

Supplementary Materials

Table S1. 310 polymorphic SSR markers validated in 24 samples of *Betula alnoides*.

Primer Name	GenBank No.	Motif	Primer Sequence	Ta (°C)	N _A	H _O	H _E	I	Size of alleles (bp)
BG0002	MH973665	(TA)8	F:TCATTCGATTGCAGCCATAACT R:TTTCGCCTTCTAAAACACCCCT	60	3	0.83	0.51	0.80	247-251
BG0004	MH973666	(AT)8	F:TCTCCTGATTACATCTACCCGA R:TGCCAGAGTGTTAGAAAGGAGT	60	3	0.30	0.45	0.78	109-119
BG0005	MH973667	(TC)8	F:TGTCTTCCACCTTTTCACCCAA R:TGGTGCATGAGTTGTAATTTCTGA	60	2	0.67	0.44	0.63	193-195
BG0006	MH973668	(TC)7	F:TAGACTGTCTACCTCGGCTCAA R:TGTTCAAAGAGTCCATCCCGAG	60	4	0.88	0.74	1.36	105-111
BG0009	MH973669	(GA)9	F:ACCAACAGGAACCCATATCACC R:CCAGAGGATAGGATAGAGGCGA	60	11	0.71	0.71	1.74	216-260
BG0011	MH973670	(TA)6	F:TGCTAGTACTCCAAGCATGAGG R:GGACAGTGGCAGAGCTTAAAGA	60	2	0.86	0.53	0.83	277-281
BG0019	MH973671	(CT)7	F:ACCCAGCTATCTATCCCATGGA R:GTTGAGTCCACAATTCAGCACC	60	3	0.62	0.61	1.02	126-130
BG0023	MH973672	(TC)7	F:AGCATTCACAGCAGATACCCAA R:TTTCTCCAGGGGATGAACAACC	60	2	0.79	0.48	0.67	259-261
BG0025	MH973673	(ATA)7	F:AGTGTTACAACAGTCGCCTGAA R:AGCTTTATTCCACTTGGCTCCA	60	3	0.06	0.33	0.61	121-130
BG0026	MH973674	(TG)6	F:GGAGTTCAGTTCTGGAGAAGGG R:TCATTTCAAATCCCTCTGGCA	60	2	0.21	0.19	0.33	243-245
BG0028	MH973675	(TA)6	F:TGTCCTCTATTCATGTATGTGGA	60	3	0.17	0.57	0.92	128-132

BG0029	MH973676	(TC)8	R:TCATTTGGGAACGAGTTTGTCA F:TACTCTTGACTGCAGGCTTGTT R:CCTCTTCCTCCTCTAGACCCAA	60	5	0.54	0.49	1.02	247-255
BG0032	MH973680	(AG)11	F:AGAGTAGCGACGTGAATCATGG R:CATGCTAGCGTGACGAATTAGC	60	10	0.92	0.81	1.83	219-237
BG0033	MH973681	(CT)11	F:GTTTTGGAACCTTCATGAGCCC R:GCCTTGTGCTTGGATTTTCCTT	60	6	0.92	0.73	1.49	169-185
BG0036	MH973682	(AG)6	F:ATGGGGATTATGTGGTTATGCT R:AGAGTGCTTTGTCTGAATCCGT	60	3	0.88	0.56	0.90	208-212
BG0037	MH973677	(AG)6	F:AGTGTGGAGTATCAGAGACCGA R:CCCCCTCTTCCTTTGCTTACTT	60	4	1.00	0.66	1.15	105-111
BG0041	MH973678	(AT)7	F:AGGAAGAAGAACATGGGTGTGG R:TGAAAATTTACCCGCGATGGAC	60	7	0.83	0.79	1.69	264-278
BG0046	MH973679	(AGA)5	F:CGAAGAAAATGACGGTGATCGG R:TGGTAAGCACTCACAAGCCTAG	60	3	0.79	0.55	0.91	192-198
BG0047	MH978853	(AGA)5	F:AGACATTTCAAGCAAAAGGCCC R:ACAGCAACTATACTCCACAGCC	60	5	0.88	0.68	1.22	221-242
BG0048	MH978852	(TTC)5	F:ACGAGTAGACTCCTAGAGATCATCA R:CGAGCGACACCAACTACCTAAT	60	4	0.63	0.58	1.14	194-209
BG0049	MH978851	(AG)6	F:CCTTGTGAGAAACAACACCAAGG R:CTCATTCAGCCCTTCACCGAC	60	4	0.92	0.35	0.68	141-147
BG0051	MH978850	(GA)6	F:TGTCTTCCTCGAGACTCAGACT R:GCATCTTTGGCATTCTTCTGGGT	60	2	0.79	0.19	0.33	242-256
BG0053	MH978849	(AT)6	F:TGTTGTCGGTTCGATAATCGGT R:CTGTGGAGTGTGGAGTATGACC	60	3	0.52	0.46	0.79	274-278
BG0054	MH978848	(TA)6	F:TCACGCCTTCCATACAACAAAA	60	8	0.50	0.79	1.82	210-224

BG0055	MH978847	(CT)6	R:GTCAGAGTAACAGGGTTGAGCA F:TCTATAGCTCGGTCGACCAAGA R:CTTCACCACTCAAGAACCCTCA	60	2	0.08	0.08	0.17	151-153
BG0058	MH978846	(AATA)6	F:TACCCAGCAGGAGAGTTGGATA R:CCAGGTAGAGCTTTAAACCCGT	60	3	0.50	0.56	0.88	244-252
BG0062	MH978845	(AT)6	F:CGTGGCATGACATGTCTGTTTT R:AGACAAGCGTAGACAAGGGAAA	60	5	0.71	0.74	1.43	268-280
BG0064	MH978844	(TTA)6	F:GCTGAACCACCTTCATAGACCA R:AATACGACACGTGTCCAGTGAA	60	4	0.38	0.63	1.13	187-199
BG0065	MH978843	(AG)6	F:TCCGGATTGTTCTAAGTCGGTG R:TCTCCTTCTTCTTCCTCTCCACT	60	2	0.63	0.43	0.62	136-138
BG0069	MH978842	(AG)7	F:CCCATTTGCCAACGCTCATAAT R:CTGTGATGTAGGCGTACCCTTT	60	2	0.58	0.42	0.67	228-230
BG0070	MH978841	(TC)12	F:CTCATACACGAACAAAGCGACC R:GTACGCCGAAAAAGAGGAGGTA	60	6	0.54	0.62	1.27	209-219
BG0071	MH978840	(ATG)6	F:GTTGTCTTCTTGTGTGCCTGTC R:ACGACCTGCATCTACATCAACA	60	7	1.00	0.82	1.79	206-224
BG0076	MH978839	(GA)6	F:GAAACCGACACACAGAGATGGA R:CCCGCATCTATCACTGCTACAT	60	3	0.17	0.16	0.34	101-105
BG0078	MH978838	(GCT)5	F:CTTTTGCTGTGCAGTGTTCTG R:CAACTTCATGGCAGCAATACCA	60	3	0.42	0.34	0.61	252-258
BG0085	MH978837	(CT)6	F:GGCCTGCACTTGTTCCATATTC R:GACTGCCAAGAATTGCCCAATT	60	2	0.04	0.04	0.10	240-242
BG0086	MH978836	(TC)12	F:CTCGTTTGGCTGTTTTCTGAGG R:TGAATGAAATCCAAGGGCGAGA	60	12	1.00	0.85	2.15	186-208
BG0089	MH978835	(TA)9	F:TAGACTGTTGCTGCTTTTTTCGC	60	2	0.13	0.12	0.27	250-254

BG0091	MH978834	(CT)12	R:TAGTGGTATGACTGTGGGCAAG F:CTCTGTTGCTGTATATGCTGCC	60	17	1.00	0.90	2.50	140-180
BG0095	MH978833	(AG)15	R:TCCATATCAAATCCCCGTCCAG F:TGTCTACTACATCCCCACAGTCT	60	11	0.88	0.88	2.25	222-250
BG0096	MH978832	(GCA)5	R:CGAGGATGCCATAATGAAGGGA F:TTAATCCGGGCAGCCTTGAATT	60	5	0.92	0.68	1.26	132-147
BG0098	MH978831	(AC)6	R:AGATTTGGACTCCGAAACTCCC F:TTAGCTCACCCTCACACAGTC	60	3	0.08	0.08	0.20	206-210
BG0099	MH978830	(TA)6	R:AGCATGCAAAGCACGTGTTTAT F:AGAGACTCAAAAGTGGGGCAAT	60	10	0.79	0.84	2.04	229-247
BG0102	MH978829	(CTGCC)6	R:GGTGGAGTTGTTGACTTGTTTCG F:AAATAGCTGCCACCGTTCACTA	60	4	0.83	0.63	1.16	194-209
BG0106	MH978828	(CT)9	R:CCCTTGTTTGTCAACCAACGAA F:TAGGCACACCCTTCTTTCGTAC	60	8	0.92	0.74	1.54	255-275
BG0118	MH978827	(GCTGT)5	R:GCTGGCTGTGAAGCAAGATTAC F:AGCGCATAGGCCTTAATACTACAA	60	6	0.92	0.74	1.48	244-269
BG0119	MH978826	(ATGT)6	R:CAAACAACCTCACAGAACGCAT F:AGATTGATCGAGACCATGACGG	60	5	1.00	0.68	1.25	241-257
BG0121	MH978825	(AG)7	R:ATAGGCACCAACTCAGGACATC F:CCAAACTAAGAAAGTCCCGAGC	60	6	0.38	0.71	1.38	220-230
BG0122	MH978824	(TA)8	R:TCTCTGGGTTTCGTAGGCTTAGA F:ACTTGAGTCGAAACCATCTAACCA	60	7	0.58	0.74	1.57	250-262
BG0124	MH978823	(AT)11	R:GACCATTGCTCCCGTTAAATCG F:GCCCAAAATATGACGCTCGATC	60	9	0.88	0.80	1.85	101-121
BG0126	MH978822	(GAA)9	R:GGTGCTCGAGCGTCAAGNCT F:ACTGTAAGGGGGTAAGGACTCA	60	3	0.54	0.50	0.87	255-264

			R:TTATTCAAGACAGCTGGAGCCC						
BG0127	MH978821	(AT)8	F:GACTCGTGTTGCGCCATTTAAT R:GGGAAGCACTAACACTCTCCAA	60	7	0.67	0.82	1.85	165-177
BG0128	MH978820	(GA)6	F:CCGAGAGAGAGAGGGAGATACC R:GTTTGGGTCATAAACGGGTCAC	60	13	0.92	0.78	1.89	224-286
BG0129	MH978819	(CT)8	F:GAGAAAGTCAGAACCCTTCGCTT R:GCAATTGATAGCCTCCTCCGTA	60	8	0.92	0.74	1.60	158-178
BG0132	MH978818	(GA)10	F:TGATTCATCGTCAGCCACAAGA R:AGCACACGTACGTACTAGTGTG	60	3	0.13	0.13	0.28	204-212
BG0141	MH978817	(TG)8	F:AACTCCACCCCTTACCTTAGT R:TTCCAACCTTTCCTTCCCCTTCC	60	3	0.38	0.40	0.72	278-282
BG0145	MH978816	(AT)6	F:ACTCCTGTAGGGCCTAGGAATT R:GAGGAGAATGGAGAGGGAGAGT	60	4	0.96	0.63	1.08	142-148
BG0148	MH978815	(TC)9	F:GTGCCAAAGTGTATTTCGGCTTT R:GCGAAGGCGTACAATGTTTGTT	60	19	0.96	0.92	2.68	179-217
BG0149	MH978814	(AT)6	F:AATAGGGACGGAACCAGTGTTG R:CCATGGCTCCCCCTTGATTTTT	60	3	0.67	0.66	1.08	138-146
BG0157	MH978813	(AAT)7	F:GGCATTGTCGCTAATTGCACTT R:TCAAAGTTGAGCTCACCTGGTT	60	5	0.75	0.71	1.35	224-236
BG0158	MH978812	(TA)6	F:CGTTTGTGCGCAGATATGGTAG R:ATTTGCAGAACCCTGGCTCTAA	60	3	1.00	0.51	0.75	221-225
BG0159	MH978811	(TA)13	F:CGTCTAATCCATCCATGCATGC R:AGACAGATCCTAGAGCTCTGCA	60	8	0.78	0.75	1.63	145-159
BG0162	MH978810	(AT)6	F:ACGTTTAGCAGATGTTGTACTTGC R:TCCAATAGCAAATCAAATACCCAAA	60	4	1.00	0.66	1.17	258-268
BG0163	MH978809	(CT)8	F:TAAAGTTGTCCCGTCCTTGCAT	60	8	0.75	0.82	1.87	237-253

			R:AGATGCATGACGAGAAGAGCAA						
BG0164	MH978808	(TC)12	F:TTTCAATTTCTCTGCGACCCCT R:GCCGCAATAGTAATCCAATCCG	60	8	0.67	0.70	1.50	259-279
BG0165	MH978807	(AG)12	F:CTCTAGGGTTGCGCATTGAAAC R:GCAGCTGCCTTTACAAGACAAA	60	8	0.75	0.65	1.42	212-230
BG0167	MH978806	(AT)6	F:GGCTTAGAAGATCCATGGCGTA R:GCGCTTCAGGTATATCCATCCT	60	3	1.00	0.64	1.05	165-169
BG0169	MH978805	(AT)8	F:GCGCCCTTCTGCAATTTCTAAT R:TGCTGAAGGAAATCCAGTGAGG	60	4	0.46	0.40	0.76	154-162
BG0174	MH978804	(GA)6	F:GAGATAGTGCTTGAGAGACCG R:ACACAACACAACACAAGTCACG	60	5	0.63	0.75	1.45	241-255
BG0175	MH978803	(ATAA)5	F:CGCTCATGTAAGCACTCCAATG R:ACTCCACTTTAACTTGCGTTGC	60	4	0.88	0.71	1.48	205-217
BG0176	MH978802	(GA)7	F:CAAGAGAGATGGAGATCGGCTG R:CTCTCAATCTCTCTCACGCC	60	5	0.46	0.60	1.19	157-179
BG0179	MH978801	(TTC)7	F:TTCAAAGGTCACCGATACGTGT R:GAATGACTGAGAATGGCAGCAC	60	4	0.50	0.64	1.10	183-195
BG0184	MH978800	(TTTC)5	F:ATATTGGCGCTTGATCCCTAGG R:AACTCTCTCGCTCTCTGTCTTG	60	4	0.83	0.68	1.24	266-278
BG0188	MH978799	(ATG)6	F:GACAAAGTCCCCAGCATTACAGT R:GCTTCATCACTCCTTTTCGAGGA	60	6	0.79	0.69	1.37	121-139
BG0189	MH978798	(AAT)7	F:AGTGGTTCATATATGGTGTCCACA R:CAGCCCACTCTAATACCGTGAA	60	4	0.67	0.52	0.88	153-165
BG0193	MH978797	(TC)6	F:TATTCCTCCGCTCTCTCTCTC R:TGCATTCCCTTGTTCCAGAA	60	4	0.54	0.43	0.81	180-188
BG0201	MH978796	(TG)6	F:AAGTGACTTTTCGTGTCAACCA	60	3	0.25	0.60	0.97	259-263

BG0205	MH978795	(AAT)7	R:ACCGGTACACAGCTTCTACAAG F:TTTTGCTGAGCCCATTTTCACT R:ATCCATGGAACTGGCTGTTCT	60	9	0.96	0.78	1.84	154-181
BG0207	MH978794	(GA)7	F:AGAAAGAGATGAGCGTTTGGGG R:CACCATCTCTCTCTCATAACGCA	60	5	0.96	0.61	1.11	101-109
BG0212	MH978793	(TA)9	F:AGGACATGCATGATGAAGTGGT R:GCCAACCCTTGATGTAAGCTTG	60	3	0.63	0.54	0.83	110-114
BG0216	MH978792	(ACC)5	F:TCTGACAAACACGTCTGGATCC R:CCCTCGATCGATGTCTCCATTT	60	5	0.92	0.72	1.44	258-276
BG0220	MH978791	(AATA)5	F:CCTATGGGCTGACACTGAATGA R:AACAAATGCAATTTTCAGGGCAC	60	2	0.29	0.25	0.41	164-168
BG0221	MH978790	(AG)6	F:TGAAGATGATGCTAGCGTCACT R:TGCCCCTAGTATTGGTCGACTA	60	3	0.08	0.08	0.20	268-272
BG0222	MH978789	(AT)7	F:ATCGATCGAGACCTAGCTAGCT R:AGGCCGTGCACTGAATATTAGT	60	4	0.50	0.42	0.79	156-162
BG0226	MH978788	(AG)10	F:CTCTCCCTTTCAAGTAGGTCGG R:CTCCATTTTGCTGTGGTTGGAG	60	6	0.38	0.42	0.90	252-262
BG0232	MH978787	(TC)6	F:TGCACCTGAAGAGTTTCCAAGT R:ACCAAAGAGTTGTGACCATAGCA	60	3	0.71	0.47	0.71	242-248
BG0233	MH978786	(TC)7	F:AAATAACGTCGTGTGGCACTTG R:TTCTCTCTACAATGGCGGAGAG	60	3	0.75	0.49	0.77	231-241
BG0236	MH978785	(AT)7	F:GGATCAACGACATCTTCCTCGA R:CGCAGATTACTTGATTCAACAAGA	60	4	0.50	0.54	0.98	158-166
BG0238	MH978784	(AG)9	F:CTACAACGCTCGTCCTCTTCTT R:CGCTGGAAGAGGGGCTAATATT	60	8	0.46	0.80	1.77	236-250
BG0239	MH978783	(CA)7	F:TACCTCTTCAAGCCAACACACA	60	4	0.17	0.80	1.77	146-152

BG0240	MH978782	(TA)8	R:CCCTTAACTAGACGTCTCAGCC F:TTTTTCGACGAGTTTTTGGCCC	60	3	1.00	0.65	1.08	275-279
BG0245	MH978781	(TC)8	R:TCTTGTAACACTCCCCTCAAGC F:GAAACAAACGGGCCCTTAGTGAA	60	6	0.71	0.81	1.75	206-216
BG0248	MH978780	(CT)6	R:ACCGGATGTACATATGCAGGAC F:GAACAGACACGTCGTTTGCATG	60	3	0.75	0.58	0.30	264-268
BG0251	MH978779	(AAT)5	R:GGATCCCGTCATGTTCCAACA F:AGCGTAAAGTGCTTTCAAATACA	60	3	0.04	0.08	0.20	214-220
BG0252	MH978778	(GA)12	R:TGCCAGTAGAAGTAATCGTGCA F:ACCTTTGGATTTGAGCAAAGACA	60	15	0.96	0.87	2.27	161-199
BG0260	MH978777	(TTC)6	R:ACTGTTAGCAATGGTCAGTGGA F:CACAAGTTACACAACCTCACGCA	60	4	0.25	0.26	0.57	142-154
BG0262	MH978776	(AT)6	R:CGAAGAAGAACAGTCTGACGGA F:GTTGTGGCAACCCGATTTTCATA	60	2	0.08	0.28	0.45	167-169
BG0267	MH978775	(TC)9	R:TTGGTTATGGTTCCCGATCAGG F:AGAGTACGGTTCGTGTGTAACC	60	4	0.50	0.42	0.80	202-218
BG0275	MH978774	(AC)8	R:CTTTTCCTGCTGCTGCTTCTTT F:ACGTATGCAGCTATCCAATGAA	60	3	0.08	0.08	0.20	276-280
BG0285	MH978773	(TA)10	R:TGTGTTAGGGTCCGAATCTAGT F:GACCCAAAAGCTCAGCAGTTTT	60	3	0.04	0.26	0.51	225-235
BG0293	MH978772	(TAAT)5	R:AGGAAATCGCCCTTGACTTATCA F:TTGAGCATGTCAAATAGCATTTCT	60	2	0.13	0.12	0.23	212-216
BG0295	MH978771	(AG)9	R:TAAAAGTACGTGCAGCTAGGCA F:TTTGCACCGGATAAAAAGCACTG	60	7	0.54	0.78	1.13	105-121
BG0296	MH978770	(AT)18	R:TATCAACGACCCTCCTCTGTCT F:CCAAGAGCCATCCTCACTCTTT	60	5	0.88	0.71	1.37	242-250

BG0299	MH978769	(GA)7	R:GTCATTGCCTCCACTCCACTAA F:CAACGCAATCTCAAACAGGTCC	60	4	0.54	0.62	1.06	272-278
BG0301	MH978768	(AT)6	R:TCCTACTCTCTAGCGTGGTTCA F:TGGAAAAGGATCCAGAGAAGCC	60	7	0.75	0.65	1.40	247-259
BG0302	MH978767	(AAT)9	R:GTATGGAGGGAAAGCTTTGCAC F:GCAGCCACCAAAGAATACACAG	60	3	0.54	0.47	0.82	215-224
BG0304	MH978766	(TA)6	R:CAACCACGCTTCTTTACTGCAA F:CCCTTCTCCCTTTCCCTCTTTC	60	3	0.21	0.50	0.86	101-113
BG0306	MH978765	(AG)9	R:ACCCCATTAATCACCTTCCCAC F:AATCCTTGGAGAACGAGTTGGG	60	7	0.88	0.74	1.53	180-200
BG0307	MH978764	(AAG)5	R:GACATTCTCGTCTCGGGTAACA F:CGGTTTGGAGAACTTGCAGAG	60	3	1.00	0.66	1.08	236-254
BG0314	MH978763	(AAT)6	R:GCCAAAGCCAAACTCAATCTCA F:TGAACTATCCTCATGGCCTTGG	60	3	0.29	0.33	0.61	132-144
BG0315	MH978762	(GA)10	R:TGAATATTTGGCCACCCCTTCA F:TGCACGTCATTTTATAGCAAACA	60	2	0.09	0.09	0.18	137-145
BG0320	MH978761	(TC)6	R:TTGAGCAGAGGGTTCAAGGATC F:CTCGAACCCCATCTTCTCCTTC	60	9	0.75	0.67	1.42	225-243
BG0324	MH978760	(TA)6	R:AAAGACAGTGTAGTCCGTGCAT F:AATTGGGTGTTTGACGTTACAG	60	10	0.50	0.63	1.47	102-128
BG0325	MH978759	(TC)7	R:AGCAATAGGAGGGGCTTAGAAA F:GGTGTACAGTGTCATGTCCCAT	60	4	0.88	0.72	1.33	117-125
BG0328	MH978758	(TA)10	R:GGAAAGGGAAGGGAAGAGGAAG F:TTGTGTGTCCGAATGAGGTGAT	60	5	0.67	0.47	0.78	170-180
BG0329	MH978757	(AT)6	R:CGACGACGAGAAAAGCAAGATG F:AAAGTGGGGTTGGAATGATCGA	60	4	0.35	0.64	1.13	233-241

BG0331	MH978756	(CT)6	R:GCCAAACATGCCCTTTCCTTTT F:TTTCCCCACTCTCATCCCAAAG	60	4	0.92	0.73	1.35	137-145
BG0334	MH978755	(TTC)5	R:GAGGATAGAAAAGAGGGCAGAGG F:CGTCATCACTGATAAGGCCACT	60	2	0.08	0.08	0.17	223-226
BG0335	MH978754	(TTG)6	R:TCGGGTTCTCGAAAAGTTACCT F:TGGTTGGAGGATTGAGACACAG	60	4	0.54	0.47	0.94	259-268
BG0337	MH978753	(CT)7	R:CCACAGCACAACAACAACAAGA F:TGTGTACTTGCAATGCAGCATC	60	3	0.25	0.23	0.46	268-272
BG0338	MH978752	(AAAT)6	R:AGAAAGAAGGGAACAGCGCTAA F:CCTCACTTGGCAGATGCAAAAA	60	6	0.75	0.80	1.67	219-239
BG0339	MH978751	(GA)6	R:GGGACATTACTAAATCCCAGAAGC F:GGAGGATCTAACGGCAGAGAAG	60	2	0.25	0.23	0.38	181-183
BG0340	MH978750	(GA)7	R:ACTCCTCAGCTCAACTCTCTCT F:GTGGAAGCCCATCAAAAGTTCC	60	13	0.88	0.74	1.75	222-250
BG0342	MH978749	(TA)6	R:CGCAAAGGCACCTTTATTGTGA F:CTTCATGCAAATGCCCACTCA	60	2	0.08	0.08	0.17	237-241
BG0345	MH978748	(AT)10	R:CCCACATGTCGAAATCTAAGC F:ACCCTTAAAAGCTTGAGGTTCAGA	60	4	0.21	0.22	0.52	158-166
BG0346	MH978747	(AG)6	R:CAGTGGAGGTTTAGGTTTCCGT F:CTTTGACTCCCCTCTCCACTTG	60	5	0.38	0.37	0.79	135-157
BG0347	MH978746	(AAAAT)5	R:CCAGCTAGCCTCTTGATCTTCA F:TGATAAAATGGGAATCAGCGGGA	60	3	0.38	0.59	1.02	130-140
BG0349	MH978745	(AAT)5	R:AACAACCTCTTGCTTGCAACGC F:CATGCCTTTGAGGGGTTTCATTG	60	2	0.28	0.50	0.69	155-161
BG0350	MH978744	(ATT)6	R:TAGGGCTAGTTCCTTACACCCA F:TCGGAAATGCAAATTGAGCTGA	60	4	0.50	0.68	1.21	196-205

BG0354	MH978743	(AG)10	R:TAATCTTAAACAACCGCAACCG F:TTAACCAAACAGTCCAGGGGAG R:ACGAGCAAAAATGTAACCGTGAA	60	7	0.58	0.66	1.32	158-179
BG0356	MH978742	(AT)8	F:TTGGGCTGCATACTCCTCAATT R:GCACTCTCTAATGCCAAACTCG	60	8	0.50	0.73	1.63	111-129
BG0362	MH978741	(TTA)12	F:ATTGAAATCTGTTGACGCCGTC R:TGTTGCGCTTTCTCTTGCAATTT	60	11	1.00	0.83	2.00	206-236
BG0367	MH978740	(AG)11	F:AGTAACCAACCTTGCTACCACT R:TTGCTACCCAACAAAGCACAAG	60	9	0.96	0.83	1.93	100-122
BG0369	MH978739	(TC)10	F:CATGCAGAACCCTCTCTTCCTT R:CCCCTCACGTTAAACAAGCAAG	60	8	0.88	0.75	1.62	219-239
BG0370	MH978738	(TC)8	F:ACACAATCCTCCAAGGTTTCATCA R:TGCATGTTTTCGCCATATTGGG	60	11	0.88	0.77	1.77	141-169
BG0374	MH978737	(TC)7	F:ATCACACAGGCTAGGGTTTCTG R:GAAAGATGACGCTCGTGGGT	60	4	0.88	0.65	1.11	130-136
BG0376	MH978736	(AG)6	F:CCCCCTTCTTCTCCCTTTCTTC R:CCGAAACTTCCCTTCTTAGGCT	60	2	0.13	0.12	0.23	131-135
BG0377	MH978735	(AC)24	F:GGCCATCCCTTCACCTTATCTT R:ACACCCAGGTAAGCACAAATCA	60	13	0.42	0.46	1.22	216-250
BG0379	MH978734	(GA)8	F:AACTTTTCTTCCATGCTCGCTG R:TTCAACAGAGATACCTCGGCAC	60	17	0.83	0.92	2.62	129-177
BG0380	MH978733	(TA)8	F:AACGGAGAAAATATTGACCATGTT R:TGGTGTGGTTTATATGATGCCCA	60	4	0.54	0.72	1.32	112-116
BG0386	MH978732	(TC)6	F:CCTCAAATGTTAGAGCTTTACGCC R:CGACATCCATTTTGGCTCGC	60	6	0.17	0.45	0.88	100-118
BG0392	MH978731	(AAT)5	F:AAATCCCATCATCCACCGTTGA	60	3	0.42	0.37	0.66	207-213

			R:ATGTCAACGTAAGCACCCAGAT						
BG0395	MH978730	(TTA)11	F:AGACTGGAATTTAACATCGACCCA R:TGGGGATAGATATTCGATCTTTTCG	60	5	0.50	0.76	1.51	272-284
BG0396	MH978729	(TGA)6	F:GGCAATTATGAAGTCATGGCTGA R:GCTTTTGCAAATGCCTAATGCT	60	2	0.88	0.50	0.69	201-204
BG0397	MH978728	(AATGGA)5	F:ACTAAATTTAAAGGGGCCGGGT R:ACCAAATTTATACGGAGCCGGT	60	3	0.79	0.57	0.93	166-178
BG0400	MH978727	(AT)6	F:CTCGAGGTTCTCAAAGTGTGGA R:CCCCACTTAAGGAAGAGGTTTC	60	4	0.71	0.59	1.05	246-254
BG0402	MH978726	(AT)7	F:TCCAGGAGTGCTCTTAAGGAGA R:GCTTGGTATCACTCCCTCAACA	60	7	0.54	0.75	1.55	231-251
BG0407	MH978725	(CT)6	F:AAGGCTTCCGTTCTCTCATCTC R:AGAGAGATGGAGTCTGCTCAGT	60	3	0.88	0.61	1.01	123-131
BG0411	MH978724	(AAAT)5	F:TGCTTGGGCCTAAAGAGGTTTA R:TGTGTAATTGCCAAGAGCTTGC	60	2	0.58	0.41	0.60	121-125
BG0412	MH978723	(ATT)5	F:TCGTGAACAACCTGTGAATTGCA R:CGTGACAAAAAGGTGGAGCTTT	60	3	0.50	0.38	0.63	262-268
BG0413	MH978722	(ATA)6	F:CCCACCCTTGTCCTGGTATTTT R:CACCCTTCCAATCTGAGGGAAT	60	2	0.38	0.30	0.48	216-219
BG0414	MH978721	(TA)7	F:GATAGCTAGGTAGGCCAGCATG R:TAGGTGGTGAATATGCTGCCAA	60	4	0.83	0.67	1.21	156-170
BG0415	MH978720	(AAT)10	F:ATCATGAGGTTGCCTGGGATTT R:TCCTTGGAACGGACTTTTCACA	60	10	0.85	0.82	1.94	190-226
BG0416	MH978719	(TG)6	F:TCCAGCTCTCTGTCTCTCTCTC R:TCGACTGCCTTGGGTAAACTT	60	4	0.83	0.67	1.21	220-230
BG0419	MH978718	(TA)8	F:GTCACCTGAATCACGATGCCAA	60	7	0.88	0.73	1.51	217-231

BG0422	MH978717	(TA)8	R:AGCACCTTAGTGGAACCATGAG F:GGTCACACGTAAAGCCACTTG	60	4	0.79	0.61	1.06	224-236
BG0426	MH978716	(GAT)5	R:TACATGCTGCCGCCTTGTATAT AGAGAGAGACAAGAAAGGGGGA	60	7	0.87	0.67	1.36	169-202
BG0427	MH978715	(AG)12	R:CAAACCCACGCAGATTCACAAT F:CTGAGGCATGTTTGGTTTGGTT	60	10	0.83	0.82	1.92	141-161
BG0432	MH978714	(TAAA)5	R:TATGAGACACGGGACTGTGAGA F:ACAAGAGCTATTGAAGAAAACACA	60	2	0.04	0.19	0.33	264-268
BG0434	MH978713	(AAATAA)7	R:GCACGTGCTAAAAGAATCTGCA F:AACCATTGTTACCAACGATGT	60	6	0.48	0.67	1.30	110-140
BG0437	MH978712	(CTT)5	R:AGTCCTGAATTGATAGGTGTGTGA F:CGCCTAGCACTAATCCATACGT	60	3	0.08	0.23	0.45	249-261
BG0438	MH978711	(CGC)5	R:AGGCTACTTCAGTGTTGCTTGA F:AGACTGAACCTGCAAAAATCGC	60	2	0.50	0.37	0.56	239-242
BG0441	MH978710	(TA)8	R:CCCCATCATCAACAACCTCCA F:TGCACCAAAACTCAAAGCAACG	60	2	0.43	0.34	0.52	167-171
BG0445	MH978709	(GA)7	R:TTCACCAACTGATGCCTTAGCT F:ACAAGATATTGACGGATGGCGA	60	2	0.33	0.23	0.45	107-109
BG0452	MH978708	(AC)6	R:ATCAAACCCAGGAATAGGCAGG F:TGCTGGTTATGCATGTATGATGT	60	2	0.58	0.41	0.60	276-278
BG0456	MH978707	(TC)10	R:GGTTTTAAAGATCCCGGCGTTT F:ATGGGCATTCTGTCTCACAAC	60	9	0.92	0.78	1.72	236-264
BG0461	MH978706	(AAAT)5	R:GTGTTTGCAGAGTTCCATGCAT F:TGGAGGAAAAATCCAGAGAGCC	60	4	0.57	0.64	1.22	249-273
BG0463	MH978705	(ATT)7	R:AGGAGTCAGCTTTTCAGTGGAG F:CCGGCTTGGAGATGTCTTTAAC	60	6	0.36	0.24	0.47	255-270

BG0470	MH978704	(AG)7	R:ACGTTAGCAGTGTTGAGATTGT F:GAAACGCATCCGAGAAAGACAC	60	6	0.83	0.60	1.15	106-126
BG0474	MH978703	(GA)6	R:GTTCCCCATCTTTGAACTTGGC F:GGTCATGGTTGAGGTACGAGTT	60	3	0.79	0.55	0.88	174-178
BG0476	MH978702	(AT)7	R:GTGTCAACAGCAGAACCAACAA F:TGGACAGGATGAAAGCGAATCA	60	5	0.83	0.61	1.11	208-226
BG0478	MH978701	(CT)6	R:ACGTGGATCAAACCTGATGGGTA F:TAATTCAGCCCACCCAAAGGAA	60	4	0.71	0.68	1.23	101-113
BG0479	MH978700	(AG)6	R:CAGGAATTTGGGTGGTTAGGGA F:CAGAAGGGCTAGTTTTGTTTCGC	60	9	1.00	0.84	1.98	163-181
BG0483	MH978699	(AG)6	R:GCACTACTCCTGTACACTACGG F:GCTGTGGGGTCTTGTTATGTA	60	2	0.13	0.12	0.23	227-229
BG0485	MH978698	(TA)6	R:GTCTACCACTTGAAGTTAGCTCCT F:TCCTAAAACGGTGTCATTTTTGAGA	60	7	0.26	0.24	0.60	269-283
BG0492	MH978697	(TA)6	R:CTAGCCGTGCACTCCATACATA F:AGGATTGACTGAAGGCTACGTG	60	9	0.75	0.68	1.55	228-250
BG0494	MH978696	(AC)7	R:GATTAGCGCTTGAAATGCCACA F:GGGAAAGAGAAAGGGTTGGTCT	60	5	0.67	0.54	1.04	103-113
BG0497	MH978695	(GT)7	R:TGAAAGTTTCTACTCCCACGGG F:AACCGCTTGTACATCCCTAAGC	60	4	0.67	0.63	1.13	247-253
BG0505	MH978694	(TTTG)5	R:TCCCTAGAGTATGAAATCTTCACAT F:CCTGTCTGCAGCATAAATACGTG	60	3	0.13	0.20	0.42	264-276
BG0509	MH978693	(GA)9	R:GCACAAATTGGCACTCATTCCT F:AGACTAGCCATGATCAACGTGT	60	7	0.88	0.71	1.49	251-263
BG0514	MH978692	(AG)6	R:CCAAGTGTGAGAACTAGCAGC F:GGAAGCAGCTCAAATCAAAGCA	60	3	0.71	0.52	0.90	144-148

BG0517	MH978691	(AT)6	R:AGAAGCGTCTGTCTCAACTCAG F:ACTACGCCACCCTACATCAATC R:CTCTGCCTCGTTGTAATCCTGA	60	9	0.83	0.76	1.63	112-142
BG0519	MH978690	(TA)6	F:AGAGTTACAAGCAGCACAAGGA R:TAGAAACGTTGGGAGTGGATGG	60	7	0.83	0.76	1.55	221-245
BG0521	MH978689	(CT)7	F:TCTTGTCGGTTCAAAAACACGC R:TTCGTTTTCTTGGAAGTTGGGC	60	3	0.91	0.58	0.95	269-273
BG0522	MH978688	(TC)7	F:ACGTCACTGAGTCCATTTACACA R:TCACACCTCGTAGGAAGTTGTG	60	4	0.83	0.58	0.99	244-252
BG0524	MH978687	(AT)13	F:ATTGCAACCACTTTAAGCGGTT R:GCAAGCCAATACTTTGCCTAGG	60	11	0.79	0.84	2.12	223-253
BG0525	MH978686	(AG)9	F:ACTTCTTGGAACCAATCAGCT R:CAGCCTGAAAGTTGTGCAATCG	60	5	1.00	0.70	1.31	257-267
BG0526	MH978685	(AT)11	F:ACTTAGGTCTTAACTAGGCACTTGA R:TCAGCACTCACTCACATGGTAC	60	9	0.75	0.61	1.27	202-226
BG0531	MH978684	(CAA)5	F:CACTCTCGCAGATCATCTCTCC R:ATTGTCCCCGCTTGTTGATAGT	60	2	0.50	0.48	0.68	187-190
BG0533	MH978683	(TCT)10	F:TCTTTCCCTTCATCTTCTGCGA R:CCCTTGTGAGAAGTACTGGGTC	60	7	0.92	0.69	1.30	162-186
BG0536	MH978682	(CT)13	F:ATTGGACTTCAGGTCATCGCAT R:ACAGAGAGTGTGTGATGGAAATCA	60	10	0.96	0.83	1.96	107-131
BG0540	MH978681	(ATT)6	F:TCCCCTGATTCCCTTCCACTAT R:CCCATTTTATGCGGTTGAATGC	60	4	0.63	0.53	0.94	107-119
BG0542	MH978680	(TAA)5	F:AGTCGTTAAACCACATAGGCCA R:AGAAAGGGGCACTTCCTTATGG	60	2	0.54	0.39	0.82	209-212
BG0544	MH978679	(AC)10	F:GAGCTGGTGTGAGAAAGTTGC	60	3	0.33	0.33	0.63	176-180

BG0545	MH978678	(AG)6	R:TGGAGTGGACCGATTCACTCTC F:CTCTGCCCTCTCAACTGTATC	60	3	0.87	0.65	1.07	264-268
BG0546	MH978677	(ATT)7	R:TTGCTCCCACATCAGAAGTACC F:TCCGAAGATGTTGGAAAACACT	60	3	0.83	0.64	1.05	170-176
BG0547	MH978676	(TC)9	R:AGTACTCTGTTCCGGCTTGGTTT F:GCTTCCTCCTCTCTTTCTACG	60	5	0.67	0.66	1.23	112-120
BG0548	MH978675	(TC)6	R:CACTCCCCCTTCATTCCATCAA F:TAAAGCACCTACAGCCTCAAC	60	2	0.29	0.30	0.48	242-244
BG0550	MH978674	(AT)6	R:GCCCAATGTTGTAGCGAGAAG F:GGGGGATCCTCTCCATTTTCATG	60	7	0.75	0.75	1.57	167-181
BG0551	MH978673	(GA)7	R:TCAATCATTGGATCGGTCATTGT F:ATCAACAAATGCTTCCACTGCC	60	4	0.63	0.55	1.02	125-139
BG0553	MH978672	(GA)6	R:GGTGGGTTCTCAGCACTCTATC F:TGTGTAGACTTTCTTTCCACCTCA	60	2	0.08	0.08	0.17	237-239
BG0554	MH978671	(TC)6	R:AGACTGGAGGCGTATTGCTAAG F:TGGGAATAGCACAACAATTGACA	60	7	0.92	0.76	1.62	115-129
BG0559	MH978670	(TA)11	R:CCGGACTGGTAGTAAAATCCCA F:GACGGTTGGTGACGTTGTTTTT	60	7	0.75	0.72	1.48	210-228
BG0562	MH978669	(AAG)5	R:AGCTGTCAACCACCACCATATT F:TTGGTTTTCTAGCACAAGTCT	60	2	0.75	0.47	0.66	272-275
BG0563	MH978668	(AT)8	R:CCACCCACATTTCAAGGCTAT F:AGCAGTATCCAAGACAACACCT	60	3	0.25	0.45	0.80	255-259
BG0566	MH985747	(AG)11	R:AGGAAGCTTTACCATTCCACAA F:AACCACGACAGCTGAGAGTAAG	60	11	1.00	0.85	2.06	132-152
BG0572	MH985748	(AG)9	R:TGCCTTCTTTGGAAAGGCATTG F:GTTTCTCTCTCTCGGTGTCGTT	60	4	0.50	0.49	0.92	253-259

			R:CTATTTTCTTCCCTCCCGCCTT						
BG0573	MH985749	(GT)7	F:CTACCCCTTACCTCAACCCCTA R:TGTTGTTGGGGTCAAAACTGTG	60	6	0.75	0.59	1.16	220-234
BG0574	MH985750	(TC)7	F:CATGTCGCTAGGTCACATGAGA R:GGTGTGTGAGAATCGTGTAGGT	60	7	0.57	0.55	1.11	199-219
BG0577	MH985751	(AT)7	F:TTTGCCGAATCATCAACGTGTT R:GACACCAAGCTAGGGAAGTTGA	60	3	0.67	0.51	0.75	133-139
BG0583	MH985752	(AAT)8	F:AGCCAAAACACAATGGGTTTCT R:CGTCACACATCAATTTGGAACCA	60	4	0.83	0.74	1.36	101-113
BG0589	MH985753	(GA)8	F:TGCTTTGGAGGCCAACATCATA R:TGCGAATAGAGGGCTTTCCAAT	60	3	0.38	0.32	0.58	222-232
BG0591	MH985754	(AAT)8	F:GCATCGCCATTCTCTCTTA ACT R:TCATGCGCCTAATTCATCCCAT	60	3	0.46	0.52	0.89	237-243
BG0592	MH985755	(AG)8	F:ACGAGTAGACTGTTGAGAACTCT R:AATGGCACTAAAACCGGGTTTG	60	4	1.00	0.72	1.33	161-173
BG0598	MH985756	(AT)7	F:ACACACACTGCCTTCTTCTTCT R:AGTCCAAAATTGCAACTTGCCA	60	4	0.79	0.67	1.19	169-175
BG0599	MH985757	(TA)8	F:CACGACACAACATGCAACATCT R:AAATCCAGAAGGGGCTAACTAG	60	5	0.79	0.66	1.26	103-111
BG0606	MH985758	(TC)6	F:TAATGTAAAGGTCTTCGGCCCC R:AGGTCCATGTCACCATGTGTAC	60	3	0.71	0.51	0.75	117-123
BG0609	MH985759	(TG)16	F:TCGTCGCGCAGTAAAAATTTGT R:TAGCGGCGATTGTTCCATTTTC	60	10	0.63	0.55	1.24	189-211
BG0611	MH985760	(TA)6	F:CGAAACGTATTTTGGAGCATATGC R:CCCCCTGAAGATTTTCGCATTG	60	3	0.33	0.30	0.55	196-200
BG0615	MH985761	(CT)7	F:AACCCTATAAAACCCCGACGAC	60	2	0.17	0.15	0.29	120-122

			R:GGAGGGAGGAGGAGAAGTTAGT						
BG0616	MH985762	(AT)6	F:AATTGGTCAGTCTTCAGGAGCC R:AGCATGTCCCTCACTTATGTGG	60	4	0.96	0.64	1.15	197-205
BG0618	MH985764	(TA)9	F:GCTGGATTGAGAGTCAGGATCA R:ACGAAGACGAGAGAGAGAGTGA	60	9	0.67	0.82	1.90	248-264
BG0620	MH985763	(AG)7	F:TCCCTTGGA AAAAGCTTTGGGA R:GATGATATGGCCCACTCAAA	60	2	0.08	0.08	0.18	283-285
BG0625	MH985765	(TC)9	F:GTCTCCAAAACCAAGCAAAGCT R:TAAACAGCTGAGTTCCCGAGT	60	6	0.88	0.66	1.30	213-225
BG0631	MH985766	(AG)8	F:TCTCCACAACGACCCTTTACTG R:GCTTGTTGAGAAGGCATTTCTGA	60	3	0.04	0.41	0.70	218-224
BG0637	MH985767	(TA)7	F:ACCAGACGGTCTGCATTA ACTT R:TGTCGATACCTTTTCACTCATCCA	60	5	0.79	0.57	1.00	125-137
BG0640	MH985768	(GA)7	F:CAATGTGGGCATGGCATAGAAG R:CTTCTGCCTCTCTCCGTTTCTT	60	2	0.67	0.44	0.63	155-157
BG0648	MH985769	(AAT)5	F:TGAAACAAATGGAGCTTTAGGGT R:GAGCTATGCCATTTGGATTGGG	60	2	0.54	0.50	0.69	131-140
BG0655	MH985770	(TA)6	F:ACTTGGGTGTTTATGCTTTTCTGT R:GTTGAGGAACCTAACAATCTATCCT	60	2	0.67	0.44	0.63	184-188
BG0657	MH985771	(GA)6	F:TCAACAAACGCGGCATAGATTC R:ACTCCACCGATTCCCTGAATTC	60	2	0.58	0.41	0.60	175-181
BG0660	MH985772	(AT)10	F:CCCCTTTATCCTGAGTCCAAGG R:GCCCCCAAATTAGTTGTTGCAT	60	8	0.92	0.79	1.75	233-247
BG0661	MH985773	(AG)7	F:GGCCTATAGCAATGTGGGTGTA R:ACATTTTCACACCTCTCCTCCC	60	2	0.29	0.25	0.41	196-198
BG0667	MH985774	(AT)7	F:GCATTGCGTGGA AATGTTGGTA	60	2	0.33	0.39	0.77	174-186

BG0683	MH985775	(TTA)6	R:GCCAAATTGTTAGCCCCAAAGT F:AGCCAAGTGTTATAGCAGACTT	60	9	0.92	0.84	1.96	226-250
BG0684	MH985776	(CT)11	R:AGAAGATGTCCAAGAACGTGCT F:TCCTCTTCTCCACAAGCAAGAC	60	17	1.00	0.88	2.39	226-262
BG0685	MH985777	(GA)7	R:TCTTGCCTCCCCATTTCAAGAA F:TTTCTGCTTCTTTGCCGTTTAC	60	6	0.92	0.62	1.14	101-117
BG0687	MH985778	(TA)6	R:CACGAGCTGCATCTCTCTCTAG F:TCTATTATAGGGGGCGGGACAT	60	7	0.79	0.64	1.35	173-191
BG0693	MH985779	(AG)13	R:GGAGGTAGAAGCTCAAACCCCTC F:ACCCTCCTAAGTTACACCAGAC	60	8	0.92	0.85	2.01	214-230
BG0694	MH985780	(TC)8	R:GGCACATGTCTGAAGAAGCTACT F:GTCCCACTAACGTGATACTCCC	60	2	0.21	0.19	0.33	101-103
BG0695	MH985781	(AGA)5	R:ACGGAGGAAATGGAGAGAGAGA F:AGTCAACTACGTTGTCCACTCC	60	2	0.50	0.37	0.56	234-237
BG0696	MH985782	(TA)8	R:CTGCTTTTGGCTGACTTCCATC F:TACATGGGTGTGCGAAAGATGA	60	5	0.96	0.64	1.17	158-166
BG0700	MH985783	(AT)7	R:ACTGTACGCAAATGTAAATTGTTCA F:AAGTTTGTCTATCTCTCTACACACA	60	4	0.92	0.67	1.22	260-270
BG0713	MH985784	(AT)8	R:GCACACTTCCACGCTTTTCTAC F:CAACAAATTGGACCATGAGGGC	60	6	0.88	0.78	1.67	143-153
BG0714	MH985785	(GA)7	R:TCTGTTCTCCATCAGTATGTTTGT F:AAAGCGATACCGAAATTCGCAG	60	10	0.83	0.77	1.79	101-123
BG0719	MH985786	(GA)7	R:ATTATTTCCACCGTCACAACCA F:AGACACGTGAAGTCAACAGTTT	60	4	0.42	0.43	0.79	168-174
BG0723	MH985787	(TATTTT)5	R:ACTCTGGTTTGGCCACTCTAAG F:GTAGGTAGGCCCATGTCTCATG	60	3	0.50	0.62	1.02	215-227

BG0732	MH985788	(CA)8	R:ACAATTGTTGCACCTTCCACTC F:AATTGGCTCCTGGGAACCTTCTT	60	5	1.00	0.72	1.36	154-162
BG0736	MH985789	(AG)6	R:TCCCAGAGTTTTGATGGTGATGA F:TCAAAAACCTCCAACCCAAGATTG	60	2	0.33	0.48	0.68	104-106
BG0738	MH985790	(AAT)5	R:TCCCCTTTGCATGACACTGTTA F:TCTAACAAAACCATGTTCCCACT	60	3	1.00	0.56	0.89	202-223
BG0742	MH985791	(TA)9	R:GTTGACTACTTCGCTGATATGCA F:TCGAGACACACTTAACAAATGGT	60	10	0.92	0.77	1.71	240-266
BG0743	MH985792	(TC)7	R:AGAGAGAGAGAGAGGGCGAAACT F:CTGATTGTGACTACGCCAACAC	60	5	0.75	0.78	1.56	262-270
BG0745	MH985793	(AG)8	R:CAAGTCTGATGCATGCTAAGCC F:TGTGTTTGATTTTAGTGCCTGCA	60	3	0.54	0.53	0.90	203-207
BG0748	MH985794	(AT)6	R:AAAGACAATCATCACCACCGCT F:GGTGGAAAGGTAGGCACATACA	60	3	0.79	0.19	0.40	231-235
BG0749	MH985795	(TCT)6	R:GACAGCCTAGTCCTAGTGATGC F:TGAAAAGGAGTCCAACAACAGAGA	60	5	0.92	0.70	1.36	135-153
BG0750	MH985796	(TA)10	R:GAGGAGAAGGCTCATGGGTATG F:TTTCTGCCATATTCTGACGTGT	60	3	0.42	0.34	0.57	151-157
BG0751	MH985797	(TA)11	R:TTGTCCACTCCCCCATAATTG F:ACCCATGGTTATGAGCGAAGAG	60	11	0.63	0.57	1.39	224-248
BG0756	MH985798	(CCA)5	R:CATATGCACAGCACAGTACTGC F:CAACCCACCTAGAAATCCACCA	60	3	0.83	0.56	0.90	188-194
BG0758	MH985799	(TC)13	R:TGCCAAGAAAGGTGGTGTATTG F:GTTGTTGAAGACAGATGGTGGC	60	10	0.79	0.83	2.02	192-230
BG0759	MH985800	(TG)15	R:GAACTCAAAACCCGTTCTCTGC F:TGCTCTATGAGGTGGTTAGCAT	60	3	0.13	0.14	0.32	238-244

			R:GATCAAAAACCCAGCATTCCCC						
BG0761	MH985801	(AT)15	F:ATCTCACCTAACATCCGCTTGC R:GGCCTCATCTTGACCCTCATAG	60	12	0.92	0.81	1.88	126-154
BG0763	MH985802	(TAT)16	F:AGTGGGGCTTCGTTCTTTCTAG R:GCTGTATGTTTGTCTGGTTTGCT	60	7	0.92	0.73	1.54	177-195
BG0765	MH985803	(GA)6	F:GACTAAATTTGCTGGCCGTACC R:CAATAGCTCTGACCGATCGGAT	60	3	0.79	0.49	0.73	236-240
BG0767	MH985804	(CT)8	F:AGCCTTGAAACTGGAAATTTTGTCT R:CCCCATCCTCCCAACCATTA	60	5	0.50	0.66	1.27	181-189
BG0768	MH985805	(AG)9	F:ATTGACTTAAAGCTGACCGGGT R:CTAGCTGTATTTCTCCGACCCC	60	8	0.92	0.79	1.80	209-225
BG0771	MH985806	(AG)10	F:ACGGCTCTCATTTGACACAATA R:GTTCTTGGCTCACAGAGGAGAG	60	6	0.88	0.60	1.10	172-184
BG0773	MH985807	(AT)6	F:ACTCTGACACCCACTTCTAGGT R:AGCCTTCATGCTGTACTCACAA	60	4	0.96	0.61	1.08	124-134
BG0779	MH985808	(CT)9	F:ATCATGTTAGAGCTGGTCGGTG R:CACCCTGAGCAACACAATTTGT	60	3	0.63	0.54	0.87	256-262
BG0780	MH985810	(CT)6	F:GTCCTACATCAAGGGCCAGAAT R:GCATTGCTCTCAAGTCTCCACT	60	4	0.88	0.57	0.98	270-282
BG0783	MH985809	(AAT)6	F:CGAATCTTGTGTTCCGATGCAT R:ATGACCTCTTTCTTCAGCAGGG	60	4	1.00	0.65	1.12	269-284
BG0786	MH985811	(AAG)7	F:TGACATTACCCGTGTTTTTGCC R:AAACCTTTCAGCTTCATGTGCC	60	5	0.71	0.54	1.02	215-227
BG0790	MH985812	(TC)6	F:GTCAGGGAAAAACACATTCCGG R:TATCACCCCTAGGCAATCCTCA	60	4	0.71	0.66	1.18	100-116
BG0793	MH985813	(AG)14	F:ACCAAGAGAGAAATCTTCTAGAACA	60	11	0.75	0.88	2.25	163-187

BG0797	MH985814	(TC)6	R:CCGCCATTGTTGTTTCGTTACT F:AAAATGGTCTCCCCTGACTTCC R:TGGGTCTGGTTTCATGCCAATA	60	6	0.96	0.70	1.44	166-182
BG0798	MH985815	(TC)6	F:GCCGTATTGCTGTCTTCTTCAC R:AAGTTAAGAAGCCCCCTCACGAG	60	3	0.50	0.48	0.72	181-187
BG0799	MH985816	(AT)12	F:AGCCTGATTAGCCCCCATAAAA R:TCCCCAATGGTCATGGCAATAA	60	6	0.63	0.74	1.56	249-261
BG0802	MH992132	(AAG)5	F:CCTGAACACACAACAATGCGAT R:CTATCACCCAGATCGTGCTGAA	60	5	0.58	0.66	1.27	251-263
BG0803	MH985818	(AT)7	F:GCGCTAAGAGTGAGTGAGAGAA R:CGCTAATCGTAAAACCGCCTTT	60	5	1.00	0.65	1.24	242-258
BG0806	MH985819	(CT)10	F:TCAGCTTATGCAGGCCTAAACA R:TATGACAAATGGAAGGCGGACA	60	8	0.88	0.74	1.67	253-269
BG0810	MH985820	(TC)9	F:AAATCTGTGAACAAGTGCTGCC R:AGGCTTGGCTTTGATACACCAT	60	4	0.50	0.44	0.85	140-146
BG0813	MH985821	(TTC)5	F:CGAGTAGACTAAAATCGCGGGT R:CCGTATGCTGATGTGTTGAGAC	60	3	0.42	0.35	0.65	224-236
BG0816	MH985822	(AT)6	F:ATCAGGTTGACAGTGCTGACAT R:AAATGTGACATGTTTCCGAGGC	60	6	0.92	0.79	1.61	159-173
BG0818	MH985823	(TC)11	F:GGAGATGCAGAGGGATCGATTT R:CAGCCAAACAGTCGAAACGAAA	60	7	0.92	0.76	1.57	210-232
BG0824	MH985824	(AT)6	F:TCACCACTCCCATATGGCAAAA R:TTGTCAAATGTCACAGCAGCAC	60	5	0.29	0.51	0.92	162-188
BG0826	MH985825	(AG)7	F:CGAGTAGACTATTTTGATTTGTGCC R:TATCAAGGACTCTGCCCAAACC	60	4	0.54	0.49	0.91	136-146
BG0828	MH985826	(TAA)12	F:GCCCCTTGATAAAAATGTCACA	60	8	0.46	0.81	1.83	250-274

BG0831	MH985827	(TC)6	R:TTTGATTCCAGGCGTTCTTTGC F:AGGCAAGGGACGTTAAGCTTAG R:GGTAACCTGCTAAGAGGTGAGG	60	7	0.75	0.66	1.32	204-218
BG0833	MH985828	(ATT)6	F:AGTTACCGCCGCCTAAAATATT R:AGAGCCAATAATAACCATTCCTTGCA	60	3	0.75	0.50	0.84	261-267
BG0842	MH985829	(AG)6	F:AATAGACCCTCCTACGTCCCTT R:CGTTCGATGACTGCCCAAATAC	60	2	0.21	0.25	0.41	247-255
BG0847	MH985830	(TC)6	F:ACTTTAAATTGTGGATGGGTCTCA R:GCTGATCACTGTTTATCATCGCA	60	4	0.21	0.20	0.46	208-218
BG0848	MH985831	(CT)6	F:AGTCAATTGTAGGGGCCGAATT R:AACACCCTCTTACAAGCTCTCG	60	5	0.75	0.65	1.19	138-152
BG0849	MH985832	(GA)6	F:TGCCTACTTCCAAATGACCGAA R:GACGCGACTCGATGTTAATACG	60	6	0.96	0.74	1.55	179-195
BG0852	MH985833	(AT)9	F:CCACCAGGGTAGAAAGCTATGG R:GCTTCTTGAGGTCATAGTTCAACG	60	7	0.92	0.80	1.69	129-143
BG0854	MH985834	(AT)8	F:TGTCATTCAGCCCAAGCCTAAT R:CCAAAATCTTGGCCCAAACCTCA	60	10	0.21	0.78	1.74	145-175
BG0856	MH985835	(AT)7	F:GAAACTTGGGTGAATCCACGTG R:TCAGGTGCATAGCATGTGACTT	60	3	0.63	0.59	1.19	236-246
BG0864	MH985836	(GA)8	F:ATTGGTAGTTGAAGTGTTGCGC R:CCTCCAGTGCCTTATCTGAGTC	60	6	1.00	0.76	1.52	204-214
BG0866	MH985837	(CTGCCC)5	F:CTGGTGCGCTACATTGTTCTTC R:TTCCCTAGGTTCCCGAAAACCTC	60	3	1.00	0.65	1.07	165-177
BG0872	MH985838	(TTA)8	F:TGATGGAGTTACGAGCTGCTTT R:TACCCTAGCCCCCAATATGACT	60	5	0.46	0.74	1.46	220-235
BG0876	MH985839	(AAT)10	F:TGGGCTGATATGGTAGTGTTCA	60	6	0.54	0.61	1.16	115-130

BG0878	MH985840	(TA)8	R:ATATTGCATTGGGCTGATGTGC F:CCTGTGACGATCGGTTCAATTC	60	5	0.38	0.37	0.77	127-137
BG0879	MH985841	(AG)13	R:CCCCATTTGGTAGAGAAGACCC F:GGAGTTAGAATGGTGCATTTGACA	60	13	1.00	0.89	2.34	215-239
BG0880	MH985842	(CT)8	R:ACCCTAACAATAGCGCACATGA F:TCAAAGACCCAGCTGTGTCTTT	60	3	0.75	0.60	0.99	221-227
BG0881	MH985843	(AGG)6	R:CCTCTCACAAAACATGCTCC F:TGGACGACAAGACTGCTGTTTA	60	8	0.50	0.66	1.48	169-196
BG0883	MH985844	(AAT)9	R:CAGGAATCCCAACTTCCCCTTT F:CCCATGCATGCTCAATGTAGTG	60	4	0.13	0.68	1.26	251-260
BG0884	MH985845	(AT)8	R:CACATGCCATCAAACGTGATCA F:AGTGATGGAAGTTCAAGGAGGT	60	5	0.67	0.50	0.93	230-238
BG0885	MH985846	(GAT)6	R:GGCATGACCCACTACTGTGAAT F:TGGTCTGATGCATGAGTACCAA	60	3	1.00	0.66	1.09	262-268
BG0887	MH985847	(GA)6	R:GGCAAGAGAACAGGCAGATTTG F:CCAAGTGAACATGCTTTTATTTGCA	60	2	0.17	0.15	0.29	204-210
BG0888	MH985848	(ATTT)5	R:CCATAAGCGACACTGAGCCTAT F:ACGTCACAGGTAAATACTGCAA	60	4	0.88	0.74	1.37	263-279
BG0889	MH985849	(TTG)5	R:GGGTGCCAGTGTGTGTGTAATA F:GGGAGGGAGAGAGACTGTCATA	60	4	0.92	0.60	1.02	275-287
BG0891	MH985850	(TAT)8	R:CCAGAGCCAGAATCCAGAATCA F:TGATACACACCAGCATGTTGGA	60	9	0.67	0.82	1.88	139-166
BG0893	MH985851	(ATT)9	R:CGTACTGGCCATTTGCTTCTTT F:CTCGAGTCAGCATGAAGGTCAT	60	6	0.96	0.82	1.75	247-265
BG0895	MH985852	(AT)6	R:TTTGAACCAGATCCTTCGGTT F:AAGCGTGCAACCCACTAATTC	60	3	0.88	0.52	0.78	188-192

R:TATAAGCTGCTGTTCCGATGCA

Note: Ta, annealing temperature; N_A, number of alleles; H_O, observed heterozygosity; H_E, expected heterozygosity; I, Shannon-Wiener diversity index.

Table S2. The PCR results for 270 SSR primer pairs in 24 samples of *Betula alnoides*.

Primer Name	Motif	Primer Sequence	Ta (°C)	N _A	Size of alleles (bp)
*BG0001	(ATC)5	F:GAACAGGTGTTGAGCATGCAAT R:TTTCGCCTTCTAAAACACCCCT	60	1	245
°BG0003	(TC)8	F:CTTCTGATGGCGTGGTATCTGA R:CGAGATCGTTAGAAGCTCTCCC	60	/	/
*BG0012	(ATT)5	F:GCACTTAAGAGGATCCGAACCT R:ATAATTTGGAGCGTTGCACGTC	60	1	161
*BG0017	(AGA)6	F:CTGCAGGTGAAAGCATTTTCGA R:TTACGGTTGAGTTGCACGAGTA	60	1	244
°BG0022	(TA)13	F:GACTACGAGTAGACTAGCACTTTGA R:ACATACCTAACCAATGTAGGACAT	60	/	/
°BG0031	(TA)7	F:ACGAGTAGACTATCCTTCGCTT R:TCAACTACAGCTCAGCATGGAG	60	/	/
*BG0038	(GA)7	F:TTTGTTTCAACCATCCTTTGCA R:ACGTCTCTCTCTTTCCTCGTT	60	1	271
*BG0042	(ATT)5	F:GGGCAATGTAGGAGTTCCAAGA R:GAAGCTTGGGTTTGATGGTCAC	60	1	138
°BG0045	(AT)10	F:CAAGTGGAAGCTAGGGTCTCA R:TCCGATATAGAACTCAATGCACACT	60	/	/
°BG0052	(AG)9	F:AAGCCAAGCTAAGTTCCAATGC	60	/	/

		R:TCTACTAACGTGGACCTCTGGT			
°BG0056	(AT)6	F:ACCCCCTTTATTTGGTCTCACC	60	/	/
		R:GACATGCAGTCCTGTCGTTATA			
*BG0057	(TCT)6	F:CAGCTTTTTATGCTTGGCTGGT	60	1	168
		R:GTAAATGGCTGCCAGGATTGAC			
*BG0059	(CA)6	F:TGGGTAGCTAGAAACAACCTTAACCA	60	1	238
		R:TCAAAGCTTGAGCAAAGATGGC			
°BG0060	(TA)9	F:GCTAAGCCAATCTTGTCTATGCC	60	/	/
		R:ATAGGACTCCTCCACACATGCA			
°BG0063	(ATT)5	F:AACAACAGCCGTCACCTCTTTG	60	/	/
		R:GCATTGCTTTGGGTTGGTGATT			
°BG0067	(TA)10	F:ATCAGAGATGAGGGAAGTGGGA	60	/	/
		R:TATCTAGGGCTGAAAATGCGGG			
*BG0068	(TTA)5	F:TGGGCTAGGATCTTCTCATGGA	60	1	280
		R:TCAAACACCTGCAGAAAGACAA			
°BG0072	(AG)10	F:ACGCTCTGGAGAAAACCTACTGG	60	/	/
		R:CGAGAAACGAGCTAGGAAAAGG			
°BG0081	(AT)6	F:CCCACCAGGTGTGTGTTTAAAC	60	/	/
		R:GGCAATGGCGAATTGTGTATGA			
*BG0084	(ATT)7	F:GAGAAGTTGCTTGTGCGGAAAT	60	1	124
		R:CAGAGGTACATGATGCCTGAGG			
*BG0092	(AC)8	F:TCAAAGTTTGGGGGTATGGGAA	60	1	240
		R:GCTCGTGGCAATTCGAATTGAA			
*BG0093	(AG)6	F:TCGGTTAATTCGGTGTCGGTAA	60	1	273
		R:CTCTCAGTCTCTCACAGTCACG			

°BG0094	(CTT)6	F:GCAAAAAGGCCTCATCAGCTTT R:TCTGAGATTCCGGCGTTATCTG	60	/	/
°BG0103	(TA)12	F:GCTGCCGCATCTACCAAATTAG R:TGCAGACATTGTTTCGATTGTTGT	60	/	/
◇BG0104	(AAT)5	F:GACCAAGCCACCTCATGACTAT R:TAAAGGTGGCCGAACAATCTCA	60	2	127-133
°BG0105	(TCT)8	F:CTTGTAAGGACTGTTGCAACCC R:AAGGCAAGCTGAAGATTTGCAG	60	/	/
◇BG0109	(ATG)7	F:AGTAGACTGACTCCTGCCATCT R:ACTCTATTGCTTCTTGGGCGAA	60	4	129-141
◇BG0110	(TA)6	F:TGATCTCAGTGCTCAAACACAGA R:ACGTGGCAGAGACTTTATGGTT	60	3	241-247
*BG0130	(TC)8	F:GAGTAGACTGTCTCGCTGAAGG R:ACGAAGACCACGCTCTTTGTAT	60	1	145
*BG0135	(CT)8	F:ACTCCTTTGGCTCCTGTCATTT R:TGGTGTAAGAATGGTTGTTGCA	60	1	236
°BG0137	(TA)7	F:GCAAATTAACCGTTAACCGCCT R:CGGTTAGGGTTTAAAACGGTGG	60	/	/
*BG0138	(AAGA)5	F:AACTCACCATTTGACTGCAAGC R:AGGTAACGGTTGTTTGAATTCCA	60	1	267
°BG0140	(TA)8	F:GCGTGGTAAAAAGTCTGCTGTT R:TCATGCATGAAATTAAGCTGACCA	60	/	/
°BG0152	(TA)12	F:AGCCCCTCTACATGTGAAATCA R:TCTCATGTAGAGGGGTCAAAGT	60	/	/
°BG0160	(TA)6	F:TACGAGTAGACTGGCTTAGGGT	60	/	/

		R:CGATGGTGAAGTCAGTTGGAGA			
*BG0168	(ATA)6	F:ATTTGCTCCCCCATAAGAACGT R:AGTCACCCGTTTATGGCTCATT	60	1	265
*BG0170	(TA)6	F:GTTACGCCGCTGTCCTTAAAAA R:AGGAAAGCAAGTGGTGGATGTA	60	1	105
°BG0178	(AT)6	F:GAGTAGACTGTAGCACCCGATG R:CGATCCACTGCATCAACACTTT	60	/	/
°BG0185	(AAAC)5	F:GACCTCTCCAGCTTGCTTCTAA R:AGCCAAAGATGGATCAAGATGGA	60	/	/
*BG0191	(AT)6	F:ACGCTCAATTTATCAAGCTGGC R:CCCTCTCGTCTCCATCAAAACA	60	1	254
*BG0192	(TC)6	F:TTCCTCCCTCACGACATCTTTG R:GGAATGAGAGATGCCTGAGAGG	60	1	122
*BG0194	(TG)6	F:GCCATTGAGGTAAGATTTGCAGT R:GTGCAAAAGTACAACCCTGGG	60	1	280
*BG0195	(ATG)5	F:TGGGCTATGATGTGAGAATGGA R:ATTAAGACAAGCACATGCCTGC	60	1	275
*BG0196	(ATA)5	F:AGCTGCTTCCTAACTAGTTTCCT R:ACCTTTTTTGCTTCCCCTAGACA	60	1	274
°BG0197	(CT)8	F:GTAGACTCCGTGTTTGGTAGCT R:CACGATTTTGGCCCTGGAAAAT	60	/	/
°BG0199	(TA)6	F:AAGATTATTGCGCGCGACATAC R:AAAAGGCGTGCCATGTGTTATT	60	/	/
*BG0200	(GA)6	F:ACAGATGCTTCATCATCGTCGT R:GATTCGGACTCGGGA ACTCTAC	60	1	210

°BG0204	(TA)16	F:GTCCACGCTAGCCTAGTTTGAA R:CCTTGCCTTATGATGCTGTTGG	60	/	/
*BG0209	(AAAT)5	F:ATGAATATAGGGAGGCCAAGGG R:TCAACAAGAAGCAGGTCAAGGA	60	1	215
*BG0210	(ATT)6	F:TGGGTTACCTGAAGAACATGCA R:TCCTCCTTTTTGGTGTATCATCT	60	1	129
°BG0213	(AG)7	F:AAAGTCAAAAACCTCAGGTGGCG R:ACAGCACCTGGGTTTGTCTATAA	60	/	/
°BG0214	(AT)12	F:CCCTGGACCTTTTGTATGGAGA R:CGATTTTGCCCCACTTTGTGTT	60	/	/
°BG0215	(TA)10	F:TATTGCCACATTCTCCGCAAAC R:CCATCACTTACTTTGAAGCACACT	60	/	/
*BG0223	(CT)6	F:CCCATGAACCCAAAGACCCATA R:CAGAGAGAGACAGAGCCCTTCT	60	1	237
°BG0224	(TTTA)5	F:TTTTGACACGGAACAACCACTG R:TCACGAGGAAAATAGTATCGCA	60	/	/
◇BG0227	(GA)6	F:TGTGCCAAGAATTGAAGGGAGA R:GGCCCGATAAAAGTCACCATTTT	60	2	270-272
°BG0228	(TC)8	F:TTTACGCTTGCAACACAGTCTG R:GAATTTGCGGAACACATTTGCA	60	/	/
*BG0229	(GTG)5	F:TCGATATCGAGCATTGCCTCAA R:CCCTCTTTATCAGCCCCCAATT	60	1	242
*BG0230	(GGCAA)5	F:ACGCTTAGAACAAGAGTGACGT R:CGACCAAGATTGCCACACTTTT	60	1	157
°BG0231	(AT)8	F:TAACCTAGACTCAGCCACTTGC	60	/	/

		R:TTTGACGGATTGCTCCATACCA			
°BG0253	(AT)6	F:CGAGTAGACTTCGAAGACCCAA R:GGCTCACTAGTCAAGCGAAGTA	60	/	/
°BG0255	(TA)6	F:AGAAGAGAAAAGAAGCCTGCAGA R:CGAATCGGCAAGTTACGTTCTC	60	/	/
°BG0257	(TC)7	F:TTCCCAAGTTGAAGTCGATGGT R:GAGAGCATCACAAGACAGGGAA	60	/	/
◇BG0268	(CCA)7	F:AAATCAAAAGCTAAGCCCGCTG R:TTTGGTTTCTGGTGGCTTAGGA	60	2	252-255
◇BG0271	(TGA)5	F:TGATGAAGTTGATTGCTCTCAAG R:GACCTTGTGTTTACACCTTGTGA	60	3	248-254
°BG0277	(AC)17	F:AATAGCCACCCCGAAATCTAC R:TGGTGTGGATTAGTCAACCCAT	60	/	/
*BG0281	(TC)6	F:TCCTTACACACTTCCACCATGC R:ATCCATCAGCCCTTTATGTGCA	60	1	116
◇BG0298	(TA)8	F:AGACTTGAGTATTTTCCATAGGCGA R:GGCGCGGCTCATTACATTAA	60	2	266-276
°BG0300	(GA)9	F:GAGGGGCTTGGGTTTTTCATTT R:GGCCTTTAGAGCATTTTCAGCA	60	/	/
*BG0308	(AT)6	F:AATGGATGTAGGCTTACCACAT R:AAGCAACACAACGCTTCAGATT	60	1	129
°BG0309	(TA)6	F:TAAGCACATGAATTCACGCCAC R:GCATAGCGCGGGTTATATGCTA	60	/	/
*BG0313	(CT)7	F:TCTTGGATAATCCTGCAACGCT R:TTGCTCTGTTTCAGACCTGTGT	60	1	240

*BG0319	(TTA)5	F:CCTGAGAGTCTGAAACTTTATTTGT R:TGCTAACAAATCCTCCTTCTCCA	60	1	151
*BG0321	(AT)10	F:ATCACTTGTCTGCATGCGATTG R:AGGTTCCCTTACACTTCTGGCAA	60	1	269
°BG0322	(TAA)7	F:ACAATGCTTAACAATGCATGCA R:TCGACATCCGACTTTGAGCATT	60	/	/
°BG0323	(ATT)8	F:CCTGGCTCTAGCTCGGATAAAG R:CCCTGAGGAAAGATTTCTGGGAA	60	/	/
◇BG0326	(TTC)5	F:ATAAAAAGACCCATGGCCGGAA R:TCTCCGTCTTTTCTCCTTGCTC	60	2	143-146
*BG0332	(AT)7	F:AGTGACTAAAACTCCTTGACACA R:AGTACCCATTGCCTTAAGGGTG	60	1	270
*BG0336	(TA)12	F:TATGGTTGGGGCAATTGCTAGT R:AGGAATTCCAGCGATCACAAGT	60	1	222
*BG0341	(AT)6	F:TTCTGGAGGGGAGTCTCGTTAT R:ACTCTCTAATGCAAACTCGGC	60	1	252
*BG0343	(TC)7	F:TTCCGACACCGATTTAACCGAT R:GTAGGCAAGAAGAAACGTCGTT	60	1	168
°BG0348	(GA)10	F:TGGCTCATAAACCACCAACCAA R:AGAGAATCTGGAGCCCCAATTG	60	/	/
*BG0351	(CT)6	F:TACGAGTAGACTCACCTCCTGG R:AAAGAGCCATCAGAATGTCCCC	60	1	145
°BG0352	(TTA)6	F:TGCAGTTTGTTAGAACATTGTTACG R:TCCCATAACACTGATACGACAATC	60	/	/
*BG0353	(CT)6	F:TTATTCCTCCTATGGTCCGTCC	60	1	177

		R:CCTTCTGGCCACTATGCAATTG			
*BG0359	(TA)7	F:GCATCAGCTCAAAAGACATGCT R:GGTTGTTGCCCAAACCTTAAAGA	60	1	230
*BG0360	(CCT)5	F:CACGTTATTTGCACACTCAGCA R:TATTCTTGGCGTTGCTTTGTGG	60	1	249
°BG0361	(CT)8	F:CTACGAGTAGACTACCGCGAAG R:GTGCCAGAGAGAAAATGGGGAG	60	/	/
◇BG0365	(TTAT)5	F:TTTCCTTCCGAGTCCCTTCTTG R:CATTGGTTTTATCCTGCAGGCC	60	2	276-280
*BG0371	(AAT)8	F:CAGGGTGATTGATGTTGGAGGA R:TTCAAGTTTGGAGCTGGAGGAG	60	1	243
*BG0372	(AG)6	F:TGGAGGAGGATGTTGGTTCAAG R:GAATCGGGTCATCACACAAACC	60	1	102
*BG0378	(AAT)5	F:GGTTGGCCTGGACTTTAGATCA R:GCATCGAATGTGGTTGATGGTA	60	1	233
*BG0382	(AT)14	F:AATTAGGCCTGGGCTGAATGAA R:TGAGGAATTTTGGGTTTAGCTAGGA	60	1	235
*BG0388	(ATT)5	F:CCATCCCTTGGTTTCTCTTTCTC R:CCGGTTGAATGCGTAAGGTTTT	60	1	256
*BG0389	(TA)6	F:AGGGGTCTGAGACTTTTGCATT R:AGATGGGGAGGGATTAGTCACA	60	1	106
°BG0390	(AAT)5	F:TCTAGCTAGGGGTGCATTCTCT R:GCATCAGAAACACAGCAGAGAC	60	/	/
*BG0401	(AT)6	F:TGACCTTGGCTTGTTTGGGTAT R:GCTAGCAGCTATGATTGCCAAC	60	1	212

°BG0404	(AC)9	F:TGTGTAACCTCAAGTTTGGGGGT R:CAACATTCTAAGCTCGCCCATG	60	/	/
°BG0405	(ATT)6	F:GCCCCAACGTACGTCACTAGTAA R:TTGGGGGTTTCAAGGCTTATTTCA	60	/	/
°BG0408	(AT)11	F:AGGCATCTTGAAAAGCTATGCT R:GGAACCTCCATCTTGAGAGAGA	60	/	/
*BG0409	(AT)9	F:GCACAGTTGGAAGGGATTATGC R:ATGTGCACATGACAGCTTGAAC	60	1	233
°BG0410	(TC)12	F:TCCTCTCCTTCTCTCACAGTCC R:GAAAGATCGACGGAGACAGTGA	60	/	/
°BG0417	(AT)12	F:ATACAGAACCGTCAGATGGCTC R:ACTTCGTTAAGGCCCCGTTTATA	60	/	/
*BG0418	(AT)12	F:TGGGCTGATGTGAATCATGACT R:ACCCCCAAAATAGAGCACTGAT	60	1	140
°BG0420	(TG)6	F:ACGAGTAGACTGAATAGAATGCA R:AGACCTGGAAGCAATAATGGCA	60	/	/
*BG0421	(TAA)5	F:ACCTAGTCCTAATTTGCGAGCA R:CCTCCCCGGTCTCAATATTCAT	60	1	247
*BG0423	(AT)6	F:CGAGTAGACTAGAGGGAGGGAG R:AGTGTGAAAGCAGTGGAGACAA	60	1	195
*BG0424	(CT)7	F:TCGACTACTCCTCTTCCCCATT R:CTCTTGACGAGAGGGAAGC	60	1	118
°BG0425	(AT)6	F:AATTCGGTTGCCAAATAAGCCC R:TTAGGCTTAGGAGTTGTGCACC	60	/	/
*BG0428	(GT)7	F:TGTTCAACATTTTAAGCTCGCCA	60	1	250

		R:GAGGGTATGCTACGAGCCATAC			
*BG0431	(GA)6	F:CAGAACTGAAGAGGATAGCCGG R:CGAAGCAGTTAAGGGCAGTAGA	60	1	128
*BG0435	(TA)11	F:TCTGCCACCATCCATTCACTAC R:TGAAAATTAACCACCCGTGTGC	60	1	200
*BG0439	(TC)7	F:TTGGGGCAAAGAACCAGAAAAGG R:AGTTTCATTCATCACGCACAGA	60	1	267
*BG0440	(TGT)6	F:TTGCATGCCATTGAGAAGCTTC R:CTGCACTTACAGTTGCTACAGA	60	1	226
*BG0442	(TC)6	F:TGGCTAATCCATTCACTGTCTCT R:TGCATCTAGCCATGGATATGAA	60	1	242
*BG0446	(AT)6	F:ACTACGAGTAGACTAAGCAAAATCA R:TTTTGAGCTTGGCTGCATTTGA	60	1	188
°BG0451	(CT)7	F:AAGCATCTTCAACAAACCTTTCA R:CTTGGTGGGTTTGGTGAAGGG	60	/	/
*BG0455	(TA)6	F:CTTCAGAAGCGCACTTTCTTGT R:GAACTGAAGCTGCAATGAAGCA	60	1	169
°BG0459	(TTA)5	F:ACGTGTCGATTTCAATTCAACCA R:AAATTGCAAGTGTGGTGGGATC	60	/	/
*BG0464	(GA)9	F:AAATATCACGGTCGGTTGTCCA R:TATTCGAGGGCTCCCATGAATG	60	1	125
*BG0466	(GA)13	F:ACTACACGTACGTAATTTTGTGTGT R:TCGTTGTCCCAATTGATAGCCA	60	1	260
*BG0473	(AG)6	F:AGAATCAGCGATTCCGTGAAGT R:GTTCAAAAACGACCTCTGTCCC	60	1	149

*BG0477	(TC)6	F:TCTTCCACTGTCTCCTCGATCT R:CAGAGAGGCACATACGAGTGAG	60	1	267
°BG0480	(AT)7	F:ACAAAATAAGAGTGGTTGGCCA R:AAAAACCAAATAGCGGGTGGC	60	/	/
°BG0481	(TA)9	F:TTGAAGGATGATTTTTACTGTCACA R:TGCCTAGCGCCAAAAATGTTTT	60	/	/
*BG0482	(ATT)7	F:ATTAGAGACCGGCTTGATGCTT R:ACGTGATATCTGTGGGCGTAAA	60	1	261
*BG0486	(TA)6	F:CGTTTGAAATCTGCCCCACTTT R:CCAAAGAGTGTCAAAGTTGCCA	60	1	259
°BG0489	(CT)6	F:CCTTGCTTGATGTGCCTTTGAA R:TGGCGGATTTTGTTTGAAGGTC	60	/	/
°BG0493	(TC)8	F:TTCCCTCCCTGAATCCTCTTCA R:ATTGGAGAGATCTTCGGGGAGA	60	/	/
*BG0495	(AT)11	F:CGCATGGCAAATATTTCCGAA R:ACCCCTACTTCACTTTCATGGT	60	1	259
*BG0501	(GA)7	F:TCAAATGTACAGGCTCATCGAT R:TTGCCTTGAACTGCGTGAAAAT	60	1	278
°BG0504	(TA)7	F:GTAGACTTGTAGGATGGGGTGG R:GTTTCATCTATAGCAAGCACGCG	60	/	/
°BG0506	(TTA)5	F:GGAGAAGAATCAAGAGCACCT R:CCCCCAACTCCCCAACTAAATT	60	/	/
°BG0507	(GCA)7	F:AGAACTGGGACTTGCGGTATT R:ATTGAGTTCCCAAGCACCTGTT	60	/	/
◇BG0515	(TC)6	F:AGGAGCAATTCAGTGAATTAACAA	60	2	170-182

		R:GCTACACTTCGACAAATATGCA			
*BG0520	(ATA)6	F:TCTCAAGAGGACTTCATGTGAAT R:CTTGAAAAAGCCCCGAGAATG	60	1	191
*BG0523	(AG)7	F:CCGAAAACCCTCCAATGCTTAA R:ATCTCCCTCTCTCAGACAGGAG	60	1	126
*BG0527	(AT)6	F:GTTGCGGAGCCTAGTAGGTTAA R:ACACACACCTTGATACATATTCT	60	1	249
°BG0528	(GA)7	F:AGCGCCAAAGAAATCAAACGAA R:CGATCTCCCTCTCTTTCTCACG	60	/	/
°BG0529	(CT)9	F:CGAGTAGACTACGTGTAAGGCC R:GAGAAATGTATCAGTGGTGCCG	60	/	/
◇BG0530	(AC)6	F:GGTGGAGGAGATGTACGACAAA R:CTGTCCCGATCGATTGTGTTTG	60	2	247-269
°BG0532	(AG)7	F:GGAAGAGGTACTGCGGTGTATT R:TTCTAACGCTTACGCTCTCGC	60	/	/
*BG0534	(GAA)5	F:ATCGGGTATAATCCGGAAAGGC R:CCCACTGTTCGTCCCTTGTTATT	60	1	164
*BG0537	(AT)11	F:TGTTAGTTTGAGAAGGCAAAGTGT R:AAGCAAGTACCTTACCTGGCAA	60	1	113
°BG0539	(AT)10	F:GGGTATATGTGATTAGCGGGG R:TGAATTAAGTGTCTCAGCCCCC	60	/	/
*BG0541	(CT)9	F:CCCAAAACCCTCCTTCCTCTC R:AATCACGCATCTCTCTCGTCTC	60	1	204
*BG0543	(CT)6	F:ACGCTTATACAGACGCATAGCA R:TGAGAACAGAGGAAGACACAGC	60	1	169

*BG0557	(CT)15	F:AAACCCGCTGCTTGTACAGATA R:TGCAATTTAAATGCAAGCCCCA	60	1	175
°BG0558	(TC)9	F:CACGTCAGCACACACCTATAT R:GGGAAGGGAGGGAGAGAGATAA	60	/	/
*BG0560	(TA)6	F:TGCCAATTTGAAGACCCTCGTA R:TTGACTTCAGTTGTGCCCCATA	60	1	189
°BG0565	(AG)6	F:GGATTCAGGCACAGAAACACAC R:GTTATCGTCATGGTTTCGCTGG	60	/	/
°BG0567	(ATC)6	F:ACTACGAGTAGACTCTTCTTTGCT R:GCTGTTGGTTCTCTCAAGCCTA	60	/	/
°BG0568	(AT)7	F:ACATAAACATTACATTTGGGAAGCT R:GATAGTTTCGAACCACCCCAA	60	/	/
°BG0570	(TA)7	F:GGTAAAGATGAGAGGCGAGAGG R:CACCCCATACCCCCTTTTTGTA	60	/	/
*BG0571	(TTA)5	F:CCAAATCCCCACAGTCGACATA R:TCGAATTTGGTGTGACAATGA	60	1	116
°BG0576	(AT)6	F:AGAAAGCCCCCAGTAATGAGTG R:CCCCCTCCCCCTAATTAGGTAT	60	/	/
°BG0578	(AT)6	F:CTCACGTACATACCTTGCCACT R:AATGGAGTTGAACTATGACCGT	60	/	/
◇BG0579	(AAG)5	F:ACGGGACTAAACACACCGATTT R:GCATCATCCATGGCTGTTTCATC	60	4	218-230
*BG0580	(CT)6	F:GGTTGTTCTTGCAAACTCTCC R:CAGGGGCAATGGCATTAAACAAA	60	1	102
*BG0582	(TA)9	F:AGAGCTAATCCCGTGTGAACAG	60	1	244

		R:TCCTCCCCTATGATGACTCGTT			
*BG0584	(TG)6	F:ACTACGAGTAGACTTATTGAACACA R:TCATGATTCCTCTGATTGGCATCA	60	1	146
*BG0586	(TC)12	F:AACAAGTTCGTCGTCGGTGATA R:CTGCAGGAGTCGAAGGATTCTT	60	1	214
*BG0587	(AC)7	F:AAGTTTGGGGGTATGCTACGAG R:ACATTCTAAGCTCGCCCAATGA	60	1	245
°BG0593	(AC)6	F:AGTTTGGGGGTATGCTATGAGC R:AGTTCCCAGATCAACCCCAAAT	60	/	/
°BG0595	(AT)13	F:AACGCTTTAAGCAGTTGCAGTT R:ACATTGTGATAGAGGGAGCCTT	60	/	/
*BG0601	(AGA)5	F:ACGAATTTATGGAGAAGGCCGA R:CCAGGATCTTCACTGGACGTAC	60	1	261
*BG0604	(TA)6	F:TTGACTATTAGTGTGGCGACCC R:CAGCTCCCAGTGATGTTTCTCT	60	1	200
°BG0605	(AT)14	F:GGACCATTCCAAAACACATGCA R:TCTGTGCTATTAGGTGTGTCTTT	60	/	/
*BG0607	(AT)7	F:CGCACGACCAGAAAATAGGAAC R:AAGCAGGTACACCATTCCTCTG	60	1	261
*BG0608	(TA)10	F:GGAGCCCTTTCACAATTGCTTT R:TGTGATGTATTACATTGTTTGAGCA	60	1	123
*BG0612	(TTA)5	F:AGCAATTCAGGCGTGAGAGTAT R:TTTACACGATCCGAGAATCCGA	60	1	274
*BG0613	(AT)7	F:CGTTTGCAATGTCAACCTCTC R:GTAAATGAGACATGCAGGCAGC	60	1	244

*BG0622	(CT)8	F:TGTTCCACCATTGATGTGGAAGTC R:AGTCTAGTCCAAGGAAAGGAGAGA	60	1	233
°BG0624	(AT)8	F:TTTTTGAAGCATGCCCACTTGC R:GGAGAGATGACACAGCTGGAAT	60	/	/
*BG0629	(TAT)5	F:GCAAGAGTATGGACAGGAGGAG R:AAGACAATTCCCAGGCGTCTAG	60	1	202
*BG0635	(ATA)5	F:GCCAAAAAACAATGCAGGTAACA R:TTAGGACACCCCTTCTGAGACA	60	1	224
°BG0636	(CA)9	F:ACTGCATCCCTCTAAAAGTGAGA R:AAGGAGGAAGAGTTGTTGGTGG	60	/	/
◇BG0641	(TCA)5	F:TTTGGACTTTCTATGCCGTCCT R:AGACTGGTTTTTCATGACACGGA	60	2	248-254
*BG0644	(GA)11	F:AGGCATTCTTCTCGGATAACCA R:CTGCCCACTAACAATGAATGCC	60	1	207
°BG0652	(AAT)6	F:AGTGTGTACAACCTGGTTACGGT R:AGCTCACGCAGACTAATGAGAA	60	/	/
*BG0653	(TA)18	F:ACTATGCATGGCTAGCTTGTGT R:ATGCATAACAACACAAGCAGGG	60	1	248
*BG0656	(AC)6	F:AAGTTTGGGGGTATGCTACGAG R:AATCACCAGTTTCCCAGATCCC	60	1	224
°BG0662	(AT)6	F:TCAGTTGAAGACCGAGTAAGGC R:ACTTCATCTTCATCTGTTCAATTCA	60	/	/
°BG0663	(TAT)5	F:AATCCCGAGTCTCAACCAAACA R:TGTGTTTGATGTCGTGGGTTTG	60	/	/
*BG0664	(TC)6	F:TGCAAATTCCGCACCTCATTTT	60	1	170

		R:GAAGTGGCGCCAAGATATCAAC			
*BG0668	(AT)11	F:ACGAGTAGACTAAATTAGGGGTCT R:AGTTGCTCGAGACTTGTGATGT	60	1	245
*BG0669	(TA)6	F:TCCTAATTCACCATCTGATTAGCT R:CCATGTGGCAAGCTTCAATGAA	60	1	241
*BG0670	(TTTC)5	F:ATTTTGGCAGTGCCTGTAAATT R:GATGGCCTTGTGAATGCAAAC	60	1	160
*BG0672	(TA)6	F:AGACTACAACATAAATCAGGCACT R:TCTCAGGTGCTATCTGACCAGA	60	1	222
*BG0677	(GTT)6	F:TGCAAGAGGTGGGATGTAAAGT R:TGTTATGGCCCCCTTTCTGGTT	60	1	123
*BG0678	(AC)6	F:CCGCAAATTCGCCCAAAGAAAA R:CGAGTTCTGAAGGGAGTTTTGC	60	1	223
°BG0679	(ATC)6	F:ACGATCTATTCTACCTCTATCAGCA R:AACACTACGGATACAAGGCTGG	60	/	/
*BG0686	(AG)7	F:TGCCCAAACAAAAAGACAAAAAGA R:AAAGAGCCGGATGTAGGTGATT	60	1	220
*BG0689	(AT)6	F:TCTCTTTTTGGTTCATGTTAGCCT R:GCGCAAACGTCTTCCATTTTCA	60	1	216
◇BG0704	(GA)6	F:CGTTTCCAAGAAGATCAACGCA R:TGGTGATGATGACTTTTTGGGC	60	2	253-257
*BG0708	(TA)7	F:GCCCAGATTTTATCATTGCCGG R:ATGGACCCCCTGATCTTGAAAC	60	1	275
°BG0709	(AT)7	F:ACAAGAGGAAATGATGGGTTTGT R:TTAGTCCCCCTCCTGAGAATGT	60	/	/

*BG0710	(CA)6	F:TCATGAGAAGACCATTCCACCG R:ACGCATAGTTCCTGCCCCATTAA	60	1	122
*BG0712	(TA)10	F:CTACTCCCTTCGAGGATCAGGA R:AGGATTTGCTTGACAGGGGTAG	60	1	166
*BG0715	(TC)9	F:GGAGGGGGTCAAAATGTTCTCT R:CCCACATGAGCACCTATTGAGA	60	1	259
*BG0716	(AT)6	F:TAAAGGCCTAAGAGCTAGCTCG R:ACCTTAATTTTGGCTAAAGACGGA	60	1	266
*BG0718	(AAT)5	F:ATAGCCTGTCCCATGCTTTCAA R:CCAAGCCGAGTCTAACATCAGT	60	1	210
*BG0720	(TA)8	F:CTCGGTAAACCACTTCCCTCAA R:TGGAAGGTAGTAAGAATTTGGGAGA	60	1	236
°BG0722	(TC)6	F:CTGTAGCTAGTGATCTGGGTGG R:CGAGAGAGATGAGAGCTCTTCG	60	/	/
*BG0724	(AT)8	F:TTAGGCAGGGTCCTTATGTTGC R:TTTAAATCGGACCAAATGGCCC	60	1	157
°BG0725	(TA)9	F:GGGTCACGTCTTTCCTCTTTCT R:GAAAAACCCAACACGTACAGCA	60	/	/
*BG0727	(TA)6	F:AAATCGCAAACCTCAAACGGACC R:GAGTGGCATATGTGAGAGCAGA	60	1	221
*BG0731	(TAT)5	F:AGTTAAATTTTCAGCTCATTCGGT R:TGTGGAGATAAATATTGGTTGGTGG	60	1	277
◇BG0734	(AT)12	F:GAGATATAAATGTGGGCATGGCA R:ATGCCTCACAACTTAGTAGGGC	60	4	248-256
*BG0735	(ATT)5	F:CGATAAGAATGGTGCAAGCCAG	60	1	223

		R:AGGGATAGAAAACCACTCATAGAGT			
*BG0740	(TA)9	F:ACATGTGGCAGACTAGCATGAA R:TCAACAAATTAGAGGACACTGCC	60	1	200
°BG0741	(AT)6	F:ACAAGCAACATGACGCAAGAAA R:CCTACCCCAGTTTCCAATGTGA	60	/	/
°BG0744	(AG)6	F:TCTATATAGAGGTCGAGCGCGA R:TTCATACCCATGGACCCAAGTG	60	/	/
°BG0746	(TA)6	F:TTAGGAGTGGCAAAAGACCCTC R:TCTTGTCTTCTGCTTCGACGAA	60	/	/
*BG0747	(TAT)5	F:TCCATTTTCGGTTCTACATGCCA R:TGCATGCCACATCTTTTCAATCA	60	1	185
*BG0752	(AAT)9	F:AAATGGTACCGAGTTTTTGGCG R:CTCTCACGCCAAGGTGAATAGT	60	1	127
*BG0753	(TC)12	F:GAGTAATGCGACGGACAACATG R:TACATTCAACGGCGGTAGTGG	60	1	151
*BG0754	(TA)6	F:GTCATGTGCCTTACAGTTGCAA R:GGTACCAACGGACATTGCAAAA	60	1	280
◇BG0755	(AT)6	F:TCCCTTGTAGCCCTCTCTCTTA R:TTGTGGTCGGTTTTGCAAAACT	60	2	271-273
°BG0762	(ATT)6	F:ACGTGTATTGGGTAAAGTCGCT R:ACCCTCACATTTTATGCTTCGT	60	/	/
*BG0764	(ATT)6	F:CGAATTTTCATGATCTCTCGGCA R:ACGTTTCAGTACGAGGCTCTTT	60	1	266
*BG0769	(AATA)5	F:AAGGTGGGTCTTTCATGCTCTT R:TGGAGTTAGCAAAATTGGCCAC	60	1	115

*BG0770	(TA)7	F:TCCCGATGAATGTTTCAGTGGA R:ACCGTCAAGAGTCCAAAACCTGT	60	1	222
*BG0772	(AT)6	F:AGGGTTGATTGAGACTGTCCT R:TCAATTTGCAAACGGCTCTTGT	60	1	222
*BG0778	(AG)16	F:GACTCATACGACCCAACCTTGT R:TTGGTTTGTGGGCAATGGTTAC	60	1	155
*BG0788	(AAT)5	F:CAAATTAGCGAACGGTAGCTCG R:AGCCGTCTAGTCAACAGATAGC	60	1	127
°BG0789	(AAT)6	F:TGGCCAATTGGGTGGTAATTTT R:AGTCCAAATACCCTCAACCACC	60	/	/
°BG0791	(TA)10	F:TACTAACCTCAAGCACATGGCC R:CATCCTGCATGTCAAGCTCAAA	60	/	/
*BG0792	(AT)13	F:AGTAGACTGGGTTCTCGTCAT R:AGGCTAATGCTCTTGCCTTTCT	60	1	221
°BG0794	(TA)6	F:TTTTTATTGGGGGTGGCTCTGT R:ACACCTACACATGGCTTTGTCT	60	/	/
°BG0796	(GA)8	F:CCTCAAAAGTACAGCGAGGACT R:TTCGGACTTTTTGTAAGCGCAG	60	/	/
*BG0800	(AT)6	F:GTGTGGCTATTCGAAACAACA R:CGTTCCTTCTCATTGTTCTC	60	1	278
*BG0804	(GAA)7	F:CGTGAGTAACGCTCTTTCACTC R:AATGTTGAGAAACGTTGGCGAG	60	1	263
°BG0807	(GT)7	F:GTTCAACATTCTAAGCTCGCCA R:GGGGGTATGATACGAGCCATAC	60	/	/
°BG0808	(TA)6	F:GGAGAGATGGGTTGATGTGTGT	60	/	/

		R:GAAGCTCATATCACCCCAGTCC			
*BG0809	(TTC)5	F:TGGTTGGGAAGTGCAATTTTCC	60	1	223
		R:CCACTTTGCCCCAAGTCAATTT			
°BG0811	(TC)8	F:CTCGAACTTGCGTCTCTCTTCT	60	/	/
		R:ATTCAAGTGACAAGATGCGTGG			
*BG0812	(AT)8	F:ACAAAGTAGACATGGAAGGCGA	60	1	252
		R:AAAATTGCTCGTCTAGGGTGGT			
*BG0814	(ATT)6	F:TTTGAAATCACTGAACCACCGC	60	1	258
		R:GTGTGCCCCCTTGTTCTACTG			
*BG0815	(TC)6	F:GACTCTAATTTCTGGGGCTCC	60	1	240
		R:TATGCACATGAGTCTAGCCAC			
°BG0820	(ATT)6	F:GTGTACAGTCGAGTTCGTTTGC	60	/	/
		R:AGTGAAGAAGATGGGTGTGTTT			
*BG0822	(AC)8	F:TCCCCCTGGTATGATCTTTCCA	60	1	221
		R:GTTCAACATTTAAGCTCGCCCA			
°BG0823	(TA)11	F:CGAGTAGACTGAGAACGAAGACA	60	/	/
		R:ATTGTACTTCACGTCAGGCCAT			
*BG0825	(ATT)5	F:AATAACATGTTGCTGTCACGCC	60	1	132
		R:TCACTTCTCCTCCAAGAAAAGAA			
*BG0827	(TA)6	F:ACTACGAGTAGACTGAATACTCACA	60	1	253
		R:AAAACAGTGTGAGCCCCAGTAA			
*BG0829	(AT)11	F:TGAACAGTACTGCTCAGCAACA	60	1	213
		R:AGGAGAGAGAAAAGGCTAGGTGT			
*BG0832	(AT)7	F:ATTCGTGGGTATTGTGCGAGTCC	60	1	150
		R:CATCATTTGACTCAATCCGGGC			

*BG0836	(TCT)5	F:TAGGAAAGGGTAGTGCTTGCAG R:TGCACATTATACCCATATTGAACAA	60	1	176
*BG0837	(TA)6	F:CGTAATCTCAAACGCACCAGTC R:GGCAATGCCTATCAATCCTTACA	60	1	223
*BG0838	(GA)8	F:CGAGTAGACTGATACTGCCGTT R:TCCTCTCCTTCTCTCACAGTCC	60	1	226
°BG0839	(TA)11	F:TCCGAAAAAGACAATGAATGCCT R:TCCACTACCGAGTTTGTTGACC	60	/	/
*BG0840	(CCT)6	F:CTGCCCATCAAAATGCAAGACA R:AGTCGAGAAATCTGTTGTGCCA	60	1	273
*BG0843	(AT)9	F:ACTCTTGGCAAATGACCTCAAG R:CTTTGAAAGACTCTTCCAATTCAGT	60	1	233
°BG0850	(AT)9	F:ACTCTCTTTGGTCTTGTTGTCCA R:CTTCCAAGTTTGATGAGTGCCG	60	/	/
*BG0851	(CTTT)5	F:CCTGGGCAGCAACACATTTAAT R:TGTGCTACATATGCTGTGATGT	60	1	226
*BG0853	(GA)6	F:CACATGCAGTGTAATTGACGCA R:GGTGAGAGTGAGGGAACATGAG	60	1	182
*BG0858	(GA)8	F:GAGTCGAGAGATAGCTTCAGGC R:TCAATGTTTCACGGTCTCACCC	60	1	221
°BG0859	(TA)6	F:AACCTCATCCATCGCTTTCAGT R:TTCTTTGGAAGACTACTGGGCC	60	/	/
*BG0860	(TC)6	F:TGTTTTCGTCTTTCTGTTGGCC R:CCGTGGTTTTTGACAGAAAGTGT	60	1	233
*BG0861	(AAT)5	F:CACAGTGGAGAGAGAGGAGAGA	60	1	215

		R:CCCCAACCCAGTTTAGCTAGTT			
°BG0862	(TC)9	F:ACGAGTAGACTTCTGCTTCAATGA	60	/	/
		R:AGCCAATGATCTGCAGCTTTTG			
°BG0865	(AG)6	F:TTGCTGGATCTCCTTGTTCAA	60	/	/
		R:AAATTTGCAGAAGAAGACAGCCCC			
*BG0869	(TA)6	F:TGCACCTCTTCCCTTTTCAGTT	60	1	106
		R:TTTCGCTTTCCCTATTCTCCCC			
*BG0870	(ATT)7	F:TCTATCAGGAACATGGCCCATG	60	1	211
		R:TGTCACAATGCCCAAGTTGAAC			
*BG0875	(TG)6	F:GGCATGTTTCAGAATGGCCAAT	60	1	123
		R:AGATCTCAAGTTGGCCCTCTTG			
°BG0886	(TA)8	F:TCAGTGCATGCATGTATGTGTG	60	/	/
		R:CATGAGTCAGTCCAGTTCCACA			
°BG0892	(CT)7	F:ATTCCTTCAAACAACGAAGCCG	60	/	/
		R:GTCTTAAGAGAGAGAAAACGAGGTGT			
*BG0894	(TC)6	F:GGTGGCAAATTGTGAGGTTAGA	60	1	212
		R:TAGGAGGAAGAGAAGGATGGGG			
°BG0896	(AT)18	F:GCTAACGCACGAAAGGATTTGT	60	/	/
		R:AGCTTTGAATTCACCTGGAGGT			
*BG0900	(TAT)5	F:CAGTGGATCCCTCCTACCTAGT	60	1	152
		R:GAAGGTGCAGATTTTCAACCCA			

Note: *, the primers generating monomorphic markers in 24 samples; °, the primers with weak fluorescence signals in amplified products of most samples; and ◇, fixed heterozygosity.

Table S3. Validation of 19 SSR markers developed previously in 24 samples of *Betula alnoides*.

Primer Name	Motif	Primer Sequence	Ta (°C)	N _A	H _O	H _E	I	Size of alleles (bp)
BAG01	(TG)8(GA)13	F: CAAGGTGCTCAGGGTGTTT R: TATCCTCTTTGGCATTGAA	52	7	0.79	0.62	0.80	241-255
BAG02	(TC)15(CA)9	F: CCTTGCTCTGCGTGATGTATTT R: CAGAATCCTCTTATTTCACAG	52	8	1.00	0.81	1.83	228-244
BAG03	(CT)17	F: TGCGTATGCTTCCAACAC R: ACCCAGAACCTGTCCACC	52	9	0.91	0.79	1.96	322-344
BAG04	(TC)21	F: TCTTTGCCTTAATGATTGTTGC R: GGCTGACGGACACTGTTTGA	52	14	1.00	0.92	2.12	209-235
BAG06	(CG)5(CA)8	F: TCGCACATACACTCACACATT R: ATGCTGCACACTTTTGATTTA	50	4	0.96	0.76	0.78	168-174
BAG09	(AT)5 G(TG)8	F: TCGTTCAGGCAACTCTATCAAT R: ATTTGTAAAGATGGATGGAGAA	54	8	0.65	0.55	0.84	273-297
BAG10	(AG)5 ... (GA)25 ... (GA)	F: ACCAACTCCTAAACCACCATAACC R: GGGAGGATTTCAACGGCATTTA	54	16	0.74	0.88	1.97	215-263
BAG12	(TCG)5	F: GTCCTCCTTCACTATTCCTTTGT R: CTTTCAGGGTAATTCTGATTTGG	52	5	0.79	0.66	0.76	163-178
BAG14	(TC)7(CT)9	F: CATTGCTTCATTTTGGCTTCTA R: TTCTGATGTGAAATACTGCTGG	50	10	1.00	0.92	0.84	250-270
BAG16	(TG)8(AG)8 T(AG)6	F: CACTAACCGCAACCAATAATCC R: ATTTGCCTTCCTACCAACTCTG	54	9	0.91	0.90	1.02	293-309
BAG17	(AG)15	F: GTTGGTAGTTGTGTGATGGA R: AGTTGTATGGATAGAAAAGT	52	9	1.00	0.94	1.30	201-217
BAG18	(GGT)5	F: GGATGGGTGACTAAGAGGGAGGA R: GCAATGGTAGACAAAGTCACAGC	50	3	0.71	0.56	0.77	248-260

BAG20	(TG)9 TT(AG)13	F: TTCTCCCACAACCCTTGATGC R: CCAGGCATCCAGTCCCTTATTA	50	11	1.00	0.84	0.98	249-273
BAG22	(TC)15	F: CGACGACGATTACAACGAGT R: TGGGTTGACATTCTAAGGGTGCT	52	11	0.88	0.77	0.95	247-275
BAG24	(TC)21	F: GAATTATTCGTGTTCAAAGTCT R: CATAACAAGCAGTCAACCCATCT	52	9	1.00	0.76	1.12	242-258
BAG25	(CT)5	F: GATCTCGCCGTCGTCTCAAC R: CCAACAGGCAACAGATACAGAGT	52	5	0.50	0.62	0.86	243-265
BAG27	(TC)10 A(CA)10	F: ATGTGGAAGAGAGGATAGAATCT R: TGGAGTTAAGAGAACACAATAGA	50	4	0.91	0.77	0.69	317-325
BAG28	(AC)7	F: ACCTATTACATTGAATTCTATGA R: ATCATCTGTTAGCTTATCATAAT	52	8	0.75	0.79	0.93	302-316
BAG29	(AC)10	F: AGGCTTTGGCTTCCCTTATT R: CGGACACTTGTTCCGATTTT	52	5	0.67	0.81	1.04	143-157

Table S4. Amplification rate of 96 SSR markers for *Betula alnoides* in six related species of genus *Betula*.

Primer Name	Species					
	<i>Betula platyphylla</i>	<i>Betula austro-sinensis</i>	<i>Betula cylindrostachya</i>	<i>Betula fujianensis</i>	<i>Betula hainanensis</i>	<i>Betula luminifera</i>
BG0009	+	+	+	+	+	+
BG0029	+	+	+	+	+	+
BG0032	+	+	+	+	+	+
BG0048	–	+	+	+	+	+
BG0070	–	+	+	+	+	+
BG0086	+	+	+	+	+	+
BG0091	+	+	+	+	+	+
BG0096	–	+	+	+	+	+
BG0106	+	+	+	+	+	+
BG0118	+	+	+	+	+	+
BG0119	–	+	+	+	+	+
BG0121	–	+	+	–	–	+
BG0128	+	+	+	+	+	+
BG0129	–	+	+	+	+	+
BG0148	+	–	+	+	+	+
BG0163	–	–	–	–	–	–
BG0165	–	+	+	+	+	+
BG0176	+	+	+	+	+	+
BG0188	+	+	+	+	+	+
BG0189	–	–		–	–	–
BG0205	–	–	–	–	–	–
BG0207	–	+	+	+	+	+

BG0222	+	+	+	+	+	+
BG0236	+	+	+	+	+	+
BG0238	-	-	-	-	-	-
BG0248	+	+	+	-	+	+
BG0252	+	+	+	+	+	+
BG0260	-	-	-	-	-	-
BG0267	-	+	+	+	+	+
BG0295	-	+	+	+	+	+
BG0296	+	+	+	+	+	+
BG0299	-	-	-	-	-	-
BG0314	-	-	+	+	+	+
BG0324	+	+	+	+	+	+
BG0325	-	+	+	+	+	+
BG0328	+	+	+	+	+	+
BG0329	-	-	+	-	-	+
BG0350	+	+	+	+	+	+
BG0354	+	+	+	+	+	+
BG0362	+	+	+	-	-	+
BG0367	+	+	+	+	+	+
BG0377	+	+	+	+	+	+
BG0386	+	+	+	-	+	+
BG0392	-	+	-	-	-	-
BG0395	-	-	-	-	-	-
BG0397	+	+	+	+	+	+
BG0400	+	+	+	+	+	+
BG0407	-	+	-	+	+	+
BG0412	-	-	+	+	+	+

BG0415	+	+	+	+	+	+
BG0416	+	+	+	+	+	+
BG0419	+	+	+	+	+	+
BG0422	-	+	+	+	+	+
BG0427	-	-	+	+	+	+
BG0432	+	-	-	-	-	+
BG0434	-	-	+	+	+	+
BG0437	-	-	+	-	-	+
BG0456	+	+	+	+	+	+
BG0461	+	+	+	+	+	+
BG0463	-	+	+	+	+	+
BG0470	+	+	+	+	+	+
BG0476	+	+	+	+	+	+
BG0478	+	+	+	+	+	+
BG0479	-	+	+	+	+	+
BG0485	-	+	+	+	+	+
BG0497	+	+	+	+	+	+
BG0505	+	+	+	+	+	+
BG0509	-	-	-	-	-	-
BG0514	+	+	+	+	+	+
BG0524	+	+	+	+	+	+
BG0525	+	+	+	+	+	+
BG0533	-	-	+	+	+	-
BG0536	-	-	-	+	+	-
BG0540	-	+	+	+	+	+
BG0544	-	+	+	+	+	+
BG0545	-	-	+	-	-	+

BG0546	+	+	+	+	+	+
BG0547	+	+	+	+	+	+
BG0548	-	-	-	-	-	-
BG0550	-	-	+	+	+	-
BG0551	-	+	+	-	-	+
BG0554	+	+	-	+	+	+
BG0559	-	+	+	+	+	+
BG0563	-	+	+	+	+	+
BG0566	+	+	+	+	+	+
BG0572	-	+	-	+	+	+
BG0573	-	+	+	+	+	+
BG0574	-	-	-	-	-	-
BG0577	+	+	+	+	+	+
BG0583	+	+	+	+	+	+
BG0589	-	-	-	+	+	+
BG0592	-	+	+	+	-	+
BG0598	-	+	+	+	+	+
BG0606	+	-	+	+	+	+
BG0888	-	+	+	+	+	+
BG0893	-	-	-	-	-	-

Note: +, present of PCR amplicons; -, absent of PCR amplicons.