Table S2. The primer sequences of the SSR markers used in the HJ DH population genetic linkage map construction

Marker	F_primer (5'--3')	R_primer (5'--3')
BEN2	GGGCAGGGAGCTAAGTAACC	AACAGCTCCACCGTTACTGG
BEN6	GTGGAAGATCGAGTGCGAAT	CCTCTGACTCCATCTCAGCC
BEN9	TGGAGCAACAACCTGTGAAG	GTGGTGAGGGAAGGAGTTGA
BEN10	AACAGCAGAGAAGCGAGGAG	GAAGAGGGATCGGAAGAAGG
BEN14	CAAGAGATCGTAGCTTCCGC	CAGTTGGCCAGAAGTGCATA
BEN16	CTGGTCCAATGAGCAAACCT	GGAGGTGGTCCTTTCTTTCC
BEN25	CGTCTACTGCCCTCAATGGT	CTAGCGAGGATTCCGATGAG
BEN28	TCGCAAACGTCATCACTCTC	GCCGTCGCGTCATATATTCT
BEN30	GGAGAATGGTAAGCGAGAAGC	TCCACACCTTGAAAGGGTTC
BEN32	GAGATGCTTCTATCGCCTGG	CTCGTCGAGGACTCTCATCC
BEN43	GTGGTGATGGTACATCTGCG	CCTTTGGTGGTAGTGGTGGT
BEN45	TGTTCGTATTCTCGCGACTG	CGATTTCCTTCAAGCTCTGC
BEN48	TGGGCTCCTACAACCGTAAC	TCTGATCCATCTGATGCTGC
BEN50	TCAATCCTCGAATCTCGCTT	CGATCCCTGGAGGATACCTT
BEN52	TTCAAGGATGAGGAAATGCC	ACAGCGAAAGGGAACAAAGA
BEN55	ACGCCATTTGCATTCTTCTC	TCTGTGCTTCCACAATCAGC
BEN59	GATTCGCTTCCCTTCCTTCT	TTGAGCTTCTCTAGCTCCGC
BEN68	CGTCACACGCCACATTATTC	AGTAATCAATCACCTGCGGC
BEN69	AACCCTGAAGAATCCCGTCT	GGTTGGCTACCAGTTTCAGG
BEN78	CTGTGGTTCCTGCTCTCTCC	AGTGAAATTGGGTTTCGCAC
BEN81	GAAAGCGGCAAAGTCATTCT	GAATCCGAAACTCCGAGACA
BEN82	AAGGATTTGCTGAGGAAGCA	CAGCATGATAACCATGGACG
BEN83	TGATCGGTCAAAGTCAACCA	GATCCACCGTGCTTCTCTGT
BEN84	TTGATCCAATAGCCATGACG	TCGAGGACGAGATGAGACCT
BEN95	GAAGACGAAGATGCCGTAGC	TGGAATTTGCTGGAGGTTTC
BEN98	ATCACTTCCGGTAATGCGAC	CTGATTTGAAGGCTCTTCCG
BEN116	ACGCTCAATCTCACAGCCTT	ATGAAACTTTCTCGGAGGCA
BEN119	ATGGACAGGAGATGGTGGAG	GGTATCCACGGCTTGTGACT

BEN123	AAAGACAAAGACTTGCGCGT	CTCCCACTCAGACTTCTCGG
BEN133	TTGGGTGGTAAGAAAGATGGA	ACTTGCTCGTGTGGAAGACC
BEN134	AGCTAAGCTAAAGGCGGAGG	AAGCCCAAATCAAGCATCTG
BEN136	TGCGAGGATCCCAAGTTTAC	CAAACTGTTTCCTTGTGGCA
BEN140	ACAGGACACGATACGGGAGA	GGCTTGCTTCAGTCCGTAAG
BEN178	CTCGCTAGGAAACGGCATAG	AGAGATCCAGCCTTTGTTGC
BEN185	GGAGGAAGGGAACAGTGTGA	TCCGGAAGTGAAGTAATCGG
BEN186	TCTTCTTCCTCCTCAGCTCG	TCTTCCTCTTCTCGCTCTCG
BEN189	TTAAACCCGGTCCTGTTCTG	CATGAGCTCAGGAGGAGGAG
BEN190	CCGGAAAGATCAGGTAACGA	AGGAGCGCTTGTGTCAATCT
BEN200	AAGCAAACAAACACATGCCA	TGCGGAAGAAGAAGAAAGGA
BEN203	TGACTCAAATCAACCTCTCACG	TTTGTCACTCGCCATCTCTG
BEN206	CGCACGCTTTATGTTCTGTC	CGTCTCCTGGTGGTACCTGT
BEN210	GCAAGGCTTTCTCACCAAGT	TGAAACAATCACGCAAAGGA
BEN211	ACACGCTCACTGGAGAATCC	TTTCGTCGGTGTAGTTGTCG
BEN216	ATTGTCTTTGCTCCGACACC	TTGAGAAGCGGCGTAGAAAT
BEN228	GACCAATCCTCCTCCTCCTC	TTGAAGAGCTGAGTCGGGAT
BEN229	TTCAAACACGGTCTCTGCAC	GTCCAGCGATTGAAGATGGT
BEN235	TCTCGATGGGAAAGTGGAAC	CATGGCACTGATCCAATCAC
BEN236	TCGGTGGAAGCTAATCTTGG	GGGATTGATCGGAACTCGTA
BEN239	GAAGGACTCGTCAAGATGGC	CAGCTGGAGTACAGATCGCA
BEN251	AAATCTGGGATCTGCACGAC	CGTATCCCTGCTGCTTCTTC
BEN253	ATCTTCGTGGCTGCGTGT	GCCAACATTCGGAAAGAGAG
BEN254	TTCAATGGAAAGATCCCGAG	TTGCAGAAGCGTAAAGCAGA
BEN260	AGTCGGCTAAGGAGAAAGCC	AACATCCACATCTCCAAGCC
BEN266	AGGAACGGTTGCTTACGAGA	ATCCCTCAGCTCACTCCTCA
BEN269	GAATGGGTACACGCCTGAGT	CCGATGTTGATGTTCCTGTG
BEN271	AGGTTCGTTGGTCGGTAGTG	TTGTGGAACGAGAACTGCTG
BEN278	AGCTGTGAGGGAGTCAAGGA	TTTCGCGGTATCTACGGAAC
BEN281	GTGGATTTCTGCTCACCCAT	ATGTGAGGAGGGTGAAGGTG

BEN284	CAAGCGGAGAGGATGAAGAG	GGAGCTTGACCTTGAGCAAC
BEN285	ATCCGGGTTTGCACATAGAG	CCAGAGGATGTTCAGTGGGT
BEN288	CAAACCGGTCACTAAACCGT	GGAAGCTGAAGAAGCACGTC
BEN296	ACGCCGTGTCAGAAGAAGAT	AACAGGCTTTAACGAGGTGG
BEN312	TAAACCTCCGCTTAAAGCCC	ATCCGACTTCGAATTCCTCC
BEN313	CGAGAGTTTGAGTGGCTGTG	TAATTCGCCGAGAGGAAGAA
BEN316	GCTTGCTTCTCTTGGCAATC	CCCACGGAGATAGATGGAGA
BEN320	CGTTGGTTTTTGCATGTTGA	GCTGCTCTCATTTTGGAAGC
BEN327	GCAAGATTCTTCCCGTTCAA	GCGATCTGATTAGCCCTTTG
BEN330	CCTTTCTGGGGATTTGATTG	ATCCGCAGATTGGATCTTTG
BEN332	CTCCGCAAGTTTCCTTTTTG	CCGACCGAGACTGGAAATTA
BEN334	GCGATAGGTGTTCAGGGAGA	TTTCGCAGTCATACTCGTCG
BEN335	ATGACTCGTGATCTCCTCGG	AAATCGAGACGTTTCTCCCA
BEN337	TTACTGAACCAACCTCGTCG	GGAGAGAGCGTCTTTGGTTG
BEN341	TGGAAACATTAGCTTGGAACC	GCAACTCGTCTTGTTTCATT
BEN343	TCTTTGGAAGATGACCCCAG	TCCAGCTTCATCATGTCTTACA
BEN348	GATTAGCTCTGGTTTCCCCC	AGAAAATCATCACCCCCTCC
BEN349	GTGTGGTCGTCAATTTGTGC	AGGAGGAGGAAGAGCAGAGG
BEN363	CCTTGGATTCAAAGAGCAGG	TCAGGGCGGAGTTTACAAAG
BEN374	CTGACGAGGCGATTAAGAGG	TCACCATCTCAGCAGTAGCG
BEN376	ATTAGGGCTGAGTCTGGGCT	GGAGCTTAACGATGTGGAACA
BEN387	TGAAAGGGTCGAATTCGTTT	ATGAGTTTCGCCTAACGACG
BEN391	ACCACCATGCCTAAGTCGTC	AACTAAGGTGGGGGATTTGG
BEN396	GTAACAGCGTCTTGCGACAG	TCCTCTGATCCACTCCATCC
BEN406	CGGGGAGGTTTTAAAGCAG	CACGGATTTGACACCCTCTT
BEN410	TGTTCCTCCACCACAACAAA	GTGCTTCTGCTTCTTTTGGC
BEN420	GCAGCAAAGGCAGGTCTACT	AGGATTGAAGGCGACAGAGA
BEN425	CCGGGAGTAACTGACCTCAA	TAGTCTCCTTACAACGCCCC
BGO001	TTCGCTATCTCTCGACCGTT	ATCCTCGCCGTGATATTCCT
BGO006	AACGGCTATGGCTTGTATGG	GACTCTTCGGTCTCGCTCAG

BGO029	GCAACTGCACAGAGTTTGGA	ATCATCGTGATTCCTCTCGC
BGO041	GAAGGACTCGTCAAGATGGC	CTGGAGTACAGATCGCAGCA
BGO044	TCGCACTTGAATCTCCCTCT	CGAGTCAACTCGGTGAGACA
BGO054	TAAGTTCTTCGCCGAGATCC	CAAGCGCAAACTCAAGCATA
BGO055	CGATCACTGCTTCACTGCAT	TAGTTAGGTGGTCGGCCAAG
BGO056	AGGTTCGTTGGTCGGTAGTG	TTGTGGAACGAGAACTGCTG
BGO078	ACTTACACCTCTTGGTGGCG	CAGCTTCTCCAAGCAGATCC
BGO090	GAGGTGTGGCTAGTGGTGGT	CGGTGAATGAAGTCCATCCT
BGO108	TCGCGTGCCAAACAATAGTA	ATTCACTTCTTCCATTGCGG
BGO114	CCTTTATTCCATTTCCGGGT	TGGACCAGCCAAGGTTAGTT
BGO120	TGGCATTTGAGTAGTGGCCT	AGTGGCCCACACTTCCATAG
BGO125	GAACCACCAAGGGAAAGTCA	CGATTCAGCTAATCCAAGCC
BGO140	GGACGTGCGGATCAAGATA	TGACAACGGGATATTCAAAGG
BGO141	TTTCCAGGGATGGTTATGGA	CCGGCTCTGATACGCATACT
BGO146	CCTAGTCCATGCTGTTTCGG	CCCAAGGAAGATGGTGAAGA
BGO151	GAGATCGTCGGTGAGAGAGC	TACAGCGGACTCCAAACCTC
BGO153	CGACGAAAGGAAGAAACCCT	AGAAGGAAAGTAGCCGCCTC
BGO156	TGTGTCAGCCACAAGAGAGG	TCGCCATGATGTTATCTGGA
BGO160	CCAGACACAACAAACATGGC	TTCGAGGAGAGTTTGGGAGA
BGO161	TTTGGTTACTAACACGCCCG	AGGACTCGAAATGGATGTGC
BGO169	CTAATCCACCACCGTCACCT	TTGTGTTTAGAGGCGCAATG
BGO178	ACTAACAAGCACCGGAGACG	AGCACCTGTAGCGGGTTCTA
BGO179	TTCTTCGCCTTACCTCCTGA	AACACAAGTGAGACATTGGCA
BGO183	AAGAAAGGTCCATGTGTCCG	CGAAATGCCAGATTCCAAAT
BGO185	GATAACCGATCGGACATTCG	AAGGCCAGTCCAACCAGAG
BGO196	GTGAAGGGAAGTCCCAGACA	TCGACCACAAGACCTGTTCA
BGO199	CAATCGAATCGACATGAACG	TGCGTTGTATTAGATGCACGA
BGR1	TGACTTTCTTGAGGGTATGC	AGCATTGGTATCCAAGACAA
BGR2	CGTACGCTTGTGTGAGTAGA	CAGCAGGTAATAACAGAGGG
BGR6	GAAGAAGCTTTACTCGGTGA	TTATGTTAGGGCTTGTCCTG

BGR8	ATAGTCATCGGAGGTCGATT	AAATCCACTTTCTCTCTCCC
BGR16	TCCGTCTCTTCTTTTCTTGA	CGCTGTAGTGTTCTTCTGGT
BGR20	CGTAACTTGTTGTTGTCACG	CCTACCATTGAAGATGGTCT
BGR23	GTCGGATCAGCTCTGTGTAT	CTCTTCTTCTCTCTCATCGC
BGR34	GGACCTTGGTTCAGTGTGTA	GAGTAGGATGGGTGCATCT
BGR35	CCGCCTAAGCTCATTAACTA	CACCTAGTCACCGGAATAAA
BGR38	TGCTCTTACTCCTCTGCTCT	CCAACTCTTCTAGGATCGC
BGR42	AGTCGCTAGAGGTTTTTCCT	CAGCACTAAGCATCTCATCA
BGR43	GTGCTCCTTTCAAATCTACG	GACAGGATGATGTGGTATCC
BGR45	ATCGTTTCTCTCTCCCTCTC	ATATCCGTTGGAGAAGACG
BGR49	GATATTGGTCGTTGGAGTTC	CCTCTCTCGCCATTACTCTA
BGR50	GATGGCCATGGAGTAGATAA	GACCCATTCGTACTTGAGTT
BGR51	GAAGGGATAGAGAGAGAGGC	GGAAGAGAAGAACAGAAGCA
BGR52	CAGAATCGGAGTAACCAACT	AAAATCACCGATCCTCTTCT
BGR54	CTTCCCTTCTTCAGTTGCT	GGTTTGAGAAATGATTCACG
BGR55	AGACGAAAAGGTTGCTTCTT	CTTTTAAGCTTCCTTCCTCC
BGR56	GGGAGGAAGATGGAGATTTA	GAACACTTATCAGCCGTTTC
BGR58	AGCAGTGTATCCGCACTATC	TAATATTGTTTGGAGCAGGC
BGR60	GAAACTGGAGAAAGGAAAGG	CCATCGTCACGAACTACATA
BGR61	GCCACAAAACTACTAGATGGA	CAAACTATCCATGTCTTCCG
BGR64	CTCCTGTAAACCACCATCAT	CTCCGTTAACAACCATCATT
BGR65	GTTGAAAGCTTACGCAGTCT	ACCTGAAGCTCTGAAACTCA
BGR66	GCTCTTCATGATGTTCCATT	CCTTAGATGAACCTACATTCG
BGR69	AGACGAGTCATCTCCATCG	GCAACATGAAGAAGAAGAGG
BGR70	AGAGAGTTTCAGGCTTTGGT	GGGAAAAGAGTGGAGAGAGT
BGR71	TCTACTTCTCTCCCTCCTCC	AGAGAGAAATGGGAGAAACC
BGR74	ACAAACACCTCGATCTCATC	GGGGGAGAGATAGATACCTG
BGR75	ACACGTCTCCATGAAAAAGA	GTTCCATGGACAGAAGAAGA
BGR80	TCGATATGTATTCAGGGGAG	GAGTCATCAGCATCTTCCTC
BGR83	TCTTTCTCAGTCCCTCTTGA	GTTCCATGCAAATCCATAGT

BGR84	CCTCCTTACCCTAACCCTAA	CCATAACCAGGTGAGGAAG
BGR87	AGGATGGTGAAGTGAAACAG	TAATCTCCGTTGATCTCCAG
BGR88	GTTCCAACCATAAGCCCT	GATAAAACCTGCGGTCAC
BGR89	ATAGTAAACCACCACAACCG	ACTATAGGCCCTCTCTGTCC
BGR93	CAAGTCAAGTCCCAATCAAC	TTGCTGAGAGAGTGATGGA
BGR98	GGTTATACCTTTTGGGAAGG	CAGTGTCTCCCTTTGTTCTC
BGR99	GGATAAGCGATACACACCTT	TATGAGATACTGGTGCGTGT
BGR100	CTTAAAATCCTCCAGGAACC	CTCTTAGCATTGGGATTAGC
BnEMS14	TTTGTGAGTGGTCTTGATTT	AATGGATAATACTGATGCTCTT
BnEMS20	CTCTATCCGAAGTGAATGATG	GTCGTCAACCCACACAAA
BnEMS57	ATGTTGGGTAAAGGCTACTG	CTGCTCTCTGTTCTGCTTATC
BnEMS59	ACACCACCGTCCAGAAGA	TATCACTCTCAAACCTCCCA
BnEMS60	TATCACTCTCAAACCTCCCA	ACACCACCGTCCAGAAGA
BnEMS82	AGAAGGAAGGTTTGCTCACT	CAACACAGAGATTGGTTCATC
BnEMS146	AGGTGATTTCTCTTCTCGGT	TACTTTGTCTGAGTGTGGTGG
BnEMS439	TCTATAGCCAGCGCTCTTAC	TAGTCATTGCACATTGCTTC
BnEMS634	GCACACACCTTTCTTTCTTC	GTCCTCGGTGCTTATGTTAG
BnEMS695	GCTGGTAAATTGTTCCATTA	CGTAAGGAAGACCAAGAACA
BnEMS812	ATTCTCTGCCTCTAGGCTTT	AAGACATGTTTGATTCCGAC
BnEMS820	ATACTGTCAAGAAGCCCAAA	AAGAATCCAACCATGGATAA
BnEMS824	CACAATCCCACTCTCAAGTT	TCCATTTCAAGAAGTAGGGA
BnEMS843	CGGAGTCCAATACGAATAAG	GGATGTTGCTAGGTAAGCAC
BnEMS860	TGGTGACTACTACTAAATCGAGA	GAGAGTAGAATGAAGCCACG
BnEMS973	GTCTTCGTTGTGTCCTCAGT	TAATGATGCTTCTCGGTCTT
BnEMS993	CCTATTCGACCACAATGAAT	GAGAGTTGGCTCGAGTGTAG
BnEMS994	TGATTCCTCTCCTCCTCATA	TGCTAGCTTCCTTCATAAGC
BnEMS1012	ACCTAACTCGCACTTCTTCA	TTGGTAGAGAAACCAGAGGA
BnEMS1036	CGTACCTGAGGCAGTTACTC	GGAATCCGTTATTTGATTGA
BnEMS1072	GATATCTTGATTAGGGTTCTTAT	GTTCTCCTGCATTTAGATCG
BnEMS1084	AAGGTGATGATGGTAAATGC	TCTCTCTGTTCGATGTCCTT

BnEMS1116	GAAATTGGCCACATGTATTT	CCAAGACCTCCCTATCTTCT
BnEMS1119	ACTGGAGTTTCAATTGGATG	CATCATCTTCAGCACTAGCA
BnEMS1124	ATGTTTCCTTTGCTCGTTAG	GAAGCCCAACATTATTCAAA
BnEMS1144	ATATCTCTCTTTGCGAACCC	TGGATCTATTAGCTGCCATT
BnEMS1156	ATCTGAACAATCAATCTCCG	TTACGATACGCTCTCCTCAT
BnEMS1171	CTGTGAGGAGAGAAAGGATG	AGCTTACAGCTTTCAACAGG
BnEMS1173	CGAAATCCTCACAATCTCAG	CGGAGATTGATTGTTCAGAT
BnEMS1184	AACGTCAGAGAAATGTGGAC	GGCATTACTCAACGGTGTAT
BnEMS1185	CTTCTTCAACCTCTCCCTTT	GTGTTGAGCTTCTTGAGGAC
BnGMS9	GGAGGAGGAAGAGGAAGATA	GGAGCTAGTGAAGCCAATAA
BnGMS87	TTCTTCACTGATCCCACTTT	TGTCTGTAGCATTGATTGGA
BnGMS131	GAAGAAGAACATGGCTTGAG	GCTTCAATTCAATCTTCACC
BnGMS133	CTTAAATTGTCCCTCCTCCT	AAGAAATGAGCTTGAAGCAG
BnGMS147	AAGCAGTGAGCACTACACAA	CTTCTTGCCTAACAATGACC
BnGMS153	CTCAATGCTAAGGATATCGG	TCTGATCTTTCAGACTCCGT
BnGMS161	GAGTCTTGCTTTATCATGCC	GATCTTTCACTTCAGCCTTG
BnGMS175	TGATCTTCCTGAGAATCAGC	GAGGAAGAAGGAGAGAGGAA
BnGMS198	AGTTTCGGATACTTTCGGAT	CATGTCGACAAGAGAAACAA
BnGMS205	AAGAGAGACAGCGTGTTGTT	GACTCTAGGAGAGTAGACGGC
BnGMS208	GGGTATTTGAGGGTATTGGT	CATGTCGACAAGAGAAACAA
BnGMS213	GTAGTACGGAGATGCGTGAT	AAAGAACGAGTTGACTTTCG
BnGMS249	AATAATAAGAAGGGATGGAA	CACCTTAAGTGGTTTCTTGC
BnGMS265	ATAATCGTCGGTTCGATGTA	GCTTTGTGTGAAGGAATTTG
BnGMS584	GTCCGTGTCGATCTACATTT	CAAGACCATTGAGCTTTCTT
BoGMS38	CCTTTGTTCAGCACCATC	CGTGGATTGAGAAGTAGCAGT
BoGMS125	GTTGGCTTCACTTCTCCTACT	GCATCTCATACATCAAAGGG
BoGMS154	CTACGGCTTCGTCTCGTC	GCTTTGCGTTACATCTTTCT
BoGMS197	CCCTCTTGATTACAACGAAA	GTATGTTTACCTGGACCTGACT
BoGMS204	CCGATAGTAGTCAAAGCCTG	GAAACCTAAACGGCACAA
BoGMS314	AGAAAGATGGAGAAGACGAAG	CGAGAAGAAGAGAGGAAAGAA

BoGMS319	GTCTTCCTTCATCCTTCTCC	GGGCAACTTCGTCATTATC
BoGMS328	TTTATTCGGTTTATTCGGTTT	GAAGGTGAGTCTTGATGGTG
BoGMS351	AGGTGGTGTAGTTGAGGAGAC	TGACAGATGGGATAAGACAAA
BoGMS373	CTCTGACGAAGATGGCTG	AAGTCTATGTTTGGATAAGGGA
BoGMS490	CTTGAGTCGTTTGTTTGTGTT	CAGAGGGAGTAGTGTTTATGG
BoGMS539	ACGACACCGTATTGATTCTC	ATCCACTCACCTCCCAGT
BoGMS545	CCTCTGTTTCTTTGCTCTTTG	GATTCATTGTGTGTGTGATGT
BoGMS560	ATGAAGAAGTGTTTGGTGAG	AAGATTGATGGAAGCAAGAA
BoGMS561	CAAAGACTAAACCAGACCAAG	ATAGGCAAGGTGAGAAGAAAG
BoGMS576	ACCTGGAGTTGAGACGGG	CAGTGTTGAGTGTTCTTCTATT
BoGMS586	GCTGTATCATCTTCTTGCTCT	TGTTTCTTTGTAGTTTGGTGG
BoGMS622	ATCTGCCTTCACCGACTT	TCTGGTTCAGTTCGTTTATTT
BoGMS680	CTCTGCGTAAGAACATCACA	CGCTAAACGACCTCTACCA
BoGMS693	CATCTCCACATCACTACTCCA	ATTACCCAATCCCAACAAA
BoGMS788	CGCATTACTATCTCCATTGTC	GGCTGTCACTCTCTTCGG
BoGMS795	AACTACCAAGTCGTGTGAGAA	CAAAGTAAGCAAGTGGAGAAA
BoGMS819	AGGGAGATGGACACATTTAG	GAGAGAGGGCAAAGAAGATAG
BoGMS829	CACACTCATCTCTGTTTCAGTT	TTCACTTCCAGCATTACGA
BoGMS876	TGATGATAACTTGTAAATCTGCT	TTCTTTGGTGGTCCTGGT
BoGMS1032	GCCGTCGTCATCTTCTAC	ATTGAGTATCCCTTCTCTGCT
BoGMS1059	TAAGCACGCAACTGTGGA	GGGTTATTTGAACGGAGTATG
BoGMS1072	CATTGTCTCGTCTGCTCAA	AGCCCATTAGTTCTCTCTCAC
BoGMS1114	CACCACTAACCTATGAACCTG	TGTCTCTTCTCCACTTTGTTG
BoGMS1153	ATTAGTGCGTATCATTGTGG	GGGTTCTTGCTCTTGGATT
BoGMS1166	TAATGGAAACGCACCAAG	AAACAATCTTAGCAGAGGAGG
BoGMS1186	GACTGGAACGACAACGACT	GCGGAGGTAGATTAGGGA
BoGMS1199	CCTTACTTCTCTGTGGTTGG	CGGGAACTTTGTGGACTT
BoGMS1200	CCGTCGTCTCTCCTAAATC	TTATTGGGTCGGTTATTCACT
BoGMS1201	GGTAACACCAATCCACTTTCT	CACTTCAAACTTCTCATCTGG
BoGMS1203	GTTATCCACGCTTTGGTG	GCAAGACACTTATTATTTGAGAC

BoGMS1230	AAGTTGTCCCTGTTCGTG	CATTCTTGGTCGGAGTTAGTT
BoGMS1246	CACTACCCGTTCGTTCAG	ACATTCAGCCACTCTGCTT
BoGMS1295	CTCCTTCTTCATTCTTCGG	AATCTCCCTATTGCTTGTTC
BoGMS1303	ACACGAGCCATCACCTACT	CTCTCCTCCTCTCTTAGCATT
BoGMS1307	TGGCGATAAAGAGGAGAAC	CGAAGAGAGAGAAACAAAGAA
BoGMS1308	ACGATTTGGTATCTTCTTTCC	GTTCCGACTAACACTCTCTCA
BoGMS1320	TCTCCAAATCCTTCTTCTCAC	CCACCTTCTCCACTAATAACC
BoGMS1373	CCACCTTCTCCACTAATAACC	TCTCCAAATCCTTCTTCTCAC
BoGMS1375	ACACACCATCTCTCTCATCTC	GGAACCTCTCTGCTCTCAA
BoGMS1382	CTTCCTGCGTCACTTTACC	AGGCTGTCTCCTCACCCA
BoGMS1399	ATGTTCCCATTTCAGAGTCA	TTATCCCAATCCTCATCATC
BoGMS1425	GGCGGCAAGACTCAATAA	ACTTTGGTTAGAGAAGAAATGA
BoGMS1464	CTGATGAACGGAGACACAG	AAGCAAAGCAGAGCATAAAC
BoGMS1484	ACCTGTTGTTCACTTCATCAC	TTGAGTCGTCACTGTTTCATT
BoGMS1558	CTACGACCTACAAGAATGCC	CATCAGTAAAGCAGAGAACAAA
BoGMS1561	AGATAACGGATGTGAGGAGA	CTTGAGAAGATTGGCTTGTT
BoGMS1575	CCAGCAGAGAATGTGCCT	TTGAAATAGACTTTGGTTTGG
BrGMS5	ATTTCGGATCATAGCTGTTCCA	TCAGAGAAACACAACACCAAGC
BrGMS38	AGGTTTGGGAGATGCAGAGTT	GCCACTGAGACTTCCTCCTCT
BrGMS124	CGAGGAGAACAGAAGGGATAGA	CGCTGGGTACAGAAACCTAAAC
BrGMS216	ACACGGGCTACAAAACAAGAGT	ATGCTTCTGATTTAACCTGGGA
BrGMS217	CATTCCGCCTAAGCTCATTAAC	CAATTTCACCTGCACCTAGTCA
BrGMS231	TGAACCACCAACGTGTTCTTAC	TTTCCCTAGATCCGCTGTCTTA
BrGMS268	TCACCATGTGTAAAAGACTCGG	TTGGCTTATCTTCTTGGGATTG
BrGMS316	TGGGACCATAAATTGGATAAGG	GTGTGGTTTGTGAGAGATGGAA
BrGMS351	TGCATCCAGACAGTTACCAAAT	TTAACGCTCATTTCACTTCCTC
BrGMS363	AAGAAGTCTCACAAACGAAGCC	AAGATCAAAACCTCATTGCCC
BrGMS375	TATTGGAGGCATCACATCTCAA	AGCTGCAACACAGAGAAAGACA
BrGMS387	GCGTAATCTCAAGCGAAACAAT	GAAGCCGACAATTCCCCT
BrGMS394	ATCTACTTTCCCTTCACCACCA	GAAATGATCTTGCTGACCACAC

BrGMS406	TCGATAGACTGAGCAACGGTAA	GGATACACATTTTGGGAGAGGA
BrGMS426	CCGTTGAAGTTGTAGAGACGAG	TGCTTGAAATACATGATACCCC
BrGMS509	TGGAGACGTGTGTTCATTTCAT	GTTCACCCCTGACATTAGTTGG
BrGMS556	GGTTGGTTCCTCCTCTTCTTCT	TTTAACTTCAGCATCTGGGGAT
BrGMS679	ACTGGCGAGAAAAGAGATGAAG	GAGAATGGGCTTTGTTAGTTGG
BrGMS725	GATCACATATTCGTCGTGTTGC	AGGAAGTGACGTGTTTCCGTAT
BrGMS726	GATCATTGCTTATCCTGCGAAT	ACGGCATGGAAACGTCTATAA
Ap1c 5pr	GCGTAGGAGGTGGTAAAGATAGC	ACACCCACATTGCATTTTACCC
BN12A	GCCGTTCTAGGGTTTGTGGGA	GAGGAAGTGAGAGCGGGAAATCA
BN25C2	AAACCTCCTCAAAAACCCCTAAACG	TCCCCTCTTTCCTCTCTCTCTAGGC
BN38A	TGGTAACTGGTAACCGACGAAAATC	ACGCTGTCTTCAGGTCCCACTC
BN9A	GAGCCATCCCTAGCAAACAAG	CGTGGAAGCAAGTGAGATGAT
BRAS005	CGTTCGTTGTTGCCCTCTACT	CTCTACACGACGGCGATAAAA
BRAS019	CTCAAGACAAACGACCAGTAA	GAGAAGAAATCGCCAAGA
BRAS021	ACCGTTGAGATCAATCCCTAT	CATCTTCCTTAATCGAAACCC
BRAS051	GAATAGCCTCGCAGAAGTAGC	CGACGGCGATAAAACGAA
BRAS063	GACGCTCATTTCACTTC	TCCTAACTAACATCATTTTGC
BRAS072	GCCATCTACACATTTATCCC	CACTAACCTTCTTGCTACCGT
BRAS074	AATTTAAACCTCATTTTCTTC	ACCTCCATTGTGTCTGAT
BRAS083	GATGTTGTTGGGGAGAATG	AAAAAGTAGGCAAGTTCAAGC
BRAS087	GCAGAATAGCCTCGCA	GGAGGAAAAGAACGTGG
BRAS120	AAAAATAAATACAGCGAACC	ACCTTTAGCAGCTAATCATC
BRMS-006	TGGTGGCTTGAGATTAGTTC	ACTCGAAGCCTAATGAAAAG
BRMS-007	AAATTGTTTCTCTTCCCCAT	GTGTTAGGGAGCTGGAGAAT
BRMS-008	AGGACACCAGGCACCATATA	CATTGTTGTCTTGGGAGAGC
BRMS-026	CCTATCCTCGGACTAATCAGAA	GTGCTTGATGAGTTTCACATTG
BRMS-049	GATCTTCTCTCCAAAACTCTCT	AAAGTCCAAGCTAAATTACAAA
BRMS97	AAGAGCAAGAGCCAAGACAGCCTAC	TGGTGATGGAGAAGTACATGGACGT
CALSSR	GTTAAGTGTGGCGTTAGAGG	CCTTGGTACATGCCACTGAA
CB10022	AACAACCAAACATAGTCCC	GTTGACTTTGACCTTGACTT

CB10028	CTGCACATTTGAAATTGGTC	AAATCAACGCTTACCCACT
CB10034	TACGGGATAGGCGACGAA	CCTAAGCGAGACGTATTG
CB10057	CTAGGCTAAGGAAGATTGTCA	TAGTTTCTTCCTCCTGCTATC
CB10196	TTGTAGGCAATGATGAGGA	GAGAGAAGGGCTCCTTTG
CB10217	CCCCATATCATCCCTACC	GCTGAACAACCCACAAAG
CB10258	ATGATGCCTAGCATGTCC	AAGCTAAAGCGAAAGAAGC
CB10297	CTCATTCCACTGCCAAAC	ACGAGTCACCATGTCAGG
CB10299	TACAGGTTCCTTGCGATG	ATGGACGAGACAACATGG
CB10330	AGGCGAGTTTACGAGGAT	ACCTGCACCAGTCATTTG
CB10347	ATCTGAACACTTTCGGCA	GGAAGCACCATGTCAGC
CB10413	CTTAGCACAACCACTCGG	GGTGATGAAGATGACGATG
CB10439	ACCTCGAAGGGTATCTGC	CGTGCAATTTCAACAACA
FITO007.2	ggtcggcacgagagctttaag	cctaaaatttaatcgcacgccg
FITO018	tgccaagctttgagtagcaa	tgccttcttccatgctttct
FITO035	aaagtcgtgggaagtatcgt	aggtgtaaggatggtggtagt
FITO095	agatttcatccacagcctc	tttgattcttgcgttctctc
FITO114	gcgatacaaagaaatccaaa	caacaaataaccaaacattga
FITO131	ctacaacgggcagggtga	aaatcccatctactggtttga
FITO135	tgtaagacaacaccattcctt	cacagtcacatccaccataac
FITO136	cctcctcctcagacttacact	tcacatccaccataaccttt
J0609	GTTGGTTAAAATCGTGTATGC	CCTACAAAAAGCAATAACGTG
MR52a	TCGACATGGATTCTACCAAA	GAACTTGCAAGCTGCAATTA
Na10-A09	TCTTGAGCAAAGAAACTTGG	CAAACTGAGCCATACACAAAGG
Na10-C01	TTTTGTCCCACTGGGTTTTC	GGAAACTAGGGTTTTCCCTTC
Na10-E02	TCGCGCATGTAATCAAAATC	TGTGACGCATCCGATCATAC
Na10-G10	TGGAAACATTGGTGTTAAGGC	CATAGATTCCATCTCAAATCCG
Na12-A01	GCATGCTCTTGATGAACGAA	GCTTCAACCTCTCAATCGCT
Na12-B02	CGCGTTGTAACTCCAAGACC	TTTTCTAAATCATCCACTGTATCC
Na12-C01	CCAGGTTACTGTTAAAGAATAAGAGAG	ATCGTCTGCGAGTCTCCTTG
Na12-C06	AACGGATGAAGAACACATTGC	TAGGGCCTGTTATTCGATGG

Na12-C08	GCAAACGATTTGTTTACCCG	CGTGTAGGGTGATCTAGATGGG
Na12-D08	ACGACGATTCAACTCATCTTC	TTAACCAACTTCGCTTTTTG
Na12-D11	AATTGCATTTTGTATCCAGCG	ACATCCCTAGGATCAATGCC
Na12-E01	ATTCCATGACTCCATTGTC	AAATCCCTTGTCTCTGTCG
Na12-E02	TTGAAGTAGTTGGAGTAATTGGAGG	CAGCAGCCACAACCTTACG
Na12-E05	CGTATGTTTGTTCCACCTGC	ACTAGCAACCACAACGGACC
Na12-E09	CATGAGAACAAGATGGGTTCG	CTGAAACTTGAGCAAAGCCC
Na12-F03	GGCGACATAGATTTGAACCG	TCCACTTTCTCTCTCTTCCCC
Na12-G05	CCGATCATACCTTTTACTCTAGCC	GATGTTCCTCTCGGTGATGC
Na12-H02	CTATGGTTCATCTTTCGCCG	GCTGCACATCCATCTCTCG
Na12-H09	AGGCGTCTATCTCGAAATGC	CGTTTTTCAGAATCTCGTTGC
Na14-B03	GATGGTCGCCGATTCAATGA	CCCATCAGCACTAGAAACCA
Na14-E02	ACTGGCTACATGAGTTTCAGTG	GAGGGAAGACAACTGGTCTCA
NIAB_SSR106	GTCTCAAGCCAACATCCATC	AACGGAACCATAAGGAGACC
Ol09-A06	TGTGTGAAAGCTTGAAACAG	TAGGATTTTTTTGTTCACCG
Ol10-B01	CCTCTTCAGTCGAGGTCTGG	AATTTGGAAACAGAGTCGCC
Ol10-D01	TCTCTGCCAAAAGCAAATAGC	CTTGGCTCTCTCTCACCACC
Ol10-D03	GCCAAAGACCTCAAAGATGG	AAGCCACGTGAAGAAAGTCC
Ol10-E05	GCCAGAAACAGGAGAAATGG	GAAGCCGAAGAAAATAAGCG
Ol10-F09	AGAGAGCGAGATTGATTGGC	AAACGACCACGAGTGATTCC
Ol11-B05	TCGCGACGTTGTTTTGTTC	ACCATCTTCCTCGACCCTG
Ol11-H09	CCCTTTTCCCCTTCTATTGG	GTGCGACTTGGAATTTCTCC
Ol12-E03	CTTGAAGAGCTTCCGACACC	GACGGCTAACAGTGGTGGAC
Ol13-G05	GTGTGCAGGAAACGATGTTC	GGGAGTTTGAAGAGAAAGCG
pMR181	AGATTTGCATGTGGTTTGAC	ATTGCTTANTGATGTTGGGAA
Ra2-G08	ATGTCCGGATAACCGAATCC	GAAGCTTTTCAATTTTTAAGTTCTCTC
Ra3-D04	AAAAGGACCTACCAATTTCGTG	CGACCCAAACTGAGCCATAC
sN0706	TCCGACGGTCAAGATTAAGG	GGCTGTGGTGGATCTAGGAA
sN13034	AGCATGTGCAGAGTGCAGAC	AAAGGAAGGCCGATGAGATT
sN1988	TTCCCTCCCTCCCTCTTAAA	CGTTGGATGCAGAGCTGTTA

sN2025	AAGGAGCAAACACAAGCGAT	GCACAAGCACTCTACGGTGA
sN2032	CACCATCACCACCTTCACAA	TGGTTCACTCATGTCTCCGA
sN2837	CACACCCTTACCACGTTCCT	GCAACAAAGCATACTTCGCA
sN3523R	CGTTGGCAAAAAGCCTACTC	CTCAGGGACGTCGTAAGAGC
sN3761	CGACAGAGGGTTCAAATGGT	CGGTGTGTAGGTCTGCTCAA
sN9425	CGCCGACTTTAAAGAGATGG	TCCTTGGGTTGGTCACTGAT
sNRA56	AATCTTCGCATACCCATTCG	GTTTGACGCGGATAACCATC
sNRA59	CAGATTCGGATTTGGGAAGA	GGCGGAAGAATCAAAGGAGT
sNRH63	GAATCAGTCACCAGGGGAGA	CCATCGCGGTAATTAAACCT
sORH13	CCTGATGTTTTGGTTGTGTCA	TCACTGTGTTTACTTGCGCC
sR0282R	AGGAAGCCCAACAGGACTTT	AATTCGATTCTCCATCGTGC
sR10417	CGGAGAAGAAACGAGCATTC	TAGGGTTTCTGACCCGATTG
sR12095	GCTGCGAGGAAATCAGAGTC	TACACACTTGATCGCGCTTC
sR12137I	TCGGAATCAGATTAAACCCG	CATTATTGAAAAACACACGCC
sR12156	TTCTTGGTGTGTCCTGCAAA	GAGCTATGGCAATCCTCCTG
sR12777	CAAGCAGTTTAAGGAACCGC	ATAATTGCATTTTGCTCCGC
sR3688	GGAGTCCACTTCATGGAGGA	CTCTTGCTCGTAGGTTTCCG
sR4047	AGAGAGGGTGTTGTTCCCAG	ATTCTTTGAATGGCCAGCAC
sR6083	CTTGTTCTTGCGTAGCCACA	ACTTTGCTCTGGCTCAGCTC
sR6293	CCAAACGCTTTTCTTTCTGC	CCAATGACGCTCCAAGATTT
sR7223	AGGACCCGACTTTCCTTGTT	ACCAAACTCGGCGTACAAAT
sR9251J	TCTCCAGTACGGGGAAGAGA	CAAAGAAGCCATGTGTGGAA
sR9411	GAGCATAGGGCAAAAACTGC	CGATGTCGCTCTCAATCTCA
sR9447	AAATTCGAAAATGCAAACGG	CCAATCTTGGAACAATAGAAGATG
sR9477	CAGCTGGTTATCCTCGGTTT	CCTCAGGTGGACAGAGAAGC
sS1867A	TCACCAGGGCTGATCTATGA	GGGTGATCTAGATGGGTGAGTG
sS2131	TTGCTTCCAGAGATCTGGTTC	TGCGACTACTAAATTGTCGTGTT
sS2277	GATCTGCGGTAGGAATCGAA	CGTGCTACATAATAGGGAAAAACC
sS2331B	TGTCCTGTTTTCTGTGCTGG	GCCAACGCTAGTTTTGCTTC