

# Supporting Information

Fujii and Toriyama 10.1073/pnas.0901860106

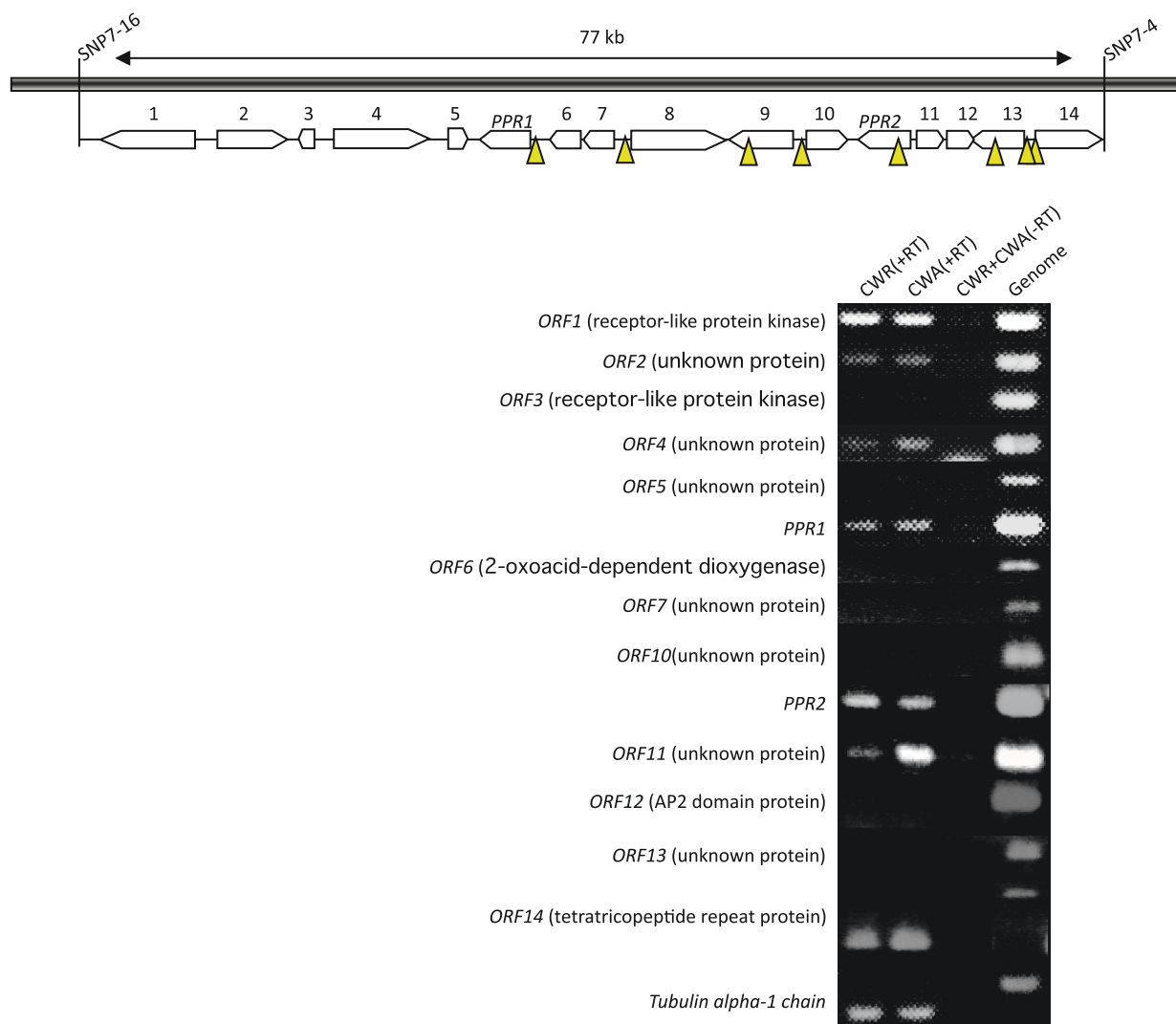


Fig. S1. Transcript detection of 14 predicted genes around the *RF17* locus.

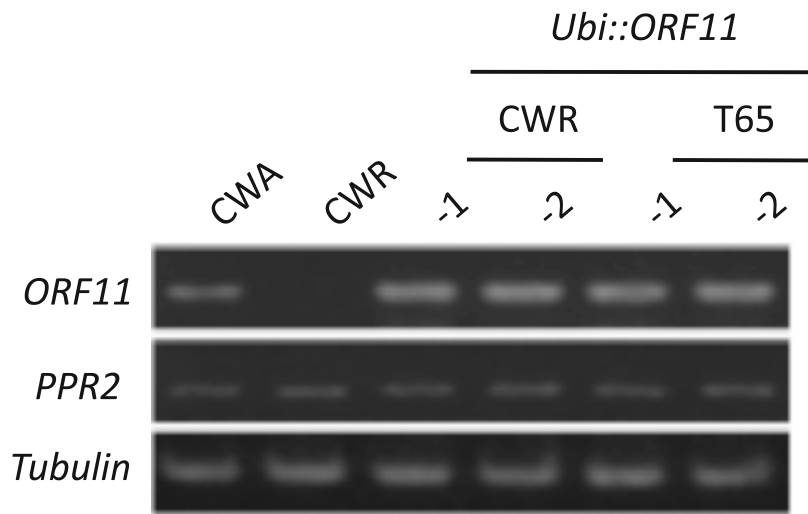
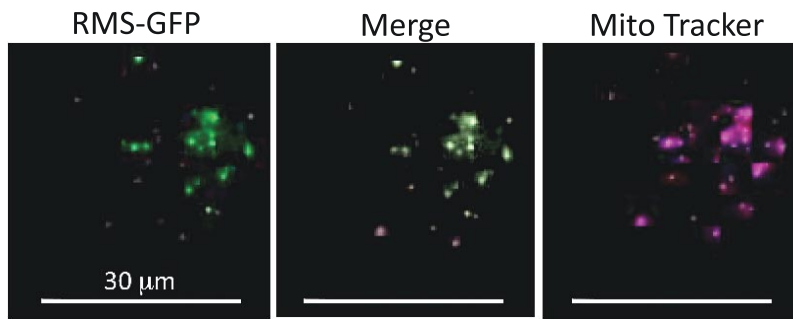


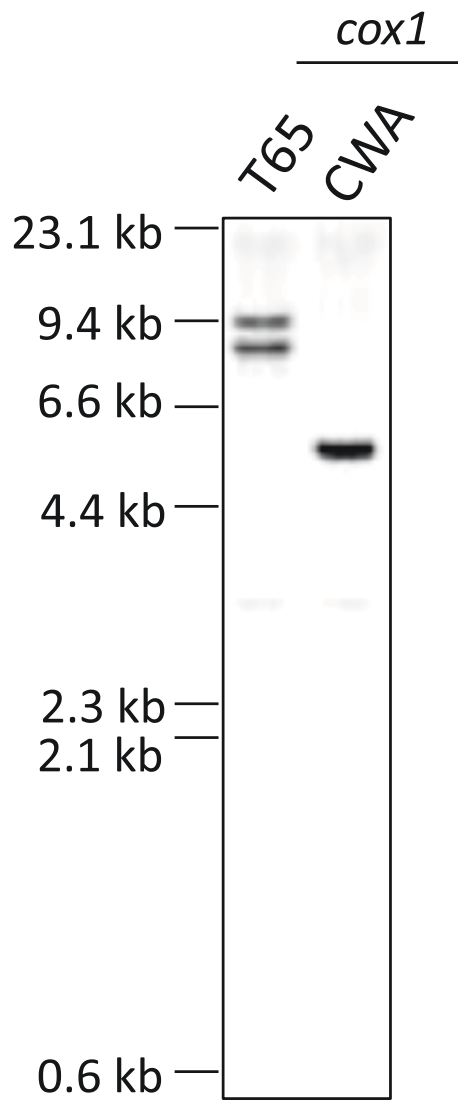
Fig. S2. Overexpression of *ORF11* in mature anthers confirmed by RT-PCR.

	140	150
FAS2_YEAST/1769-1832	AKEAVF	KSLGVKSLGGGA
FAS2_CANAL/1768-1831	AKEAVF	KALGVESKGAGA
ACPS_BRAJA/5-76	AKEACSK	ALGTGIRRGVW
ACPS_BACSU/5-73	AKEAFSK	AFGTGIGRQLS
ACPS_CHLPN/6-73	GKEAVAK	ALGTGIGSVVA
ACPS_BORBU/4-70	AKESLIK	ALSPLLQYKIN
ACPS_MYCTU/6-73	AKEAVIK	AWSGSRFAQRP
P78615_EMENI/1743-1806	AKEAVF	KSLGVCSKGAGA
PSF1_BACPU/107-169	MKEAFIK	LTCKGIS-YGL
O64506_ARATH/471-538	LKEAYVK	ALGKGFSGAPF
GSP_ANEMI/103-165	IKESYIK	AKGKMY-IP
STCJ_EMENI/1429-1495	AKEAVFK	CLQTVSKGAGA
Q9ZB56_PROMI/118-182	LKEAYIK	SRGIGLSEEL
O31302_CORAM/10-89	AKEAFIK	AWSQAIYQKPP
FAS2_PENPA/1740-1803	AKEAVF	KSLGVSSKGAGA
Q9FOY4_XANAL/160-226	AKESLFA	AYSAVGRYFD
LYS5_YEAST/133-197	LKESYTK	FTGTGLNTDLS
Y495_SYNY3/107-171	AKEAFL	KATGKISGGLN
O33901_9GAMM/81-145	LKESYIK	AKGLGLALS
LP14_BACSU/104-166	MKESFI	KQAGKGLS-LPL
ACPS_RICPR/5-74	AKEAVSK	AFVGI GRGIN
ACPS_ECOLI/6-73	VKEAAKA	FCTGIRNGLA
PPT2_YEAST/15-100	LKECSL	KALCCCVSKHDL
YDF2_SCHPO/123-188	CKEAIL	KALGIGLSGNPL
ACPS_STAA8/5-74	TKEAFS	KALGTGLGKHVA
Q22171_CAEEL/119-190	LKEAIL	KATGVGIMKDLN
ORF11/139-154	AAEAALK	SLGTERMRDVG

Fig. S3. Alignment of C-terminal amino acids of the ACPS catalytic domain. Amino acids 139-156 of ORF11 are shown.



**Fig. S4.** Mitochondrial localization of *ORF11* (= RMS) indicated by the merged image of RMS-GFP and the Mito tracker Red fluorescence.



**Fig. S5.** Southern blot analysis of mitochondrial *cox1*. Total DNA isolated from T65 and CWA was digested with *S*all and hybridized with a digoxigenin-labeled *cox1*.



**Table S1. Pollen germination frequency on stigmas after anthesis**

Line	No. of stigmas observed ( <i>n</i> )	No. of stigmas with pollen germination ( <i>a</i> )	Frequency of stigmas with pollen germination ( <i>a/n</i> ), %	No. of pollen per stigma ( <i>b</i> )	No. of germinating pollen per stigma ( <i>c</i> )	Frequency of pollen germination ( <i>c/b</i> ) $\pm$ SD, %
CWR	7	7	100.00	152.6	118.1	77 $\pm$ 11
CWA	7	0	0.00	0.4	0	0 $\pm$ 0
T65	7	7	100.00	151	121.7	81 $\pm$ 10
RNAi-ORF11-2	18	4	22.20	1.3	0.4	31 $\pm$ 2
RNAi-ORF11-3	23	6	26.00	1.7	0.5	29 $\pm$ 28
RNAi-PPR2-1	12	0	0.00	0.7	0	0 $\pm$ 0
RNAi-PPR2-3	16	0	0.00	0.4	0	0 $\pm$ 0

Table S2. Primer sequences of PCR markers used in this study

Marker name	Forward primer sequence	Reverse primer sequence	Chromosome	Position, cM	Polymorphism detection	BAC clone accession no. in NCBI
Markers used for marker-assisted selection of the CMS lines and CWR						
RM3252	GGTAACTTTGTTCCCATGCC	GGTCAATCATGCATGCAAGC	1	0.3		
RM8068	AAACCTCTCGTGTAAATTAG	TGAACATTTATTGATATGGTA	1	9.5		
RM1167	GAACATAAACCATGCGGGAG	AGCTAGTGGCAAAAGTGTGC	1	22.6		
RM8146	GACTCCTCCAAGTGCAACG	GTAGCTTCCCCACAATGTCA	1	25.4		
RM6466	CGAACGAGAATCCCTCATG	ATTGCACCAAGAGGAGATCG	1	49.0		
RM1287	GGAAGCATGCAATAGCC	GGCCGTAGTTTTGCTACTGC	1	58.1		
RM8003	ATCATGTTAATTAATGTCTAG	TGCTAAAAGGTTATTTTTAC	1	73.7		
RM8144	AAAAGTAGCTATATTTGGGA	GTGAGGAAATTATCGAAACAG	1	95.7		
RM3475	GTCGTTTTGCCTAGTTGAGC	TTCTCGGTGTATGGGTCTC	1	107.6		
RM8097	TACATACACGTTTATGTGCC	CGAGCGTAGGAAGACTACC	1	129.0		
RM1216	TTCCCAATGGAACAGTGAC	AGGGTCTACCACCGATCTC	1	132.1		
RM8085	TGCGTTTGCATTTCTTTTA	GGAAAGTTGTGTTCTTTGGC	1	139.9		
RM8062	CAAATTAATCCATCCATTATT	GAGGAGATGCTAGTTAATTAC	1	155.2		
RM6321	GGCTCTACCTCGCTGTTGTC	ACGAATATAACCTGCGGCAG	1	181.8		
RM8136	ATGTAAGCTAGGTAGAGCTG	GCGTACGTACGTAAGTAATA	1	181.8		
RM3340	TCTTGGCAAGCTCTCTCTC	CCATCATCTCGATCTTGACG	2	0.0		
RM7033	GTGCCAACACTGCACTAAC	GTTGGCGGTGATTCTGATG	2	7.9		
RM4355	GGGTAGAGAGTAGAAGGCA	TATATGGCAAGCCTAGCG	2	19.0		
RM6911	GGTGATTGCTATTTAACTTC	ACTTTTTCCAAATTATGCT	2	42.1		
RM6023	AAGGAAGCAGCGATGTGAAG	GAGCTAGAGATCACCTGGCG	2	81.7		
RM3515	GGAAAGAAGATATGCCATGC	AGAGAGAATCAGAAACACCAA	2	95.2		
RM1367	CGTAGGATCGGAGTTGTTGC	CCTAGCTGCTACCACCAAGC	2	110.9		
RM5631	CGTCCAAGAAATATTGCAGT	GTGAGACAGAATCCTTACGC	2	118.1		
RM5303	GCCATTTCTGCTCTTTCTTA	GTTTGCATGGAGAAGAAGAA	2	126.4		
RM3789	ATTAAGGGCAGGGGCATATC	CATTGACTGGTGTGGTCAGG	2	150.5		
RM3850	AAGTTGAGAATGAGGGACAA	TTCGGAAGTAAAAGGTAAT	2	156.3		
RM3248	AGAAGGTTGCTTTCTTGGCC	CTTGCAAGGTCTGTTGCATC	2	157.9		
RM4108	GTCCCTCGCTTATATCTAG	CAACTCTGCTAAACGAATTA	3	1.1		
RM6297	TTCTTCTCTCTCTCGCTCG	CCAAAGCAACCCATCTCAAC	3	7.9		
RM1338	AGAGGGAATTAGATTGGATT	GGTCCACTTCTTCTTCTAT	3	40.3		
RM6676	GTTACGGTCCAATAAGAAAT	CTTCAAGCTTACGAAAACA	3	65.4		
RM3223	CCGACGCTCAAGATCGTC	GAGAGAGAGGAGGGGAGAGG	3	86.0		
RM6146	ATCTTCTCCGGTCTCCCTC	AAGGAGGGAGGAGGCGTAG	3	86.0		
RM5626	ATCAGTCGGTCATAAAGCC	ACCTTCTTCTGCTGCTG	3	99.0		
RM2334	CATGCATCTGATCTGATTAT	TGTGAAGAGTACAAGTAGGG	3	115.6		
RM3856	TTGCATAACAAGATGAACAA	TTAATTGCGGATTTTTTATT	3	127.4		
RM6759	TGGAAAATTTGATGACATA	TATGGGGTATCCATAATCTC	3	144.5		
RM7389	AGCGACGGATGCATGATC	TTGAGCCGGAGGTAGTCTTG	3	164.4		
RM3585	TTGATGAGAGTGAACCAGCG	CGTTTATGCAGAACAACCCC	3	164.4		
RM3586	GAAGAGAGAGCCAGAGCCAG	ACACGATCGAGCTAGAAGACG	3	164.4		
RM7535	GACGAAAACCGGTCGAATTC	TCCAACAAGAGTGAGCATGC	4	6.8		
RM1359	AACGAATTCTATTTTGCCTC	TTCTTCTCATTTCAATTCGC	4	56.1		
RM3558	ACGAGAGATCTTCTTTCGAC	CCTCTATTTATGCCTCTACGC	4	69.8		
RM3866	AGTTGGTCATCTACCAGAGC	GATCTTCTGCTCAGAAAG	4	70.9		
RM3276	TCCGTCTCGACTCTCCATC	GATGAGACACCACGGACATG	4	102.4		
RM3335	TAATCCACTGTGTCATTTAA	ACCATCATCTTGTACCTAGT	4	113.2		
RM5879	ACCAGAGATCGATTGGTAGC	GGCTGCCTATCGAGGCTAAC	4	129.6		
RM1248	ACAAGCAGCTAATGGTTGGG	GTGATTTTGGCTCAGGTGAG	5	3.0		
RM7373	AACTCCTCCTTCTTCTGTC	ACAGGTTGATCGATCTTGCC	5	3.0		
RM5874	GAAAAGATCCTGCTCGTTG	GATCATCGCCAGAGCTC	5	30.7		
RM3777	GCTCCCAAATCTTGGTCTTG	TCTCACCTCTTCCCTACAAGC	5	31.5		
RM3853	AACATATGCTATGTGCCCTT	GGAGTTATCAGCAAATGCTC	5	31.5		
RM3322	CTTCTCCACCCATGCCAC	CCTGCAACGAACACCCAC	5	32.0		
RM3419	ATCTTGGTGAACAGTGCTC	CTGCTGCTATTCCTCAAGAC	5	36.4		
RM3437	AACCACCTAGGTTTCTCCCC	TAGCAACGAGGTTATTGGGC	5	60.7		
RM3800	GAATGAACCAATCCAAATGA	CCTGGAAGTGTGTATGATC	5	87.4		
RM4501	GCACAAATGTCTCTGTCTAA	AGAGTACGAAACGGTACAAG	5	89.6		
RM1054	ACTTACATCTGAGGTGCATA	GCATTGCAGATTACAGATAC	5	122.0		
RM8109	CATTGTTTAAAGTGCATAATTG	ACCATGACATGGCACATT	6	1.7		
RM2615	CAGAGTGCTTTAGACAATCA	AAATTGTAAGAGATTCTGC	6	32.7		
RM6857	ATGTTTTCTTTTTTGGAGG	AGAGGAAAAGATGAGGGGAA	6	34.3		



Marker name	Forward primer sequence	Reverse primer sequence	Chromosome	Position, cM	Polymorphism detection	BAC clone accession no. in NCBI
RM6836	TTGTTGTATACCTCATCGAC	AGGGTAAGACGTTTAACTTG	6	54.1		
RM5745	ATGCCAAGTGGACGATGTAC	ACATGTGGGTAGTGGGATGG	6	64.9		
RM6818	GTCGCATTCGTCTCCACC	ACCATTTCCAGATGACTCGG	6	65.8		
RM1161	AAACTGTTTTACCCCTGGCC	ATCCCCTTCTGCGGTAACAAC	6	65.8		
RM2229	AGCACCTAAGCATCTAGCAC	CATGTACCCAAAACAATTA	6	65.8		
RM5087	AAGGAGTTAGTGGGGGATAA	GAGATGAGATCCGAACCTCT	6	65.8		
RM3827	TAGTCTCGAGGACGGATTG	CTGGCCTTTCTTCAATCTGC	6	80.4		
RM5314	ATCCCACAATAACCCCTTGC	TGGTTGAGAGGTTGGATGG	6	91.9		
RM5753	AACATGCTCAACTTCTGGGC	GCTAGGTACGATCCAGCTGC	6	124.4		
RM508	AGAAGCCGGTTCATAGTTCATGC	ACCCGTGAACCACAAAGAACG	6	<8.2		
RM7083	AACTCAGGCACAGCCAAACAGC	CCACCTCTACTGTACGGTCTCG	6	<8.2		
RM19262	GGAAAGACCAGTTTAGAGCAATGG	AGCTAGATCCCTGTGTTTACACG	6	<8.2		
RM8059	CTTGATGCATCCACGGTACG	AACCAACGAACCAACGGAAAGC	6	<8.2		
RM8060	GGTTGTGCTGAATACTGTCCATAAGC	CAGGTAACCGGTGAAGATGTGC	6	<8.2		
RM3132	TTTGAGGAGAGTCTTGGGTTTGG	CTCCACTTCTCTTCACTCCCTTCC	6	<8.2		
RM4784	TACTGCAGAATTCCTGTGAGACG	GTACAAATTCCTGTTCTGAGAGC	6	<8.2		
RM7399	CAGATATGATGTTCTTGCCCTTGC	GCTTGCCAGATCACCTACCTACC	6	<8.2		
RM2353	CCTGGAGCAACTGTGGTACAAGC	AGCCACACTTGTGGTAGGTTTGG	6	<8.2		
RM6663	CCTCATCGGTGCGAACAC	ATACAGTGAAGCGTGTCCGG	7	0.0		
RM3196	ACCATGTCAGCAACCAC	ACATGTCTGATCGAGCTTCC	7	0.0		
RM1093	AGGTTGATGAACCCGATGAG	CTAGCTGCAGAACGGAGGAG	7	2.5		
RM3394	CCCTTACGTGCAGTACATTG	ATGCAGGCTACTTACTAGCG	7	2.5		
RM8263	TTTGCTGTCCCTTGTTC	TGCAATTCAAAGTCTTAGGG	7	35.7		
RM6872	GGATGAACACTGATGATGGC	ACCTCCACCAGATATCCAC	7	35.7		
RM6728	GGGTATGTGTCTGCTATTTTA	GAAATCTGGAATTTCCCTA	7	42.6		
RM6767	ACATTCTTGATCTACGTGGC	AATTATGGTTGCTAGGTTGG	7	60.8		
RM1973	GAGTTGGAAGGATATTTAA	TGGAGCCTAGAGAATACATA	7	71.3		
RM1330	CAGAGCTGTGGAAGAGGAG	CTCCTCAAACCGACTTC	7	96.1		
RM1364	AAGAAATCAAACACATGA	AAAACATCTACTTTGATCCA	7	101.8		
RM5720	CCTGATAAATTGACAGTTAC	GAGAGTAGGAGTTGATAACA	7	115.5		
RM1306	TGCCAATTACCTTCCCCTAC	TGCTCCGATTGCTGCTATG	7	116.1		
RM5911	CCCTTTTTAAGTCTGGGG	GGTGCCTCCTTCAAAGTTG	8	0.0		
RM6369	CAAGCTAGGGCTGCATAAGC	GCTTACCTACTACTCTCAC	8	0.5		
RM1235	GAAAACTAAAAAGCAGAGGA	AAGCTATCCATTTTGGATTA	8	12.8		
RM3572	AGTGCTGTCTGTTTTTGGC	CCCCTCCCTTCTTCTTTG	8	32.7		
RM4085	ACGAACTACTCATGTGTAA	CGAGTCTAGAATCCATATAA	8	35.7		
RM6215	CAGCAGAGAGATGACGCAAG	AAACCCAAAACCCCTCGTCTC	8	66.5		
RM5485	CTTCCACAAGCTTGGCTAGG	AATGCCATCCCCTACTCATG	8	96.6		
RM8058	ATATGATTTTCTCAAACAAC	CCAAACTACTAAACAGTACA	8	99.1		
RM3120	ATCGATGGAAGCTTTTGC	GGATGTACAAGAGCTTAGGAG	8	127.2		
RM3496	CGCTGAAAATACTGAATTGA	AGATGCATTTATTCCGAAAG	8	127.2		
RM3840	GAGGAAGAGGAAGGGACTCACC	TTGCGTCTACTGCTACTTCTCC	8	127.2		
RM7400	TGCAGCAGAAACACGAAGAG	AACTCGCCATCATCTCCAAG	8	127.2		
RM1328	GAATGGGATTAGACGATTTG	CCATGAGTGACATCAAAGG	9	0.0		
RM8206	TCTTTCTGGATCATTGGATG	ACTCTGCCAAGGATAACAAG	9	3.2		
RM6475	AGATCAAAGCAACGGCTAGC	GAACAGAGAGGGGACGTGTC	9	42.5		
RM5657	TATGTGCATTTGTAAGGTGA	GCTTTAGATTATTGAGCGAG	9	49.3		
RM1189	AACTGCCCATTTGTCTGTC	GACTCCGGACTAGACCAATC	9	58.3		
RM7424	AGAAGCCCATCTAGCAGCAG	TCAAGCTAGCCACACAGCTG	9	60.8		
RM5786	AAATCAGGAAAGTTTCTCAGC	AGAGACACAGGCAAGTCATC	9	77.2		
RM2144	ACATTATGAAACGGAGGAAG	GAAATGATGCATCAGCATTA	9	91.5		
RM6364	GTTCAATTCGTCTTCTCGG	TCTGATTCTTCTTCTCCG	10	0.0		
RM3311	AAGTATCCCTGTCTCACGCC	AGGTAGAGGGAGGGAGGGAG	10	19.0		
RM6704	CACACATTGCATTACGAGGG	CAGGGGCAGCTTGAATACTG	10	48.1		
RM1873	CTGACAGGACATTAATAAAC	CCTCATCTTAATCTCTTTA	10	48.4		
RM5352	CATGGTGCAAGTATGGATC	GTCTCTGCTGCAACACATCG	10	71.4		
RM3451	CGGCGAGATAACAATTCTCC	GCGTGATGATATGGTATCGG	10	72.8		
RM4771	ACGTTGATTTCAATCAGGTC	ACGCTAACTGAGAAACATGG	10	83.8		
RM5768	TTAGAGATGGGCCTAGCAGC	CACCCCTCATCACCATGACAC	10	94.1		
RM1761	ACGCTTAAAGAACATTTGAT	GCGATTAACCTTTAACCATT	11	0.3		
RM7557	GTGTACTGCCATGAAAGGCC	GAAGTGCCTTTGAGGAGAG	11	9.2		
RM1812	CAGCTAGTGAGCTCCTAGTG	GCTAACCCACCACTTATTC	11	10.3		
RM5599	CTCACAAATACCCATCCAC	AATTTTGTGCTGTTGTGAA	11	19.8		

Marker name	Forward primer sequence	Reverse primer sequence	Chromosome	Position, cM	Polymorphism detection	BAC clone accession no. in NCBI
RM3625	CTTGCAATTCAATTGCTTAC	GGTGGCCTAGTAAAATAAA	11	34.8		
RM3428	ATTCATGCTTCCTTTCAGTG	GATTAAGTGGTTTGCCATTTG	11	56.2		
RM6091	GCTGTCCTGCTTGAATCC	TGGTAGGCTGGTGACATGC	11	56.2		
RM5349	AGGGCATGCTTACATCCAAC	CATTTGCTTCTATGCCCCAG	11	79.1		
RM5961	GTATGCTCCTCCTCACCTGC	ACATGCGACGTGATGTGAAC	11	79.9		
RM4069	ACAATAATCTTCAAAGATGC	AATCATTGTGAAGTCAATC	11	112.1		
RM1233	GTGTAATCATGGGCACGTG	AGATTGGCTCCTGAAGAAGG	11	112.9		
RM7240	GCGACGACGAAGCTACCTAC	ACGTTTCGGGTTTCATGCC	11	112.9		
RM5926	ATATACTGTAGGTCCATCCA	AGATAGTATAGCGTAGCAGC	11	117.9		
RM1880	ACCACTAAATAAGCACATAC	GGCATCATACATTAATAATAC	12	9.4		
RM3483	CCTAGCTTTCAGGAGCAAG	CCCACAATGAGAAAACAGTTG	12	10.0		
RM8214	CCTAGCTTTCAGGAGCAAG	CCCACAATGAGAAAACAGTTG	12	10.0		
RM3472	ATCGCAAGAATCCGTGAAG	CGCTTTTGAGCTCGCCTC	12	27.6		
RM3455	TGAATCCACACTCGCAGATC	GCCAGTCCACGATTGGTC	12	38.1		
RM7619	CTTGGTATGTATTGGCAGCG	GAGGCAATAGGAGGGGAGAG	12	38.1		
RM5746	TCGCTACGTCGACTGATTTG	ATATCATCAGTCGGCAGCAG	12	39.4		
RM7003	GGCAGACATACAGCTTATAGGC	TGCAAATGAACCCCTCTAGC	12	41.8		
RM6973	CAACTCCAGCTTCGCCAAC	CGGCCACACCTAAATAAACG	12	49.3		
RM1337	GCTGAGGAGTATCCTTTCTC	ACCATAGGAAGATCATCACA	12	51.5		
RM1261	GTCCATGCCCAAGACACAAC	GTTACATCATGGGTGACCCC	12	61.6		
RM1246	AGCTCGATCCCCTAGCTCTC	TTGGAGAAGGTCACTGCC	12	65.3		
RM7102	CGGCTTGAGAGCGTTTTTAG	TACTTGGTTACTCGGGTCGG	12	71.9		
RM6869	GAGCTCCTGTAGTGACCCG	ATCAGCCTCGCAGCTTC	12	75.8		
RM3331	CCTCCTCATGAGCTAATGC	AGGAGGAGCGGATTTCTCTC	12	89.5		
RM7376	TCACCGTCACTCTTAAGTC	GGTGGTTGTGTCTGTTTGG	12	89.5		
RM1103	CAGCTGTGCTACTACCCG	CTACTCCACGTCCATGCATG	12	91.4		
RM5609	CGCCAGTGTGCAATATGATG	TCTTGGTGCAGTAGGTGCAC	12	93.0		
RM6947	ATTAACGTCCTACTGCTGGC	GCTAGGTTAGTGGTGCAGGG	12	93.0		
RM5479	TGATGCCTCCTAAGCTCACC	ACTTCTCCCCTCTCTGCTCC	12	95.4		
RM1264	CGGATAAGGACAAAGCAAGC	GTAGTACTGTGGACCAACCCG	12	104.2		
RM6953	ATGTCTCAACGGACGTAGGC	CTTGATGCAAGAACTGCTGC	12	104.2		
RM2197	ACTGAGAACTTAAATCATCG	GAACAACCTTGAAGAGAAAAC	12	109.2		
Markers used for high-resolution mapping of <i>Rf17</i>						
AT4-1	ACTGAAGCAAGTGACGTACG	CACCACTAGTCCACTAGTTC			PCR	AL606588
SNP7-21	GGAAGAAGTGATTCGCTCAAC	GGGTAGGGTGATTCAGATGC			PCR-RFLP( <i>SpeI</i> )	AL731582
SNP7-26	GGTATGTATGATCAGCTGCC	GATAGTAGGCCCTTTGCTTG			PCR-RFLP( <i>MspI</i> )	AL731582
SNP7-5	CGGTGTCTGTTATTATCTCC	TTATTCCTCTGGAGGGTGCA			PCR-RFLP( <i>MseI</i> )	AL731582
SNP7-4	CCACCACTGATGCCAACTAC	ATGACATGCGAACAGCTCAC			PCR-RFLP( <i>HhaI</i> )	AL731582
INDEL7-1	AACTCCACATGCATGCCATC	CTGTACTCGCTTTGAGATGC			PCR	AL731582
INDEL7-18	GTCATTCTCCGTAACAAGCG	TCCATTGGAACACTCCCTC			PCR	AL731582
INDEL7-2	ATTTGCGGGCTCATAATGGG	AGAAAGCCCCGACACTCCATT			PCR	AL731582
SNP7-14	CGGCTACGAATTTTCAGTAGC	ATCTCGTCGAAAACAAGCC			PCR	AL731582
SNP7-16	GAGCCAACTGCAACGAGTTC	GTGGTACCATCCTAGTATCC			PCR	AL731582
SNP7-17	ACGTCCCCATTGCTTTTGTG	TTGATCGTGGCGATTGATGG			PCR	AL731582
S13322*	TGGTGCGACGACATTCCTGAGAT	AGGGTCTGTCGGGTGTTAGATTGC			PCR-RFLP( <i>HaeIII</i> )	AL606595
INDEL8-1	ACAGAGACCAATTTCCCTC	TGCTCGATGTCGAAGTCGCC			PCR	AL606595
INDEL8-2	GTGGGTTGTCTTCTACTG	GTTTCTGTGCTAGGAATGCC			PCR	AL606595
RM3839 (1)	AATGGGACCAGAAAGCACAC	AAAAAGAGCATGGGGGCTAC			PCR	AL606595
SNP8-4	AGGTGTACAGGCTTGAATGC	AGAGCACGTAGGAGAGGATG			PCR	AL606595
GT10-1	GCAGTCAAATCCGATGGTAG	ATTAGATGCGTCAACTCCACGA			PCR	AL606623
TG10.5-1	TGGTAGAAAACCTCAACCCC	CGAGATCTACTCACTTCTCG			PCR	AL606623
INDEL5-2	GAGGCACATGAGCAGATTGA	ATCAGTAGCCGTGGAACACC			PCR-RFLP( <i>MspI</i> )	AL606441
INDEL6-1	CATAGCCGGCCAGAACTAAG	TAGCTAGCGCTGCAGAAGTG			PCR-RFLP( <i>HhaI</i> )	AL606447
INDEL6-4	TTGGTATGTGCTCGAATCCA	TGATTGACAGCCAAACAGGA			PCR-RFLP( <i>HhaI</i> )	AL606447

\*See <http://rgp.dna.affrc.go.jp/publicdata/caps/index.html>.

**Table S3. Primer sequences for RT-PCR**

Gene name	RAP-DB accession no.	Forward primer sequence	Reverse primer sequence
<i>ORF11 (RMS)</i>	Os04g0475900	ACTCGGTTCCAGGCGATGGTGGAA	GGTGGCTAAACTTGGCCAGCCAAAAC
<i>PPR2</i>	Os04g0475800	TCGTTACCACGGTAGATAGACTCAT	CCCACATCTTCTCCTTGCATAATCC
Tubulin	Os07g0574800	TACAACGGTTGGCGTCGCAC	AACTGCGCACACGGTCCAG