Table S1. Polymorphic markers for polymorphic screening.

Chromosome	Primer	Location (Mb)	Polymorphism (+/-)	Forward sequence (5'–3')	Reverse sequence (5'-3')
1	RM1282	0.55	+	TCGTGCAGGAGGTCTTCATGG	TTGAGGATGGTAACGAACCTTGC
	RM283	4.89	+	GGCATGAGAGTCTGTGATGTTGG	TAGTACTGCTCCATCTGCCTTGG
	RM3174	5.09	-	GCTTCAGGAGCTCTCCAAAGAGG	CTAGCTCCGTGTCAGCAACACC
	RM1201	7.2	-	GCTACGTACGAGCCCTAGTTACCG	TACCGCGCCACATATACACAACC
	RM581	9.11	+	ATGCGTGATCAACAATCGAGAACG	CCATAGCCGATGGATTGAAAGTGG
	RM580	9.6	-	GAAATGGACTCGCTCCTAAACTGG	ACGAACTAGAGCATGGGCACTCC
	RM493	12.28	+	GTACGTAAACGCGGAAGGTGACG	CGACGTACGAGATGCCGATCC
	RM562	14.63	+	GGAAAGGAAGAATCAGACACAGAGC	GTACCGTTCCTTTCGTCACTTCC
	RM513	16.09	-	CTATTGGGCGTTGGTCTAGTGG	CAACGAAATCATCCCTAGCTTCC
	RM466	17.27	-	CCTCACCATTGATCTCCATCACC	ACTTGCCCTCCTCTTCTCAACG
	RM5964	17.6	+	TCTTCCAGGATCCGCCTTCTCC	GGAAGATCTCCCGCAGCTCACC
	ZTQ5	21.88	+	GGGTAGTCAATTAGTGGATTGAGG	ATTCCCAAGCCGTATGGC
	RM5718	22.29	-	TTTCGGACATGCGTAGTTGTAGG	CGTACGTGAAGCAATAAGGTGAGC
	RM6716	23.1	+	CCTATGCGATCTCCTATTTGG	CGAGTCAGACACGTACTACTGC
	RM11414	25.9	-	GGAAAGTAGAGAGAAGAACTCAGC	CACTACTTGTAGGTCAACATACCG
	RM3475	26.04	-	ATGTTGTCGAGTCGTGGTAATGC	TATTCCTCGGTGTATGGGTCTCC
	RM7202	26.2	-	AGGCTTCGACAATGACGTTTGG	TTTCTAAGCCATGAGAGCGAACG
	RM3143	26.82	-	AAAGCCTGGATAAGATGGTTCG	CTGTAGTTGCTGTTTGCCTGTCC
	RM1232	27.63	-	TCACTGGCTGTCTCTGTGGAGTGG	CGCTTTGCTTCCCTCCTCTGC
	RM443	28.34	-	GCGAAGCCCAATCTGAAGAAGC	CCAGTCCCAGAATGTCGTTTCG
	RM11575	29.38	-	GACGTGGGTGTTTGTATTTACG	TGTACCTAACAGGTTGATGTGG
	RM11608	29.88	-	GTATAATGGTGTGTGTCAGTGTGTGC	ACTGTGAGCCTGTGAGCCTACC
	RM11635	30.54	-	TTGTCACCCTTACTAGGATCAGC	GTGTGACTCTTGATGTAACTCAGC

Chromosome	Primer	Location (Mb)	Polymorphism (+/-)	Forward Sequence (5'–3')	Reverse Sequence (5'–3')
	RM128	30.7	-	TGATTTCTTGGAAGCGAAGAGTGAGG	CCTCCTTGTGCTCAGCCATGC
	RM1268	31.4	+	GCTGTCACTGACCGAGCGTAGG	TCGAGAGATCCAATCCAGTTTGC
	RM11694	31.9	-	GCGTCTATGCGTATCTTCATCTTACC	CAACTCTGCTAGTGTGCCTCTGC
	RM11706	32.1	+	CTTTGACCAGGACAATCTAGC	CTATTATACCGTGAGGTGTGTACC
	RM11709	32.2	-	CAGCCCGGCAGTCTATATTTCG	ACTGACGACGGGCTAGTGTTCC
	RM11717	32.34	-	TCAATAGAACCCATACGTCAGTCG	CATGCCACGGTTACTCCTACG
	RM212	33	-	AAGGTCAAGGAAACAGGGACTGG	AGCCACGAATTCCACTTTCAGC
	RM11745	33.2	-	CTCCTACATGTCCACGATAACAGC	AGGAGGGTGAGTGAATGTGTCC
	RM5389	35.73	-	TGTGCTATTGCGCGAGATTATCC	CATCACCGCTCCAACTCATGC
	RM3602	39	-	GGCTTGTGTTACTGCGATCTCC	GGTTCACTGCTCAATAGTCACAGG
	RM12177	41.3	-	CGGAATGGGATGGAACAGAAGG	AGGGAACAAAGAGGGCGAAAGG
	M33	42.4	+	CTTGAGTTCGAAGCGAGAAGACG	CACTTGAGCTCGAGACGTAGCC
	RM12245	42.72	-	TCCATCACTGGCACTGCTTGC	GTTCTTGCCGTCGTTGTCATTAGG
1	RM12246	42.73	-	ATCTGGACAACAACTCTAGCATCG	TCCTGCCCTTCCTTTCTTTACG
	RM12247	42.73	-	ATCTGGACAACAACTCTAGCATCG	TCCTGCCCTTCCTTTCTTTACG
	RM12248	42.76	-	CATTATCTGAATCCGGAGGAAGTAGC	ACACAAACCCTCGCCTCAACC
	RM12249	42.76	-	CATTATCTGAATCCGGAGGAAGTAGC	ACACAAACCCTCGCCTCAACC
	RM1067	42.91	-	CTAGGTGGAGCAGAGACAACAGC	TAACCGATGGAGAGAGAATGTCTAGC
	M69	42.92	+	CTCTACAGCTTGAGTTTGGTACATCC	GTGTTGGTGAGCTAGCTGTTGC
	RM12270	42.95	-	CTAGTCGGCATGGGTTTGAAGC	GTCTGCAAGTGGGTGAAGATGG
	RM12271	42.97	-	GAGATATTGGGCGAGTGCGAAGG	ATGTTGGCCGCTGCAAATCC
	M76	43.03	+	GTCGACGGCTTCCTCAAGATTGG	TGAGACCTCTGTGAAGGCACTCG
	RM12281	43.06	-	ACGGTTGGAAGAGAGAATGATCG	GCCCTGTAGGTAAGGAAGGAAAGG
	RM12282	43.12	-	CTAGCTAGTCAAACAAGGTAGTCC	CTAGTGTGGCGAGTAGTAGTGG

	RM12283	43.14	−	TGCTCAGCAGTGGCTCATCC	TGTGATGTCCCAGCGAATAGC
	M86	43.17	+	CTCACTCACTGACCCACAACTCC	TTAAGATGATGGCTCCTCTCTGC
	RM12288	43.2	−	AGCTCGGCCCTTGTGCTTCC	GCTGGCCCATCAGAGTCAGAGC
2	RM279	2.88	-	CCTCTCACTCACGTGGACTCTCC	CCTCACCCTAGGCTTTGATATGC
	RM1075	3.83	-	GCATGGAGACCTTAATATCCAACTCC	GATAGACGATCGAGTTGGGTTGC
	RM3732	4.41	-	GGCCCATCCACAAACTCAGATGG	CTAACGGATCATGCAGAGAGGAGACC
	RM3294	5.2	-	ATAGACGGATGGCACGAGATGC	ATGTGTTCAGTTCAGTGGTGAGTGG
	RM6378	5.47	-	CTGATCATCTCATGCCTCCTACG	TCCATCTCCCAATATGACCAACC
	RM12733	6.75	-	CAAGCAGCATAGAGAGTCATCTCG	TGAGTTGACCGGAATTTGACC
	RM174	7	-	ATAAGCGACGCCAAGACAAGTCG	GGAAGCAAGAAGGAAAGAGAGATGG
	RM145	7.71	-	CACTGCTTTGCTCTCCAGTCTCC	CAACATCTCCGTCAGAATCAAGC
	ZTQ17	8.55	-	ACATCAATTCTTCTGTTGTGCC	CAACTGATCTGAGCGTGGG
	RM5699	8.98	-	TATTGGTATGTGTGGGATCG	CTGGTGTACCTATATGGATTGC
	ZTQ18	9.78	+	AGCGATCCTTGGTGAGAGC	TGACCAGCACAAGGTGAGC
	RM324	11.39	+	GATTCCACGTCAGGATCTTCTGG	GCTCACCAGTTGAGATTGAAAGG
	RM300	13.19	-	GGGCTTAAGGACTTCTGCGAACC	AGCGATCCACATCATCAAATCG
	RM6374	15.28	-	TCACCAGACTCAACAAAGGATCG	TTCACCTTTCTTCTCCCTCATTCC
	RM5812	15.99	-	ATTGCCCTTTGGTAGGAGATACG	TCCCTATGGAAGGAAGAAGATGG
	ZTQ23	17.46	+	CAGAAGCACTTCCCTCATAAGTC	TTCGGCCAACTTTCCTGC
	RM13508	22.4	-	AAGGGAGAGCTTAACCAGCAAGC	TGCCGAGTTTATCTGAACTTGAGG
	RM5430	22.82	+	TAAAAACTGAGCCGTGAGCC	ACCATGGGGAGCTGCTTC
	RM3874	23.86	+	AAGCTGGGTGATCTTAGTTTGG	GAGAGTAGTGGCTATTTGCTTGC
	RM3515	24.04	+	CATGCTAGTAAGCAAAGGGCAACG	TTGCACGTCCAACTGTCCAAGC
	RM1920	25.46	-	GCCTGGTAAGTGGTAATGTAATGG	GTGAATTCCTCCTTGGTCTTGG
	RM1385	26.64	-	GACAGGTAAGGTGTGGTGGTAAGG	AAACCTTTCTCAAACGCACACG

Chromosome	Primer	Location (Mb)	Polymorphism (+/-)	Forward sequence (5'–3')	Reverse sequence (5'–3')
2	RM599	27.11	-	CTGCAGCTCTTCCCAGAGAACC	CGCGGCAGAGTAGCAGAACC
	RM13769	27.63	-	CCACCATTCGGTAATGAGATCG	GACGTGGTGATAGATGGTTCTGG
	RM497	29.05	+	GCTGCTTGTGTTGTTGTTGTCG	CACAGGCTCCTCTTCACCTATGG
	RM6	29.58	-	GTCCCCTCCACCCAATTC	TCGTCTACTGTTGGCTGCAC
	RM5472	30.64	-	TTTCACTCAAGACCAGACCTGTACG	GCACGTCATTGTAGTGACTAGTGAGG
	RM3263	32.66	-	GGAGCAGTGGATGGATCTGAGG	GCACCACCAATCTACTCCTATTGTGC
	RM5460	33.77	-	ACAACCACAGCTGCTTGAATTGC	AGAGGAACCCACTGCCCTTGC
	RM213	34.66	-	ACAAGCAGATACTGACTGATGC	CTTCTTTGCATCCAGACTTCC
	RM207	35.39	+	ATCCTAGTGGATAAGGCACAGACTGG	CCCTTGCTCTTCCACCTCATCC
3	RM4108	0.53	-	CATGCATGCAACTCTGCTAAACG	ATCAGGATCCAGGAAATCGAACC
	RM132	1.01	-	CTTTCTCTCGCCTACGCCTTCC	TCGACGAGGTTGATCAGTAGGG
	RM6297	1.74	+	CTCTCCTCTCGCTCGCTGTTCC	GAGTGGTAATTGGGCTTGGATGG
	ZTQ26	2.13	-	TTAACCCAGCACGATTACTAGC	GTCCGAGCCCATGTAGTGTAG
	ZTQ75	2.15	-	GTATCAGACGATCAGACACCACC	GCGTGAGTAGTAAAGAGGACAGC
	ZTQ76	2.35	+	GTGTCAATTATCGGAGAATGGAG	AACTAGCAGTGCTCCCTACTCC
	RM1332	2.45	-	ATGCAACAGGGAGGTGCTTGG	TGAATCTGAAGATGCCCAAGAGG
	RM5628	3.12	-	CATGTAATCGCACCATGTTTGG	CACAATGTCGACCTCCAATATGC
	RM5474	3.8	-	GTGGGTTTGTGTTTGGAGAGACG	GTGTTGGTGAGCATAGCAGTTGG
	ZTQ72	3.83	+	CTCTGCACGGAGCAATAGC	ATGACTCAACCTAGTTTACCCTTTC
	RM175	3.86	-	GACGGAGGAGTTCGAGAGGAAGC	GTGAAGCGACTAGGCGGAGAAGG
	RM489	4.33	-	GAACAGGGACACAATGATGAGG	GACGATCGGACACCTAATTACAGC
	RM6038	4.82	-	CCGTCGTGTCGTACTGGTAGTCC	TCCACAGCCTACCTAGCTTCTCC
	RM1324	6.03	-	CCAAGTGTGTCCGAGCTTAGTGC	TGAGTCAAAGCGAAAGTCAACAGG
	ZTQ70	6.82	+	CCTGTAGGTCAGCAATATACACG	GCATAATGATGGGACACCAAG

	ZTQ31	8.25	-	GGCCTCTCGAACACAGCC	GTCTATCAGGACCTGAGCAAGG
	RM157	9.49	+	GTCTTCCTCCTCCTCACGAATCC	CGGCTTCTTCTCTGCCTTGG
	ZTQ32	9.96	-	CTCATGCTTGGGTCTCGC	GGCAGCAGGTGAGAATCG
	LJH-3	10.29	+	AAGCCGAACCACAAAGCTAG	AGGAACAATCGTTTCATCATCC
	RM1284	10.59	+	CCTCCTTCGTAAGGGAACATATCC	TCAATTGCACCTCTCCTTGAAGC
	ZTQ33	11.48	-	CCTATACCATGAATGATTCGCC	GGAGGCAGTTGATCGAGTTG
	RM5928	12.57	+	CTTACCTTCTGAAATGGAGGTAGC	CAAGGTGAAAGACGAAGAATGC
	RM3257	13.27	-	CTATCCGGAATTGGACCCAGACC	ACTGGCGGTCATGGAGATACAGC
	RM15045	14.7	-	TTTGTCCTAGTTCCCTGCTGTTGC	AGCTTAGACAGCCCGAGAATGC
	RM15040	14.48	-	CAAACAAATCGTGGATGGATGG	CGCACACACGCAAATATATAGTCC
	RM1164	14.69	-	TTTCTGGCGACGTGATTTGTCG	CAATTCGGAAGAGCAAACATGACC
	RM2835	14.89	-	GACGTACTTCCTTCGTTTTA	TAAGTGATTTTGTGCATTTG

Chromosome	Primer	Location (Mb)	Polymorphism (+/-)	Forward sequence (5'–3')	Reverse sequence (5'–3')
3	ZTQ35	15.5	+	GCACATGCCCGCGTATATG	TTAGCATCCCAATGTGTAGGAG
	RM3400	17.07	-	GGGTGCACCTTTGTATCTGTGC	TGACAGAGGTAAAGCAGCAGTAGTCG
	RM15281	18. 48	−	CGGGCTTATATCTTTGGCAAATGG	GCCTCCTCCCTCCTTTCTCG
	RM15315	20. 2	−	CTCGACCAAACAGACCAGTAGGG	ATCGCCGCTTAGGAGAATCTGG
	RM15382	21.97	+	GGACAACGAGATAAACGAAAGG	GTCAAGAAGTTCGACAGGATCG
	RM8208	22.2	-	TGTAAATGCCTGAGTGCCTACCC	AGCTAAACCGCTAGGGCCTTCC
	RM6483	22.21	-	CCTACATAGAGCGTGTTCTTCTGC	GCACACTCTCCTCTCTGACTCC
	RM15414	22.34	+	TCCATCATATGCTCTGCTCTCTGC	CCTCCCTTCCTCCAGATCACC
	RM5864	22.39	-	AGGGAGTAACTAACAAGGTCACAAGG	GCATAAATTCAGCTCCGTACAAGG
	RM15626	25.8	-	TGGGTTTCGGGATACAAATGC	CCCGTTTAGGTTGATGGTTACG
	RM15632	25. 88	−	GTTGAGGCCGGAGATGATGAGC	CCGCCTATATAATGGCGCTCTCG
	RM15644	26.24	-	GAGCTTGCCGGTGATCAGATGG	CCGGGTTCTTCCTCAACTTCTCC

	LJH-4	26.75	+	TTCAGAACGACAACCTCTACAGG	AATAGCACCATAGTGTTTAGCAGC
4	RM2416	0.94	-	CAACGCCATTGAAACGACTAGG	GCAAGCACAGTTAGGCTCTTAATTCC
	J50-58	4.65	+	CGCAATCAATCAATCCAATC	CCTACTCATCATAATCTTGGG
	RM6487	4.67	-	CCGTGGAGAAGAAGCTGTAGACG	CTTCCCAACCTCAACCTCTCG
	RM3471	6.31	-	AGAAACAGAGGGAGGGAGCAGAGG	GATCCCGACAGATGGTGACTTGC
	RM3536	7.97	-	GCGACAGAGATGCGGGAAGAGC	TCACACATCCAACGGTCCAAATCC
	RM401	13.21	+	GCATGAGCTGCTCTCATTATTGTCC	GAAACGAACCAAACGTTCATCG
	RM3317	13.71	+	AACAGCAACCTGACAGAAGAATGG	TATGTGGCTTCTCGTTGAGTTGG
	RM5900	13.82	-	TGTTGAAGGAGATACACCGAAACC	TAGGATGTTAAAGCGCCACTTGC
	RM5687	15.91	-	AGAGAAGAAGGGAAGGAGGAAGG	AGTGACTTGTGGGTGACTTGTGG
	RM1100	17.95	-	TCTCGCTCTCGCTGTTTCTCC	TGCCTCTGGGATTTGGATGG
	RM16820	18.61	+	CCCTGCACCTGGATTCTCTCTCC	ATTGACGCACAGACAAGAACAAGACG
	RM1155	20.51	-	GACAGGGAGTGTGGCAACTATGC	GATCACAGACAATCATGGGTTGG
	RM5687	20.88	-	AGAGAAGAAGGGAAGGAGGAAGG	AGTGACTTGTGGGTGACTTGTGG
	RM3337	21.9	-	GGGAAGAGGAAGAGAGGAGAGAGC	GTGCTGAGAAGCCTGAGATTTGG
	RM3524	22.89	+	CTGTCTCCGTCTTCCTCACTCG	TGGAGAAATCTCCCTTCCTGAGC
	RM3785	24.22	-	GCAAGCAGCAAGAGCGAAGAGG	CTCAAGGCCGCCTCTCAAATCC
	RM3735	26.39	-	AACTCCTCCCTTGCTGCCTCTCC	CGAGAGGTCCTTCCACGTCAGC
	RM17308	27.44	-	AGGACTGAGGACGGCGAAGG	CGAAGAATCCGCGACACTAACG
	RM7187	27.65	-	CACACCAACTTCTCGCGGTAAACG	CACAGCGAACGTGGTGTCTTCG
	RM3170	27.79	-	GCAGTGTCATTCTCATGAAACCTACC	CAGACTCCAAAGCACCCATAACC
	RM5320	27.99	+	GTACAAGCAAACGCTTCCCAAGG	ACGACATGTGCCGGTAGATCAGG
	ZTQ37	29.34	+	CATGAGATAACGATGCCTCG	TGTTCTGGACCATATACGATACG
	RM6955	29.78	-	AAGATCCACCGTCATCCTCTGC	GGTGTGATGCTACTTGTCAGAAACG

Chromosome	Primer	Location (Mb)	Polymorphism (+/-)	Forward sequence (5'–3')	Reverse sequence (5'–3')
4	ZTQ38	31.09	+	TGCGAATGCTTGAATGGATC	CAAGGCTCACTTCCTAGATCAAG
	RM6909	32.06	+	TTTGGGATAAATGGGAGAGG	TCAGCTGGTTATTATGGAGAGG
	RM5611	32.67	-	GGAAGACACATCTTACACCGTTCC	CAGCCACTCTGATCTCGTGTCC
	RM1153	33.03	-	TGGAGGAGCGGTGGTACTCG	CCGGTGGACCTAACAAATTACGC
	RM3648	33.3	+	CGAGAAGCCGAAGAGGAAGAGAGC	CCAACAGATCCATCTCAACCAACTCC
	RM3399	34.92	+	CTCTCCTCCCTCCCTCTTGTCG	AATACCCAACACACAGGCTACGC
	RM6303	35.29	-	GCCTCAGCCTCAAGCTCTGC	ATCCACCTTCCTGCTTGCTACC
5	RM2010	1.18	-	GCAATACACGCCAATCTTCTAGG	TTGGGATGGAGGTAGTATTGTGC
	RM153	1.58	+	CCTCGAGCATCATCATCAGTAGG	TCCTCTTCTTGCTTGCTTCTTCC
	RM405	3.01	-	TATGCTTTCTGTCAGCTTCC	CTGCTGTGAAAGAGTTGACG
	RM169	7.4	+	CACCTCCTCCAAGATCCTTATGC	CTCTCTGTCTCGCTGTCTGTTGC
	RM2744	8.3	-	TGGCTGGCACTCTACCTTGTACC	ATTCAGGGATGAGCTTGTCTTGG
	RM6082	8.89	-	GCGGGTGCTTATGTCACCTACACG	AATGAGGGTGGGAGCGATGTCC
	S113-17	13.5	+	CTACATTTCCCTATTGGACTGGG	GAGCCCACCCAGTGGTTC
	RM6724	13.7	-	GCGATTAGCGGTTACACAGATGG	TCAAGTACGCTTCTTGCCTATACACC
	RM6645	14.94	+	CTCCGGGATGCCATAGTTTCG	AAGCTTCCTCTCGATCGTCTTCG
	RM598	16.81	+	TTTCCGGACAGCTGGATTATAGC	GATTGAGGCAGAGAGACCTAATTCC
	RM1237	18.01	+	CAGCACACATACTCTGGCTCTCC	CCGCGAGCTTTAGAAGAGAAGG
	RM5948	18.97	-	GTTAGAACCCGATGTTGGTGTTGG	GGACATCAAGAACAGGAGACCTAGC
	RM459	20.23	-	CCTCCAGTATCGATCACCAAAGC	CGAAAGAAAGTCATAGCACGATGG
	RM3575	21.3	+	ACAGCCTCAAATTGTGAGCAAGG	GCTGTATGATCTGTATCCATCCATCC
	RM5642	22.24	-	AAAAACCGGCTAATCCCTCC	TTCGATGGGATTGATCGC
	C2	22.26	+	GAACAGAAAGGGTAGTGCCAAC	CTCATAAGCAAGTTGTCCAATGG
	RM3476	23.76	-	TGATAGTTGACAATGCAGGAGAGG	TCGATCCGGAAGTTATTTCTGC

Chromosome	Primer	Location (Mb)	Polymorphism (+/-)	Forward sequence (5'–3')	Reverse sequence (5'–3')
	RM421	24.03	-	GCATAGCTATCCAGAATCCATTGACC	AGACGTAGCTCAGGTGAAACATCC
	RM3664	27.6	+	GGGCTGTTGCCTTAAACTGTCC	TATGAATTGCTACAGGCCATGC
	RM3170	27.8	+	GCAGTGTCATTCTCATGAAACCTACC	CAGACTCCAAAGCACCCATAACC
	RM1054	29	-	ATCGTCTCGTCTCTCTGCTGTGC	CATATGTACCGCAACCTCACTTGG
	RM18911	24.12	-	CCTCGACGTACGGAAGAGGAAACG	CCGGAATCCTCGACGAGACG
	ZTQ51	29.3	-	AGGATACACCCATCCACATTG	GTCACATGAGGTCAGCGAGG
6	RM19313	1.47	-	TGCCATCTCATAAACCCACTAACC	CTGAGATACGCCAACGAGATACC
	RM587	2.29	+	TTCCCATCTGCACTACCATAATCC	GAGCAGAGATGTGCTTTGCTACC
	RM584	3.4	+	TATGTGGTTGGCTTGCCTAGTGG	TGCCCATATGGTCTGGATGTGC
	RM7420	3.96	+	CACAAAGCAAGCACCCAGAAGG	TCATGGCGTGAAGGAAGGAAGG
	RM7420	3.95	-	CACAAAGCAAGCACCCAGAAGG	TCATGGCGTGAAGGAAGGAAGG
	RM6734	3.96	-	GGGCTTGGACTTGGAGTCTTGG	GACCAGGACCGATCCATCTCC
6	RM19457	3.97	-	CACGGCACGATACATAAACAACAGG	AGGCATGGCCCATAGGTAGTTGG
	RM19458	3.97	-	CTGCTTCTCGCAGGATAACACG	AAACAAGCCGAGCAGAAGATGC
	RM19459	4.6	-	AGCTAGCAACGCCCTGAGATGC	TGCGTCCTCGTCGTCTATCTTCC
	RM19549	5.1	+	CCTGGTACTAACCATGTGATTGAGC	AACGTCAGAGTCTCACCACAAGC
	RM19558	5.3	+	CATCTGATCTCGCATGCACTTGG	GTCTCTCTGCCGCTGGATCG
	RM19570	5.4	-	CCCAGATATTCTGTGTGATCATGAGG	GAGTGAATGTGAGCCGTCTATTGG
	RM3370	6.64	+	GTGTCTTAGAGCATATAACG	AAATCTTGAAAAATTCTTCT
	RM5531	7.17	-	TTTGTGTTGGTAAGTTGCTTC	TTAAGGAGAGTGTTTTCTTTTCTC
	RM3330	11.06	-	CGTTCGAGCAGAACCATCTACC	CCTCTTCCGCTCCACTCTCC
	RM3183	12.44	-	GTGGTGCTAGTATGGACGAGAGG	CGGTTGGTAGACTGTAAACAAAGTGC
	ZTQ53	13.4	-	CGACCTGTAGCTGCCACC	TGGGCTCCTTCTGAGATAGTTG
	RM7193	20.2	-	ATGTGGGAATTTCTAGCCCC	CCCTAGTTTTCCAAATGGCC

	RM3187	20.57	-	GCGGCTCTACGAGCTCCTCTACTGG	GAGCTTTGTCAGCGGATTTGTTCG
	RM3827	22.29	+	TAGGTAGGACCGTGCTTCATTGC	CCCTGGCCTTTCTTCAATCTGC
	RM5957	24.52	-	ACAAGACGTTGCCAACCATCC	CCAACGGTGGTGGTAGTGATAGC
	RM5371	25.44	+	GCAGAGGATGCCCACTTAATTCC	GGGCTAGCTTTAGCTGCGTTGC
	RM3567	25.61	-	ACCACGCGTCATTGACATCC	ATGGGATGAAACTGCCACAACC
	RM30	26.86	-	GTCACATTCCGTTTCCCATCATTCC	CCTCACCTCACCACACGACACG
	RM6458	27.56	-	TTGTCACGAGAGATGTGAGAGTGAGC	GGGTCTTCGAGGATGGAGTTGG
	ZTQ55	28.04	-	TGGTGAGGTTACCTAAAGGTCAG	AGCCGGAGAAGGATGACC
	RM400	28.43	-	TTACACCAGGCTACCCAAACTCG	TTGCTGAGTTCCCTCGTCTATCC
	RM6224	28.78	-	GAATCGCCTCCCTCCAACTCG	CTCATCGCTGTCCGGTGTTCC
	RM7412	29.16	-	CGAGTGGATCAGCAAATCTACAGC	CAGCATCAGGCTTGTGTTAATGG
	RM20701	30.34	-	GAGAAGAAATTCAGAGAGCAGAGC	CAACCACATGATCCATATGACG
	RM494	31.08	-	GGGATCGAGATAGACATAGACC	TCTGTACAGTGTCATTCCTTCC
7	RM20824	0.49	-	TAGTTGAGTACACCACACAGATGC	CCTTGAGTTTCTGCCTACAAGC
	RM6663	2.07	-	ACAAATACAGTGGAAGCGTGTCG	GAACACGTCTGGGAGCACTACG
	RM427	2.67	+	TTGAGCTGATGAGAGTTGGTTGC	CTGTCACTAGCTCTGCCCTGACC
	RM4098	3.15	-	GAAGATGCAGAGCACGGAAGC	GTGTTCGTTTCGGATTAGAGTTGG
	RM8263	4.65	-	TACGTTACGGTTCACTTCATGG	GGCCAAGACAACTTCAAGACC
	RM6081	5.59	-	GACCAAGACGAGCCAAGAAGAGACC	ACCCTGAACACCACGCACTCC
	RM5672	6.38	-	ATATAGAGGCAACCACTTAGCC	TACACCCTACAAGGAAACAAGC
	RM3583	8.08	-	ACCATGAGGTCCACTTGATACGC	GCCATGTCATCATCTGATCTCTTTCC
	RM5436	9.12	+	TGAGCTGCACAAGACAGACAAGC	ACCATTTGAACAGGATGGACTGG
	RM6222	10.06	-	CTGGGCCAACACGTTTGAGTTCC	CCTCCTATCCGGAGAAGGACTTGG
	RM1135	16.93	-	GTATAGCCAACCAAGCAAGATAGC	GATGCCTAGACACACATGTAAGC

Chromosome	Primer	Location (Mb)	Polymorphism (+/-)	Forward sequence (5'–3')	Reverse sequence (5'–3')
7	RM445	17.46	-	GCCTTGTCCCTAGCTAATCATTTCC	GGCTCGAATCTACGAACAACAGC
	RM320	18.69	-	TACAGCAGGGTGGAATATCGACAAGC	TCGTTGTAACGCGTGGATATTTGG
	RM11	19.25	-	ATCGGTGCTTGGCTGGATAGC	CCACCTTCTTCTCCTCCTCTTCC
	RM2966	19.73	+	CTGGACGATTTAACTGGAGATTGC	TCCCGTACGTATGTATGGTTTGC
	RM3826	20.8	-	AGTCTCCGCAACACAGAGTCAGC	TGAAGAGAAGTGCGTGATTCTTCC
	ZTQ65	21.1	-	CCATCGTGCTGATGCTCC	TCGAGTGGCGTAGTCTAGTCG
	RM1279	21.61	-	TCGGGTATAATTATCGCAGCACACG	ATGGATGGTACGAGGACGAGAGC
	RM455	22.35	-	CCACAAATTAATCCGGATCACACC	AGCATTGTGCAATCACGAGAAGG
	RM7564	22.75	-	CGCACAAACAAGTAAACGACACC	CATGCTAGCTTGGATGTGTAGTGC
	ZTQ66	23.6	+	ACACCAGCCATCACCTGTTAC	GAGTAAGAGCGGGCTGGC
	RM21931	24.63	+	CCTGCATTTCCTTTCAACTCATGG	GTGTTCTTGTGATCGTGCTCTCG
	RM3589	25.1	-	CTGGTCTGGATTTGAAGTCTCACC	CAATGTCCAAGATCAGGGTAGAGG
	RM21991	25.84	-	CACCGTACAGATCGGAACCAGAGC	CATGCTCGCCAAGTCCAGAGC
	CY7-6	25.69	+	ACTGCCAAAGATGTGAAGCTAA	AATTCACCTTTGGAACAATGGA
	RM8261	25.86	-	AGCTCGACGACTGGATGGTACG	GGTGCTTCTCCTGCAAACACG
	RM21992	25.85	-	ATGGGTGAGGCTTTAAACACAGG	TAAGCCAGTCCATTGGCAAACC
	RM8261	25.86	-	AGCTCGACGACTGGATGGTACG	GGTGCTTCTCCTGCAAACACG
	RM21996	25.87	-	AGCAGCAGTGCAGGAGTAGTAGC	CGAAGAAAGTATAGCCACCATGC
	RM3552	26.35	-	GTAACACTCTGCACACCACAATGG	TGAGCTGGGACAGAGGAGAGG
	RM22037	26.39	+	AATGGAGGTGCGATACATTCTGC	GATATATGCATAAGCGGTGTGTGG
	RM22039	26.4	-	GATCAACGAACCCACCACACC	CGCGTCTTGTATATGCACTTGATCC
	RM22040	26.4	-	AATGGAGCTCCTGACTCTAAAGC	TGCATCTCCTACAGAAACAAGG
	RM22060	26.93	+	CGAACCGCCTTCTCCACTGC	TGTTGGTGTCCCTCTCCTAATTCTCG
	RM22065	27.02	-	GAAGTTAATTGAGCTTGGCGATGG	AGCACGTGGAACAGAAAGAAAGG

	CY7-15	27.39	-	TCGCTCGTCAATTCTCTCCAC	ATGCATAATACGGAGTAGTGAAC
	CY7-4	27.48	-	CCACAAAGGCGAGAGTCCAA	TGGGTGTCGTAGCCCTCTT
	RM22071	27.57	+	TAGGCAATTAGGCTCCACGAAGG	TGGCACTACGTCGATAAAGAATGC
	CY7-8	27.62	-	GGACTGTTGAATTGGGCCTC	GCACACAGAAATAGTTACCTTCT
	CY7-14	27.71	-	GGGACGACGAAATGGAAGG	CGAGACGAGTTAAGCCGCT
	CY7-30	27.73	-	TCTGTTGCAGGATGCTCTAAA	TGAAGCATGGTACAGCAATAAA
	RM22087	27.79	+	GATCCTCTCGTCTTCATCTTCTATCC	TCGCTTTCCAAACCTCTTAGAACC
	RM5720	28.66	-	GACTCGTCACTGACACTGATACG	CTTGTTAGGAAGAGCATTCTGC
	RM1357	28.85	-	CGATCCTCAAGCTCCAAATTTCC	CGTCACTGCACCCATAACTGC
	RM22143	28.89	-	CTCTTTGGATTTCTGCCCTTCG	TGGTCCTTCGAGAGGTTCTCTAGC
	RM7601	29.03	-	GTTTGTTGCGTCGAATGGAAAGC	CGGCTTGTGAATTTGCTTGTGG
	RM420	29.43	-	CCTCTCACTCTGCCTGCTCTACC	TCTCTAACTCTTGAGTGACAGCAACC
	CY7-5	29.62	+	GGATTCTGCTTACAACATGAAG	TCCTTATTTGTACTAGGCTTTG

Chromosome	Primer	Location (Mb)	Polymorphism (+/-)	Forward sequence (5'–3')	Reverse sequence (5'–3')
8	RM152	0.68	-	AAGGAGAAGTTCTTCGCCCAGTGC	GCCCATTAGTGACTGCTCCTAGTCG
	RM38	2.11	-	ACGAGCTCTCGATCAGCCTAGC	CACTCCATGGAAGAGGCAAGC
	RM1270	3.07	+	ACTACCACGGACCAAAATAC	AGATCATCAGCATCAACTCC
	ID43	3.53	+	GGCGGTATTACTAAGAGGACCA	GCATGTTGGAAATGGAGTGAA
	LJH-8	8.13	+	GCCACTACGATGACTACGCTAG	CGGCTTGAGATTGATTGATTG
	RM6429	8.38	-	GATGTTGGTGTGCAGGGTGTAGG	GTCACCACCCTCTACGTACGTTCC
	RM8243	8.93	-	TCTACCTTAGCTGTCCTGAATTGG	CACATACCTGTTCCGTTTGATCC
	RM3481	9.12	+	CCTCACGTCGTGCTCTCCAACC	CCTCGTCGCGTTCGTCAACC
	LJH-9	10.14	-	GAGCCTAGCAATCAACTGATTG	CGGGCTTCATGCTCAGAA
	RM7027	15.84	+	CTCCAAACTGTGAAAGATGG	CTCTAGGACCTGGACTTTATGG
	RM6382	16.91	-	GCCGCAGTGAGGAAGAAGAACG	GACGTCAAGTCCGCCAACATCC

	RM5767	18.82	-	GTCCGACTCACCTCCCTCTTGC	CCTCATCCTCTCCACGCTCTCC
	RM3153	18.98	-	GTGTGATGGTGACGGATTACATGTGC	CATGCTGCAGAATTTCCATGTTGG
	RM223	20.65	-	GCTGGGCCTATATGGACTTTCG	AGGCAAGTCTTGGCACTGTAAGC
	RM210	22.47	+	GACAACTCCATATCAACGCAAAGC	GAGGATGGTTGTTCACTTGTTTGG
	RM1309	19.18	-	GAGGACACTGACGACAGCTTGG	CGCGCAAATCATTAAGTTCAGG
	RM8264	19.83	-	TTCTACGGAATTTCTCCCTCTGG	CTAATCAATCTCTCGCGTTCTTGG
	RM5808	20.26	-	GGGAGTAGGAGGGAGGGAGAAAGAGG	CAGAACCAGCGAGGGAAACACC
	RM515	20.28	-	CGAGATACGGTGAATGACACACG	ACCAATCAGAGAGCACACACAGG
	SSR08-10	24.7	-	AATTTGTAAGTTGCCAAGGACA	ATCGCGCTGCTTCTGAAAC
	RM419	25.82	+	TTCCTTCCCAGTGATTTCTCTCC	CCCTTTCTCCTCCTTTGGTATGC
	SSR08-1	25.9	-	GGAAGAGAGCTGATTCAGGAGA	AGTCCAGGTTAGTCGTAGCTGAG
	RM1345	26.14	+	CGCACAAACCAAACACACAACC	CTCGTGTCGTCTTCACCAAAGC
	RM5493	26.14	-	GCGGTAACAAACCAACCAACC	AAAGCAGGACACAGTCACACAGG
	SSR08-2	26.2	-	GCAGTAATACGTCCGTGCAAT	ACATGGAGTAAATCTGAACATAGC
	SSR08-3	26.2	-	CATGTGGTTCCCTCCTCCT	TGAGCATCCCGTGCTGTC
	SSR08-4	26.2	-	CCAAGTAACTAACCCGTCAAGA	AGTCACACAGGCTACCTCACC
	RM1615	26.27	-	AAACGTAGACGAAGATCACCTGTGC	TTCGAGAGTGATCAGTACCCTTCTCC
	Ind08-hp19	26.6	-	CACTTCTGGATATGAGAAGCTCAGTT	AGCTGAAACATGCGTGTTTAATG
	Ind08-hp28	26.91	-	CAAAGCGAGCAGCAAACTCA	TACGCCAGTGCTTGCGTG
	RM3754	26.96	+	CTCGAGCTACATGAGCCAATGC	GCCTCCTAACATGAAGACCATATCC
	Ind08-hp30F	27	-	CATGTTCCCACCTGTATAATGACTT	GTGGCGTATATGGTTACTCACTTATTA
	Ind08-hp22	27.2	-	GCCAGCATCCATCATGCTT	ACCGTCCCTAATGCCACAC
	Ind08-hp34	27.2	-	CTTGCTCTCCACCATGCCG	TGCATTGTAATCATACTGTGTTACATG
	Ind08-hp35	27.3	-	CGATCTATTCGTGTGTTTACGTGT	ATCACCAGCGCATCTGCC
	RM3376	27.32	+	GGAGGGAGTACTAGCTATTTACAGG	CAGAGGGACTCTTATGATGACG

	SSR08-26	27.4	-	GGCCTGTCTCGGTCTGAT	AGCACTTAGGATTAGCGGTG
	SSR08-28	27.5	-	GAATGCAAGCTCGCAACTA	AGGAGATTGGATTGCTGTACC

Chromosome	Primer	Location (Mb)	Polymorphism (+/-)	Forward sequence (5'–3')	Reverse sequence (5'–3')
9	RM23679	0.82	+	TCACAGCTTAGTGCATGTTGAGC	GATTCACCTGGCAATGAGAACG
	RM7007	1.1	-	GCAGTGGTGGTAAGGTAAGAAATGC	TGGAAATGGAGGAGAAGAAGAGG
	RM3609	1.1	+	GTCGCAGGGACTAGTTAGTTAATGG	TGGCATCTTCTTGGTTGTTAGC
	RM5688	1.6	-	GGTGATGATGAGTGTTTGATGC	TGACAGTAGTAGTTCAGCAGTGTCC
	RM6021	5.3	-	GAGGAGCTGCTTGTACCGTGTGC	GAAGCCACCCTCTCCTCCATCC
	RM444	5.87	+	TGCATCTTTCACCGTAGTCCTAGC	CTTGCTGGAGCTCGTAGATGC
	RM464	6.57	-	GAAGCAGGAAACAAGAAGAGAAGG	GTCTTCACCACAGTAAATGCTTGC
	RM6920	6.95	-	TGGTTGTCGATTTGTTGTCAGC	CGAAGTCATGCGAAACTCATGC
	RM5515	7.14	-	AGACCCTTGGCTACTGATTCC	AAGGTTCCACGAAAGATCTAGG
	RM5526	7.31	-	CACATGATCCTCCACCCACTAGC	GCCTGGCCTCTCTTATCTGTCTACC
	RM24006	9.28	-	CGATTGCCATTCCTTAGTACCAAACG	AGTTCATCTCCTCAAGCAGCAAGC
	ind 9-19	9.18	+	TCCAAGAGGTCCCGTAGC	GCAATCCGATGGCTATAACT
	RM7390	10.47	-	TGAGAGCTCGTAGGAAGTGTCC	CAGAGTCAGCAATCGCTAAGG
	RM27926	11.21	-	GCCATCACTGTACCTTGTTCTTGG	CAATGCCGACGAGTTCTTCTCC
	RM1896	11.76	-	CAAGTCGTTCTCTCGCCTACTGC	CATTGGAATGGAGGATGATAGTGG
	RM524	12.92	-	ATCATAGCCCAGACCAAGAATGC	AGATGAAGAGCAGGAACCGTAGG
	RM7039	14.63	-	CTTCCAGTGAGGTGACTCTACGC	ATGCACATTTGCCATTCTACCG
	ind12	14.64	+	TTGAGGCTTATCTGGCTCTTA	TACTTACTCCCTCCGTCCAA
	zj04	15	-	TCCTTAATTTAAGATGAAGAAGTCA	TAAAGGATCTTCATTGATGATCTT
	xs02	15	-	GCGAGGGTGAGGGCTC	CCGACGCCTATCCACC
	RM5122	15.24	-	ATATCACTGGGCAGACGGAGAGC	ACAGCCCACAGATCACAACAGC
	RM3700	15.37	+	CCTTTGCCGCCTTCTCTTGG	ACGAGTTCCCGGTTAACCTTACG

	RM434	15.61	-	TCTCTAGTTGCCTCATCCCTCTAACC	GGCTCAACCTCTATATTTGCTGATCG
	RM2819	16.22	-	TGTGGCCAGTTGAACATCATACC	GTCGAAACAAAGGAGGTGGTTCC
	RM7175	16.87	-	CGTGTCCATTGTGTGAAGCTACG	ACGTGGTGCCTCCTTTCAAACC
	RM3778	17.26	-	GGAGCTCGCGCAAGAGATGG	TCAACTCCGAATCCAATTCCTTCC
	RM242	18.64	+	AAACACATGCTGCTGACACTTGC	TTACTAGATTTACCACGGCCAACG
	RM108	19.01	-	CTCCTCAGGCTTCCCTCTCTTGG	ATCCCGAGATTTGCTTCTCTTGC
	RM6491	19.74	-	GGTGTTCCTGCGTGGCTTCG	GTTCCCGCGCTTTGTCTGTCC
	RM201	19.9	+	GTACTCTCGCCGTTCACAACTCC	TTAGTGACCGGGATGACACAGC
	RM24666	20.36	-	CTAGTGCACACGGGCGACAAGC	CTCCAGATGAGACGAGACCACACG
	RM6816	22.21	-	TCGCTCTCCATTGATAGCTAGACC	AGTGGCGCGATACTGTAAGAACC
	RM205	22.42	+	CCTAAGAGGAGCCATCTAACAACTGG	CTTGGATATACTGGCCCTTCACG
10	RM5095	0.052	-	CTATATGACTATGCGAATGG	ACAAATGCAACTAAGGTAGA
	XYD1-2	4.2	-	GGGATGCTGAGAATGTTGG	ATGCACGCTGGTGACATTG
	RM6271	4.44	+	AATGAGGTGTGGCGGTGTCG	AGTACTCATGCAAGCGGAAATGC

Chromosome	Primer	Location (Mb)	Polymorphism (+/-)	Forward sequence (5'–3')	Reverse sequence (5'–3')
10	RM6646	5.36	+	GGCAGTTTGATGTTGGAGAACTGC	ATTCAGCGACGACATGCACACC
	RM25108	5.61	-	ACCAGTGTCTCGTTGTGAGTAGC	ACTTCGAATAATGCGGTTGC
	RM25158	7.93	-	ACATGTAGGGTGTAGATTGTGG	ATTGTGCTAACTCCTCTGAGC
	XYD-5	10.15	+	TGCGTTTCCCACATACATGG	CAATCACATTCTACTAACTTCTGCC
	RM3311	10.69	+	CACTCGATGAGGCAATTTGAAGC	ATCATCCAAGTATCCCTGTCTCACG
	RM25167	8.35	-	CTCTGATCGATCTCAGCTTCTCC	ATCACGTTCGTTCACGTTTGG
	RM5348	8.55	-	TCACCGAATCCGATAGGAGTACC	CCTAAAGTGTATGGGCTGGAATGG
	RM4455	11.22	-	TGCTCCGGAGATGTAGACTATGTCG	TTCGTGGGTGATGGATATCTGC
	RM6142	12.35	-	CCTGCTTCTCCCTCCTGTACCC	GCGAGCAAATACAGAGGCTACTACC
	RM5758	12.47	-	GCCCTGATATTCAATGGATGC	AAGCGGTATTGGTGATTGTTGG

	XYD-4	12.93	-	GAATGGAGTAGAGGATTTCCAATAG	TGCTCTGCCATGTAACTCCG
	RM8201	13.83	-	CCCACTATGCTGGTACACATCTTTCG	CCTCTTCCGCTTCGCCTTCG
	RM5147	14.02	-	CTAGGTATAGGGTATCGTCTTGG	AGGTCCTGACAATAAACTACCG
	RM1083	14.67	-	GAGGCATCAAAGATGAGGAAGAAGG	GGGTTCACAAACCATTTAGGATGTGG
	RM596	14.77	-	ATGGTCTCCACCGTCTTCTCG	TTCATCTACACGGACGAATTGC
	RM3470	16.84	-	ACTACACCTTGATGTGATCTCC	CAGAGGCAGAGCTACTATTGC
	RM6128	19.83	-	GGAGGAGGTGTAGGCCATAGAACG	AATCCCAACCCACCACCTCTCC
	RM147	20.5	-	ATCGAAACCCTAGCTCCTACACC	GATCTTCCTCGAGAACGTCATCC
	RM3123	21.83	-	ACGCTCTTAATTGATCCGTTCG	CAAAGTCCAGTTCCGTTGATCC
	RM591	22.45	-	CTCATAGGTGGGTTAGTTTCTTGG	GCTGGTTTACAACTTGCTACTCTACC
	RM4771	22.57	-	AACTGAGAAACATGGGACAGAAGC	CTCAACCACACCCTCATTCACC
	RM6179	25.87	-	GCGCCGCCGAGATGATAAGC	AGCGGCATCTCGTCCATCTCC
11	RM7173	0. 44	-	TTTCTGTGGGTCCTCATCTTCTCTCC	CAATGTGTGATGTCGGATTCTTGG
	111	0.53	-	AGGGTCACTCTTGCGTATGAA	GTGCTAAGTGGCAATGATATAAGAG
	RM3717	1.17	-	ATCCCTTTCCCTCAACCAAATCC	AGCAAGCTCTACCTTTGCTGTCG
	RM1240	1.46	-	CACTCACATGCTCAAATGGATCG	CACCTGATCAAGCCATATCACTCC
	RM6288	2.17	-	GGCCCAGCAGCAGTACATGG	ATTGGGTAGTGCATCGGGTACG
	RM1812	2.41	-	CCTACCTCCAGTGAGAGCTAACC	ACGTGCATTTGTGTGGTTTAGG
	RM6085	3.04	-	GATGATGGCGACCACCAGTAGG	CCAGCAGCTAAACCCTTCTTGC
	RM1124	3.85	-	CTAGGGATCGGTAGACCCAATCG	TGGTGATGGCACTTTAGACAGAAGG
	RM4504	5.47	-	CCTTGGATGACAATGTTGAGAACAGC	CTGGCTGCATTGTAATTGATGAGC
	RM3625	6.66	-	TGCAATTTCATCCACCCATCTCG	ACGAGTGCACGCTGTCATTGG
	RM3701	8.1	-	GAAAGAGGAGGAAGAGCTAGAGG	CCATATGTACGGAGTGTGTTTACC
	CZ-9	9.7	+	CCGCTATCTTCTCCCTACGTG	GGAGTTGTAATAGGTGGTAGAGGG
	RM4862	9.98	-	ATCACAGTGTTGATCCATCTCC	CAATCCTAAGAAGGGTATCTGG

	113	10.63	+	GCTTAATGCTTCTCGATATGGG	GAAACTTCGGCTCCTCACA

Chromosome	Primer	Location (Mb)	Polymorphism (+/-)	Forward sequence (5'–3')	Reverse sequence (5'–3')
11	RM26480	10.64	-	CACCACCACCAGTGCCTATCG	TGCATATGGGCCTCTAAACATGC
	RM3428	13.94	+	GCCATTGACACCAAATGATCACC	GGCATATAAGGTCCATGGTGAATTGG
	RM26662	15.26	-	AACTCCACCTTTACCCACACTGC	CGCCAGTAGGAAGGAGATGATAAGG
	RM26668	15.43	+	ACGAAGCGTCCTGCATCATCC	CCTTCCAACCGAAATTTGAGAGG
	RM26710	16.4	-	ATCTACTCCGCCACCACCACAGC	CTCTACCTCTCCCTCTCGCCTTCC
	RM7303	16.98	-	GCGTTCGTCCAGATGAAGTTCG	GCTTGTGCAGCAGGGAAGATACC
	CZ-10	17.64	+	CTAACGGGAGTACCCACTGAAC	GGGTTGTGTTTCAGTGAGACTG
	RM457	19.53	-	GCACAAGTTGATACTCTCCTCTGACG	CCACCATTATCTGCTCCATCACC
	RM1219	20.66	-	CGACGAGGAATGGAGGAGTTTGG	TCCTATGTTTCAAACCTGCCCTCACG
	SWU11-31	21.22	+	GACAAACCGAGCCATACGG	GGGTTAATTTGATCCGTGCC
	RM206	21.63	-	ATCGATCCGTATGGGTTCTAGC	GTCCATGTAGCCAATCTTATGTGG
	SWU11-44	21.71	-	GTAAAGCGGTGAACCACACTG	TACGCAAGTGGATGACGGA
	SWU11-48	21.82	+	GCAGCTCTTCCAAGTGACTTG	GTAAAGAGCCCAAATCTGGC
	SWU11-49	22.03	+	GTTGCCAAATGATGCTTAGTTG	GTTTGCACATTCCAGTAGTAGCC
	SWU11-36	22.27	+	CACAGGCCCGATTTGGT	AGCGCGAGCAGATTAGGG
	RM7277	24.68	-	TGTCTGACTAGCACTGCTGAACG	GCAGCTTAAGAGCGTTTGTAGGG
	RM2191	25.12	-	TAGTTGTTCGGAGAACATGG	ACACAAAGACACCTCGTATGC
	RM4069	26.67	-	CCGAGACTTCAGAGTGCTCACC	CTATATTGCCGTGGCTCATTAGTGG
	RM27248	26.79	-	CAGCGACTGCTTATGGTTTACCC	CTGAATAAACGGCGGCATAAAGG
	RM1233	27	-	ATGGGCACGTGTAATTCATTCG	ATCCTCGAAAGTAGGAGTAGGAAAGC
	RM144	28.8	-	CATGTTGTGCTTGTCCTACTGC	AGCTAGAGGAGATCAGATGGTAGTGC
12	RM5367	0.16	-	ATTCCTCACGCCCACTGTACC	AGTGATATCCAACCCGAACTTGC
	RM6335	0.48	-	GGATCTCCAATTCTCGATTCATCC	CCTCCCTCCATCTTCTTGATTGC

	RM3609	1.1	-	GTCGCAGGGACTAGTTAGTTAATGG	TGGCATCTTCTTGGTTGTTAGC
	RM247	3.18	-	AAGGCGAACTGTCCTAGTGAAGC	CAGGATGTTCTTGCCAAGTTGC
	RM6296	3.2	-	TTAAGCCCACGTTTCTCTTGTCC	CTCGCTAGGGTTAGGGTTTCAGG
	RM27568	3.23	-	TGTCATGTCGAGGATCGGAAGC	GAAACGATCTGGTTGCCTTCTCC
	RM27573	3.27	-	GCCTCAACAAGATTCGATTCACC	AAATCGGGTTCGGACTTATCAGG
	RM3472	3.52	-	CACACACTCTCTCAATCTCAACACC	AGAAGCGAGAGGAGGGAGATAGC
	RM491	3.58	-	CACATGATGCGTAGCGAGTTGC	TTATGCCTCTCCCTTCCCAATTCC
	RM3455	4.92	-	TGAATCCACACTCGCAGATCG	AAATCAGCTCGGAGGGAACAGC
	RM7119	6.69	-	CTGAGACCATGACGGGATAAACACC	GGCCTCAGATCATCACAACTTGG
	RM7003	6.77	-	CTCTAGCTCTCTCATGGATGG	AATCATAGGGCAGACATACAGC
	RM2935	7.4	-	CTTTGCACATGCGTCGTTGC	AAACTGCACATGGCCTCTCAGG
	RM101	8.82	-	AAGTAGTGGTCGAAGTGTGTATCG	GGTGAATGGTCAAGTGACTTAGG
	ind5	10.1	+	ATATGACGGACGGTTAAGTGTTGAA	AGCAAGCTGTTTGGAACTTGTATGT

Chromosome	Primer	Location (Mb)	Polymorphism (+/-)	Forward sequence (5'–3')	Reverse sequence (5'–3')
12	RM27871	8.84	-	AGGCTAGGATGAGCAGGAGAAGG	GGTGGGCCCTATATTCCAAGC
	ind19	11.18	-	GGAGTAACTTGGAAGGAGGTAATA	TATGAAAGAACACTCAGGCGA
	RM1337	11.93	+	AGTGGCCCGAACCTGTATAACC	GAGCAGGTGCAATGCTGAGG
	RM27966	12.12	-	TCTGAGCCAACAGTAAGAGTCAGG	TGTCACCCGTAGTGTTTGTACGG
	RM247	12.32	-	AAGGCGAACTGTCCTAGTGAAGC	CAGGATGTTCTTGCCAAGTTGC
	RM1261	17.53	-	ATGGTAGAGACACAAGTCCATGC	GACAAATTGGTGTAGGTGAAGG
	IND-34	18.1	+	ACCCTAACCACAAATATCGCCTA	AGGATGTGGCGGTAGAATGCA
	RM1246	19.11	-	GGCTCACCTCGTTCTCGATCC	CATAAATAAATAGGGCGCCACACC
	RM28349	21	-	GAGAGGAGAGGGAGAGAGATGC	CATGCTTACCTACTCTGTCCAACG
	RM1986	21.24	-	TCTGTGGAGAAGAAATGGATCTCG	CATCTCTCCTCTAGGCGGATTGG
	RM3326	21.77	-	AGAGCGCCGTTCCTTCTCTTTCTCC	AGGAGGGAGAGCACGTGAGAGAGG

	RM4589	22.02	-	GTTTAAACATGGGAGGTGTCAACC	CGGGCATCACTGAAATACCG
	RM7018	22.19	-	GTTTAAACATGGGAGGTGTCAACC	CGGGCATCACTGAAATACCG
	RM6869	22.3	+	GGCTAGCCAGGTCTTGGAGAGG	CACCATGAGCTCCTTGTAGTGACC
	CZ-12	22.58	+	CTCATACATGCTACCATGATATGG	CCATGTTAGATCCGTCCTACAAG
	RM3813	23.31	-	ACCGTTAGATGACACAAGCAACG	GGTTAGCAAGACTGGAGGAGACG
	RM7376	23.47	-	CCTAGGTGGTTGTGTTCTGTTTGG	CGTCACCTCTTAAGTCAACACATCG
	RM3331	23.49	-	ACGAGAGGGAGGAGAGAGAAACG	GGAGAGCCACAGGAACAGATCG
	RM1103	23.57	-	GTCGGTGTGTACTCCGTGTTTGG	CATATGCAGTGGTCAGTGGAGTGG
	RM2854	23.62	-	AGCATGAGACCCACATATCAGC	CCTATCTTAGAGTGCCATCTAGTTCC
	RM6410	23.98	+	GGAAGAAGCATCTGCAGTAGTAGACG	GAATTAGCCGACAGCGTCTTGG
	RM5609	24	-	GGAGGCCAGGGAAGAAGAAGG	TTGTGCCGCCTTTGGAATTAGC
	RM3226	24.11	-	GCTCTCGTGAAAGACCTACATCATGC	AGCTGCTTGGCGAAAGTTCTGG
	RM3739	25	-	CTAAGATCCAACGGGTTCTGTGC	TTGTGTGCACTTCGTCTTCAACC
	RM1264	26.17	-	GAGATCATCGTAAGTCCTCCTTCC	GGATAAGGACAAAGCAAGCAAGC
	RM28782	26.91	-	TAAGCTATCTTCGCAGGCGGATGG	GGATCTGCCACCTCACCATTGC
	RM28817	27.35	-	GAAGAACAGAGCTGAGGGTGAGG	GTACCATGGATGGAAGGTCATGC
	RM28819	27.39	-	GAACGTCTCGTTCCCTATCACG	TCCACTCACTCATCTCTCCTTGC
	RM2197	27.42	-	AGCATGAAAGTAGCGGCAGACC	GCTTCTTCTCGTGTGTCATTTGG
	RM28821	27.44	-	GCACTCCACATTGTTGTCATCC	TTGTGAAACGGAGGGAGTAGC
	RM28824	27.5	-	CCCTTCTCTTCTCCTGTACCC	GGTTCCTAGGTGTCATCTTAGTGC

Table S2. Polymorphic markers for gene pool screening.

Chromosome	Primer	Location (Mb)	Polymorphism (+/-)	Forward sequence (5'–3')	Reverse sequence (5'–3')
1	RM1282	0.55	+	TCGTGCAGGAGGTCTTCATGG	TTGAGGATGGTAACGAACCTTGC
	RM283	4.89	+	GGCATGAGAGTCTGTGATGTTGG	TAGTACTGCTCCATCTGCCTTGG
	RM581	9.11	+	ATGCGTGATCAACAATCGAGAACG	CCATAGCCGATGGATTGAAAGTGG

	RM493	12.28	+	GTACGTAAACGCGGAAGGTGACG	CGACGTACGAGATGCCGATCC
	RM562	14.63	+	GGAAAGGAAGAATCAGACACAGAGC	GTACCGTTCCTTTCGTCACTTCC
	RM5964	17.6	+	TCTTCCAGGATCCGCCTTCTCC	GGAAGATCTCCCGCAGCTCACC
	ZTQ5	21.88	+	GGGTAGTCAATTAGTGGATTGAGG	ATTCCCAAGCCGTATGGC
	RM6716	23.1	+	CCTATGCGATCTCCTATTTGG	CGAGTCAGACACGTACTACTGC
	RM1268	31.4	+	GCTGTCACTGACCGAGCGTAGG	TCGAGAGATCCAATCCAGTTTGC
	RM11706	32.1	+	CTTTGACCAGGACAATCTAGC	CTATTATACCGTGAGGTGTGTACC
	M33	42.4	+	CTTGAGTTCGAAGCGAGAAGACG	CACTTGAGCTCGAGACGTAGCC
	M69	42.92	+	CTCTACAGCTTGAGTTTGGTACATCC	GTGTTGGTGAGCTAGCTGTTGC
	M76	43.03	+	GTCGACGGCTTCCTCAAGATTGG	TGAGACCTCTGTGAAGGCACTCG
	M86	43.17	+	CTCACTCACTGACCCACAACTCC	TTAAGATGATGGCTCCTCTCTGC
2	ZTQ18	9.78	+	AGCGATCCTTGGTGAGAGC	TGACCAGCACAAGGTGAGC
	RM324	11.39	+	GATTCCACGTCAGGATCTTCTGG	GCTCACCAGTTGAGATTGAAAGG
	ZTQ23	17.46	+	CAGAAGCACTTCCCTCATAAGTC	TTCGGCCAACTTTCCTGC
	RM5430	22.82	+	TAAAAACTGAGCCGTGAGCC	ACCATGGGGAGCTGCTTC
	RM3874	23.86	+	AAGCTGGGTGATCTTAGTTTGG	GAGAGTAGTGGCTATTTGCTTGC
	RM3515	24.04	+	CATGCTAGTAAGCAAAGGGCAACG	TTGCACGTCCAACTGTCCAAGC
	RM497	29.05	+	GCTGCTTGTGTTGTTGTTGTCG	CACAGGCTCCTCTTCACCTATGG
	RM207	35.39	+	ATCCTAGTGGATAAGGCACAGACTGG	CCCTTGCTCTTCCACCTCATCC
3	RM6297	1.74	+	CTCTCCTCTCGCTCGCTGTTCC	GAGTGGTAATTGGGCTTGGATGG
	ZTQ76	2.35	+	GTGTCAATTATCGGAGAATGGAG	AACTAGCAGTGCTCCCTACTCC
	ZTQ72	3.83	+	CTCTGCACGGAGCAATAGC	ATGACTCAACCTAGTTTACCCTTTC
	ZTQ70	6.82	+	CCTGTAGGTCAGCAATATACACG	GCATAATGATGGGACACCAAG
	RM157	9.49	+	GTCTTCCTCCTCCTCACGAATCC	CGGCTTCTTCTCTGCCTTGG
	LJH-3	10.29	+	AAGCCGAACCACAAAGCTAG	AGGAACAATCGTTTCATCATCC

	RM1284	10.59	+	CCTCCTTCGTAAGGGAACATATCC	TCAATTGCACCTCTCCTTGAAGC
	RM5928	12.57	+	CTTACCTTCTGAAATGGAGGTAGC	CAAGGTGAAAGACGAAGAATGC
	ZTQ35	15.5	+	GCACATGCCCGCGTATATG	TTAGCATCCCAATGTGTAGGAG
	RM15382	21.97	+	GGACAACGAGATAAACGAAAGG	GTCAAGAAGTTCGACAGGATCG
	RM15414	22.34	+	TCCATCATATGCTCTGCTCTCTGC	CCTCCCTTCCTCCAGATCACC
	LJH-4	26.75	+	TTCAGAACGACAACCTCTACAGG	AATAGCACCATAGTGTTTAGCAGC
4	J50-58	4.65	+	CGCAATCAATCAATCCAATC	CCTACTCATCATAATCTTGGG
	RM401	13.21	+	GCATGAGCTGCTCTCATTATTGTCC	GAAACGAACCAAACGTTCATCG
	RM3317	13.71	+	AACAGCAACCTGACAGAAGAATGG	TATGTGGCTTCTCGTTGAGTTGG

chromosome	primer	location (Mb)	polymorphism (+/-)	Forward sequence(5'-3')	Reverse sequence(5'-3')
4	RM16820	18.61	+	CCCTGCACCTGGATTCTCTCTCC	ATTGACGCACAGACAAGAACAAGACG
	RM3524	22.89	+	CTGTCTCCGTCTTCCTCACTCG	TGGAGAAATCTCCCTTCCTGAGC
	RM5320	27.99	+	GTACAAGCAAACGCTTCCCAAGG	ACGACATGTGCCGGTAGATCAGG
	ZTQ37	29.34	+	CATGAGATAACGATGCCTCG	TGTTCTGGACCATATACGATACG
	ZTQ38	31.09	+	TGCGAATGCTTGAATGGATC	CAAGGCTCACTTCCTAGATCAAG
	RM6909	32.06	+	TTTGGGATAAATGGGAGAGG	TCAGCTGGTTATTATGGAGAGG
	RM3648	33.3	+	CGAGAAGCCGAAGAGGAAGAGAGC	CCAACAGATCCATCTCAACCAACTCC
	RM3399	34.92	+	CTCTCCTCCCTCCCTCTTGTCG	AATACCCAACACACAGGCTACGC
5	RM153	1.58	+	CCTCGAGCATCATCATCAGTAGG	TCCTCTTCTTGCTTGCTTCTTCC
	RM169	7.4	+	CACCTCCTCCAAGATCCTTATGC	CTCTCTGTCTCGCTGTCTGTTGC
	S113-17	13.5	+	CTACATTTCCCTATTGGACTGGG	GAGCCCACCCAGTGGTTC
	RM6645	14.94	+	CTCCGGGATGCCATAGTTTCG	AAGCTTCCTCTCGATCGTCTTCG
	RM598	16.81	+	TTTCCGGACAGCTGGATTATAGC	GATTGAGGCAGAGAGACCTAATTCC
	RM1237	18.01	+	CAGCACACATACTCTGGCTCTCC	CCGCGAGCTTTAGAAGAGAAGG
	RM3575	21.3	+	ACAGCCTCAAATTGTGAGCAAGG	GCTGTATGATCTGTATCCATCCATCC

	C2	22.26	+	GAACAGAAAGGGTAGTGCCAAC	CTCATAAGCAAGTTGTCCAATGG
	RM3664	27.6	+	GGGCTGTTGCCTTAAACTGTCC	TATGAATTGCTACAGGCCATGC
	RM3170	27.8	+	GCAGTGTCATTCTCATGAAACCTACC	CAGACTCCAAAGCACCCATAACC
6	RM587	2.29	+	TTCCCATCTGCACTACCATAATCC	GAGCAGAGATGTGCTTTGCTACC
	RM584	3.4	+	TATGTGGTTGGCTTGCCTAGTGG	TGCCCATATGGTCTGGATGTGC
	RM7420	3.96	+	CACAAAGCAAGCACCCAGAAGG	TCATGGCGTGAAGGAAGGAAGG
	RM19549	5.1	+	CCTGGTACTAACCATGTGATTGAGC	AACGTCAGAGTCTCACCACAAGC
	RM19558	5.3	+	CATCTGATCTCGCATGCACTTGG	GTCTCTCTGCCGCTGGATCG
	RM3370	6.64	+	GTGTCTTAGAGCATATAACG	AAATCTTGAAAAATTCTTCT
	RM3827	22.29	+	TAGGTAGGACCGTGCTTCATTGC	CCCTGGCCTTTCTTCAATCTGC
	RM5371	25.44	+	GCAGAGGATGCCCACTTAATTCC	GGGCTAGCTTTAGCTGCGTTGC
7	RM427	2.67	+	TTGAGCTGATGAGAGTTGGTTGC	CTGTCACTAGCTCTGCCCTGACC
	RM5436	9.12	+	TGAGCTGCACAAGACAGACAAGC	ACCATTTGAACAGGATGGACTGG
	RM2966	19.73	+	CTGGACGATTTAACTGGAGATTGC	TCCCGTACGTATGTATGGTTTGC
	ZTQ66	23.6	+	ACACCAGCCATCACCTGTTAC	GAGTAAGAGCGGGCTGGC
	RM21931	24.63	+	CCTGCATTTCCTTTCAACTCATGG	GTGTTCTTGTGATCGTGCTCTCG
	CY7-6	25.69	+	ACTGCCAAAGATGTGAAGCTAA	AATTCACCTTTGGAACAATGGA
	RM22037	26. 39	+	AATGGAGGTGCGATACATTCTGC	GATATATGCATAAGCGGTGTGTGG
	RM22060	26.93	+	CGAACCGCCTTCTCCACTGC	TGTTGGTGTCCCTCTCCTAATTCTCG
	RM22071	27.57	+	TAGGCAATTAGGCTCCACGAAGG	TGGCACTACGTCGATAAAGAATGC
	RM22087	27.79	+	GATCCTCTCGTCTTCATCTTCTATCC	TCGCTTTCCAAACCTCTTAGAACC
	CY7-5	29.62	+	GGATTCTGCTTACAACATGAAG	TCCTTATTTGTACTAGGCTTTG

Chromosome	Primer	Location (Mb)	Polymorphism (+/-)	Forward sequence (5'–3')	Reverse sequence (5'–3')
8	RM1270	3.07	+	ACTACCACGGACCAAAATAC	AGATCATCAGCATCAACTCC
	ID43	3.53	+	GGCGGTATTACTAAGAGGACCA	GCATGTTGGAAATGGAGTGAA

	LJH-8	8.13	+	GCCACTACGATGACTACGCTAG	CGGCTTGAGATTGATTGATTG
	RM3481	9.12	+	CCTCACGTCGTGCTCTCCAACC	CCTCGTCGCGTTCGTCAACC
	RM7027	15.84	+	CTCCAAACTGTGAAAGATGG	CTCTAGGACCTGGACTTTATGG
	RM210	22.47	+	GACAACTCCATATCAACGCAAAGC	GAGGATGGTTGTTCACTTGTTTGG
	RM419	25.82	+	TTCCTTCCCAGTGATTTCTCTCC	CCCTTTCTCCTCCTTTGGTATGC
	RM1345	26.14	+	CGCACAAACCAAACACACAACC	CTCGTGTCGTCTTCACCAAAGC
	RM3754	26.96	+	CTCGAGCTACATGAGCCAATGC	GCCTCCTAACATGAAGACCATATCC
	RM3376	27.32	+	GGAGGGAGTACTAGCTATTTACAGG	CAGAGGGACTCTTATGATGACG
9	RM23679	0.82	+	TCACAGCTTAGTGCATGTTGAGC	GATTCACCTGGCAATGAGAACG
	RM3609	1.1	+	GTCGCAGGGACTAGTTAGTTAATGG	TGGCATCTTCTTGGTTGTTAGC
	RM444	5.87	+	TGCATCTTTCACCGTAGTCCTAGC	CTTGCTGGAGCTCGTAGATGC
	ind 9-19	9.18	+	TCCAAGAGGTCCCGTAGC	GCAATCCGATGGCTATAACT
	ind12	14.64	+	TTGAGGCTTATCTGGCTCTTA	TACTTACTCCCTCCGTCCAA
	RM3700	15.37	+	CCTTTGCCGCCTTCTCTTGG	ACGAGTTCCCGGTTAACCTTACG
	RM242	18.64	+	AAACACATGCTGCTGACACTTGC	TTACTAGATTTACCACGGCCAACG
	RM201	19.9	+	GTACTCTCGCCGTTCACAACTCC	TTAGTGACCGGGATGACACAGC
	RM205	22.42	+	CCTAAGAGGAGCCATCTAACAACTGG	CTTGGATATACTGGCCCTTCACG
10	RM6271	4.44	+	AATGAGGTGTGGCGGTGTCG	AGTACTCATGCAAGCGGAAATGC
	RM6646	5.36	+	GGCAGTTTGATGTTGGAGAACTGC	ATTCAGCGACGACATGCACACC
	XYD-5	10.15	+	TGCGTTTCCCACATACATGG	CAATCACATTCTACTAACTTCTGCC
	RM3311	10.69	+	CACTCGATGAGGCAATTTGAAGC	ATCATCCAAGTATCCCTGTCTCACG
11	CZ-9	9.7	+	CCGCTATCTTCTCCCTACGTG	GGAGTTGTAATAGGTGGTAGAGGG
	113	10.63	+	GCTTAATGCTTCTCGATATGGG	GAAACTTCGGCTCCTCACA
	RM3428	13.94	+	GCCATTGACACCAAATGATCACC	GGCATATAAGGTCCATGGTGAATTGG
	RM26668	15.43	+	ACGAAGCGTCCTGCATCATCC	CCTTCCAACCGAAATTTGAGAGG

	CZ-10	17.64	+	CTAACGGGAGTACCCACTGAAC	GGGTTGTGTTTCAGTGAGACTG
	SWU11-31	21.22	+	GACAAACCGAGCCATACGG	GGGTTAATTTGATCCGTGCC
	SWU11-48	21.82	+	GCAGCTCTTCCAAGTGACTTG	GTAAAGAGCCCAAATCTGGC
	SWU11-49	22.03	+	GTTGCCAAATGATGCTTAGTTG	GTTTGCACATTCCAGTAGTAGCC
	SWU11-36	22.27	+	CACAGGCCCGATTTGGT	AGCGCGAGCAGATTAGGG
12	ind5	10.1	+	ATATGACGGACGGTTAAGTGTTGAA	AGCAAGCTGTTTGGAACTTGTATGT
	RM1337	11.93	+	AGTGGCCCGAACCTGTATAACC	GAGCAGGTGCAATGCTGAGG
	IND-34	18.1	+	ACCCTAACCACAAATATCGCCTA	AGGATGTGGCGGTAGAATGCA
	RM6869	22.3	+	GGCTAGCCAGGTCTTGGAGAGG	CACCATGAGCTCCTTGTAGTGACC
	CZ-12	22.58	+	CTCATACATGCTACCATGATATGG	CCATGTTAGATCCGTCCTACAAG
	RM6410	23.98	+	GGAAGAAGCATCTGCAGTAGTAGACG	GAATTAGCCGACAGCGTCTTGG

Table S3. Primers synthesized for fine mapping on chromosome 1.

No.	Primer	Physical location (Mb)	Polymorphism (+/-)	Forward sequence (5'–3')	Reverse sequence (5'–3')
1	M36	42.539	-	GTTATTACTGCTTCCTCCGTTTCACG	TGGTTCCCAACAACTGATGTAGC
2	M37	42.562	-	CGTCCTCATCGTCATCATCTCG	GGATGAGGAAGGACGTAGACATGC
3	M38	42.567	-	TCTCCCATCTCCCATATTCCCATCC	GCGCATGACGTCGGAGATCG
4	M39	42.579	-	TGCGAGCCATCACCAACTACG	ACCATGAGCTGCTGGATCAGG
5	M40	42.579	-	GAGATTATCGCCGTTGATACCG	CTCTTCCTCGGCTTCTTGTCG
6	ZJ-1	42.604	-	TTGCAGATGGGTTAATATACATCT	TTGACGTGAAAGAGCAGGAG
7	ZJ-3	42.614	-	CCACCTCCTGCCACTGAC	CGATGCACTGTTTAATTTGTTC
8	ZJ-4	42.614	-	GAAGAAGACGACACTGCCC	CGGAACATGACGAACGAC
9	ZJ-5	42.614	-	CCACCTCCTGCCACTGAC	CGATGCACTGTTTAATTTGTTC
10	M41	42.615	-	GGATACTCTATGTTCCTCTGCTGTGC	GTCTCCGCCGTCTCGTAAACC
11	ZJ-10	42.615	-	CGGTATTGGATACTCTATGTTCC	CCGTGTCCTTGAAGGACAG

12	ZJ-11	42.617	-	ATACAGTGACAGACATTGAATTGG	CATAAGTCAATATCTGCCTCCC
13	ZJ-12	42.617	-	ATACAGTGACAGACATTGAATTGG	CATAAGTCAATATCTGCCTCCC
14	ZJ-14	42.623	-	TAGGTCATGCCATCATCTTTG	GCGAGCCTGTAGTAGAAGCA
15	ZJ-16	42.635	-	CCTGGATGTGTATGGATTGG	GGTAGCTTTACCTATGTTATCCAAG
16	ZJ-17	42.636	-	ACCACTAAAGTCTCTTTCATTGC	GAGGAGAAGATCACCAACTACG
17	ZJ-18	42.637	-	CTTGATGAACAGCGACGC	CCGTCGATCACACACCAG
18	RM6490	42.651	-	TTTCTTCTTCCGGTAGCCAAAGC	GGTGGGATGATGATGATTGTATGG
19	ZJ-22	42.651	-	GGTAGCCAAAGCTGGATGA	GGATGATGATGATTGTATGGG
20	ZJ-23	42.656	-	GGAGAGGGCTGGTAATAGGA	CCCTATCCCTATCGCAACC
21	RM6491	42.656	-	GGCAGGAGAGGGAGAGAGAAAGG	GGAGAGCAGGACGCAGAAGAGG
22	ZJ-27	42.657	-	TCTCCAAACGATAGCTCCG	GTCTATGCCATTGCCACTTG
23	M44	42.659	-	AGTCCATCCAAGTCTATTGCATCC	GCCCTTCACAAATTGTTCTTCG
24	M50	42.78	-	ACTACTACTGCAGCTTCCAGTCC	AATTTACTACGTTCGGGTGAGG
25	ZJ-29	42.782	-	AATCAGGCGGACGTGCAGTAGT	TGTTTCTCGGTAGTGAGGGAAACG
26	M51	42.783	-	TTAGTGGGTCTGATCATTGTGTCAGG	TGTTTCTCGGTAGTGAGGGAAACG
27	M52	42.8	-	GACTGTGACCTAATCACACGCACAGC	GCCGTGCAAACTGCAAAGTCG
28	M53	42.818	-	TCTGGAGGTTGAAAGCTGAAACG	CGACTATGTCGGTGCCAAATGC
29	M54	42.825	-	TGGCTTCGAAAGTGAGGGTAGC	GTGTACTTGGTGATGGAACACAGC
30	M55	42.852	-	CCTCCCGTAAATAGTCCATACAGC	CTTCACGCATCCACTGATTATTCC
31	M56	42.858	-	ACTATGACTGGTGGGCCCTTCG	CGAGGAGGAGGAGGAGCTTTGG
32	ZJ-21	42.875	-	TTTGGTTCGGCCTGAAGAAGG	GGAGTTTACAGTTGAGGGAGCATTC
33	ZJ-9	42.922	+	CAGATGGAGTACATGAAGTGCCAATG	GCATTGTGTCAACAACTCAGGTCC
34	ZJ-25	42.979	+	CACGGTAATGTGCTAAAGCTCCTG	GTGGGTTGTGGAGAGACAACCTG
35	ZJ-30	42.983	+	CAAGAAGCTCAACCAGGACGGCTTC	GAGAGTAGAGTTGAGGCACCGAATCG
36	ZJ-32	43.096	-	TAGATGCCGACGGATGATGATG	GCATATACTACAAGAGGCAGTACAAG

Table S4. Primers used for qPCR analysis.

Gene	Primers	Forward sequence (5'–3')	Reverse sequence (5'–3')	Sizes of Amplicons	Reference
LOC_Os03g50885	*ACTIN*	GACCCAGATCATGTTTGAGACCT	CAGTGTGGCTGACACCATCAC	131bp	Ren, Li, et al., 2013
LOC_Os03g11614	*OsMADS1*	TCTTGGTGAGGATTTGGGC	CCTTGCTCTTCAGATCAAACAG	137bp	Ren, Li, et al., 2013
LOC_Os01g66030	*OsMADS2*	GGGATAGTGAACGTGAATGATAAAC	GGACATTCAATCCAGTGGTGG	308bp	Sang, Li, et al.,2012
LOC_Os05g34940	*OsMADS4*	CCAATCTGCGGGACAAGA	AGCCAAATTGGCAGTGCTC	261bp	Sang, Li, et al.,2012
LOC_Os02g45770	*OsMADS6*	AGAGAAAGACGCAACTGATGATGG	AGGCTTGCTGCATGGCTCTG	141bp	Ren, Li, et al., 2013
LOC_Os03g54160	*OsMADS14*	CCATTAACGAGCTTCAACGG	TGGTATGGATCTGAAGCCTCC	314bp	Sang, Li, et al.,2012
LOC_Os07g01820	*OsMADS15*	AGTACGCCACTGACTCCAGG	TGCTGGCCCCTCACATTC	382bp	Sang, Li, et al.,2012
LOC_Os06g49840	OsMADS16	CCGCTACCAGCAAGCCAT	CTTGTAGGTTTCAGTCTGTGTGG	247bp	Sang, Li, et al.,2012
LOC_Os03g54170	*OsMADS34*	GCTTCGCAAGATGCTGCC	GTAGCCAGTGGAGCTAAATCCTC	140bp	Ren, Li, et al., 2013
LOC_Os08g06480	*ASP1*	AATTGGAGTCTTCGAAGCAGAG	ACAACCATGGGGTAAACACTTC	108bp	Kwon,Yu, et al.,2012
LOC_Os07g04670	*G1*	CGCGGCATCTCCTATCACAA	CGCTCCCGAAGTCGCAGTA	205bp	Liu,Li,et al., 2016
LOC_Os03g11600	*DL*	CCCATCTGCTTACAACCGCTT	GTTGGAGGTGGAAACCGTCG	151bp	Ren, Li, et al., 2013