

Supplementary data:

Development of molecular map and identification of QTLs linked to *Fusarium* wilt resistance in chickpea

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Table 1. List of SSR markers used for screening parental polymorphism in the present study.

	SSR ID	Forward primers (5'–3')	Reverse primers (5'–3')
1	EST SSR 1	GAAAAGCGGAGAAAGTGTGC	AAACTCTCTCTCCCACGCCT
2	EST SSR 2	AAGCATCAGAAGAATCAGACAGG	CTTCCTCCTCGAGATCCTCC
3	EST SSR 3	ATGAAATTGCTCCGTTGAGG	GGGATTTGATTCTGGAAGA
4	EST SSR 4	CGAGGATCTCTGGGAAATGA	AAGCGTGCTGCTTCAGAAAT
5	EST SSR 5	TGGTTACAAATGTACAATGCCA	GGCAGATTCTCACCCCTACA
6	EST SSR 6	GGGTGTGGATAGCAATGGTT	AGCTCAATTGCCAGGAAGAA
7	EST SSR 7	ATCACTTCTTGCCATGTCCC	GGTGGTGAATGAGGAGAAA
8	EST SSR 8	AATTAGGGTTGGATGGAGGG	CTCCGAACCACTACGCTTC
9	EST SSR 9	AGTGGTGGAAGTATCCGTGG	AAGGATGAAAAACAGAGGGTG
10	EST SSR 10	GGTTCATTTCAAAGCGGAA	CTTCCTTCAAACCAAGCCAA
11	EST SSR 11	CCTCTTCAAACCATCCTCACA	TCTCGAGCGATCCATCTTTT
12	EST SSR 12	CAAAGCCTGGTTCTTCATCA	GGAAAGTAGCCTGAGGTGCAA
13	EST SSR 13	TCTTTCGCTTTCCTCCCTC	GGTGGAAAGCGTTATTGAGA
14	EST SSR 14	AATACGCATCCAATCCATCC	GTGTGGTGTGCACAGAGTT
15	EST SSR 15	ACCATTTCTCCTGTGTGG	CATAGCCACAGCCATTGAAA
16	EST SSR 16	GCTTGTGCATGGAAGACAAA	GGCAGTGATAAATACTGCCCA
17	EST SSR 17	TTTTTCATCCATCACATCACA	TTGATGCTTTTACAACGTCGC
18	EST SSR 18	CAAAGTAAACCCACCGCTA	ACCGCAATATGGAACACGAT
19	EST SSR 19	CGTTTCTCGCTCTGGAGGTA	TTTCGTTGGTTACACGGTCA
20	EST SSR 20	CCTAATCACCACCACCACC	ATGCAACCCATTTTGGAGAA
21	EST SSR 21	GGTTTTGAGAGAGAGTGC GG	TCTTCCGCAAAAACAAAACC
22	EST SSR 22	GCCTCATGCATCACAAGAAA	GCATTTTGCATGTTTGAACC
23	EST SSR 23	CCAACCAATGAAAGCTAGGC	TCCTATACCAATCCCCACA
24	EST SSR 24	TCACTCCCTCGATCCTCAAC	AGAAACTTGGCAAAAGCAGC
25	EST SSR 25	GAAGTGAAGGAGGAAGTTGG	ACATCTCCGAACTCGACCAC
26	EST SSR 26	CTGCATCAACCACACCAATC	CAACGGATAATGCACTCCCT
27	EST SSR 27	TAGTTGCTGCCTTCGGAAT	GGCGGATACTACTTTGTCGC
28	EST SSR 28	TCGCATAGAAGATGTCGTCG	ACGTAATCGATGACGAGGT
29	EST SSR 29	CCTCGCCAAATAATCTCAGG	CCGAAGAGCAGAGGAAGATG
30	EST SSR 30	ACATTGTTGGTTCGTGTTTGC	GGGTGATGTTGGAAGGATGA
31	EST SSR 31	ACAGAGAGGGAGGTTCTGTC	CCCTTCTTCCATGTACCACC
32	EST SSR 32	TCCCCTGAAACTGTCACAAA	CACCTGGAGAAGCTGAAATTG
33	EST SSR 33	GTCCCCCGCAGTTACTGTTA	GTAATTGTGAAGCCGGTCTGT
34	EST SSR 34	CGGTAAGAGAAGAAGCCACG	TGCATTCAATTCAATTCCACA
35	EST SSR 35	CGCAACTTCTCCCTTTCATC	TCATGGATTTCCCTTTGCTC
36	EST SSR 36	TCAACCCTGTTTTGGTTTCT	TTGTTCTTATTGTCAACAACCC
37	EST SSR 37	GTGTTGGAGTTGGAGGAGGA	CTTGTGCTGTTGTGCACCT
38	EST SSR 38	AATGGTGGTGGTTTGAAGG	CCATTCGCACTTTTGTCTT
39	EST SSR 39	GTGGCCAGGTGAGAGAAGAG	ATGGTAGTTTGGCGGTGAAG
40	EST SSR 40	TTGATGAGGAAGATGGAGGG	TTGATGAGGAAGATGGAGGG
41	EST SSR 41	GACTAAGGCCTCAAAAACCC	ATCACCACCTTCTGCATCCC
42	EST SSR 42	TCCCAACCTCTTTTCCCTTT	AAACGGTGTGACCATAGGAA
43	EST SSR 43	TTCTCCAATTTCTCCCTTTTGA	AATTGAGCCTTTTGCATTG
44	EST SSR 44	GACTAAGGCCTCAAAAACCC	ATCACCACCTTCTGCATCCC

Table 1 (contd)

	SSR ID	Forward primers (5'–3')	Reverse primers (5'–3')
45	EST SSR 45	GCAGTGGAGGTGAATTCGAT	GGGTGCACCTGTTTCAGAAT
46	EST SSR 46	GCGATCTCTCGAAAACCTA	GAACGCAAACCACATGATTG
47	EST SSR 47	TGAACCCAACAAGGAACCAT	CCCCATGTGCTAAAAGCAAC
48	EST SSR 48	CCGATACCGGAGGATGTAGA	CCCAAACCTCGACCTTGTGT
49	EST SSR 49	TATGCTGCTGCAACTCCAAC	ACACAACCTGCTCATTGCTG
50	EST SSR 50	CGAAGCATAACAGTTGATG	GGGATCTTGTTCACGCTGT
51	EST SSR 51	TCCATTCCAACCTTAACCACA	GGAATGGAAGAAGAGAAGGGA
52	EST SSR 52	CGCATCTTCAATTCCATCCT	GGGCCAACTCAAAAGTTTC
53	EST SSR 53	TCAAAGGGAAAGGATTTTGG	AGGGTCCCTCAGTATTGCCT
54	EST SSR 54	AACCCATTTTGCAATCTGCT	CGTGAGGAGAGAGTTCCAC
55	EST SSR55	TTTTCCCTTTATCGCATGG	TAGGGGAAGGCAAATGTACG
56	EST SSR 56	CTCTTGCAACTTCCCCACTC	AAAGCAAAGGAGGGTTTGGT
57	EST SSR 57	ATCACAACGTGGTGGTAGCC	TCTTCTTCTCCTGGGGATCA
58	EST SSR 58	CAGGCCTTGTGTGTTGAGGT	TTCTCCTCGATTTCAATGGG
59	EST SSR 59	TAATGAAAATTGTGGGAGAAG	TGACCCTCTGTCTACTCAT
60	EST SSR 60	CGCCACAACAACACCATATC	CGAAAGAAATTGATGCGAGA
61	EST SSR 61	TGCTGGTCTTGTAGCTGGTG	GCAGCTTGTAAGGGTTTGG
62	EST SSR 62	AGATCCACCTCCACCTTGTG	TTGGAGGTTGTGTGTGGA
63	EST SSR 63	ACACCACCCACAGTAGGAA	GGGACAAGTCAGTCCGGTAA
64	EST SSR 64	CGGCCATTGAAATTGAAAA	GTTGGAAACAACACGCCTT
65	EST SSR 65	CCTCAAGTGCAACAAAACAA	TGCAAACATTTTACACCAGA
66	EST SSR 66	TTTCAACAATGCCAACAAA	TCGAAGAAGGGGAAGAAACA
67	EST SSR 67	ACCATTGTTTGGGCATTC	CGAATTGAGGGTCTTCCAA
68	EST SSR 68	ACGGTCAGTGAGCTGCTTCT	TCCCAATCCTAGTACCACG
69	EST SSR 69	CCAGTTGTTGCCTCGGTATT	CAGGTTGATGTCCGAATGTG
70	EST SSR 70	GCATCACAAGCTTCAACAGC	TTTTGGGTTGATGGGTGATT
71	EST SSR 71	CGTCGTTACATACCAAACG	CCAGAAGGAGATCCTGAACG
72	EST SSR 72	CGGTGATGAACCTGTTGTTG	AAGCCACTCAAGACGCTGTT
73	EST SSR 73	TTCCAGATCTCCGGTAGGTG	ACTCTCCACTCTCCCAACA
74	EST SSR 74	CATTCCCATATTTCTCCG	AAGACAATCGAATCCAACGG
75	EST SSR 75	AAACTTGAGGGCAAGCCTTT	CAAAACACAGAGTTGAAGGAACA
76	EST SSR 76	GAGCATCATAAGCGACGTGA	CCGCCAATCATATCCATTCT
77	EST SSR 77	CAGGAACCAAGATTGCAAGA	GGGAAAGAGTTCAAAACCCA
78	EST SSR 78	GGGACAAGTCAGTCCGGTAA	ACACCACCCACAGTAGGAA
79	EST SSR 79	ATCAGCGACAACACTACAACA	TAATTGAGAATCGGGTTCG
80	EST SSR 80	TCCTCCAACAACAACACCAA	AGGAGGAACCTTTGAAACCC
81	EST SSR 81	CGGTGTGAATTTGGTGTATGA	CAACAACAACCGAACGAGTG
82	EST SSR 82	TCACCATCGTGTGATGGACT	TTGTTGGGTCTCTTTTGT
83	EST SSR 83	AAACACAGATGTCGTCGCAA	CCTGATATTCGGCAACACG
84	EST SSR 84	CCGGCTTAATGAAAGAGGAA	GACCATGGGATGGATGTTTC
85	EST SSR 85	GGTTTTGAGCGTGGTTTGTAT	TGCAAAAATGTGAAGCACAGA
86	EST SSR 86	CGTTACGATATTCGGGTGCT	GCTTCCCTTACGCTTAACCC
87	EST SSR 87	TGATGATTTTGTGATGGTTTGA	GCTGCATCACAGAAAGTTGG
88	EST SSR 88	CTTGCAATGCACCTTCTCCA	TGCAGAAGGAATTGTGCTTG
89	EST SSR 89	GACGCTTCCAGAAGATTGC	CCACTGGAATGGAGGAAAAA
90	EST SSR 90	CTGGTCCAAAAGATCACAGCA	CTTTCACCCCCAACAACT
91	EST SSR 91	ACGGTGAATTCATCCAGAC	ATCATTGCTGTGAAAGCACG
92	EST SSR 92	ATGATGCTACTGGAGGTGGC	CCCAAATCCTCCTCTTCTC
93	EST SSR 93	CCATCACCACCAACCTAAC	AGAAGAGAGGGCGGAGTAGG
94	EST SSR 94	TCACCATGCCATTAACTCCA	GTGCCAGGAGAAGGTCTCAG
95	EST SSR 95	GCTGGTACCACCCGAACATA	GTGAAGTAACGGGATCCAA
96	EST SSR 96	TGAGCGATGTTACGTGTTGAG	TGGTGGACATGAGAGGATGA
97	ca4958_TC16800	TGGTTTGTGCCTGAGAGAGA	TCCAAACAAGACCTGATGA
98	ca4958_TC16812	TCGCTTCTGTAAACGACTGG	GCAAACAACAACAACAACA
99	ca4958_TC16903	AAGTGGCTATCAGGGGTGTC	GGGGGAGAGTGACACTGAAT
100	ca4958_TC16909	CCTGACGGGAAAATCATAG	TGACTCAGAATCGGACAAGG
101	ca4958_TC17100	TTGGAACATCCCATCAGGTA	TCCTCTCCGTGTGTAACAG
102	ca4958_TC17173	TCACTTCTTCCACCAACCA	ATCCTCAAATGGATCCAACC
103	ca4958_TC17568	TTGGGCTCTTCTCCTTCTTC	CAACAATGTCACCCAGCTTT
104	ca4958_TC17608	GGAAAGGGATGTTGGATGTT	ACCATGATACCTCACCACCA
105	ca4958_TC17719	GCGAGAATTTGCCATTTGTT	TAATTTGGTGGCTGTTTCCA
106	ca4958_TC17933	TCTAGGGGTTCTGTGTAGTG	GCCATCAATCTTCTCCTCT
107	ca4958_TC17959	TTCGCTTCATTGAATGTGG	CGATCACAAGTCAGAACAAGG
108	ca4958_TC18003	CCACCCTCGTTACCTCTCTT	TTGGGTCTCTCCTCTCTCGT

Table 1 (contd)

	SSR ID	Forward primers (5'–3')	Reverse primers (5'–3')
109	ca4958_TC18114	CACTCCAATGGCTAATCTGC	ACAATCTCCGGTGGTGTTTT
110	ca4958_TC18156	TGTTTTCTTTGCTGCTCCA	GCTGCCACTTGTTCATATC
111	ca4958_TC18156	TGTTTTCTTTGCTGCTCCA	GCAAAATTGAGAGGTGGAATG
112	ca4958_TC18452	TGCAACTCCACTTTCCTTCA	CCAACACTGCAAACACACAC
113	ca4958_TC18471	ATGGGACCCACACAGGTAGT	TGGTTTGATCAACTCCATGA
114	ca4958_TC18703	CACCCTCCACTTTTCCACTT	TGGAATTTGCTGTGAAGATCA
115	ca4958_TC18714	TGGAACAGATCAATTTGTGAA	TGCTATGGCAATGGTAAAGG
116	ca4958_TC18714	CCGCTGTTCTGATTTTGTAT	TCCAGTTCTCCCAATCTCAA
117	ca4958_TC18917	ACCTTCAGACTCCGGTTATT	AATGCAGATGAATGCGAGAG
118	ca4958_TC18930	CAAATGGCAGCTATTCATTC	TTGCTGACCAGGAAACAGAG
119	ca4958_TC23243	GAAGATGAACGGTGGTTGTG	GCACTCCACATGAACATGAA
120	ca4958_TC23820	CACTTCGCCACTAAGTCACC	TGGACTGAAAAAGGAGACTCG
121	ca4958_TC24185	TCTCGAAGAATGTGGTGCTC	AAAGTTAGGCGTCCACCTG
122	ca4958_TC24913	CAATTCATCATGAGGGTGG	TCTATCTTTTCCCCCAAAGG
123	ca4958_TC25280	TCTTCACAAAACCGCCATAA	GGTGGGTTTGTGTTGGGTTTA
124	ca4958_TC28113	AAGGGTTGGTGGATCAAAA	TGGCATAAAAAGTTTGGTTTCA
125	ca4958_TC28408	GCTCAGTGGAGAGAGAGTGG	AAGGCTTCTCCTTGATCACAA
126	ca4958_TC29834	AAACGCATTGATACGGATTG	CAGATCTGAGGAGGAGGAG
127	ca4958_TC31257	AGAAACCGAGGTTGATGGAG	TGACCACCTAAAGCTTGTCTT
128	ca4958_TC31939	ATGCTGATACTGTGCGAAGC	TGTTGTTGTTTCTCCTTTTCG
129	ca4958_TC32962	CGTCGTCATCTTCATTTCAA	AACGACGACGACGATAACAA
130	ca4958_TC33024	GTAGAGGTGGAGGTGGTGGT	CCATACCTGAACCATACCC
131	ca4958_TC33024	AAGGGTATGGTGGAGGATCA	ACCACCTCACCTTTTCCAC
132	ca4958_TC09239	TCTGCATTATTACTACTACTCATC	TCATGATTATGATTACTTTTCATT
133	ca4958_TC06880	TCATTTTGTGGGATTTTCAA	TCCCTAATCATCACTCACTCA
134	ca4958_TC14433	ATGCTCCATGGTGGTCATAA	ACGAGCTCCAATTCACATAA
135	EST_icc1882_con0917	CATCACAATCCCTTCTTCAA	GAAGAGAGGAGGGAGAGAGAG
136	ca4958_TC05038	TTCCGTTTTCAAACCCAAAC	AACAGAGAGCTCCGAATCCA
137	ca4958_TC05167	CCAGTTGTTGCCTCGGTATT	CAGGTTGATGTCCGAATGTG
138	ca4958_TC14801	CAGATTCCAAACGTGCAGTG	ATTGCAATGTGAACCCACAA
139	ca4958_TC16913	TCCATTCCAACCTTAACCACA	GGAATGGAAGAAGAGAAGGGA
140	ca4958_TC16245	GGCCACGAAAACATCAAGT	TTGGAAATGGGTTCTCAACA
141	ca4958_TC10205	TAGTTGCTGCCTTCGGAAC	GGCGGATACTACTTTGTGCG
142	ca4958_TC08452	AGCTTCTTTTGGCTGTGG	GAAGCATGTTTGTGCAACT
143	ca4958_TC07232	AATGGAGCTTGAATCTGGGA	TGGGAAGCTTGTGAAAGTGA
144	ca4958_TC10126	TTTCGTCCCCAATCCAATA	ATTGGTCCCAATGTCTTGA
145	ca4958_TC15151	TTTTTCATCCATCACATCATCA	TTGATGCTTTACAACGTGCG
146	ca4958_TC03453	TCACAACCACCTGTAGCAGC	TGACCCTTTTGGGGTCAGTA
147	ca4958_TC05036	TCGAGGAAGATTGCAGGAGT	ATTGCTATTTTGGTCCGACG
148	ca4958_TC06179	TGCTCATTTCAAACCGGAA	CTTCTTCAAACCAAGCCAA
149	ca4958_TC07757	TGAACAAAGGACCACACACC	TGTTCCAAGAAAAGCAGGGA
150	ca4958_TC07870	TTTTTCCCTTTATCGCATGG	TAGGGGAAGGCAAATGTACG
151	ca4958_TC10124	CCCAGATACAATGCATACGCT	CCGATTTTCTTCTCAACA
152	ca4958_TC10363	TGCAGCAGAGCATCAAATCT	GTTGTCTGAAGGTCCCAAAA
153	ca4958_TC11468	CGGTGATGAACCTGTTGTTG	AAGCCACTCAAGACGCTGTT
154	ca4958_TC12179	ATTGCCATGAGAAATGGAGG	CCAGAAGATCCAAAGCCTGA
155	ca4958_TC15401	GTCTTGGGAACCTTGCCTTA	GATGCGTAACTACAACCGCA
156	ca4958_TC15544	AAACTTGAGGGCAAGCCTTT	CAAAACACAGAGTTGAAGGAACA
157	ca4958_TC15615	AACCCATTTTGCAATCTGCT	CGCTGAGGAGAGAGTCCAC
158	ca4958_TC16715	CCAAAACCATTTTCTTCAATC	TATGGATCGGAAGACGAACC
159	ca4958_TC18432	TACGGAGGCTATTTGATGGTC	CACCTTCCACTCCTTTGTGC
160	ca4958_TC03722	GATTCACCAAACCAAGCCAT	AAAGAGTGCAGGGGATGTTG
161	ca4958_TC05739	TCATCTGGGAAAAGGGAGTG	AAGGACCTCATCAAACAGAA
162	ca4958_TC06046	CAGGCCTTGTGTTGAGGT	TTCTCCTCGATTCAATGGG
163	ca4958_TC08447	TCCATTTCTTCTTTTCTCT	GGTAGAAGGTGCTTGACCGA
164	ca4958_TC09085	GGCTGGGTTGATTTATGGTG	AGACAGCAAGCAAGCAGTGA
165	ca4958_TC11130	TGCTGGTCTGTAGCTGGTG	GCAGCTGTAAAGGGTTGG
166	ca4958_TC11140	AGTCTTGGTGGTGTTCGG	TCTACCCCAAGTGCATTCTT
167	ca4958_TC11147	TGGGCATCTCAGAAAATGCT	ATTTGGGCTGAGAAGGTTT
168	ca4958_TC12117	TTTCAACAATGCCAACCAAAA	TCGAAGAAGGGGAAGAAACA
169	ca4958_TC12490	TGCAAGTTAACACGAGACC	TTCCAGCAAATTTGGAACC
170	ca4958_TC14627	TTATGAGGCGGCATAAAAGG	TTGAATGTTCCATGACACG
171	ca4958_TC17527	GCGTTTTGGTTTTGGAAAGA	AACTTGCAGCCAACACTTCC
172	ca4958_TC11653	TCACCATCGTGTGATGGACT	TTGTTGGGCTCTTTTGTGTTT

Table 1 (contd)

	SSR ID	Forward primers (5'–3')	Reverse primers (5'–3')
173	ca4958_TC11038	CCACCTCTTCCCATCACTCA	TCATGGAGAATCCCAGATCC
174	ca4958_TC00696	TGGGGTGTGTTTTCTTTCTC	ACAGATCAGTAGCCCGTGAA
175	ca4958_TC01951	CACATGGAAGACCACCACTT	TGTTTCACATTTCCCTGCAT
176	ca4958_TC02355	GGGCATAAAGAGGTGGTGT	AACCCGAGATCATGAGGATT
177	ca4958_TC02355	TGTTGTTGTTCCCTCTTCG	CCACTCGTGACGGTAGTGTT
178	ca4958_TC02624	AAGTGGCCATTGGTATCCTC	ACGGTCACCAGAACTTGTGTG
179	ca4958_TC02706	CATTGCTAATTGTGCTGAGGA	GAATGCGCAGAGATCCATAA
180	ca4958_TC02857	GATCGGAGGAAGAATCGAAA	TTGGATGTGGATGCTTATGG
181	ca4958_TC03008	CCCTTTGGTGATTTTGAACC	CATTGATTGCCACAACACT
182	ca4958_TC03244	TCCGATCTGTTGTTTCTGC	GCCATGAAATGAAACCCCTA
183	ca4958_TC03560	TCCCAAAACAATACCAACCA	GGAAAAGGTTCCATTTTGG
184	ca4958_TC03875	GGGGAAAAGTCGAAATTGAA	CACCCCTTCCCTTATTTGCAT
185	ca4958_TC03897	GGAACCAGGAAGAGCCATTA	CGCCTCGTAGAAGCAGATAC
186	ca4958_TC03990	TGGCTTCTCCATCAAAACAA	TTCCGACCTTATCAATGGAA
187	ca4958_TC04232	TTACATTGTGTGATCCTTCACC	TTCCCTTATTCATTTATTTGAACC
188	ca4958_TC04313	TTTGGGTCGTTTGTTTTGAA	CCGCCATAACCCCTTTTCTT
189	ca4958_TC04502	CAATGCAAGTTCAAATGGAGA	TTGTCTCCCAACCAACTCAA
190	ca4958_TC04586	TTGAACTCCCTTGTGAGGA	CCTCACATGATATTCTCCAAA
191	ca4958_TC04757	GTGGAGGAGGTGAAGGTGAT	CCTCCCCCACCATATGTTTA
192	ca4958_TC05016	TTGCTGCATCATTCTGTCA	TCAGCATCATCAGAGGGTTC
193	ca4958_TC05274	CGGGTTTAGGTTGGACTGAT	CCGTTACCCCTTATGGCATCT
194	ca4958_TC05331	TTCCAGTTTGTGCGAGGTGTA	AGGAGGTTGAGCTGATTTGAA
195	ca4958_TC05934	GGTTTTGTGTTTGTCTGGTA	TCAAACCTTTGTTTCAGAACAC
196	ca4958_TC06040	CCAAGGTGTTCCCTTCTTCC	CGGGTTGAGGTACCGAGTTA
197	ca4958_TC06482	CTCTACTTTGGCATGAAACCA	TTGAATGGAGCAATGAATCC
198	ca4958_TC07057	AGCTAGGTGGGGAATGTGAC	GGGCTTAATTCACGGACAG
199	ca4958_TC07193	AGGGTGAAGGATCCAAAGTG	TGATATTCGGGTTCAAATGC
200	ca4958_TC07193	AGGGTGAAGGATCCAAAGTG	TGATATTCGGGTTCAAATGC
201	ca4958_TC07410	GCCTGAATTTGGGAATCTG	CGAGCGTTTTCTCTTCCTTG
202	ca4958_TC07421	AAATCTCCACCACCTCGAAT	ATATCACCGGTGGTTTTGGA
203	ca4958_TC07645	GCAGCAATTCAAAACATTG	CCTTGAGCAGCCCAATAAAG
204	ca4958_TC07722	GATGATGGTCTTTGGCATCC	GGCAAAGTTTCGACAGATAA
205	ca4958_TC07975	TATCCGCAATGTCAGTGTCC	TGGAGCGAAGAATACCACAA
206	ca4958_TC07975	CCATTTTCTTGTGCTGTTCG	TAGAACCCTTGGCAGAGCAA
207	ca4958_TC08322	TCCTTCAAGCCCTAGTTTGG	GCTTCTGTTTCTGTCCCATT
208	ca4958_TC08531	TGAAGGCGAGATGCTGTAG	GCTTCTGTGTGCTGGTAGA
209	ca4958_TC08568	GATCGGAAGTTTGGTGGATT	CCCCCTTCTATACTTCCAA
210	ca4958_TC08885	GCACCAATTTTTCTTTTTGAA	TGAAATTTGGTTTTGGGTTG
211	ca4958_TC08918	CCCAACCCCTTCACATTTTA	GCTGACAGTTTTCCGTTTGA
212	ca4958_TC08953	TTGCCCTCTTCTTCTCTC	GCGACCAAGACAGATGAAGAT
213	ca4958_TC08953	TTGCCCTCTTCTTCTCTC	GCGAGCAAGACAGTGAAGAT
214	ca4958_TC09117	TGGAGCATGGAACCTAAAT	GGTGCTCTTCTCCTTTCACC
215	ca4958_TC09222	CAGAACTCTTTGCCATTGCT	ATCAAGTGGTGGCAAATCAA
216	ca4958_TC09378	GGGATTATCTTCGGTGACG	AGACGAAGGTTATCCCAAT
217	ca4958_TC09444	CCCAGTTCTCTTCCATACCA	TCACCATTTGTGTGAGGATT
218	ca4958_TC09513	GCTCCGGGCTCTATTAACCT	TACGAAGATGCAGACGAAGC
219	ca4958_TC09806	GAGTCTCCCAATTCCTTCA	AAGGAGGAACACAAGGGGTA
220	ca4958_TC09904	CAACAACAGCATCAACAACAA	TGATGCAAATGGTGAGGATT
221	ca4958_TC09904	CCCTCCTTTTTCTTCAATCA	TTCTCTGCCATGGTGAAATC
222	ca4958_TC10046	TTGGTGAATGAGGATGAACTTA	GCTATGTATCCACTTGCTATGTTT
223	ca4958_TC10273	ATGCCCTGGGAATTCATTGTT	GCCACGTTTTGTTGTGTTTT
224	ca4958_TC10422	TGTGGCGATGAAAGTTTGT	AACCAAATGCACCACTCTCA
225	ca4958_TC10535	GTCCATGTCAACCTTTGCAG	GCAAATGCATTAATTTGCAC
226	ca4958_TC10802	TTTTCTTGTTCGAGCTTG	TTTGTGATTCTGTGTTGGA
227	ca4958_TC10910	CAGGACAAGACAGGCTACTGA	GCATTTCCGGTTATGATCC
228	ca4958_TC11191	AGATAGTTGCACGCCTTTGA	AAGGGTGTCTGCCAATCTC
229	ca4958_TC11203	ACAGCAGGTGCATCAAAAG	TGGGCACTTTACAATCTTGC
230	ca4958_TC11243	TTGCTGACTTCTATTTGATG	AATCGTCGCCATTGGTAGTT
231	ca4958_TC11253	CCCACTGATGTTTGAAGG	AGCTTTTTCGCCGTTAATG
232	ca4958_TC11327	GCCGATCTTCCACAGTGAG	TGTCGAAGATGGACACTGCT
233	ca4958_TC11367	TGCAACAATGAATGGAACA	TTGGTATCTTCTGGACGGTTA
234	ca4958_TC11369	CGTGTGTTGAGGATGAGAG	TCAGATCTGTTTTCGCCAGA
235	ca4958_TC11613	GGATGCGGTGTTGAACATAC	TTTGGTTCTTGAGCTTGGA
236	ca4958_TC11838	TTTGTGTTGATCATATTGGA	GTGGTAGAGGACCCACCATT

Table 1 (contd)

	SSR ID	Forward primers (5'–3')	Reverse primers (5'–3')
237	ca4958_TC11910	TTTTGAACCAAGGCTTTGAA	GGAAATTGTGGTACACCTTGG
238	ca4958_TC11988	AATCAAAAACCAACACGACGA	CTGCTTCGCCTTTCTCCTAA
239	ca4958_TC12039	TCCCTTGTCTCTTTGGTGAA	TCGATTCATCTCCTCATTGG
240	ca4958_TC12240	AGGTTTTTATGAGAGGCGTCA	GCCAAGGTGGAACCAATTAC
241	ca4958_TC12253	CCTCATCTCCTTTGCCTGAT	TAGACCCGGAACTTTGATCC
242	ca4958_TC12253	TCTGTCGAAAACAAGCCAAC	TGCTTTGGTGGCGTCAATTAG
243	ca4958_TC12255	GGATGTCACCGTACACGTTAG	TCTGATCAATCACCTTCTCG
244	ca4958_TC12255	GGATGTCACCGTACACGTTAG	TCTGATCAATCACCTTCTCG
245	ca4958_TC12644	TGGTGGAGGGAAGATAAAGG	GAATGTGGCTGAGTTCAACG
246	ca4958_TC12848	AATGCTTGCTAGGGGACAAT	TGGTGATGATGATGATGGTG
247	ca4958_TC13118	TGACAAAAGTCCAAGACTCCA	AGAAAAAGTCCCACATCATGG
248	ca4958_TC13754	ATGAGACTGTGGGACCCAAT	ACTGCCTGAATCGCTACCAT
249	ca4958_TC13761	TTGGTTAGATCGGATTAGTGGTT	TTCATTTCTCTCTTTTCTTTTT
250	ca4958_TC13876	CAAAGCTTGGGTTACTCCAT	TTGGTTCTATCGATGGTCTCC
251	ca4958_TC14483	GCAAGCATTCTTCCACAGA	CCCTCCTTTCCCTCTCTTCT
252	ca4958_TC14528	GAAGAGCCATGGTGACAGAA	CAACTTCTCCACACCCTTCA
253	ca4958_TC14781	TGGTGAGTGGAGCTGAAGAG	GCGGTTCTCCTCTAAGCAAT
254	GSSR4	AACCACATTTGTTGTCGCTG	CAAAATAAATGAAGGAGAGAATAAAGC
255	GSSR6	TGAGTGTGTACTGGGGTGAAA	AACACGCCCCCTTCTTATCCT
256	GSSR7	GCGAAAAAGACAACGAAAGC	TCATCGGATTGGTCTCTTC
257	GSSR9	GACAAGCCTCCGTGTGATTT	ATCGACGTCGCTAAATGCTT
258	GSSR11	CTGTTACGTGCAATGGATGC	TCGGTATGACACAAAAATGTGA
259	GSSR12	GACCTAGTCCGCGACTCAAC	AGACCCAAACATGTCCGTAATA
260	GSSR13	TCATGCAACAGACGAATTGA	AACATGTTATAAAACGTAAGGCG
261	GSSR14	CAATCAAGCTCGTATGGAACA	CATCAATTATCAACTACCAATTTTC
262	GSSR15	TGTGACAAAACAATAACGTGTCA	CGTCAAAGTTAACGCAAGTTGAG
263	GSSR18	CCCTCAAGCAACCCATAAAT	TTGACACCATATGTGTTCTCCC
264	GSSR19	TGTCACAAACATGTAAGACAGTTGTT	AAGATTTGGCTGGCTTCATC
265	GSSR21	CCTTGCGTGAGTTTGACGTA	CATCGCGGTCATGTGAGTTA
266	GSSR24	TCATTTTTGAATGTCCATGCTT	TCAATTTCTTATACTTTTCGCAACA
267	GSSR27	GCAAAGTGAATTTGTGGGT	AAAACATCAATTTACCATCATTCA
268	GSSR37	CGAACACTGATGCCAAACAA	AAAATGTATTTTATGAGTTTGGCCTAT
269	GSSR39	GTGCACACGGGTTACACAGT	GTGCGGTGGTTGAAGGTAGT
270	GSSR40	TCACTTTTACATTACACAAAGGATT	CATGTCTTTTGATATACTACCTCCACA
271	GSSR41	CCAAGCTATAGTGCAATCATCGT	AGGAGGCCCTTTGAAAAATCA
272	GSSR42	AAAACATCATGTGCTGGTGC	CAGCTCATCCTCCTACTGTGG
273	GSSR47	CCACCAAATCCGTCAACTT	TGTTCCATCATATTTTCAACCG
274	GSSR50	CCAAAAGGTTACGTTCAAAAAGA	GCTTTTTGCATTTGTTTCCAA
275	GSSR57	AACGCTTTCCCTACCAATTTTT	GGAGGAAAGTCGTTAACAAAAGA
276	GSSR58	TTATATAAAATTCGATATGCAGGATCT	TCTCAATTCAACTTCCACTCAA
277	GSSR60	TTTTTCTTTTCCATAATGTGCG	CACCGGTTCAATTTTCGATT
278	GSSR62	TTTTTGTTACAACCATTTTTGGAT	GAAGCTATTTTGAATCTTTTGTAA
279	GSSR68	GAGCTCAATAATTGGATTAGATTTATG	TGGTACAAAAATACCAGGATCAA
280	GSSR69	GCCCAGTCTCCTCCTTTT	ACGTCACCTCCCTCCACAA
281	GSSR77	TGTCACAAAAGACTAGGCTAGGA	AATTTTGTAAACGACCAACAACA
282	GSSR81	GAAATTGAACCCACAATTCCA	AATTGGCAACGGTGAGAAAA
283	GSSR82	TCAATTTTGAACGAGAAGTGAATC	CCAAAGAGTCTACTAGCGGAACA
284	GSSR85	TGTGAGTCGTGCACAATAAAAA	TGTTTATCAGGTTCAAGCCG
285	GSSR87	GAAGGAAATATATCCCTTACAAGTGTG	ACGGTAAACTATAAGACGTGTGCG
286	GSSR94	TAAAACCTTATTTTGCCGGA	GGGATAACGCCAAGGACATA
287	GSSR106	TGAAATTCAGCAACGAAATGA	CCCAGTAACCGCTCTCTCTG
288	GSSR107	GCAGGGGCTATATGGATTTG	GCATGAATTCAGCAGAAGAAAA
289	GSSR114	TTATCCCCTAAGCCTCGCTA	CCACGTCGGTTCTCTTTGAT
290	TR 2	GGCTTAGAGTTCAAAGAGAGAA	AACCAAGATTGGAAGTTGTG
291	TR 56	TGATTCTCTCACGTGAATTC	ATTTTGATTACCGTTGTGGT
292	TR 20	ACCTGCTTGTTTAGCACAAT	CCGCATAGCAATTTATCTTC
293	TR 24	AACAACCTCCTCTTATTTTCCA	CAGTAAAAATCAGCCCAAAC
294	TR 29	GCCCCTGAAAAATAAAAAAG	ATTTGAACCTCAAGTTCTCG
295	TR 59	AAAAGGAACCTCAAGTGACA	GAAAATGAGGGAGTGAGATG
296	TA 42	ATATCGAAATAAATAACAACAGGATGG	TAGTTGATACTGGATGATAACCAAAA
297	TA 53	GGAGAAAATGGTAGTTAAAGAGTACTAA	AAAAATATGAAGACTAACTTTGCATTTA
298	TA 186	ACAAAATTCTAAAAGTTCCTTCTACCA	GTTGTTAGTCGAATAATTGAGAAAAAGA
299	TS 45	TGACACAAAATTGTCTCTTGT	TGTTCTTAACGTAACCTAA
300	TA 135	TGGTTGGAAATTGATGTTTT	GTGGTGTGAGCATAATTCAA