

Supplementary Table S3. List of the SSR motifs identified from the 423 *S. endobioticum* pathotype 18(T1) DNA contigs and the corresponding primers.

Contig*†	Motifs	Forward primer (FP)	Reverse primer (RP)	expected product size bp
3673	(CTATA)3	CACTGCGGTGCAACCTACTA	AATGGCCAAGAGAAAGAGCA	152
3673	(AT)7	ACTGTCCGTCTCCTGCATTC	GTCCCCCTGTGTCTTTACGA	388
3673	(TGG)4	TGTCATTCGTTTGTGGCAAT	ATCTATGCAGCGCCTCAACT	225
3673	(GCTTCT)3	AAATTTAAACACCGCATCGC	GTTCGTGTTTTTGGGCTTGT	194
3673	(AGCA)3	GGACCAGTTGCCAATGAGTT	GGTTATGGAGGGGCTATGGT	356
3673	(GAA)4	ATGATTTTCGAGTGGGACGAC	AATACTCGCACACACACCCA	273
3673	(GAG)4	GAAGTGGGTGCTGCAATTTT	AGCTTGGTATTCTCGCCTCA	336
79482	(TTGGCC)3	TAACTGAATTTTCCACGCCC	AATGCTGCAGACTCGGAAGT	292
79482	(CCAGCA)3	ATTAGTGGCAATACGGGCAG	GGTTGCAGATAATGGCGAAT	355
79482	(CGA)8	ATTCGCCATTATCTGCAACC	CCGTTGCGCTAGTACTGACA	387
79482	(CTA)4	AGAGGACGGTTGTTGGTGAC	AGAAAACCTGGTGTGAACGG	347

79482	(TG)8	GAAGAGTCGGAAAGCAGTCG	AATGCTGATCCAAAGCCATC	380
79482	(GGCGAT)3	AGAATGCAGGGAGGGAAAGT	CATCGCATTGCATTTTCATTC	361
79482	(CCCAT)3	TCTCGACCTAGATGGGATGG	TGTATCGTTTGAGTGCGTCC	367
79482	(GCCGAG)3-(GAC)4-(ACG)4	CCAGGCGATCATCCAGTAGT	ACATCCTTGACGGTTCGTTC	343
79482	(GTGA)3-(GGGC)4	AGGTGCTGCGACAGGTCTAT	CTCCAAAGCCGACTACAAGC	158
79482	(TGG)4	CTTCTTCCACTTCCAGTCGC	CTGAGCCAGCCACAAATACA	394
4884	(CGCA)5	TCAGCTTTGCTGACGATCTG	ACGCCAACGAATGGTAGAAC	349
4884	(GTG)4	CTCGTTGCTCTGATGTTCCA	GGAACGTGAACGTGTCATTG	351
4884	(CCAT)3	TTGGATTGACCGGTAAGAGG	CATCTCGGGTAAGCATGGAT	172
4884	(CACG)3	CTGACGTTTGGGTCACAATG	ATAGGATTGGACGCATGAGG	331
3553	(TCCA)3	TCGGGTTCGGTATTTACCAA	GAGTGTCTGTGTCGGGGTTT	321
3553	(GAA)4	CTTGTAGCCTGGAGCAAAGG	CGTTGAAGGCTGTTGAGACA	303
3553	(CTC)4	AGCCTAAACGCCTGACTGAA	CAACGTCACCTACCACATCG	263
3553	(TAGC)3	CAAAAATGCAACGTGGACAG	AGTCGTGGATGGAACGAAAC	366

4761	(CCAT)3	CAGCAACAGAAGGCAACAAA	CATTTAAATCGGCCATGCTT	216
4761	(TCG)4	TGAACAAGCGCGTAAAGATG	CTGGATCTGGTTCCGGAGTA	254
214772	(AAG)4-(GTCACC)4	CGCCAATGTTACTGTTGCAC	GGAGCTACTGCTCTCGCAAT	387
214772	(ACT)4	CACATGTGAAGGTTCAACGG	GAAGCGAAAGACCGTCGTAG	219
214772	(GCG)4	CACAAAGTCCTTGAGGAGGC	GCAATCATCCACCATCACAG	362
310502	(GATG)3	TGTGTAATTCAGCGAGCAGC	CCAAGTTTCCTTCCCCTCA	321
213091	(ATCA)3	TCATAGCGCCCGCTACTACT	CTGGATGGCTGATGGTTTTT	334
213091	(TATG)4	CTGCTTCCAGAGCCTATTCG	ACTCGGTAGAGCCTTGACCA	398
213091	(TTCGT)3	AGGATCGGGTGGGGTTATAG	TTCACAGAGACGAACATCGC	374
213091	(CCACTC)3	TCGTGATTGCTTGCTTGTTT	GTGGTAGTAATGCTGGGCGT	287
213091	(CTCATG)3	ACTATGTGCTGTGGCTGTCG	ACATCCAAGGCAGTCGTACC	366
38217	(TAG)4	ATGGTGAATATGCCCGAAAG	CTGCCATCCTTTCATTCGAT	195
38217	(CAA)4-(CAA)4-(CAA)6	TCTCCTTTCTTGCTCGGT	CCCAGCTGCTTTCATTCAT	311
38217	(AAT)4	GGCGTGATTGGAGTTGAAAT	GGCTACAATGGAGTCGGTGT	246

2977	(GCT)4-(ACCC)3	TCACTGCTGGAAACGATGTC	TTCAACGAGCACTTGGACAG	350
2977	(AGG)4	GATTCGAGCAACAGGAGGAG	GAACTCAAACCACCAGCCAT	153
2977	(AAT)4	ACTTGGAAGCCGAACTTGAA	ACTATCATCCGCATCACCT	329
2255	(TGC)4	GTTCTAGCGCTGCTCGTTCT	GATCTACGTTGCTGCGTTCA	334
2255	(CCA)4	ATCGTGGATCTCCACACACA	GGTTGGTGTGATTGAGCCT	329
2255	(CGTGCC)3	CAGCACAACGATCAGAGCAT	TCGAATGACATCTGAGCTGC	299
134542	(TGCTG)4	CGTGATGGGCTCTTTACGTT	AATGGCTGCTAACCACGAGT	334
134542	(CCGCA)3	GACTTGGACGACCTGGATGT	ATCCTGGATGGTTGGTTTGA	353
134542	(AGGG)3	GCGGACTCATACACCAGGAT	TGCAACCCTCAAAAATCTCC	355
134542	(CATA)3	TGTGTCCCTACAATCCACGA	GAAGACGTGACCCATCGAAT	366
407616	(CCAA)4	GTCGCAAATGCTGCTGATTA	CGATAAAATGGCTTGGTCGT	373
407616	(CACGAG)3	GTCGTGCATTCAAGTCGAGA	GTCGCTCGAGGCTTTACAAC	259
407616	(TGGA)3	TGAGGGGACCATCCTACTTG	ATGCCTATTCGGATCAGTCG	390
397081	(TCATC)3	GAACGGATGAACGGAGTTGT	ATCGATATGCTGGGATCGAG	234

397081	(GCGG)3	CCGTACGTTACGAACTCGGT	GGATGCCGTAAGTCGTCATT	134
397081	(CGACG)3	CAAAGCGAATCAGGGATCAT	TCGAGGGAAGTATCAATGGC	193
397081	(CCGTT)3	CGACGTACTTGACAACCCCT	CGGACTATATGCGCTTGGAT	380
442158	(CAACAG)3	GGCCCAACAGCAAGTACAGT	CCATTCTTGCGACTTCCAAT	365
442158	(GA)10	GGGTGCGTACGATCACTTTT	TGAGCTAGGTGCAGATGGTG	148
3881	(TCA)4	TAATTTGCCATTCTGCCCAT	TCAACCAAGTTCTAACCGCC	316
3881	(GTG)4	GATGAACCTTTGGGTCGAGA	AAAGCACGACCACGTCCTAC	341
3881	(GTGGC)9-(GGAT)6	TTGGCAACAAAAGAGCAGTG	CGCCTAGCACAACAACCTGAC	334
3881	(ATAC)3-(TACT)5	CAGCCGTGCGCATATAGTCT	ACAGAGAGAAGCCCAATGGA	366
3881	(TGCGG)3	TGGAAGAGGGCCTGAATATG	ATGAGCGCCATAAAGTGGTC	260
345443	(TCA)4	CAGTGATGCCCAAGGTACT	AACAGTGATGGTCCGAAAGC	369
345443	(CATA)3	CCATAGGGGAGGCCAATTAT	TCTCTTTCTGGGCAGCATTT	314
345443	(CATG)3	GGTACGCACCTCCACAAGAT	ATTGACCCTACTGCAAACGG	362
107447	(GACCAT)4	ACAGGTGGTCGTCCAATAGC	TGATTCCGTATGCCTGATGA	170

107447	(TGGG)3	CTCACAAGGCCGGTATTCAT	ATCTGCTGCAGCCTTGATTT	340
107447	(CAAAA)6	GAGCAGTATGCCAGGAAAGC	GTAGGCATGAGGGACGACAT	385
107447	(CCCCCT)3	GCTGTGCATTGCTGTTCTGT	TACCAACAGGTTACCGGCTC	333
107447	(GCCC)4	CGTCGATGTGCCTATGTGTC	ACAGGTACTCCAGACACGGG	296
107447	(CTG)4	CCATATCCCAGAAGCCAAGA	TTTAAACCTCGGGTGATTTCG	364
380499	(GAT)4	GGAGTCTCGTGTCCGATCAT	TTTTATTGTGTTTCGTCGCCA	333
705	(GGA)4	TGTCAGAGATGCATTAGCGG	CCTGTCCTGTCCTGTCCTGT	229
705	(TCA)4	CTGTACGAATGCGCAAGAAA	ATGGTACAACCTGTCGAGGGC	312
705	(CTGC)3	TGCTCTAGCGAGACAAGCAA	TGATGGACATGCAAGGTTGT	293
705	(AGT)4-(TGAG)5	GTGTTATGCCGTTGGCTTTT	CCTGATCTTGCCTGACCAAT	339
693	(TAA)4	ATCCCAGTAGTCGTGCCATC	CTGTGCTGTGCAACACATTG	391
693	(AGC)4	GGTGGTCTTGGCAGTAGAGC	AACCTCCACCATCAAGTTCG	384
439619	(GGT)4	AGAGACAAGGGCGTTGCTAA	TACTAACCCCGGAGCTGATG	328
439619	(TGGG)3	AAGCTTTCTGATAACGCCGA	AAAAGGCCATTGCTGCTAGA	357

2723	(AGGAGC)3	ATGCAATGTCAGCAAACAGC	TGACTATCTGCGAGACGTGG	303
2723	(TGGAT)4	CCACGTCTCGCAGATAGTCA	CCATCCAGCCTGTCTTCAAT	300
2723	(AAG)4	CGCAACAACAGAGAACGAAA	GTAGAAGAGATAGGGCGGGG	290
2723	(TGA)4	GTCATGACGTCGTGGTCAAC	AATCGACATGGGGTGGTTTA	384
2723	(TGA)4	GCTGCTGCTGATGGTGATAA	GGCAACTACACAGCAAGCAA	275
2723	(GCAAT)3	TAATCAGAGCACCGTTGCAG	TTTTGCTTGATGCATGTGGT	332
2723	(AAG)4	TGCTTGTTACATCGCTTTGG	CATCCAAGCTTCAATGCTGA	378
334133	(GTA)6	GCAGCTATCAGACCGAGGAC	TTGGACTTTACCTGAACGGG	253
334133	(CCT)5	TCTGGTTCGGCCAAGTTTAC	CTGGTGCTTCGACCTTCTTC	340
334133	(TCCGC)3	GCGTAGATGTCCCAGCATT	GCCCTGGGTTGCCTATATTT	149
334133	(TGCGAA)3	TTCCGCATCATAGTCCATCA	ACTGGCACGACGAAGGATAG	292
334133	(ATT)4	CACTTGCGAGTGTGTGTGTG	ATTCAGTTTTTCGCTGGATCG	331
2711	(GCTGGT)3-(TCGG)4	GCACATATGCGTGTTATGCC	ATGCCAAGGGATATGGATGA	279
2711	(GACC)5	ATCGTACATCGTACCGCACA	CCTGGACTAGCTGATGGCTC	367

2711	(GAT)4	CGGAAGCACATCAAAGGATT	CCTCATCCTCGTAGCTTTTCG	201
411368	(CATC)3	AGAGACCCCGACACTCACAC	TCCAAATCGGTGATAAGGGA	359
411368	(GTT)4	CGTCTGCGAGTGATGACATT	CACGGTACGTCATACGTTGG	371
411368	(AACA)3	TGCCAGCTCAGCATAATGTC	GCTTGTTTCCAGTTTTCCCA	262
2785	(CATC)3	ATGTATAGAAGGCGATGCGG	GTTGCAAAGGATGGAAGGAA	249
2785	(ATG)4	AGCCTTTGAAGTCGACAGGA	TGCGCATGCGTATTGTTATT	344
2785	(GAT)4	GAATGGGAAGATGAGGACGA	ATCATTCAACCAATCGGCTC	357
2785	(GGA)4	TGACGAAGACGACGAAGATG	GTGGCAACAATGTTTCATCG	286
7711	(GCT)4	AGTCATATACAAACGCCGCC	ACTGACAAGACCGCTGGAAT	323
143809	(CGGT)3	TGAATCCTGCATCTTGCTTG	CAAAGCACTTGCAGTTTGGA	359
2894	(CATGGG)3-(GGGC)3	CGAATGGTGTGTTTTGAAGCCT	TGATCAAGGACGGAAAGACC	338
2733	(CCTCCA)3	AGGGAATGAGCAGCTAAGCA	CGAATGTCTTGCAGTCAGGA	306
2733	(CCAT)3	GGTAACAGGCGTAGTTGGGA	GGGTTCGGTTTGTGGATATG	367
2733	(GGATGC)3	GGATGAGCTCAGAGGTTTCG	TTCTGTGCTCAGCATCATCC	143

5509	(GTAC)3	CTTACGCGCTAGGTTGAAGG	ACGCTCCTGATAACCGTGTC	375
5509	(CACG)3	GACCGAAAACTTCCGATGA	CTCGCTCATATGGTGTCATGT	216
5509	(ATC)4	GGCGATGGAGCACTATCAAT	GCAAAAGCATGCTGCAAATA	270
473917	(ATGG)3	CGGTTGATCAAGCAGACAGA	TCACTAGTGCATGTAGCGGG	306
473917	(AAG)4	GAAGTCAGGATAGCCGCAAG	AGCAAATGCCATTCTACGCT	360
384599	(GGGGC)3	CTCGCATCAACTCGTTCGTA	TCGCTGTATTTGCTGAAACG	365
459	(CCAA)3	TGTGGCTGGTTAGTGTGCAT	ATAGTAGTGATGCGGTGGGC	328
459	(TGCAA)3	AAGCCGTCAAACGATACACC	TCAGTGCATGAGACCAGAGG	379
136	(AATC)3	AACCAGCGATACCTCATTGC	ACAGGCGCAGGACTACAGAT	280
271657	(ATTG)3	GACGCGGTTTCAGTATTTGGT	AATCGATCAGTGCCAAGGTC	369
271657	(GCG)5	CCATTCTCTCCCAAACGGTA	AGGGAGCTGTGTCACCAGAC	368
271657	(GCAAT)3	TATCAGCAACGACGCGTAAG	GAACACGGACTCCCCATCTA	321
8071	(AAACT)3	AAGGGACCGAGGAAGGAATA	AGCAACAGCACTCAAAGGCT	389
8071	(AATA)3	GGACACCGGCATGGTTATAC	ACGCTGGAAAATCCAGAATG	379

575255	(GGT)4	CGAACGACCTCAAGAAGAGG	AGCCTAGGAGACGATGCAGA	241
5274	(TTCC)3	TGTTGTGAGCAAAAACGAGC	GTGCTGACGACGAAGATGAA	327
5274	(ACA)4	CTTCGCCATCTGAAGACTCC	CCAAGCACCATTTAAGCCAT	368
5274	(GACC)3	TCTAGTGATCATCGCGCAAC	GATTGGTTGGTTGGTTGGTC	354
5274	(CCGA)3 -(CCAA)4	TGCTTGTGATGAATGAAGGC	GCCAGGGTAGAAAGCAACAG	346
5274	(GTTG)3	AGTTGGCGGCGTATTATCAC	CATCACACACCTTGTTTGGC	293
3244	(ATTGG)4	AAGGGTGGTGACTGTCCTTG	CGAATAAGGCAAATGCGACT	252
3244	(CATC)3	ATATACCACGAAACCGCTGC	TAGCTATCGCTGGATGAGCA	247
207	(ACGCA)3-(TCGC)3	AGTGTGCCAACCCATCTAGC	GTTGCAGGTCTAGGAGGTCG	329
207	(GAGTGG)3	AGGAAAAGGCTCGGTGGTAT	CCTCGCCACATACGGATACT	313
207	(TGGACA)3	GCCCATGCACTATGGATCTC	GGAATGCGGACAAAGTTCAT	316
2341	(GGTGC)3	GGCGACCACAGTTGAATTTT	TAGCCCTCTTGGTCGTCAAC	366
2341	(GGGGGA)3	ATTTGGATATTGGAGGTGCG	CACTCACACTGTCCAACGCT	369
2341	(TGCT)3-(AGCC)4-(CTGCCC)3	CACTCCATGTCTGCTGTGCT	AAGGACTCGACAGAAGCCAA	243

2341	(GGGGA)3	CCATCCACATCTGTGTCAGC	GCACCAATCATGAGAGGGAT	264
2341	(CCAA)5	AAGGTCGCAACAAGCTCCTA	GTATGGGCGGTCAGCTATGT	382
2341	(GATAG)3-(GATGG)4	ATATGCTACAAAGGCAGCGG	GCAGACTATCAACGCAGCAA	267
2341	(CGAA)3	TGCTGAATATTTGCGTCTCG	GTTGAACAACACGCTGCACT	241
5068	(GCT)4	TTCTGCGTGGGCTTCTTAGT	AGTACACGCTCATGGCACAG	305
5675	(CAT)4	CAGCTTCAGCATCCACTTCA	TTGTGATAGTTTCCCTGGC	189
5675	(CATC)3	TCGACAGTCATGAGCGAAAC	CCATGGGGAGATGAATGAAG	366
383309	(TGTAT)3-(TGA)4	TCCCATGGACTGTGTAACGA	CGAGATTTGATGAGCAAGCA	272
383309	(CGCCAA)3	GCGACGCTAGAGTAACCCTG	CACTCTGCCTCGGAAGTAGG	193
383309	(GCGAC)3	GACACCCGTCAAAGTCCATT	AATTGAAATCCAGCACGGAC	365
383309	(TCTT)3	ATGGCAATCCTCAAGCTGTT	AAGACACGAAATCAGGTCCG	363
383309	(CGGG)3	TAAGCAACACAATTCCGCAC	CGAATCGACGACGTGACTAA	382
140904	(CTT)4	GAGGTAGCGACAGCAGTTCC	ATTCGGGTGAGATTTTGTGC	366
4278	(GGCG)3	AGCATTGATTTCAAGCGGAT	TACACCGAAGACGAGAGCCT	356

4278	(TCG) ⁵	AGATCAGCTCAAAAAGGCCA	ACACAGCATAACACGCCAGAG	352
4278	(CTGGTG) ³	CTCTGGCGTGTATGCTGTGT	TATTTGCGCATCATGTGGTT	350
4278	(TCG) ⁴	GCAAGCTCACACATAGGCAA	TAATAGGGTAATGCGTCGCC	304
4278	(TGCCC) ³	TACATGATGGTACGCCTGGA	GCGGTATGTCTGGTGTGTTG	326
4278	(GCTGGT) ³	ACGCCTTACACATCTCCACC	GGTGACGAACCGGACAGTAT	327
4278	(CCG) ⁵	GGGTGGCTTACTGGAACTCA	TCATGGTCGAGACGCTGTAG	391
4278	(GTT) ⁴ -(TTG) ⁵	GAGTCCGTCAAGTTGGCAAT	TGCTGCCGAAGCCTACTATT	327
4278	(ATGT) ³ -(TGGA) ³ -(TGACG) ³	GAAAAGGGCCCTCTAACCTG	AGCAAACGAAATAGGTGCGT	347
365657	(AAAG) ³	GCAGACGTGCTATCAGGACA	ATCATTGGTTTGCCTTTTGC	313
612913	(CAGC) ³	TCGATTGTGATTTGAGCAG	ATACCTACCGAAGCGAGGGT	255
612913	(CGCGA) ³	ATTTGATTGTCTGCGGGAAG	GATGCACGATGAGGAATGTG	378
6665	(GGTC) ³	ATGCGGAACCGTGTATAAGC	ACTTTGCGTGGGAAATTGAC	376
200477	(TAG) ⁷	GGATTGTTTGGTGCGATTTT	TTCCTGCCATCCAACCTTTTC	364
14106	(GTT) ⁴	GACCCCTTGTTGAGCAGGTA	TTGGCATCATCAACTTTGGA	199

342892	(GCT)4	GTGGTGGCTCGACAGATTTT	ATGGACGTGAGACCTCAACC	154
342892	(GCATG)3	GGATAGGCGTTGTGTCCATT	CTGTGAGCAACCTGGAGTGA	345
353437	(TGGAT)3	CTGAAAACCTGCAGCCATGAA	ACCTTTGGGATCGCCTACTT	278
353437	(TCG)4	GCAAAAGCCCGTAAGATCAA	GGTGAGCAATGTAATGGGCT	233
353437	(CGTGC)3	CCGACTGGACTGACTGGACT	ATAGCGGGTGGCATAAGAGA	376
353437	(GGAGT)3	CTGAAATCCATGGCGAATTT	GCATCTACGCTGCGACATTA	245
602	(TTTG)3	AAATTACATCCGCAACAGGC	ACTTGGCATTGGTTGGAGAC	377
602	(AGG)4	CTGAAGGAGTTGTTAGCCGC	TCGTTCCTTTTTGAGACGCT	150
602	(CCTC)3	TGACACTGACGATGGCTCTC	TCAACTTGCACAGGCTCATC	266
602	(TTTGT)3-(TGGA)4	TTTCAGAATGAAGGGGGATG	GTGGTAAGCCGTTGATCGTT	398
78108	(ATC)6	GCTCCCATCTTCTTCAGCAC	AGCTGAACGAATACCGTTGG	328
78108	(CTG)5	GCTTTGCAGAATAAGCCAGG	CCATGGTGCGTGTTAGTGTC	336
78108	(CACGC)5	CGCACTTTCTGACGTGATGT	CTAGAGGGGTAAAAACCCGC	370
105	(TCCG)3	AGCAGAAAAACCAGCTCGAA	TGGATTGGCGTATTCTCTCC	387

105	(CGTTA)3	GGAGAGAATACGCCAATCCA	AGGAATTGGCGAGAGTGCTA	176
105	(AGT)5-(TAG)4	ACGAGAAAACATCAATGCCC	TCAGCACGTCAAGTCGTTTC	208
184220	(GT)7	GTGTTTGGGCTCATGGAAGT	ACGGCATGCAAGTCAGTATG	370
184220	(GACA)3	TGATTGCTGATGGAAATGGA	TGCATATTCGATTTGGACGA	328
3502	(TACT)3	GATGACGGCAGTCTTGGATT	TTGCATCTTTCGTTCTGCAC	344
3502	(CAT)4	CCAAGCAGAGAATCCCATGT	ACGGGTCTGGGCTTATTCTT	376
432007	(TCCCC)4	AGAGGCTTGTTAGGGGGTGT	CACGGGCTTTTCAAATCAGT	271
432007	(CCTT)3	CATGTGCCAATAACACAGCC	CACGGGCTTTTCAAATCAGT	219
432007	(TGCT)3	GCAGAATGCACTGGAACAGA	TGTCGTGTACATCCCCAAGA	301
804791	(CTCTTC)3	GAATGCTTGTGCATCGCTTA	TCTACTCGCTTCGCTTCACA	260
630365	(TGCT)3	AACAAGGCATCGAGAGCAGT	CTTCGTCAATGATCCGTCCT	271
630365	(TGG)5	GTGAGACGGGGAGATGTTGT	GGATTACCAGTACCGCTCCA	124
630365	(TGG)4	GCGTTGTGTCATTCCCTGCTA	CCTATATGCGCGAAAACCAT	292
630365	(GCTCCT)3	ATGCAGTGGATAAGGCCAAC	TTGAAGTCGACACAGAACGG	369

630365	(GCT)5	CCGTTCTGTGTCGACTTCAA	ATGGGCAAGAAATTGTCGAG	216
9066	(GTG)4	TGCATCGACTGGCTGTAGTC	GCGCATAGCATAGCATAGCA	365
9066	(CTATG)4	TAGTACTGCAGAGGGCGGTT	ATCTCCACACTGGTCTGCCT	340
9066	(ACG)5	GTGCGTGTGTCTCTCATCGT	GGGGATTTGAACATGAATGG	193
9066	(ACC)4	AAGGTGGGATTTTCAGTGTCG	TTAGCATCATTACCCTCGGC	316
61960	(ACTTTT)3	ATACGGTGTGGTTGGTGGAT	CGTATGATCGAACCATGTCTG	159
61960	(AAC)9	GTGTAGTGGCAAGTGGCAGA	ACCCTCCATGCAAAGTTCAC	354
61960	(GTGC)3 -(GAGC)4	GAAGCTACATGCGTTGGTGA	ATGCAACATCGAGACAGCAG	252
61960	(ATTA)3	TGCTCGAGTGACAGGTTTTG	GGAATTGCATTGTTTTGCCT	378
61960	(GGCAT)6	ATGTCGGCATTTCATGACAAA	GATTGTCCCAAGCCACTGTT	388
61960	(TTA)6-(GTGGC)3-(CTCG)3	CCGACCAGTATAACGCCTGT	TAGGGCACATATGCAGTGGA	285
2035	(TGG)6	ACCCCGTCTTTTCCTTGTCT	ACTATGGCGAAACAAATCCG	253
2035	(TTGG)4	CAGGATGACCCAAGACCAGT	CAAAGTTCGGCATCAAGGTT	231
2035	(AGGAC)4	CCAAAGGCATCGTCATAGGT	CTTTTCTTTTGGCTGCGTTC	375

427183	(CTA)4	CCTCTTCATCCCCATCTTCA	AGACGGTGTCGAGCAGAGAT	366
177654	(GTTT)3	GGCACTTCTAGCCACCTCTG	ATCAACAGTAAACGTCGGGC	396
177654	(CTTG)3	CTACTTTCACCAGCGCCTTC	CCAAGTCACTCCACCACCTT	258
639	(GAT)4	TTCATGAAACGAGTGGGTCA	GTAGACTGTGTTGGGCGGTT	350
3129	(CAGG)3	TATGATGCACATTGAGGCGT	TCGTGGTGCCAAACTGTAAA	388
3129	(AGC)4 -(AAC)4	GAAACGACAACGGGAAAAGA	CAGATCTGTGGTGGGTGTTG	322
3129	(GCAT)4	TACACGATCCACTGGCACAT	TTCCTGAATTCGGTCAGAGG	324
3129	(GGGA)3	ACGCACTTTCGAATTTGTCC	GTGAAGTGGAAGAGGCTTGC	218
2749	(TCAA)3	ATGGCCATGACGATTTTCTC	CTGCCTTTATTCCCCAGACA	306
512973	(ATT)6	TGCAAGAGCCAACACTTGTC	GCTTTCAGTTGGGATTGGAA	380
512973	(GTC)5	CGTCATAGACAAGGCGCATA	CAAGCACAAACACACGATCC	396
512973	(TCG)5	ACTTTGGGTTCGGTGATGAAG	AGAGCAGCCGAAAGTGTTGT	322
733333	(TAC)4	TTGAAGCTGACTGTTGTCCG	TGCCATTTATGTTACCATGAGC	180
268975	(CTACC)3	CAAGGAGCCTGTCAACCAAT	ATACTCTGGCAGTCGAGCGT	251

596961	(CAT)4	TATTCGCCTTTGATGAAGCC	TGCTGGGGGAGATATTCTTG	198
419237	(TCT)4	GCAAAACACTCTCTAGGCGG	TGCTTCTGTGAATGGAGACG	370
419237	(CCAA)3	TCAACGCGAAAAGTGTCAAG	AGAAGACAAGATCCGCCTCA	396
419237	(GCGA)3	GTGGAACCTGGCATTTCAGT	CGGGATTAGATGCATGTGTG	313
419237	(CCGT)4	TTGTGAAAGCATGCGGTTAG	GATGGAGAAGATGAGGCAGC	397
5826	(GAA)5	CCTATTGCGCATTCCAAGAT	GGCACTCTGTACACCCACCT	334
2746	(ACGC)4	GCGCGATCTAGGAAGTTTTG	GATTGCAATGTGTCAATCGG	203
730054	(CAGCA)3	GTTGAAGACTCGCACAAGCA	GGGTACATGAGCAATGAGGG	258
730054	(ACAT)3	GATCATCATCGTGCGTCTTG	TGGGACAAGTACAATGGCAA	336
730054	(GT)8	GCAGGTTTGAAAAGAGCTGG	GCATACGACTGAAGACGCAA	347
2696	(GCG)4	CGTTTCGTAGGAATTGGGAA	AAGTACCCGTCACGACCAAG	353
5508	(AGT)4	GCACTTTGCGTTCAATGAGA	TGGGAATGCTGAATGACAAA	378
527896	(GATG)3	ACTGCTTACCATTGTTGCC	TGTGACTATGCCATGTCGGT	385
771441	(TGCG)4	TTCGACAAATTGCTTGCTTG	ACAGCCTCCTGCTGAGACAT	376

632089	(GCAGG)3-(ATGG)3	TCAAGCGTCAGTCGTCAGTC	ACAAGCATGCACAAGCAGAC	208
632089	(CAT)4	ACAGACAGAGGGGTTGGTTG	ATCTCGAGTACTGAGCCCGA	364
7715	(TCA)5	ACCCCATCATCCATCAGTA	CCGGGTATCCTGTTTCTCAA	296
7715	(ACC)5-(CAC)4	TTCAACCAGCATCATTTCCA	CAAGGTAGCAGCCTCGAAAC	319
7715	(ACA)6	TGCGCTGATTTTGTGCTTAC	CAATCTGTCTTTTCGCACCA	266
5954	(GAT)4	TGTATGCGACGTGCCTAGAG	GGCTAAAGTCGTGGGTGAAG	395
5954	(GTACG)3	GGGATCCAATTCAAGCAGAA	GGAGCAACGGATTTACCTCA	388
5735	(GAT)4	AGCCCTTGGAAGTACTTGA	AATGTAGCACGCGCAGTATG	340
2580	(TGGA)3-(GT)7	AATGGGGTTAGTAGGCTCCG	CATACACGTGGTAGCAACGG	216
11155	(AGC)6	GCGTGTGAACAAAAGCAGAA	ATGACCATGAACGATGGGAT	355
81447	(TGAT)3	GGAAAAGGCCAGATGAATGA	GGCATACGAGTATCGTCCGT	376
81447	(GTCGC)3	CTGACATCCGACAACACCTG	TCACAATCCAAAATGCCTGA	152
678375	(ATAAT)3	ATTTGTCGCCATCTCATTCC	CGGTACATGCAGTTCACCAC	271
678375	(GCT)4	ATCGGTCCCATATCCTCCTC	CCATTTGGAACCTTTGCCTA	200

678375	(GAAAA)3	TTGACATTTTCAGGGTGGTGA	TTTACGCGCTTTAGCCAAGT	155
656761	(TATG)3	CCAGTCACATCGTCTGCTGT	ATTGCCGTTGATGGGTAGAG	305
23998	(GATGCG)3	CATTTGGGAATGATTTTGCC	GTTGCACCCGTCTCATTCT	321
23998	(TAT)4	TGGCACTGGAGAGCTTACCT	AGCCGGCAACTTAGATGAGA	155
8367	(GATG)3	TTGTTGGTGGAAATTGACGA	CGACTAATGCTCCAGAAGCC	231
3560	(CGCGT)3	GCTCACTAGGCCAGAGTTGG	ATGGCGTTAGGTTTCAGGTTG	247
3560	(CCGG)3	CAACCTGAACCTAACGCCAT	GTCGGTAAGCCGCAAGTTAG	326
7990	(GCCA)3	GATGATTCCGAGGAGGATGA	AGTGCTTCATACCCCACCAG	210
68758	(ATAC)4	GGTTCCACTTACGTAGGCCA	ATGATGCGGATGACATGAGA	172
68758	(CT)8	CTAGCACTCTCACATGCCCA	CAAGAAACGACTTGATCGCA	332
494235	(CGATGG)3	GGAGGATGTCGTGAGTGGAT	ACAAGCCCTGGACCTCCTAC	264
451711	(TGTGT)3	TGGGTTTGGGACGTTTAGAG	GTCTGAGTGCATATCTGCCA	286
451711	(ACAGAC)3	TGGCAGATACGCACTCAGAC	ACTCATGCCCAAACCTCGAAC	333
277434	(CAGC)3	GCCTCGCTCTGATGACTACC	AATTCCTCGTATGAGGTCGTG	235

818598	(TGG)4	ATCGGTGCTGATGTTTGTCA	GTAAGCCCACGAAATAGGCA	299
18355	(CCA)4	GTGGTGCTTGCTGTTGACTG	GTCCGGCAAGTACAAACCAT	297
18355	(TAA)4	AGCCAATGGCAATGGTAAAG	ACTCTCCGGTCAATCCTCCT	392
5674	(CGA)5	TTAGGGCTGCGAGAAGACAT	TTCTTTTGCTGCCTCCACTT	249
7289	(GGT)6	TAGGTCGTTCTCGTGGGTTC	CCATCATTGCCTCTCCAGTT	311
7289	(CAA)5	AACTGGAGAGGCAATGATGG	TCTACCAACAATCTTCCGCC	141
75331	(GTAAC)3	GAGGAATGGTTGTGGCTGAT	ATTGTGGATGATGGGTGGAT	400
75331	(AGT)6	AACCATGGGAGAGTTTGCAG	GGGCGTTAGATTGTATGCGT	326
332905	(TGC)4	TGCCTCTTGTGACAGTTTGC	TACCACCGCACATAACCAGAA	321
332905	(AT)8	TCTCGACATTCAGGCTGTTG	GCACTTCAGCCATGCAATTA	384
29983	(AGC)6	CACCCTGGGATACTCGACAT	CTTTTTCCTTGCGAGAGTGG	392
699449	(CGCCG)4	ACGAAAAGCGTGACAGTGTG	TGGTTGCGTTGTCAAAACAT	200
9599	(GTTG)3	TCAATAGCGGCCAGGTTTAC	CACTCAGCACTTTCGTTCCA	343
9599	(CAG)4	ATTCGTGTCTCGGACGAAGT	TAGTGACAGTGGATGCCGAG	313

492	(TGCAGG)3	GATTCCGTTCTCGCTGGAT	AATAAGCGCCAGTTTCAACG	303
626	(CTA)5-(TGT)4-(CTA)7-(TAC)5- (CTG)4	CCACCACCGCTACTACCACT	GGAACATGTTGGCTGGAGAT	295
15315	(CAA)4	TCTGTGCACTTTTGCCAGTC	TGGAGATTCCATACATCGCA	288
11982	(CATGGT)3	CTCCACATACGCATTGGTTG	GACAGATCGACAGACAGGCA	333
11982	(GCA)4	CCCTGTAAGAGTATCCGGCA	TGATGAAGAACTGGCGACTG	375
11982	(CAA)4	GCTGTCGTAGTTGGCATCAA	GATCCCATACCGACAACCTCG	397
11982	(AGG)4	ATAAACCGTTGGTGTTCGCT	GAAATGCGCTCAACTTGACA	344
5561	(GCTAT)3	AAGAGGCCATGTTTCAGGATG	GTTTACCGCGCGAATATGAT	335
2826	(ATG)5	ACAAGCAAACCCAAGGAATG	ACTCGGTTGGATGAGTGGAC	375
2826	(CAG)5	TATTCCAAGGTCCTCGATGC	CTGATCCCGACGAATAGGAA	261
4633	(CCA)4-(CCA)5	CCCAAATACGTACCACCACC	AACCAGTGCGATTGAGAACC	386
474225	(GAC)4	GAAGCTGGAGTTGACGAAGG	ACTCCCTAGATCGTCCCGTT	337
474225	(GATGTT)3	TCGAGGGATATGGAGAGGTG	CAACATGTGCGAGCAAGAGT	355

16161	(GTGG)3	AGAGTCAGCTCCATGCGATT	GTATCGCTGAAGACGAAGCC	242
16161	(TCGCA)3	AGCGAGAACGAAGCTAGCAG	ATCAGGCGTCTCCACACTCT	343
12570	(CAGGG)3	CGTATCCTCTCAGCCTCCAG	ACACCCCAGTCCAGTAGCAC	249
113713	(GGTGTA)3	TTGTGGGTGGAACACTTTCA	ACCAACCCTGCGTATGTCTC	263
113713	(GCGG)4	TGGATTCGCGGGATAAGTAG	TCGCCCTAGCTCAAAAGGTA	278
113713	(GCAAG)3-(GCAGG)3	AGCTATGGGAGCGAAAGTGA	GCGTGAAAAGGCATTATCGT	239
113713	(GCGG)5-(TGGCG)3	ACGATAATGCCTTTTCACGC	AGCCAAGTCTCCAAATCCCT	270
113713	(TGGA)3	TATGTCGAGTGAGTGAGCGG	AGCCAAGTCTCCAAATCCCT	164
13625	(ATGGAT)3	TGCAGAATCGCTCACTTTTG	ACAGCCGCCTTTTCACTAGA	292
9746	(GACC)3	CATAGCCAGACAGCCAGACA	GTGAGCTGGCAAGGATCTTC	373
654	(GAAG)3	TTTCTTTCCTTGCAGGCACT	CCAACCTGTACGGAAATTGG	298
654	(ATG)4	AACGCAGCGTCTTCTTTGAT	CAGGCACGTATCATTGTGG	222
284478	(GAGGG)3-(AGGAT)4	TACATCGCGTTGTGTGGTTT	ACACCTTCATCCATCAAGCC	339
284478	(TCGC)6	TTTGATGTGTCGGAAGACCA	CTCGTATTGTGCAGTTGCGT	382

284478	(GCAAC)5	ATGGCCGTCCTGCTACTAGA	CTGGGTGGTTCTGAGATGGT	325
2978	(CGTTGG)3	GCATGGAACACATGGAATGA	GAGACGGAGTCGGATTGGTA	343
4865	(GATTGC)7	CGATTTTTGGCAGTGGATTT	TCTTTCCCGTTATGGACCAG	333
4865	(GCGT)3	AGCTTTGAATGGGGATGATG	GTGAAGCATCCAAGCCTAGC	247
6416	(CAGC)3	GGGTCTAGGCTGGTTGATGT	AATTCCCGTATGAGGTCGTG	150
910783	(TCA)5	TACGCCAAAGCACACATAGC	AGACCACATGGTTGGTTGGT	391
910783	(ACCA)3	CTATCCGGAAAGGCACTTCA	AATACGCGATCCCACAACCTC	228
9650	(GGGGCA)3	GAGGATACAAAGGGCGTTGA	CTGTTTGACATTGACGCCAC	260
9650	(ATGGT)4	CGATGTGCAGAGTTGAGCAT	AGTTGCATGAATGACCCCTC	349
11965	(CATC)3	AAGAGCTGCCTCATTTCCA	TTCTGACATTTGCTTCGTCG	192
17	(AATC)3	AAATTTCGCCACCACAAAAG	CAACATGTGCAATAGTGGGC	221
14710	(GGGAT)4	GTTTCGCAAGATGCAGCATAA	ATGAGCATGAGCATGACGAG	373
14710	(GAC)6	AAGCGGGACTCTAGCATTGA	TGTTCCAATCTGCTCAGACG	355
16731	(AGT)4-(TCAC)3	GTGGATGGACTGCCTCATTT	TCTTGCTGCTCATTCACCAC	299

4669	(AAGC)4	CCACAGTAAAATGGTCGCCT	GTCGTGGGCTGGATAGACAT	379
18731	(AAT)4	CATAGGCACTCACGATGCAG	CTGTGGACGGTACTTGCAGA	228
25357	(CAGAA)3	TCAAAAGACCCGTTAGCACC	CGTCAGAATGTTTCCCCACT	396
25357	(GCAC)3	GCATGATACCTCTGCACCCT	CGTCAGAATGTTTCCCCACT	330
36697	(AGGT)3	CCTGAGAGTTTCTTGCCTGG	TTGACACTACCTGCTCGTCG	279
671	(TACA)4	CAAGCGATTGGCATTGTATG	GCATTGGAAACAAACCGTCT	334
13140	(CATGTG)3	TTGATGGGCTTGAAGGATTC	AAACGCTCTGCGTATGGTCT	329
34155	(ACTAT)3	CGGTTTGCCAGGTGTATTCT	GGTCAAGGATTCGGAGATCA	186
31566	(GCACT)3	ACTTTCCACACCTGCTCCAT	TGGTTGTGTGCCTATTGCAT	161
31566	(AGG)5	GTCACCGTCCTGGACAAGAT	TACAATCGACGGATGTCCAA	352
12082	(CAAA)3	GTCTTTTGCAACTCACGCAA	GTCAGAAGAAGCGGAGGTTG	342
37981	(CCA)4	TTCTCTGACCCCCAGACATC	GTCGAACGTGGAGGAGGATA	202
37981	(CTTC)3	TATCCTCCTCCACGTTCGAC	TCGTCTTGTTCAATCTTGCG	296
24880	(CCGC)4	ATATCGCCATGCTTGAAAGG	AGCGTTGTCGTATGTAGCCC	353

30120	(CTGTGT)3	TCCTACGCGTCAAGGACTCT	ACAGGATATTGCACTTGCCC	381
55495	(CGG)4	TCAGCATGCAGACACAAACA	ACGACTCCCACATGTACGGC	367
28590	(GTCGTT)3	ATCCCGTTCGTCGTAGACAC	CACGAGGTCAGACACCACAC	348
14963	(AATGT)3	TACAGGTCGCGCAGTCATTA	GCCTTTTGGTCAACGGATAA	200
14168	(CAT)4	CTCTCCGCTGAGTATGCGTT	CAGCGGTTGAAACCGATTAT	212
512270	(ATT)4	CGAAGACAGAAAACATGCGA	GTCGCTAAGCAGTCCTTTGG	297
512270	(CTGCAT)3	CATCGTGTCATTTCGCAGACT	AGACGATACCATTTCCGACG	258
442391	(ACAGG)3	CGCACACCGGCTATTTCTAT	CCATCATGCAACAACCAGAC	389
442391	(GTGGCT)3	AATATGACAAGGCGAGCAGG	GTCGGATAATCGAGTGCGTT	365
385013	(ATGT)3	AACCGTTTCGTGGAATCATC	TTCAGCAGTGCCACTTTGTC	308
385013	(AAG)4	TTGCAAACAGCGTAAAGCAG	GAAGTGCAGAATGCCTCACA	399
57759	(ACA)8	ACTCCAAAAGCATCACCACC	ATGTGTGGTTGAGAAAGGGC	243
57759	(CTGGGA)4	CGATACATGGCGTACCACAC	GTCCTCGAACACCAGAAAGC	361
57759	(CGTCG)4	ATTACCCGTGCCACAGAAAC	GGCTAGTCAACCGATCCTGA	338

57759	(GGAT) ³	CAGGTGTCGCTTCAAGTTCA	TGGTAAGCTCGCTCTTCCAT	384
57759	(GGGGGC) ³	ACAAGAGATGGTACGTGGGG	ATAATACCTGTCGCCCTCCC	139

* The contig numbers are repeatedly represented for those contigs in which multiple simple sequence repeats were found.

† The 41 SSR motifs evaluated in the five German pathotypes are included in the manuscript text and are not listed here.