Appendix A PCR primers and characterization of SNP loci

Primer number, Contig and SNP	Primer sequence (5’-3’)	*T*m(°C)	*T*a(°C)	Amplicon size (bp)
5, T2-31299, C/T	FI: AAAGGCGGCGGGTCC***C***TT	61.9	62	T 211
	RI: GGGGTATGCGGGATATTC***G***CG	63.9		C 241
	FO: CCCCGTTGTACGACGAGAATCGTA	63.7		Outer 413
	RO: GGTGAAGTCTCTCCTCCGGCCTTT	65.4		
9, T3-30695, G/A	FI: TCAACAAGTACAATAGGAAA***C***CG	56.6	54	G 197
	RI: AACAGGATCCTGGGTATAG***C***AT	58.2		A 293
	FO: ATGTGACTCAGCCTCGTTATGTA	58.4		Outer 445
	RO: CTGGTAAAGAGACTGACAAGCTTAA	58.7		
11, T2-32906, C/G	FI: GTCGGGGAAATCAAAGAA***T***GC	58.0	61	C 215
	RI: CAGACTCCAACTGCGATTGAG***T***AC	62.0		G 252
	FO: CTGATGGTGATGAGTCGAGGATAG	62.0		Outer 422
	RO: ATCAGACGTGTCCTCAGTACCCTT	62.0		
15, T1-26224, C/T	FI: ACTACAAGGTCAAAAAACTAGTCTC***G***TC	60.6	56	C 171
	RI: AGAAGAAAAGCAGAAAGC***C***GA	56.1		T 248
	FO: TTAACTATGATCTCCCTACTCAACCC	60.4		Outer 370
	RO: CAGTTACAAACCTCAAATGCAAAAT	55.4		
21, T2-26968, G/A	FI: ACCGCCTCATGAACCTGCTG***A***AG	63.7	63	G 180
	RI: GAACCCGAACTGGGTGTGG***G***TT	63.8		A 267
	FO: GCGTTTGAGCTTTCAGAGCGGATT	62.0		Outer 402
	RO: GGTGTACCCCACCGACATTCTGATC	65.3		
25, T3-31578, T/C	FI: GACTCTTTTGTGTCATCCTCT***C***CT	60.3	60	T 151
	RI: CACTTGCTGCAAGTTTATC***A***CG	58.2		C 178
	FO: CTCAATTGGGGATGTAATACTTGAG	58.7		Outer 283
	RO: AGAACTGGAGTTAGGTGAGAGAGGT	62.0		
26, T2-30620, T/C	FI: CAGGACCCCGATGATAAG***G***TT	60.0	57	T 210
	RI: TGCTTGATATTTCATACTGCAA***A***CG	57.1		C 261
	FO: ATCCATATGGAAGCCAAAACCTAGT	58.7		Outer 425
	RO: AACAGTCGGATCTATTCAACTCGAC	60.3		
27, T3-35667, C/T	FI: ACCGGTCATGAATGATTG***T***GT	56.1	60	T 213
	RI: GTGGTTCTTCTTAGTCTCCA***G***GG	62.0		C 249
	FO: ACTTTGTTCATCAAATCTGTGCTCT	57.1		Outer 418
	RO: GGTACTATAAAGGGGAGGAGGACA	62.0		
30, T3-29141, C/T	FI: TGGAACTCAGACTCCAAAT***T***GC	58.2	57	C 208
	RI: GAACCAAGCCTTGAAAGG***A***CA	58.0		T 242
	FO: GGAAGCCCAGGTAGTCGTTTAATAT	60.3		Outer 407
	RO: ATATCTTCCCCAGTCAATTCAAATG	57.1		

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Primer number, Contig and SNP	Primer sequence (5’-3’)	*T*m(°C)	*T*a(°C)	Amplicon size (bp)
34, T1-26603, T/C	FI: CAGACAGTTGAAATAACAATGCAC***C***TC	60.5	59	C 226
	RI: TTGTTTCAACCCGAGGAA***C***GA	58.0		T 279
	FO: GTTGTTAATGATTCCATAATCGCGG	58.7		Outer 457
	RO: TGGAAATGTTGAACGTGATGAGTCT	58.7		
38, T2-28199, G/A	FI: AACTACTACCCAAAATGCCCTCAG***A***CG	63.5	60	G 215
	RI: TCCACGCCGAGAGCTAGC***G***CT	65.8		A 164
	FO: CTGAGGGCATTAACCACAACGGTGT	63.6		Outer 331
	RO: TGCTCTTGTACTTGCCGTTGCTGAG	63.6		
41, T3-32657, T/C	FI: CCACTGTACGAGAGGGACAAC***G***TC	65.4	57	C 190
	RI: TTCCATTCCCCTGCAGGATTT***T***TA	58.6		T 272
	FO: TCGGAAGAGACCAAGCTATCTGAGC	63.6		Outer 414
	RO: CAAGTGCGAGATATGGATGATGAGC	62.0		
49, T3-23002, C/T	FI: ATGTCTTCTTGGTCCTGG***C***AT	58.0	55	T 167
	RI: GGAGAACAACTACCAGAATATGGAG***T***AG	62.0		C 117
	FO: ATAGATTTTGGGACTGTCACATGAT	57.1		Outer 235
	RO: GATTCTTGGAAAATGGGAGGTATTA	57.1		
55, T3-30010, G/A	FI: GTGCAGGAGGTGAAAAAC***G***CA	60.0	58	A 186
	RI: GTTCAACAAAATCCCCTTCTGGA***A***AC	60.4		G 213
	FO: TACCAAATGTTGAAGCTAGCAGCCA	60.3		Outer 352
	RO: CCCGCCAAAAGAAATCTTGAACTAG	60.3		
62, T1-25257, G/A	FI: AAAAATCAGTAGTGATAATAATTTGTC***A***CG	56.6	59	G 215
	RI: GCAGCATACGAGGACAAC***C***AT	60.0		A 284
	FO: GATATAATACTGCAAAAGCACCAAGC	58.8		Outer 448
	RO: ATTGGAGTTCAAGATCCAGTAATGC	58.7		
67, T1-29128, G/C	FI: GCAATCACACCCGCACTA***G***AG	61.9	54	G 197
	RI: GCTTTAATTTAGGGGGTATG***C***GG	60.2		C 261
	FO: GGGTCCTCACTACATGAACAAGCTT	62.0		Outer 414
	RO: TCATGTTTGGTGCATTGGATAATTT	55.4		
89, T2-31924, T/A	FI: GCTAAAATTATCGGAAGCATAA***G***CT	57.1	55	T 198
	RI: AAATAATGATTCTCTCATCACTGTT***C***CT	57.6		A 236
	FO: AATTCTTCAGGTCAAACACCTTGTA	57.1		Outer 381
	RO: TTATTGAAATAGTTGCTGCATGTGA	55.4		
93, T3-35889, T/C	FI: AAGGTACCAAAAAAAAATCTGT***G***TC	55.4	56	C 188
	RI: AAATCTTCAATCACAGGCA***A***AA	52.6		T 222
	FO: TTCATTGGACCTAATTAAGAGTTCA	55.4		Outer 363
	RO: AAGTACATGATGTCACTTAAGCATGT	57.3		

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Primer number, Contig and SNP	Primer sequence (5’-3’)	*T*m(°C)	*T*a(°C)	Amplicon size (bp)
101, T2-30832, A/G	FI: ACGGGCCTTCCCACTCCC***C***CA	67.8	64	A 200
	RI: TTTACCAATCCTTGCATGATGGTTGAG***T***CC	63.4		G 289
	FO: CGTGACCTTTATCGTTGCCCCGAATC	65.1		Outer 438
	RO: CCCCCAAGGATCCTCTGGTGAGGAA	66.9		
110, T3-34224, T/C	FI: CCATCAAGCCCAAGAACAC***T***AC	60.1	54	C 220
	RI: TTATCTTCATCTACATCTTCATCT***G***CA	57.4		T 298
	FO: AGGAGAAATGGGAGAATATAAACAAGT	57.4		Outer 469
	RO: TGCAAAACAGCTTCTTAACACCTAT	57.1		
112, T1-26622, G/T	FI: AGTTACCTTGACTTCATCAAGGACTAT***A***TG	60.7	58	G 161
	RI: CTTCCAAGGCCCAATCCCC***G***CA	65.7		T 207
	FO: GAATGGTTGAAGCAGCCTGTTTTCA	60.3		Outer 316
	RO: TTTCGTTGCGAAAAGTGTAAGGGTG	60.3		
113, T1-28028, G/C	FI: GAACCCCATCGTCGGATTC***G***TC	63.8	57	C 234
	RI: CCAGCAAGGGTAAATTGTTCTGT***C***CC	63.6		G 188
	FO: CTTGAGAAACGTGCACAACGCGTTAT	62.0		Outer 374
	RO: CGCTCTCGGAGACAACAATGGGTAT	63.6		
116, T2-24666, T/G	FI: ACCACCTCGCATCTTACGC***C***TT	61.9	64	T 176
	RI: CAATTCAGTAATCAAAGGTGTGGA***C***CC	62.0		G 219
	FO: GTGCTTCCGCTTAGACATGTGCTTT	62.0		Outer 346
	RO: ACCGTCTGAAACTGTTCAGCATGAA	60.3		
123, T1-28812,T/A	FI: TTTTTTTTGTTCAGTGAGAGTC***C***CT	57.1	58	T 206
	RI: CCATTGCAGTGAACCTTACATAC***T***CT	60.4		A 287
	FO: GAACAAACCGGAAAATAAAATCAAA	53.8		Outer 442
	RO: GATCATGCATAACAAAAACAACAGC	57.1		
125, T2-26567, A/C	FI: AACGGATTATTTGCTCACATG***C***CC	60.3	64	C 202
	RI: GCTCGGACCTGCTCCTTC***G***TT	63.9		A 274
	FO: TGCATGAATTCGGGGAGATGATAAA	58.7		Outer 431
	RO: ATGGTACTCCAGACCCTTCCACTGG	65.3		
126, T2-33341, A/G	FI: ACTGAACGAAATAATGAGAATATGCC***A***TA	57.8	60	A 236
	RI: TGGGAGTGACAGAGGGGC***T***AC	63.9		G 291
	FO: CTGCTCACACTCCAAGAAAATGAAC	60.3		Outer 477
	RO: AGATCCAAAAGGCATCATCTTGAAC	58.7		
128, T3-28938, A/C	FI: AATAAAACATATTATGCTTCCTCCTT***T***TA	55.0	54	A 213
	RI: AACAACAAATATATCTCTAAATTCTCT***T***CG	5.6		C 279
	FO: ACTGAATTCTTTACCGAGTATGGAG	58.7		Outer 433
	RO: TATTTTTTGGTTTTAAATCTCGGTG	53.8		

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Primer number, Contig and SNP	Primer sequence (5’-3’)	*T*m(°C)	*T*a(°C)	Amplicon size (bp)
131, T1-22617, G/A	FI: CTTTAATATCCCAGGGTGATGTG***T***AG	60.4	60	G 171
	RI: TACGAGTCGAGCTTCTTC***G***CT	60.0		A 254
	FO: ATATACATAACTGAGAGGAGCCCCC	62.0		Outer 378
	RO: ACCATTGATATCCCCTACTTCCTTC	60.3		
140, T3-32052, C/G	FI: AATGAACACAGCCATGTCAAAGT***A***TC	58.8	60	C 167
	RI: CACATCAGAGTAAAAAAAAACACGA***A***TC	57.6		G 227
	FO: CGGATTTCATGAAAGTGTATGCAG	58.6		Outer 340
	RO: AATAATCTATAACGCCCGGTTCAAA	57.1		
147, T1-27404, A/G	FI: TTCGTATTTTATTAGACATTGT***T***AG	52.1	53	G 183
	RI: CGGATAGTGAGTTCTCTA***G***GT	58.0		A 271
	FO: TAAGAGAGAAGCTAGCAGATTC	56.3		Outer 408
	RO: CTTGAGTACTCTGCTGAATAGAT	56.6		
148, T1-27856, G/C	FI: AGGTTCTTGCACAGCTTG***T***TC	58.0	56	C 199
	RI: TTCGGAGAGGAGTGAACAGT***A***AC	60.2		G 278
	FO: CATTATCATCGTCTTCTTCATCATC	57.1		Outer433
	RO: GAAGTAATTGTTCCAGCTCTAAGGA	58.7		
152, T3-23789, T/C	FI: GTTGGTTGTGATGGGGAG***G***AC	61.9	57	C 211
	RI: CAACAGTTCTCTATTGAATCATAAACT***G***CA	59.3		T 266
	FO: CCTGCTCTCCCAACCAAGTTAATAG	62.0		Outer 426
	RO: GATTATGAACTGCTTCCAGACTCCC	62.0		