | D |
|---|---|---|---|---|
| 83 | Hnrnpd | heterogeneous nuclear ribonucleoprotein D(Hnrnpd) | Mus musculus | GO:0001889~liver development,GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0010628~positive regulation of gene expression,GO:0010629~negative regulation of gene expression,GO:0021549~cerebellum development,GO:0042752~regulation of circadian rhythm,GO:0043488~regulation of mRNA stability,GO:0045727~positive regulation of translation,GO:0048255~mRNA stabilization,GO:0048511~rhythmic process,GO:0051592~response to calcium ion,GO:0051602~response to electrical stimulus,GO:0061158~3'-UTR-mediated mRNA destabilization,GO:0071230~cellular response to amino acid stimulus,GO:0071392~cellular response to estradiol stimulus,GO:0071732~cellular response to nitric oxide,GO:0097167~circadian regulation of translation,GO:1901355~response to rapamycin,GO:1904383~response to sodium phosphate,GO:1904586~cellular response to putrescine,GO:1990828~hepatocyte dedifferentiation, |
| 84 | Hnrnpr | heterogeneous nuclear ribonucleoprotein R(Hnrnpr) | Mus musculus | GO:0007623~circadian rhythm,GO:0043086~negative regulation of catalytic activity,GO:0061014~positive regulation of mRNA catabolic process,GO:0061157~mRNA destabilization, |
| 85 | Hspa4 | heat shock protein 4(Hspa4) | Mus musculus | GO:0001933~negative regulation of protein phosphorylation,GO:0009408~response to heat,GO:0010628~positive regulation of gene expression,GO:0010629~negative regulation of gene expression,GO:0032092~positive regulation of protein binding,GO:0043066~negative regulation of apoptotic process,GO:0043392~negative regulation of DNA binding,GO:0045040~protein import into mitochondrial outer membrane,GO:0051131~chaperone-mediated protein complex assembly,GO:0060548~negative regulation of cell death, |
| 86 | Iars | isoleucine-tRNA synthetase(Iars) | Mus musculus | GO:0001649~osteoblast differentiation,GO:0006412~translation,GO:0006418~tRNA aminoacylation for protein translation,GO:0006428~isoleucyl-tRNA aminoacylation, |
| 87 | Ilf2 | interleukin enhancer binding factor 2(Ilf2) | Mus musculus | GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0006955~immune response,GO:0045893~positive regulation of transcription, DNA-templated, |

|  | E | F | G |
|---|---|---|---|
| 83 | GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0005829~cytosol,GO:0019013~viral nucleocapsid,GO:0030529~intracellular ribonucleoprotein complex,GO:0070062~extracellular exosome, | GO:0000166~nucleotide binding,GO:0003676~nucleic acid binding,GO:0003677~DNA binding,GO:0003680~AT DNA binding,GO:0003682~chromatin binding,GO:0003723~RNA binding,GO:0003729~mRNA binding,GO:0008134~transcription factor binding,GO:0035925~mRNA 3'-UTR AU-rich region binding,GO:0042162~telomeric DNA binding,GO:0042826~histone deacetylase binding,GO:0044822~poly(A) RNA binding, | IPR000504:RNA recognition motif domain,IPR012677:Nucleotide-binding, alpha-beta plait,IPR012956:CARG-binding factor, N-terminal, |
| 84 | GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0019013~viral nucleocapsid,GO:0030425~dendrite,GO:0030426~growth cone,GO:0030529~intracellular ribonucleoprotein complex,GO:0043679~axon terminus,GO:0071013~catalytic step 2 spliceosome, | GO:0000166~nucleotide binding,GO:0003730~mRNA 3'-UTR binding,GO:0044822~poly(A) RNA binding, | IPR000504:RNA recognition motif domain,IPR006535:HnRNP R/Q splicing factor,IPR012677:Nucleotide-binding, alpha-beta plait, |
| 85 | GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005811~lipid particle,GO:0005829~cytosol,GO:0070062~extracellular exosome, | GO:0000166~nucleotide binding,GO:0001085~RNA polymerase II transcription factor binding,GO:0005515~protein binding,GO:0005524~ATP binding,GO:0032403~protein complex binding,GO:0033613~activating transcription factor binding, | IPR013126:Heat shock protein 70 family,IPR018181:Heat shock protein 70, conserved site, |
| 86 | GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0005829~cytosol,GO:0016020~membrane,GO:0070062~extracellular exosome, | GO:0000049~tRNA binding,GO:0000166~nucleotide binding,GO:0002161~aminoacyl-tRNA editing activity,GO:0004812~aminoacyl-tRNA ligase activity,GO:0004822~isoleucine-tRNA ligase activity,GO:0005524~ATP binding,GO:0016874~ligase activity,GO:0051020~GTPase binding, | IPR001412:Aminoacyl-tRNA synthetase, class I, conserved site,IPR002300:Aminoacyl-tRNA synthetase, class Ia,IPR002301:Isoleucine-tRNA ligase,IPR009008:Valyl/Leucyl/Isoleucyl-tRNA synthetase, class Ia, editing domain,IPR009080:Aminoacyl-tRNA synthetase, class 1a, anticodon-binding,IPR013155:Valyl/Leucyl/Isoleucyl-tRNA synthetase, class I, anticodon-binding,IPR014729:Rossmann-like alpha/beta/alpha sandwich fold,IPR023586:Isoleucine-tRNA ligase, type 2, |
| 87 | GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005730~nucleolus,GO:0005737~cytoplasm,GO:0016020~membrane,GO:0030529~intracellular ribonucleoprotein complex, | GO:0003677~DNA binding,GO:0003723~RNA binding,GO:0003725~double-stranded RNA binding,GO:0005524~ATP binding,GO:0016740~transferase activity,GO:0044822~poly(A) RNA binding, | IPR006116:2-5-oligoadenylate synthetase, N-terminal,IPR006561:DZF, |

|  | H | I | J | K |
|---|---|---|---|---|
| 83 |  |  | Acetylation,Alternative splicing,Biological rhythms,Complete proteome,Cytoplasm,Direct protein sequencing,DNA-binding,Isopeptide bond,Methylation,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,Ribonucleoprotein,RNA-binding,Transcription,Transcription regulation,Ubl conjugation,Viral nucleoprotein,Virion, | chain:Heterogeneous nuclear ribonucleoprotein D0,domain:RRM 1,domain:RRM 2,modified residue,sequence conflict,splice variant, |
| 84 |  |  | Complete proteome,Proteomics identification,Reference proteome,Ribonucleoprotein,Signal,Viral nucleoprotein,Virion, |  |
| 85 | mmu04612:Antigen processing and presentation, |  | Acetylation,ATP-binding,Coiled coil,Complete proteome,Cytoplasm,Direct protein sequencing,Methylation,Nucleotide-binding,Phosphoprotein,Proteomics identification,Reference proteome,Stress response, | chain:Heat shock 70 kDa protein 4,modified residue, |
| 86 | mmu00970:Aminoacyl-tRNA biosynthesis, |  | Acetylation,Aminoacyl-tRNA synthetase,ATP-binding,Complete proteome,Cytoplasm,Ligase,Nucleotide-binding,Phosphoprotein,Protein biosynthesis,Proteomics identification,Reference proteome, | binding site:ATP,chain:Isoleucyl-tRNA synthetase, cytoplasmic,modified residue,short sequence motif:"HIGH" region,short sequence motif:"KMSKS" region, |
| 87 |  |  | 3D-structure,Activator,Complete proteome,Cytoplasm,DNA-binding,Methylation,Nucleus,Phosphoprotein,Reference proteome,Transcription,Transcription regulation, | chain:Interleukin enhancer-binding factor 2,compositionally biased region:Poly-Glu,domain:DZF,modified residue, |

|  | A | B | C | D |
|---|---|---|---|---|
| 88 | Ilk | integrin linked kinase(Ilk) | Mus musculus | GO:0001558~regulation of cell growth,GO:0001658~branching involved in ureteric bud morphogenesis,GO:0001954~positive regulation of cell-matrix adhesion,GO:0003151~outflow tract morphogenesis,GO:0006468~protein phosphorylation,GO:0006469~negative regulation of protein kinase activity,GO:0007050~cell cycle arrest,GO:0007229~integrin-mediated signaling pathway,GO:0007569~cell aging,GO:0008284~positive regulation of cell proliferation,GO:0010667~negative regulation of cardiac muscle cell apoptotic process,GO:0010761~fibroblast migration,GO:0014044~Schwann cell development,GO:0014912~negative regulation of smooth muscle cell migration,GO:0016310~phosphorylation,GO:0018105~peptidyl-serine phosphorylation,GO:0021675~nerve development,GO:0022011~myelination in peripheral nervous system,GO:0030030~cell projection organization,GO:0030335~positive regulation of cell migration,GO:0030513~positive regulation of BMP signaling pathway,GO:0032288~myelin assembly,GO:0032956~regulation of actin cytoskeleton organization,GO:0034446~substrate adhesion-dependent cell spreading,GO:0042327~positive regulation of phosphorylation,GO:0043066~negative regulation of apoptotic process,GO:0043206~extracellular fibril organization,GO:0043406~positive regulation of MAP kinase activity,GO:0043410~positive regulation of MAPK cascade,GO:0043491~protein kinase B signaling,GO:0043524~negative regulation of neuron apoptotic process,GO:0045197~establishment or maintenance of epithelial cell apical/basal polarity,GO:0045663~positive regulation of myoblast differentiation,GO:0045669~positive regulation of osteoblast differentiation,GO:0045773~positive regulation of axon extension,GO:0045893~positive regulation of transcription, DNA-templated,GO:0048662~negative regulation of smooth muscle cell proliferation,GO:0048812~neuron projection morphogenesis,GO:0050772~positive regulation of axonogenesis,GO:0050775~positive regulation of dendrite morphogenesis,GO:0051291~protein heterooligomerization,GO:0051897~positive regulation of protein kinase B signaling,GO:0070527~platelet aggregation,GO:0090263~positive regulation of canonical Wnt signaling pathway,GO:2000178~negative regulation of neural precursor cell proliferation, |
| 89 | Inca1 | inhibitor of CDK, cyclin A1 interacting protein 1(Inca1) | Mus musculus | GO:0008285~negative regulation of cell proliferation,GO:0045736~negative regulation of cyclin-dependent protein serine/threonine kinase activity,GO:2001235~positive regulation of apoptotic signaling pathway, |
| 90 | Kank2 | KN motif and ankyrin repeat domains 2(Kank2) | Mus musculus | GO:0000122~negative regulation of transcription from RNA polymerase II promoter,GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0006915~apoptotic process,GO:0008285~negative regulation of cell proliferation,GO:0033147~negative regulation of intracellular estrogen receptor signaling pathway,GO:0043069~negative regulation of programmed cell death,GO:0051497~negative regulation of stress fiber assembly,GO:0070563~negative regulation of vitamin D receptor signaling pathway,GO:2000134~negative regulation of G1/S transition of mitotic cell cycle, |
| 91 | Kank3 | KN motif and ankyrin repeat domains 3(Kank3) | Mus musculus | GO:0051497~negative regulation of stress fiber assembly, |
| 92 | Katnal2 | katanin p60 subunit A-like 2(Katnal2) | Mus musculus | GO:0031122~cytoplasmic microtubule organization,GO:0051013~microtubule severing, |

|  | E | F | G |
|---|---|---|---|
| 88 | GO:0001725~stress fiber,GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0005886~plasma membrane,GO:0005911~cell-cell junction,GO:0005925~focal adhesion,GO:0016020~membrane,GO:0030017~sarcomere,GO:0030027~lamellipodium,GO:0030054~cell junction,GO:0030424~axon,GO:0031012~extracellular matrix,GO:0042995~cell projection,GO:0043025~neuronal cell body,GO:0043034~costamere,GO:0043195~terminal bouton,GO:0043198~dendritic shaft,GO:0043234~protein complex, | GO:0000166~nucleotide binding,GO:0004672~protein kinase activity,GO:0004674~protein serine/threonine kinase activity,GO:0004871~signal transducer activity,GO:0005178~integrin binding,GO:0005515~protein binding,GO:0005524~ATP binding,GO:0016301~kinase activity,GO:0016740~transferase activity,GO:0017124~SH3 domain binding,GO:0019901~protein kinase binding, | IPR000719:Protein kinase, catalytic domain,IPR001245:Serine-threonine/tyrosine-protein kinase catalytic domain,IPR002110:Ankyrin repeat,IPR011009:Protein kinase-like domain,IPR020683:Ankyrin repeat-containing domain, |
| 89 | GO:0005634~nucleus,GO:0005737~cytoplasm, | GO:0004861~cyclin-dependent protein serine/threonine kinase inhibitor activity,GO:0030332~cyclin binding, | IPR026238:Inhibitor of CDK interacting with cyclin A1, |
| 90 | GO:0005737~cytoplasm,GO:0005739~mitochondrion, |  | IPR002110:Ankyrin repeat,IPR020683:Ankyrin repeat-containing domain,IPR021939:Kank N-terminal motif, |
| 91 | GO:0005737~cytoplasm, |  | IPR002110:Ankyrin repeat,IPR020683:Ankyrin repeat-containing domain,IPR021939:Kank N-terminal motif, |
| 92 | GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005856~cytoskeleton,GO:0005874~microtubule, | GO:0000166~nucleotide binding,GO:0005524~ATP binding,GO:0008568~microtubule-severing ATPase activity,GO:0016787~hydrolase activity, | IPR003593:AAA+ ATPase domain,IPR003959:ATPase, AAA-type, core,IPR006594:LisH dimerisation motif,IPR027417:P-loop containing nucleoside triphosphate hydrolase,IPR027497:Katanin p60 ATPase-containing subunit A-like 2, |

|  | H | I | J | K |
|---|---|---|---|---|
| 88 | mmu03320:PPAR signaling pathway,mmu04510:Focal adhesion,mmu05100:Bacterial invasion of epithelial cells,mmu05213:Endometrial cancer, |  | Acetylation,ANK repeat,ATP-binding,Cell junction,Cell membrane,Cell projection,Complete proteome,Cytoplasm,Kinase,Membrane,Nucleotide-binding,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,Serine/threonine-protein kinase,Transferase, | binding site:ATP,chain:Integrin-linked protein kinase,domain:Protein kinase,modified residue,nucleotide phosphate-binding region:ATP,region of interest:Interaction with LIMS1,region of interest:PH-like; mediates interaction with TGFB1I1,repeat:ANK 1,repeat:ANK 2,repeat:ANK 3,repeat:ANK 4,repeat:ANK 5,sequence conflict, |
| 89 |  |  | Alternative splicing,Complete proteome,Nucleus,Phosphoprotein,Reference proteome, | chain:Protein INCA1,modified residue,short sequence motif:Nuclear localization signal,splice variant, |
| 90 |  |  | Alternative splicing,ANK repeat,Apoptosis,Coiled coil,Complete proteome,Cytoplasm,Methylation,Mitochondrion,Phosphoprotein,Reference proteome,Repeat,Transcription,Transcription regulation, | chain:KN motif and ankyrin repeat domain- containing protein 2,modified residue,repeat:ANK 1,repeat:ANK 2,repeat:ANK 3,repeat:ANK 4,repeat:ANK 5,sequence conflict,splice variant, |
| 91 |  |  | ANK repeat,Coiled coil,Complete proteome,Phosphoprotein,Proteomics identification,Reference proteome,Repeat, | chain:KN motif and ankyrin repeat domain- containing protein 3,compositionally biased region:Poly-Ser,repeat:ANK 1,repeat:ANK 2,repeat:ANK 3,repeat:ANK 4,repeat:ANK 5, |
| 92 |  |  | Alternative splicing,ATP-binding,Complete proteome,Cytoplasm,Cytoskeleton,Hydrolase,Microtubule,Nucleotide-binding,Reference proteome, | chain:Katanin p60 ATPase-containing subunit A- like 2,domain:LisH,nucleotide phosphate-binding region:ATP,splice variant, |

| | A | B | C | D |
|---|---|---|---|---|
| 93 | Lama5 | laminin, alpha 5(Lama5) | Mus musculus | GO:0001658~branching involved in ureteric bud morphogenesis,GO:0001738~morphogenesis of a polarized epithelium,GO:0001755~neural crest cell migration,GO:0001942~hair follicle development,GO:0007155~cell adhesion,GO:0007229~integrin-mediated signaling pathway,GO:0007517~muscle organ development,GO:0009887~organ morphogenesis,GO:0016331~morphogenesis of embryonic epithelium,GO:0016477~cell migration,GO:0030155~regulation of cell adhesion,GO:0030198~extracellular matrix organization,GO:0030324~lung development,GO:0030334~regulation of cell migration,GO:0034446~substrate adhesion-dependent cell spreading,GO:0042127~regulation of cell proliferation,GO:0042384~cilium assembly,GO:0042475~odontogenesis of dentin-containing tooth,GO:0045995~regulation of embryonic development,GO:0048754~branching morphogenesis of an epithelial tube,GO:0060271~cilium morphogenesis,GO:0060445~branching involved in salivary gland morphogenesis,GO:0090002~establishment of protein localization to plasma membrane, |
| 94 | Lgals1 | lectin, galactose binding, soluble 1(Lgals1) | Mus musculus | GO:0002317~plasma cell differentiation,GO:0006915~apoptotic process,GO:0007157~heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules,GO:0010812~negative regulation of cell-substrate adhesion,GO:0010977~negative regulation of neuron projection development,GO:0031295~T cell costimulation,GO:0033555~multicellular organismal response to stress,GO:0034120~positive regulation of erythrocyte aggregation,GO:0042493~response to drug,GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB signaling,GO:0045185~maintenance of protein location,GO:0045445~myoblast differentiation,GO:0046598~positive regulation of viral entry into host cell,GO:0048678~response to axon injury,GO:0071333~cellular response to glucose stimulus,GO:0071407~cellular response to organic cyclic compound, |
| 95 | Lmnb1 | lamin B1(Lmnb1) | Mus musculus | GO:0031662~positive regulation of cyclin-dependent protein serine/threonine kinase activity involved in G2/M transition of mitotic cell cycle,GO:0046330~positive regulation of JNK cascade,GO:1904609~cellular response to monosodium L-glutamate, |
| 96 | Lpp | LIM domain containing preferred translocation partner in lipoma(Lpp) | Mus musculus | GO:0007155~cell adhesion, |
| 97 | Luc7l2 | LUC7-like 2 (S. cerevisiae)(Luc7l2) | Mus musculus | GO:0006376~mRNA splice site selection, |
| 98 | Map3k19 | mitogen-activated protein kinase kinase kinase 19(Map3k19) | Mus musculus | GO:0006468~protein phosphorylation,GO:0016310~phosphorylation,GO:0030036~actin cytoskeleton organization, |

| | E | F | G |
|---|---|---|---|
| 93 | GO:0005576~extracellular region,GO:0005578~proteinaceous extracellular matrix,GO:0005604~basement membrane,GO:0005605~basal lamina,GO:0005610~laminin-5 complex,GO:0005615~extracellular space,GO:0005634~nucleus,GO:0031012~extracellular matrix,GO:0043259~laminin-10 complex,GO:0070062~extracellular exosome, | GO:0005102~receptor binding,GO:0005178~integrin binding,GO:0005515~protein binding, | IPR000034:Laminin B type IV,IPR000742:Epidermal growth factor-like domain,IPR001791:Laminin G domain,IPR002049:EGF-like, laminin,IPR008211:Laminin, N-terminal,IPR009254:Laminin I,IPR010307:Laminin II,IPR013320:Concanavalin A-like lectin/glucanase, subgroup, |
| 94 | GO:0005576~extracellular region,GO:0005578~proteinaceous extracellular matrix,GO:0005615~extracellular space,GO:0005622~intracellular,GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005829~cytosol,GO:0009986~cell surface,GO:0031012~extracellular matrix,GO:0070062~extracellular exosome, | GO:0001948~glycoprotein binding,GO:0004871~signal transducer activity,GO:0005515~protein binding,GO:0005534~galactose binding,GO:0030246~carbohydrate binding,GO:0030395~lactose binding,GO:0042803~protein homodimerization activity,GO:0043236~laminin binding,GO:0044822~poly(A) RNA binding, | IPR001079:Galectin, carbohydrate recognition domain,IPR013320:Concanavalin A-like lectin/glucanase, subgroup, |
| 95 | GO:0005634~nucleus,GO:0005635~nuclear envelope,GO:0005637~nuclear inner membrane,GO:0005638~lamin filament,GO:0005652~nuclear lamina,GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0005882~intermediate filament,GO:0016020~membrane,GO:0016363~nuclear matrix,GO:0031965~nuclear membrane, | GO:0005198~structural molecule activity,GO:0008432~JUN kinase binding,GO:0043274~phospholipase binding, | IPR001322:Lamin Tail Domain,IPR001664:Intermediate filament protein,IPR018039:Intermediate filament protein, conserved site, |
| 96 | GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005925~focal adhesion,GO:0030054~cell junction, | GO:0005515~protein binding,GO:0008270~zinc ion binding,GO:0046872~metal ion binding, | IPR001781:Zinc finger, LIM-type, |
| 97 | GO:0005634~nucleus,GO:0005685~U1 snRNP,GO:0016607~nuclear speck,GO:0071004~U2-type prespliceosome, | GO:0003729~mRNA binding,GO:0019899~enzyme binding,GO:0044822~poly(A) RNA binding, | IPR004882:LUC7-related, |
| 98 | GO:0005737~cytoplasm, | GO:0000166~nucleotide binding,GO:0004672~protein kinase activity,GO:0004674~protein serine/threonine kinase activity,GO:0004702~receptor signaling protein serine/threonine kinase activity,GO:0005524~ATP binding,GO:0016301~kinase activity,GO:0016740~transferase activity, | IPR000719:Protein kinase, catalytic domain,IPR001245:Serine-threonine/tyrosine-protein kinase catalytic domain,IPR002110:Ankyrin repeat,IPR008271:Serine/threonine-protein kinase, active site,IPR011009:Protein kinase-like domain,IPR017441:Protein kinase, ATP binding site,IPR020683:Ankyrin repeat-containing domain, |

| | H | I | J | K |
|---|---|---|---|---|
| 93 | mmu04151:PI3K-Akt signaling pathway,mmu04510:Focal adhesion,mmu04512:ECM-receptor interaction,mmu05145:Toxoplasmosis,mmu05146:Amoebiasis,mmu05200:Pathways in cancer,mmu05222:Small cell lung cancer, | | 3D-structure,Basement membrane,Cell adhesion,Coiled coil,Complete proteome,Direct protein sequencing,Disulfide bond,Extracellular matrix,Glycoprotein,Laminin EGF-like domain,Reference proteome,Repeat,Secreted,Signal, | chain:Laminin subunit alpha-5,disulfide bond,domain:Laminin EGF-like 1,domain:Laminin EGF-like 10,domain:Laminin EGF-like 11; truncated,domain:Laminin EGF-like 12,domain:Laminin EGF-like 13,domain:Laminin EGF-like 14,domain:Laminin EGF-like 15,domain:Laminin EGF-like 16; first part,domain:Laminin EGF-like 16; second part,domain:Laminin EGF-like 17,domain:Laminin EGF-like 18,domain:Laminin EGF-like 19,domain:Laminin EGF-like 2,domain:Laminin EGF-like 20,domain:Laminin EGF-like 21,domain:Laminin EGF-like 22,domain:Laminin EGF-like 3,domain:Laminin EGF-like 4,domain:Laminin EGF-like 5,domain:Laminin EGF-like 6,domain:Laminin EGF-like 7,domain:Laminin EGF-like 8,domain:Laminin EGF-like 9,domain:Laminin G-like 1,domain:Laminin G-like 2,domain:Laminin G-like 3,domain:Laminin G-like 4,domain:Laminin G-like 5,domain:Laminin IV type A,domain:Laminin N-terminal,glycosylation site:N-linked (GlcNAc...),modified residue,region of interest:Domain II and I,region of interest:Domain IV 1 (domain IV B),short sequence motif:Cell attachment site,signal peptide, |
| 94 | | | 3D-structure,Acetylation,Apoptosis,Complete proteome,Extracellular matrix,Lectin,Phosphoprotein,Reference proteome,Secreted, | binding site:Beta-galactoside,chain:Galectin-1,domain:Galectin,modified residue,region of interest:Beta-galactoside binding,sequence conflict, |
| 95 | | | Acetylation,Coiled coil,Complete proteome,Direct protein sequencing,Disulfide bond,Intermediate filament,Isopeptide bond,Lipoprotein,Membrane,Methylation,Nucleus,Phosphoprotein,Prenylation,Reference proteome,Ubl conjugation, | chain:Lamin-B1,compositionally biased region:Glu-rich (highly acidic; could be involved in chromatin binding),lipid moiety-binding region:S-farnesyl cysteine,modified residue,region of interest:Coil 1A,region of interest:Coil 1B,region of interest:Coil 2,region of interest:Head,region of interest:Linker 1,region of interest:Linker 2,region of interest:Rod,region of interest:Tail,sequence conflict,short sequence motif:Nuclear localization signal, |
| 96 | | | Acetylation,Activator,Alternative splicing,Cell adhesion,Cell junction,Complete proteome,Cytoplasm,Isopeptide bond,LIM domain,Metal-binding,Methylation,Nucleus,Phosphoprotein,Reference proteome,Repeat,Ubl conjugation,Zinc, | chain:Lipoma-preferred partner homolog,compositionally biased region:Pro-rich,domain:LIM zinc-binding 1,domain:LIM zinc-binding 2,domain:LIM zinc-binding 3,modified residue,sequence conflict,splice variant, |
| 97 | | | Alternative splicing,Coiled coil,Complete proteome,Hydroxylation,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome, | chain:Putative RNA-binding protein Luc7-like 2,compositionally biased region:Arg/Ser-rich,modified residue,sequence conflict,splice variant,zinc finger region:C2H2-type; atypical, |
| 98 | | | ANK repeat,ATP-binding,Complete proteome,Kinase,Nucleotide-binding,Proteomics identification,Reference proteome,Serine/threonine-protein kinase,Transferase, | |

| | A | B | C | D |
|---|---|---|---|---|
| 99 | Mapk1 | mitogen-activated protein kinase 1(Mapk1) | Mus musculus | GO:0000165~MAPK cascade,GO:0000189~MAPK import into nucleus,GO:0006351~transcription, DNA-templated,GO:0006468~protein phosphorylation,GO:0006915~apoptotic process,GO:0006974~cellular response to DNA damage stimulus,GO:0007049~cell cycle,GO:0007165~signal transduction,GO:0007507~heart development,GO:0008284~positive regulation of cell proliferation,GO:0009636~response to toxic substance,GO:0009887~organ morphogenesis,GO:0010800~positive regulation of peptidyl-threonine phosphorylation,GO:0014032~neural crest cell development,GO:0016310~phosphorylation,GO:0018105~peptidyl-serine phosphorylation,GO:0018107~peptidyl-threonine phosphorylation,GO:0019233~sensory perception of pain,GO:0019858~cytosine metabolic process,GO:0030278~regulation of ossification,GO:0030335~positive regulation of cell migration,GO:0030878~thyroid gland development,GO:0031647~regulation of protein stability,GO:0031663~lipopolysaccharide-mediated signaling pathway,GO:0032212~positive regulation of telomere maintenance via telomerase,GO:0032496~response to lipopolysaccharide,GO:0032872~regulation of stress-activated MAPK cascade,GO:0033598~mammary gland epithelial cell proliferation,GO:0035556~intracellular signal transduction,GO:0038127~ERBB signaling pathway,GO:0042473~outer ear morphogenesis,GO:0043330~response to exogenous dsRNA,GO:0043627~response to estrogen,GO:0045596~negative regulation of cell differentiation,GO:0045727~positive regulation of translation,GO:0045893~positive regulation of transcription, DNA-templated,GO:0048538~thymus development,GO:0050852~T cell receptor signaling pathway,GO:0050853~B cell receptor signaling pathway,GO:0051090~regulation of sequence-specific DNA binding transcription factor activity,GO:0051493~regulation of cytoskeleton organization,GO:0051973~positive regulation of telomerase activity,GO:0060020~Bergmann glial cell differentiation,GO:0060291~long-term synaptic potentiation,GO:0060324~face development,GO:0060425~lung morphogenesis,GO:0060440~trachea formation,GO:0060716~labyrinthine layer blood vessel development,GO:0061308~cardiac neural crest cell development involved in heart development,GO:0070371~ERK1 and ERK2 cascade,GO:0070849~response to epidermal growth factor,GO:0071310~cellular response to organic substance,GO:0072584~caveolin-mediated endocytosis,GO:0090170~regulation of Golgi inheritance,GO:0097011~cellular response to granulocyte macrophage colony-stimulating factor stimulus,GO:1904355~positive regulation of telomere capping,GO:2000641~regulation of early endosome to late endosome transport, |
| 100 | March8 | membrane-associated ring finger (C3HC4) 8(March8) | Mus musculus | GO:0000209~protein polyubiquitination,GO:0002250~adaptive immune response,GO:0002376~immune system process,GO:0002495~antigen processing and presentation of peptide antigen via MHC class II,GO:0016567~protein ubiquitination,GO:0045347~negative regulation of MHC class II biosynthetic process, |

| | E | F | G |
|---|---|---|---|
| 99 | GO:0005622~intracellular,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0005739~mitochondrion,GO:0005769~early endosome,GO:0005770~late endosome,GO:0005794~Golgi apparatus,GO:0005815~microtubule organizing center,GO:0005829~cytosol,GO:0005856~cytoskeleton,GO:0005901~caveola,GO:0005925~focal adhesion,GO:0015630~microtubule cytoskeleton,GO:0030424~axon,GO:0031143~pseudopodium,GO:0032839~dendrite cytoplasm,GO:0043204~perikaryon,GO:0043234~protein complex,GO:0070062~extracellular exosome,GO:0072686~mitotic spindle, | GO:0000166~nucleotide binding,GO:0001784~phosphotyrosine binding,GO:0004672~protein kinase activity,GO:0004674~protein serine/threonine kinase activity,GO:0004707~MAP kinase activity,GO:0005515~protein binding,GO:0005524~ATP binding,GO:0008134~transcription factor binding,GO:0008353~RNA polymerase II carboxy-terminal domain kinase activity,GO:0016301~kinase activity,GO:0016740~transferase activity,GO:0019901~protein kinase binding,GO:0019902~phosphatase binding,GO:0031435~mitogen-activated protein kinase kinase kinase binding,GO:0042802~identical protein binding, | IPR000719:Protein kinase, catalytic domain,IPR003527:Mitogen-activated protein (MAP) kinase, conserved site,IPR008271:Serine/threonine-protein kinase, active site,IPR008349:Mitogen-activated protein (MAP) kinase, ERK1/2,IPR011009:Protein kinase-like domain,IPR017441:Protein kinase, ATP binding site, |
| 100 | GO:0005764~lysosome,GO:0005765~lysosomal membrane,GO:0005768~endosome,GO:0016020~membrane,GO:0016021~integral component of membrane,GO:0030659~cytoplasmic vesicle membrane,GO:0031410~cytoplasmic vesicle,GO:0031901~early endosome membrane, | GO:0004842~ubiquitin-protein transferase activity,GO:0008270~zinc ion binding,GO:0016874~ligase activity,GO:0042289~MHC class II protein binding,GO:0046872~metal ion binding,GO:0061630~ubiquitin protein ligase activity, | IPR011016:Zinc finger, RING-CH-type,IPR013083:Zinc finger, RING/FYVE/PHD-type, |

|  | H | I | J | K |
|---|---|---|---|---|
| 99 | mmu04010:MAPK signaling pathway,mmu04012:ErbB signaling pathway,mmu04014:Ras signaling pathway,mmu04015:Rap1 signaling pathway,mmu04022:cGMP-PKG signaling pathway,mmu04024:cAMP signaling pathway,mmu04062:Chemokine signaling pathway,mmu04066:HIF-1 signaling pathway,mmu04068:FoxO signaling pathway,mmu04071:Sphingolipid signaling pathway,mmu04114:Oocyte meiosis,mmu04150:mTOR signaling pathway,mmu04151:PI3K-Akt signaling pathway,mmu04261:Adrenergic signaling in cardiomyocytes,mmu04270:Vascular smooth muscle contraction,mmu04320:Dorso-ventral axis formation,mmu04350:TGF-beta signaling pathway,mmu04360:Axon guidance,mmu04370:VEGF signaling pathway,mmu04380:Osteoclast differentiation,mmu04510:Focal adhesion,mmu04520:Adherens junction,mmu04540:Gap junction,mmu04550:Signaling pathways regulating pluripotency of stem cells,mmu04611:Platelet activation,mmu04620:Toll-like receptor signaling pathway,mmu04621:NOD-like receptor signaling pathway,mmu04650:Natural killer cell mediated cytotoxicity,mmu04660:T cell receptor signaling pathway,mmu04662:B cell receptor signaling pathway,mmu04664:Fc epsilon RI signaling pathway,mmu04666:Fc gamma R-mediated phagocytosis,mmu04668:TNF signaling pathway,mmu04713:Circadian entrainment,mmu04720:Long-term potentiation,mmu04722:Neurotrophin signaling pathway,mmu04723:Retrograde endocannabinoid signaling,mmu04724:Glutamatergic synapse,mmu04725:Cholinergic synapse,mmu04726:Serotonergic synapse,mmu04730:Long-term depression,mmu04810:Regulation of actin cytoskeleton,mmu04910:Insulin signaling pathway,mmu04912:GnRH signaling pathway,mmu04914:Progesterone-mediated oocyte maturation,mmu04915:Estrogen signaling pathway,mmu04916:Melanogenesis,mmu04917:Prolactin signaling pathway,mmu04919:Thyroid hormone signaling pathway,mmu04921:Oxytocin signaling pathway,mmu04930:Type II diabetes mellitus,mmu04960:Aldosterone-regulated sodium reabsorption,mmu05010:Alzheimer's disease,mmu05020:Prion diseases,mmu05034:Alcoholism,mmu05132:Salmonella infection,mmu05133:Pertussis,mmu05140:Leishmaniasis,mmu05142:Chagas disease (American trypanosomiasis),mmu05145:Toxoplasmosis,mmu05152:Tuberculosis,mmu05160:Hepatitis C,mmu05161:Hepatitis B,mmu05164:Influenza A,mmu05200:Pathways in cancer,mmu05203:Viral carcinogenesis,mmu05205:Proteoglycans in cancer,mmu05210:Colorectal cancer,mmu05211:Renal cell carcinoma,mmu05212:Pancreatic cancer,mmu05213:Endometrial cancer,mmu05214:Glioma,mmu05215:Prostate cancer,mmu05216:Thyroid cancer,mmu05218:Melanoma,mmu05219:Bladder cancer,mmu05220:Chronic myeloid leukemia,mmu05221:Acute myeloid leukemia,mmu05223:Non-small cell lung cancer,mmu05230:Central carbon me- |  | Acetylation,Apoptosis,ATP-binding,Cell cycle,Complete proteome,Cytoplasm,Cytoskeleton,Direct protein sequencing,Kinase,Magnesium,Nucleotide-binding,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Serine/threonine-protein kinase,Transferase,Ubl conjugation, | active site:Proton acceptor,binding site:ATP,chain:Mitogen-activated protein kinase 1,compositionally biased region:Poly-Ala,domain:Protein kinase,modified residue,nucleotide phosphate-binding region:ATP,short sequence motif:TXY, |
| 100 |  |  | Adaptive immunity,Complete proteome,Cytoplasmic vesicle,Endosome,Immunity,Ligase,Lysosome,Membrane,Metal-binding,Phosphoprotein,Proteomics identification,Reference proteome,Transmembrane,Transmembrane helix,Ubl conjugation pathway,Zinc,Zinc-finger, | chain:E3 ubiquitin-protein ligase MARCH8,transmembrane region,zinc finger region:RING-CH-type, |

| | A | B | C | D |
|---|---|---|---|---|
| 101 | Mat2a | methionine adenosyltransferase II, alpha(Mat2a) | Mus musculus | GO:0006556~S-adenosylmethionine biosynthetic process,GO:0006730~one-carbon metabolic process,GO:0007623~circadian rhythm,GO:0009725~response to hormone,GO:0034214~protein hexamerization,GO:0042493~response to drug,GO:0051291~protein heterooligomerization,GO:0051591~response to cAMP, |
| 102 | Mcm6 | minichromosome maintenance complex component 6(Mcm6) | Mus musculus | GO:0006260~DNA replication,GO:0006268~DNA unwinding involved in DNA replication,GO:0006270~DNA replication initiation,GO:0007049~cell cycle, |
| 103 | Mcm7 | minichromosome maintenance complex component 7(Mcm7) | Mus musculus | GO:0006260~DNA replication,GO:0006268~DNA unwinding involved in DNA replication,GO:0006270~DNA replication initiation,GO:0006974~cellular response to DNA damage stimulus,GO:0007049~cell cycle,GO:0008283~cell proliferation,GO:0042325~regulation of phosphorylation,GO:0042493~response to drug,GO:0071364~cellular response to epidermal growth factor stimulus,GO:0071466~cellular response to xenobiotic stimulus, |
| 104 | Mdh1 | malate dehydrogenase 1, NAD (soluble)(Mdh1) | Mus musculus | GO:0002230~positive regulation of defense response to virus by host,GO:0005975~carbohydrate metabolic process,GO:0006099~tricarboxylic acid cycle,GO:0006107~oxaloacetate metabolic process,GO:0006108~malate metabolic process,GO:0006734~NADH metabolic process,GO:0019674~NAD metabolic process,GO:0019752~carboxylic acid metabolic process,GO:0055114~oxidation-reduction process,GO:0098779~mitophagy in response to mitochondrial depolarization,GO:0098792~xenophagy, |
| 105 | Mki67 | antigen identified by monoclonal antibody Ki 67(Mki67) | Mus musculus | GO:0006259~DNA metabolic process,GO:0007049~cell cycle,GO:0007088~regulation of mitotic nuclear division,GO:0007126~meiotic nuclear division,GO:0008283~cell proliferation,GO:0014070~response to organic cyclic compound,GO:0030212~hyaluronan metabolic process,GO:0031100~organ regeneration,GO:0034605~cellular response to heat,GO:0051983~regulation of chromosome segregation,GO:0072574~hepatocyte proliferation,GO:1902275~regulation of chromatin organization,GO:1990705~cholangiocyte proliferation, |
| 106 | Mllt4 | DExD-box helicase 39A(DDX39A) | Homo sapiens | GO:0000398~mRNA splicing, via spliceosome,GO:0006369~termination of RNA polymerase II transcription,GO:0006405~RNA export from nucleus,GO:0006406~mRNA export from nucleus,GO:0006974~cellular response to DNA damage stimulus,GO:0010468~regulation of gene expression,GO:0010501~RNA secondary structure unwinding,GO:0031124~mRNA 3'-end processing, |
| 107 | Mybbp1a | MYB binding protein (P160) 1a(Mybbp1a) | Mus musculus | GO:0001649~osteoblast differentiation,GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0006913~nucleocytoplasmic transport,GO:0022904~respiratory electron transport chain,GO:0032922~circadian regulation of gene expression,GO:0042149~cellular response to glucose starvation,GO:0045892~negative regulation of transcription, DNA-templated,GO:0048511~rhythmic process,GO:0071158~positive regulation of cell cycle arrest,GO:0072332~intrinsic apoptotic signaling pathway by p53 class mediator,GO:2000210~positive regulation of anoikis, |

| | E | F | G |
|---|---|---|---|
| 101 | GO:0005829~cytosol,GO:0048269~methionine adenosyltransferase complex, | GO:0000166~nucleotide binding,GO:0004478~methionine adenosyltransferase activity,GO:0005524~ATP binding,GO:0016597~amino acid binding,GO:0016740~transferase activity,GO:0046872~metal ion binding, | IPR002133:S-adenosylmethionine synthetase,IPR022628:S-adenosylmethionine synthetase, N-terminal,IPR022629:S-adenosylmethionine synthetase, central domain,IPR022630:S-adenosylmethionine synthetase, C-terminal,IPR022631:S-adenosylmethionine synthetase, conserved site,IPR022636:S-adenosylmethionine synthetase superfamily, |
| 102 | GO:0000784~nuclear chromosome, telomeric region,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0042555~MCM complex, | GO:0000166~nucleotide binding,GO:0003677~DNA binding,GO:0003678~DNA helicase activity,GO:0003697~single-stranded DNA binding,GO:0004003~ATP-dependent DNA helicase activity,GO:0004386~helicase activity,GO:0005515~protein binding,GO:0005524~ATP binding,GO:0016787~hydrolase activity,GO:0042802~identical protein binding, | IPR001208:Mini-chromosome maintenance, DNA-dependent ATPase,IPR004039:Rubredoxin-type fold,IPR008049:DNA replication licensing factor Mcm6,IPR012340:Nucleic acid-binding, OB-fold,IPR018525:Mini-chromosome maintenance, conserved site,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |
| 103 | GO:0000784~nuclear chromosome, telomeric region,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0005829~cytosol,GO:0016020~membrane,GO:0042555~MCM complex, | GO:0000166~nucleotide binding,GO:0003677~DNA binding,GO:0003678~DNA helicase activity,GO:0003697~single-stranded DNA binding,GO:0004003~ATP-dependent DNA helicase activity,GO:0004386~helicase activity,GO:0005515~protein binding,GO:0005524~ATP binding,GO:0016787~hydrolase activity, | IPR001208:Mini-chromosome maintenance, DNA-dependent ATPase,IPR003593:AAA+ ATPase domain,IPR008050:DNA replication licensing factor Mcm7,IPR012340:Nucleic acid-binding, OB-fold,IPR018525:Mini-chromosome maintenance, conserved site,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |
| 104 | GO:0005615~extracellular space,GO:0005737~cytoplasm,GO:0005739~mitochondrion,GO:0005813~centrosome,GO:0005829~cytosol,GO:0043209~myelin sheath,GO:0070062~extracellular exosome, | GO:0003824~catalytic activity,GO:0016491~oxidoreductase activity,GO:0016615~malate dehydrogenase activity,GO:0016616~oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor,GO:0030060~L-malate dehydrogenase activity,GO:0051287~NAD binding, | IPR001236:Lactate/malate dehydrogenase, N-terminal,IPR001252:Malate dehydrogenase, active site,IPR001557:L-lactate/malate dehydrogenase,IPR010945:Malate dehydrogenase, type 2,IPR011274:Malate dehydrogenase, NAD-dependent, cytosolic,IPR015955:Lactate dehydrogenase/glycoside hydrolase, family 4, C-terminal,IPR016040:NAD(P)-binding domain,IPR022383:Lactate/malate dehydrogenase, C-terminal, |
| 105 | GO:0000775~chromosome, centromeric region,GO:0000793~condensed chromosome,GO:0005634~nucleus,GO:0005694~chromosome,GO:0005730~nucleolus,GO:0005737~cytoplasm,GO:0016020~membrane, | GO:0000166~nucleotide binding,GO:0003677~DNA binding,GO:0005524~ATP binding,GO:0008022~protein C-terminus binding,GO:0044822~poly(A) RNA binding, | IPR000253:Forkhead-associated (FHA) domain,IPR008984:SMAD/FHA domain,IPR012568:K167R, |
| 106 | GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005681~spliceosomal complex,GO:0005737~cytoplasm,GO:0016020~membrane, | GO:0003676~nucleic acid binding,GO:0004004~ATP-dependent RNA helicase activity,GO:0005515~protein binding,GO:0005524~ATP binding,GO:0016887~ATPase activity,GO:0042802~identical protein binding,GO:0044822~poly(A) RNA binding, | IPR001650:Helicase, C-terminal,IPR011545:DNA/RNA helicase, DEAD/DEAH box type, N-terminal,IPR014001:Helicase, superfamily 1/2, ATP-binding domain,IPR014014:RNA helicase, DEAD-box type, Q motif,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |
| 107 | GO:0005634~nucleus,GO:0005730~nucleolus,GO:0005737~cytoplasm,GO:0016020~membrane,GO:0042564~NLS-dependent protein nuclear import complex,GO:0043231~intracellular membrane-bounded organelle, | GO:0001047~core promoter binding,GO:0003677~DNA binding,GO:0003714~transcription corepressor activity,GO:0003887~DNA-directed DNA polymerase activity,GO:0005515~protein binding,GO:0008134~transcription factor binding,GO:0008270~zinc ion binding,GO:0043565~sequence-specific DNA binding,GO:0044822~poly(A) RNA binding, | IPR007015:DNA polymerase V,IPR016024:Armadillo-type fold, |

| | H | I | J | K |
|---|---|---|---|---|
| 101 | mmu00270:Cysteine and methionine metabolism,mmu01100:Metabolic pathways,mmu01230:Biosynthesis of amino acids, | PIRSF000497:methionine adenosyltransferase, | Acetylation,ATP-binding,Complete proteome,Magnesium,Metal-binding,Nucleotide-binding,One-carbon metabolism,Phosphoprotein,Potassium,Proteomics identification,Reference proteome,Transferase, | binding site:ATP,chain:S-adenosylmethionine synthetase isoform type-2,metal ion-binding site:Magnesium,metal ion-binding site:Potassium,modified residue,nucleotide phosphate-binding region:ATP,sequence conflict, |
| 102 | mmu03030:DNA replication,mmu04110:Cell cycle, | | Acetylation,ATP-binding,Cell cycle,Complete proteome,Direct protein sequencing,DNA replication,DNA-binding,Glycoprotein,Helicase,Hydrolase,Nucleotide-binding,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome, | chain:DNA replication licensing factor Mcm6,domain:MCM,modified residue,nucleotide phosphate-binding region:ATP, |
| 103 | mmu03030:DNA replication,mmu04110:Cell cycle, | | Acetylation,ATP-binding,Cell cycle,Complete proteome,DNA replication,DNA-binding,Glycoprotein,Helicase,Hydrolase,Nucleotide-binding,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome, | chain:DNA replication licensing factor mcm7,domain:MCM,modified residue,nucleotide phosphate-binding region:ATP,region of interest:Interaction with ATRIP,region of interest:Interaction with RAD17, |
| 104 | mmu00020:Citrate cycle (TCA cycle),mmu00270:Cysteine and methionine metabolism,mmu00620:Pyruvate metabolism,mmu00630:Glyoxylate and dicarboxylate metabolism,mmu01100:Metabolic pathways,mmu01130:Biosynthesis of antibiotics,mmu01200:Carbon metabolism,mmu04964:Proximal tubule bicarbonate reclamation, | PIRSF000102:L-lactate/malate dehydrogenase, | Acetylation,Complete proteome,Cytoplasm,Direct protein sequencing,Methylation,NAD,Oxidoreductase,Phosphoprotein,Proteomics identification,Reference proteome,Tricarboxylic acid cycle,Ubl conjugation, | active site:Proton acceptor,binding site:NAD,binding site:Substrate,chain:Malate dehydrogenase, cytoplasmic,modified residue,nucleotide phosphate-binding region:NAD,sequence conflict, |
| 105 | | | Acetylation,Alternative splicing,ATP-binding,Cell cycle,Chromosome,Complete proteome,DNA-binding,Isopeptide bond,Nucleotide-binding,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,Ubl conjugation, | |
| 106 | | SM00487:DEXDc,<br>SM00490:HELICc, | Acetylation,Alternative splicing,ATP-binding,Complete proteome,Cytoplasm,Helicase,Hydrolase,Isopeptide bond,mRNA processing,mRNA splicing,Nucleotide-binding,Nucleus,Phosphoprotein,Polymorphism,Proteomics identification,Reference proteome,RNA-binding,Ubl conjugation, | chain:ATP-dependent RNA helicase DDX39,compositionally biased region:Poly-Glu,domain:Helicase ATP-binding,domain:Helicase C-terminal,modified residue,nucleotide phosphate-binding region:ATP,sequence conflict,sequence variant,short sequence motif:DECD box,short sequence motif:Q motif, |
| 107 | | | Acetylation,Activator,Biological rhythms,Citrullination,Complete proteome,Cytoplasm,Direct protein sequencing,Nucleus,Phosphoprotein,Reference proteome,Repressor,Transcription,Transcription regulation, | chain:Myb-binding protein 1A,compositionally biased region:Asp-rich,modified residue,mutagenesis site,region of interest:Interaction with MYB,region of interest:Required for nuclear and nucleolar localization,sequence conflict,short sequence motif:Nuclear export signal 1,short sequence motif:Nuclear export signal 2, |

|  | A | B | C | D |
|---|---|---|---|---|
| 108 | Myh10 | myosin, heavy polypeptide 10, non-muscle(Myh10) | Mus musculus | GO:0000281~mitotic cytokinesis,GO:0001701~in utero embryonic development,GO:0001764~neuron migration,GO:0001778~plasma membrane repair,GO:0003279~cardiac septum development,GO:0006887~exocytosis,GO:0006930~substrate-dependent cell migration, cell extension,GO:0007097~nuclear migration,GO:0007155~cell adhesion,GO:0007409~axonogenesis,GO:0007411~axon guidance,GO:0007420~brain development,GO:0007507~heart development,GO:0007512~adult heart development,GO:0008283~cell proliferation,GO:0008360~regulation of cell shape,GO:0021592~fourth ventricle development,GO:0021670~lateral ventricle development,GO:0021678~third ventricle development,GO:0021680~cerebellar Purkinje cell layer development,GO:0030036~actin cytoskeleton organization,GO:0030048~actin filament-based movement,GO:0030239~myofibril assembly,GO:0031032~actomyosin structure organization,GO:0031175~neuron projection development,GO:0035904~aorta development,GO:0050885~neuromuscular process controlling balance,GO:0055003~cardiac myofibril assembly,GO:0055015~ventricular cardiac muscle cell development,GO:0060041~retina development in camera-type eye,GO:0060976~coronary vasculature development, |
| 109 | Myl9 | myosin, light polypeptide 9, regulatory(Myl9) | Mus musculus | GO:0070527~platelet aggregation, |
| 110 | Mylk | myosin, light polypeptide kinase(Mylk) | Mus musculus | GO:0002230~positive regulation of defense response to virus by host,GO:0006468~protein phosphorylation,GO:0006939~smooth muscle contraction,GO:0014820~tonic smooth muscle contraction,GO:0016310~phosphorylation,GO:0030335~positive regulation of cell migration,GO:0032060~bleb assembly,GO:0035690~cellular response to drug,GO:0035865~cellular response to potassium ion,GO:0051928~positive regulation of calcium ion transport,GO:0060414~aorta smooth muscle tissue morphogenesis,GO:0071277~cellular response to calcium ion,GO:0071476~cellular hypotonic response,GO:0090303~positive regulation of wound healing,GO:0098779~mitophagy in response to mitochondrial depolarization,GO:0098792~xenophagy, |
| 111 | Myo18a | myosin XVIIIA(Myo18a) | Mus musculus | GO:0007030~Golgi organization,GO:0016477~cell migration,GO:0031032~actomyosin structure organization,GO:0043066~negative regulation of apoptotic process,GO:0048194~Golgi vesicle budding,GO:0050714~positive regulation of protein secretion,GO:0090161~Golgi ribbon formation,GO:0090164~asymmetric Golgi ribbon formation, |
| 112 | Ncl | nucleolin(Ncl) | Mus musculus | GO:0001525~angiogenesis,GO:0006897~endocytosis,GO:0032760~positive regulation of tumor necrosis factor production,GO:0043066~negative regulation of apoptotic process,GO:0045944~positive regulation of transcription from RNA polymerase II promoter,GO:0071222~cellular response to lipopolysaccharide,GO:0071364~cellular response to epidermal growth factor stimulus,GO:1901838~positive regulation of transcription of nuclear large rRNA transcript from RNA polymerase I promoter,GO:2000232~regulation of rRNA processing,GO:2000778~positive regulation of interleukin-6 secretion, |

|  | E | F | G |
|---|---|---|---|
| 108 | GO:0001725~stress fiber,GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005739~mitochondrion,GO:0005819~spindle,GO:0005829~cytosol,GO:0005886~plasma membrane,GO:0005903~brush border,GO:0005938~cell cortex,GO:0015629~actin cytoskeleton,GO:0016459~myosin complex,GO:0016460~myosin II complex,GO:0030027~lamellipodium,GO:0030424~axon,GO:0030426~growth cone,GO:0030496~midbody,GO:0031594~neuromuscular junction,GO:0032154~cleavage furrow,GO:0042641~actomyosin,GO:0042995~cell projection,GO:0043005~neuron projection,GO:0043025~neuronal cell body,GO:0043197~dendritic spine,GO:0070062~extracellular exosome,GO:0097513~myosin II filament, | GO:0000146~microfilament motor activity,GO:0000166~nucleotide binding,GO:0003774~motor activity,GO:0003779~actin binding,GO:0005515~protein binding,GO:0005516~calmodulin binding,GO:0005524~ATP binding,GO:0030898~actin-dependent ATPase activity,GO:0043531~ADP binding,GO:0051015~actin filament binding, | IPR000048:IQ motif, EF-hand binding site,IPR001609:Myosin head, motor domain,IPR002928:Myosin tail,IPR004009:Myosin, N-terminal, SH3-like,IPR008989:Myosin S1 fragment, N-terminal,IPR027401:Myosin-like IQ motif-containing domain,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |
| 109 | GO:0001725~stress fiber,GO:0016459~myosin complex,GO:0016460~myosin II complex,GO:0030018~Z disc, | GO:0005509~calcium ion binding,GO:0032036~myosin heavy chain binding,GO:0046872~metal ion binding, | IPR002048:EF-hand domain,IPR011992:EF-hand-like domain,IPR018247:EF-Hand 1, calcium-binding site, |
| 110 | GO:0001725~stress fiber,GO:0005737~cytoplasm,GO:0005856~cytoskeleton,GO:0005911~cell-cell junction,GO:0030027~lamellipodium,GO:0032154~cleavage furrow,GO:0042995~cell projection,GO:0070062~extracellular exosome, | GO:0000166~nucleotide binding,GO:0003779~actin binding,GO:0004672~protein kinase activity,GO:0004674~protein serine/threonine kinase activity,GO:0004687~myosin light chain kinase activity,GO:0005516~calmodulin binding,GO:0005524~ATP binding,GO:0016301~kinase activity,GO:0016740~transferase activity,GO:0019899~enzyme binding,GO:0046872~metal ion binding, | IPR000719:Protein kinase, catalytic domain,IPR003598:Immunoglobulin subtype 2,IPR003599:Immunoglobulin subtype,IPR003961:Fibronectin, type III,IPR007110:Immunoglobulin-like domain,IPR008271:Serine/threonine-protein kinase, active site,IPR011009:Protein kinase-like domain,IPR013098:Immunoglobulin I-set,IPR013783:Immunoglobulin-like fold,IPR017441:Protein kinase, ATP binding site, |
| 111 | GO:0000139~Golgi membrane,GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0005793~endoplasmic reticulum-Golgi intermediate compartment,GO:0005794~Golgi apparatus,GO:0005802~trans-Golgi network,GO:0005856~cytoskeleton,GO:0005903~brush border,GO:0016020~membrane,GO:0016459~myosin complex,GO:0042641~actomyosin, | GO:0000166~nucleotide binding,GO:0003774~motor activity,GO:0005524~ATP binding,GO:0043531~ADP binding,GO:0044822~poly(A) RNA binding,GO:0051015~actin filament binding, | IPR000048:IQ motif, EF-hand binding site,IPR001478:PDZ domain,IPR001609:Myosin head, motor domain,IPR002928:Myosin tail,IPR027401:Myosin-like IQ motif-containing domain,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |
| 112 | GO:0001650~fibrillar center,GO:0001651~dense fibrillar component,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005730~nucleolus,GO:0005737~cytoplasm,GO:0005938~cell cortex,GO:0009986~cell surface,GO:0016020~membrane,GO:0030529~intracellular ribonucleoprotein complex,GO:0036464~cytoplasmic ribonucleoprotein granule,GO:0070062~extracellular exosome, | GO:0000166~nucleotide binding,GO:0003676~nucleic acid binding,GO:0003677~DNA binding,GO:0003697~single-stranded DNA binding,GO:0003723~RNA binding,GO:0005102~receptor binding,GO:0005509~calcium ion binding,GO:0005515~protein binding,GO:0008022~protein C-terminus binding,GO:0035368~selenocysteine insertion sequence binding,GO:0042134~rRNA primary transcript binding,GO:0042162~telomeric DNA binding,GO:0042393~histone binding,GO:0042802~identical protein binding,GO:0043236~laminin binding,GO:0043565~sequence-specific DNA binding,GO:0044822~poly(A) RNA binding,GO:1990631~ErbB-4 class receptor binding, | IPR000504:RNA recognition motif domain,IPR012677:Nucleotide-binding, alpha-beta plait, |

| | H | I | J | K |
|---|---|---|---|---|
| 108 | mmu04530:Tight junction, | | Acetylation,Actin-binding,ATP-binding,Calmodulin-binding,Cell adhesion,Cell projection,Cell shape,Coiled coil,Complete proteome,Methylation,Motor protein,Myosin,Nucleotide-binding,Phosphoprotein,Proteomics identification,Reference proteome, | chain:Myosin-10,domain:IQ,domain:Myosin head-like,modified residue,nucleotide phosphate-binding region:ATP, |
| 109 | mmu04022:cGMP-PKG signaling pathway,mmu04024:cAMP signaling pathway,mmu04270:Vascular smooth muscle contraction,mmu04510:Focal adhesion,mmu04530:Tight junction,mmu04670:Leukocyte transendothelial migration,mmu04810:Regulation of actin cytoskeleton,mmu04921:Oxytocin signaling pathway, | | Acetylation,Calcium,Complete proteome,Metal-binding,Motor protein,Muscle protein,Myosin,Phosphoprotein,Reference proteome,Repeat, | chain:Myosin regulatory light polypeptide 9,domain:EF-hand 1,domain:EF-hand 2,domain:EF-hand 3,modified residue,sequence conflict, |
| 110 | mmu04020:Calcium signaling pathway,mmu04022:cGMP-PKG signaling pathway,mmu04270:Vascular smooth muscle contraction,mmu04510:Focal adhesion,mmu04611:Platelet activation,mmu04810:Regulation of actin cytoskeleton,mmu04921:Oxytocin signaling pathway,mmu04971:Gastric acid secretion, | | Actin-binding,Alternative initiation,Alternative promoter usage,Alternative splicing,ATP-binding,Calcium,Calmodulin-binding,Cell projection,Complete proteome,Cytoplasm,Cytoskeleton,Disulfide bond,Immunoglobulin domain,Kinase,Magnesium,Metal-binding,Nucleotide-binding,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,Serine/threonine-protein kinase,Transferase, | active site:Proton acceptor,binding site:ATP,chain:Myosin light chain kinase, smooth muscle,compositionally biased region:Glu-rich,domain:Fibronectin type-III,domain:Ig-like C2-type 1,domain:Ig-like C2-type 2,domain:Ig-like C2-type 3,domain:Ig-like C2-type 4,domain:Ig-like C2-type 5,domain:Ig-like C2-type 6,domain:Ig-like C2-type 7,domain:Ig-like C2-type 8,domain:Ig-like C2-type 9,domain:Protein kinase,modified residue,nucleotide phosphate-binding region:ATP,region of interest:5 X 12 AA approximate tandem repeats,region of interest:5 X 28 AA approximate tandem repeats,region of interest:Actin-binding (calcium/calmodulin- insensitive),region of interest:Actin-binding (calcium/calmodulin- sensitive),region of interest:Calmodulin-binding,repeat:1-1,repeat:1-2,repeat:1-3,repeat:1-4,repeat:1-5; truncated,repeat:2-1,repeat:2-2,repeat:2-3,repeat:2-4,repeat:2-5,sequence conflict,splice variant, |
| 111 | | | Alternative splicing,ATP-binding,Coiled coil,Complete proteome,Cytoplasm,Cytoskeleton,Golgi apparatus,Motor protein,Myosin,Nucleotide-binding,Phosphoprotein,Proteomics identification,Reference proteome, | chain:Myosin-XVIIIa,domain:IQ,domain:Myosin head-like,domain:PDZ,modified residue,nucleotide phosphate-binding region:ATP,sequence conflict,short sequence motif:Interaction with actin,splice variant, |
| 112 | | | Acetylation,Complete proteome,Cytoplasm,Direct protein sequencing,DNA-binding,Isopeptide bond,Methylation,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,RNA-binding,Ubl conjugation, | chain:Nucleolin,compositionally biased region:Arg/Gly/Phe-rich,compositionally biased region:Asp/Glu-rich (acidic),domain:RRM 1,domain:RRM 2,domain:RRM 3,domain:RRM 4,modified residue,region of interest:8 X 8 AA tandem repeats of X-T-P-X-K-K-X-X,repeat:1,repeat:2,repeat:3,repeat:4,repeat:5; truncated,repeat:6,repeat:7,repeat:8,sequence conflict, |

| | A | B | C | D |
|---|---|---|---|---|
| 113 | Ndufa4 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4(Ndufa4) | Mus musculus | GO:0006810~transport,GO:0055114~oxidation-reduction process, |
| 114 | Nmral1 | NmrA-like family domain containing 1(Nmral1) | Mus musculus | |
| 115 | Nolc1 | nucleolar and coiled-body phosphoprotein 1(Nolc1) | Mus musculus | GO:0007000~nucleolus organization, |
| 116 | Nop58 | NOP58 ribonucleoprotein(Nop58) | Mus musculus | GO:0000154~rRNA modification,GO:0006608~snRNP protein import into nucleus,GO:0042254~ribosome biogenesis,GO:0048254~snoRNA localization, |
| 117 | Npm1 | nucleophosmin 1(Npm1) | Mus musculus | GO:0000055~ribosomal large subunit export from nucleus,GO:0000056~ribosomal small subunit export from nucleus,GO:0000448~cleavage in ITS2 between 5.8S rRNA and LSU-rRNA of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA),GO:0006281~DNA repair,GO:0006334~nucleosome assembly,GO:0006407~rRNA export from nucleus,GO:0006884~cell volume homeostasis,GO:0006913~nucleocytoplasmic transport,GO:0006950~response to stress,GO:0007098~centrosome cycle,GO:0007569~cell aging,GO:0008104~protein localization,GO:0008284~positive regulation of cell proliferation,GO:0008285~negative regulation of cell proliferation,GO:0009303~rRNA transcription,GO:0010608~posttranscriptional regulation of gene expression,GO:0010629~negative regulation of gene expression,GO:0010667~negative regulation of cardiac muscle cell apoptotic process,GO:0010824~regulation of centrosome duplication,GO:0010825~positive regulation of centrosome duplication,GO:0010826~negative regulation of centrosome duplication,GO:0016049~cell growth,GO:0019827~stem cell population maintenance,GO:0031328~positive regulation of cellular biosynthetic process,GO:0031398~positive regulation of protein ubiquitination,GO:0031647~regulation of protein stability,GO:0031648~protein destabilization,GO:0032071~regulation of endodeoxyribonuclease activity,GO:0042273~ribosomal large subunit biogenesis,GO:0042274~ribosomal small subunit biogenesis,GO:0043066~negative regulation of apoptotic process,GO:0043085~positive regulation of catalytic activity,GO:0043516~regulation of DNA damage response, signal transduction by p53 class mediator,GO:0043523~regulation of neuron apoptotic process,GO:0043524~negative regulation of neuron apoptotic process,GO:0044387~negative regulation of protein kinase activity by regulation of protein phosphorylation,GO:0045727~positive regulation of translation,GO:0045740~positive regulation of DNA replication,GO:0045860~positive regulation of protein kinase activity,GO:0045893~positive regulation of transcription, DNA-templated,GO:0046599~regulation of centriole replication,GO:0048025~negative regulation of mRNA splicing, via spliceosome,GO:0050680~negative regulation of epithelial cell proliferation,GO:0050821~protein stabilization,GO:0051054~positive regulation of DNA metabolic process,GO:0051092~positive regulation of NF-kappaB transcription factor activity,GO:0051259~protein oligomerization,GO:0051260~protein homooligomerization,GO:0051726~regulation of cell cycle,GO:0060699~regulation of endoribonuclease activity,GO:0060735~regulation of eIF2 alpha phosphorylation by dsRNA,GO:1900264~positive regulation of DNA-directed DNA polymerase activity,GO:1902751~positive regulation of cell cycle G2/M phase transition,GO:1904751~positive regulation of protein localization to nucleolus,GO:2000381~negative regulation of mesoderm development, |
| 118 | Nup107 | nucleoporin 107(Nup107) | Mus musculus | GO:0000973~posttranscriptional tethering of RNA polymerase II gene DNA at nuclear periphery,GO:0006355~regulation of transcription, DNA-templated,GO:0006406~mRNA export from nucleus,GO:0006606~protein import into nucleus,GO:0006810~transport,GO:0015031~protein transport,GO:0051028~mRNA transport,GO:0051292~nuclear pore complex assembly, |

| | E | F | G |
|---|---|---|---|
| 113 | GO:0005739~mitochondrion,GO:0005743~mitochondrial inner membrane,GO:0005747~mitochondrial respiratory chain complex I,GO:0005751~mitochondrial respiratory chain complex IV,GO:0016020~membrane,GO:0070062~extracellular exosome,GO:0070469~respiratory chain, | GO:0004129~cytochrome-c oxidase activity,GO:0008137~NADH dehydrogenase (ubiquinone) activity,GO:0032403~protein complex binding, | IPR010530:NADH-ubiquinone reductase complex 1 MLRQ subunit, |
| 114 | GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0048471~perinuclear region of cytoplasm, | | IPR008030:NmrA-like,IPR016040:NAD(P)-binding domain, |
| 115 | GO:0005654~nucleoplasm,GO:0005730~nucleolus,GO:0015030~Cajal body,GO:0030532~small nuclear ribonucleoprotein complex, | GO:0005515~protein binding,GO:0044822~poly(A) RNA binding, | IPR006594:LisH dimerisation motif,IPR007718:SRP40, C-terminal, |
| 116 | GO:0005634~nucleus,GO:0005730~nucleolus,GO:0005732~small nucleolar ribonucleoprotein complex,GO:0005737~cytoplasm,GO:0015030~Cajal body,GO:0016020~membrane,GO:0030529~intracellular ribonucleoprotein complex,GO:0031428~box C/D snoRNP complex,GO:0032040~small-subunit processome,GO:0070761~pre-snoRNP complex, | GO:0001094~TFIID-class transcription factor binding,GO:0030515~snoRNA binding,GO:0044822~poly(A) RNA binding,GO:0051117~ATPase binding, | IPR002687:Nop domain,IPR012974:NOP5, N-terminal,IPR012976:NOSIC, |
| 117 | GO:0001652~granular component,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005730~nucleolus,GO:0005737~cytoplasm,GO:0005813~centrosome,GO:0005829~cytosol,GO:0005856~cytoskeleton,GO:0005925~focal adhesion,GO:0015934~large ribosomal subunit,GO:0015935~small ribosomal subunit,GO:0016020~membrane,GO:0016363~nuclear matrix,GO:0016607~nuclear speck,GO:0030529~intracellular ribonucleoprotein complex,GO:0031616~spindle pole centrosome, | GO:0002039~p53 binding,GO:0003676~nucleic acid binding,GO:0003677~DNA binding,GO:0003713~transcription coactivator activity,GO:0003723~RNA binding,GO:0004860~protein kinase inhibitor activity,GO:0005515~protein binding,GO:0005524~ATP binding,GO:0005547~phosphatidylinositol-3,4,5-trisphosphate binding,GO:0008134~transcription factor binding,GO:0019843~rRNA binding,GO:0019899~enzyme binding,GO:0019901~protein kinase binding,GO:0030957~Tat protein binding,GO:0042393~histone binding,GO:0042803~protein homodimerization activity,GO:0043023~ribosomal large subunit binding,GO:0043024~ribosomal small subunit binding,GO:0043422~protein kinase B binding,GO:0044822~poly(A) RNA binding,GO:0046982~protein heterodimerization activity,GO:0047485~protein N-terminus binding,GO:0051059~NF-kappaB binding,GO:0051082~unfolded protein binding, | IPR004301:Nucleoplasmin,IPR024057:Nucleoplasmin core domain, |
| 118 | GO:0000775~chromosome, centromeric region,GO:0000776~kinetochore,GO:0000777~condensed chromosome kinetochore,GO:0005634~nucleus,GO:0005643~nuclear pore,GO:0005654~nucleoplasm,GO:0005694~chromosome,GO:0005813~centrosome,GO:0016020~membrane,GO:0016021~integral component of membrane,GO:0031080~nuclear pore outer ring,GO:0031965~nuclear membrane,GO:0034399~nuclear periphery, | GO:0005487~nucleocytoplasmic transporter activity,GO:0017056~structural constituent of nuclear pore, | IPR007252:Nuclear pore protein 84/107, |

|  | H | I | J | K |
|---|---|---|---|---|
| 113 | mmu00190:Oxidative phosphorylation,mmu01100:Metabolic pathways,mmu04932:Non-alcoholic fatty liver disease (NAFLD),mmu05010:Alzheimer's disease,mmu05012:Parkinson's disease,mmu05016:Huntington's disease, |  | 3D-structure,Acetylation,Complete proteome,Direct protein sequencing,Electron transport,Membrane,Mitochondrion,Mitochondrion inner membrane,Phosphoprotein,Proteomics identification,Reference proteome,Respiratory chain,Transport, | chain:NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4,modified residue, |
| 114 |  |  | Alternative splicing,Complete proteome,Cytoplasm,Direct protein sequencing,NADP,Nucleus,Proteomics identification,Reference proteome, | binding site:NADP,binding site:NADP; shared with dimeric partner,chain:NmrA-like family domain-containing protein 1,disulfide bond,nucleotide phosphate-binding region:NADP,region of interest:Interaction with ASS1,sequence conflict,splice variant, |
| 115 |  |  | Coiled coil,Complete proteome,Proteomics identification,Reference proteome, |  |
| 116 | mmu03008:Ribosome biogenesis in eukaryotes, |  | Coiled coil,Complete proteome,Isopeptide bond,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Ribonucleoprotein,Ribosome biogenesis,Ubl conjugation, | chain:Nucleolar protein 58,compositionally biased region:Lys-rich,domain:Nop,modified residue,sequence conflict, |
| 117 |  |  | 3D-structure,Acetylation,ADP-ribosylation,Chaperone,Complete proteome,Cytoplasm,Cytoskeleton,Direct protein sequencing,Disulfide bond,DNA-binding,Isopeptide bond,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,RNA-binding,Ubl conjugation, | chain:Nucleophosmin,compositionally biased region:Asp/Glu-rich (acidic),compositionally biased region:Asp/Glu-rich (highly acidic),compositionally biased region:Met-rich,cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO),modified residue,region of interest:Required for interaction with SENP3,region of interest:Required for nucleolar localization,short sequence motif:Nuclear localization signal, |
| 118 | mmu03013:RNA transport, |  | Acetylation,Centromere,Chromosome,Complete proteome,Kinetochore,Membrane,Methylation,mRNA transport,Nuclear pore complex,Nucleus,Phosphoprotein,Protein transport,Proteomics identification,Reference proteome,Translocation,Transmembrane,Transmembrane helix,Transport, | chain:Nuclear pore complex protein Nup107,modified residue, |

|  | A | B | C | D |
|---|---|---|---|---|
| 119 | Parp1 | poly (ADP-ribose) polymerase family, member 1(Parp1) | Mus musculus | GO:0000723~telomere maintenance,GO:0006259~DNA metabolic process,GO:0006273~lagging strand elongation,GO:0006281~DNA repair,GO:0006284~base-excision repair,GO:0006302~double-strand break repair,GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0006471~protein ADP-ribosylation,GO:0006974~cellular response to DNA damage stimulus,GO:0007005~mitochondrion organization,GO:0007179~transforming growth factor beta receptor signaling pathway,GO:0010332~response to gamma radiation,GO:0010613~positive regulation of cardiac muscle hypertrophy,GO:0010990~regulation of SMAD protein complex assembly,GO:0016540~protein autoprocessing,GO:0023019~signal transduction involved in regulation of gene expression,GO:0032042~mitochondrial DNA metabolic process,GO:0032869~cellular response to insulin stimulus,GO:0033148~positive regulation of intracellular estrogen receptor signaling pathway,GO:0034599~cellular response to oxidative stress,GO:0036211~protein modification process,GO:0040009~regulation of growth rate,GO:0042769~DNA damage response, detection of DNA damage,GO:0043504~mitochondrial DNA repair,GO:0044030~regulation of DNA methylation,GO:0045944~positive regulation of transcription from RNA polymerase II promoter,GO:0048148~behavioral response to cocaine,GO:0051103~DNA ligation involved in DNA repair,GO:0051901~positive regulation of mitochondrial depolarization,GO:0060391~positive regulation of SMAD protein import into nucleus,GO:0070212~protein poly-ADP-ribosylation,GO:0071294~cellular response to zinc ion,GO:0071451~cellular response to superoxide,GO:0071560~cellular response to transforming growth factor beta stimulus,GO:1900182~positive regulation of protein localization to nucleus,GO:1901216~positive regulation of neuron death,GO:1903376~regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway,GO:1903516~regulation of single strand break repair,GO:1903827~regulation of cellular protein localization,GO:1904044~response to aldosterone,GO:1904357~negative regulation of telomere maintenance via telomere lengthening,GO:1904646~cellular response to beta-amyloid,GO:1904762~positive regulation of myofibroblast differentiation,GO:1905077~negative regulation of interleukin-17 secretion,GO:1990966~ATP generation from poly-ADP-D-ribose,GO:2000679~positive regulation of transcription regulatory region DNA binding,GO:2001170~negative regulation of ATP biosynthetic process, |
| 120 | parp1 | poly (ADP-ribose) polymerase family, member 1(Parp1) | Mus musculus | GO:0000723~telomere maintenance,GO:0006259~DNA metabolic process,GO:0006273~lagging strand elongation,GO:0006281~DNA repair,GO:0006284~base-excision repair,GO:0006302~double-strand break repair,GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0006471~protein ADP-ribosylation,GO:0006974~cellular response to DNA damage stimulus,GO:0007005~mitochondrion organization,GO:0007179~transforming growth factor beta receptor signaling pathway,GO:0010332~response to gamma radiation,GO:0010613~positive regulation of cardiac muscle hypertrophy,GO:0010990~regulation of SMAD protein complex assembly,GO:0016540~protein autoprocessing,GO:0023019~signal transduction involved in regulation of gene expression,GO:0032042~mitochondrial DNA metabolic process,GO:0032869~cellular response to insulin stimulus,GO:0033148~positive regulation of intracellular estrogen receptor signaling pathway,GO:0034599~cellular response to oxidative stress,GO:0036211~protein modification process,GO:0040009~regulation of growth rate,GO:0042769~DNA damage response, detection of DNA damage,GO:0043504~mitochondrial DNA repair,GO:0044030~regulation of DNA methylation,GO:0045944~positive regulation of transcription from RNA polymerase II promoter,GO:0048148~behavioral response to cocaine,GO:0051103~DNA ligation involved in DNA repair,GO:0051901~positive regulation of mitochondrial depolarization,GO:0060391~positive regulation of SMAD protein import into nucleus,GO:0070212~protein poly-ADP-ribosylation,GO:0071294~cellular response to zinc ion,GO:0071451~cellular response to superoxide,GO:0071560~cellular response to transforming growth factor beta stimulus,GO:1900182~positive regulation of protein localization to nucleus,GO:1901216~positive regulation of neuron death,GO:1903376~regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway,GO:1903516~regulation of single strand break repair,GO:1903827~regulation of cellular protein localization,GO:1904044~response to aldosterone,GO:1904357~negative regulation of telomere maintenance via telomere lengthening,GO:1904646~cellular response to beta-amyloid,GO:1904762~positive regulation of myofibroblast differentiation,GO:1905077~negative regulation of interleukin-17 secretion,GO:1990966~ATP generation from poly-ADP-D-ribose,GO:2000679~positive regulation of transcription regulatory region DNA binding,GO:2001170~negative regulation of ATP biosynthetic process, |
| 121 | Pbx1 | pre B cell leukemia homeobox 1(Pbx1) | Mus musculus | GO:0001655~urogenital system development,GO:0001658~branching involved in ureteric bud morphogenesis,GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0006694~steroid biosynthetic process,GO:0007275~multicellular organism development,GO:0007548~sex differentiation,GO:0008284~positive regulation of cell proliferation,GO:0009887~organ morphogenesis,GO:0009952~anterior/posterior pattern specification,GO:0009954~proximal/distal pattern formation,GO:0010971~positive regulation of G2/M transition of mitotic cell cycle,GO:0030154~cell differentiation,GO:0030278~regulation of ossification,GO:0030325~adrenal gland development,GO:0030326~embryonic limb morphogenesis,GO:0035162~embryonic hemopoiesis,GO:0042127~regulation of cell proliferation,GO:0045665~negative regulation of neuron differentiation,GO:0045944~positive regulation of transcription from RNA polymerase II promoter,GO:0048536~spleen development,GO:0048538~thymus development,GO:0048568~embryonic organ development,GO:0048706~embryonic skeletal system development, |

| | E | F | G |
|---|---|---|---|
| 119 | GO:0000784~nuclear chromosome, telomeric region,GO:0005634~nucleus,GO:0005635~nuclear envelope,GO:0005654~nucleoplasm,GO:0005667~transcription factor complex,GO:0005730~nucleolus,GO:0005737~cytoplasm,GO:0005739~mitochondrion,GO:0016020~membrane,GO:0043234~protein complex, | GO:0003677~DNA binding,GO:0003682~chromatin binding,GO:0003910~DNA ligase (ATP) activity,GO:0003950~NAD+ ADP-ribosyltransferase activity,GO:0005515~protein binding,GO:0008134~transcription factor binding,GO:0008270~zinc ion binding,GO:0016740~transferase activity,GO:0016757~transferase activity, transferring glycosyl groups,GO:0019899~enzyme binding,GO:0019901~protein kinase binding,GO:0030331~estrogen receptor binding,GO:0042802~identical protein binding,GO:0042826~histone deacetylase binding,GO:0044822~poly(A) RNA binding,GO:0046332~SMAD binding,GO:0046872~metal ion binding,GO:0047485~protein N-terminus binding,GO:0051287~NAD binding,GO:0070412~R-SMAD binding,GO:1990404~protein ADP-ribosylase activity, | IPR001357:BRCT domain,IPR001510:Zinc finger, PARP-type,IPR004102:Poly(ADP-ribose) polymerase, regulatory domain,IPR008288:NAD+ ADP-ribosyltransferase,IPR008893:WGR domain,IPR012317:Poly(ADP-ribose) polymerase, catalytic domain,IPR012982:PADR1, |
| 120 | GO:0000784~nuclear chromosome, telomeric region,GO:0005634~nucleus,GO:0005635~nuclear envelope,GO:0005654~nucleoplasm,GO:0005667~transcription factor complex,GO:0005730~nucleolus,GO:0005737~cytoplasm,GO:0005739~mitochondrion,GO:0016020~membrane,GO:0043234~protein complex, | GO:0003677~DNA binding,GO:0003682~chromatin binding,GO:0003910~DNA ligase (ATP) activity,GO:0003950~NAD+ ADP-ribosyltransferase activity,GO:0005515~protein binding,GO:0008134~transcription factor binding,GO:0008270~zinc ion binding,GO:0016740~transferase activity,GO:0016757~transferase activity, transferring glycosyl groups,GO:0019899~enzyme binding,GO:0019901~protein kinase binding,GO:0030331~estrogen receptor binding,GO:0042802~identical protein binding,GO:0042826~histone deacetylase binding,GO:0044822~poly(A) RNA binding,GO:0046332~SMAD binding,GO:0046872~metal ion binding,GO:0047485~protein N-terminus binding,GO:0051287~NAD binding,GO:0070412~R-SMAD binding,GO:1990404~protein ADP-ribosylase activity, | IPR001357:BRCT domain,IPR001510:Zinc finger, PARP-type,IPR004102:Poly(ADP-ribose) polymerase, regulatory domain,IPR008288:NAD+ ADP-ribosyltransferase,IPR008893:WGR domain,IPR012317:Poly(ADP-ribose) polymerase, catalytic domain,IPR012982:PADR1, |
| 121 | GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005667~transcription factor complex,GO:0005737~cytoplasm, | GO:0000978~RNA polymerase II core promoter proximal region sequence-specific DNA binding,GO:0001077~transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding,GO:0003677~DNA binding,GO:0003700~transcription factor activity, sequence-specific DNA binding,GO:0005515~protein binding,GO:0043565~sequence-specific DNA binding,GO:0046982~protein heterodimerization activity, | IPR001356:Homeodomain,IPR005542:PBX,IPR009057:Homeodomain-like,IPR017970:Homeobox, conserved site, |

| | H | I | J | K |
|---|---|---|---|---|
| 119 | mmu03410:Base excision repair, | PIRSF000489:poly (ADP-ribose) polymerase, | Acetylation,ADP-ribosylation,Alternative initiation,Complete proteome,Direct protein sequencing,DNA damage,DNA repair,DNA-binding,Glycosyltransferase,Isopeptide bond,Metal-binding,NAD,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,S-nitrosylation,Transcription,Transcription regulation,Transferase,Ubl conjugation,Zinc,Zinc-finger, | chain:Poly [ADP-ribose] polymerase 1,domain:BRCT,domain:PARP alpha-helical,domain:PARP catalytic,modified residue,region of interest:Automodification domain,sequence conflict,short sequence motif:Nuclear localization signal,splice variant,zinc finger region:PARP-type 1,zinc finger region:PARP-type 2, |
| 120 | mmu03410:Base excision repair, | PIRSF000489:poly (ADP-ribose) polymerase, | Acetylation,ADP-ribosylation,Alternative initiation,Complete proteome,Direct protein sequencing,DNA damage,DNA repair,DNA-binding,Glycosyltransferase,Isopeptide bond,Metal-binding,NAD,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,S-nitrosylation,Transcription,Transcription regulation,Transferase,Ubl conjugation,Zinc,Zinc-finger, | chain:Poly [ADP-ribose] polymerase 1,domain:BRCT,domain:PARP alpha-helical,domain:PARP catalytic,modified residue,region of interest:Automodification domain,sequence conflict,short sequence motif:Nuclear localization signal,splice variant,zinc finger region:PARP-type 1,zinc finger region:PARP-type 2, |
| 121 | mmu05202:Transcriptional misregulation in cancer, | | 3D-structure,Activator,Alternative splicing,Complete proteome,Developmental protein,Differentiation,Direct protein sequencing,DNA-binding,Homeobox,Nucleus,Proteomics identification,Reference proteome,Sexual differentiation,Steroidogenesis,Transcription,Transcription regulation, | chain:Pre-B-cell leukemia transcription factor 1,compositionally biased region:Poly-Ala,DNA-binding region:Homeobox; TALE-type,helix,splice variant,strand, |

|  | A | B | C | D |
|---|---|---|---|---|
| 122 | Pcna | proliferating cell nuclear antigen(Pcna) | Mus musculus | GO:0000122~negative regulation of transcription from RNA polymerase II promoter,GO:0006260~DNA replication,GO:0006272~leading strand elongation,GO:0006275~regulation of DNA replication,GO:0006281~DNA repair,GO:0006287~base-excision repair, gap-filling,GO:0006298~mismatch repair,GO:0006974~cellular response to DNA damage stimulus,GO:0019985~translesion synthesis,GO:0031297~replication fork processing,GO:0032077~positive regulation of deoxyribonuclease activity,GO:0033993~response to lipid,GO:0034644~cellular response to UV,GO:0045739~positive regulation of DNA repair,GO:0045740~positive regulation of DNA replication,GO:0071466~cellular response to xenobiotic stimulus,GO:1902990~mitotic telomere maintenance via semi-conservative replication, |
| 123 | Pes1 | pescadillo ribosomal biogenesis factor 1(Pes1) | Mus musculus | GO:0000463~maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA),GO:0000466~maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA),GO:0006364~rRNA processing,GO:0007000~nucleolus organization,GO:0008283~cell proliferation,GO:0033365~protein localization to organelle,GO:0042254~ribosome biogenesis,GO:0051726~regulation of cell cycle, |
| 124 | Pfdn2 | prefoldin 2(Pfdn2) | Mus musculus | GO:0006457~protein folding,GO:0051495~positive regulation of cytoskeleton organization, |
| 125 | Ppid | peptidylprolyl isomerase D (cyclophilin D)(Ppid) | Mus musculus | GO:0000122~negative regulation of transcription from RNA polymerase II promoter,GO:0000413~protein peptidyl-prolyl isomerization,GO:0006457~protein folding,GO:0006461~protein complex assembly,GO:0006810~transport,GO:0006915~apoptotic process,GO:0015031~protein transport,GO:0034389~lipid particle organization,GO:0042981~regulation of apoptotic process,GO:0043065~positive regulation of apoptotic process,GO:0045070~positive regulation of viral genome replication,GO:0050714~positive regulation of protein secretion,GO:0061077~chaperone-mediated protein folding,GO:0071492~cellular response to UV-A, |
| 126 | Ppp1ca | protein phosphatase 1, catalytic subunit, alpha isoform(Ppp1ca) | Mus musculus | GO:0005975~carbohydrate metabolic process,GO:0005977~glycogen metabolic process,GO:0005979~regulation of glycogen biosynthetic process,GO:0005981~regulation of glycogen catabolic process,GO:0006417~regulation of translation,GO:0006470~protein dephosphorylation,GO:0007049~cell cycle,GO:0007143~female meiotic division,GO:0009987~cellular process,GO:0016311~dephosphorylation,GO:0030324~lung development,GO:0032922~circadian regulation of gene expression,GO:0042752~regulation of circadian rhythm,GO:0043153~entrainment of circadian clock by photoperiod,GO:0048511~rhythmic process,GO:0048754~branching morphogenesis of an epithelial tube,GO:0051301~cell division,GO:2001241~positive regulation of extrinsic apoptotic signaling pathway in absence of ligand, |
| 127 | Ppp1cb | protein phosphatase 1, catalytic subunit, beta isoform(Ppp1cb) | Mus musculus | GO:0005975~carbohydrate metabolic process,GO:0005977~glycogen metabolic process,GO:0005979~regulation of glycogen biosynthetic process,GO:0005981~regulation of glycogen catabolic process,GO:0006470~protein dephosphorylation,GO:0007049~cell cycle,GO:0030155~regulation of cell adhesion,GO:0032922~circadian regulation of gene expression,GO:0042752~regulation of circadian rhythm,GO:0043153~entrainment of circadian clock by photoperiod,GO:0048511~rhythmic process,GO:0051301~cell division, |

| | E | F | G |
|---|---|---|---|
| 122 | GO:0000307~cyclin-dependent protein kinase holoenzyme complex,GO:0000784~nuclear chromosome, telomeric region,GO:0005622~intracellular,GO:0005623~cell,GO:0005634~nucleus,GO:0005652~nuclear lamina,GO:0005654~nucleoplasm,GO:0005657~replication fork,GO:0005737~cytoplasm,GO:0005813~centrosome,GO:0043596~nuclear replication fork,GO:0043626~PCNA complex,GO:0070062~extracellular exosome,GO:0070557~PCNA-p21 complex, | GO:0000701~purine-specific mismatch base pair DNA N-glycosylase activity,GO:0003677~DNA binding,GO:0003682~chromatin binding,GO:0003684~damaged DNA binding,GO:0005515~protein binding,GO:0008134~transcription factor binding,GO:0019899~enzyme binding,GO:0030331~estrogen receptor binding,GO:0030337~DNA polymerase processivity factor activity,GO:0030971~receptor tyrosine kinase binding,GO:0032139~dinucleotide insertion or deletion binding,GO:0032405~MutLalpha complex binding,GO:0035035~histone acetyltransferase binding,GO:0042802~identical protein binding,GO:0070182~DNA polymerase binding, | IPR000730:Proliferating cell nuclear antigen, PCNA,IPR022648:Proliferating cell nuclear antigen, PCNA, N-terminal,IPR022649:Proliferating cell nuclear antigen, PCNA, C-terminal,IPR022659:Proliferating cell nuclear antigen, PCNA, conserved site, |
| 123 | GO:0000793~condensed chromosome,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005694~chromosome,GO:0005730~nucleolus,GO:0005737~cytoplasm,GO:0016020~membrane,GO:0030687~preribosome, large subunit precursor,GO:0070545~PeBoW complex, | GO:0003723~RNA binding,GO:0005515~protein binding,GO:0043021~ribonucleoprotein complex binding,GO:0044822~poly(A) RNA binding, | IPR001357:BRCT domain,IPR010613:Pescadillo, |
| 124 | GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005730~nucleolus,GO:0005737~cytoplasm,GO:0005739~mitochondrion,GO:0005829~cytosol,GO:0016272~prefoldin complex,GO:0070062~extracellular exosome, | GO:0044183~protein binding involved in protein folding,GO:0051082~unfolded protein binding, | IPR002777:Prefoldin beta-like,IPR009053:Prefoldin,IPR027235:Prefoldin subunit 2, |
| 125 | GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005730~nucleolus,GO:0005737~cytoplasm,GO:0005739~mitochondrion, | GO:0003755~peptidyl-prolyl cis-trans isomerase activity,GO:0005528~FK506 binding,GO:0008134~transcription factor binding,GO:0016018~cyclosporin A binding,GO:0016853~isomerase activity,GO:0019899~enzyme binding,GO:0030331~estrogen receptor binding,GO:0030544~Hsp70 protein binding,GO:0031072~heat shock protein binding,GO:0042277~peptide binding,GO:0051879~Hsp90 protein binding, | IPR002130:Cyclophilin-like peptidyl-prolyl cis-trans isomerase domain,IPR011990:Tetratricopeptide-like helical,IPR013026:Tetratricopeptide repeat-containing domain,IPR019734:Tetratricopeptide repeat,IPR020892:Cyclophilin-type peptidyl-prolyl cis-trans isomerase, conserved site,IPR023114:Elongated TPR repeat-containing domain,IPR023566:Peptidyl-prolyl cis-trans isomerase, FKBP-type,IPR024936:Cyclophilin-type peptidyl-prolyl cis-trans isomerase, |
| 126 | GO:0000164~protein phosphatase type 1 complex,GO:0000784~nuclear chromosome, telomeric region,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005730~nucleolus,GO:0005737~cytoplasm,GO:0005886~plasma membrane,GO:0005911~cell-cell junction,GO:0042587~glycogen granule,GO:0043005~neuron projection,GO:0043025~neuronal cell body,GO:0043197~dendritic spine,GO:0043204~perikaryon,GO:0070062~extracellular exosome,GO:0070688~MLL5-L complex,GO:0072357~PTW/PP1 phosphatase complex, | GO:0004721~phosphoprotein phosphatase activity,GO:0004722~protein serine/threonine phosphatase activity,GO:0005515~protein binding,GO:0008157~protein phosphatase 1 binding,GO:0016787~hydrolase activity,GO:0016791~phosphatase activity,GO:0032403~protein complex binding,GO:0043021~ribonucleoprotein complex binding,GO:0046872~metal ion binding, | IPR004843:Metallophosphoesterase domain,IPR006186:Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase, |
| 127 | GO:0000164~protein phosphatase type 1 complex,GO:0000784~nuclear chromosome, telomeric region,GO:0005634~nucleus,GO:0005730~nucleolus,GO:0005737~cytoplasm,GO:0005925~focal adhesion,GO:0042587~glycogen granule,GO:0070062~extracellular exosome,GO:0070688~MLL5-L complex,GO:0072357~PTW/PP1 phosphatase complex, | GO:0004721~phosphoprotein phosphatase activity,GO:0004722~protein serine/threonine phosphatase activity,GO:0005515~protein binding,GO:0016787~hydrolase activity,GO:0016791~phosphatase activity,GO:0017018~myosin phosphatase activity,GO:0019901~protein kinase binding,GO:0046872~metal ion binding,GO:0050115~myosin-light-chain-phosphatase activity, | IPR004843:Metallophosphoesterase domain,IPR006186:Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase, |

| | H | I | J | K |
|---|---|---|---|---|
| 122 | mmu03030:DNA replication,mmu03410:Base excision repair,mmu03420:Nucleotide excision repair,mmu03430:Mismatch repair,mmu04110:Cell cycle,mmu05161:Hepatitis B,mmu05166:HTLV-I infection, | | Acetylation,Complete proteome,DNA damage,DNA repair,DNA replication,DNA-binding,Isopeptide bond,Methylation,Nucleus,Phosphoprotein,Reference proteome,Ubl conjugation, | chain:Proliferating cell nuclear antigen,cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin),modified residue,sequence conflict, |
| 123 | | | Acetylation,Chromosome,Coiled coil,Complete proteome,Isopeptide bond,Nucleus,Proteomics identification,Reference proteome,Ribosome biogenesis,rRNA processing,Ubl conjugation, | chain:Pescadillo homolog,compositionally biased region:Glu-rich,domain:BRCT,modified residue,region of interest:Required for 28S ribosomal RNA processing,region of interest:Sufficient for interaction with MAP1B,region of interest:Sufficient for nucleolar localization, |
| 124 | | | Chaperone,Coiled coil,Complete proteome,Cytoplasm,Mitochondrion,Nucleus,Proteomics identification,Reference proteome, | chain:Prefoldin subunit 2,sequence conflict, |
| 125 | | | Acetylation,Apoptosis,Chaperone,Complete proteome,Cyclosporin,Cytoplasm,Direct protein sequencing,Isomerase,Nucleus,Phosphoprotein,Protein transport,Proteomics identification,Reference proteome,Repeat,Rotamase,TPR repeat,Transport, | chain:40 kDa peptidyl-prolyl cis-trans isomerase,domain:PPIase cyclophilin-type,modified residue,repeat:TPR 1,repeat:TPR 2,repeat:TPR 3, |
| 126 | mmu03015:mRNA surveillance pathway,mmu04022:cGMP-PKG signaling pathway,mmu04024:cAMP signaling pathway,mmu04114:Oocyte meiosis,mmu04261:Adrenergic signaling in cardiomyocytes,mmu04270:Vascular smooth muscle contraction,mmu04390:Hippo signaling pathway,mmu04510:Focal adhesion,mmu04611:Platelet activation,mmu04720:Long-term potentiation,mmu04728:Dopaminergic synapse,mmu04750:Inflammatory mediator regulation of TRP channels,mmu04810:Regulation of actin cytoskeleton,mmu04910:Insulin signaling pathway,mmu04921:Oxytocin signaling pathway,mmu04931:Insulin resistance,mmu05031:Amphetamine addiction,mmu05034:Alcoholism,mmu05168:Herpes simplex infection,mmu05205:Proteoglycans in cancer, | | Acetylation,Biological rhythms,Carbohydrate metabolism,Cell cycle,Cell division,Complete proteome,Cytoplasm,Direct protein sequencing,Glycogen metabolism,Hydrolase,Manganese,Metal-binding,Nucleus,Phosphoprotein,Protein phosphatase,Reference proteome, | active site:Proton donor,chain:Serine/threonine-protein phosphatase PP1-alpha catalytic subunit,metal ion-binding site:Iron,metal ion-binding site:Manganese,modified residue, |
| 127 | mmu03015:mRNA surveillance pathway,mmu04022:cGMP-PKG signaling pathway,mmu04024:cAMP signaling pathway,mmu04114:Oocyte meiosis,mmu04261:Adrenergic signaling in cardiomyocytes,mmu04270:Vascular smooth muscle contraction,mmu04390:Hippo signaling pathway,mmu04510:Focal adhesion,mmu04611:Platelet activation,mmu04720:Long-term potentiation,mmu04728:Dopaminergic synapse,mmu04750:Inflammatory mediator regulation of TRP channels,mmu04810:Regulation of actin cytoskeleton,mmu04910:Insulin signaling pathway,mmu04921:Oxytocin signaling pathway,mmu04931:Insulin resistance,mmu05031:Amphetamine addiction,mmu05034:Alcoholism,mmu05168:Herpes simplex infection,mmu05205:Proteoglycans in cancer, | | Acetylation,Biological rhythms,Carbohydrate metabolism,Cell cycle,Cell division,Complete proteome,Cytoplasm,Direct protein sequencing,Glycogen metabolism,Hydrolase,Manganese,Metal-binding,Nucleus,Phosphoprotein,Protein phosphatase,Proteomics identification,Reference proteome, | active site:Proton donor,chain:Serine/threonine-protein phosphatase PP1-beta catalytic subunit,metal ion-binding site:Iron,metal ion-binding site:Manganese,modified residue, |

|  | A | B | C | D |
|---|---|---|---|---|
| 128 | Ppp1cc | protein phosphatase 1, catalytic subunit, gamma isoform(Ppp1cc) | Mus musculus | GO:0005977~glycogen metabolic process,GO:0006470~protein dephosphorylation,GO:0007049~cell cycle,GO:0030182~neuron differentiation,GO:0032922~circadian regulation of gene expression,GO:0042752~regulation of circadian rhythm,GO:0043153~entrainment of circadian clock by photoperiod,GO:0046822~regulation of nucleocytoplasmic transport,GO:0051301~cell division, |
| 129 | Prdx4 | peroxiredoxin 4(Prdx4) | Mus musculus | GO:0007283~spermatogenesis,GO:0008584~male gonad development,GO:0019471~4-hydroxyproline metabolic process,GO:0022417~protein maturation by protein folding,GO:0030198~extracellular matrix organization,GO:0045454~cell redox homeostasis,GO:0055114~oxidation-reduction process,GO:0072593~reactive oxygen species metabolic process,GO:2000255~negative regulation of male germ cell proliferation, |
| 130 | Prpf38a | PRP38 pre-mRNA processing factor 38 (yeast) domain containing A(Prpf38a) | Mus musculus | GO:0006397~mRNA processing,GO:0008380~RNA splicing, |
| 131 | Prpf8 | pre-mRNA processing factor 8(Prpf8) | Mus musculus | GO:0000244~spliceosomal tri-snRNP complex assembly,GO:0000398~mRNA splicing, via spliceosome,GO:0006397~mRNA processing,GO:0008380~RNA splicing,GO:0071222~cellular response to lipopolysaccharide,GO:0071356~cellular response to tumor necrosis factor, |
| 132 | Pycrl | pyrroline-5-carboxylate reductase-like(Pycrl) | Mus musculus | GO:0006561~proline biosynthetic process,GO:0008652~cellular amino acid biosynthetic process,GO:0009972~cytidine deamination,GO:0055114~oxidation-reduction process,GO:0055129~L-proline biosynthetic process, |
| 133 | Qars | glutaminyl-tRNA synthetase(Qars) | Mus musculus | GO:0006418~tRNA aminoacylation for protein translation,GO:0006425~glutaminyl-tRNA aminoacylation,GO:0007420~brain development,GO:0043066~negative regulation of apoptotic process, |

| | E | F | G |
|---|---|---|---|
| 128 | GO:0000777~condensed chromosome kinetochore,GO:0000784~nuclear chromosome, telomeric region,GO:0005730~nucleolus,GO:0005739~mitochondrion,GO:0005741~mitochondrial outer membrane,GO:0005925~focal adhesion,GO:0016607~nuclear speck,GO:0030496~midbody,GO:0032154~cleavage furrow,GO:0043197~dendritic spine,GO:0070688~MLL5-L complex,GO:0072357~PTW/PP1 phosphatase complex, | GO:0004721~phosphoprotein phosphatase activity,GO:0004722~protein serine/threonine phosphatase activity,GO:0005515~protein binding,GO:0005521~lamin binding,GO:0008022~protein C-terminus binding,GO:0008157~protein phosphatase 1 binding,GO:0016791~phosphatase activity,GO:0019903~protein phosphatase binding,GO:0019904~protein domain specific binding,GO:0032403~protein complex binding,GO:0044822~poly(A) RNA binding,GO:0046872~metal ion binding,GO:0047485~protein N-terminus binding, | IPR004843:Metallophosphoesterase domain,IPR006186:Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase, |
| 129 | GO:0005576~extracellular region,GO:0005615~extracellular space,GO:0005623~cell,GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005739~mitochondrion,GO:0005783~endoplasmic reticulum,GO:0005790~smooth endoplasmic reticulum,GO:0005829~cytosol,GO:0070062~extracellular exosome, | GO:0004601~peroxidase activity,GO:0016209~antioxidant activity,GO:0016491~oxidoreductase activity,GO:0042803~protein homodimerization activity,GO:0051920~peroxiredoxin activity, | IPR000866:Alkyl hydroperoxide reductase subunit C/ Thiol specific antioxidant,IPR012336:Thioredoxin-like fold,IPR013766:Thioredoxin domain,IPR019479:Peroxiredoxin, C-terminal, |
| 130 | GO:0005634~nucleus,GO:0005681~spliceosomal complex,GO:0031965~nuclear membrane,GO:0071011~precatalytic spliceosome, | GO:0044822~poly(A) RNA binding, | IPR005037:Pre-mRNA-splicing factor 38,IPR024767:Pre-mRNA-splicing factor 38, C-terminal, |
| 131 | GO:0005634~nucleus,GO:0005681~spliceosomal complex,GO:0005682~U5 snRNP,GO:0016020~membrane,GO:0016607~nuclear speck,GO:0030529~intracellular ribonucleoprotein complex,GO:0030532~small nuclear ribonucleoprotein complex,GO:0071013~catalytic step 2 spliceosome, | GO:0000386~second spliceosomal transesterification activity,GO:0003676~nucleic acid binding,GO:0003723~RNA binding,GO:0017070~U6 snRNA binding,GO:0030619~U1 snRNA binding,GO:0030620~U2 snRNA binding,GO:0030623~U5 snRNA binding,GO:0044822~poly(A) RNA binding,GO:0070530~K63-linked polyubiquitin binding,GO:0097157~pre-mRNA intronic binding, | IPR000555:JAB1/Mov34/MPN/PAD-1,IPR012337:Ribonuclease H-like domain,IPR012591:Pre-mRNA-processing-splicing factor 8,IPR012592:PROCN,IPR012984:PRO, C-terminal,IPR019580:Pre-mRNA-processing-splicing factor 8, U6-snRNA-binding,IPR019581:Pre-mRNA-processing-splicing factor 8, U5-snRNA-binding,IPR019582:RNA recognition motif, spliceosomal PrP8,IPR021983:PRP8 domain IV core, |
| 132 | GO:0005737~cytoplasm,GO:0005829~cytosol, | GO:0004126~cytidine deaminase activity,GO:0004735~pyrroline-5-carboxylate reductase activity,GO:0005515~protein binding,GO:0016491~oxidoreductase activity,GO:0042802~identical protein binding, | IPR000304:Pyrroline-5-carboxylate reductase,IPR008927:6-phosphogluconate dehydrogenase, C-terminal-like,IPR016040:NAD(P)-binding domain, |
| 133 | GO:0005737~cytoplasm,GO:0005739~mitochondrion,GO:0005829~cytosol,GO:0017101~aminoacyl-tRNA synthetase multienzyme complex, | GO:0003723~RNA binding,GO:0004819~glutamine-tRNA ligase activity,GO:0005524~ATP binding,GO:0019901~protein kinase binding, | IPR000924:Glutamyl/glutaminyl-tRNA synthetase, class Ib,IPR001412:Aminoacyl-tRNA synthetase, class I, conserved site,IPR004514:Glutamine-tRNA synthetase, class Ib,IPR007638:Glutaminyl-tRNA synthetase, class Ib, non-specific RNA-binding domain 2,IPR007639:Glutaminyl-tRNA synthetase, class Ib, non-specific RNA-binding domain, N-terminal,IPR011035:Ribosomal protein L25/Gln-tRNA synthetase, anti-codon-binding domain,IPR014729:Rossmann-like alpha/beta/alpha sandwich fold,IPR020056:Ribosomal protein L25/Gln-tRNA synthetase, beta-barrel domain,IPR020058:Glutamyl/glutaminyl-tRNA synthetase, class Ib, catalytic domain,IPR020059:Glutamyl/glutaminyl-tRNA synthetase, class Ib, anti-codon binding domain,IPR020061:Glutamyl/glutaminyl-tRNA synthetase, class Ib, alpha-bundle domain, |

|  | H | I | J | K |
|---|---|---|---|---|
| 128 | mmu03015:mRNA surveillance pathway,mmu04022:cGMP-PKG signaling pathway,mmu04024:cAMP signaling pathway,mmu04114:Oocyte meiosis,mmu04261:Adrenergic signaling in cardiomyocytes,mmu04270:Vascular smooth muscle contraction,mmu04390:Hippo signaling pathway,mmu04510:Focal adhesion,mmu04611:Platelet activation,mmu04720:Long-term potentiation,mmu04728:Dopaminergic synapse,mmu04750:Inflammatory mediator regulation of TRP channels,mmu04810:Regulation of actin cytoskeleton,mmu04910:Insulin signaling pathway,mmu04921:Oxytocin signaling pathway,mmu04931:Insulin resistance,mmu05031:Amphetamine addiction,mmu05034:Alcoholism,mmu05168:Herpes simplex infection,mmu05205:Proteoglycans in cancer, |  | 3D-structure,Acetylation,Alternative splicing,Biological rhythms,Carbohydrate metabolism,Cell cycle,Cell division,Centromere,Chromosome,Complete proteome,Cytoplasm,Direct protein sequencing,Glycogen metabolism,Hydrolase,Kinetochore,Manganese,Metal-binding,Mitochondrion,Nucleus,Phosphoprotein,Protein phosphatase,Proteomics identification,Reference proteome,Signal, | active site:Proton donor,chain:Serine/threonine-protein phosphatase PP1-gamma catalytic subunit,metal ion-binding site:Iron,metal ion-binding site:Manganese,modified residue,sequence conflict,splice variant, |
| 129 |  |  | 3D-structure,Antioxidant,Complete proteome,Cytoplasm,Direct protein sequencing,Disulfide bond,Oxidoreductase,Peroxidase,Proteomics identification,Redox-active center,Reference proteome,Secreted,Signal, | active site:Cysteine sulfenic acid (-SOH) intermediate,chain:Peroxiredoxin-4,disulfide bond,domain:Thioredoxin,signal peptide, |
| 130 | mmu03040:Spliceosome, |  | Alternative splicing,Coiled coil,Complete proteome,mRNA processing,mRNA splicing,Nucleus,Phosphoprotein,Reference proteome,Spliceosome, | chain:Pre-mRNA-splicing factor 38A,compositionally biased region:Arg-rich,modified residue,sequence conflict,splice variant, |
| 131 | mmu03040:Spliceosome, |  | Acetylation,Complete proteome,Methylation,mRNA processing,mRNA splicing,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Ribonucleoprotein,RNA-binding,Spliceosome, | chain:Pre-mRNA-processing-splicing factor 8,domain:MPN,modified residue,region of interest:Involved in interaction with pre-mRNA 5' splice site,region of interest:Required for interaction with EFTUD2 and SNRNP200,sequence conflict, |
| 132 | mmu00330:Arginine and proline metabolism,mmu01100:Metabolic pathways,mmu01130:Biosynthesis of antibiotics,mmu01230:Biosynthesis of amino acids, | PIRSF000193:pyrroline-5-carboxylate reductase, | Acetylation,Amino-acid biosynthesis,Complete proteome,Cytoplasm,NADP,Oxidoreductase,Proline biosynthesis,Reference proteome, | chain:Pyrroline-5-carboxylate reductase 3,modified residue,sequence conflict, |
| 133 | mmu00970:Aminoacyl-tRNA biosynthesis,mmu01100:Metabolic pathways, |  | Aminoacyl-tRNA synthetase,ATP-binding,Complete proteome,Ligase,Nucleotide-binding,Protein biosynthesis,Proteomics identification,Reference proteome, |  |

| | A | B | C | D |
|---|---|---|---|---|
| 134 | Qk | quaking(Qk) | Mus musculus | GO:0001570~vasculogenesis,GO:0006397~mRNA processing,GO:0006417~regulation of translation,GO:0006810~transport,GO:0007275~multicellular organism development,GO:0007286~spermatid development,GO:0008366~axon ensheathment,GO:0008380~RNA splicing,GO:0010628~positive regulation of gene expression,GO:0010667~negative regulation of cardiac muscle cell apoptotic process,GO:0010976~positive regulation of neuron projection development,GO:0030154~cell differentiation,GO:0042552~myelination,GO:0042692~muscle cell differentiation,GO:0042759~long-chain fatty acid biosynthetic process,GO:0048255~mRNA stabilization,GO:0048714~positive regulation of oligodendrocyte differentiation,GO:0051028~mRNA transport,GO:0061158~3'-UTR-mediated mRNA destabilization, |
| 135 | Rab11b | RAB11B, member RAS oncogene family(Rab11b) | Mus musculus | GO:0001881~receptor recycling,GO:0006810~transport,GO:0006897~endocytosis,GO:0007264~small GTPase mediated signal transduction,GO:0015031~protein transport,GO:0032402~melanosome transport,GO:0033572~transferrin transport,GO:0035773~insulin secretion involved in cellular response to glucose stimulus,GO:0044070~regulation of anion transport,GO:0045054~constitutive secretory pathway,GO:0045055~regulated exocytosis,GO:0071468~cellular response to acidic pH,GO:0090150~establishment of protein localization to membrane,GO:1990126~retrograde transport, endosome to plasma membrane,GO:2000008~regulation of protein localization to cell surface,GO:2001135~regulation of endocytic recycling, |
| 136 | Rab5c | RAB5C, member RAS oncogene family(Rab5c) | Mus musculus | GO:0006810~transport,GO:0007032~endosome organization,GO:0007264~small GTPase mediated signal transduction,GO:0015031~protein transport,GO:0030100~regulation of endocytosis,GO:0048227~plasma membrane to endosome transport, |
| 137 | Rac1 | RAS-related C3 botulinum substrate 1(Rac1) | Mus musculus | GO:0001934~positive regulation of protein phosphorylation,GO:0002093~auditory receptor cell morphogenesis,GO:0002551~mast cell chemotaxis,GO:0003382~epithelial cell morphogenesis,GO:0006897~endocytosis,GO:0006911~phagocytosis, engulfment,GO:0006935~chemotaxis,GO:0006972~hyperosmotic response,GO:0007010~cytoskeleton organization,GO:0007015~actin filament organization,GO:0007155~cell adhesion,GO:0007186~G-protein coupled receptor signaling pathway,GO:0007264~small GTPase mediated signal transduction,GO:0007411~axon guidance,GO:0008283~cell proliferation,GO:0008361~regulation of cell size,GO:0010592~positive regulation of lamellipodium assembly,GO:0010762~regulation of fibroblast migration,GO:0010811~positive regulation of cell-substrate adhesion,GO:0014041~regulation of neuron maturation,GO:0016358~dendrite development,GO:0016477~cell migration,GO:0021799~cerebral cortex radially oriented cell migration,GO:0021831~embryonic olfactory bulb interneuron precursor migration,GO:0021894~cerebral cortex GABAergic interneuron development,GO:0022604~regulation of cell morphogenesis,GO:0030032~lamellipodium assembly,GO:0030036~actin cytoskeleton organization,GO:0030041~actin filament polymerization,GO:0030334~regulation of cell migration,GO:0030838~positive regulation of actin filament polymerization,GO:0031529~ruffle organization,GO:0032707~negative regulation of interleukin-23 production,GO:0034446~substrate adhesion-dependent cell spreading,GO:0035567~non-canonical Wnt signaling pathway,GO:0043552~positive regulation of phosphatidylinositol 3-kinase activity,GO:0043652~engulfment of apoptotic cell,GO:0045216~cell-cell junction organization,GO:0045453~bone resorption,GO:0045740~positive regulation of DNA replication,GO:0048168~regulation of neuronal synaptic plasticity,GO:0048532~anatomical structure arrangement,GO:0048812~neuron projection morphogenesis,GO:0048813~dendrite morphogenesis,GO:0048870~cell motility,GO:0048873~homeostasis of number of cells within a tissue,GO:0051496~positive regulation of stress fiber assembly,GO:0051668~localization within membrane,GO:0051894~positive regulation of focal adhesion assembly,GO:0051932~synaptic transmission, GABAergic,GO:0060071~Wnt signaling pathway, planar cell polarity pathway,GO:0060263~regulation of respiratory burst,GO:0060999~positive regulation of dendritic spine development,GO:0071260~cellular response to mechanical stimulus,GO:0071526~semaphorin-plexin signaling pathway,GO:0071542~dopaminergic neuron differentiation,GO:0072659~protein localization to plasma membrane,GO:0090023~positive regulation of neutrophil chemotaxis,GO:0090103~cochlea morphogenesis,GO:0097178~ruffle assembly,GO:1900026~positive regulation of substrate adhesion-dependent cell spreading,GO:1904948~midbrain dopaminergic neuron differentiation, |

| | E | F | G |
|---|---|---|---|
| 134 | GO:0005634~nucleus,GO:0005737~cytoplasm, | GO:0003676~nucleic acid binding,GO:0003723~RNA binding,GO:0003729~mRNA binding,GO:0017124~SH3 domain binding,GO:0044822~poly(A) RNA binding, | IPR004087:K Homology domain,IPR004088:K Homology domain, type 1, |
| 135 | GO:0005622~intracellular,GO:0005737~cytoplasm,GO:0005739~mitochondrion,GO:0005768~endosome,GO:0005815~microtubule organizing center,GO:0005886~plasma membrane,GO:0005913~cell-cell adherens junction,GO:0008021~synaptic vesicle,GO:0016020~membrane,GO:0016023~cytoplasmic, membrane-bounded vesicle,GO:0016235~aggresome,GO:0030054~cell junction,GO:0030670~phagocytic vesicle membrane,GO:0030672~synaptic vesicle membrane,GO:0031410~cytoplasmic vesicle,GO:0045202~synapse,GO:0045335~phagocytic vesicle,GO:0055037~recycling endosome,GO:0055038~recycling endosome membrane,GO:0070062~extracellular exosome, | GO:0000166~nucleotide binding,GO:0003924~GTPase activity,GO:0005515~protein binding,GO:0005525~GTP binding,GO:0019003~GDP binding,GO:0031489~myosin V binding,GO:0098641~cadherin binding involved in cell-cell adhesion, | IPR001806:Small GTPase superfamily,IPR005225:Small GTP-binding protein domain,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |
| 136 | GO:0005622~intracellular,GO:0005765~lysosomal membrane,GO:0005768~endosome,GO:0005769~early endosome,GO:0005811~lipid particle,GO:0005886~plasma membrane,GO:0016020~membrane,GO:0030139~endocytic vesicle,GO:0031410~cytoplasmic vesicle,GO:0031901~early endosome membrane,GO:0042470~melanosome,GO:0043231~intracellular membrane-bounded organelle,GO:0070062~extracellular exosome, | GO:0000166~nucleotide binding,GO:0003924~GTPase activity,GO:0005515~protein binding,GO:0005525~GTP binding,GO:0019003~GDP binding, | IPR001806:Small GTPase superfamily,IPR005225:Small GTP-binding protein domain,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |
| 137 | GO:0000139~Golgi membrane,GO:0000242~pericentriolar material,GO:0001891~phagocytic cup,GO:0005622~intracellular,GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005802~trans-Golgi network,GO:0005829~cytosol,GO:0005884~actin filament,GO:0005886~plasma membrane,GO:0005925~focal adhesion,GO:0016020~membrane,GO:0016021~integral component of membrane,GO:0016023~cytoplasmic, membrane-bounded vesicle,GO:0019897~extrinsic component of plasma membrane,GO:0030027~lamellipodium,GO:0031012~extracellular matrix,GO:0031410~cytoplasmic vesicle,GO:0031901~early endosome membrane,GO:0032587~ruffle membrane,GO:0036464~cytoplasmic ribonucleoprotein granule,GO:0042470~melanosome,GO:0042995~cell projection,GO:0060091~kinocilium,GO:0070062~extracellular exosome, | GO:0000166~nucleotide binding,GO:0003676~nucleic acid binding,GO:0003924~GTPase activity,GO:0004519~endonuclease activity,GO:0005515~protein binding,GO:0005525~GTP binding,GO:0017137~Rab GTPase binding,GO:0019899~enzyme binding,GO:0019901~protein kinase binding,GO:0030742~GTP-dependent protein binding,GO:0031996~thioesterase binding,GO:0042826~histone deacetylase binding,GO:0051022~Rho GDP-dissociation inhibitor binding,GO:0051117~ATPase binding, | IPR001427:Ribonuclease A,IPR001806:Small GTPase superfamily,IPR005225:Small GTP-binding protein domain,IPR023411:Ribonuclease A, active site,IPR023412:Ribonuclease A-domain,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |

| | H | I | J | K |
|---|---|---|---|---|
| 134 | | | 3D-structure,Alternative splicing,Complete proteome,Cytoplasm,Developmental protein,Differentiation,Methylation,mRNA processing,mRNA splicing,mRNA transport,Nucleus,Phosphoprotein,Reference proteome,RNA-binding,SH3-binding,Translation regulation,Transport, | chain:Protein quaking,domain:KH,mutagenesis site,sequence conflict,short sequence motif:Nuclear localization signal,short sequence motif:SH3-binding,splice variant, |
| 135 | mmu04144:Endocytosis,mmu04152:AMPK signaling pathway,mmu04962:Vasopressin-regulated water reabsorption, | | Acetylation,Cell junction,Citrullination,Complete proteome,Cytoplasmic vesicle,Direct protein sequencing,Endosome,GTP-binding,Lipoprotein,Membrane,Methylation,Nucleotide-binding,Prenylation,Protein transport,Proteomics identification,Reference proteome,Synapse,Transport, | chain:Ras-related protein Rab-11B,lipid moiety-binding region:S-geranylgeranyl cysteine,modified residue,nucleotide phosphate-binding region:GTP,propeptide:Removed in mature form,short sequence motif:Effector region, |
| 136 | mmu04014:Ras signaling pathway,mmu04144:Endocytosis,mmu04145:Phagosome,mmu04962:Vasopressin-regulated water reabsorption,mmu05146:Amoebiasis,mmu05152:Tuberculosis, | | 3D-structure,Cell membrane,Complete proteome,Direct protein sequencing,Endosome,GTP-binding,Lipoprotein,Membrane,Nucleotide-binding,Prenylation,Protein transport,Proteomics identification,Reference proteome,Transport, | chain:Ras-related protein Rab-5C,helix,lipid moiety-binding region:S-geranylgeranyl cysteine,modified residue,nucleotide phosphate-binding region:GTP,short sequence motif:Effector region,strand,turn, |
| 137 | mmu04010:MAPK signaling pathway,mmu04014:Ras signaling pathway,mmu04015:Rap1 signaling pathway,mmu04024:cAMP signaling pathway,mmu04062:Chemokine signaling pathway,mmu04071:Sphingolipid signaling pathway,mmu04145:Phagosome,mmu04151:PI3K-Akt signaling pathway,mmu04310:Wnt signaling pathway,mmu04360:Axon guidance,mmu04370:VEGF signaling pathway,mmu04380:Osteoclast differentiation,mmu04510:Focal adhesion,mmu04520:Adherens junction,mmu04620:Toll-like receptor signaling pathway,mmu04650:Natural killer cell mediated cytotoxicity,mmu04662:B cell receptor signaling pathway,mmu04664:Fc epsilon RI signaling pathway,mmu04666:Fc gamma R-mediated phagocytosis,mmu04670:Leukocyte transendothelial migration,mmu04722:Neurotrophin signaling pathway,mmu04810:Regulation of actin cytoskeleton,mmu04932:Non-alcoholic fatty liver disease (NAFLD),mmu04972:Pancreatic secretion,mmu05014:Amyotrophic lateral sclerosis (ALS),mmu05100:Bacterial invasion of epithelial cells,mmu05132:Salmonella infection,mmu05200:Pathways in cancer,mmu05203:Viral carcinogenesis,mmu05205:Proteoglycans in cancer,mmu05210:Colorectal cancer,mmu05211:Renal cell carcinoma,mmu05212:Pancreatic cancer,mmu05231:Choline metabolism in cancer,mmu05416:Viral myocarditis, | | Cell membrane,Complete proteome,Cytoplasm,Disulfide bond,Endonuclease,GTP-binding,Hydrolase,Isopeptide bond,Lipoprotein,Membrane,Methylation,Nuclease,Nucleotide-binding,Prenylation,Proteomics identification,Reference proteome,Transmembrane,Transmembrane helix,Ubl conjugation, | chain:Ras-related C3 botulinum toxin substrate 1,lipid moiety-binding region:S-geranylgeranyl cysteine,modified residue,mutagenesis site,nucleotide phosphate-binding region:GTP,propeptide:Removed in mature form,short sequence motif:Effector region, |

| | A | B | C | D |
|---|---|---|---|---|
| 138 | Rack1 | receptor for activated C kinase 1(Rack1) | Mus musculus | GO:0001649~osteoblast differentiation,GO:0001934~positive regulation of protein phosphorylation,GO:0006412~translation,GO:0006417~regulation of translation,GO:0006915~apoptotic process,GO:0006919~activation of cysteine-type endopeptidase activity involved in apoptotic process,GO:0007049~cell cycle,GO:0007275~multicellular organism development,GO:0007369~gastrulation,GO:0008104~protein localization,GO:0010629~negative regulation of gene expression,GO:0017148~negative regulation of translation,GO:0030178~negative regulation of Wnt signaling pathway,GO:0030308~negative regulation of cell growth,GO:0030335~positive regulation of cell migration,GO:0030822~positive regulation of cAMP catabolic process,GO:0032436~positive regulation of proteasomal ubiquitin-dependent protein catabolic process,GO:0032464~positive regulation of protein homooligomerization,GO:0032880~regulation of protein localization,GO:0033137~negative regulation of peptidyl-serine phosphorylation,GO:0035556~intracellular signal transduction,GO:0040008~regulation of growth,GO:0042998~positive regulation of Golgi to plasma membrane protein transport,GO:0043065~positive regulation of apoptotic process,GO:0043473~pigmentation,GO:0043547~positive regulation of GTPase activity,GO:0048511~rhythmic process,GO:0050765~negative regulation of phagocytosis,GO:0051302~regulation of cell division,GO:0051343~positive regulation of cyclic-nucleotide phosphodiesterase activity,GO:0051726~regulation of cell cycle,GO:0051898~negative regulation of protein kinase B signaling,GO:0051901~positive regulation of mitochondrial depolarization,GO:0071333~cellular response to glucose stimulus,GO:0071363~cellular response to growth factor stimulus,GO:0090003~regulation of establishment of protein localization to plasma membrane,GO:1903208~negative regulation of hydrogen peroxide-induced neuron death,GO:2000114~regulation of establishment of cell polarity,GO:2000543~positive regulation of gastrulation,GO:2001244~positive regulation of intrinsic apoptotic signaling pathway, |
| 139 | Ranbp3 | RAN binding protein 3(Ranbp3) | Mus musculus | GO:0006810~transport,GO:0015031~protein transport,GO:0046827~positive regulation of protein export from nucleus,GO:0046907~intracellular transport, |
| 140 | Rangap1 | RAN GTPase activating protein 1(Rangap1) | Mus musculus | GO:0007165~signal transduction,GO:0046826~negative regulation of protein export from nucleus,GO:0048678~response to axon injury,GO:0071375~cellular response to peptide hormone stimulus,GO:1904117~cellular response to vasopressin, |
| 141 | Rbbp4 | retinoblastoma binding protein 4(Rbbp4) | Mus musculus | GO:0000183~chromatin silencing at rDNA,GO:0006260~DNA replication,GO:0006335~DNA replication-dependent nucleosome assembly,GO:0006336~DNA replication-independent nucleosome assembly,GO:0006338~chromatin remodeling,GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0007049~cell cycle,GO:0016569~covalent chromatin modification,GO:0031497~chromatin assembly,GO:0043044~ATP-dependent chromatin remodeling,GO:0060416~response to growth hormone, |
| 142 | Rbbp7 | retinoblastoma binding protein 7(Rbbp7) | Mus musculus | GO:0000122~negative regulation of transcription from RNA polymerase II promoter,GO:0000183~chromatin silencing at rDNA,GO:0006260~DNA replication,GO:0006338~chromatin remodeling,GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0016569~covalent chromatin modification,GO:0030308~negative regulation of cell growth,GO:0045892~negative regulation of transcription, DNA-templated,GO:0048545~response to steroid hormone,GO:0070370~cellular heat acclimation, |

|  | E | F | G |
|---|---|---|---|
| 138 | GO:0001891~phagocytic cup,GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005739~mitochondrion,GO:0005829~cytosol,GO:0005886~plasma membrane,GO:0005913~cell-cell adherens junction,GO:0015935~small ribosomal subunit,GO:0016020~membrane,GO:0030425~dendrite,GO:0030496~midbody,GO:0042995~cell projection,GO:0043005~neuron projection,GO:0043025~neuronal cell body,GO:0043204~perikaryon,GO:0044297~cell body,GO:0048471~perinuclear region of cytoplasm,GO:0070062~extracellular exosome,GO:1990630~IRE1-RACK1-PP2A complex, | GO:0004872~receptor activity,GO:0005080~protein kinase C binding,GO:0005515~protein binding,GO:0008200~ion channel inhibitor activity,GO:0008656~cysteine-type endopeptidase activator activity involved in apoptotic process,GO:0019899~enzyme binding,GO:0019903~protein phosphatase binding,GO:0030292~protein tyrosine kinase inhibitor activity,GO:0030971~receptor tyrosine kinase binding,GO:0035591~signaling adaptor activity,GO:0042169~SH2 domain binding,GO:0042803~protein homodimerization activity,GO:0044822~poly(A) RNA binding,GO:0098641~cadherin binding involved in cell-cell adhesion, | IPR001680:WD40 repeat,IPR015943:WD40/YVTN repeat-like-containing domain,IPR017986:WD40-repeat-containing domain,IPR019775:WD40 repeat, conserved site,IPR020472:G-protein beta WD-40 repeat, |
| 139 | GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0005829~cytosol, | GO:0008536~Ran GTPase binding,GO:0070412~R-SMAD binding, | IPR000156:Ran binding domain,IPR011993:Pleckstrin homology-like domain, |
| 140 | GO:0000775~chromosome, centromeric region,GO:0000776~kinetochore,GO:0000777~condensed chromosome kinetochore,GO:0005634~nucleus,GO:0005635~nuclear envelope,GO:0005643~nuclear pore,GO:0005694~chromosome,GO:0005737~cytoplasm,GO:0005829~cytosol,GO:0005856~cytoskeleton,GO:0005913~cell-cell adherens junction,GO:0016020~membrane,GO:0030425~dendrite,GO:0031965~nuclear membrane,GO:0043231~intracellular membrane-bounded organelle,GO:0044614~nuclear pore cytoplasmic filaments,GO:0048471~perinuclear region of cytoplasm,GO:0072686~mitotic spindle,GO:1904115~axon cytoplasm,GO:1990723~cytoplasmic periphery of the nuclear pore complex, | GO:0005096~GTPase activator activity,GO:0008536~Ran GTPase binding,GO:0031625~ubiquitin protein ligase binding,GO:0098641~cadherin binding involved in cell-cell adhesion, | IPR001611:Leucine-rich repeat,IPR009109:Ran-GTPase activating protein 1, C-terminal,IPR027038:Ran GTPase-activating protein, |
| 141 | GO:0000790~nuclear chromatin,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0016581~NuRD complex,GO:0016589~NURF complex,GO:0033186~CAF-1 complex,GO:0035098~ESC/E(Z) complex,GO:0043234~protein complex, | GO:0000978~RNA polymerase II core promoter proximal region sequence-specific DNA binding,GO:0000980~RNA polymerase II distal enhancer sequence-specific DNA binding,GO:0005515~protein binding,GO:0008094~DNA-dependent ATPase activity,GO:0031492~nucleosomal DNA binding,GO:0042826~histone deacetylase binding, | IPR001680:WD40 repeat,IPR015943:WD40/YVTN repeat-like-containing domain,IPR017986:WD40-repeat-containing domain,IPR019775:WD40 repeat, conserved site,IPR020472:G-protein beta WD-40 repeat,IPR022052:Histone-binding protein RBBP4, |
| 142 | GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0016581~NuRD complex,GO:0035098~ESC/E(Z) complex, | GO:0003723~RNA binding,GO:0005515~protein binding, | IPR001680:WD40 repeat,IPR015943:WD40/YVTN repeat-like-containing domain,IPR017986:WD40-repeat-containing domain,IPR019775:WD40 repeat, conserved site,IPR020472:G-protein beta WD-40 repeat,IPR022052:Histone-binding protein RBBP4, |

| | H | I | J | K |
|---|---|---|---|---|
| 138 | mmu05162:Measles, | | Acetylation,Apoptosis,Biological rhythms,Cell cycle,Cell membrane,Cell projection,Complete proteome,Cytoplasm,Developmental protein,Direct protein sequencing,Gastrulation,Growth regulation,Membrane,Nucleus,Phosphoprotein,Reference proteome,Repeat,Translation regulation,WD repeat, | chain:Guanine nucleotide-binding protein subunit beta-2-like 1,modified residue,repeat:WD 1,repeat:WD 2,repeat:WD 3,repeat:WD 4,repeat:WD 5,repeat:WD 6,repeat:WD 7,sequence conflict, |
| 139 | mmu05166:HTLV-I infection, | | Acetylation,Complete proteome,Cytoplasm,Nucleus,Phosphoprotein,Protein transport,Reference proteome,Transport, | chain:Ran-binding protein 3,domain:RanBD1,modified residue,sequence conflict, |
| 140 | mmu03013:RNA transport, | | 3D-structure,Acetylation,Centromere,Chromosome,Coiled coil,Complete proteome,Cytoplasm,Cytoskeleton,GTPase activation,Isopeptide bond,Kinetochore,Leucine-rich repeat,Membrane,Nucleus,Phosphoprotein,Reference proteome,Repeat,Ubl conjugation, | chain:Ran GTPase-activating protein 1,compositionally biased region:Asp/Glu-rich (highly acidic),cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO),helix,modified residue,mutagenesis site,repeat:LRR 1,repeat:LRR 2,repeat:LRR 3,repeat:LRR 4,repeat:LRR 5,repeat:LRR 6,sequence conflict,short sequence motif:SUMO conjugation,site:Hydrophobic interaction with UBC9, |
| 141 | | | Acetylation,Cell cycle,Chromatin regulator,Complete proteome,DNA replication,Isopeptide bond,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,Repressor,Transcription,Transcription regulation,Ubl conjugation,WD repeat, | chain:Histone-binding protein RBBP4,cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin),modified residue,repeat:WD 1,repeat:WD 2,repeat:WD 3,repeat:WD 4,repeat:WD 5,repeat:WD 6, |
| 142 | | | Acetylation,Chaperone,Chromatin regulator,Complete proteome,Direct protein sequencing,DNA replication,Isopeptide bond,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,Repressor,Transcription,Transcription regulation,Ubl conjugation,WD repeat, | chain:Histone-binding protein RBBP7,cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin),modified residue,repeat:WD 1,repeat:WD 2,repeat:WD 3,repeat:WD 4,repeat:WD 5,repeat:WD 6,repeat:WD 7, |

|  | A | B | C | D |
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| 143 | Rbm14 | RNA binding motif protein 14(Rbm14) | Mus musculus | GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0016575~histone deacetylation,GO:0043153~entrainment of circadian clock by photoperiod,GO:0045944~positive regulation of transcription from RNA polymerase II promoter,GO:0046600~negative regulation of centriole replication,GO:0046822~regulation of nucleocytoplasmic transport,GO:0060395~SMAD protein signal transduction,GO:0097167~circadian regulation of translation,GO:0098534~centriole assembly, |
| 144 | Rbm39 | RNA binding motif protein 39(Rbm39) | Mus musculus | GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0006397~mRNA processing,GO:0008380~RNA splicing, |
| 145 | Rbp1 | retinol binding protein 1, cellular(Rbp1) | Mus musculus | GO:0002138~retinoic acid biosynthetic process,GO:0006776~vitamin A metabolic process,GO:0006810~transport,GO:0030852~regulation of granulocyte differentiation,GO:0033189~response to vitamin A,GO:0042572~retinol metabolic process,GO:0042573~retinoic acid metabolic process, |
| 146 | Rcc2 | regulator of chromosome condensation 2(Rcc2) | Mus musculus | GO:0007049~cell cycle,GO:0007067~mitotic nuclear division,GO:0007229~integrin-mediated signaling pathway,GO:0010762~regulation of fibroblast migration,GO:0010971~positive regulation of G2/M transition of mitotic cell cycle,GO:0030334~regulation of cell migration,GO:0034260~negative regulation of GTPase activity,GO:0045184~establishment of protein localization,GO:0048041~focal adhesion assembly,GO:0051301~cell division,GO:0051895~negative regulation of focal adhesion assembly,GO:0051987~positive regulation of attachment of spindle microtubules to kinetochore,GO:0072356~chromosome passenger complex localization to kinetochore,GO:0090630~activation of GTPase activity,GO:1900025~negative regulation of substrate adhesion-dependent cell spreading,GO:1900027~regulation of ruffle assembly, |
| 147 | Rsl1d1 | ribosomal L1 domain containing 1(Rsl1d1) | Mus musculus | GO:0000470~maturation of LSU-rRNA,GO:0001649~osteoblast differentiation,GO:0006412~translation,GO:0032880~regulation of protein localization,GO:0042981~regulation of apoptotic process,GO:2000772~regulation of cellular senescence, |
| 148 | Rtcb | RNA 2',3'-cyclic phosphate and 5'-OH ligase(Rtcb) | Mus musculus | GO:0001701~in utero embryonic development,GO:0001890~placenta development,GO:0006388~tRNA splicing, via endonucleolytic cleavage and ligation,GO:0006396~RNA processing,GO:0008033~tRNA processing, |
| 149 | Sept7 | septin 7(Sept7) | Mus musculus | GO:0000281~mitotic cytokinesis,GO:0007049~cell cycle,GO:0007067~mitotic nuclear division,GO:0016476~regulation of embryonic cell shape,GO:0030865~cortical cytoskeleton organization,GO:0031270~pseudopodium retraction,GO:0048668~collateral sprouting,GO:0051291~protein heterooligomerization,GO:0051301~cell division,GO:0060271~cilium morphogenesis,GO:0060997~dendritic spine morphogenesis,GO:1902857~positive regulation of nonmotile primary cilium assembly, |

|  | E | F | G |
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| 143 | GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005667~transcription factor complex,GO:0005730~nucleolus,GO:0005737~cytoplasm,GO:0048471~perinuclear region of cytoplasm, | GO:0000166~nucleotide binding,GO:0003676~nucleic acid binding,GO:0003723~RNA binding,GO:0003730~mRNA 3'-UTR binding,GO:0030374~ligand-dependent nuclear receptor transcription coactivator activity,GO:0036002~pre-mRNA binding,GO:0044822~poly(A) RNA binding, | IPR000504:RNA recognition motif domain,IPR012677:Nucleotide-binding, alpha-beta plait, |
| 144 | GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005815~microtubule organizing center,GO:0015630~microtubule cytoskeleton, | GO:0000166~nucleotide binding,GO:0003676~nucleic acid binding,GO:0003713~transcription coactivator activity,GO:0003723~RNA binding,GO:0005515~protein binding,GO:0044822~poly(A) RNA binding, | IPR000504:RNA recognition motif domain,IPR003954:RNA recognition motif domain, eukaryote,IPR006509:Splicing factor, CC1-like,IPR012677:Nucleotide-binding, alpha-beta plait, |
| 145 | GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0005829~cytosol,GO:0044297~cell body, | GO:0005215~transporter activity,GO:0005501~retinoid binding,GO:0008289~lipid binding,GO:0016918~retinal binding,GO:0019841~retinol binding, | IPR000463:Cytosolic fatty-acid binding,IPR000566:Lipocalin/cytosolic fatty-acid binding protein domain,IPR011038:Calycin-like,IPR012674:Calycin, |
| 146 | GO:0000775~chromosome, centromeric region,GO:0005634~nucleus,GO:0005694~chromosome,GO:0005730~nucleolus,GO:0005737~cytoplasm,GO:0005856~cytoskeleton,GO:0005874~microtubule,GO:0005886~plasma membrane,GO:0016020~membrane,GO:0030496~midbody,GO:0031901~early endosome membrane,GO:0034506~chromosome, centromeric core domain,GO:1990023~mitotic spindle midzone, | GO:0008017~microtubule binding,GO:0019901~protein kinase binding,GO:0019904~protein domain specific binding,GO:0031267~small GTPase binding,GO:0044822~poly(A) RNA binding,GO:0048365~Rac GTPase binding, | IPR000408:Regulator of chromosome condensation, RCC1,IPR009091:Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II, |
| 147 | GO:0005634~nucleus,GO:0005730~nucleolus,GO:0005913~cell-cell adherens junction,GO:0016020~membrane,GO:0022625~cytosolic large ribosomal subunit, | GO:0003723~RNA binding,GO:0005515~protein binding,GO:0044822~poly(A) RNA binding,GO:0098641~cadherin binding involved in cell-cell adhesion, | IPR016094:Ribosomal protein L1, 2-layer alpha/beta-sandwich,IPR023674:Ribosomal protein L1, superfamily, |
| 148 | GO:0005634~nucleus,GO:0005635~nuclear envelope,GO:0005737~cytoplasm,GO:0005789~endoplasmic reticulum membrane,GO:0072669~tRNA-splicing ligase complex, | GO:0000166~nucleotide binding,GO:0003972~RNA ligase (ATP) activity,GO:0005524~ATP binding,GO:0008452~RNA ligase activity,GO:0016874~ligase activity,GO:0017166~vinculin binding,GO:0044822~poly(A) RNA binding,GO:0046872~metal ion binding, | IPR001233:RtcB family,IPR027513:tRNA-splicing ligase RtcB, eukaryotic, |
| 149 | GO:0000775~chromosome, centromeric region,GO:0000776~kinetochore,GO:0000777~condensed chromosome kinetochore,GO:0001725~stress fiber,GO:0005634~nucleus,GO:0005694~chromosome,GO:0005730~nucleolus,GO:0005737~cytoplasm,GO:0005819~spindle,GO:0005856~cytoskeleton,GO:0005886~plasma membrane,GO:0005913~cell-cell adherens junction,GO:0005929~cilium,GO:0005930~axoneme,GO:0005938~cell cortex,GO:0005940~septin ring,GO:0015629~actin cytoskeleton,GO:0015630~microtubule cytoskeleton,GO:0016020~membrane,GO:0030496~midbody,GO:0031105~septin complex,GO:0031513~nonmotile primary cilium,GO:0032154~cleavage furrow,GO:0032156~septin cytoskeleton,GO:0032160~septin filament array,GO:0042995~cell projection,GO:0043005~neuron projection,GO:0043209~myelin sheath,GO:0043234~protein complex,GO:0043679~axon terminus,GO:0044297~cell body,GO:0045202~synapse,GO:0070062~extracellular exosome, | GO:0000166~nucleotide binding,GO:0005515~protein binding,GO:0005525~GTP binding,GO:0042802~identical protein binding,GO:0046982~protein heterodimerization activity,GO:0098641~cadherin binding involved in cell-cell adhesion, | IPR008115:Septin 7,IPR016491:Septin,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |

| | H | I | J | K |
|---|---|---|---|---|
| 143 | | | Acetylation,Alternative splicing,Complete proteome,Cytoplasm,Isopeptide bond,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,RNA-binding,Transcription,Transcription regulation,Ubl conjugation, | chain:RNA-binding protein 14,compositionally biased region:Ala-rich,domain:RRM 1,domain:RRM 2,modified residue,region of interest:TRBP-interacting domain,sequence conflict,splice variant, |
| 144 | | | 3D-structure,Acetylation,Activator,Alternative splicing,Complete proteome,mRNA processing,mRNA splicing,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,RNA-binding,Transcription,Transcription regulation, | chain:RNA-binding protein 39,compositionally biased region:Arg/Ser-rich (RS domain),compositionally biased region:Poly-Ala,domain:RRM 1,domain:RRM 2,domain:RRM 3,modified residue,region of interest:Activating domain,region of interest:Interaction with ESR1 and ESR2,region of interest:Interaction with JUN,region of interest:Interaction with NCOA6,sequence conflict,splice variant, |
| 145 | | | Complete proteome,Cytoplasm,Reference proteome,Retinol-binding,Transport,Vitamin A, | binding site:Retinoic acid,chain:Retinol-binding protein 1, |
| 146 | | | Acetylation,Cell cycle,Cell division,Centromere,Chromosome,Complete proteome,Cytoplasm,Cytoskeleton,Microtubule,Mitosis,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat, | chain:Protein RCC2,modified residue,repeat:RCC1 1,repeat:RCC1 2,repeat:RCC1 3,repeat:RCC1 4,repeat:RCC1 5,repeat:RCC1 6,repeat:RCC1 7, |
| 147 | | | Acetylation,Coiled coil,Complete proteome,Nucleus,Phosphoprotein,Reference proteome, | |
| 148 | | | ATP-binding,Complete proteome,Cytoplasm,Ligase,Manganese,Metal-binding,Nucleotide-binding,Nucleus,Phosphoprotein,Reference proteome,tRNA processing,Zinc, | chain:UPF0027 protein C22orf28 homolog,modified residue,sequence conflict, |
| 149 | | PIRSF006698:septin, | Acetylation,Cell cycle,Cell division,Cell projection,Centromere,Chromosome,Cilium,Coiled coil,Complete proteome,Cytoplasm,Cytoskeleton,Direct protein sequencing,GTP-binding,Kinetochore,Mitosis,Nucleotide-binding,Phosphoprotein,Proteomics identification,Reference proteome, | binding site:GTP,binding site:GTP; via amide nitrogen and carbonyl oxygen,chain:Septin-7,modified residue,nucleotide phosphate-binding region:GTP, |

|  | A | B | C | D |
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| 150 | Sept9 | septin 9(Sept9) | Mus musculus | GO:0007049~cell cycle,GO:0051291~protein heterooligomerization,GO:0051301~cell division,GO:1902857~positive regulation of nonmotile primary cilium assembly, |
| 151 | Set | SET nuclear oncogene(Set) | Mus musculus | GO:0006334~nucleosome assembly,GO:0043524~negative regulation of neuron apoptotic process,GO:0045892~negative regulation of transcription, DNA-templated, |
| 152 | Sf3b1 | splicing factor 3b, subunit 1(Sf3b1) | Mus musculus | GO:0000245~spliceosomal complex assembly,GO:0000398~mRNA splicing, via spliceosome,GO:0001825~blastocyst formation,GO:0006397~mRNA processing,GO:0008380~RNA splicing,GO:0009952~anterior/posterior pattern specification, |
| 153 | Sf3b3 | splicing factor 3b, subunit 3(Sf3b3) | Mus musculus | GO:0000398~mRNA splicing, via spliceosome,GO:0006397~mRNA processing,GO:0008380~RNA splicing,GO:0042177~negative regulation of protein catabolic process, |
| 154 | Slc25a4 | solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 4(Slc25a4) | Mus musculus | GO:0006412~translation,GO:0006810~transport,GO:0008637~apoptotic mitochondrial changes,GO:0010667~negative regulation of cardiac muscle cell apoptotic process,GO:0055085~transmembrane transport,GO:0060546~negative regulation of necroptotic process,GO:0061051~positive regulation of cell growth involved in cardiac muscle cell development,GO:1902109~negative regulation of mitochondrial membrane permeability involved in apoptotic process,GO:2000277~positive regulation of oxidative phosphorylation uncoupler activity, |
| 155 | Slc25a5 | solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5(Slc25a5) | Mus musculus | GO:0006412~translation,GO:0006810~transport,GO:0007059~chromosome segregation,GO:0008284~positive regulation of cell proliferation,GO:0055085~transmembrane transport,GO:1901029~negative regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway, |
| 156 | Smarcc1 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1(Smarcc1) | Mus musculus | GO:0006323~DNA packaging,GO:0006337~nucleosome disassembly,GO:0006338~chromatin remodeling,GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0007399~nervous system development,GO:0008286~insulin receptor signaling pathway,GO:0009887~organ morphogenesis,GO:0016569~covalent chromatin modification,GO:0030850~prostate gland development,GO:0032435~negative regulation of proteasomal ubiquitin-dependent protein catabolic process,GO:0043044~ATP-dependent chromatin remodeling,GO:0045893~positive regulation of transcription, DNA-templated,GO:0045944~positive regulation of transcription from RNA polymerase II promoter, |

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| 150 | GO:0001725~stress fiber,GO:0005737~cytoplasm,GO:0005856~cytoskeleton,GO:0005874~microtubule,GO:0005913~cell-cell adherens junction,GO:0005930~axoneme,GO:0015629~actin cytoskeleton,GO:0031105~septin complex,GO:0031513~nonmotile primary cilium,GO:0048471~perinuclear region of cytoplasm, | GO:0000166~nucleotide binding,GO:0005525~GTP binding,GO:0098641~cadherin binding involved in cell-cell adhesion, | IPR005225:Small GTP-binding protein domain,IPR016491:Septin,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |
| 151 | GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0005783~endoplasmic reticulum,GO:0005829~cytosol,GO:0043234~protein complex,GO:0048471~perinuclear region of cytoplasm, | GO:0003677~DNA binding, | IPR002164:Nucleosome assembly protein (NAP), |
| 152 | GO:0000785~chromatin,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005681~spliceosomal complex,GO:0005686~U2 snRNP,GO:0005689~U12-type spliceosomal complex,GO:0016021~integral component of membrane,GO:0016363~nuclear matrix,GO:0030532~small nuclear ribonucleoprotein complex,GO:0034693~U11/U12 snRNP,GO:0071004~U2-type prespliceosome,GO:0071013~catalytic step 2 spliceosome, | GO:0003682~chromatin binding,GO:0003729~mRNA binding,GO:0005515~protein binding,GO:0044822~poly(A) RNA binding, | IPR011989:Armadillo-like helical,IPR015016:Splicing factor 3B subunit 1,IPR016024:Armadillo-type fold, |
| 153 | GO:0005634~nucleus,GO:0005681~spliceosomal complex,GO:0005689~U12-type spliceosomal complex,GO:0005730~nucleolus,GO:0071013~catalytic step 2 spliceosome, | GO:0003676~nucleic acid binding,GO:0003723~RNA binding, | IPR004871:Cleavage/polyadenylation specificity factor, A subunit, C-terminal,IPR017986:WD40-repeat-containing domain, |
| 154 | GO:0005634~nucleus,GO:0005739~mitochondrion,GO:0005741~mitochondrial outer membrane,GO:0005743~mitochondrial inner membrane,GO:0016020~membrane,GO:0016021~integral component of membrane,GO:0043209~myelin sheath, | GO:0003735~structural constituent of ribosome,GO:0005215~transporter activity,GO:0005515~protein binding,GO:0019899~enzyme binding, | IPR002067:Mitochondrial carrier protein,IPR002113:Adenine nucleotide translocator 1,IPR018108:Mitochondrial substrate/solute carrier,IPR023395:Mitochondrial carrier domain, |
| 155 | GO:0005634~nucleus,GO:0005739~mitochondrion,GO:0005743~mitochondrial inner membrane,GO:0016020~membrane,GO:0016021~integral component of membrane,GO:0031012~extracellular matrix,GO:0042645~mitochondrial nucleoid,GO:0043209~myelin sheath,GO:0070062~extracellular exosome,GO:0071817~MMXD complex, | GO:0003735~structural constituent of ribosome,GO:0005215~transporter activity,GO:0031625~ubiquitin protein ligase binding,GO:0044822~poly(A) RNA binding, | IPR002067:Mitochondrial carrier protein,IPR002113:Adenine nucleotide translocator 1,IPR018108:Mitochondrial substrate/solute carrier,IPR023395:Mitochondrial carrier domain, |
| 156 | GO:0000790~nuclear chromatin,GO:0001741~XY body,GO:0005622~intracellular,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0016514~SWI/SNF complex,GO:0043234~protein complex,GO:0071564~npBAF complex,GO:0071565~nBAF complex,GO:0090544~BAF-type complex, | GO:0000978~RNA polymerase II core promoter proximal region sequence-specific DNA binding,GO:0000980~RNA polymerase II distal enhancer sequence-specific DNA binding,GO:0003677~DNA binding,GO:0003682~chromatin binding,GO:0005515~protein binding,GO:0031492~nucleosomal DNA binding,GO:0047485~protein N-terminus binding, | IPR000953:Chromo domain/shadow,IPR001005:SANT/Myb domain,IPR001357:BRCT domain,IPR007526:SWIRM domain,IPR009057:Homeodomain-like,IPR011991:Winged helix-turn-helix DNA-binding domain,IPR017884:SANT domain, |

| | H | I | J | K |
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| 150 | mmu05100:Bacterial invasion of epithelial cells, | PIRSF006698:septin, | Acetylation,Alternative splicing,Cell cycle,Cell division,Complete proteome,Cytoplasm,Cytoskeleton,Direct protein sequencing,GTP-binding,Nucleotide-binding,Phosphoprotein,Proteomics identification,Reference proteome, | binding site:GTP; via amide nitrogen and carbonyl oxygen,chain:Septin-9,modified residue,nucleotide phosphate-binding region:GTP,splice variant, |
| 151 | | | Acetylation,Alternative splicing,Chaperone,Coiled coil,Complete proteome,Cytoplasm,DNA-binding,Endoplasmic reticulum,Isopeptide bond,Methylation,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Ubl conjugation, | chain:Protein SET,compositionally biased region:Asp/Glu-rich (highly acidic),cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin),modified residue,sequence conflict,splice variant, |
| 152 | mmu03040:Spliceosome, | | Acetylation,Citrullination,Coiled coil,Complete proteome,Isopeptide bond,Membrane,mRNA processing,mRNA splicing,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,Spliceosome,Transmembrane,Transmembrane helix,Ubl conjugation, | chain:Splicing factor 3B subunit 1,modified residue,region of interest:Interaction with PPP1R8,repeat:HEAT 1,repeat:HEAT 10,repeat:HEAT 11,repeat:HEAT 2,repeat:HEAT 3,repeat:HEAT 4,repeat:HEAT 5,repeat:HEAT 6,repeat:HEAT 7,repeat:HEAT 8,repeat:HEAT 9, |
| 153 | mmu03040:Spliceosome, | | Alternative splicing,Complete proteome,mRNA processing,mRNA splicing,Nucleus,Phosphoprotein,Reference proteome,Spliceosome, | chain:Splicing factor 3B subunit 3,modified residue,sequence conflict,splice variant, |
| 154 | mmu04020:Calcium signaling pathway,mmu04022:cGMP-PKG signaling pathway,mmu05012:Parkinson's disease,mmu05016:Huntington's disease,mmu05166:HTLV-I infection, | | Acetylation,Complete proteome,Direct protein sequencing,Isopeptide bond,Membrane,Mitochondrion,Mitochondrion inner membrane,Phosphoprotein,Reference proteome,Repeat,S-nitrosylation,Transmembrane,Transmembrane helix,Transport, | binding site:Nucleotide,chain:ADP/ATP translocase 1,cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin),modified residue,repeat:Solcar 1,repeat:Solcar 2,repeat:Solcar 3,sequence conflict,short sequence motif:Substrate recognition,transmembrane region, |
| 155 | mmu04020:Calcium signaling pathway,mmu04022:cGMP-PKG signaling pathway,mmu05012:Parkinson's disease,mmu05016:Huntington's disease,mmu05166:HTLV-I infection, | | Acetylation,Chromosome partition,Complete proteome,Direct protein sequencing,Membrane,Methylation,Mitochondrion,Mitochondrion inner membrane,Reference proteome,Repeat,Transmembrane,Transmembrane helix,Transport, | binding site:Nucleotide,chain:ADP/ATP translocase 2,modified residue,repeat:Solcar 1,repeat:Solcar 2,repeat:Solcar 3,short sequence motif:Substrate recognition,transmembrane region, |
| 156 | | | Acetylation,Alternative splicing,Chromatin regulator,Coiled coil,Complete proteome,Isopeptide bond,Methylation,Neurogenesis,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Transcription,Transcription regulation,Ubl conjugation, | chain:SWI/SNF complex subunit SMARCC1,compositionally biased region:Glu-rich,compositionally biased region:Poly-Ala,compositionally biased region:Poly-Pro,compositionally biased region:Pro-rich,domain:SANT,domain:SWIRM,modified residue,sequence conflict,splice variant, |

| | A | B | C | D |
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| 157 | Smarcc2 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2(Smarcc2) | Mus musculus | GO:0000122~negative regulation of transcription from RNA polymerase II promoter,GO:0006337~nucleosome disassembly,GO:0006338~chromatin remodeling,GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0006357~regulation of transcription from RNA polymerase II promoter,GO:0007399~nervous system development,GO:0016569~covalent chromatin modification,GO:0021882~regulation of transcription from RNA polymerase II promoter involved in forebrain neuron fate commitment,GO:0043044~ATP-dependent chromatin remodeling,GO:0045892~negative regulation of transcription, DNA-templated,GO:0045893~positive regulation of transcription, DNA-templated, |
| 158 | Smarce1 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1(Smarce1) | Mus musculus | GO:0006337~nucleosome disassembly,GO:0006338~chromatin remodeling,GO:0007399~nervous system development,GO:0016569~covalent chromatin modification,GO:0022008~neurogenesis,GO:0043044~ATP-dependent chromatin remodeling,GO:0045892~negative regulation of transcription, DNA-templated, |
| 159 | Smc3 | structural maintenance of chromosomes 3(Smc3) | Mus musculus | GO:0006275~regulation of DNA replication,GO:0006281~DNA repair,GO:0006974~cellular response to DNA damage stimulus,GO:0007049~cell cycle,GO:0007052~mitotic spindle organization,GO:0007062~sister chromatid cohesion,GO:0007064~mitotic sister chromatid cohesion,GO:0007067~mitotic nuclear division,GO:0007126~meiotic nuclear division,GO:0007165~signal transduction,GO:0019827~stem cell population maintenance,GO:0032876~negative regulation of DNA endoreduplication,GO:0051276~chromosome organization,GO:0051301~cell division,GO:0051321~meiotic cell cycle, |
| 160 | Snd1 | staphylococcal nuclease and tudor domain containing 1(Snd1) | Mus musculus | GO:0001649~osteoblast differentiation,GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0006401~RNA catabolic process,GO:0031047~gene silencing by RNA,GO:0098609~cell-cell adhesion, |
| 161 | Snrnp70 | small nuclear ribonucleoprotein 70 (U1)(Snrnp70) | Mus musculus | GO:0000398~mRNA splicing, via spliceosome,GO:0043484~regulation of RNA splicing,GO:0048026~positive regulation of mRNA splicing, via spliceosome,GO:0071300~cellular response to retinoic acid,GO:0071356~cellular response to tumor necrosis factor,GO:0071560~cellular response to transforming growth factor beta stimulus, |
| 162 | Snrpd3 | small nuclear ribonucleoprotein D3(Snrpd3) | Mus musculus | GO:0000245~spliceosomal complex assembly,GO:0000387~spliceosomal snRNP assembly,GO:0006396~RNA processing,GO:0006397~mRNA processing,GO:0006479~protein methylation,GO:0008380~RNA splicing, |

|  | E | F | G |
|---|---|---|---|
| 157 | GO:0000790~nuclear chromatin,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0016514~SWI/SNF complex,GO:0017053~transcriptional repressor complex,GO:0043234~protein complex,GO:0071564~npBAF complex,GO:0071565~nBAF complex,GO:0090544~BAF-type complex, | GO:0000978~RNA polymerase II core promoter proximal region sequence-specific DNA binding,GO:0000980~RNA polymerase II distal enhancer sequence-specific DNA binding,GO:0003677~DNA binding,GO:0003682~chromatin binding,GO:0005515~protein binding,GO:0031492~nucleosomal DNA binding, | IPR000953:Chromo domain/shadow,IPR001005:SANT/Myb domain,IPR001357:BRCT domain,IPR007526:SWIRM domain,IPR009057:Homeodomain-like,IPR011991:Winged helix-turn-helix DNA-binding domain,IPR017884:SANT domain, |
| 158 | GO:0000790~nuclear chromatin,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0016514~SWI/SNF complex,GO:0017053~transcriptional repressor complex,GO:0043234~protein complex,GO:0071564~npBAF complex,GO:0071565~nBAF complex,GO:0090544~BAF-type complex, | GO:0000978~RNA polymerase II core promoter proximal region sequence-specific DNA binding,GO:0000980~RNA polymerase II distal enhancer sequence-specific DNA binding,GO:0003677~DNA binding,GO:0003723~RNA binding,GO:0005515~protein binding,GO:0008080~N-acetyltransferase activity,GO:0016922~ligand-dependent nuclear receptor binding,GO:0031492~nucleosomal DNA binding,GO:0047485~protein N-terminus binding, | IPR009071:High mobility group (HMG) box domain, |
| 159 | GO:0000775~chromosome, centromeric region,GO:0000785~chromatin,GO:0000800~lateral element,GO:0000922~spindle pole,GO:0005604~basement membrane,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005694~chromosome,GO:0005737~cytoplasm,GO:0008278~cohesin complex,GO:0008280~cohesin core heterodimer,GO:0016363~nuclear matrix,GO:0030893~meiotic cohesin complex,GO:0034991~nuclear meiotic cohesin complex, | GO:0000166~nucleotide binding,GO:0003682~chromatin binding,GO:0005515~protein binding,GO:0005524~ATP binding,GO:0036033~mediator complex binding,GO:0045502~dynein binding,GO:0046982~protein heterodimerization activity, | IPR003395:RecF/RecN/SMC,IPR010935:SMCs flexible hinge,IPR024704:Structural maintenance of chromosomes protein,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |
| 160 | GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005739~mitochondrion,GO:0005913~cell-cell adherens junction,GO:0016020~membrane,GO:0016442~RISC complex,GO:0042470~melanosome,GO:0070062~extracellular exosome,GO:0097433~dense body, | GO:0003676~nucleic acid binding,GO:0004518~nuclease activity,GO:0005515~protein binding,GO:0044822~poly(A) RNA binding,GO:0098641~cadherin binding involved in cell-cell adhesion, | IPR002071:Thermonuclease active site,IPR002999:Tudor domain,IPR016071:Staphylococcal nuclease (SNase-like), OB-fold,IPR016685:RNA-induced silencing complex, nuclease component Tudor-SN, |
| 161 | GO:0000243~commitment complex,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005681~spliceosomal complex,GO:0005685~U1 snRNP,GO:0005737~cytoplasm,GO:0016607~nuclear speck,GO:0019013~viral nucleocapsid,GO:0030529~intracellular ribonucleoprotein complex,GO:0071004~U2-type prespliceosome,GO:0071011~precatalytic spliceosome, | GO:0000166~nucleotide binding,GO:0003676~nucleic acid binding,GO:0003723~RNA binding,GO:0003729~mRNA binding,GO:0030619~U1 snRNA binding,GO:0044822~poly(A) RNA binding,GO:1990446~U1 snRNP binding, | IPR000504:RNA recognition motif domain,IPR012677:Nucleotide-binding, alpha-beta plait,IPR022023:U1 small nuclear ribonucleoprotein of 70kDa N-terminal, |
| 162 | GO:0000243~commitment complex,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005681~spliceosomal complex,GO:0005682~U5 snRNP,GO:0005683~U7 snRNP,GO:0005685~U1 snRNP,GO:0005686~U2 snRNP,GO:0005687~U4 snRNP,GO:0005689~U12-type spliceosomal complex,GO:0005697~telomerase holoenzyme complex,GO:0005737~cytoplasm,GO:0005829~cytosol,GO:0019013~viral nucleocapsid,GO:0030529~intracellular ribonucleoprotein complex,GO:0034709~methylosome,GO:0034715~pICln-Sm protein complex,GO:0034719~SMN-Sm protein complex,GO:0070062~extracellular exosome,GO:0071010~prespliceosome,GO:0071011~precatalytic spliceosome,GO:0071013~catalytic step 2 spliceosome,GO:0097526~spliceosomal tri-snRNP complex, | GO:0003723~RNA binding,GO:0019899~enzyme binding,GO:0030620~U2 snRNA binding,GO:0044822~poly(A) RNA binding,GO:0070034~telomerase RNA binding,GO:0071208~histone pre-mRNA DCP binding,GO:0071209~U7 snRNA binding,GO:1990446~U1 snRNP binding, | IPR001163:Ribonucleoprotein LSM domain,IPR010920:Like-Sm (LSM) domain,IPR027141:U6 snRNA-associated Sm-like protein LSm4/Small nuclear ribonucleoprotein Sm D1/D3, |

|  | H | I | J | K |
|---|---|---|---|---|
| 157 |  |  | Acetylation,Alternative splicing,Chromatin regulator,Coiled coil,Complete proteome,Isopeptide bond,Neurogenesis,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Transcription,Transcription regulation,Ubl conjugation, | chain:SWI/SNF complex subunit SMARCC2,compositionally biased region:Glu-rich,compositionally biased region:Poly-Ala,compositionally biased region:Poly-Gln,compositionally biased region:Poly-Glu,compositionally biased region:Pro-rich,domain:SANT,domain:SWIRM,modified residue,sequence conflict,splice variant, |
| 158 |  |  | Chromatin regulator,Coiled coil,Complete proteome,DNA-binding,Isopeptide bond,Methylation,Neurogenesis,Nucleus,Phosphoprotein, Reference proteome,Ubl conjugation, | chain:SWI/SNF-related matrix-associated actin- dependent regulator chromatin subfamily E member 1,compositionally biased region:Glu-rich,DNA-binding region:HMG box,modified residue, |
| 159 | mmu04110:Cell cycle,mmu04114:Oocyte meiosis, | PIRSF005719:structural maintenance of chromosomes protein, | 3D-structure,Acetylation,ATP-binding,Cell cycle,Cell division,Centromere,Chromosome,Coiled coil,Complete proteome,DNA damage,DNA repair,Meiosis,Mitosis,Nucleotide-binding,Nucleus,Phosphoprotein,Reference proteome, | chain:Structural maintenance of chromosomes protein 3,compositionally biased region:Ala/Asp-rich (DA-box),modified residue,mutagenesis site,nucleotide phosphate-binding region:ATP,region of interest:Flexible hinge,sequence conflict, |
| 160 | mmu05203:Viral carcinogenesis, | PIRSF017179:RNA-induced silencing complex, nuclease component Tudor-SN, | Acetylation,Complete proteome,Cytoplasm,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,Transcription,Transcription regulation, | chain:Staphylococcal nuclease domain-containing protein 1,domain:TNase-like 1,domain:TNase-like 2,domain:TNase-like 3,domain:TNase-like 4,domain:Tudor,modified residue,sequence conflict,short sequence motif:Nuclear localization signal, |
| 161 | mmu03040:Spliceosome, |  | Acetylation,Alternative splicing,Complete proteome,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Ribonucleoprotein,RNA-binding,Viral nucleoprotein,Virion, | chain:U1 small nuclear ribonucleoprotein 70 kDa,compositionally biased region:Arg/Asp/Glu-rich (mixed charge),compositionally biased region:Arg/Glu-rich (mixed charge),compositionally biased region:Poly-Gly,domain:RRM,modified residue,sequence conflict,splice variant, |
| 162 | mmu03040:Spliceosome,mmu05322:Systemic lupus erythematosus, |  | Acetylation,Complete proteome,Cytoplasm,Methylation,mRNA processing,mRNA splicing,Nucleus,Reference proteome,Repeat,Ribonucleoprotein,RNA-binding,Spliceosome,Viral nucleoprotein,Virion, | chain:Small nuclear ribonucleoprotein Sm D3,compositionally biased region:Arg/Lys-rich (basic),modified residue,region of interest:5 X 2 AA tandem repeats of [RM]-G,repeat:1,repeat:2,repeat:3,repeat:4,repeat:5, |

| | A | B | C | D |
|---|---|---|---|---|
| 163 | Sptan1 | spectrin alpha, non-erythrocytic 1(Sptan1) | Mus musculus | GO:0031532~actin cytoskeleton reorganization,GO:0051693~actin filament capping, |
| 164 | Srrm2 | serine/arginine repetitive matrix 2(Srrm2) | Mus musculus | GO:0006397~mRNA processing,GO:0008380~RNA splicing, |
| 165 | Srsf10 | serine/arginine-rich splicing factor 10(Srsf10) | Mus musculus | GO:0000375~RNA splicing, via transesterification reactions,GO:0000398~mRNA splicing, via spliceosome,GO:0006355~regulation of transcription, DNA-templated,GO:0006376~mRNA splice site selection,GO:0006397~mRNA processing,GO:0006406~mRNA export from nucleus,GO:0008380~RNA splicing,GO:0016482~cytosolic transport,GO:0048024~regulation of mRNA splicing, via spliceosome,GO:0048025~negative regulation of mRNA splicing, via spliceosome, |
| 166 | Srsf6 | serine/arginine-rich splicing factor 6(Srsf6) | Mus musculus | GO:0000380~alternative mRNA splicing, via spliceosome,GO:0000381~regulation of alternative mRNA splicing, via spliceosome,GO:0006376~mRNA splice site selection,GO:0006397~mRNA processing,GO:0008380~RNA splicing,GO:0010629~negative regulation of gene expression,GO:0010837~regulation of keratinocyte proliferation,GO:0032868~response to insulin,GO:0045617~negative regulation of keratinocyte differentiation,GO:0048025~negative regulation of mRNA splicing, via spliceosome,GO:0060501~positive regulation of epithelial cell proliferation involved in lung morphogenesis,GO:0060548~negative regulation of cell death,GO:0061041~regulation of wound healing,GO:2000675~negative regulation of type B pancreatic cell apoptotic process, |
| 167 | Stip1 | stress-induced phosphoprotein 1(Stip1) | Mus musculus | |
| 168 | Strap | serine/threonine kinase receptor associated protein(Strap) | Mus musculus | GO:0000122~negative regulation of transcription from RNA polymerase II promoter,GO:0000387~spliceosomal snRNP assembly,GO:0006397~mRNA processing,GO:0008380~RNA splicing,GO:0010633~negative regulation of epithelial cell migration,GO:0010719~negative regulation of epithelial to mesenchymal transition,GO:0030277~maintenance of gastrointestinal epithelium,GO:0030512~negative regulation of transforming growth factor beta receptor signaling pathway,GO:0050680~negative regulation of epithelial cell proliferation,GO:0060394~negative regulation of pathway-restricted SMAD protein phosphorylation, |
| 169 | Sub1 | SUB1 homolog (S. cerevisiae)(Sub1) | Mus musculus | GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0006357~regulation of transcription from RNA polymerase II promoter,GO:0060395~SMAD protein signal transduction, |

| | E | F | G |
|---|---|---|---|
| 163 | GO:0005737~cytoplasm,GO:0005856~cytoskeleton,GO:0005886~plasma membrane,GO:0005913~cell-cell adherens junction,GO:0005916~fascia adherens,GO:0015630~microtubule cytoskeleton,GO:0016020~membrane,GO:0016328~lateral plasma membrane,GO:0030018~Z disc,GO:0030863~cortical cytoskeleton,GO:0032437~cuticular plate,GO:0033270~paranode region of axon,GO:0043209~myelin sheath,GO:0043231~intracellular membrane-bounded organelle,GO:0043234~protein complex,GO:0070062~extracellular exosome,GO:1903561~extracellular vesicle, | GO:0003779~actin binding,GO:0005509~calcium ion binding,GO:0005515~protein binding,GO:0005516~calmodulin binding,GO:0019905~syntaxin binding,GO:0030507~spectrin binding,GO:0032403~protein complex binding,GO:0046872~metal ion binding,GO:0046982~protein heterodimerization activity,GO:0047485~protein N-terminus binding,GO:0098641~cadherin binding involved in cell-cell adhesion, | IPR001452:Src homology-3 domain,IPR002017:Spectrin repeat,IPR002048:EF-hand domain,IPR011992:EF-hand-like domain,IPR013315:Spectrin alpha chain, SH3 domain,IPR014837:EF-hand, Ca insensitive,IPR018159:Spectrin/alpha-actinin,IPR018247:EF-Hand 1, calcium-binding site, |
| 164 | GO:0005634~nucleus,GO:0005681~spliceosomal complex,GO:0015030~Cajal body,GO:0016607~nuclear speck,GO:0071013~catalytic step 2 spliceosome, | GO:0044822~poly(A) RNA binding, | IPR013170:mRNA splicing factor, Cwf21,IPR024945:Spt5 C-terminal domain, |
| 165 | GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005829~cytosol,GO:0016607~nuclear speck,GO:0030425~dendrite,GO:0043025~neuronal cell body,GO:0043679~axon terminus, | GO:0000166~nucleotide binding,GO:0003676~nucleic acid binding,GO:0003723~RNA binding,GO:0044822~poly(A) RNA binding,GO:0051082~unfolded protein binding, | IPR000504:RNA recognition motif domain,IPR012677:Nucleotide-binding, alpha-beta plait, |
| 166 | GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0016607~nuclear speck, | GO:0000166~nucleotide binding,GO:0003676~nucleic acid binding,GO:0003723~RNA binding,GO:0005515~protein binding,GO:0036002~pre-mRNA binding,GO:0044822~poly(A) RNA binding, | IPR000504:RNA recognition motif domain,IPR012677:Nucleotide-binding, alpha-beta plait, |
| 167 | GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005829~cytosol,GO:0043209~myelin sheath,GO:0043234~protein complex, | GO:0005515~protein binding,GO:0008022~protein C-terminus binding,GO:0030544~Hsp70 protein binding,GO:0044822~poly(A) RNA binding,GO:0051087~chaperone binding, | IPR001440:Tetratricopeptide TPR-1,IPR006636:Heat shock chaperonin-binding,IPR011990:Tetratricopeptide-like helical,IPR013026:Tetratricopeptide repeat-containing domain,IPR013105:Tetratricopeptide TPR2,IPR019734:Tetratricopeptide repeat, |
| 168 | GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005829~cytosol,GO:0032797~SMN complex,GO:0034719~SMN-Sm protein complex, | GO:0005102~receptor binding,GO:0005515~protein binding,GO:0016301~kinase activity,GO:0044822~poly(A) RNA binding, | IPR001680:WD40 repeat,IPR015943:WD40/YVTN repeat-like-containing domain,IPR017986:WD40-repeat-containing domain,IPR019775:WD40 repeat, conserved site,IPR020472:G-protein beta WD-40 repeat, |
| 169 | GO:0005634~nucleus,GO:0005667~transcription factor complex,GO:0005730~nucleolus,GO:0070062~extracellular exosome, | GO:0001205~transcriptional activator activity, RNA polymerase II distal enhancer sequence-specific binding,GO:0003677~DNA binding,GO:0003697~single-stranded DNA binding,GO:0003713~transcription coactivator activity,GO:0044822~poly(A) RNA binding, | IPR003173:Transcriptional coactivator p15,IPR009044:ssDNA-binding transcriptional regulator, |

| | H | I | J | K |
|---|---|---|---|---|
| 163 | | | Acetylation,Actin capping,Actin-binding,Alternative splicing,Calcium,Calmodulin-binding,Coiled coil,Complete proteome,Cytoplasm,Cytoskeleton,Direct protein sequencing,Metal-binding,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,SH3 domain, | calcium-binding region:1,calcium-binding region:2,chain:Spectrin alpha chain, brain,domain:EF-hand 1,domain:EF-hand 2,domain:EF-hand 3,domain:SH3,modified residue,repeat:Spectrin 1,repeat:Spectrin 10,repeat:Spectrin 11,repeat:Spectrin 12,repeat:Spectrin 13,repeat:Spectrin 14,repeat:Spectrin 15,repeat:Spectrin 16,repeat:Spectrin 17,repeat:Spectrin 18,repeat:Spectrin 19,repeat:Spectrin 2,repeat:Spectrin 20,repeat:Spectrin 21,repeat:Spectrin 22,repeat:Spectrin 23,repeat:Spectrin 3,repeat:Spectrin 4,repeat:Spectrin 5,repeat:Spectrin 6,repeat:Spectrin 7,repeat:Spectrin 8,repeat:Spectrin 9,sequence conflict,site:Cleavage; by mu-calpain,splice variant, |
| 164 | | | Acetylation,Alternative splicing,Coiled coil,Complete proteome,Direct protein sequencing,Methylation,mRNA processing,mRNA splicing,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Spliceosome, | chain:Serine/arginine repetitive matrix protein 2,compositionally biased region:Ala-rich,compositionally biased region:Arg-rich,compositionally biased region:Lys-rich,compositionally biased region:Pro-rich,compositionally biased region:Ser-rich,modified residue,region of interest:Sufficient for RNA-binding,sequence conflict,splice variant, |
| 165 | mmu03040:Spliceosome, | | Alternative splicing,Complete proteome,mRNA processing,mRNA splicing,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,RNA-binding, | chain:Splicing factor, arginine/serine-rich 13A,compositionally biased region:Arg/Ser-rich (RS domain),domain:RRM,modified residue,sequence conflict,splice variant, |
| 166 | mmu03040:Spliceosome,mmu05168:Herpes simplex infection, | | Acetylation,Complete proteome,mRNA processing,mRNA splicing,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,Repressor,RNA-binding, | |
| 167 | mmu05020:Prion diseases, | | Acetylation,Complete proteome,Cytoplasm,Direct protein sequencing,Isopeptide bond,Nucleus,Phosphoprotein,Reference proteome,Repeat,TPR repeat,Ubl conjugation, | chain:Stress-induced-phosphoprotein 1,domain:STI1 1,domain:STI1 2,modified residue,repeat:TPR 1,repeat:TPR 2,repeat:TPR 3,repeat:TPR 4,repeat:TPR 5,repeat:TPR 6,repeat:TPR 7,repeat:TPR 8,repeat:TPR 9,sequence conflict,short sequence motif:Bipartite nuclear localization signal, |
| 168 | mmu03013:RNA transport, | | Complete proteome,Cytoplasm,Kinase,mRNA processing,mRNA splicing,Nucleus,Phosphoprotein,Receptor,Reference proteome,Repeat,Transferase,WD repeat, | chain:Serine-threonine kinase receptor- associated protein,modified residue,repeat:WD 1,repeat:WD 2,repeat:WD 3,repeat:WD 4,repeat:WD 5,repeat:WD 6,repeat:WD 7,sequence conflict, |
| 169 | | | Acetylation,Activator,Complete proteome,Direct protein sequencing,DNA-binding,Isopeptide bond,Nucleus,Phosphoprotein,Reference proteome,Transcription,Transcription regulation,Ubl conjugation, | chain:Activated RNA polymerase II transcriptional coactivator p15,compositionally biased region:Lys-rich,compositionally biased region:Ser-rich,modified residue,region of interest:Interaction with ssDNA,region of interest:Regulatory,sequence conflict,site:Cleavage, |

| | A | B | C | D |
|---|---|---|---|---|
| 170 | Tbx2 | T-box 2(Tbx2) | Mus musculus | GO:0000122~negative regulation of transcription from RNA polymerase II promoter,GO:0001947~heart looping,GO:0003007~heart morphogenesis,GO:0003148~outflow tract septum morphogenesis,GO:0003151~outflow tract morphogenesis,GO:0003203~endocardial cushion morphogenesis,GO:0003256~regulation of transcription from RNA polymerase II promoter involved in myocardial precursor cell differentiation,GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0007219~Notch signaling pathway,GO:0007275~multicellular organism development,GO:0007521~muscle cell fate determination,GO:0007569~cell aging,GO:0008016~regulation of heart contraction,GO:0008284~positive regulation of cell proliferation,GO:0035050~embryonic heart tube development,GO:0035909~aorta morphogenesis,GO:0036302~atrioventricular canal development,GO:0042733~embryonic digit morphogenesis,GO:0045892~negative regulation of transcription, DNA-templated,GO:0048596~embryonic camera-type eye morphogenesis,GO:0048738~cardiac muscle tissue development,GO:0060021~palate development,GO:0060045~positive regulation of cardiac muscle cell proliferation,GO:0060465~pharynx development,GO:0060560~developmental growth involved in morphogenesis,GO:0060596~mammary placode formation,GO:0090398~cellular senescence,GO:1901208~negative regulation of heart looping,GO:1901211~negative regulation of cardiac chamber formation, |
| 171 | Tcof1 | treacle ribosome biogenesis factor 1(Tcof1) | Mus musculus | GO:0006810~transport,GO:0042790~transcription of nuclear large rRNA transcript from RNA polymerase I promoter, |
| 172 | Tjp1 | tight junction protein 1(Tjp1) | Mus musculus | GO:0001825~blastocyst formation,GO:0007605~sensory perception of sound,GO:0032496~response to lipopolysaccharide,GO:0042493~response to drug,GO:0043116~negative regulation of vascular permeability,GO:0045471~response to ethanol,GO:0071000~response to magnetism,GO:0071333~cellular response to glucose stimulus,GO:0090557~establishment of endothelial intestinal barrier,GO:0098609~cell-cell adhesion, |
| 173 | Tjp2 | tight junction protein 2(Tjp2) | Mus musculus | GO:0050892~intestinal absorption,GO:0071847~TNFSF11-mediated signaling pathway,GO:0090557~establishment of endothelial intestinal barrier,GO:0090559~regulation of membrane permeability,GO:2001205~negative regulation of osteoclast development, |
| 174 | Tln1 | talin 1(Tln1) | Mus musculus | GO:0007016~cytoskeletal anchoring at plasma membrane,GO:0007044~cell-substrate junction assembly,GO:0007155~cell adhesion,GO:0030866~cortical actin cytoskeleton organization,GO:0070527~platelet aggregation,GO:0098609~cell-cell adhesion, |

| | E | F | G |
|---|---|---|---|
| 170 | GO:0005634~nucleus,GO:0005667~transcription factor complex, | GO:0000978~RNA polymerase II core promoter proximal region sequence-specific DNA binding,GO:0001078~transcriptional repressor activity, RNA polymerase II core promoter proximal region sequence-specific binding,GO:0003677~DNA binding,GO:0003700~transcription factor activity, sequence-specific DNA binding,GO:0005515~protein binding,GO:0043565~sequence-specific DNA binding, | IPR001699:Transcription factor, T-box,IPR002070:Transcription factor, Brachyury,IPR008967:p53-like transcription factor, DNA-binding,IPR018186:Transcription factor, T-box, conserved site,IPR022582:Transcription factor, T-box, region of unknown function, |
| 171 | GO:0005634~nucleus,GO:0005730~nucleolus,GO:0005737~cytoplasm, | GO:0044822~poly(A) RNA binding, | IPR003993:Treacher Collins syndrome, treacle,IPR006594:LisH dimerisation motif,IPR017859:Treacle-like, Treacher Collins Syndrome, |
| 172 | GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005886~plasma membrane,GO:0005911~cell-cell junction,GO:0005912~adherens junction,GO:0005913~cell-cell adherens junction,GO:0005921~gap junction,GO:0005923~bicellular tight junction,GO:0009986~cell surface,GO:0014704~intercalated disc,GO:0016020~membrane,GO:0016323~basolateral plasma membrane,GO:0016324~apical plasma membrane,GO:0016327~apicolateral plasma membrane,GO:0030054~cell junction,GO:0031674~I band,GO:0043296~apical junction complex,GO:0045177~apical part of cell,GO:0046581~intercellular canaliculus, | GO:0005515~protein binding,GO:0005516~calmodulin binding,GO:0008022~protein C-terminus binding,GO:0019904~protein domain specific binding,GO:0098641~cadherin binding involved in cell-cell adhesion, | IPR000906:ZU5,IPR001452:Src homology-3 domain,IPR001478:PDZ domain,IPR005417:Zona occludens protein,IPR005418:Zona occludens protein ZO-1,IPR008144:Guanylate kinase,IPR008145:Guanylate kinase/L-type calcium channel,IPR011511:Variant SH3,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |
| 173 | GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005886~plasma membrane,GO:0005911~cell-cell junction,GO:0005913~cell-cell adherens junction,GO:0005921~gap junction,GO:0005923~bicellular tight junction,GO:0009986~cell surface,GO:0016020~membrane,GO:0030054~cell junction, | GO:0005515~protein binding,GO:0008022~protein C-terminus binding,GO:0019904~protein domain specific binding,GO:0030674~protein binding, bridging,GO:0098641~cadherin binding involved in cell-cell adhesion, | IPR001452:Src homology-3 domain,IPR001478:PDZ domain,IPR005417:Zona occludens protein,IPR005419:Zona occludens protein ZO-2,IPR008144:Guanylate kinase,IPR008145:Guanylate kinase/L-type calcium channel,IPR011511:Variant SH3,IPR027417:P-loop containing nucleoside triphosphate hydrolase, |
| 174 | GO:0001726~ruffle,GO:0005737~cytoplasm,GO:0005815~microtubule organizing center,GO:0005856~cytoskeleton,GO:0005886~plasma membrane,GO:0005913~cell-cell adherens junction,GO:0005925~focal adhesion,GO:0009986~cell surface,GO:0016020~membrane,GO:0030054~cell junction,GO:0032587~ruffle membrane,GO:0042995~cell projection,GO:0070062~extracellular exosome, | GO:0003779~actin binding,GO:0005178~integrin binding,GO:0005200~structural constituent of cytoskeleton,GO:0005515~protein binding,GO:0017166~vinculin binding,GO:0030274~LIM domain binding,GO:0032403~protein complex binding,GO:0051015~actin filament binding,GO:0098641~cadherin binding involved in cell-cell adhesion, | IPR000299:FERM domain,IPR002404:Insulin receptor substrate-1, PTB,IPR002558:I/LWEQ domain,IPR006077:Vinculin/alpha-catenin,IPR011993:Pleckstrin homology-like domain,IPR014352:FERM/acyl-CoA-binding protein, 3-helical bundle,IPR015009:Vinculin-binding site-containing domain,IPR015224:Talin, central,IPR015710:Talin-1,IPR018979:FERM, N-terminal,IPR019747:FERM conserved site,IPR019748:FERM central domain,IPR019749:Band 4.1 domain, |

|  | H | I | J | K |
|---|---|---|---|---|
| 170 |  |  | Complete proteome,Developmental protein,DNA-binding,Nucleus,Phosphoprotein,Reference proteome,Transcription,Transcription regulation, | chain:T-box transcription factor TBX2,compositionally biased region:Ala-rich,DNA-binding region:T-box, |
| 171 | mmu03008:Ribosome biogenesis in eukaryotes, |  | Acetylation,Complete proteome,Isopeptide bond,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,Transport,Ubl conjugation, | chain:Treacle protein,compositionally biased region:Ala-rich,compositionally biased region:Lys-rich,compositionally biased region:Poly-Ala,compositionally biased region:Poly-Lys,compositionally biased region:Poly-Ser,domain:LisH,modified residue,region of interest:10 X approximate tandem repeats,repeat:1,repeat:10,repeat:2,repeat:3,repeat:4,repeat:5,repeat:6,repeat:7,repeat:8,repeat:9,sequence conflict, |
| 172 | mmu04520:Adherens junction,mmu04530:Tight junction,mmu04540:Gap junction,mmu05132:Salmonella infection, |  | 3D-structure,Calmodulin-binding,Cell junction,Cell membrane,Complete proteome,Cytoplasm,Gap junction,Membrane,Phosphoprotein,Proteomics identification,Reference proteome,Repeat,SH3 domain,Tight junction, | chain:Tight junction protein ZO-1,compositionally biased region:Poly-Pro,domain:Guanylate kinase-like,domain:PDZ 1,domain:PDZ 2,domain:PDZ 3,domain:SH3,domain:ZU5,modified residue, |
| 173 | mmu04530:Tight junction, |  | 3D-structure,Cell junction,Cell membrane,Complete proteome,Membrane,Nucleus,Phosphoprotein,Reference proteome,Repeat,SH3 domain,Tight junction, | chain:Tight junction protein ZO-2,compositionally biased region:Poly-Glu,domain:Guanylate kinase-like,domain:PDZ 1,domain:PDZ 2,domain:PDZ 3,domain:SH3,helix,modified residue,region of interest:Interaction with SCRIB,sequence conflict,strand, |
| 174 | mmu04015:Rap1 signaling pathway,mmu04510:Focal adhesion,mmu04611:Platelet activation,mmu05166:HTLV-I infection, |  | 3D-structure,Acetylation,Cell junction,Cell membrane,Cell projection,Coiled coil,Complete proteome,Cytoplasm,Cytoskeleton,Membrane,Phosphoprotein,Proteomics identification,Reference proteome, | chain:Talin-1,domain:FERM,domain:I/LWEQ,helix,modified residue,region of interest:Interaction with LAYN,region of interest:Interaction with SYNM,sequence variant,strand,turn, |

| | A | B | C | D |
|---|---|---|---|---|
| 175 | Tmcc2 | transmembrane and coiled-coil domains 2(Tmcc2) | Mus musculus | |
| 176 | Tmsb10 | thymosin, beta 10(Tmsb10) | Mus musculus | GO:0007015~actin filament organization,GO:0030036~actin cytoskeleton organization,GO:0042989~sequestering of actin monomers, |
| 177 | Top2a | topoisomerase (DNA) II alpha(Top2a) | Mus musculus | GO:0000712~resolution of meiotic recombination intermediates,GO:0000819~sister chromatid segregation,GO:0002244~hematopoietic progenitor cell differentiation,GO:0006259~DNA metabolic process,GO:0006265~DNA topological change,GO:0006266~DNA ligation,GO:0006268~DNA unwinding involved in DNA replication,GO:0006312~mitotic recombination,GO:0006974~cellular response to DNA damage stimulus,GO:0007059~chromosome segregation,GO:0016925~protein sumoylation,GO:0030261~chromosome condensation,GO:0030263~apoptotic chromosome condensation,GO:0040016~embryonic cleavage,GO:0042752~regulation of circadian rhythm,GO:0043065~positive regulation of apoptotic process,GO:0044774~mitotic DNA integrity checkpoint,GO:0045070~positive regulation of viral genome replication,GO:0045870~positive regulation of single stranded viral RNA replication via double stranded DNA intermediate,GO:0045944~positive regulation of transcription from RNA polymerase II promoter,GO:0048511~rhythmic process, |
| 178 | Tpm1 | tropomyosin 1, alpha(Tpm1) | Mus musculus | GO:0001701~in utero embryonic development,GO:0003065~positive regulation of heart rate by epinephrine,GO:0008360~regulation of cell shape,GO:0009790~embryo development,GO:0030049~muscle filament sliding,GO:0030336~negative regulation of cell migration,GO:0031529~ruffle organization,GO:0032781~positive regulation of ATPase activity,GO:0034614~cellular response to reactive oxygen species,GO:0042060~wound healing,GO:0043462~regulation of ATPase activity,GO:0045214~sarcomere organization,GO:0045785~positive regulation of cell adhesion,GO:0051496~positive regulation of stress fiber assembly,GO:0051693~actin filament capping,GO:0055010~ventricular cardiac muscle tissue morphogenesis,GO:0060048~cardiac muscle contraction,GO:1904706~negative regulation of vascular smooth muscle cell proliferation,GO:1904753~negative regulation of vascular associated smooth muscle cell migration, |
| 179 | Tpr | translocated promoter region, nuclear basket protein(Tpr) | Mus musculus | GO:0000122~negative regulation of transcription from RNA polymerase II promoter,GO:0000189~MAPK import into nucleus,GO:0006404~RNA import into nucleus,GO:0006405~RNA export from nucleus,GO:0006606~protein import into nucleus,GO:0006810~transport,GO:0006913~nucleocytoplasmic transport,GO:0006999~nuclear pore organization,GO:0007049~cell cycle,GO:0007067~mitotic nuclear division,GO:0007094~mitotic spindle assembly checkpoint,GO:0010965~regulation of mitotic sister chromatid separation,GO:0015031~protein transport,GO:0031453~positive regulation of heterochromatin assembly,GO:0031990~mRNA export from nucleus in response to heat stress,GO:0034605~cellular response to heat,GO:0035457~cellular response to interferon-alpha,GO:0042307~positive regulation of protein import into nucleus,GO:0045947~negative regulation of translational initiation,GO:0046827~positive regulation of protein export from nucleus,GO:0046832~negative regulation of RNA export from nucleus,GO:0051028~mRNA transport,GO:0051301~cell division,GO:0070849~response to epidermal growth factor,GO:0090267~positive regulation of mitotic cell cycle spindle assembly checkpoint,GO:0090316~positive regulation of intracellular protein transport,GO:1901673~regulation of mitotic spindle assembly, |
| 180 | Tuba1a | tubulin, alpha 1A(Tuba1a) | Mus musculus | GO:0007017~microtubule-based process, |

| | E | F | G |
|---|---|---|---|
| 175 | GO:0016020~membrane,GO:0016021~integral component of membrane, | | IPR019394:Predicted transmembrane/coiled-coil 2 protein, |
| 176 | GO:0005623~cell,GO:0005737~cytoplasm,GO:0031941~filamentous actin, | GO:0003785~actin monomer binding, | IPR001152:Thymosin beta-4, |
| 177 | GO:0000228~nuclear chromosome,GO:0000793~condensed chromosome,GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005730~nucleolus,GO:0005814~centriole,GO:0009330~DNA topoisomerase complex (ATP-hydrolyzing),GO:0043234~protein complex, | GO:0000166~nucleotide binding,GO:0000287~magnesium ion binding,GO:0003677~DNA binding,GO:0003682~chromatin binding,GO:0003916~DNA topoisomerase activity,GO:0003918~DNA topoisomerase type II (ATP-hydrolyzing) activity,GO:0005080~protein kinase C binding,GO:0005524~ATP binding,GO:0008022~protein C-terminus binding,GO:0008094~DNA-dependent ATPase activity,GO:0008144~drug binding,GO:0008301~DNA binding, bending,GO:0016853~isomerase activity,GO:0019899~enzyme binding,GO:0042803~protein homodimerization activity,GO:0042826~histone deacetylase binding,GO:0043130~ubiquitin binding,GO:0043565~sequence-specific DNA binding,GO:0043566~structure-specific DNA binding,GO:0044822~poly(A) RNA binding,GO:0046872~metal ion binding,GO:0046982~protein heterodimerization activity, | IPR001241:DNA topoisomerase, type IIA,IPR002205:DNA topoisomerase, type IIA, subunit A/C-terminal,IPR003594:Histidine kinase-like ATPase, ATP-binding domain,IPR006171:Toprim domain,IPR012542:DTHCT,IPR013506:DNA topoisomerase, type IIA, subunit B, domain 2,IPR013757:Type IIA DNA topoisomerase subunit A, alpha-helical domain,IPR013758:DNA topoisomerase, type IIA, subunit A/ C-terminal, alpha-beta,IPR013759:DNA topoisomerase, type IIA, central domain,IPR013760:DNA topoisomerase, type IIA-like domain,IPR014721:Ribosomal protein S5 domain 2-type fold, subgroup,IPR018522:DNA topoisomerase, type IIA, conserved site,IPR020568:Ribosomal protein S5 domain 2-type fold,IPR024946:Arginine repressor C-terminal-like domain, |
| 178 | GO:0001725~stress fiber,GO:0005737~cytoplasm,GO:0005856~cytoskeleton,GO:0005862~muscle thin filament tropomyosin,GO:0030016~myofibril,GO:0031941~filamentous actin,GO:0032059~bleb,GO:0032587~ruffle membrane,GO:0043234~protein complex, | GO:0003779~actin binding,GO:0005200~structural constituent of cytoskeleton,GO:0042803~protein homodimerization activity,GO:0047485~protein N-terminus binding,GO:0051015~actin filament binding, | IPR000533:Tropomyosin, |
| 179 | GO:0000775~chromosome, centromeric region,GO:0000776~kinetochore,GO:0005622~intracellular,GO:0005634~nucleus,GO:0005635~nuclear envelope,GO:0005643~nuclear pore,GO:0005694~chromosome,GO:0005737~cytoplasm,GO:0005856~cytoskeleton,GO:0005868~cytoplasmic dynein complex,GO:0016020~membrane,GO:0019898~extrinsic component of membrane,GO:0031965~nuclear membrane,GO:0034399~nuclear periphery,GO:0042405~nuclear inclusion body,GO:0044615~nuclear pore nuclear basket,GO:0072686~mitotic spindle, | GO:0003682~chromatin binding,GO:0003729~mRNA binding,GO:0005487~nucleocytoplasmic transporter activity,GO:0005515~protein binding,GO:0015631~tubulin binding,GO:0031072~heat shock protein binding,GO:0042803~protein homodimerization activity,GO:0044822~poly(A) RNA binding,GO:0051019~mitogen-activated protein kinase binding,GO:0070840~dynein complex binding, | IPR012929:Tetratricopeptide, MLP1/MLP2-like,IPR015866:Serine-tRNA synthetase, type1, N-terminal, |
| 180 | GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005856~cytoskeleton,GO:0005874~microtubule,GO:0005881~cytoplasmic microtubule,GO:0036464~cytoplasmic ribonucleoprotein granule,GO:0043209~myelin sheath,GO:0055037~recycling endosome,GO:0070062~extracellular exosome, | GO:0000166~nucleotide binding,GO:0003924~GTPase activity,GO:0005200~structural constituent of cytoskeleton,GO:0005525~GTP binding,GO:0019904~protein domain specific binding, | IPR000217:Tubulin,IPR002452:Alpha tubulin,IPR003008:Tubulin/FtsZ, GTPase domain,IPR008280:Tubulin/FtsZ, C-terminal,IPR017975:Tubulin, conserved site,IPR018316:Tubulin/FtsZ, 2-layer sandwich domain,IPR023123:Tubulin, C-terminal, |

|  | H | I | J | K |
|---|---|---|---|---|
| 175 |  |  | Coiled coil,Complete proteome,Membrane,Methylation,Phosphoprotein,Proteomics identification,Reference proteome,Transmembrane,Transmembrane helix, | chain:Transmembrane and coiled-coil domains protein 2,modified residue,transmembrane region, |
| 176 |  | PIRSF001828:thymosin beta, | Acetylation,Actin-binding,Complete proteome,Cytoplasm,Cytoskeleton,Phosphoprotein,Proteomics identification,Reference proteome, | modified residue,peptide:Thymosin beta-10, |
| 177 |  |  | Acetylation,ATP-binding,Biological rhythms,Complete proteome,DNA-binding,Isomerase,Isopeptide bond,Magnesium,Metal-binding,Nucleotide-binding,Nucleus,Phosphoprotein,Reference proteome,Topoisomerase,Ubl conjugation, | active site:O-(5'-phospho-DNA)-tyrosine intermediate,binding site:ATP,chain:DNA topoisomerase 2-alpha,modified residue,nucleotide phosphate-binding region:ATP, |
| 178 | mmu04260:Cardiac muscle contraction,mmu04261:Adrenergic signaling in cardiomyocytes,mmu05206:MicroRNAs in cancer,mmu05410:Hypertrophic cardiomyopathy (HCM),mmu05414:Dilated cardiomyopathy, |  | Acetylation,Actin-binding,Alternative splicing,Coiled coil,Complete proteome,Cytoplasm,Cytoskeleton,Isopeptide bond,Muscle protein,Phosphoprotein,Proteomics identification,Reference proteome, | chain:Tropomyosin alpha-1 chain,cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin),modified residue,splice variant, |
| 179 | mmu03013:RNA transport,mmu05200:Pathways in cancer,mmu05216:Thyroid cancer, |  | Acetylation,Cell cycle,Cell division,Centromere,Chromosome,Coiled coil,Complete proteome,Cytoplasm,Cytoskeleton,Kinetochore,Membrane,Methylation,Mitosis,mRNA transport,Nuclear pore complex,Nucleus,Phosphoprotein,Protein transport,Proteomics identification,Proto-oncogene,Reference proteome,Translocation,Transport, |  |
| 180 | mmu04145:Phagosome,mmu04540:Gap junction, |  | Acetylation,Complete proteome,Cytoplasm,Cytoskeleton,Direct protein sequencing,GTP-binding,Isopeptide bond,Microtubule,Nitration,Nucleotide-binding,Phosphoprotein,Reference proteome, | chain:Tubulin alpha-1A chain,modified residue,nucleotide phosphate-binding region:GTP,sequence conflict,site:Involved in polymerization, |

| | A | B | C | D |
|---|---|---|---|---|
| 181 | Txn1 | thioredoxin 1(Txn1) | Mus musculus | GO:0000103~sulfate assimilation,GO:0000122~negative regulation of transcription from RNA polymerase II promoter,GO:0006351~transcription, DNA-templated,GO:0006355~regulation of transcription, DNA-templated,GO:0006457~protein folding,GO:0006662~glycerol ether metabolic process,GO:0006810~transport,GO:0009314~response to radiation,GO:0033138~positive regulation of peptidyl-serine phosphorylation,GO:0033158~regulation of protein import into nucleus, translocation,GO:0034599~cellular response to oxidative stress,GO:0043388~positive regulation of DNA binding,GO:0045454~cell redox homeostasis,GO:0046826~negative regulation of protein export from nucleus,GO:0055114~oxidation-reduction process,GO:1903206~negative regulation of hydrogen peroxide-induced cell death, |
| 182 | Txnl1 | thioredoxin-like 1(Txnl1) | Mus musculus | GO:0000103~sulfate assimilation,GO:0006457~protein folding,GO:0006662~glycerol ether metabolic process,GO:0006810~transport,GO:0034599~cellular response to oxidative stress,GO:0045454~cell redox homeostasis,GO:0055114~oxidation-reduction process, |
| 183 | Uba1 | ubiquitin-like modifier activating enzyme 1(Uba1) | Mus musculus | GO:0006464~cellular protein modification process,GO:0006974~cellular response to DNA damage stimulus,GO:0019941~modification-dependent protein catabolic process, |
| 184 | Ube2i | ubiquitin-conjugating enzyme E2I(Ube2i) | Mus musculus | GO:0000122~negative regulation of transcription from RNA polymerase II promoter,GO:0006464~cellular protein modification process,GO:0007049~cell cycle,GO:0007059~chromosome segregation,GO:0007067~mitotic nuclear division,GO:0007275~multicellular organism development,GO:0010469~regulation of receptor activity,GO:0016032~viral process,GO:0016925~protein sumoylation,GO:0033145~positive regulation of intracellular steroid hormone receptor signaling pathway,GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB signaling,GO:0043161~proteasome-mediated ubiquitin-dependent protein catabolic process,GO:0045892~negative regulation of transcription, DNA-templated,GO:0051091~positive regulation of sequence-specific DNA binding transcription factor activity,GO:0051301~cell division,GO:1903755~positive regulation of SUMO transferase activity, |
| 185 | Ube2m | ubiquitin-conjugating enzyme E2M(Ube2m) | Mus musculus | GO:0006464~cellular protein modification process,GO:0043525~positive regulation of neuron apoptotic process,GO:0045116~protein neddylation, |
| 186 | Usp5 | ubiquitin specific peptidase 5 (isopeptidase T)(Usp5) | Mus musculus | GO:0006508~proteolysis,GO:0006511~ubiquitin-dependent protein catabolic process,GO:0016579~protein deubiquitination,GO:0032436~positive regulation of proteasomal ubiquitin-dependent protein catabolic process,GO:0071108~protein K48-linked deubiquitination, |
| 187 | Wbp11 | WW domain binding protein 11(Wbp11) | Mus musculus | GO:0006364~rRNA processing,GO:0006396~RNA processing,GO:0006397~mRNA processing,GO:0008380~RNA splicing,GO:0045292~mRNA cis splicing, via spliceosome,GO:1903146~regulation of mitophagy,GO:1903955~positive regulation of protein targeting to mitochondrion, |

|  | E | F | G |
|---|---|---|---|
| 181 | GO:0005576~extracellular region,GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005739~mitochondrion,GO:0005829~cytosol,GO:0030424~axon,GO:0030425~dendrite,GO:0043025~neuronal cell body,GO:0070062~extracellular exosome, | GO:0005515~protein binding,GO:0015035~protein disulfide oxidoreductase activity,GO:0015037~peptide disulfide oxidoreductase activity,GO:0016671~oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor,GO:0019899~enzyme binding,GO:0044822~poly(A) RNA binding, | IPR005746:Thioredoxin,IPR012336:Thioredoxin-like fold,IPR013766:Thioredoxin domain,IPR017937:Thioredoxin, conserved site, |
| 182 | GO:0000502~proteasome complex,GO:0005623~cell,GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005739~mitochondrion,GO:0070062~extracellular exosome, | GO:0015035~protein disulfide oxidoreductase activity,GO:0015036~disulfide oxidoreductase activity,GO:0016671~oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor, | IPR005746:Thioredoxin,IPR008979:Galactose-binding domain-like,IPR010400:PITH domain,IPR012336:Thioredoxin-like fold,IPR013766:Thioredoxin domain,IPR017937:Thioredoxin, conserved site, |
| 183 | GO:0000792~heterochromatin,GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005739~mitochondrion,GO:0005765~lysosomal membrane,GO:0005829~cytosol,GO:0010008~endosome membrane,GO:0030057~desmosome,GO:0030867~rough endoplasmic reticulum membrane,GO:0070062~extracellular exosome, | GO:0000166~nucleotide binding,GO:0004839~ubiquitin activating enzyme activity,GO:0004842~ubiquitin-protein transferase activity,GO:0005515~protein binding,GO:0005524~ATP binding,GO:0008641~small protein activating enzyme activity,GO:0016874~ligase activity,GO:0044822~poly(A) RNA binding, | IPR000011:Ubiquitin/SUMO-activating enzyme E1,IPR000594:UBA/THIF-type NAD/FAD binding fold,IPR016040:NAD(P)-binding domain,IPR018074:Ubiquitin-activating enzyme, E1, active site,IPR018075:Ubiquitin-activating enzyme, E1,IPR018965:Ubiquitin-activating enzyme e1, C-terminal,IPR019572:Ubiquitin-activating enzyme, |
| 184 | GO:0001650~fibrillar center,GO:0005634~nucleus,GO:0005635~nuclear envelope,GO:0005654~nucleoplasm,GO:0005737~cytoplasm,GO:0005829~cytosol,GO:0016604~nuclear body,GO:0016605~PML body,GO:0030425~dendrite,GO:0045202~synapse,GO:1990234~transferase complex, | GO:0000166~nucleotide binding,GO:0004842~ubiquitin-protein transferase activity,GO:0005515~protein binding,GO:0005524~ATP binding,GO:0008022~protein C-terminus binding,GO:0008134~transcription factor binding,GO:0016874~ligase activity,GO:0019789~SUMO transferase activity,GO:0019899~enzyme binding,GO:0043398~HLH domain binding,GO:0043425~bHLH transcription factor binding,GO:0044822~poly(A) RNA binding,GO:0061656~SUMO conjugating enzyme activity,GO:0071535~RING-like zinc finger domain binding, | IPR000608:Ubiquitin-conjugating enzyme, E2,IPR016135:Ubiquitin-conjugating enzyme/RWD-like,IPR023313:Ubiquitin-conjugating enzyme, active site,IPR027230:SUMO-conjugating enzyme Ubc9, |
| 185 | GO:0005737~cytoplasm,GO:0070062~extracellular exosome, | GO:0000166~nucleotide binding,GO:0004842~ubiquitin-protein transferase activity,GO:0005524~ATP binding,GO:0016874~ligase activity,GO:0018169~ribosomal S6-glutamic acid ligase activity,GO:0019788~NEDD8 transferase activity, | IPR000608:Ubiquitin-conjugating enzyme, E2,IPR016135:Ubiquitin-conjugating enzyme/RWD-like,IPR023313:Ubiquitin-conjugating enzyme, active site, |
| 186 |  | GO:0004843~thiol-dependent ubiquitin-specific protease activity,GO:0005515~protein binding,GO:0008233~peptidase activity,GO:0008234~cysteine-type peptidase activity,GO:0008270~zinc ion binding,GO:0016787~hydrolase activity,GO:0036459~thiol-dependent ubiquitinyl hydrolase activity,GO:0043130~ubiquitin binding,GO:0046872~metal ion binding, | IPR001394:Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2,IPR001607:Zinc finger, UBP-type,IPR009060:UBA-like,IPR013083:Zinc finger, RING/FYVE/PHD-type,IPR015940:Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote,IPR016652:Ubiquitinyl hydrolase,IPR018200:Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2, conserved site, |
| 187 | GO:0005634~nucleus,GO:0005654~nucleoplasm,GO:0005681~spliceosomal complex,GO:0005730~nucleolus,GO:0005737~cytoplasm,GO:0016607~nuclear speck,GO:0043231~intracellular membrane-bounded organelle, | GO:0005515~protein binding,GO:0008599~protein phosphatase type 1 regulator activity,GO:0019888~protein phosphatase regulator activity,GO:0044822~poly(A) RNA binding,GO:0050699~WW domain binding, | IPR019007:WW domain binding protein 11, |

|  | H | I | J | K |
|---|---|---|---|---|
| 181 |  | PIRSF000077:thioredoxin, | Acetylation,Activator,Complete proteome,Cytoplasm,Disulfide bond,Electron transport,Nucleus,Redox-active center,Reference proteome,S-nitrosylation,Secreted,Transcription,Transcription regulation,Transport, | active site:Nucleophile,chain:Thioredoxin,disulfide bond,domain:Thioredoxin,modified residue,sequence conflict,site:Contributes to redox potential value,site:Deprotonates C-terminal active site Cys, |
| 182 |  |  | Complete proteome,Cytoplasm,Disulfide bond,Electron transport,Nucleus,Phosphoprotein,Proteasome,Redox-active center,Reference proteome,Transport, | chain:Thioredoxin-like protein 1,disulfide bond,domain:Thioredoxin,modified residue,sequence conflict, |
| 183 | mmu04120:Ubiquitin mediated proteolysis,mmu05012:Parkinson's disease, |  | 3D-structure,Acetylation,ATP-binding,Complete proteome,Cytoplasm,Direct protein sequencing,Ligase,Mitochondrion,Nucleotide-binding,Nucleus,Phosphoprotein,Reference proteome,Repeat,Ubl conjugation,Ubl conjugation pathway, | active site:Glycyl thioester intermediate,chain:Ubiquitin-like modifier-activating enzyme 1,helix,modified residue,nucleotide phosphate-binding region:ATP,region of interest:2 approximate repeats,repeat:1-1,repeat:1-2,sequence conflict,strand,turn, |
| 184 | mmu03013:RNA transport,mmu04064:NF-kappa B signaling pathway,mmu04120:Ubiquitin mediated proteolysis,mmu05206:MicroRNAs in cancer, |  | 3D-structure,Acetylation,ATP-binding,Cell cycle,Cell division,Chromosome partition,Complete proteome,Cytoplasm,Developmental protein,Host-virus interaction,Isopeptide bond,Ligase,Mitosis,Nucleotide-binding,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,Ubl conjugation,Ubl conjugation pathway, | active site:Glycyl thioester intermediate,chain:SUMO-conjugating enzyme UBC9,cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin),helix,modified residue,region of interest:Interaction with SUMO1,site:Interaction with RANBP2,site:Substrate binding,strand,turn, |
| 185 | mmu04120:Ubiquitin mediated proteolysis, |  | Acetylation,ATP-binding,Complete proteome,Ligase,Methylation,Nucleotide-binding,Phosphoprotein,Proteomics identification,Reference proteome,Ubl conjugation pathway, | active site:Glycyl thioester intermediate,chain:NEDD8-conjugating enzyme UBC12,modified residue,region of interest:Interaction with UBA3, |
| 186 |  | PIRSF016308:ubiquitin-specific protease (ubiquitin carboxyl-terminal hydrolase), | Acetylation,Complete proteome,Disulfide bond,Hydrolase,Metal-binding,Phosphoprotein,Protease,Proteomics identification,Reference proteome,Repeat,Thiol protease,Ubl conjugation pathway,Zinc,Zinc-finger, | chain:Ubiquitin carboxyl-terminal hydrolase 5,domain:UBA 1,domain:UBA 2,modified residue,zinc finger region:UBP-type, |
| 187 | mmu03040:Spliceosome, |  | Acetylation,Coiled coil,Complete proteome,Cytoplasm,Methylation,mRNA processing,mRNA splicing,Nucleus,Phosphoprotein,Proteomics identification,Reference proteome,rRNA processing, | chain:WW domain-binding protein 11,compositionally biased region:Asp-rich,compositionally biased region:Poly-Lys,compositionally biased region:Pro-rich,modified residue,sequence conflict,short sequence motif:PGR, |

|  | A | B | C | D |
|---|---|---|---|---|
| 188 | Ywhab | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide(Ywhab) | Mus musculus | GO:0006605~protein targeting,GO:0035308~negative regulation of protein dephosphorylation,GO:0043085~positive regulation of catalytic activity,GO:0045744~negative regulation of G-protein coupled receptor protein signaling pathway,GO:0045892~negative regulation of transcription, DNA-templated,GO:0051220~cytoplasmic sequestering of protein,GO:0051291~protein heterooligomerization,GO:0098609~cell-cell adhesion, |

|  | E | F | G |
|---|---|---|---|
| 188 | GO:0005634~nucleus,GO:0005737~cytoplasm,GO:0005829~cytosol,GO:0005913~cell-cell adherens junction,GO:0005925~focal adhesion,GO:0016020~membrane,GO:0017053~transcriptional repressor complex,GO:0030659~cytoplasmic vesicle membrane,GO:0042470~melanosome,GO:0043234~protein complex,GO:0048471~perinuclear region of cytoplasm,GO:0070062~extracellular exosome, | GO:0003714~transcription corepressor activity,GO:0004497~monooxygenase activity,GO:0005515~protein binding,GO:0008022~protein C-terminus binding,GO:0019899~enzyme binding,GO:0019904~protein domain specific binding,GO:0032403~protein complex binding,GO:0042826~histone deacetylase binding,GO:0050815~phosphoserine binding,GO:0051219~phosphoprotein binding,GO:0098641~cadherin binding involved in cell-cell adhesion, | IPR000308:14-3-3 protein,IPR023409:14-3-3 protein, conserved site,IPR023410:14-3-3 domain, |

|  | H | I | J | K |
|---|---|---|---|---|
| 188 | mmu04110:Cell cycle,mmu04114:Oocyte meiosis,mmu04151:PI3K-Akt signaling pathway,mmu04390:Hippo signaling pathway,mmu05161:Hepatitis B,mmu05203:Viral carcinogenesis, | PIRSF000868:14-3-3 protein, | 3D-structure,Acetylation,Alternative initiation,Coiled coil,Complete proteome,Cytoplasm,Direct protein sequencing,Monooxygenase,Nitration,Oxidoreductase,Phosphoprotein,Proteomics identification,Reference proteome, | chain:14-3-3 protein beta/alpha,chain:14-3-3 protein beta/alpha, N-terminally processed,modified residue,sequence conflict,site:Interaction with phosphoserine on interacting protein,splice variant, |