

Supplementary Table S2. List of *S. endobioticum* ESTs/contigs used in the verification through PCR analysis, the corresponding primers and the analysis steps performed to identify polymorphic markers.

Number	Contig / ESTs	EST /Contig description	Forward /Reverse primers	PCR product (bp)	Analysis for SNPs between the five pathotypes by
1	4599	Translation initiation factor elf	5' GAATTGGCTTCCCAGATGAA 3' 5' AGCGGAAACCCCAAGATAGT 3'	552	SSCP
2	1693	Glutamine synthetase	5' TCACTACTTCGGGGCCATAC 3' 5' GAGTAGCTCGGCGTACTTGG 3'	1744	No
3	12661	Retinoblastoma-binding protein 5-like	5' TCGTTGTCTGCACCTACCTG 3' 5' TGATTGGCAGTCACTTCAGC 3'	1418	Sequencing
4	1481	Cell cycle control protein (Cwf4)	5' GGGAGGAGTCACAACCTGGAA 3' 5' TGAGTTCGAAGCCAGATCCT 3'	944	No
5	13680	ptk9 protein tyrosine kinase 9	5' CCACCCTGACCAAGGAACTA 3'	840	No

			5' TGAATGACGTTTGCTTTTGC 3'		
6	8109	Translationally-controlled tumor protein	5' GCAGTGAAGGACATTGACGA 3'	713	No
			5' ACAACTGATGCACGCCATAC 3'		
7	5558	Cell division control protein	5' ATGAAGCAATTGGGAACCAG 3'	1000	Sequencing
			5' TTTCACGGCTCTGTGTTGAG 3'		
8	1024	Glyceraldehyde-3-phosphate dehydrogenase	5' ATCGGATACCAGGCAAACAG 3'	939	No
			5' GACCTGAGCTACTGCCTTGG 3'		
9	5523	Tumor susceptibility gene	5' AATCCACGTCACCATCCTTC 3'	363	No
			5' GGGATTCCATTTTTGTGGTG 3'		
10	12394	Mitogen-activated protein kinase kinase	5' TGGAGCTGTCCATGCAGTAG 3'	806	No
			5' TCCAATCGGCTATTTCAACC 3'		
11	9843	Cancer susceptibility candidate protein 1	5' ATGGTCCAAC TGCTGAGAGG 3'	617	SSCP
			5' GTCAGTTTCGAGACGCATCA 3'		
12	14451	Cell division cycle 123 homolog	5' AACCCATTCCGTGAATCAAC 3'	236	SSCP

			5' TCATCGATGGTCCTTCCTTC 3'		
13	17308	Activating signal cointegrator 1	5' CTGGGGAATGCTTCACTTGT 3'	413	SSCP
			5' CTTCGGCTCTTTTCTGTTGG 3'		
14	5552	Sporulation protein RMD1	5' TTCGACCCATCTCGTCTACC 3'	957	Sequencing
			5' GGCCTGTTAGTGCCATTGTT 3'		
15	19475	Glucose-repressible alcohol dehydrogenase transcriptional effector	5' TTCTGCTCCTCATCAACGTG 3'	2000	No
			5' CCTGCACCAGCAGACATAGA 3'		
16	1252	Pkinase-domain-containing protein	5' TCATACGTGGCATCCGTAAA 3'	816	No
			5' GCGAAGTTTCTTGGAACGAG 3'		
17	30469	Endoplasmic reticulum auxin efflux carrier	5' CATCAAAGCGATGGGAAGAC 3'	850	No
			5' CTCTCTTTCCCCCGAAAAAC 3'		
18	4756	Yabby like transcription factor	5' ACGGACATTGAGCTCCTCAT 3'	368	SSCP
			5' GCCTAAGGTCGCTAAAGCTG 3'		
19	1644	S-adenosylmethionine synthase	5' ATCGATCGACTTTGGACCAG 3'	1458	No

			5' GCTGGCTGCTATCACAATGA 3'		
20	5806	Trehalose-phosphatase TPS2 /Glycosyl transferase	5' AAACGAGCGGAGCAGTATGT 3' 5' AAGACGGCCTTGTTGATTTG 3'	303	SSCP
21	639	Cyclin B /cell division cycle protein	5' ATGAGCTTTCTGCGAAGAGG 3' 5' ATGATGGTGCGAACATGAAA 3'	690	SSCP
22	565	gtp-binding nuclear protein gsp1 ran	5' GCTTCAACACCTGGGACACT 3' 5' GGTTGTACTGGGCAATCAGG 3'	800	No
23	30149	Signal induced proliferation associated /Rap/Ran GTPase-activating	5' CACCTCGTATCCTTGCCATT 3' 5' GCACGAATCACAGGAGTTCA 3'	886 (No product)	-
24	24122	Multifunctional tryptophan biosynthesis protein	5' TGGGCGTGAGACATAACAAG 3' 5' CCTCAGGCAGAGTAATGGGTA 3'	168	SSCP
25	7067	GATA-binding transcription factor/ Cutinase palindrome-binding	5' ACTCGAGATTCTTCCGCAA 3' 5' TTGGCGAGACCACAGCTTAT 3'	1023	Sequencing
26	23722	Endonuclease/exonuclease/phosphatase	5' GCGGGAGATCATTACGTTTG 3'	212	SSCP

		family protein	5' CCCTTTGTTCCCGACAAC 3'		
27	21536	Cell fusion protein/chitin biosynthesis protein	5' CTGCCGAATGGAGCTTTAAC 3' 5' GGCATAACAACAGGCTCGAT 3'	205	SSCP
28	5607	Symbiosis associated/microtubule/autophagy	5' ACTTGAGAGAGCAGCGAGGA 3' 5' CTGGAGGCTGAGAGGATACG 3'	340	SSCP
29	20547	Block of proliferation 1	5' AGAGACTGCAACCAGGGGTA 3' 5' TCCGTCGTCACTGCAAGTAG 3'	224	SSCP
30	17092	<i>Tryptophan biosynthesis protein</i>	5' TATCGCCGTCCAAGTTTACC 3' 5' CACATCAACGACATCCCAAC 3'	224	SSCP
31	25285	Transforming growth factor beta regulator 1	5' CCGGACCTGATAAAGAACCA 3' 5' GGTAGTGGCCGAAATCTCAA 3'	450	SSCP
32	6501	Transforming growth factor-beta receptor-associated protein 1	5' TGTTATCGACCACAGGACCA 3' 5' GCCGATATGAATGGAACCAG 3'	267	SSCP
33	9408	TMS membrane protein/tumor	5' GCTAACAATGTGGCAAGCAA 3'	769	No

		differentially expressed protein	5' ATATCGCTCGGCTGGATCTT 3'		
34	14425	TMS membrane protein/tumor differentially expressed protein	5' GTGGCGAGACATATCCTGGT 3' 5' CAAGCTGCATGTCGATGTTT 3'	446	Sequencing and SSCP
35	6369	Ras oncogene	5' AAATGACGAATGACCGGTGT 3' 5' GATGGTTGGCAACAAGTGTG 3'	390	SSCP
36	19219	Ras oncogene family	5' GTGTCGTGACCAAGGACCA 3' 5' GCAAAAAGTACCCCCAAACA 3'	445	No
37	22719	Ras oncogene family	5' CAACATTTTGGCGGATCTCT 3' 5' AAGTGCGGTACGAGATGGAG 3'	326	No
38	14639	<i>tRNA isopentenyltransferase</i>	5' ATCCAAGCCATGAAGATTGC 3' 5' TAAGGTGTGCTTCCCATTCC 3'	510	SSCP
39	340296	erg24 ergosterol biosynthesis protein	5' CACAAATACCAGGCCGACTT 3' 5' CATAAGGCACACGGTTTGTG 3'	4615	Sequencing
40	4884	Serrate RNA effector molecule	5' TCGACATACAGCAGCCAAAG 3'	3619	Sequencing

			5' CCGGTAAC TCACTCGGTCAT 3'		
41	669	Actin partial	5' CAGTAAGGTCACGACCAGCA 3'	350	SSCP
			5' CCAAGGCCAACAGAGAGAAG 3'		
42	855	855 Heat shock protein 90	5' CAAGTCCTTGACCGATCCAT 3'	600	SSCP
			5' AATGTCGCTTCACGATTTCC 3'		
43	963	Mitochondrial processing peptidase subunit beta	5' TTGATCGATTTCCCAAGGAG 3'	180	SSCP
			5' ATCCAAAGAGAATGGCATCG 3'		
44	1590	MCM-domain-containing protein	5' GAACCCATTAGACCTTCTCG 3'	400	SSCP
			5' ACGGTGGAGATGAAGCCATA 3'		
45	938	26S protease regulatory subunit6	5' CATACGACGGCTTCCTTCAT 3'	248	SSCP
			5' TTTCCAAGCTGGTCAAATCC 3'		
46	8897	Ca ²⁺ -transporting atpase	5' ACACCCATAATCTCGGCAAC 3'	238	SSCP
			5' TGTCATGTTGCCAACCAAGT 3'		
47	676	Actin partial	5' GCCAAGTCAAGACGGAGAAT 3'	400	SSCP

			5' GGAGCATCCTGTCCTCCTAA 3'		
48	92	26s protease regulatory subunit 7-like	5' GACGTAGCAATGCTGGATCA 3'	600/350	SSCP
			5' GCTATTGGAGGTGCACGATT 3'		
49	253	Heat shock protein partial	5' TCATCCACTGCTCAGACCAC 3'	200	SSCP
			5' TGGAGCCACCAACAAGTACA 3'		
50	6373	duf887-domain-containing protein	5' TGCTTGCTGGACTACCTGTG 3'	324	SSCP
			5' CGGAGCAGCAAAGTACATCA 3'		
51	1379 (1142)	ATP-dependent RNA helicase	5' AAATCCCGCTCGTACCTATCCTTTC 3'	465	Sequencing
			5' GGTGGCGGATAGAAAGACAA 3'		
52	365018 (4432)	AAA+ ATPase domain-containing protein	5' AAAGTGCAGCCCTCTTCAAAACGTGAAGGT 3'	285	Sequencing
			5' ACATACTTTGTTGAGCAACTCGGGTCCCTT 3'		
53	9476 (1581)	ATP-binding cassette transporter 1 (ABC1)	5' GGGATCAAAGTCATCAAGCTTTATGCATGG 3'	766	Sequencing
			5' CACCAATCTCAGTCAAATCACCACCCGGCA 3'		
54	1644 (12467)	Methionine adenosyltransferase	5' ATTTCAACAGACGCCAAACTCGACTACC 3'	790	Sequencing
			5' CCACATACACTGACACGGGCTCTGCGAC 3'		

55	2773	RuvB-like 2	5' TGGAACGAATCGGTGCTCATTACATATTC 3'	1235	Sequencing
			5' GTAGACTCTCTTGATATCCTCTACATCCAC 3'		
56	913	14-3-3 family protein	5' AAGTACCTTTCCCGCAACTTCCCATTGAGC 3'	1363	Sequencing
	(12984)		5' GCAACCTCCTATCTGTTGCCTACAAGAACG 3'		
57	2158	Diphosphomevalonate decarboxylase	5' GGATGCATGTATGCCATGAAAGCCACTCCA 3'	1413	Sequencing
	(2920)		5' GACACTTTCGTAACCACGTAACCACACCAA 3'		
58	9555	fthfs-domain-containing protein	5' TACTTTGCCCCGTAGATTGGCCGGCACTGGA 3'	1087	Sequencing
	(2730)		5' GAGTGATTGCCGATGCGACATGACAGGCAG 3'		
59	276	CK1/CK1/CK1-D protein kinase	5' AAAGCTCAACAAGACACAGAAGTTGGACGG 3'	742	Sequencing
	(2090)		5' GGACATACCCTAGGGATTCCAGATCATCAC 3'		
60	385013	H/ACA ribonucleoprotein complex subunit 4	5' GACAAACCAGCAAATCCATCATCACACGAA 3'	1100	Sequencing
	(2816)		5' TTTCTTTTTTCGGTTCCTCGCCCGGAGGTGG 3'		
61	297	agc_ndr_protein_kinase	5' ACCAGTCGCATTCTTTGCCATACCCTTTTT 3'	688	Sequencing
	(1917)		5' ATAAAGGTCATTGGAAAGGGTGCATTCGGC 3'		
62	5507	Clathrin_heavy_chain_1	5' GCTCAATGTTGTGAGAAAGCAGGCTTGTAT 3'	853	Sequencing
	(2409)		5' GGTTCCTTTTCAAAAAGGCTTCCGCATTAT 3'		

63	1747 (2191)	wd repeat-containing protein slp1	5' CCTCTTGACTTCTTTACCAAGTCAGACGT 3' 5' GCGAGGGCACATATCCAGGGTAGGAGTAAT 3'	733	Sequencing
64	14539 (2495)	Pantothenate kinase	5' CGAAGGCCGGAACCATTACAGTATGAAGAC 3' 5' GTAGCTGCTCGTTGTTTCGAATCTTCTTGA 3'	890	Sequencing
65	1174 (2445)	v-type atpase	5' CTGATAAGTGCCATAGGACAGTAACCCACC 3' 5' CACCAGGAATGGCCGTAGTACCACCTTGTA 3'	799	Sequencing
66	1360 (3004)	Malate synthase	5' AAATCACAGGACCGGTAGACAGGAAGATGG 3' 5' GCCATAACTGACTACGAGAAATCTCAGCGG 3'	1112	Sequencing
67	1104 (1111)	Glycine-dehydrogenase	5' CTTTGCAATATCAATGGCAGCAATACCGGC 3' 5' GGTCACCTATCCATCAACGTATGGTGTCTT 3'	557	Sequencing
68	1124 (2338)	Splicing factor 3B	5' GAATCGACATGAGAAAGTGCAAGAGAATTG 3' 5' CCTGACTGCCAATGTACAAAGAATTAAAGA 3'	758	Sequencing
69	3763 (2984)	Peptidyl-prolyl cis-trans isomerase	5' GCGAGACATGCAACGACTAAACACGCTTTA 3' 5' ATGTCATCTTTGGTCGAGTTGTATCCGGCC 3'	1117	Sequencing
70	3140	Endosomal_integral_transmembrane	5' GTTGGACACAGGGAGGACGAGATGTTAGAG 3' 5' ATAGAATCCAGATGCTCCCGCCGTCATAAA 3'	1058	Sequencing

	(3013)				
71	2854	Peptidase fungalysin domain-containing	5' CCCTCGCCCAACTATTCGATACAAATACTA 3'	1283	Sequencing
	(2985)	protein	5' CCAATAAAACAAGTTGGTAATGGAACCGTC 3'		
72	1039	t-complex-chaperonin containing TCP1	5' GGCATCGCTACTGCATAATCGCCTCAGGAT 3'	1284	Sequencing
	(272)		5' TGGCATTCTTGACTGCTCGTAAACCATCGC 3'		
73	10688	ste-ste11-cdc15-protein-kinase	5' CTCTCGGGAGCCATCCAGTATGGACTGCCA 3'	1050	Sequencing
	(338)		5' ACTCGGTCATTGATGAATATGTGCTTGGAG 3'		
74	3295	Fatty acid activator Faa4	5' CCCCAACTCGGCCACGTCATTCAAAGTCAT 3'	790	Sequencing
	(2550)		5' CAAAGCAGCCACGTGGCCGTACTGGCATCT 3'		
75	4647	Mitochondrial outer membrane translocase	5' ATGTCACACATTGGATCGACTTCTGTAGCC 3'	700	Sequencing
	(2993)	receptor	5' GATTCTGCCATGATGGACTTTGAAAAGGCC 3'		
76	2578	Trafficking protein	5' GGTTCAATTGTTTGTTCGCTTCGTTTCAT 3'	820	Sequencing
	(1464)		5' CTTTGTGATTGTCGGACATAGGGACAATCC 3'		
77	442391	Beta-Casp domain-containing protein	5' AAGGGGCGGTAGATGTTTGATACCCGCCTT 3'	757	Sequencing
	(2188)		5' CATCTCGTTTGAATCACCATGAACCAAAAC 3'		

78	9123 (1309)	map-kinase	5' GAAGATTTGTGATTTTCGGTCTAGCCCCGAGG 3' 5' TGGCGCAGTTTCGCGGTGTCGGGCTGCTAA 3'	613	No
79	639 (2896)	G2-M-B-type-cyclin-Cdc13	5' TCAGCAGCAGGAGGGCAACATTATTGTGAT 3' 5' TCTACCACATACTCTGAGACCATGACCGGA 3'	889	No
80	7197 (1810)	Phospholipid-transporting-atpase	5' CAACAATGGGCCCAAGCATATGCCAAAGCA 3' 5' CCATCACCAATGGCTAGAGTTACAGCTCGG 3'	659	No
81	6970 (3586)	ccaat-binding-factor	5' CTTGTTAAGAAAACACAAACAGGCTAGCGG 3' 5' CGGCCACAAATTCGAGCCATTCCGAGCACT 3'	615	No
82	18118 (1893)	Chitinsynthase	5' GCCATTGACCAACCAAATGATTTGGGCCAA 3' 5' CTGCGGATCAAAGTTGCTCAATCCCTTGGT 3'	636	No
83	3832 (2750)	saps-domain-containing protein	5' CTGCAGGAATGCAAGGCCCATATGCTAAA 3' 5' TATCTCACTACAATACCTCCGAATGAGCTC 3'	765	No
84	59 (1894)	RNA-binding domain-containing protein	5' ACGATATTGGCTGCAAAAAGTTTGGTTGGG 3' 5' CCTACCGATCGTGAAAGTGGCAGAGTCAAG 3'	753	No
85	1210	Protein kinase	5' TGATTACAGCAGTACACAGGTGCCTCGTGG 3' 5' CTCCAGCATCTGTTCCAAGCGCCAAGTAAA 3'	1186	No

	(2810)				
86	359	pka-protein kinase cAMP-dependent	5' GGAATAAATGGTGGATGGATTCTACCTTCA 3'	899	No
	(1509)		5' CGTCGAGAATCTGTCTTGTTCGGTAGAAGAT 3'		
87	303	T-complex protein 1 epsilon subunit1	5' GCATAGTGAAAAAGCACCCCTCAAGTCTCAC 3'	1636	No
	(534)		5' TTTACCAACTGAGTAGCCAGCAAGAACTGG 3'		
88	10240	GMP-synthase	5' ATCTTGCTCTGGTTCGCCGTATTCGGTCTAT 3'	1438	No
	(2963)		5' CGGACAGCACCTATTCCCATTCTATTGTAC 3'		
89	999	d-3-phosphoglycerate dehydrogenase	5' ATAGCACCCCTGGCATCGGACATTTGCTTC 3'	823	No
	(4664)		5' CTCCATTCAAGTAACTCTCGCTCAGTTGCC 3'		
90	6204	Casein kinase1	5' ACAGAGATCCTAAAACCAAACAACACATTC 3'	974	No
	(2802)		5' TTCGTCGTCACCGCCACAGAATAGCTTC 3'		
91	1737a	t-complex protein 1 subunit	5' CCAGGACATCTATTACGTTACGTTGCCT 3'	804	No
	(395)		5' GCTGAAAGAGAGAAAATGAAGGCAAAGGTA 3'		
92	1975	Ribosome biogenesis abc transporter arb1	5' CGTGACTTATCTGGTGGTTGGAGAATGAGG 3'	722	No
	(5432)		5' TATTTGCACAGCTTCAGTCTGGTGTGACGA 3'		

92	1583	Aminophospholipid-transporting P-type	5' GAAGATCCTCCCAAACATGGTGTGCGAGAA 3'	744	No
	(2925)	ATPase	5' CACTGGTTTACGAGGCGGTAATCTCATTAG 3'		
94	1035	Arginine N-methyltransferase	5' CTTCGGCATCCACGAAGAAATGCTCAAAGA 3'	502	No
	(4825)		5' TCTGGCCATACTGAATCCGTAAACGTTATC 3'		
95	465	H/ACA ribonucleoprotein complex subunit 4	5' GCTGCTCAAGAATTATGACAAGCTACATGT 3'	1042	No
	(2618)		5' GTACCTATCCAATTTCCCTTCCTTGACC 3'		
96	1304	Heat shock protein hsp60	5' AATGAAATTCGACCGGGGTTTCATATCACC 3'	749	No
	(776)		5' GCCTTGAGCAGTGCAGTGCCGCCACCA 3'		