

Accessory Publications

Table S1. The SRAP primers used in this study.

Upper primers		Lower primers	
Code	Sequence (5'-3') ^a	Code	Sequence (5'-3') ^a
A	em-AAT	1	me-ATA
B	em-TGC	2	me-AGC
C	em-GAC	3	me-AAT
D	em-TGA	4	me-ACC
E	em-AAC	5	me-AAG
F	em-GCA	6	me-TAG
G	em-ATG	7	me-TTG
H	em-AGC	8	me-TGT
I	em-ACG	9	me-TCA
J	em-TAG	10	me-TAC
K	em-TCG		
L	em-GTC		
M	em-GGT		
N	em-CAG		
O	em-CTG		
P	em-CGG		
Q	em-CCA		

^a The core sequences of primers for amplification were: em-=GACTGCGTACGAATT; me-=TGAGTCCAAACCGG.

Table S2. The AFLP primers used in this study

<i>EcoR</i> I primers ^a		<i>Pst</i> I primers ^a		<i>Mse</i> I primers ^a	
Code	Sequence (5'-3')	Code	Sequence (5'-3')	Code	Sequence (5'-3')
E1	E-AAA	P1	P-AGA	M1	M-CAA
E2	E-AAT	P2	P-AGT	M2	M-CAT
E3	E-AAC	P3	P-CAC	M3	M-CAC
E4	E-AAG	P4	P-CAG	M4	M-CAG
E5	E-ATA	P5	P-CCA	M5	M-CTA
E6	E-ATT	P6	P-CTG	M6	M-CTT
E7	E-ATC	P7	P-GCA	M7	M-CTC
E8	E-ATG	P8	P-GCT	M8	M-CTG
E9	E-ACA	P9	P-GGA	M9	M-CCA
E10	E-ACT	P10	P-GGT	M10	M-CCT
E11	E-ACC	P11	P-GTT	M11	M-CCC
E12	E-ACG	P12	P-TGA	M12	M-CCG
E13	E-AGA	P13	P-TGT	M13	M-CGA
E14	E-AGT	P14	P-TGC	M14	M-CGT
E15	E-AGC			M15	M-CGC
E16	E-AGG			M16	M-CGG

^aThe core sequences of primers for amplification were: E-= GACTGCGTACCAATT C;
P-= GACTGCGTACATGCAG; M-= GATGAGTCCTGAGTAA.

Table S3 Characteristics of detected QTLs for each trait measured in two different locations

Trait	QTL	location	LG	Closest neighboring locus	Marker interval	Maximum LOD score	Additive value	Dominant Value	Percentage variance explained	Functional markers
PH	Qph1.1	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	1	CB10597	CB10597/AUXDR-2	2.85	-2.56	-5.10	10.41	-
	Qph2.1	Wuhan	2	BKCOAS	BKCOAS/CN33b	3.16	5.11	13.20	17.31	BKCOAS
		Jingmen	-	-	-	-	-	-	-	-
	Qph2.2	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	2	J10-2-280	J10-2-280/B4-1-330	2.68	5.39	-2.13	6.55	-
	Qph2.3	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	2	CN34	CN34/J2-4-180	2.82	4.59	-2.06	5.80	-
	Qph2.4	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	2	DNAPL-2	DNAPL-2/P4-5-260	2.89	2.61	2.69	6.19	DNAPL-2
Qph4.1	Qph4.1	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	4	RM5-300	RM5-300/DNAJ	2.85	3.71	3.61	10.78	-
	Qph6.1	Wuhan	6	VHSD	CB10006/VHSD	2.93	4.55	6.58	8.22	VHSD
		Jingmen	-	-	-	-	-	-	-	-
	Qph7.1 ^a	Wuhan	7	CB10526	F7-1-130/CB10526	5.59	7.18	0.50	13.64	-
		Jingmen	7	F7-1-130	F7-1-130/CB10526	4.80	4.64	6.15	11.35	-
	Qph7.2	Wuhan	7	RM5-130	Ra2-A01/CB10569	6.10	12.26	0.18	19.68	-
		Jingmen	7	B5-1-280	Ra2-A01/RM5-130	4.42	3.93	1.48	9.81	-
	Qph7.3	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	7	B5-2-270	CN64/RabGAP-1	4.26	3.82	3.75	10.40	RabGAP-1
HPB	Qph9.1	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	9	PM8-112	PM8-112/CB10298	2.72	-2.72	2.67	8.29	-
	Qph9.2	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	9	CB10311	CB10311/CHS-1	2.52	-1.55	-4.35	5.79	-
	Qph10.1	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	10	NAM-2	C5-1-550/NAM-2	3.30	2.07	-5.54	6.56	NAM-2
	Qph15.1	Wuhan	15	Ra1-F06	Ra1-F06/Na10-E08	2.54	-1.30	5.82	5.86	-
		Jingmen	-	-	-	-	-	-	-	-
	Qph19.1	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	19	PM1-230	L9-1-340/LADC	3.88	6.32	-9.12	12.33	LADC
HPB	Qhpbl.1	Wuhan	1	AUXDR-1	AUXDR-1/Na14-F11a	2.81	3.71	-5.43	6.74	AUXDR-1
		Jingmen	-	-	-	-	-	-	-	-
	Qhpbl.2	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	1	CB10597	CB10597/AUXDR-2	2.60	-8.90	1.35	10.02	-
	Qhpb2.1	Wuhan	2	AUXR	AUXR/EIF-4F	2.51	2.55	2.51	5.75	AUXR
		Jingmen	-	-	-	-	-	-	-	-
	Qhpb2.2	Wuhan	2	J2-4-180	CN34/DNAPL-2	3.00	1.74	4.42	6.84	DNAPL-2
		Jingmen	-	-	-	-	-	-	-	-
	Qhpb3.1	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	3	Q6-3-850	N1-1-280/Q6-3-850	3.44	0.83	-6.63	10.67	-
LMI	Qhp7.1	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	7	KEMP	BRMS-036/C2H2T-2	5.59	2.62	8.64	18.24	KEMP,C2H2T-2
	Qhp7.2	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	7	SUC-2	SUC-2/RPSaA	10.21	-3.34	9.26	21.55	SUC-2, RPSaA
	Qhp7.3	Wuhan	7	PM9-130	BRAS004/RabGAP-2	5.50	4.66	1.21	11.47	C2H2T-1, RabGAP-2
		Jingmen	7	PM9-130	BRAS004/RabGAP-2	3.95	4.68	-0.32	9.22	C2H2T-1, RabGAP-2
	Qhp7.4	Wuhan	7	B5-1-280	CN67/CB10569	6.39	5.45	0.64	13.98	-
		Jingmen	7	B5-1-280	CN67/RM5-130	4.38	4.76	-0.27	10.26	-
	Qhp7.5	Wuhan	7	P9-3-160	P9-3-160/PM3-248	4.79	15.7	6.45	12.35	-
		Jingmen	-	-	-	-	-	-	-	-
LMI	Qlmi2.1	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	2	CN34	CN34/J2-4-180	2.83	3.17	-1.48	6.73	-
	Qlmi7.1	Wuhan	7	BRMS-036	BRMS-036/KEMP	4.23	3.53	-4.48	14.37	KEMP
		Jingmen	7	KEMP	BRMS-036/KEMP	7.27	4.69	-6.02	22.60	KEMP
	Qlmi7.2	Wuhan	7	SUC-2	SUC-2/CB10526	4.67	3.27	-3.30	8.69	SUC-2, RPSaA
		Jingmen	7	SUC-2	SUC-2/RPSaA	5.68	6.02	-4.70	12.11	SUC-2, RPSaA
	Qlmi7.3	Wuhan	7	BRAS004	BRAS004/C2H2T-1	12.30	-1.31	-0.63	5.06	-
		Jingmen	-	-	-	-	-	-	-	-
	Qlmi7.4	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	7	RabGAP-2	RabGAP-2/Ra2-A01	2.64	-1.88	-1.29	6.38	RabGAP-2
Qlmi7.5	Qlmi7.5	Wuhan	7	B5-1-280	B5-1-280/RM5-130	2.79	-2.47	0.70	6.04	-
		Jingmen	-	-	-	-	-	-	-	-
	Qlmi7.6	Wuhan	7	AT103	J8-1-580/AT103	2.99	-1.65	-0.54	5.67	AT103
		Jingmen	7	J8-1-580	P9-3-160/PM3-248	2.89	-3.35	-4.71	7.16	-
	Qlmi10.1	Wuhan	10	NAM-2	C5-1-550/NAM-2	2.77	2.22	-2.28	5.28	NAM-2
		Jingmen	-	-	-	-	-	-	-	-
Qlmi13.1	Qlmi13.1	Wuhan	13	FERRIT-1	FERRIT-1/CN38b	5.40	-3.49	2.37	15.24	FERRIT-1
		Jingmen	-	-	-	-	-	-	-	-

Table S3 (Continued)

Trait	QTL	location	LG	Closest neighboring locus	Marker interval	Maximum LOD score	Additive value	Dominant Value	Percentage variance explained	Functional markers
	Qlmi13.2	Wuhan	13	PM9-450	PM9-450/CN38a	5.92	-4.70	3.66	18.88	-
		Jingmen	-	-	-	-	-	-	-	-
	Qlmi13.3	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	13	CPS	BRAS051b/H9-3-150	3.70	-1.87	-1.59	11.08	CPS
Qlmi14.1	Wuhan	14	RRM-2	RRM-2/PM9-134	4.28	5.16	-4.78	36.68	RRM-2	
	Jingmen	14	RRM-2	PM4-130/RRM-2	2.71	6.44	-6.11	26.54	THRX, RRM-2	
	Qlmi19.1	Wuhan	19	LADC	PM1-230/OI12-A04	4.56	3.40	-5.11	14.42	LADC
		Jingmen	-	-	-	-	-	-	-	-
	Qlmi19.2	Wuhan	19	J2-250	J2-2-250/PM1-500	3.60	9.99	-4.36	18.26	-
		Jingmen	-	-	-	-	-	-	-	-
ELMI	Qelmi1.1	Wuhan	1	SCPT	ACT2-2/SCPT	3.29	2.72	-2.29	6.20	ACT2-2, SCPT
		Jingmen	-	-	-	-	-	-	-	-
	Qelmi2.1	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	2	CN34	CN34/J2-4-180	2.84	2.71	-0.86	6.35	-
	Qelmi6.1	Wuhan	6	G10-1-160	CB10006/G10-1-160	2.56	2.96	0.07	9.02	-
		Jingmen	-	-	-	-	-	-	-	-
	Qelmi6.2	Wuhan	6	VHSD	G10-1-160/VHSD	2.68	3.49	-1.32	14.16	VHSD
		Jingmen	-	-	-	-	-	-	-	-
	Qelmi7.1	Wuhan	7	BRMS-036	BRMS-036/KEMP	4.76	3.66	-4.11	11.75	KEMP
		Jingmen	7	KEMP	BRMS-036/KEMP	4.19	2.61	-4.61	13.40	KEMP
SMI	Qelmi7.2	Wuhan	7	RPSaA	SUC-2/F7-1-130	4.84	3.09	-3.59	8.88	SUC-2, RPSaA
		Jingmen	-	-	-	-	-	-	-	-
	Qelmi7.3	Wuhan	7	BRAS004	BRAS004/C2H2T-1	2.72	-1.53	-0.43	5.12	-
		Jingmen	-	-	-	-	-	-	-	-
	Qelmi10.1	Wuhan	10	NAM-2	C5-1-550/NAM-2	2.81	2.32	-2.16	5.33	NAM-2
		Jingmen	-	-	-	-	-	-	-	-
	Qelmi13.1	Wuhan	13	FERRIT-1	FERRIT-1/CN38b	4.40	-3.09	1.90	12.40	FERRIT-1
		Jingmen	-	-	-	-	-	-	-	-
	Qelmi13.2	Wuhan	13	PM9-450	CN38b/CN38a	5.40	-4.95	4.02	18.12	-
		Jingmen	-	-	-	-	-	-	-	-
SDMI	Qsmi2.1	Wuhan	2	BKCOAS	BKCOAS/CN33b	2.99	4.75	13.27	21.83	BKCOAS
		Jingmen	-	-	-	-	-	-	-	-
	Qsmi2.2	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	2	AUXR	AUXR/EIF-4F	3.27	4.10	-0.09	9.13	AUXR, EIF-4F
	Qsmi2.3	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	2	CN34	C3-3-125/CN34	5.51	4.51	-1.59	11.63	-
	Qsmi2.4	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	2	DNAPL-2	DNAPL-2/P4-5-260	2.67	2.00	1.48	5.78	DNAPL-2
	Qsmi6.1	Wuhan	6	VHSD	VHSD/STPOZ	3.72	6.84	-1.23	18.12	VHSD
		Jingmen	-	-	-	-	-	-	-	-
Qsmi7.1	Qsmi7.1	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	7	BRMS-036	BRMS-036/KEMP	3.91	4.62	-3.06	13.08	KEMP
	Qsmi9.1	Wuhan	9	RM5-375	O7-4-140/RM5-375	3.51	5.84	-8.40	12.06	-
		Jingmen	-	-	-	-	-	-	-	-
	Qsmi10.1	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	10	RM11-220	PM8-120/RM11-210	3.25	5.04	-2.34	7.66	-
	Qsmi12.1	Wuhan	12	GAPA	CN35/PM1-358	6.97	-4.17	8.15	13.39	GAPA
		Jingmen	-	-	-	-	-	-	-	-
	Qsmi14.1	Wuhan	14	PTPTP	PTPTP/CB10355	2.82	5.47	-2.47	7.45	PTPTP
		Jingmen	-	-	-	-	-	-	-	-
Qsdmi2.1	Qsdmi2.1	Wuhan	2	PM5-450	H9-1-270/AUXR	5.07	0.10	0.04	9.15	AUXR
		Jingmen	-	-	-	-	-	-	-	-
	Qsdmi2.2	Wuhan	2	J10-2-280	EIF-4F/J10-2-280	3.47	0.07	0.01	6.00	EIF-4F
		Jingmen	-	-	-	-	-	-	-	-
	Qsdmi7.1	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	7	BRMS-036	BRMS-036/KEMP	3.18	-0.02	0.12	12.16	KEMP
	Qsdmi7.2	Wuhan	-	-	-	-	-	-	-	-
Qsdmi7.3	Jingmen	7	RPSaA	SUC-2/F7-1-130	5.70	-0.14	0.14	11.43	SUC-2, RPSaA	
	Wuhan	7	BRAS004	CB10526/C2H2T-1	8.25	0.10	0.03	14.57	C2H2T-1	
	Jingmen	-	-	-	-	-	-	-	-	-

Table S3 (Continued)

Trait	QTL	location	LG	Closest neighboring locus	Marker interval	Maximum LOD score	Additive value	Dominant Value	Percentage variance explained	Functional markers
SDMI	Qsdmi7.4	Wuhan	-	-	-	-	-	-	-	-
	Jingmen	7	RabGAP-2	BRAS004/Ra2-A01	3.42	0.08	0.01	7.74	C2H2T-1, RabGAP-2	
	Qsdmi7.5	Wuhan	7	CN67	Ra2-A01/B5-1-280	12.04	0.14	-0.03	20.47	-
	Jingmen	-	-	-	-	-	-	-	-	
	Qsdmi7.6	Wuhan	7	AT103	PM3-248/CN64	7.10	0.11	0.01	12.76	AT103
	Jingmen	-	-	-	-	-	-	-	-	
	Qsdmi7.7	Wuhan	-	-	-	-	-	-	-	
	Jingmen	7	CN64	CN64/B5-2-270	2.57	0.08	-0.03	5.37	-	
	Qsdmi8.1	Wuhan	8	Ra2-E11	Ra2-E11/Ra2-E12	3.69	-0.09	0.01	5.55	-
	Jingmen	-	-	-	-	-	-	-	-	
FB	Qfb2.1	Wuhan	10	CYPRT-2	CYPRT-2/Na12-E09	2.72	0.10	-0.05	4.48	CYPRT-2
	Jingmen	-	-	-	-	-	-	-	-	
	Qfb3.1	Wuhan	-	-	-	-	-	-	-	
	Jingmen	3	BRMS-042	BRMS-042/CAS1	2.58	0.51	-0.32	5.71	-	
	Qfb6.1	Wuhan	6	KRCP-1	CB1030/KRCP-1	2.74	-0.65	0.69	5.47	KRCP-1
	Jingmen	-	-	-	-	-	-	-	-	
	Qfb6.2	Wuhan	6	VHSD	G10-1-160/VHSD	2.70	0.14	0.89	9.78	VHSD
	Jingmen	-	-	-	-	-	-	-	-	
	Qfb7.1	Wuhan	7	RM5-130	CN67/CB10569	7.18	1.10	0.22	16.76	-
	Jingmen	-	-	-	-	-	-	-	-	
SFB	Qfb12.1	Wuhan	12	BRAS051c	I9-2-180/CN35	11.64	1.58	-1.54	27.39	-
	Jingmen	12	I9-2-180	CN75/CN35	4.47	0.93	-0.87	12.47	-	
	Qfb12.2	Wuhan	12	CB10057	PM1-358/OII2-F11a	5.58	1.19	-1.02	14.12	-
	Jingmen	12	CB10057	PM1-358/OII2-F11a	5.28	1.04	-0.91	14.96	-	
	Qfb12.3	Wuhan	-	-	-	-	-	-	-	
	Jingmen	12	CB10302	CB10302/O7-2-240	4.22	0.94	-0.54	15.05	-	
	Qfb13.1	Wuhan	-	-	-	-	-	-	-	
	Jingmen	13	K4-3-120	K4-3-120/ATPS	3.10	-0.36	-0.09	7.28	ATPS	
	Qfb14.1	Wuhan	-	-	-	-	-	-	-	
	Jingmen	14	RRM-2	RRM-2/PM9-134	2.59	-0.92	0.79	28.48	RRM-2	
SS	Qsfb2.1	Wuhan	-	-	-	-	-	-	-	-
	Jingmen	2	AUXR	AUXR/EIF-4F	3.47	8.82	6.86	3.02	AUXR,EIF-4F	
	Qsfb2.2	Wuhan	-	-	-	-	-	-	-	-
	Jingmen	2	CN34	CN34/J4-4-180	3.46	11.12	0.23	7.14	-	
	Qsfb6.1	Wuhan	6	CN59	CN59/Na12-B12	3.72	-35.67	15.02	6.76	-
	Jingmen	-	-	-	-	-	-	-	-	
	Qsfb6.2	Wuhan	6	P1-2-220	IRONT/athA-1	6.09	-67.70	18.99	12.14	IRONT,CDKC-1, athA-1, athA-2
	Jingmen	-	-	-	-	-	-	-	-	
	Qsfb6.3	Wuhan	6	G10-1-160	OMET-1/VHSD	4.70	3.68	26.72	14.43	OMET-1,VHSD
	Jingmen	-	-	-	-	-	-	-	-	
Qss	Qsfb7.1	Wuhan	7	KEMP	KEMP/SUC-2	4.20	16.16	7.07	9.48	KEMP, C2H2T-2, SUC-2
	Jingmen	-	-	-	-	-	-	-	-	
	Qsfb7.2	Wuhan	7	CB10526	RPSaA/CB10526	3.46	16.88	7.04	7.87	RPSaA
	Jingmen	-	-	-	-	-	-	-	-	
	Qsfb12.1	Wuhan	-	-	-	-	-	-	-	-
	Jingmen	12	ANL2	APL-1/CN75	2.82	22.77	-22.42	9.59	APL-1, ANL2, CHS-2, APL-2,	
	Qsfb13.1	Wuhan	-	-	-	-	-	-	-	-
	Jingmen	13	APRR2-1	CPS/K4-3-120	3.18	-10.49	2.40	4.48	CPS, APRR2-1	
	Qss2.1	Wuhan	-	-	-	-	-	-	-	-
	Jingmen	2	J10-2-280	J10-2-280/B4-1-330	2.62	-0.29	-0.38	6.61	-	
Qss2.2	Qss2.2	Wuhan	-	-	-	-	-	-	-	-
	Jingmen	2	DNAPL-2	DNAPL-2/C3-2-120	3.92	-0.04	-1.42	10.74	DNAPL-2, LD	
	Qss7.1	Wuhan	7	SUC-2	SUC-2/F7-1-130	3.51	0.74	-1.17	6.42	SUC-2, RPSaA
	Jingmen	-	-	-	-	-	-	-	-	
Qss7.2	Qss7.2	Wuhan	7	CN62	CN62/RM2-180	3.35	0.97	-0.14	6.64	-
	Jingmen	-	-	-	-	-	-	-	-	

Table S3 (Continued)

Trait	QTL	location	LG	Closest neighboring locus	Marker interval	Maximum LOD score	Additive value	Dominant Value	Percentage variance explained	Functional markers
SS	Qss10.1	Wuhan	10	B8-1-180	B8-1-180/pMR33	2.64	-0.07	-0.89	5.75	-
		Jingmen	-	-	-	-	-	-	-	-
	Qss12.1	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	12	UXS-3	A2-310/PM3-187	3.28	0.94	-0.45	9.67	UXS-3
	Qss12.2	Wuhan	12	CB10204	CB10204/N4-2-180	5.35	1.61	-1.62	18.37	-
SW	Qsw7.1	Wuhan	7	BRMS-036	BRMS-036/KEMP	2.92	-0.04	-0.12	7.26	-
		Jingmen	-	-	-	-	-	-	-	-
	Qsw7.2	Wuhan	7	RPSaA	C2H2T-2/RPSaA	5.55	0.17	-0.27	9.26	SUC-2, RPSaA, C2H2T-2
		Jingmen	7	SUC-2	SUC-2/RPSaA	5.31	0.27	-0.14	10.26	SUC-2, RPSaA
	Qsw7.3	Wuhan	7	BRAS004	F7-1-130/C2H2T-1	3.99	-0.10	-0.07	6.75	C2H2T-1
		Jingmen	-	-	-	-	-	-	-	-
	Qsw7.4	Wuhan	7	CN67	Ra2-A01/B5-1-280	3.49	-0.12	-0.02	6.12	-
		Jingmen	-	-	-	-	-	-	-	-
	Qsw7.5	Wuhan	7	PM3-248	J8-1-580/AT103	4.39	-0.29	-0.13	9.66	AT103
		Jingmen	-	-	-	-	-	-	-	-
	Qsw7.6	Wuhan	7	RabGAP-1	B5-2-270/OI10-D03c	3.33	-0.14	-0.19	7.28	RabGAP-1
		Jingmen	-	-	-	-	-	-	-	-
	Qsw7.7	Wuhan	7	PM3-292	PM2-340/GCIP1	8.6	-0.25	-0.06	18.12	GCIP1
		Jingmen	-	-	-	-	-	-	-	-
Qsw7.8	Wuhan	7	CN62	CN62/CN63d	8.96	-0.26	0.00	17.66	-	-
		Jingmen	7	CN63d	CN62/CN63d	4.51	-0.13	-0.05	12.13	-
	Qsw7.9	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	7	RM2-184	RM2-184/CN63b	2.94	-0.17	-0.06	12.55	-
	Qsw12.1	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	12	PM3-175	PM3-175/RM14-355	3.03	-0.05	-0.15	6.84	-
	Qsw14.1	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	14	CB10355	PTPTP/CB10355	2.90	0.14	-0.09	5.62	PTPTP
	Qsw14.2	Wuhan	14	PM9-134	RRM-2/PM9-134	5.49	0.29	-0.32	25.86	RRM-2
		Jingmen	-	-	-	-	-	-	-	-
YP	Qyp2.1	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	2	AUXR	AUXR/EIF-4F	2.75	0.91	0.08	7.56	AUXR
	Qyp2.2	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	2	CN34	CN34/J2-4-180	3.99	0.96	-0.16	8.75	-
	Qyp6.1	Wuhan	6	IRONT	IRONT/P1-2-220	2.81	-2.10	0.46	5.74	IRONT
		Jingmen	-	-	-	-	-	-	-	-
	Qyp6.2	Wuhan	6	VHSD	VHSD/STPOZ	3.11	6.29	1.94	32.08	VHSD
		Jingmen	-	-	-	-	-	-	-	-
	Qyp7.1	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	7	KEMP	KEMP/C2H2T-2	2.52	0.98	-0.66	7.04	KEMP
	Qyp7.2	Wuhan	7	RPSaA	RPSaA/CB10526	4.87	6.57	-1.74	15.74	RPSaA
		Jingmen	-	-	-	-	-	-	-	-
	Qyp9.1	Wuhan	9	CHS-1	CHS-1/RPPOB-3	2.55	0.76	-5.97	14.13	RPPOB-3
		Jingmen	-	-	-	-	-	-	-	-
Qyp9.2	Wuhan	9	athb-1	Na10-F01b/athb-1	2.71	2.20	-6.12	9.92	athb-1	-
		Jingmen	-	-	-	-	-	-	-	-
	Qyp13.1	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	13	ATPS	K4-3-120/ATPS	4.23	-0.07	-1.02	15.51	ATPS
	Qyp14.1	Wuhan	14	RM7-165	PM9-134/PM4-362	3.08	5.99	-5.64	36.00	-
		Jingmen	-	-	-	-	-	-	-	-
SP	Qsp2.1	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	2	AUXR	AUXR/J10-2-280	4.62	14.31	7.51	12.22	AUXR, EIF-4F
	Qsp2.2	Wuhan	-	-	-	-	-	-	-	-
		Jingmen	2	CN34	CN34/J2-4-180	4.89	16.04	-0.51	10.39	-
	Qsp6.1	Wuhan	6	CN59	CN59/Na12-H07	2.65	-28.21	10.40	5.13	-
		Jingmen	-	-	-	-	-	-	-	-
	Qsp6.2	Wuhan	6	P1-2-220	IRONT/athA-1	4.27	-41.29	11.96	8.34	IRONT, CDKC-1. athA-1, athA-2
		Jingmen	-	-	-	-	-	-	-	-
	Qsp6.3	Wuhan	6	VHSD	VHSD/STPOZ	5.72	25.41	45.66	26.20	VHSD
		Jingmen	-	-	-	-	-	-	-	-
Qsp7.1	Wuhan	7	BRMS-036	BRMS-036/KEMP	4.51	22.56	-13.38	8.57	-	-
		Jingmen	-	-	-	-	-	-	-	-
Qsp13.1	Wuhan	-	-	-	-	-	-	-	-	-
		Jingmen	13	APRR2-1	CPS/K4-3-120	3.44	-13.35	3.59	13.67	CPS, APRR2-1

^a the bold face refers to stable QTLs across locations

Table S4 Functional markers involved in QTLs for agronomic traits and functions of them

Markers	Traits	Function
Cell cycle (1/1)^a		
DNAPL-2	HPB, PH, SMI, SS	DNA primase, large subunit family
Cellular organization (6/5)		
ACT2-2	ELMI	
athA-1	SP, SFB	Encodes an actin that is constitutively expressed in vegetative structures but not pollen
athA-2	SP, SFB	cellulose synthase catalytic subunit (Ath-A) (At4g39350; T22F8.250) mRNA, complete cds.
athb-1	YP	cellulose synthase catalytic subunit (Ath-A) (At4g39350; T22F8.250) mRNA, complete cds.
KEMP	ELMI, LMI, SDMI, SMI, YP, SFB, HPB	Arabidopsis thaliana cellulose synthase, catalytic subunit (Ath-B)(At5g05170) mRNA, complete cds.
VHSD	SFB, ELM, FB, PH, SMI, SP, YP	kinesin motor protein-related
Development systemic (3/3)		
ANL2	SFB	VHS domain-containing protein / GAT domain-containing protein
LD	SS	
NAM-2	ELMI, LMI, PH	
Energy metabolism (2/2)		
GAPA	SMI	Encodes a homeodomain protein of the HD-GLABRA2 group.
THRX	LMI	Wassilewskija Luminidependens mRNA
General metabolism (10/9)		
APL-1	SFB	no apical meristem (NAM) family protein
APL-2	SFB	
BKCOAS	PH, SMI	
CDKC-1	SP, SFB	
CPS	ELMI, LMI, SFB, SP	
PTPTP	SMI, SW	glyceraldehyde-3-phosphate dehydrogenase A subunit (G)
SCPS-2	SDMI	thioredoxin family protein
SCPT	ELMI	
UXS-3	SS	
ATPS	FB, YP	
Protein fate (2/1)		
CYPRT-2	SDMI	Apl3 gene
CYPRT-3	SDMI	Apl3 gene
Protein synthesis (3/3)		
EIF-4F	FB, SP, SMI, SFB, SDMI	beta-ketoacyl-CoA synthase family protein, KCS1 fatty acid elongase 3-ketoacyl
RPPOB-3	YP	cyclin-dependent kinase, putative / CDK,putative (At5g6)
RPSaA	ELMI, HPB, SFB, YP, LMI, SDMI, SS, SW	cyclase ent-kaurene synthetase A(GA1-BN-1) g
Secondary metabolism (2/2)		
CHS-2	SFB	phosphate/triose-phosphate translocator precursor
OMET-1	SFB	sucrose-phosphate synthase
Signal transduction (2/1)		
RabGAP-1	FB, PH, SW	serine C-palmitoyltransferase
RabGAP-2	HPB, SDMI, LMI	UDP-glucuronic acid decarboxylase
Subcellular localization (1/1)		
LADC	ELMI, LMI, PH	Arabidopsis thaliana cellulose synthase, catalytic subunit (Ath-B)(At5g05170) mRNA, complete cds.
Systemic response and sensing (1/1)		
AUXR	HPB, SDMI, YP, FB, SMI, SP, SFB	
Transcription (6/4)		
APRR2-1	SFB	
APRR2-1	SP	
AT103	LMI, SDMI, SW, FB	APRR2 mRNA for pseudo-response regulator 2
C2H2T-1	SDMI, SW, HPB	APRR2 mRNA for pseudo-response regulator 2
C2H2T-2	SFB, HPB, SW	Encodes a putative ZIP protein with varying mRNA accumulation in leave
RRM-2	LMI, ELM, FB, LMI, SDMI, SW	zinc finger (C2H2 type) family protein
Transport (3/3)		
FERRIT-1	ELMI, LMI	zinc finger (C2H2 type) family protein
IRONT	YP, SP, SFB	RNA recognition motif (RRM)-containing protein
SUC-2	SFB, ELM, HPB, LMI, SDMI, SS, SW	Encodes a ferretin protein that is targeted to the chloroplast
unknown (3/3)		
AUXDR-1	HPB	transporter, putative, similar to iron-phytosiderophore transporter protein yellow stripe 1 (<i>Zea mays</i>)
GCIP1	SW	sucrose transporter SUC1 mRNA
KRPC-1	FB	expressed protein, similar to auxin down-regulated protein ARG10
		GCIP-interacting family protein
		kelch repeat-containing protein

^a the number of functional markers^b the number of functional genes or ESTs