

Supplemental Table S1. Repeat motifs, amplicon size, primer sequences and annealing temperatures of simple sequence repeat markers developed from the 'Jefferson' hazelnut genome sequence.

Locus	Repeat motif	Size	Primers (5' - 3')	T _m (°C)
GB401	(AACC) ₄	183-196	[6FAM] CCTTTTCGCTCATCATATCCA TTTGTGTGTGGGTGTAGATTCC	60
GB402	(ACGC) ₄ (TCCT) ₄	166-170	[HEX]AGTACGAAAACGCGTGTCAAA AACAAACAAAACAAACGCC	59
GB403	(ACGT) ₄	152-156	[HEX]TAATAAATGGCTCCCGAAGAGA GGGTTTAGAGAAGCTCCCTCAT	60
GB404	(AGCA) ₄	122-126	[6FAM]AGAGGGCTCGGCTCTACATAA CTCGATCTCATCCTTGCTTGTT	60
GB405	(AGCT) ₄	173-177	[HEX]GGCCCTATAAATACCTTCTTCTCC CTCTCTCTCTCTCTCTCAAGCC	59
GB407	(AGGG) ₅	175-191	[HEX]CACAGCCTTCTTCCATCTCTTT TGCTCTCTTTTCTTCTCTCTGC	59
GB408	(AGTG) ₅	158-166	[HEX]AGATCAGCTAGAAGCAATTCGG TTGGATAACTTGGGGCTGTTT	60
GB409	(ATCC) ₄	157-161	[HEX]TCTCCTCCCCTCTCATCCTT AACGGCTGAAAAGAATAGCATC	60
GB410	(ATCC) ₄ AG(CCAT) ₄	157-173	[HEX]CCTCTACTATCTAGGAAGCCCCA ACTTTGGCCTTTTGGACTTTG	60
GB413	(CCAG) ₄	187-197	[6FAM]CTGCTTCATGTGGAAATGTTGT ACATAGGGTAGAGCTGTGGAGC	60
GB414	(CCAT) ₆	106-118	[6FAM]CAAGAGAGAGGGATGGTACGTT AGAGGAAGAGGATTGATGGATG	59
GB416	(CCTC) ₅	239-257	[NED]ACCGTATGCTGATTTGTATGGG CTGTGTTCTCTTTTCTCTCCAC	60
GB417	(CTAG) ₄	174-178	[6FAM]TACTGTGAAATGTGGTCACTGC ATGTTGCAGAATTGAAGGAAAA	59
GB418	(CTAG) ₅	205-217	[6FAM]TATTGGAGCCACAGAAGACGTA GAAGCGCACTGGAGTTTATTTT	59
GB420	(CTAG) ₇	211-227	[NED]CAATAGGTGTAGATGACGTGGC AACGAGTTTAAGCAACAATCCC	59
GB421	(CTGC) ₄	230-232	[NED]AGAGACCGCCATCATTCTAAAG ATTAAGATCACAACCTGGCTGGG	59
GB422	(CTTC) ₄	221-237	[6FAM]CTCTCTCCTTGGCACTCACAC CTTTGATGGGTTTGTCTTTCT	60
GB423	(GAGC) ₅	285-297	[6FAM]GTCAAAGCTGAGGAATGGTTTT TCGGTTGTCACTTGGTCAATTA	59
GB424	(GATA) ₅	278-286	[6FAM]ATCACCTCACATGACACACCTC GCTGAAGAGCCATAAACAGACC	59

Supplemental Table S1 (cont'd).

Locus	Repeat motif	Size	Primers (5' - 3')	Tm (°C)
GB425	(GATG) ₄	295-299	[6FAM]CTTAGGTTTACGTGGCTGTTCC TCCGAGGTGTGATGTTAAGAAA	60
GB426	(GCCT) ₆	285-300	[6FAM]AAACTGGAAGAGAAAAGTGCGAG GAACTGACCTGGCTTGAGTCTT	60
GB427	(GCTA) ₄	199-203	[6FAM]TTCTTCTTCTTCTTCAAACGCC TAAAAGCGTGGCAGTAAATCCT	60
GB428	(GCTA) ₅	240-244	[NED]TGATCTGTGTAAGGGAAAGAAGC TAATGGACCCAAAGAAACCAAC	59
GB429	(GCTA) ₆	241-265	[NED]TCCTTCTCCAAACATCTTGA TCTAATCCATCCACAATGGTTC	59
GB430	(GGAT) ₄	292-304	[6FAM]CTGAGCAAGCCAATAAAGCAT ATCCGGTTCTTCCACAATACAT	59
GB431	(GGCA) ₄	368-379	[6FAM]TCATAGCAAAGGGAATCATCAC GTTTATTGTGGTGTGGGTTCTG	59
GB432	(GGGA) ₅	312-321	[HEX]AAACAAGGGAAATCGTGCC AGGATGAGCTGTGAAAGAAAGG	59
GB433	(GGTT) ₅	147-152	[6FAM]GTCAAACCGTGGTAAAGGAAAA AGAAACCCGAACCTAACCTAGC	60
GB434	(GTAT) ₅ (CATG) ₄	335-347	[HEX]AACCATCTCCCTTCTCTGTTGA GCCGAGGTGAGTAAATGGATAC	60
GB435	(GTAT) ₅	89-98	[6FAM]ATTCTATTTCGCACCAAGCAAG ACTTTACCATCACATCAATGGC	59
GB436	(GTCG) ₅	122-126	[6FAM]AACAGCAAACTACCGATGGAT CTCGTGCAAATGTTGAAAAGTC	59
GB437	(GTGA) ₇	334-340	[HEX]GCTTCTTGGAGGGTTCTGC GCCAGAGCGTAAGAGAGAGAGA,	59
GB438	(GTGC) ₄	311-319	[HEX]AGAAGAAAAGAAGGGACTGAAGC GCTGGTATGAAATTAGCCAAGG	59
GB441	(TGCG) ₅	178-182	[HEX]CATTGCCATCGGTGTATGTG ATGCTTTGGGGCTTCTAAATCT	60
GB444	(GTCT) ₅	305-321	[6FAM]GCAGAAGCAAACAAAACATATCG TGTCAGGGTTAAGGACTGTTCA	59
GB445	(AGAC) ₄	135-139	[HEX]CCATACTTGCTTCAGAGATGAGAA CGAGCTTACATGGATTTTGGAT	60
GB446	(CCAT) ₄	130-134	[6FAM]AAAGGGTCTGGTTAATGAGTGC GCTCTCTTCGCTCAAAGTACAA	59
GB447	(AAGCA) ₄	172-187	[NED]TGGTAAGAGCATTAACCCACAA AGCTGGCAATGAAACATCTTCT	60

Supplemental Table S1 (cont'd).

Locus	Repeat motif	Size	Primers (5' - 3')	Tm (°C)
GB448	(ACACA) ₄	179-184	[NED]ATTCGTTTCATCCCCATTACTTG ACGTCCAGAAAACAAACATCCT	60
GB450	(AACC) ₅	327-339	[HEX]GACAACTAGGTGGCAAACAGC TTTAGTTGATTGGCTGGAAGAA	60
GB452	(ACGC) ₅	203-214	[6FAM]TATACCATCCCCGTTTGCAT CTATCCAGCTGCCATGTGAA	60
GB454	(AGCC) ₅	245-249	[NED]GCGTGGATCAAAGATTGTCA CTCCGGGGAGAACTGTGTA	60
GB456	(AGCT) ₅	104-112	[6FAM]AAAAGCCACACCCACTTCAC GGATGGCTCAACACATACCA	60
GB457	(AGGA) ₄	197-201	[6FAM]GACAATCAGTGGCTGCAAAA TTGTTGTTGTTGTTCCAAAGC	59
GB458	(AGGC) ₄	295-302	[6FAM]TTAGCTGGCTGGTTTGTGTG AGCGTTGAGGAAAAAGGTGA	60
GB461	(CCTG) ₅	273-281	[6FAM]CTAAATCGTGCCGTTGGTTT TTCAAACCTTGGTGATCCGTAA	60
GB462	(CGCT) ₄	224-234	[6FAM]AAACCCTAGGCGAAATCGAG TCCAAACGAACAACACGAAA	60
GB463	(CTAG) ₄	283-296	[6FAM]TGCAGGTACTCCAGCTCCTT TAAGTTGGCTTGGTGGTGCT	60
GB465	(CTCA) ₅	263-277	[NED]GGCGGAGCTAATAGGAAACA TGTGGGTCAATGTGGGTTC	60
GB466	(GAGG) ₄	102-110	[6FAM]TCCATGATCAGGTCTGCTTG TCATCCCATAGAGCAAACCTCAA	60
GB467	(GCAC) ₄	336-352	[HEX]AAAGGACAGGCTGCTTTCAA TGAGGTTTTAACC AAAACACAAAA	60
GB468	(GCAT) ₄	355-377	[HEX]GTCGGACGGCTAATGAAGAA CACACAAC TATTTGGGTTTGAA	60
GB469	(GCAT) ₅	328-340	[HEX]GCTAGCGTGTCACTCTGAGGAT AGACCGAAACTGGTGCATTT	60
GB470	(GCGA) ₄	381-400	[6FAM]CAAACCTTTGACCTCCTCCA GGGCCAAACAGAAACAGAGA	60
GB473	(GGGA) ₄	189-198	[6FAM]GGGGTCCCTTAAACGAAAAA GAGACGATTAAATCAACAGCTTG	60
GB475	(GTCT) ₅	183-187	[HEX]GCTTTGGCGAGAACTACGTC CTGCAAATGCCCAATGAAAT	60
GB476	(TGCA) ₄	295-298	[6FAM]TTTTGGCTTTTGGGTTTGAA CCCATTCCATTGCTGTTTCT	60

Supplemental Table S1 (cont'd).

Locus	Repeat motif	Size	Primers (5' - 3')	Tm (°C)
GB477	(TGCA) ₄	337-345	[HEX]TTTATGGCCTGCATTCCTC GAGAAGATGCTGGGGAGGTT	60
GB478	(TGCA) ₆	383-394	[6FAM]AGGCGTCTCACCCAATAAAA TGTTTTAGCCCCAAGAATC	60
GB480	(TGCT) ₅	263-277	[NED]TGGAGGCACCCCAACTAATA GGGCCTTTGAGAAAAACAAA	60
GB482	(TGTA) ₄	132-140	[6FAM]TGTTTCATTTTCTTTCGGATCTT TCAGTTGGGGGTAGAGATCG	60
GB483	(TGTA) ₆	355-359	[HEX]TAATGCCATGAACCACCAAAA AGACGTTTCCTCTGCCAAAA	60
GB501	(ACCCA) ₅	178-188	[6FAM]TCCACTTTGTTTAGATCCTCTGC AAAAGCGTGTGTTCAAGAGTCA	60
GB504	(AGAAG) ₄	178-193	[HEX]ACCCCAAGAGGTGTTTGGTATT GAAACGTGAATGGTGGACAAGT	60
GB505	(AGAAG) ₄	271-286	[6FAM]TCTTGAGACCTCAATGCACTA TTGGACTCTCATTATTCTACGGC	60
GB526	(CATCA) ₅	88-98	[HEX]CAACCGCCATTTTCAATCTACT AACGGCTGACGAAGTTGC	60
GB527	(CCATT) ₄	110-125	[HEX]GGAAACAGAGCAGGAAAAGGAT GGTTAAGATCGTTGTGGGACAT	60
GB532	(CCCTC) ₄	360-377	[HEX]CTCTTCGTGGTTTGGGTAAAA AGGCGATTCTTTGGATGAGTT	60
GB533	(CCCTC) ₅	121-131	[HEX]GTCAGTCCCAGTGATCCAGAG CTGAAAACAATAGGGTGGTCCT	60
GB535	(CCTGC) ₄	203-218	[NED]ACTTGACACTTGGCACTACAGG GGGTTTTGATATTCCTTTCACG	60
GB537	(CCTTG) ₄	181-186	[6FAM]GTCCTTTTCCAATCTCTTTCCC GGAGGTCAGTAGAGCAAGGTGA	61
GB544	(CTGCA) ₅	389-394	[6FAM]CTGGGCATGATAAAACCATAAG ACGGAGGCAGAGCATAAGTATT	60
GB545	(CTGGT) ₄	190-195	[HEX]ATTCCCTCACCACCCATTTT AAAGGTGCATGACAATTACGTG	60
GB548	(CTTTG) ₄	146-151	[6FAM]GAAACTCTCTCACAGCAATTTCG ATGGTGAATGATCTCCCTAACA	59
GB551	(GAAAG) ₄	121-131	[HEX]CCTCGATAAAGAGAGAAGTGGC GAAGGAAAACATCACGCAATAG	59
GB560	(GAGAA) ₅	164-174	[6FAM]AGAAAGGGAAGAAACGACCAC GCACACACACACACAGAGTT	60

Supplemental Table S1 (cont'd).

Locus	Repeat motif	Size	Primers (5' - 3')	Tm (°C)
GB563	(GAGAG) ₅	185-195	[HEX]GTCAAGTCTCAGGTAGATCGGC ATCGTTCAGATTGGTACACGG	60
GB565	(GAGGG) ₄	176-181	[HEX]AAGCAGTATCTTCCGACCAAAA GCTCTTTCTCCAACCATTGTCT	60
GB568	(GATGT) ₄	90-108	[HEX]CAGGACATGGAGCATTAGAACC CATGCACGGCCATTGAGT	62
GB577	(GGCCC) ₄	165-170	[6FAM]CTCCTATACCAGGCCACATCC TGGAGTAGTTGCAGAGTGATGG	61
GB580	(GGGTT) ₄	184-189	[HEX]TGTGCCTGATGAAAATACTGGT CCTAATGGGCTTCTTGGTGTAG	60
GB581	(GGGTT) ₄	105-115	[HEX]AGCTTAATCGCCGGATAGTG AAGATGATGAACCCATTCCAAC	60
GB587	(GTGCG) ₄	175-185	[HEX]TAGTTGTCTAGGGTTTTGTGC GTCTTGAGCTGGTCCTTGAAAT	60
GB594	(TATGC) ₅	172-186	[6FAM]TGGTCTTACTCTCCTCGTAGGG GTGTTTTGTGATTTCAGCAGGA	60
GB601	(AATTCC) ₄	157-169	[HEX]CCACTCCACTCTCCCTATCTTC AATCTGGTTCTGGCAAATGG	60
GB602	(CAATGT) ₄	234-246	[NED]CCGATGGAGATCGAAAGAGA GGCGCGATTGTAAATCAAAA	60
GB603	(CCCAAG) ₅	162-180	[HEX]AGAAAGAGATAGGCTTTTGGGC AATACCTCCTACATAGCCACCG	59
GB604	(GTGACA) ₄	191-197	[HEX]GAGACCAGTCGCATGAAGAAAT GGAAGTTTAGGCACCAAGGAC	60
GB605	(TAGCCA) ₅	118-124	[6FAM]TCGATAGTGGGCATTCTACAAA CAAACTCAAAGACAAGACGC	59
GB606	(CTTCTA) ₄	316-330	[6FAM]AAGGAGGAGTGTCTTACCC TCCATGACAATCACTGCAGAA	60
GB609	(GAAATT) ₄	311-341	[6FAM]TTTTTGGAGCCAGAGAATGC ATGGAGTACCGCTCGTATGG	60
GB610	(CCAAAC) ₄	86-103	[6FAM]GAACACCCCAAGTAGATCCAAC GAATCATGCTATGTCAATGGCT	59
GB613	(GATTGT) ₅	121-139	[6FAM]GGTGAAGGTCTAGTTTTGTGCC GCCGTACCACGTCTAAAGAAAG	60
GB614	(GGTTGA) ₄	365-371	[HEX]TAAACCTGCACATTTCGTCAACT CTGCTTTGTGCTTCTCATTT	60
GB615	(CAGGCT) ₅	269-287	[NED]GACCAGGAACAGGAACAGGA ACGAGAGCCGTCTTCAAAAAG	60

Supplemental Table S1 (cont'd).

Locus	Repeat motif	Size	Primers (5' - 3')	T _m (°C)
GB616	(CTCCTG) ₄	359-365	[HEX]AAGTCAGAAAACCTGAAACCCC GTTGCTATGAGATGGTTGCTTG	60
GB617	(GCAGAG) ₄	100-118	[6FAM]TCGTATGAAGTGCAAGAGGGTT CTCTCAGCTCTCACCCCATGT	61
GB618	(GTCCCA) ₄	322-328	[6FAM]GACGACATCGTTTCCTGCTT CAAGTGTCACACCGAACCAC	60
GB619	(ACTAGG) ₅	138-150	[6FAM]AGAGGAAGAGAGAGGGTTTCGAG CCACTCATCACACGCTAACATT	60
GB620	(TCACTT) ₄	199-221	[6FAM]TCTTGGGCTCCAAGCACTAC TACGCATTTGGACGTCTCTG	60
GB621	(GAGTCG) ₄	100-117	[6FAM]ACTCTTTCAGCACCCCTCTCCTT GGAACCGCTCTCGGTGAT	61
GB622	(CCACAA) ₅	113-125	[6FAM]CAAACAAGAAAGATGGGTGAGC CATAGTGTCTGCGTTGGGAACT	60
GB623	(TCCTTC) ₄	377-383	[HEX]CATCAATCAGAATCACTGCCAT TAGGAAAAGGGTAAGGTCGTCA	60
GB624	(CAAGAC) ₄	263-269	[NED]ACCTCAAATCTATGCAAAACGC AGGTGGAATCTCTGCTCACAAAC	61
GB625	(AAGCCC) ₄	224-244	[6FAM]CACGAGGAGACTGACGACAA GCGACCTTTGGAGTTGAGAG	60
GB626	(CTGAAC) ₄	139-146	[HEX]TCTATCTCCTCCTCCATACTCCG CAACCTCTCTGTTGGGCTTG	61
GB627	(CTCTTC) ₄	348-360	[HEX]GCAGCAGGTTGTGTCCACT ATTTGCGTCTTCGTAAGTTGGT	60
GB628	(GTGATG) ₄	342-360	[HEX]GCCAGTTCAAAAGATTCCATGT AAAACCCAAACATCATAAACCAA	60
GB631	(TTCTCT) ₄	92-98	[6FAM]CAACAGAGCTAAACGAGAGGAAA CGAAATGAGCTTCGACTAGGAT	60
GB633	(GGGATA) ₄	116-122	[6FAM]GTCAATCCCAAAGACGATAAGC TCTGGTGCGACTAACATCCTC	60
GB634	(CGAGAG) ₄	375-386	[NED]AAAACCACGATTGGAGATGG AAATACCGTCCATCGTGTGG	60
GB635	(GTCGTT) ₆	130-144	[6FAM]CCCATAAAACCTAATCCCCTTT CTGCTATGAATACGAAACGCAA	60
GB636	(GAAGAG) ₄	250-262	[NED]GCTTCTCTGTCCTCCACACC TCACCGTAATCCTCGTCCTC	60
GB638	(GTGGGA) ₅	318-324	[6FAM]CACGGTGCAGCTCTTATGTG TCTAGGTTTGTGTCCTGTGAATG	60

Supplemental Table S1 (cont'd).

Locus	Repeat motif	Size	Primers (5' - 3')	T _m (°C)
GB639	(CATCCA) ₄	362-374	[HEX]TCTCGGCAGCAGCAAGAT TTCTTTTGGTCCTTAGTGCGAT	60
GB640	(GAAGCC) ₄	346-360	[HEX]GGCCCTTTCTCCGTAAATAAAC GTGGATGCAGTTTGAATGTCAG	60
GB641	(ACACTC) ₄	139-152	[HEX]GTTGTAGCTGAGGGAGGGTCTA AGCCTAATTTGCGGGGAA	60
GB642	(GCAACA) ₄	361-367	[NED]CGATCCCTCCGAAACTGTTA TCGCAGAGCACGTAGATGAC	60
GB643	(CAGCCA) ₄	232-250	[NED]TGAAAGGTAGCTGATGGGGTAT AAGCGTCCATGACAACAAAAC	60
GB644	(CACTCC) ₄	239-257	[NED]TCAGACACCTGATCCCAAAAC GCGTGGTATTAAAGGGAGAGTG	60
GB645	(AATGGC) ₄	286-298	[6FAM]TTAACGCAGGTGGGTTGAAT ATTGATTTGCATGCACCGTA	60
GB646	(GCCTGT) ₄	273-291	[6FAM]GTAGCAGACGCAGAGTCACG GAGAGGCATGAGAGGTCTGG	60
GB647	(GTTTGG) ₄	165-177	[HEX]CTTCTCTGGCGATCAAGAAACT TCAAATATCACGTTCTCCTCC	60
GB648	(CTCTCC) ₅	257-277	[NED]CCTTTTACCAACAGCCCTCTTA CCAACAAACTCACAATAGATAGCG	60
GB649	(GTGAGT) ₅	251-264	[NED]GGACATCTTTGGTGAGATGTGA TAGCTGAGGGAGGGTCTACG	60
GB650	(CATGGG) ₄	314-332	[6FAM]TTAACCCAGCCGAGTTTCC CTCTCGCGTACACATGATCC	60
GB652	(CCACAA) ₄	210-230	[6FAM]CAAACGCTGGCCCTTTATTA CTGTTGAGCTTGCAGAGAATG	60
GB653	(GATGGT) ₄	199-209	[6FAM]AGGTTTTGATTTTGCCATCG TCCACCATTGGAATCCTACC	60
GB654	(AGGGAG) ₄	273-279	[6FAM]AGGGGTCCATCCCATTAGAA ATCTTTCTGGTTGCAGCTTGAT	60
GB655	(AGCCCG) ₄	235-253	[6FAM]TCATATCTGGCTACTCAGGCAA GACTCTGTCTGGCAACATTT	60
GB657	(CACTCC) ₄	192-203	[6FAM]ATAGCCCTCCATGCCACTACT CGTAAATGAAACAAGCCATCTG	60
GB658	(TCCACC) ₄	330-351	[HEX]ACCACAAAATCAAGCCTTCG CAAGTGAAAATGGGCCAGAT	60
GB659	(CACTCC) ₄	210-222	[6FAM]AATAGCAAAGGAAGCAAGGACA GTTGGTGTGGGGAGATGAGT	60

Supplemental Table S1 (cont'd).

Locus	Repeat motif	Size	Primers (5' - 3')	Tm (°C)
GB660	(GACGGT) ₄	209-221	[6FAM]GGTCTGTGTGGCTCCTGTTT GTTTCGTAGAAGCGCAGGTC	60
GB661	(AAGGAG) ₄	205-217	[6FAM]AGCTTTCACGAGACCCAGAA GCCAAAGCCCATATCAGAAA	60
GB662	(TGATGC) ₄	252-264	[NED]GGGATTGAGTTGGCCCTAAT AGCCGAAGGATATCGCTGA	60
GB663	(TCTTCC) ₄	133-139	[HEX]GCACTCTTTGTAGATGACCATGA GGTGGGGATAAGAAGAAGATGA	59
GB664	(GATGCC) ₄	302-308	[6FAM]AATAAGAAAAGGCCCGAGGA TTTAGCCACATTTGCCATT	60
GB665	(GTGGGC) ₅	175-193	[HEX]AAGGAAGGTAGCTGTTGTCGTC TATCCTCAACGTATCCACCTCC	60
GB666	(CCACTT) ₄	181-196	[HEX]CTGCTTGCCTGAGACGAAT GCAGACCCATTACACAGAGATG	60
GB668	(GACTCG) ₄	177-183	[HEX]AAGACGACGCTAACACGTTCTC TCTTCGGATTTAACACCTTTCG	60
GB669	(GGTAGT) ₄	111-117	[6FAM]GTGGAATAAGCAAGAGTGGGTC CTCTACTGTGCAGCTCGATCAC	60
GB670	(TGGCGA) ₄	253-270	[NED]AAATGGGTTTGGTGCGAA ATGTAAATAAGCGTGGGACCAT	60
GB671	(TTGGGC) ₅	234-302	[NED]TTCCAGTTTAAGACCAGACAAGC CACATTTGGGAAGACCCTAAAA	60
GB672	(GATCAC) ₄	218-230	[6FAM]AAAACATGGTGAGATTTGGGAC CATGAAAACGGCTCTGGATTA	60
GB673	(TCACCA) ₅	354-377	[HEX]CAACAATGGGAATGTTGCAG GGGCCAATAGCAAAAGTTCA	60
GB674	(CCAACC) ₄	163-173	[HEX]GCATGGTGTGAAAGCAAGAATA GAAAACAGGGGTTCGATCAAT	60
GB675	(CACCAA) ₅	344-362	[HEX]ACCTCCATTAACACGCCTTG AGAAGGCTAGGCTCACACCA	60
GB676	(ATGAGG) ₄	339-345	[6FAM]ATGGGGTTGATTGTGAGAGC GCTTGTCAAATTGGGTGGTAA	60
GB678	(CCCAGG) ₄	193-225	[6FAM]CCCATGTTCTGTTGTAGCATTT TTATGACCCATGACACGAAGAG	60
GB702	(ACCGA) ₄	181-191	[HEX]ACACTCGCTCCGAATTTTCA TTCCTCTGCTACTGCCGTCT	61
GB704	(AGAAC) ₄	107-117	[HEX]AAAGCATAAGCAGAGATAGTCAAACA GTTATTTGTTGCTATTGATTTTT	60

Supplemental Table S1 (cont'd).

Locus	Repeat motif	Size	Primers (5' - 3')	Tm (°C)
GB705	(AGAAG) ₄	217-220	[NED]CGGTGGGAATTCAAAATCTG CAGATTCAATGTTATGGTCATTTT	60
GB706	(AGAGA) ₅	369-378	[6FAM]CTCGACAGTCCTCTCCTGCT AGTTGTTTCACTGCCCTCCA	60
GB707	(AGATG) ₄	207-241	[NED]AGTCCTGTGAAATGGGTTGG TTGTTCTTCGGCTCTGTGAA	60
GB708	(CAAAC) ₄	152-172	[HEX]CTAACAGGCATGAGGCATGA TTTGTAAGAAATGGGCAACACA	60
GB709	(CACCA) ₄	261-269	[6FAM]GTGGATGACTGGACGTTGTG TTGCGGATTCTTCATCATCA	60
GB710	(CAGCT) ₄	121-126	[HEX]TTCTCTACGTGGCCGTTTTTC TGCTCCTCTCCTCCTCACTC	60
GB712	(CCAAT) ₅	124-139	[6FAM]CGCACTCTGCTTCACTTTCA GAACCCCTCGCTCTAATTC	60
GB716	(CTACT) ₅	140-151	[6FAM]ACAAGCTTGACGACCAAACC TGGTGCAAATGGGTATCAAA	60
GB717	(CTCAT) ₅	214-224	[HEX]AAGCACGTTTAGGCCTCTCA GGTGTGCACAACCTTATGTGGTAA	60
GB718	(CTCCC) ₄	393-405	[6FAM]CGAAGACAGAGAGGGAGGTG AGGGGCTTAGAGGCATGAAT	60
GB719	(CTCCT) ₅	297-311	[6FAM]TTTTTCTCTTTGGTTTTGCTTTTT TGGTCTCTATTGGGACTTTGC	60
GB720	(CTCGG) ₅	366-376	[HEX]TGGGGTGTAAGATGTGCCTA CGGGCACACACATATATCCA	60
GB721	(CTTCC) ₄	374-388	[6FAM]TCCAATAAAAACAGCGCAAT GGAAGCATATGTGGGTGGTT	59
GB722	(CTTCT) ₄	254-265	[NED]TCCTTGTGAACCTGGAGGAC CCTAAATTGGACGCGTTGAT	60
GB723	(CTTGT) ₄	257-262	[NED]CCAGGAATGTCGCTACCACT TTGTTGGTCACCTTCCTATGC	60
GB724	(GAGAG) ₄	209-221	[NED]GCTGCGTGAGACTGTGAGAG CTTGATGCGTGGCTAAAGGT	60
GB725	(GAGAT) ₅	312-317	[6FAM]CAATCAGAATTGCCCAAGGT TCAAGGAAAAGGCCAATCAC	60
GB726	(GCCAC) ₄	240-268	[NED]GGATTCCAAGTCAAGCCATC GCTCATGCACAGAGAGGTGA	60
GB727	(GCTTG) ₄	372-388	[HEX]TGATCCAAAGCACATCAGGA GCGCAGGAGAATGGTTTACT	60

Supplemental Table S1 (cont'd)

Locus	Repeat motif	Size	Primers (5' - 3')	T _m (°C)
GB728	(GGAAA) ₅	117-132	[HEX]CACGGTATTTTAATTTTGAGTCCA AAAAACTGCGGTGACTGTCC	60
GB729	(GGCGT) ₅	278-287	[NED]TCCCCGTCTAATCCCTCTTC GGTCGTCGTGGTCCTAATTC	60
GB732	(TCACA) ₄	203-208	[HEX]TGGAAAGCAGTGTGACGTTTC TCTTGCAAGTGCAAAATTGG	60
GB733	(TCATC) ₄	331-341	[6FAM]TTGCTTGCCGTACAGAACAC GCATTTTGTGGGTGCTTT	60
GB734	(TCATT) ₄	344-349	[HEX]GCATAGAGACCAGGGCAGAC ATTTGAGGCGTCCAGCATAA	60
GB735	(TCTCT) ₅	163-168	[6FAM]AAAGCAGTAGAGTCCATCTCCG TGGGTTAGTTGACTTGGGATTT	60
GB737	(TGAGT) ₅	377-392	[6FAM]AGCTGCTGTGCAGACTTTGA GGCAAGCAAAGCTGAGTTTC	60
GB739	(TGGGA) ₅	290-305	[6FAM]GATCACAAGGCGACCATTTTC GACGTTTTGGAAACGGAAAA	60
GB740	(TGGGT) ₆	336-356	[HEX]TGGCTCCAAGTATTGACATCC GAGGGGTTATGGAGCTAGCAG	60
GB741	(TTCCT) ₄	339-351	[HEX]ATCCAGAGGGCTAGGCTGTT GAGATCGATGGATGTGGTGA	60
GB742	(TTCGG) ₅	348-375	[HEX]CGGAGAGAACAGACGGAGTC GGTGGGAATTTAACGGCTCT	60
GB743	(TTGCT) ₄	204-210	[NED]CGAACGAATCTCCACCTGTT ATCTCCCCAACACAATCCAG	60
GB744	(TTGGC) ₄	131-144	[6FAM]CTCCCTCTGTGATGATGATTT GAAAAGAAAAGCCAAGCCAAAC	61
GB745	(TTGTG) ₄	313-325	[6FAM]CGTGTTCTACAGCCGATTGA CCCTACCACCATCACTTGCT	60
GB746	(TTTCC) ₄	289-299	[6FAM]AGATCGACCTGGACAAGTGC CCCCACATCCTATTCACTTT	60
GB747	(GCTTT) ₄	181-187	[HEX]GAAACTGTGGCCGATTTCTATT AGGAGAAGCAACCCCAATCT	60
GB748	(TTTGG) ₅	334-343	[HEX]CGTTTTAGCAAGGTGGGATGT TTTCCGTCCACCTTTTTGAC	60
GB749	(AACAG) ₄	269-274	[6FAM]CCCAATTGGAATCCTTGAGA TGAACCTCCATCACCACGTA	60
GB750	(AACCG) ₅	209-220	[NED]GCACACACACCAGATCCAAC GGGTTTGTAGGAGGTGCGTA	60
GB751	(AAGAG) ₄	272-277	[6FAM]GGGTTTCACCGGGAGATATT CTCTCCCAACAAGACCCAAA	60
GB752	(AGCAA) ₄	350-358	[HEX]GCAGCTTTTCCTAAGCTCCA CATGCCTCAAACCTCCCAAAT	60