Information on primers in 25 nuclear simple sequence repeats(nSSR) loci

Locus	Ta(°C)	Motif	Primer Sequence (5'-3')	Allele	Reference
MSQ13	56	TC	TGGCTGCACCTATGGCTCTTAG ACACTCAGACCCACCATTTTTCC	188-226	Dow *et al*. 1995
QpZAG16	56	TC	CTTCACTGGCTTTTCCTCCT TGAAGCCCTTGTCAACATGC	131-189	Steinkellner *et al*. 1997
QrZAG7	56	AG	CAACTTGGTGTTCGGATCAA GTGCATTTCTTTTATAGCATTCAC	108-154	Kampfer *et al*. 1998
QrZAG11	56	AG	CCTTGAACTCGAAGGTGTCCTT GTAGGTCAAAACCATTGGTTGACT	241-283	Kampfer *et al*. 1998
QrZAG30	56	GA	TGCTCCGTCATAATCTTGCTCTGA GCAATCCTATCATGCACATGCACAT	160-208	Kampfer *et al*. 1998
QrZAG87	56	TC	TCCCACCACTTTGGTCTCTCA GTTGTC AGCAGTGGGATGGGTA	99-123	Kampfer *et al*. 1998
QrZAG96	56	AG	CCCAGTCACATCCACTACTGTCC GGTTGGGAAAAGGAGATCAGA	160-238	Kampfer *et al*. 1998
PIE271	56	AG	CACACTCACCAACCCTACCC GTGCGGTTGTAGACGGAGAT	197-247	Durand *et al*. 2010
QpZAG9	56	TG	GCAATTACAGGCTAGGCTGG GTCTGGACCTAGCCCTCATG	220-274	Steinkellner *et al*. 1997
QpZAG110	56	AG	GGAGGCTTCCTTCAACCTACT GATCTCTTGTGTGCTGTATTT	193-267	Steinkellner *et al*. 1997
QrZAG112	56	GA	TTCTTGCTTTGGTGCGCG GTGGTCAGAG ACTCGGTAAGTATTC	98-116	Kampfer *et al*. 1998
QmC02241	56	GA/TC	TCAGTGACCACACGTCACCTCTC GTTTCTTGGCCATGTTTTGATGG	169-211	Ueno *et al*. 2008
CN725667	56	CCA/TTC	GCTAAGCTCCAAGCCATTTGTGA GTTTCCGATGACGTGGATGTAATCTCC	194-272	Ueno, S. & Tsumura, Y. 2008
CR627959	56	GA/TGC	GCTCCCTGGTAGTCGGCTAAAGA GTTTCAATTGGGACAACATGGAAGCAT	232-296	Ueno, S. & Tsumura, Y. 2008
GOT011	56	GA	CCCCACCGTCTACTCTCAAA GCGTTCACCACGTCCATAAT	197-225	Durand *et al.* 2010
GOT012	56	GT	TGATGATCCCAAACCACAAA AAGGCTGCAGGACTTTTCAA	204-254	Durand *et al.* 2010
GOT021	56	AT	AGAAAGTTCCAGGGAAAGCA CTTCGTCCCCAGTTGAATGT	110-150	Durand *et al.* 2010
GOT040	56	TC	AAGGCACTCGTCGCTTTCTA ACCGATTTGAAGCTCGAGAA	242-298	Durand *et al.* 2010
PIE163	56	TC	GAGAGGCATGTGGAACCAAG CAAGCATAGGTGGTGGAACC	230-264	Durand *et al.* 2010
FIR026	56	GT/GA	CTTCATGCACCAATTCCTCA GGCCATGTATGTGTGCAAAA	201-215	Durand *et al.* 2010
WAG066	56	TC	AACCTGTTTGGCTTCGTGTG AACAAAAGATTGGGAGGTGC	128-224	Durand *et al.* 2010
WAG068	56	TC/TG	TCTGCAACAAAACCAAAACAC CGGAGGAGAGAGTCAGCAAC	154-210	Durand *et al.* 2010
POR017	56	GA	CCCATATCCCTCTACGAAAGAA CTGGAGATGACATAGTGTCTCAAA	126-170	Durand *et al.* 2010
POR025	56	AG	CACACAAACCCATATGATCTGAA TCTCTTTCGATCCCTTCTGC	105-145	Durand *et al.* 2010
FIR015	56	GT	ACCCTAAAACCCCAATCACC CGGATCTTCGGCTATTCTTG	112-148	Durand *et al.* 2010

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