

Supplementary Table S1. Sequence of primers, number of loci and number of polymorphic loci of amplification products generated with 103 SSR primers across boysenberry genotype.

Marker	Primer sequences		Number of loci	Number of polymorphic loci	Polymorphic rate (%)	Reference
	Forward	Reverse				
EMFv8	TGACCCGATACAAGACAAAACCG	CACTCATGTCGGTAGCCATTCTC	1.00	0.00	0.00	Castro <i>et al.</i> (2013)
EMFxaACO1B	GCCACTCCATTGTTATCAACC	GTTTGCTCCACACTCTGTACTTCC	1.00	0.00	0.00	Castro <i>et al.</i> (2013)
EMFxaCAD1B	GAATGAATGGGGTTTCTCTACC	GTTTGCTCCCTACTTCTGTA ACTTCACC	1.00	0.00	0.00	Castro <i>et al.</i> (2013)
mRaCIRRIV2A8	TAAAAAGGCGCAACAGTCG	AGACACAGAAACAGGCATCG	1.00	0.00	0.00	Castro <i>et al.</i> (2013)
ERubLR_SQ01_B06	CCTCTACACCACCCCATCAG	CGTCATCGTCATCTCTCTCG	1.00	0.00	0.00	Woodhead <i>et al.</i> (2008)
ERubLR_SQ01_F09	GGCATAACCAAGACGTTCTC	GTCTTTGGTGGTGCTTGAGG	1.00	0.00	0.00	Woodhead <i>et al.</i> (2008)
ERubLR_SQ01_G16	GCACCCTAATCTCCATGACC	CCGCTGTAGTTCCTGTAGGC	1.00	0.00	0.00	Woodhead <i>et al.</i> (2008)
ERubLR_SQ01_I08	GCTTCAGGAAGCTCGATCAC	TCACCTAAGCACCTAATTAAGGAAG	1.00	0.00	0.00	Woodhead <i>et al.</i> (2008)
ERubLR_SQ01_I20	TCTTTTGCGGTGGCTACAAG	CAACCCGAAGTCTACAACAGC	1.00	0.00	0.00	Woodhead <i>et al.</i> (2008)

ERubLR_SQ01_M20	TTACGAACACCCATTAATTTAAGTC	AATCCTGAGACCGACGAGTG	1.00	0.00	0.00	Woodhead <i>et al.</i> (2008)
ERubLR_SQ01_N03	GATTCAAATCCAGTAGACCAGTACC	CATTGAGACCCACCTCTTGG	2.00	2.00	100	Woodhead <i>et al.</i> (2008)
ERubLR_SQ01_P18	CCACTTTATTTGATTTATTCCATCC	ACGGACAAAAGTGGGTATGC	1.00	0.00	0.00	Woodhead <i>et al.</i> (2008)
ERubLR_SQ02_B19	CTCCGCAGACATTCCTTCTC	GCTTCAGGAAGCTCGATCAC	1.00	0.00	0.00	Woodhead <i>et al.</i> (2008)
ERubLR_SQ053_E02	GTCACACAAGGCTACCAAG	ATTGAACTGGTCAACAATGC	1.00	0.00	0.00	Woodhead <i>et al.</i> (2008)
ERubLR_SQ053_H01	CTATTGCAAGGATACCAAGC	GTTGCAACATGACAATTCC	2.00	1.00	50.00	Woodhead <i>et al.</i> (2008)
ERubLR_SQ062_E01	GCAGGAGTTGGACGAGTAG	TTCCAGATCAAACAAGACC	1.00	0.00	0.00	Woodhead <i>et al.</i> (2008)
ERubLR_SQ071_E10	GAGGAGAAGATTGTGAATCG	ACACACCTCCCAGACATAAC	1.00	0.00	0.00	Woodhead <i>et al.</i> (2008)
ERubLR_SQ072_H02	TGGCAATCAACCACTCTGTG	CAAACCTGACAAACGCTCTTCC	1.00	0.00	0.00	Woodhead <i>et al.</i> (2008)
ERubLR_SQ073_C07	ATGGCTTGTAGGTTTCACTC	CATTTGCTCAAACGATTATG	1.00	0.00	0.00	Woodhead <i>et al.</i> (2008)
ERubLR_SQ074_D05	CTTCTTTCCAACCGATTTTC	ACGAATTGATTTTCATCAACC	1.00	0.00	0.00	Woodhead <i>et al.</i> (2008)
ERubLR_SQ074_E09	CACTAGGTCGATCAAGAAGC	CTGCCATAGAAACAAACGAC	1.00	0.00	0.00	Woodhead <i>et al.</i> (2008)

ERubLR_SQ191_A05	GTTTGCTTCCTTTCGTAGTC	TATACTAATGGCCACCTTGG	4.00	3.00	75.0	Woodhead <i>et al.</i> (2008)
ERubLR_SQ193_G09	GTTTCGTCATCGTCATCTCTC	AGAAAACCAAACCCCTCTAC	1.00	0.00	0.00	Woodhead <i>et al.</i> (2008)
RubEndo_SQ004_N23	CACTGCAAGGTGTCGTTTGT	ATAGCTCCGGCAATCCATC	1.00	0.00	0.00	Woodhead <i>et al.</i> (2008)
RubPara_SQ005_K23	AGGTGAGGTGGGAGATGATG	ATCCTCGGTTCTCCAAAAT	1.00	0.00	0.00	Woodhead <i>et al.</i> (2008)
RubPara_SQ007_O09	CATGGAAAACCATGCATCATA	GCTTTGTCCAAAAGTGCTGT	1.00	0.00	0.00	Woodhead <i>et al.</i> (2008)
RubPara_SQ008_D04	TTGAGAACCATGCCTACATATCTT	GCTGGAAATGGATTGAATGG	1.00	0.00	0.00	Woodhead <i>et al.</i> (2008)
RhM001	GGTTCGGATAGTTAATCCTCCC	CCAACTGTTGTAAATGCAGGAA	1.00	0.00	0.00	Castillo <i>et al.</i> (2010)
RhM003	CCATCTCCAATTCAGTTCTTCC	AGCAGAATCGGTTCTTACAAGC	1.00	0.00	0.00	Castillo <i>et al.</i> (2010)
RhM011	AAAGACAAGGCGTCCACAAC	GGTTATGCTTTGATTAGGCTGG	1.00	0.00	0.00	Castillo <i>et al.</i> (2010)
RhM021	CAGTCCCTTATAGGATCCAACG	GAACTCCACCATCTCCTCGTAG	1.00	0.00	0.00	Castillo <i>et al.</i> (2010)
RhM023	CGACAACGACAATTCTCACATT	GTTATCAAGCGATCCTGCAGTT	1.00	0.00	0.00	Castillo <i>et al.</i> (2010)
RhM043	GGACACGGTTCTAACTATGGCT	ATTGTCGCTCCAACGAAGATT	1.00	0.00	0.00	Castillo <i>et al.</i> (2010)
RiM015	CGACACCGATCAGAGCTAATTC	ATAGTTGCATTGGCAGGCTTAT	1.00	0.00	0.00	Castillo <i>et al.</i> (2010)
RiM017	GAAACAGGTGGAAAGAAACCTG	CATTGTGCTTATGATGGTTTCG	1.00	0.00	0.00	Castillo <i>et al.</i> (2010)

RiM019	ATTCAAGAGCTTAACTGTGGGC	CAATATGCCATCCACAGAGAAA	2.00	1.00	50.00	Castillo <i>et al.</i> (2010)
RiM036	AGCAACCACCACCTCAACTAAT	CTAGCAGAATCACCTGAGGCTT	1.00	0.00	0.00	Castillo <i>et al.</i> (2010)
RubfruitC1	CACGAGCTTCATCCTCTTCC	ATCCAAAGCTTTTGCGATTG	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
RubfruitE4	TCAAGGCTCCTGCTTTAACC	CGCAGAGTTGGAGACATGAA	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
RubfruitE8	CATAACCTCCAGTGGTTCC	TGATGATGTCGATGCAGGTT	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
RubfruitG7	GGCACGAGTCAAGCTCTCT	TGGTTTGTGGTTTTGAAGCA	2.00	2.00	100	Graham <i>et al.</i> (2004)
Rubleaf102	GCACGAGCCTCATCATCTTC	GATGTTCGGGCCTTTTGTA	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubleaf107	GCGGCAAGCTCATATACTCC	GGCAAGCTTGAATGAATCCT	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubleaf86	GGAACCTTGGAGCCACCTAC	TCGGCAGGTTATTCATTTGT	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubleaf97	AACAAAGCTCCTCGACCAGA	TCGAGATGGTCAGTCCAACA	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus103a	TGCAGATTTTGGTGGTGAAG	CCATTGCACAAAACCAATGA	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus105b	GAAAATGCAAGGCGAATTGT	TCCATCACCAACACCACCTA	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus107a	GCCAGCACCAAAAACCTACA	TTTACCGTCAAGAAGAAAGC	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus110a	AAACAAAGGATAAAGTGGGAAGG	TGTCAGTTGGAGGGAGAACA	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus116a	CCAACCCAAAAACCTTCAAC	GTTGTGGCATGGCCTTTTAT	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus117b	CCAAGTAAACCTCATGCAC	ACTTGGTCCTGTTGGTCTGG	1.00	0.00	0.00	Graham <i>et al.</i> (2004)

Rubus119a	GAGCAAAACAAACACAGATCAAA	CTCCAAGTAGTCACGCAGCA	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus124a	ATGAGCGCGAAATGTGGTAT	GTGGAAGTTGTTGTCGCTCA	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus126b	CCTGCATTTTTCTGTATTTTGG	TCAGTTTTCTTCCCACGGTTA	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus145a	TGTCACAGCTTTCTGGTTTC	GGCATCTGTGCGGTAAAAAT	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus167a	AACCCTAAGCCAAGGACCAT	CACCACCCATGACAGTCAGA	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus16a	TGTTGTACGTGTTGGGCTTT	GGGTGTTTGCCAGTTTCAGT	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus194h	TGTGTTGTTCTCTGCAACCA	AGCCCTTACTTTTCTGCAA	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus22a	TGTGGACGACCATAACTTGC	TCGGCATTTATACACACACACA	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus237b	CATGCTTGCATGATCACCAC	TGAGCCATAAATTTAGAGGGATT	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus243a	TGAGCGAGATGATTGGAGTG	TATGTGGTGATCATGCAAGC	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus24a	ACACACGCACGTACAGCACT	GCGCAGTCAAGTGGACTTTT	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus251a	GCATCAGCCATTGAATTTCC	CCCACCTCCATTACCAACTC	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus256e	CAACCTGAAAACCAAACCTCG	CTGAGAGCCTGAGAGGTGGT	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus259f	TGGCACAAGAAGCCTGTAAC	TCCCATATCCCTCAGCATT	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus25a	GCCAAACACACCGTTATCTTG	CATTACCACACGCTTGATGC	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus262a	TGCATGAAGGCGATATAAAGG	TCCGCAAGGGTTGTATCCTA	1.00	0.00	0.00	Graham <i>et al.</i> (2004)

Rubus26a	AACACCGGCTTCTAAGGTCT	GATCCTGGAAAGCGATGAAA	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus270a	GCATCAGCCATTGAATTTCC	CCCACCTCCATTACCAACTC	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus275a	CACAACCAGTCCCGAGAAAT	CATTCATCCAAATGCAACC	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus277a	GCCCCATCCTGTACAAAGAA	TTGCAACAAAGGTACGTAATGG	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus285a	TCGAGAAGCTTGCTATGCTG	GGATACCTCAATGGCTTTCTTG	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus2a	TGAGGGAAGAAGAGGCAAGA	CACGTGTGACCCCAATGATA	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus45c	GAGGGGCAATTAAGGGTTT	TGTTGTAATTTGGTTTATCCTTGG	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus49a	CAGCCAACCATCATCAGCTA	TTGTTTTCAGGAGGCAGGAC	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus4a	AGCGAATTGCATCTCTCTCTC	GCACTGAAAAATCATGCATCTG	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus6a	TGCATGTGACTTTGCATCTCT	GCACTGAAAAATCATGCATCTG	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubus98d	GGCTTCTCAATTTGCTGTGTC	TGATTTGAAATCGTGCGGTTA	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubusr19a	GCAGATCAATGAAAGCCCATT	CGGATCCTCCAACCTTCAT	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubusr43a	TGCCTAAAGTTTGCTGTGTA	TCGAATGTAAGTGCAGTGC	2.00	2.00	100	Graham <i>et al.</i> (2004)
Rubusr47a	AAGCAGGACACCTCAGATGC	CAGCCAACCATCATCAGCTA	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubusr56a	TGGAGATTCCAAATAAACAAATACCC	TGTGTAAACCGTTGGATGAA	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
Rubusr59b	CTCCTCCTCTTTCCTCGTCA	AAGTGCTGCTGATGTGTTGC	1.00	0.00	0.00	Graham <i>et al.</i> (2004)

Rubusr76b	CTCACCCGAAATGTTCAACC	GGCTAGGCCGAATGACTACA	1.00	0.00	0.00	Graham <i>et al.</i> (2004)
RH_MEa0001dD07	TCACCCACCTACTTTCCCAG	GTGATTCGGAGGTGGACTGT	1.00	0.00	0.00	Lewers <i>et al.</i> (2008)
RH_MEa0007aB01	TGGTGGTTCACCGTTCACTA	GAAATGCTTGAAGCCGAGAG	4.00	4.00	100	Lewers <i>et al.</i> (2008)
RH_MEa02cA01	CCCCAAACTCCAAAATCTCA	TTCTGCTCATCTTTGGGGTC	1.00	0.00	0.00	Lewers <i>et al.</i> (2008)
RH_MEa02bA10	GGCTGAGCTGAGCTTTGAAC	TCCTCTCAAATTACCACCGC	1.00	0.00	0.00	Lewers <i>et al.</i> (2008)
RH_MEa11cF09	ATGCATTAAAACCCTCGCAC	TCCTCTCAAATTACCACCGC	1.00	0.00	0.00	Lewers <i>et al.</i> (2008)
RH_MEa12cE03	TGCGTGACGGTAATAGTGGA	GATTATCGGCAATCCCAGAA	3.00	3.00	100	Lewers <i>et al.</i> (2008)
RH_MEa13aE07	GCCTGACCCGTTTTTACACA	AATTAGGACCATCCCCAAGG	1.00	0.00	0.00	Lewers <i>et al.</i> (2008)
RH_MEa13bD09	GGGTATCTGTTCAGCAAGGC	CCAAATTCCTTCTTTGCAGC	1.00	0.00	0.00	Lewers <i>et al.</i> (2008)
RH_MEa13cG02	GTGAAGGAGCTCAAGAACGG	CCCGACAACATTGCAAACCTA	1.00	0.00	0.00	Lewers <i>et al.</i> (2008)
RH_MEa14bF07	GTGAAGGAGCTCAAGAACGG	TACATCACCCGACACCATTG	4.00	3.00	75.50	Lewers <i>et al.</i> (2008)
RH_MEa15dA03	TACCCTCATGTCCTCCCAAG	TTCAGCTTCTTCTTCTGCTGG	1.00	0.00	0.00	Lewers <i>et al.</i> (2008)
RH_MEa13bG01	CCCTCCATCTCCACCATAAA	GTAAGGCCACCCCATTGAG	1.00	0.00	0.00	Lewers <i>et al.</i> (2008)
RH_MEa15aD04	CCCTCAGCATCTCCTCTACG	GAGAAGAGCGAACCCAGATG	4.00	4.00	100	Lewers <i>et al.</i> (2008)
RH_MEa10bE05	CCTTGAGAGAGCCTCCAAAC	TCTCTCCACGAAGGAGCATT	1.00	0.00	0.00	Lewers <i>et al.</i> (2008)
RH_MEa08cA04	CACTCTCGCTTGCTTGTCTG	GATTCAAAGGCCGTCAAAAA	1.00	0.00	0.00	Lewers <i>et al.</i> (2008)

RH_MEa12aF05	TTGAAGTTCGAAGTGGGCTT	ATGTTGCGGAACCTTTCTTG	1.00	0.00	0.00	Lewers <i>et al.</i> (2008)
RH_MEa13cF08	TTTGTCTCCGTCTTTTGGCC	CCTCCGAAGAAAAACAGCAG	2.00	2.00	100	Lewers <i>et al.</i> (2008)
RH_MEa01cD05	GGCACTTTTAGTCGCAGCTC	TCCTGGTCTTTTTCCTGCAA	1.00	0.00	0.00	Lewers <i>et al.</i> (2008)
RH_MEa12cC08	TTGGGCTTGCAAGACTTTTT	ATGTTTGGCTTGGGATGTC	1.00	0.00	0.00	Lewers <i>et al.</i> (2008)
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Total			123	27	21.95	
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