

Supplementary Tables

Table 1 Sequences of molecular markers

Marker name	Chr	Position (M) ^a	Forward (5'-3')	Reverse (5'-3')	Product size (bp)
01M0.45	1	0.45	TGCATGCACATTCATTTTAT	GCACAGAGCTAGGGTACAAT	200
M001	1	3.3	TCACCCGATATCCCATCAT	TAAGACGGATGGTCAAAACG	191
M004	1	7.4	GAGCTATGTTGTTATGTCGT	TAGTCACTTAGTCGTGATCG	178
M005	1	9.4	CCTCGCAAATGAAGTTCTTG	CCGAAAGAAGTTACAGGAGT	131
RM10813	1	12.9	AACCCGCTAACAGATTCAAA	TTGGAAATGTGCTCAACTGA	389
M008	1	18.7	CGCACATCTGAAATATGC	TGTCATCCATATCAGGAC	194
RM11258	1	22.9	GCTCCACCATTTCATCCATACA	CAATATCAGCCTAGCACAAA	167
RM488	1	24.8	CAGCTAGGGTTTTGAGGCTG	TAGCAACAACCAGCGTATGC	110
M012	1	28	CCACGAGTAGAGCTACTATG	AGCCCGTTTAATGATCATGC	164
M013	1	32.1	CAATGACCACGTCAAGCATAA	TCCATCCATTTTCAGCCTTTC	146
RM226	1	34	GAAGCTAAGGTCTGGGAGAA	AATGGCCTTAACCAAGTAGG	289
RM11865	1	36.3	CAACTCATTTCGGCTTCTCTT	GCAATTGCATGAGTTGGAAT	395
RM12021	1	39.1	TAATTTCTGGCACGTACGC	GTAGCGATGCAACTACCAGT	464
M015	2	1.8	GGGTGTTGGTTATATCACCT	AATCTAGTTTGCTGGCGTGC	185
M01763	2	3.94	TGCACCCAAGAAAAATATAA	GCCAAGCATATTTTGATCTC	171
RM12678	2	5.8	AGGAGAGCAGCCCACTACTC	TCTGAGAGGCTACCCGCAT	559
M05076	2	7.68	CTATTCATCATATCGGCTGG	AGCTTGTCTTCCGCTCGT	147
02M11.16	2	11.16	AAGCGTAACTTTTCGTTTTT	ATACTGTCACGGTCCTTCAA	149
M018	2	15.2	GTATTGGTATGCCACTATGC	CGAAAGCATATGCACGGCAG	157
RM1211	2	18.55	GACACGGGTTATCAGTGATGTCAG C	GCCATCACGCATGTTAGTTAGAAAC G	154
RM13429	2	21.2	ACTCACACCTATGTGTCCGTT	AAGGAGTGCTCTAGAAAATCG	296
M020	2	28	ATGTCAAGTTGAGAACGTGA	AGCATGAACATTTGCCAGAG	158
RM250	2	32.79	GGTCAAACCAAGCTGATCA	GATGAAGGCCTTCCACGCAG	219
RM14124	2	34.2	CTCAGTCAGCAACTCAGCATGG	ATCCTCTCCTGCTCAATTTG	191
M023	3	0.33	TTCAATCCCTTCCGAACC	AGCTTGGCTGAAATGATC	113
RM14391	3	2.7	GGGAGCAAATTTGATAGGTA	ATGTGACTGCTGCTGGAATTA	293
03M6.79	3	6.79	GGGAAGTGCAAGAAAAATAA	ACAAAACCTTAAAGTGGCAGC	142

03M10.7 5	3	10.75	CTAAAATTGTGAGGGACTCG	GCTTCTGATTAGAGACAGCG	139
RM6929	3	12.9	TTCTTTCGAGGGTACGTAGAGG	CTAGCTAGCCAGTAGCTGAT	185
RM1524 7	3	17.7	GGACTTCACACGGAGAGTTAG	ATCTGAACGGCTGAGATTTGT	312
RM5488	3	21.19	GGGTCAGCTGCACACATAGAACC	TCTTCAGCTCTCCCTCTCCTTCC	168
03M24.2 9	3	24.29	ATCCAATGACTGAAAGATGC	TTTAAGGAAAAACCAGTCG	164
M033	3	27.5	TCAGTGAACCAGCCACATGA	CTTTCGCGGTTCTTGGAGCA	154
03M33.1	3	33.31	TCATTTTCCTATCTGTGCAA	AGGTTCGATTCACTTCAAAA	155
03M36.3	3	36.3	ATTTAGCTCCCCTCTGTTC	CATTCTGAGTGAGTTGAGCA	173
RM1635 4	4	2	ACAAGTGATCACAATGGCTC	CTTATGCTCTCATGGTAGTGT	258
M037	4	4.6	CACATGATCTGGCTTTCATT	ATGCATACGTCGAAATCT	179
M04658	4	8.34	CAATTCCTCCATCTCTGT	CCAAATAGGAAAATCAATGC	143
S12020	4	11.3	TGTTGATTCGATGACCACC	ACCCTGTCAAATAACTCGTC	1270
RM1664 9	4	13.6	CTCCCTTCATGCGTAAGCTCT	GCAAACAGGATCCTCCACAAA	342
M09496	4	18.75	CTAAACCTGGTCCAAAGAAA	TCAAGCCAAATATGGAAGAC	159
RM1694 3	4	20.4	CTCCATGCGGTGACCATGTTAG	GATGAGCAGGAGCAGAGGAG	387
04M23.6 1	4	23.61	CCCAATTTCCAATCATTTA	GTCCTAAAAGCAATGACAGC	152
M038	4	28.7	GGCAATGTCAGTTCCTGATTT	AGGACGAGCACAAACATACCC	181
M039	4	32.2	GGTGCCTTCGTGAAGGATT	TCAAGTGCTCTTTTCCATGTG	152
RM1783 6	5	1.7	TTCGGCTTCCAATGTTCAAT	ATATCGTGGCTTTCGCTGACG	238
05M4.28	5	4.28	ACAGTAAAACGAACTGCTCC	TTGTTACTTCCCCATTCTAA	130
M040	5	7.8	TCGGTGGATTTTCATGAGAG	GTGCAACTTTGCATTGTCC	142
05M10.2 4	5	10.24	TTTAAGTCCTGTGCTGTCC	ACCCACTCAATTCATCTAGC	152
M06502	5	14.33	GTCCAATTCTGAAACAGCAC	AGACTTTGAATTTGCACGAT	161
M09668	5	19.23	GATGGACTCGAGGAGGAC	TATCTTCACCTTTTTAGCCG	161
M13153	5	24.21	TCAAGAGGAGACCATAACCA	TAACAGGGCTGATATGTTCC	182
05M26.6 2	5	26.62	CTGGAGAGAAAACAATGGAG	CTTTTAGAATGGGTGACCTG	135
M16113	5	28.63	CTCACCAAATGAGCTGAGAT	TGCTCCCTGTTTCTTCTTC	185
RM1923 4	6	0.2	ACTCCCTCGTCTCTAGAGTT	GTTGGGAGTCTATCCCATCG	299
6M4.57	6	4.54	TATAAGGGAATGAATTCGTC	TTTGACTCGATGGAGTTTTT	130
M051	6	8.1	GGTGTGGTTTAGGCTGTCA	GTCTCTCATCAGTGACGACT	132

M056	6	11	CAAGAGATTGATGCTTGTTG	CTGCTTCAATTGGAGAGACA	136
6M13.5	6	13.5	GCCAGTTCCTCAACTGTCA	CACTCCGAGTCTTCTTCC	129
06M17.5	6	17.5	AGACGAGCACCTAAGAACAA	GGGGCTAAGCTGATATTTTT	143
06M20.9	6	20.9	CAGCCATAAGCTACTGACTA	CTGGGAATTCTGTCAAATGA	160
M14082	6	24.072	TACCCTCAAATTCGATGTAG	GTCAGACCGACGAAGGAG	168
M060	6	28.7	TGACGCGACGCGCACGTT	GACAAGGTTAATCACACAGG	148
06M30.3 8	6	30.38	GCCACGAGACTTAGAACAAC	TAGTAATGGGCCGTACTAGC	175
M063	7	1.5	ACTACCTACATCCCTCTATG	CTGACATGCTTTTCTCACTG	103
M070	7	6.9	GCATGTGATTTGGTTGTGCA	CCACAAGAGATTCTAGCAGA	198
RM2130 9	7	8.6	GAGTGGATTTACTGACAAGC	GATTCTCTTGGAGCCCATAC	531
RM2139 2	7	11	GCAAGTGAGAGTTAACAAGT	GATCAGGTGACATACACATC	189
07M15.3	7	15.3	TGATATAACTGAAGCTCCGC	TGGATTAGGTTTTCACTTGG	164
07M20.1 1	7	20.11	ACCTTGACAGTCTTGTGTCC	CCGGAATATACTGATGCTCT	162
07M24.3	7	24.3	CATAGGATCGAATTTTCCTG	CAAACCTATCCTTATGAGC	138
08M0.01	8	0.01	GATGTTCCAAAAGGCTACTG	ATGTGCAACTACAATTTGCC	173
RM2241 6	8	3.3	CCCAGCTCTCTAAGCATTCT	TAACCTTCCGCTCTCACACA	336
M077	8	5.3	GGTGGTCTTGATTCCCTTGT	GAAACAGATCAGCCTCACTG	165
RM8271	8	7.6	AGCAGCTCCGATTGTGTTAG	AATGGCGTCTGTGGTACTTT	360
RM72	8	15.2	CCGGCGATAAAACAATGAG	GCATCGGTCCTAACTAAGGG	166
08M18.4 1	8	18.41	CGGTTATTATGCCTGAGTT	AAGATGAGTGGTCAAACATT	143
08M21.0 3	8	21.03	ACAGGTCTAATCAACCGCT	ATTAGTCGGTTTCCGTACAA	162
08M25.5 7	8	25.57	ACCTGAATTCATCATGGAT	AAGAGATTTTGTGTAGATGT	137
RM2364 9	8	28.3	GAGCGTCATGTCGTACTGTGG	AAGAGAGTGTTTGGGAACT	385
RM2377 8	9	3.9	AACACAGCCTAAAGGTGTTT	GCTTCGGCCCTATAGTCTTC	328
9M7	9	6.6	ATTCTTGTGAGGACGGGAGG	GAGAGGCGGTTACCATCTGC	113
9M10.51	9	10.51	GGTGAGAGATCTTGAGTTCG	TATCAAAATTAACAACCGGG	189
RM566	9	14.65	AATATGGTGGCGGTACATCC	TGATCGAGCCAACAACAACCTGG	143
M087	9	16.9	TGGCCACAGCATGGTAAAAA	CCCACATGTCAGTATGCGTA	90
RM201	9	19.87	GTACTIONCGCCGTTCAACTCC	TTAGTGACCGGGATGACACAGC	395
09M22.8 1	9	22.81	AGTTCGGTTAACCCTCTTTC	AACCCCAATACACAACAGAG	134

M093	10	0.06	CAGCCACTGCGACCTTAGTC	GTCCCATTTTTGCCACTTTC	159
M094	10	4.9	TATGAATGAAAGGGCCAACG	ACGGAGTCTTCCCTCTGTCC	138
RM2514 6	10	7.1	GTAGAGGAGAGAGACCAGA	TATCCAAGCGAATTCACACC	223
M095	10	9.9	GCGCATCCATGCATATCCAA	GACAAGGTGTTGCCCAAGAA	156
10M12.6 6	10	12.66	ATCAGCAGTTGTTTCACGA	TTTGAGAGGAAAGAAAGAGC	141
RM2542 5	10	14.4	CCAGCCCAAACAGCTCTTGC	GGGCACTGTTTGTCTTTCTGT	155
RM2553 9	10	16.7	AAGCCCTATCATTGTCTTTC	CACCCATCTTGCATTATCAG	283
M098	10	21	TAGCCCGTAGGCACTCAACT	CGGGTGCTGTGGAAGATTAT	128
11M2.51	11	2.51	AATTACAACAGAACTACAT	GATGAATGTTTCATTGGCTCT	130
M04308	11	6.25	ATTCTAAGGGAGGGACGTAG	CTCATGTTTTCTTCCCGTT	192
11M11.1 6	11	11.16	GCCATGTTTAATTTCTCTCG	GTATTGAGAGAGGGCGCATA	142
M101	11	13.3	GTTGGGGCTTAATATTGTGG	GCTGTAAACCACAAGTCTA	166
11M20.7 7	11	20.77	AATGGTGAAAGTCACACCTC	CGCAAGATTAACATGAACA	135
11M24.4 2	11	24.42	GGGCTCTGGATAAATCTCT	AACGGAAAATGCTAAACAAA	143
M104	11	28.1	CAGTTTACATGTTGGCTGAG	GGAGCTCTATGAGAACTATG	152
M105	12	0.12	CACATTGTCACATCAATCATT	GGACATACGGTTGCTGCAGT	130
L1251	12	4.6	GTAGCTAAGGCCAAAATGGGCA	CATGGAATTCCTCTCCAAAT	313
M04442	12	7.19	TGGCTAGAAAATAGTGGGAA	CCAGTTATCCACGATGAAAT	179
12M13.0 5	12	13.05	ATTAGAAGACGAGGACATGC	AAACCATGGCTGAATAAAGA	140
M09955	12	16.7	CTGCACGGATTGTATGATAA	ACACAACATGCAAATCTTGA	169
M109	12	20.6	TAGCAAGCAGCATGGTCTCT	AATCGTCTCGACCGATCTTT	137
M110	12	22.8	CTGTCAAATGCGTTCGAT	AATGCCATTCCCCTGAATTT	184
12M27.4 7	12	27.47	TAGCCCAATCATTGTCTTTC	TACTTGACAGGTGATCAAAA	139

Note: ^a Physical position of the markers on the chromosomes referred to Nipponbare genomic DNA sequences.