Supplementary Table 1. List of SSR markers used in linkage genetic mapping.

Primer Name		Primer Sequence (5'→3')	Repeat motif	Expected Product Size (bp)
WH_SSR_W0254_0187	F:	CTGTGGGCTATATGGCAA	$(AC)_5$	165
	R:	CAGAGAGTGGAGGAGGACTAGAA		
WH_SSR_W1846_0062	F:	GACTGATAGGACCTGGACTTTG	$(AC)_{10}$	173
	R:	GAACAGAGGAAACCAAGAGC		
WH_SSR_W0144_0368	F:	CTGGATACCAAGCACAAAGG	$(AG)_{16}$	176
	R:	TGCGTTCTCATCTCTAACCC		
WH_SSR_W0383_0164	F:	GAACTTGTCGTTCAGAACTCCC	$(AC)_{10}$	193
	R:	CTGATGTGGGTAGAAAGCCT		
WH_SSR_W0058_0134	F:	GTTGGTCATGAGAATCCACC	$(AC)_5$	196
	R:	ATTCTCCGTGCAGAACGTC		
WH_SSR_W0058_0445	F:	TGGCCAGTGTTGAGGTAATG	$(AC)_{20}$	189
	R:	GCGAAGGGATTTCTTAGAGC		
WH_SSR_W0210_1375	F:	TCGGGAAGATTTTCGAGC	$(AG)_5$	199
	R:	AATGGAGATGGTCCACACAG		
WH_SSR_W0033_0435	F:	GTCAGTGTGCAAAGAGAGGTC	$(AC)_6$	150
	R:	GGTCCCTATAAAGTCCGATTCC		
WH_SSR_W0067_0153	F:	GAATCTGGGCGAAGAGTATGTC	$(AG)_6$	162
	R:	AACTGAACCAGTTAACCGCC		
WH_SSR_W0234_0277	F:	CGTCCTGGAACAAACCAA	$(AC)_5$	175
	R:	GATCAGGGCGTGTTAAAGC		
WH_SSR_W0341_1656	F:	CTGGCATTTGTATCTCCCAC	$(AC)_{17}$	188
	R:	CGATGCGTGATTCGTAGA		
WH_SSR_W0103_1927	F:	GGCAAAGAACTTTGGAGAGC	$(AG)_5$	172
	R:	CTCTTTCTCGCTGTGTGTGT		
WH_SSR_W0316_0715	F:	GTCGTCTCTACTTTCTGCTGCT	$(AG)_8$	181
	R:	CTCTTAGTCCACGTGTTTACGC		
WH_SSR_W1849_0798	F:	GTGGGTGTTTTAGTGACGACTG	$(AG)_{13}$	158
	R:	TCTGTAGGAAGAAGAGCGTCC		
WH_SSR_W0335_0233	F:	ATGTTAGTGACCGAGGTGAGAG	$(AG)_{24}$	177
	R:	TTTAACGGTCCGGGTTTC		
WH_SSR_W0105_0155	F:	GATCGATTCGACAGAGAGAGAC	$(AG)_5$	154
	R:	GTCGGCGTCGAAGATACTC		
WH_SSR_W0132_2218	F:	GTTGTTCCTCTGACTCATGCTG	$(AG)_9$	183
	R:	ATCTCACACCCAACAAACCC		
WH_SSR_W0041_0887	F:	CGACACAAGGGTAGAAGAAGAG	$(AG)_6$	184
	R:	CTGTTTTCCTGCTCAGTTCC		
WH_SSR_W0022_0397	F:	AATCGTCCTCCTTCACCATC	$(AG)_6$	175
	R:	GCCTTAGGAGAGTCCTACTGTGT		
WH_SSR_W0666_0163	F:	AGCTGCCTCTTTATGCAGG	$(AG)_5$	155
	R:	GGTTTTGTCGTGAACTGACC		
WH_SSR_W0061_0294	F:	CAAATCTTGGCGGTCTCA	$(AG)_{23}$	193
	R:	GTGATCAAAGTCATGGAGGG		

Supplementary Table 1. Continued

Primer Name		Primer Sequence (5'→3')	Repeat motif	Expected Product Size (bp)
WH_SSR_W2221_0008	F:	ATTGGGGTGGGAGTTTCTC	$(AG)_5$	173
	R:	CCCAACTCCATCCATCAGTA		
WH_SSR_W0285_0258	F:	CTCTCCGACGCCTGATAAT	$(AG)_{14}$	164
	R:	CCTTCTCTGCAACACTCCTC		
BT_SSR_W0301_0157	F:	TGAGAGAGAGTGGGAAAGTGAC	$(AG)_{19}$	192
	R:	TAAGATCCAGCCGAACTAGC		
BT_SSR_W0341_2084	F:	AGACAGCAGTAGGCGAGAAAAC	$(AG)_8$	189
	R:	CTCTCCAGCTGAACTCCTCTT		
BT_SSR_W0341_1309	F:	GGGGCGGACTAGAAAATAAG	$(AG)_7$	152
	R:	CTTCTTCTCTCTCACCTGTCGT		
BT_SSR_W0121_0613	F:	CGCTCTAATTTCGGCTAGTG	$(AC)_9$	180
	R:	AGAATCGGGTAGTCCACCTT		
BT_SSR_W0099_1972	F:	GGTTTGGCGGCTAATATAGG	$(AG)_{11}$	171
	R:	GACAGTGGCCTGACCAAAT		
BT_SSR_W0921_1221	F:	GAAGGACGTAAAGCGGATTG	$(AG)_{19}$	167
	R:	CTCAGCAGCTCCAGACAACTTA		
BT_SSR_W0921_0348	F:	GTAACCCTAGTCGTCGTTCTTG	$(AG)_{15}$	160
	R:	GGGTACCCTACATGCTTCACT		
BT_SSR_W0087_1229	F:	AACACTCTAAGTGGCCCTACC	$(AC)_6$	191
	R:	GATTCTCCCTGATTTCTGCC		
BT_SSR_W0257_0571	F:	GTGCAGCCCCTACATCATAGT	$(AC)_9$	170
	R:	TGGTCTAGCTCCTAACCACTGT		
BT_SSR_W1851_0632	F:	GGTACGCTTTACTTCGTCCTTC	$(AC)_8$	160
	R:	GCGGTAGAGGGAGTACAAATCT		
BT_SSR_W0803_0295	F:	CTATCTCCCTCTCCCTCCTAGTT	$(AC)_{16}$	176
	R:	CAACTTTGTGGTTCTGCCTC		
BT_SSR_W0144_1512	F:	GCTTTGCCTTTCAGCTTC	$(AG)_5$	178
	R:	GTAAAACCAAAGCCTCCCTG		
BT_SSR_W0132_1223	F:	CTAGAAAACCCGGGATCG	$(AG)_9$	187
	R:	TTAACAGCCAACAGACGGAG		
BT_SSR_W0132_1701	F:	GTTGAGTTCGACAAGGCAGT	$(AG)_{11}$	180
	R:	CCATGCCACCATGTTTCT		
BT_SSR_W1584_1671	F:	CTTATCTTAGTTCACCCCACGC	$(AG)_5$	192
	R:	TTTAGGCCCCAAACTCCTAC		
BT_SSR_W1584_1249	F:	GTCAAAGGAAGACGGACTACTG	$(AG)_7$	174
	R:	CCATTGAGTTCTGAGTGGCT		
BT_SSR_W0210_0814	F:	CTCTCGCTCTCTGAAGTCAAGT	$(AC)_{14}$	176
	R:	CTGTAGCTATTGTGCCCTCTTC		
BT_SSR_W0307_0212	F:	TAGCCGATCGATGTACAAGC	$(AC)_5$	180
	R:	GGAACTTTTTCTGACCCCC		
BT_SSR_W0126_1671	F:	CAGTAATGAGCCTCAGCGAT	$(AC)_8$	172
	R:	GCTGGAACTGGATCGGTAT		

Supplementary Table 1. Continued

Primer Name		Primer Sequence (5'→3')	Repeat motif	Expected Product Size (bp)
BT_SSR_W0285_2323	F:	GTTTGGAAGAGATCAGGAGAGG	$(AG)_9$	155
	R:	CCACAGTTAGCTCGATGACA		
BT_SSR_W0309_1120	F:	GAAAACCTGCCGTAGTAGTCAC	$(AC)_5$	187
	R:	CTGACTAGGCAAATACCTCCTG		
BT_SSR_W1370_0085	F:	CCGGCCAAAAGATCAACT	$(AC)_5$	191
	R:	TCTCAGTCTGTGAGAGAGGCTAC		
BT_SSR_W0049_0285	F:	GAACTTTGCTTCTGGAGCTG	$(AC)_9$	168
	R:	CCCAAAGATATTGACTGGGG		
BT_SSR_W2219_0632	F:	TCTCACTCTCATGGCTGACA	$(AG)_{11}$	168
	R:	ATATTCGAGGGGAGCTTTCG		
BT_SSR_W2219_0007	F:	CTCTCCCTGTTGGGGTAGTTAT	$(AG)_{22}$	177
	R:	GGAACACAGTTTCTGCACTCTC		
BT_SSR_W1799_0071	F:	AATCAGATCCTGGACTCTCCTC	$(AC)_{11}$	184
	R:	CACCAGCTGCTGTGAGTATTGT		
BT_SSR_W0001_0274	F:	ACCGGCTTGATAGGAGAAAG	$(AC)_7$	197
	R:	CCTAGGAGAGTTCATCTGGTTC		
BT_SSR_W0337_1237	F:	GAATCCAGCCGTTCCATAAG	$(AG)_{16}$	167
	R:	GTCACTCCTTCTGAGCTCCTC		
BT_SSR_W0085_0135	F:	CCTGCTTCATCATCAAGGG	$(AG)_{16}$	196
	R:	CCACACCTCTTATCTCCATCAC		
BT_SSR_W0159_1920	F:	GGAAGGAGAGGAAAACCGTTAG	$(AG)_{11}$	188
	R:	AAATCACTCCCTCCCTACTCTC		
BT_SSR_W0159_2263	F:	CCAAAATCCCGAGCTATCTG	$(AG)_5$	179
	R:	CCCACGTGTTTCCATTACTC		
BT_SSR_W0243_0176	F:	CAACCATCTGCACAGAGAACTG	$(AG)_{15}$	168
	R:	GAAGAGTCTGGTTAGCATGGTG		
BT_SSR_W0047_1139	F:	GGAAGGAACTGGAAGGTGAT	$(AG)_8$	170
	R:	TTAATCCTCCTCCTCTCGTACC		
BT_SSR_W0115_1829	F:	GAGAGGAGAGAGATGTATGGGAC	$(AG)_8$	193
	R:	ATTTTCTCCCTCTCACCCAC		
BT_SSR_W0389_0329	F:	AGCTGAGGTGAACTTAGACGAG	$(AG)_{14}$	150
	R:	ATATGAGCTGCTGCTGTCCT		
BT_SSR_W0107_0407	F:	GAAGATGGTACTGTCTGTCCGT	$(AG)_7$	198
	R:	AGAGGAGAGAGAGTGGTCCAGTT		
BT_SSR_W0105_0311	F:	AACAGAAGACCACCTGCATC	$(AG)_{11}$	192
	R:	GGTGAAATCCCTCCATGACTAC		
BT_SSR_W1569_0020	F:	CTTGCTTGCCTCTGGTTAAG	$(AG)_6$	181
	R:	GTTTTTCCCTCATGTACCCC		
BT_SSR_W0230_0692	F:	GTGGATGCTCCAGCTCTTC	$(AG)_{18}$	179
	R:	GTACGGACGTCAGGTTTCAG		
BT_SSR_W0010_0362	F:	GATGCAAACACACACAGCC	$(AG)_6$	199
	R:	ATTCATGAGACGCTCTGGAC		

Supplementary Table 1. Continued

Primer Name		Primer Sequence (5'→3')	Repeat motif	Expected Product Size (bp)
BT_SSR_W0126_1230	F:	TGGAAGCGTATGAGTGAAGG	$(AG)_6$	153
	R:	CCTCCGGATTAGGACTAGGAT		
BT_SSR_W0069_0517	F:	GTTCTGGAGTTCAGTGAAGGG	$(AG)_5$	181
	R:	CTCGAAAGGGGATGTCTTG		
BT_SSR_W0324_0155	F:	GTTGCTGGCCATACTGCT	$(AG)_5$	196
	R:	GCTGGCTTTTTGTCGCCT		
BT_SSR_W0258_0225	F:	GAGTTGGGATTCTATCGTGC	$(AG)_{13}$	200
	R:	CCAAAACCATAGGAGGAGTC		
BT_SSR_W0800_0036	F:	CAAGGTGAGAAAGTGTGGCT	$(AG)_{13}$	162
	R:	GAGCCCTCGACGTTTTGTTA		
BT_SSR_W0396_0037	F:	GGCAGAGAAATCAGAGCTAACG	$(AG)_{14}$	189
	R:	ACACAACACAACCAGGCAG		
BT_SSR_W0233_0336	F:	CTATGCATGGTTGAGAGGACAG	$(AG)_5$	156
	R:	GTTATAGGCCCACACCTCATAG		
WB_SSR_W0062_0058	F:	GTGCTCATTGACATACAGGAGG	$(AC)_6$	175
	R:	GTAGAGATAAGTCCGGTTGTGC		
WB_SSR_W0341_4203	F:	GGTACTGGTGGCAGTTATGG	$(AC)_8$	186
	R:	GCTCCCAGTATTCTGAGTGAGAG		
WB_SSR_W0061_0376	F:	GCGTGCAAATTGTAGCAG	$(AG)_7$	189
	R:	CTACCTTAAACCTGTGGTGCTC		
WB_SSR_W0335_0233	F:	ATGTTAGTGACCGAGGTGAGAG	$(AG)_{24}$	177
	R:	TTTAACGGTCCGGGTTTC		
WB_SSR_W0230_0814	F:	CGAAAGGGTCTTTTCTAGCACC	$(AG)_6$	194
	R:	GCTAGGACCAGAACATAAGAGC		
WB_SSR_W0080_0197	F:	CATTGAAACAGCCAGAGGTC	$(AG)_{16}$	168
	R:	GATAAGCCACTAACACCACCAC		
WB_SSR_W0200_0211	F:	GTGGTCCTATTTCGGGGAT	$(AG)_{11}$	200
	R:	CTCAGAAGTTGAGCAGGACAAG		
WB_SSR_W0309_1962	F:	GGTGTGTTGAGGGAAGTTTG	$(AG)_{30}$	190
	R:	CACCACCGGAGAAACTCA		
WB_SSR_W0193_0482	F:	CGATGTGAATCGGTGGTT	$(AG)_{17}$	198
	R:	CACCGGTGAGTTACCAACTT		
WB_SSR_W0339_0949	F:	CAGCAGTTAGGTACTTGGGGT	$(AG)_{35}$	183
	R:	TATCTCCCTGTTTCCCTACCTC		
WH_SSR_001*	F:	CACAGCAGGATTTTCGAGAG	$(AC)_7$	172
	R:	CGTCTTTTGGGGTACGAGTAG		
WH_SSR_002*	F:	AAAGTGATACGACGACGAGG	$(AG)_{13}$	197
	R:	GAGAAACTCAGGCAACCAGA		
BT_SSR_003*	F:	GCAGCAAGATTTCACACC	$(AC)_7$	178
	R:	GAGCTGTTGTATTGTGGGTAGC		
BT_SSR_004*	F:	GGGAGAGAGCCTAAAGATCAAG	$(AG)_{10}$	187
	R:	CCAGTTTACCCTCCATGTTG		

Supplementary Table 1. Continued

Primer Name		Primer Sequence (5'→3')	Repeat motif	Expected Product Size (bp)
BT_SSR_005*	F:	AAACCTAAACCCAGCAGGAC	$(AG)_5$	192
	R:	AACATCTCTCCGCCTAGGTTAC		
BT_SSR_006*	F:	GGGGAATGGAGATTACCAGA	$(AG)_{10}$	172
	R:	ATCCAGTGGCTGACAAGGT		
BT_SSR_007*	F:	GGAAACCCTAACCCTCGTT	$(AG)_{15}$	177
	R:	GTGACGGCGCATAATATCTC		
BT_SSR_008*	F:	GAGAAGTTGAAACCTCGCTG	$(AG)_7$	171
	R:	CCAAGTGACCCAACCTAAAG		

*primer#81~88 are didn't matched on the current 'Wonwhang' scaffold version

Supplementary Table 2. SSR markers used in the mapping. Includes linkage group, position, gene description, number of alleles and PIC value.

	Primer Name	Linkage group	Genetic position (cM)	Putative function*	Number of alleles	PIC value
1	BT_SSR_W0085_0135	Chr01	69.8	CASP-like protein POPTRDRAFT_822486	3	0.346
2	BT_SSR_W1370_0085	Chr01	93	protein IQ-DOMAIN 1	2	0.385
3	WH_SSR_W1849_0798	Chr01	162	probable leucine-rich repeat receptor-like protein kinase IMK3	4	0.675
4	WH_SSR_W0144_0368	Chr02	36.8	protein PHLOEMPROTEIN2-LIKE A 10	3	0.627
5	WH_SSR_W2221_0008	Chr02	82.4	V-type proton ATPase subunit c1	2	0.495
6	WB_SSR_W0335_0233	Chr02	119.6	subtilisin-like protease SBT5.4	3	0.639
7	WB_SSR_W0200_0211	Chr02	129.1	WD repeat-containing protein 76	4	0.708
8	BT_SSR_W0230_0692	Chr02	207.4	cyclin-dependent kinase F-1	3	0.491
9	WB_SSR_W0230_0814	Chr02	208	strigolactone esterase D14	4	0.717
10	BT_SSR_006	Chr02	216.2	probable inactive leucine-rich repeat receptor-like protein kinase At5g20690	3	0.486
11	BT_SSR_W0144_1512	Chr02	263.9	probable beta-1,4-xylosyltransferase IRX14	2	0.469
12	WH_SSR_W0103_1927	Chr02	361	cytochrome P450 86B1	3	0.618
13	BT_SSR_W0049_0285	Chr03	104.9	GDSL esterase/lipase At5g55050	4	0.616
14	WH_SSR_W0061_0294	Chr03	112.3	transmembrane emp24 domain-containing protein p24beta3	3	0.509
15	WH_SSR_W0105_0155	Chr03	158.1	vacuolar protein sorting-associated protein VTA1 homolog	3	0.657
16	BT_SSR_W0087_1229	Chr04	31.4	homeobox protein HD1	3	0.508
17	WH_SSR_W0041_0887	Chr04	40	scarecrow-like protein 27	2	0.498
18	BT_SSR_W0309_1120	Chr04	158.4	DEAD-box ATP-dependent RNA helicase 3	2	0.492
19	WB_SSR_W0309_1962	Chr04	167.5	kinesin-4	3	0.65
20	BT_SSR_W0115_1829	Chr05	90.1	probable BOI-related E3 ubiquitin-protein ligase 2	3	0.501
21	BT_SSR_007	Chr05	103.3	ankyrin repeat and SAM domain-containing protein 6	2	0.486
22	WH_SSR_W0234_0277	Chr05	105.4	protein FAR1-RELATED SEQUENCE 7	2	0.5
23	BT_SSR_W0341_2084	Chr05	118.6	dedicator of cytokinesis protein 11	3	0.501
24	BT_SSR_W0301_0157	Chr05	121.1	nuclear-pore anchor	3	0.504
25	BT_SSR_W0341_1309	Chr05	122.8	vacuolar-sorting receptor 6	3	0.504
26	WH_SSR_W0285_0258	Chr05	150.8	60S ribosomal protein L11	4	0.648
27	BT_SSR_W0337_1237	Chr06	45,1	phosphoacetylglucosamine mutase	3	0.491
28	BT_SSR_004	Chr06	109	serine/threonine-protein kinase HT1	3	0.495
29	WH_SSR_W0067_0153	Chr06	158.3	protein TPLATE	3	0.419
30	BT_SSR_W0099_1972	Chr07	119.5	cytosolic endo-beta-N-acetylglucosaminidase	3	0.508
31	BT_SSR_W0921_0348	Chr07	129.6	transcription factor bHLH36	3	0.506
32	BT_SSR_W0921_1221	Chr07	130.7	mitogen-activated protein kinase kinase kinase YODA	3	0.506
33	BT_SSR_W0803_0295	Chr08	0	protein NRT1/ PTR FAMILY 4.3	3	0.508
34	BT_SSR_W2219_0007	Chr09	45.8	protein ALTERED XYLOGLUCAN 4	3	0.486
35	BT_SSR_W2219_0632	Chr09	48	homeobox-leucine zipper protein HAT7	3	0.482
36	BT_SSR_W0210_0814	Chr09	50.2	myb-related protein Myb4	3	0.486
37	BT_SSR_W0010_0362	Chr09	64.9	PLASMODESMATA CALLOSE-BINDING PROTEIN 1	3	0.498
38	WH_SSR_W0254_0187	Chr09	79.9	probable protein S-acyltransferase 19	4	0.769
39	BT_SSR_W1799_0071	Chr09	94.3	zinc finger protein NUTCRACKER	3	0.482

Supplementary Table 2. Continued

	Primer Name	Linkage group	Genetic position (cM)	Putative function*	Number of alleles	PIC value
40	BT_SSR_W0396_0037	Chr09	111.9	mannan endo-1,4-beta-mannosidase 2	2	0.495
41	WH_SSR_W0022_0397	Chr10	3.6	NAC domain-containing protein 17	2	0.444
42	BT_SSR_W0047_1139	Chr10	11.1	dynamin-related protein 3A	2	0.482
43	WB_SSR_W0341_4203	Chr10	49	WAT1-related protein At4g08300	3	0.601
44	WH_SSR_W0341_1656	Chr10	61.2	YTH domain-containing family protein 2	3	0.635
45	BT_SSR_W0324_0155	Chr10	189.2	polyadenylate-binding protein RBP45B	3	0.508
46	WB_SSR_W0193_0482	Chr10	201	glycogen phosphorylase 1	3	0.623
47	WH_SSR_W0058_0134	Chr10	206.3	subtilisin-like protease	4	0.769
48	WH_SSR_W0058_0445	Chr10	207	major latex allergen Hev b 5	4	0.697
49	BT_SSR_W0307_0212	Chr11	63.9	putative UDP-glucose flavonoid 3-O-glucosyltransferase 3	3	0.495
50	BT_SSR_W0233_0336	Chr11	69.3	pentatricopeptide repeat-containing protein At5g48910	2	0.478
51	BT_SSR_W1584_1671	Chr11	82.5	TMV resistance protein N	3	0.504
52	WB_SSR_W0061_0376	Chr11	235.9	2-methyl-6-phytyl-1,4-hydroquinone methyltransferase	3	0.649
53	BT_SSR_008	Chr12	275.5	flowering locus T (FT2) gene	5	0.721
54	BT_SSR_W1851_0632	Chr13	14.6	G-type lectin S-receptor-like serine/threonine-protein kinase At2g19130	2	0.486
55	BT_SSR_W0001_0274	Chr13	41.9	protein tesmin/TSO1-like CXC 2	3	0.586
56	BT_SSR_W0121_0613	Chr13	188.4	1-Cys peroxiredoxin	2	0.482
57	WB_SSR_W0339_0949	Chr14	29.2	myb-related protein Zm 38	3	0.592
58	BT_SSR_W0069_0517	Chr15	23	separase	2	0.498
59	BT_SSR_W0107_0407	Chr15	24	putative methylesterase 14	3	0.509
60	WH_SSR_W0666_0163	Chr15	112.7	2-alkenal reductase (NADP(+)-dependent)	3	0.509
61	BT_SSR_003	Chr15	143.5	serine carboxypeptidase II-3	4	0.621
62	BT_SSR_W1569_0020	Chr15	144.3	1-aminocyclopropane-1-carboxylate synthase 8	3	0.498
63	BT_SSR_W0159_2263	Chr16	11.2	protein TIFY 6A	3	0.482
64	BT_SSR_W0159_1920	Chr16	12.2	auxin efflux carrier component 3	3	0.476
65	BT_SSR_W0132_1701	Chr16	17.9	beta-glucosidase 40	3	0.482
66	BT_SSR_W0132_1223	Chr16	20	E3 ubiquitin-protein ligase MARCH9	2	0.482
67	WH_SSR_W1846_0062	Chr16	25	BTB/POZ domain-containing protein At1g67900	2	0.498
68	BT_SSR_W0800_0036	Chr16	30.4	NAC transcription factor 25	2	0.478
69	BT_SSR_W0243_0176	Chr17	55.2	protease Do-like 9	4	0.513
70	BT_SSR_W0258_0225	Chr17	70	protein IQ-DOMAIN 1	3	0.498
	Total				205	
	Mean				2.93	0.54

*Gene description obtained from homepage http://www.ncbi.nlm.nih.gov/