Supporting Information Table S1 Information of 188 SSR markers used in linkage analysis of *mn2-m1* in this study

Marker	**Name**[a]	**Motif**	**Chr. Bin**	**Forward Primer (5’-3’)**	**Reverse Primer (5’-3’)**	**Physical Position (bp)**	**P**
bnlg1014		AG	1.01	CACGCTGTTTCAGACAGGAA	CGCCTGTGATTGCACTACAC	7079849-7080009	
umc1071		TACGA	1.01	AGGAAGACACGAGAGACACCGTAG	GTGGTTGTCGAGTTCGTCGTATT	7878600-7878713	
umc2226		TGG	1.02	TGCTGTGCAGTTCTTGCTTCTTAC	AGCTTCACGCTCTTCTAGACCAAA	22057442-22057529	
bnlg1484		AG	1.03	GTAAAAGACGACGACATTCCG	GACGTGCACTCCGTTTAACA	35267947-35268064	
umc1479		AGA	1.03	CTGGCTCTTCAAGTGTAAAGGAGG	GGCCTTTTTCTTAGCTTCCTCATC	43358230-43358427	
bnlg1866		AG	1.03	CCCAGCGCATGTCAACTCT	CCCCGGTAATTCAGTGGATA	51903802-51903914	
umc1917		CTG	1.04	ACTTCCACTTCACCAGCCTTTTC	GGAAAGAAGAGCCGCTTGGT	63745297-63745438	
umc2228		AGC	1.04	GTGAGGTGAAAATGAAGCTGGAAC	ACCATACCTCTCTGAACATGAGCC	75378258-75378414	
umc2025		AGCT	1.05	CGCCGTAGTATTTGGTAGCAGAAG	TCTACCGCTCCTTCGTCCAGTA	93193678-93193806	
bnlg1057		AG	1.06	TTCACCGCCTCACATGAC	GCAACGCTAGCTAGCTTTG	192990681-192990924	
umc1122		CGT	1.06	CACAACTCCATCAGAGGACAGAGA	CTGCTACGACATACGCAAGGC	204149535-204149696	
bnlg1556		AG	1.07	ACCGACCTAAGCTATGGGCT	CCGGTTATAAACACAGCCGT	211390201-211390353	
umc1245		AGCAG	1.07	TGGTTATGTGCATGATTTTTCCTG	CATGCGTCTGATCTTCAGAATGTT	233337336-233337481	
phi423298		CCG	1.08	GGGCTGCTACTTTGACAAGGAC	CCTCCATCATCCGCTGGTA	237684047-237684180	
umc2240		AC	1.08	CGCCTTTGTAACCCAGACTCATTA	CGGATGTTGCCAAGTACATCATATC	252138180-252138322	
phi011		AGC	1.09	TGTTGCTCGGTCACCATACC	GCACACACACAGGACGACAGT	262992745-262992972	
umc1774		GT	1.1	ATGGGACTATGCATGGTATTTTGG	TACACCATACGTCACCAGGTTCAC	283221017-283221170	
umc1553		AG	1.11	TGAATGGAAGAGAAGGGAAATCTG	GCTCTGTACATCCTTAGCGACACA	292175969-292176125	
phi064		ATCC	1.11	CCGAATTGAAATAGCTGCGAGAACCT	ACAATGAACGGTGGTTATCAACACGC	302190922-302191019	
umc1819		CAAC	1.12	GCTGCTCTAAAATCATGCTGATAAAA	TATTCAGCAATGTATTCCCCCTGT	304071538-304071643	
umc1605		GGC	1.12	GGAGAAGCACGCCTTCGTATAG	CCAGGAGAGAAATCAACAAAGCAT	304199039-304199185	
phi402893		AGC	2	GCCAAGCTCAGGGTCAAG	CACGAGCGTTATTCGCTGT	475294-475514	

umc2246		CCTCCT	2	AGGCTCCAGCTCTAGGGGAGT	GTGAACTGTGTAGCGTGGAGTTGT	957610-957755	
phi96100		ACCT	2.01	AGGAGGACCCCAACTCCTG	TTGCACGAGCCATCGTAT	2812985-2813263	
umc1165		TA	2.01	TATCTTCAGACCCAAACATCGTCC	GTCGATTGATTTCCCGATGTTAAA	4004896-4005045	
phi098		AG	2.02	GAGATCACCGGCTAGTTAGAGGA	GTATGGTTGGGTACCCGTCTTTCTA	4277584-4277719	
umc1261		TG	2.02	AGAAGTGCGTATGCTACAGTGGTG	CCTAGTGGTGGAGTTCTAGGCAAA	13851568-13851677	
umc1518		TAT	2.02	TAGCTCCTTTGCGCTATTCAGTCT	GGCAGTGTTTTCTTTTGAAGTGCT	15192178-15192258	
umc1185		GC	2.03	AGTAAAAGAGGCAAGGACTACGGC	GCGGCGATATATACGAGGTTGT	22071419-22071554	
bnlg2248		AG	2.03	CCACCACATCCGTTACATCA	ACTTTGACACCGGCGAATAC	24435557-24435800	
umc1024		GA	2.04	CCTTTTTCGCCTCGCTTTTTAT	TCGTCGTCTCCAATCATACGTG	30533723-30533894	
bnlg1175		AG	2.04	ACTTGCACGGTCTCGCTTAT	GCACTCCATCGCTATCTTCC	44208669-44208837	
bnlg1909		AG	2.05	CCTGACCCTGTTCCTGAAAA	GTGTGTCTGGAGCTGTTCGA	49590702-49590872	
umc1003		TAAA	2.05	AATAGATTGAATAAGACGTTGCCC	TGTTCCAATGCTTTTGTACCTCTA	111723292-111723409	
umc1658		AC	2.06	AGAGATGGGGTAGAAATAGACGGC	CTCTCTGCTTTCTCTTCTCTTGCG	168257146-168257281	
nc003		AG	2.06	ACCCTTGCCTTTACTGAAACACAACAGG	GCACACCGTGTGGCTGGTTC	179168084-179168191	
bnlg1633		AG	2.07	GTACCTCCAGGTTTACGCCA	TCAACTTCTCATGCACCCAT	204817082-204817244	
bnlg2077		AG	2.07	GACCAGAGGATGGGGAAATT	GTAGGCACATGCACATGAGG	208916522-208916661	
umc1526		TCG	2.08	TTTTACAAGCGTGAGAGCAAGAAA	AACTGTCTGGAACAAGAAACCGAG	215376801-215376913	
bnlg1940		AG	2.08	CCTTTTGTTTCAGGCCGTTA	CAGCAGCCTGATGATGAACA	225870808-225871022	
bnlg1520		AG	2.09	TCCTCTTGCTCTCCATGTCC	ACAGCTGCGTAGCTTCTTCC	230692469-230692638	
umc1736		GCAT	2.09	CCATCCACCACTAGAAAGAGAGGA	TTAATCGATCGAGAGGTGCTTTTC	237891744-237891883	
phi101049		AGAT	2.1	CCGGGAACTTGTTCATCG	CCACGTCCATGATCACACC	243421854-243422090	
umc2105		CCAT	3	ACATACATAGGCTCCCTTTTTCCG	TCCCGTGACACTCTCTTTCTCTCT	751829-751988	
umc2255		AGCA	3.01	GCTACGCTTAAGTATCACGGCAAC	CTGCTGAGGAGAAGTGATCCTGTT	1001831-1001943	
umc1394		AT	3.01	CCCGAGTCAGAAAAACATTCACTT	CCTAACCTGAAGAAGGGAGGTCAT	1699025-1699118	
phi104127		ACCG	3.01	CTTTGCTGCTGCTTCCTACG	AACCAGTGACGTACACAAAGCA	2712196-2712351	

umc1458		GCT	3.02	CCAATAAACAAATCATCTCCCCCT	TGCTATGCTATGTACAGGGACAGG	3949519-3949609	
umc1183		AG	3.02	GCATGTACACAACACAACCTTTCA	ATGTCATTTTTGGCTTCTCGAAAT	4148936-4149092	
bnlg1325		AG	3.03	CTAAATGCGCAGCAGTAGCA	TGCTCTGCAACAACTTGAGG	4749806-4749976	
bnlg1523		AG	3.03	GAGCACAGCTAGGCAAAAGG	CTCGCACGCTCTCTCTTCTT	5053195-5053386	
bnlg1904		AG	3.04	AGGAGCATGCACTTGGTTCT	ACTCAACTGATGGCCGATCT	9812103-9812278	
nc030		CT	3.04	CCCCTTGTCTTTCTTCCTCC	CGATTAGATTGGGGTGCG	17163486-17163588	
umc1655		ACT	3.04	ACGCAAGTACAAAATTACTGCGGA	ATTAACGGCATGCTTGTAGCCTAA	25809000-25809150	
umc1600		TAA	3.05	CATATTGATAGGCTAGGCAAATGGC	CAATACAAGTTTGGTCCCAAATAAGC	126925142-126925291	
bnlg1505		AG	3.05	GAAAGACAAGGCGAAGTTGG	GCTTCTGAACTGGATCGGAG	153033814-153033982	
bnlg1798		AG	3.06	AAGTTGGTGGTGCCAAGAAG	AAAAGGTCCACGTGAACAGG	178090575-178090672	
umc2268		CGC	3.06	ATCTCCCCACAGATCTCGCC	CTTGAAGGACTCCTGCTTGATCTC	184712987-184713117	
umc1399		CTAG	3.07	GCTCTATGTTATTCTTCAATCGGGC	GGTCGGTCGGTACTCTGCTCTA	201469527-201469639	
umc1844		TC	3.08	GGCATGGGTCTCTCATAAAGTCAT	CGACGTATATGGCTGAGAACCCTA	210465572-210465707	
bnlg1108		AG	3.08	GGATTCCTTTATGACGGGGT	AGTAACAACCAAGGCATCGG	214571759-214571894	
umc1320		GAAC	3.08	TGCGAAATCTGTATACCATAGGCA	CTCTTTTAGCAGTGTGCCGAATTT	217221798-217221896	
bnlg1257		AG	3.09	CGGACGATCTTATGCAAACA	ACGGTCTGCGACAGGATATT	221547824-221548045	
bnlg1496		AG	3.09	CTGGGCAGACAGCAACAGTA	AGCCAAAGACATGATGGTCC	227285747-227285903	
umc1136		GCA	3.1	CTCTCGTCTCATCACCTTTCCCT	CTGCATACAGACATCCAACCAAAG	234431477-234431614	
phi072		AAAC	4	ACCGTGCATGATTAATTTCTCCAGCCTT	GACAGCGCGCAAATGGATTGAACT	1284193-1284334	
bnlg1370		AG	4	TATTTAATTTAGTGTGGAGCTCACG	CGAGGGTCAGTTGTTGCTCT	2514725-2514928	
umc1276		GGC	4.01	CTACCTTGTTCCTAGGGCCGTCTA	ACGCAATTATTACTGCCACACGTC	3674158-3674259	
bnlg1318		AG	4.01	TTATGTGTGCAGAACGACTCG	AGCATGGCAGAGAAGGTGAT	5694252-5694398	
umc2150		AAG	4.02	GTTGTTCACTTTCCAAAACCCTTG	GCCTTGTGCTTCTTGGAGTGTT	6142102-6142221	
umc1509		TG	4.02	CTTTCTGCAGATTCACCGTTTCTT	TTGGTTCTTTTGACCATAGACAAGC	6225371-6225498	
nc004		AG	4.03	TGCGAAGAAGCAGTAGCAAA	TGGAGGTAGAAGACGCACG	14333261-14333409	

umc1550		CT	4.03	CGGGGTAATTGGGTACATAACCTC	GTGCCTCCAACGCCTAGTTTTT	15973865-15974002	
umc1067		GCC	4.04	ACTTGTACTACGCAGGACAGTTCG	AGCCTCTGTCTGGATGACTGAAC	22850799-22850956	
umc1652		CCG	4.04	GAGAGCAGTAGCACTGACCCTTTC	CACTCGACCTCGATCGGAAC	27893918-27894062	
nc005		CT	4.05	CCTCTACTCGCCAGTCGC	TTTGGTCAGATTTGAGCACG	38554708-38554831	
bnlg1937		AG	4.05	AATGCTCGGTCCACAGAATC	AACTGGAGCCAAAAGTGGTG	39883469-39883640	
umc1299		AAG	4.06	CTTGGGTTCTTCTCTCCTATGGGT	CGCTACAAACAAGTGGCGTTTAAT	162657076-162657213	
umc1869		GGT	4.06	CGAGCGCTCTAGACACGATTTT	GAACTGGAGGAGCGAGCATGTAT	164543449-164543592	
bnlg1189		AG	4.07	CGTTACCCATTCCTGCTACG	CTTGCTCGTTTCCATTCCAT	180087254-180087465	
bnlg2162		AG	4.08	GTCTGCTGCTAGTGGTGGTG	CACCGGCATTCGATATCTTT	189138622-189138794	
umc1051		GA	4.08	CTGATCTGACTAAGGCCATCAAAC	AATGATCGAAATGCCATTATTTGT	196012928-196013048	
umc2287		CT	4.09	CTAGCTAGTAACAGAGCATCGCGG	CTGAGGTGTAGGATCGAGCAAGT	237006217-237006371	
umc1503		GAC	4.09	TTCATGACACACAAACCACAGATG	GCACCCTAGCAGACTACAACATCC	242136560-242136750	
umc1699		CA	4.1	CTTTTGCTCAAACACGGGAAATAC	AGGCATTGAGCGATATGTTTGTTT	243344016-243344151	
umc1050		AAT	4.11	CGATACACATCCATCTTCAGGTAGC	GCCTTTGTACCAATACAAGCCAAG	245525566-245525668	
bnlg1890		AG	4.11	ACCGGAACAGACGAGCTCTA	GTCCTGCAAAGCAACCTAGC	245797540-245797668	
umc1253		TTC	5	GAGGTAGGCGTCGTATGCTCTAAA	AACGTGACTTACAAGGTTGCGTTC	924533-924633	
bnlg1006		AG	5	GACCAGCGTGTTGATCCC	GGAGACCCCGACTCTCTCTC	2204781-2205011	
phi024		CCT	5.01	ACTGTTCCACCAAACCAAGCCGAGA	AGTAGGGGTTGGGGATCTCCTCC	4364137-4364300	
umc1478		GGAG	5.01	GAAGCTTCTCCTCTCGCGTCTC	CAGTCCCAGACCCTAGCTCAGTC	4605655-4605792	
umc2115		TGCCA	5.02	CTGTCTGTCTACCCAACCCAACAG	GGGGATAGGCGTGTGTATGTACTG	12794913-12795068	
umc2388		GCC	5.02	GTGAGGGACTGGAAGGAGGTGTA	CTTCCATCGCTTTCGCGTACT	18632416-18632657	
umc1597		CCT	5.03	ACAACCGCTGCGTAAACGAAT	AGAGATTAGGCGAGCGAGGG	20155011-20155117	
umc1274		TGC	5.03	TTGAGTCTGGTACTGCGTATGAGG	TAGCACTCCAACAGCAAGAGTTTG	61859104-61859219	
phi109188		AAAG	5.03	AAGCTCAGAAGCCGGAGC	GGTCATCAAGCTCTCTGATCG	66605424-66605585	
umc2066		TTCTT	5.04	ACATGGGCCGATGACTAAGAATAG	CTGAGTACACACATGTCACACAGTTG	134790483-134790622	

bnlg2323		AG	5.04	ACCGTCTCAGCAAAATGGTC	CCGCCTTCACTATGGTCAAT	155423208-155423388	
umc2303		CGG	5.05	AGAAGAAGGTGGAGGTCCAAGACT	CTGGTATCTGATCAGGGTGCG	183210754-183210909	
umc1155		AG	5.05	TCTTTTATTGTGCCCGTTGAGATT	CCTGAGGGTGATTTGTCTGTCTCT	184662385-184662530	
umc1019		CT	5.06	CCAGCCATGTCTTCTCGTTCTT	AAACAAAGCACCATCAATTCGG	196011475-196011576	
mmc0481		GA	5.06	GCACCTGCGAGACTAGG	TGTTTGAGCCGTTCTAGACT	197724698-197724821	
phi058		CCG	5.07	AGGTGCTGGACACAGACTTCAAC	ACTGAGATCCAGGCTCCTCTTC	210408036-210408183	
bnlg1118		AG	5.07	CAGAGTTGATGAACTGAAAAAGG	CTCTTGCTTCCCCCCTAATC	215859921-215860153	
umc1792		CGG	5.08	CATGGGACAGCAAGAGACACAG	ACCTTCATCACCTGCAACTACGAC	218451914-218452029	
umc2143		TTC	5.08	ACACACAACAGAGCCTTTTGTTCA	AAGAAAAGGACACCAAACCAAACA	219983072-219983220	
umc2307		CAG	5.09	GTCGACATCGTCTTCCCCAAG	GTAGGAAGCCACGTACGGCTC	221714353-221714565	
umc1153		TCA	5.09	CAGCATCTATAGCTTGCTTGCATT	TGGGTTTTGTTTGTTTGTTTGTTG	222667071-222667180	
umc1002		TA	6	AGCTAGCTATACACCGCCAGG	TCAGTTTGGAACAGGGAAAAGTA	1424859-1425004	
bnlg1600		AG	6	CGATCAGTGCGTGGAGAGTA	TAGGCATGCATTGTCCATTG	31276710-31276914	
bnlg1538		AG	6.01	CAGCCGAAGACGAAGCC	GTGGTGAACGAACGAGCAA	73927627-73927856	
umc1186		GCT	6.01	TCAAGAACATAATAGGAGGCCCAC	AGCCAGCTTGATCTTTAGCATTTG	85713814-85714029	
umc1083		GA	6.02	CTTTCCTCTCTGGAGCGTGTATTG	ATATGTTGCAGAACCATCCAGGTC	91334205-91334316	
bnlg2191		AG	6.02	CACACAATCCCCACAAAAAA	CGAAACATCCAGGAAACTGC	95868219-95868352	
umc1887		CGA	6.03	CTTGCCATTTTAATTTGGACGTTT	CGAAGTTGCCCAAATAGCTACAGT	105967402-105967492	
umc1857		TAA	6.04	TTCCTTGCCAACAAATACAAGGAT	GTTCATTGCTTCATCTTGGAACCT	110501317-110501462	
phi031		GTAC	6.04	GCAACAGGTTACATGAGCTGACGA	CCAGCGTGCTGTTCCAGTAGTT	112978836-112979057	
bnlg1617		AG	6.05	CGTGCACGGTACAGAAAGAA	AGAAAGCCACGTACCCCTTT	122796308-122796457	
umc1379		GAG	6.05	AAGTCGTAGTCAGCGAGGGCTT	GAACCACAGCTATGCTCGCC	142778091-142778202	
phi025		CT	6.05	GCAACATCCTGGAGAGCCACTACAAGG	ACAGCCTGTTTTCCTGGACAGTGAACTC	150031751-150031967	
umc1762		TC	6.06	CTTACTCCAGGCACTCCATACCAT	ATCCAGGTGAATGGTGTTTACGAT	159108024-159108173	
umc1520		GA	6.06	AGCAAATATATGAGCAATTAAGAACAGG	GTGTCGCCACCTATAATTTGATGA	162528019-162528168	

phi299852		AGC	6.07	GATGTGGGTGCTACGAGCC	AGATCTCGGAGCTCGGCTA	166029577-166029687	
umc2165		TTC	6.07	AGAACACCAAATGGTGACGTTATGT	CTAGCTCGTCTTCCCTGTGGTCT	168306415-168306573	
phi089		ATGC	6.08	GAATTGGGAACCAGACCACCCAA	ATTTCCATGGACCATGCCTCGTG	170403453-170403539	
umc2324		CAC	6.08	GATCCTCTGTCGCCAAACACTAAG	AGATGGTGACGATGAGTGATGAAC	171779778-171779923	
umc1545		AAGA	7	GAAAACTGCATCAACAACAAGCTG	ATTGGTTGGTTCTTGCTTCCATTA	1464029-1464107	
mmc0171		GA	7	AATCCTACTTGCTGCCAAAGC	CTTTGAGCTTTTTGTGTGGAC	5207414-5207594	
umc2364		GGA	7.01	AACCTCAAGATCACCAACATCCTC	CACCCTGCTGTCAGATGGATACTT	8342910-8343181	
umc1066	**P1**	**GCCAGA**	**7.01**	**ATGGAGCACGTCATCTCAATGG**	**AGCAGCAGCAACGTCTATGACACT**	**11075651-11075794**	P
bnlg1094	**P2**	**AG**	**7.02**	**GTGAAGAACGATGACGCAGA**	**CAGCAACGCTCTCACATTGT**	**39161032-39161208**	P
umc1433		AG	7.02	TTGTCAGACAGAACCCACACATTT	TTTTTGGCTTCTTTTGTTGTGGAT	85541908-85541997	
bnlg1805		AG	7.03	GCCCGTTTGCTAAGAGAATG	TGTTCGAGCATTTGCTCTTG	158942590-158942846	
phi114		GCCT	7.03	CCGAGACCGTCAAGACCATCAA	AGCTCCAAACGATTCTGAACTCGC	160761101-160761236	
bnlg1666		AG	7.04	GCTGGTAGCTTTCAGATGGC	TGTCCCTCCTCCAGTTTCAC	164321068-164321184	
phi328175		AGG	7.04	GGGAAGTGCTCCTTGCAG	CGGTAGGTGAACGCGGTA	168545414-168545543	
umc2222		AT	7.05	CCAACAACCTTGCTACCATAGTCC	TACATGGTCCTGTGACAAACTTGC	177465624-177465754	
umc2197		ACC	7.05	CGACCTCTTTGCTGTCTCATTTTT	CAAGCAATTTCCCCATCTCATACT	177955729-177955884	
phi045		AAC	7.05	CTACTACATGCGATCACGGACCAT	AACCAGTTCCAGTCTCCACTGAGT	179352645-179352790	
umc1139		GAC	8.01	TTTGTAATATGGCGCTCGAAAACT	GAAGACGCCTCCAAGATGGATAC	3221837-3221984	
umc1075		ATTGC	8.01	GAGAGATGACAGACACATCCTTGG	ACATTTATGATACCGGGAGTTGGA	4714946-4715086	
bnlg1194		AG	8.02	GCGTTATTAAGGCAAGCTGC	ACGTGAAGCAGAGGATCCAT	8759773-8759910	
umc1034		GA	8.02	GTGTTTCCGTTTCGCTGATTTTAC	TCATCCATGTGACAGAGACGACTT	20552080-20552200	
umc1904		TAAGC	8.03	CAGCCACTCGTTTATGGAGGTTTA	TGTTACTAGTCGATCTGATGCCCA	71472405-71472534	
bnlg1863		AG	8.03	GGCGTTCGTTTTGCACTAAT	CGACACAGTTGACATCAGGG	93874354-93874483	
umc1858		TA	8.04	GTTGTTCTCCTTGCTGACCAGTTT	ATCAGCAAATTAAAGCAAAGGCAG	115241780-115241935	
bnlg2046		AG	8.04	TTGGTGAAACGGTGAAATGA	CTGGTGAGCTTCACCCTCTC	120245684-120245913	

umc1562		TC	8.05	CAAAGCAGTACAATATGACCCCAG	CGTACGTCCCATAAAGATGAGAAA	129742951-129743072	
bnlg1812		AG	8.05	CGAGAAGACTTGCGTGAACA	TTACGTGCGTCGTCAGAATC	142736470-142736639	
umc1149		AG	8.06	TACAGTAGGGATTCTTGCAGCCTC	GTGGGACCTTGTTGCTTCCTTT	165203613-165203743	
umc2395		CGA	8.06	ATCACATCTTGCGTTGTCATTTTG	ATGGATTCTTTCCGGCCTCTC	168953977-168954132	
bnlg1823		AG	8.07	TGTGACTCCATACCGCACAT	CTCATCATGTTGTACATGGCG	173024014-173024196	
umc1268		GCG	8.07	ACGAACAACCTAGCACAGTCCTAAA	CAAGGCGGTTACCAAGTTTACATC	174293415-174293508	
umc2218		TC	8.08	CACGGTGCTGTACACAACTAAAGG	TATCCTCGGAAGCGAACGAA	176060753-176060880	
bnlg1056		AG	8.08	ATCGTTGTTGGGTACACGGT	ACGGGTAGTGGTGAAGATGC	177137417-177137506	
phi233376		CCG	8.09	CCGGCAGTCGATTACTCC	CGAGACCAAGAGAACCCTCA	179043680-179043819	
umc1279		CCT	9	GATGAGCTTGACGACGCCTG	CAATCCAATCCGTTGCAGGTC	1257282-1257379	
umc1867		TC	9.01	TGGTCTTCTTCGCCGCATTAT	ATAAGCTCGTTGATCTCCTCCTCC	4690756-4690865	
phi028		GAA	9.01	TCTCGCTGTCCTTCGATTAGTACGG	AATGCAGGCGATGGTTCTCCGGCCT	10912650-10912720	
phi017		TAC	9.02	CGTTGGCGACCAGGGTGCGTTGGAT	TGCAACAGCCATTCGATCATCAAAC	11219882-11219980	
bnlg1372		AG	9.02	AGCGGTGCTCAAATAGGAG	CGCCGGCTTCCCTCAC	13848886-13849128	
umc1191		CT	9.03	AAGTCATTGCCCAAAGTGTTGC	ACTCATCACCCCTCCAGAGTGTC	92001550-92001702	
umc1688		GGA	9.03	AGCAGTAGCCGCAAGCAGAG	ATCTGGAGCTGCGTGCTGTC	99140509-99140814	
umc1571		CAA	9.04	CACCGAGGAGCACGACAGTATTAT	GCACTTCATAACCTCTCTGCAGGT	109931288-109931375	
bnlg1012		AG	9.04	GAGTGAGCGTGCGGAGTC	AACAGGCCAAACTCCTCCTC	118033787-118034005	
umc1657		GACGG	9.05	ATGGATGAATATGATCCCACGG	GATCCGCACGTAGCTTTTCG	135492211-135492370	
umc1231		GA	9.05	CTGTAGGGCTGAGAAAAGAGAGGG	CGACAACTTAGGAGAACCATGGAG	135613607-135613715	
umc2345		CATC	9.06	AAAAAGAGCAGCGGAACGTG	GTCGTGCTGGCTACTCTGCTG	148178184-148178306	
umc1366		TCC	9.06	GTCACTCGTCCGCATCGTCT	CCTAACTCTGCAAAGACTGCATGA	149059685-149059797	
umc1804		AG	9.07	GCGGCGAGGTTAAAGGAAAA	GGTGTTTAGACACGCAGACACAAC	152400281-152400368	
umc2099		ATGC	9.07	AGGTCATCAAGATGCAGAGGGAG	TCAAGGTACGAAGCCTGACGAC	154861822-154861975	
umc1277		AATA	9.07	TTTGAGAACGGAAGCAAGTACTCC	ACCAACCAACCACTCCCTTTTTAG	157948237-157948375	

umc1505		AAAAC	9.08	TTACACAGAAGCCCATTTGAAGGT	GGATGGTTGTTGGTGGTGTAGAAT	158185823-158185987	
phi041		AGCC	10	TTGGCTCCCAGCGCCGCAAA	GATCCAGAGCGATTTGACGGCA	2229783-2229985	
umc1318		GTC	10.01	ACTTCGTCTAGTGTCCCTCCGTT	TGCCAGATTAAAAGCAACACAAGA	3854317-3854467	
umc2053		CGA	10.01	ATCTCTCCCTCGCTCTCCTTCTC	AGCAGCAGGTTGGTCGAATG	4297670-4297766	
umc1152		ATAG	10.02	CCGAAGATAACCAAACAATAATAGTAGG	ACTGTACGCCTCCCCTTCTC	4672467-4672637	
phi059		ACC	10.02	AAGCTAATTAAGGCCGGTCATCCC	TCCGTGTACTCGGCGGACTC	8782022-8782169	
umc2069		GCG	10.02	ACAACCTCCTCCACGACCAAAC	GTAGAGGTCCCACTTGTTCCCAAT	10856416-10856766	
bnlg1655		AG	10.03	ATTAAAATCTTGCTGATGGCG	TTCTGTTCCCGCCTGTACTT	85291039-85291160	
phi062		ACG	10.04	CCAACCCGCTAGGCTACTTCAA	ATGCCATGCGTTCGCTCTGTATC	112727512-112727671	
bnlg2336		AG	10.04	GGTAGGGGAAAAAACATGCA	TGATAAAGTTCTCTATTTGTCTGCC	127158854-127158965	
bnlg1250		AG	10.05	CCATATATTGCCGTGGAAGG	TTCTTCATGCACACAGTTGC	133411543-133411744	
umc1506		AACA	10.05	AAAAGAAACATGTTCAGTCGAGCG	ATAAAGGTTGGCAAAACGTAGCCT	134476821-134476948	
bnlg1028		AG	10.06	AGGAAACGAACACAGCAGCT	TGCATAGACAAAACCGACGT	139930325-139930473	
umc1061		TCG	10.06	AGCAGGAGTACCCATGAAAGTCC	TATCACAGCACGAAGCGATAGATG	140378278-140378380	
umc1196		CACACG	10.07	CGTGCTACTACTGCTACAAAGCGA	AGTCGTTCGTGTCTTCCGAAACT	144424283-144424437	
bnlg1185		AG	10.07	CGGTCCAGGCAGGTTAATTA	GACTCGAGGACACCGATTTC	149279000-149279134	

[a] Marker name used in map-based cloning of *mn2-m1*; Chr., Chromosome; P, Polymorphic both between the two parents and the two DNA pools.