

**Table S1.** Data on 25 SSR loci and their PCR primer pairs used to genotype *Fragaria* and *Rubus* specimens.

Locus	Gene	GenBank accession number	Motif and number of repeats	SSR location	Primer binding site location <sup>1</sup>	Forward (F) and reverse (R) primer nucleotide sequences	T, C°	Allele size, bp		
								expected	in <i>Fragaria</i>	in <i>Rubus</i>
<i>RiG001</i>	aromatic polyketide synthase (PKS3)	AF292369	(AT) <sub>6</sub>	in	in-ex2	F: TGTCCGATCCTTTCTTTGG R: CGCTTCTTGATCCTTGACTTGT	55	345	-	0, 349, 351
<i>FaF3H01</i>	flavonoid 3'-hydroxylase	KC708489	(AT) <sub>8</sub> (AACAA) <sub>2</sub> (TTCTT) <sub>2</sub>	5'UTR	5'UTR-5'UTR	F: TCCACATCTCTCTCCCATTCAT R: GGTGTGCCGAAGAGTTAGTAGG	60	359	300-357	-
<i>FaFH01</i>	flavanone 3-hydroxylase	AY691919	(ATTTT) <sub>2</sub>	in1	ex1-ex2	F: TCATCGTTTCCAGCCATTTAC R: ATGCCTCCTTCTCTAAACCCAT	60	376	346-378	0, 341-372
<i>RcFH01</i>	flavanone-3-hydroxylase	EU255776	(TATG) <sub>3</sub>	in2	in2-ex3	F: GGTCCAAGTGCATTCCATATTAC R: GTTCTTGAATCTCCCGTTGCT	60	262	-	0, 255-299
<i>FaFS01</i>	flavonol synthase	DQ834905	(CT) <sub>12</sub> -(CA) <sub>12</sub> (AAGAC) <sub>2</sub>	in2 ex3	ex2-ex3	F: CATCCCTAATGCCCTAGTCATC R: TGTACTTCGGTGGATTCTCCTT	60	304	272-315	0, 291-336
<i>FaFS02</i>	flavonol synthase	DQ834905	(GGAAG) <sub>2</sub>	ex1	ex1-ex1	F: AAGCTCCTCAAACAAATCTTCG R: GTAGTTAATGGCAGAAGGTGGC	60	273	253, 271	271
<i>FaDR01</i>	dihydroflavonol 4-reductase	AY575057	(ATT) <sub>14</sub>	5'UTR	5'UTR-5'UTR	F: GCCCACCTCGTAACCTTGTACT R: CTTTCATGGGTGTCTTGTTGT	60	263	0, 237-293	-
<i>RhDR01</i>	dihydroflavonol 4-reductase	JF764809	(TTGT) <sub>3</sub>	in2	in2-in2/ex3	F: TTTGTGTTTGAAGGAGCACATC R: ATTGCTTACCCAACCAGTCATT	60	400	-	-
<i>RhDR02</i>	dihydroflavonol 4-reductase	JF764809	(CTTCC) <sub>2</sub>	in1	ex1-in1/ex2	F: ATTCATCGGCTCTTGTTTATG R: CTTACCTTCTTCTGATTTCGCT	60	191	-	-
<i>FaLR01</i>	leucoanthocyanidin reductase	DQ834906	(CAAAT) <sub>2</sub>	in2	ex2-in2	F: ATCACCTAGTCGAAGCCATTA R: GGTCATCAGTCCAAACACAGAA	60	138	0, 126-136	0, 134, 136
<i>FaAS01</i>	anthocyanidin synthase	AY695818	(CTTGG) <sub>2</sub>	ex2	in-ex2	F: ATACGTTTTGCTAAGTGGCGTC R: CTGAGGGCATTGTTGGGTAGTAG	60	211	207	-
<i>RiAS01</i>	anthocyanidin synthase	KX950789	(ATCTC) <sub>2</sub>	ex2	ex2-ex2	F: TCAACAAGGAGAAGGTGAGGAT R: CCGTTAGGAGAGATGAAAGCAG	60	334	261-333	261-357
<i>FaAR01</i>	anthocyanidin reductase	DQ664193	(TGCTG) <sub>2</sub> (CATTT) <sub>2</sub>	ex4 in4	ex4-ex5	F: AATCTGCTTCTGGTCGGTACAT R: AGAGAGTATGGTCTTCGCCTTG	60	244	227-242	250
<i>RhAR01</i>	anthocyanidin reductase	KR732618	(GCTGC) <sub>2</sub>	ex5	ex5-ex5/in5	F: AATCTGCTTCTGGTCGGTACAT R: GGTTAAAGGGAGGGCTTACTCA	60	122	-	-
<i>FaFG01</i>	flavonoid 3-O-glucosyltransferase	AY695816	(TACG) <sub>3</sub> (CGC) <sub>4</sub>	5'UTR ex1	5'UTR-ex1	F: CTGAAGAGTGGTTGTTGGATTG R: TGCTTGGTGTGAAGAAAGAGA	60	323	293-345	-

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								expected	in <i>Fragaria</i>	in <i>Rubus</i>
<i>RhUF01</i>	UDP-glucose flavonoid 3-O-glycosyltransferase-like protein	JF764808	(GAG) <sub>7</sub> (ACAAGC) <sub>2</sub>	ex2	ex2–ex2	F: AGGAGCTGAAGAAAAGACTCCA R: AAAGTCCTCTAGGTTTCCCCTG	60	275	-	267-279
<i>FaMY01</i>	transcription factor MYB10	EU155162	(TTTAT) <sub>2</sub> (GT) <sub>5</sub> (TA) <sub>6</sub> (TA) <sub>5</sub> (AAATC) <sub>2</sub>	in2	in2–in2	F: CTACGGCTTATTCTTGCCTAGC R: TGTCAAACCTACACCGTTCAAG	60	383	0, 370-385	-
<i>FaMY02</i>	transcription factor MYB10	EU155162	(AT) <sub>32</sub> -(GT) <sub>5</sub> (TTTCT) <sub>2</sub>	in2	in2–ex3	F: TTGAACGGTGTAGGTTTGACAT R: TTCTTCACATCATTGGCAGTTC	60	310	0, 267-335	-
<i>RiMY01</i>	transcription factor MYB10	EU155165	(TAATA) <sub>2</sub> (CT) <sub>7</sub> (AT) <sub>15</sub>	in1	ex1/in1–ex2	F: GTTCCTCTCCAAGCAGGTTATT R: TGCAAAGTCTCCTCTCTTGATG	59	330	206-239	0, 228-385
<i>RiHL01</i>	basic helix loop helix regulatory protein (bHLH)	EU862822	(TACTA) <sub>2</sub>	in	ex1–in	F: TTGCAGAGGAATGAGCAACTTA R: CAAACTATGGAACAAACGAGGA	60	336	291-299	286-338
<i>RiTT01</i>	transparent testa glabra 1 (TTG1) protein	HM579852	(CAC) <sub>5</sub>	ex	ex–ex	F: ACTCCACACAAGAATCCCATCT R: CTGTTGTTCAAGACCGAAATTG	60	379	-	379, 382
<i>FaCH01</i>	class II chitinase	AF147091	(CAAAA) <sub>2</sub> (CATCTT) <sub>2</sub> (TCTTCC) <sub>2</sub>	ex1	5'UTR–ex1	F: TGCTGATGCTAACTTCCTTTGA R: ATGCAGTGTGCTCCTTGTGTAG	60	324	310-329	0, 320-329
<i>FaCH02</i>	class II chitinase	AF147091	(AATTAT) <sub>2</sub> (AGGCA) <sub>2</sub> (GAAGCC) <sub>2</sub>	ex2	in–ex2	F: TGAGAAATGGATGTTGTTCCAC R: AGCACATATCGACCTACCATGA	60	279	259-282	-
<i>FaTG01</i>	ToyoGluIII gene for β-1,3-glucanase	AB106362	(TCAAGT) <sub>2</sub>	ex2	ex2–ex2	F: AGGATGAGGATTTATGAGCCAA R: AGGGTCCAAAAGGGTTGTATCT	60	327	309, 324	318-336
<i>FaBG01</i>	β-1,3-glucanase (BG2-2)	AY989818	(GAGAG) <sub>2</sub> (GCGGGA) <sub>2</sub> (GA) <sub>9</sub>	5'UTR	5'UTR–5'UTR	F: TTACCTAGCTCAAGAGGGAGCA R: GTTTGGAAAGCCACACTTTT	60	364	328-388	-

<sup>1</sup>based on the reference sequence; in – intron, ex – exon