

Supplementary Table S1-2

Table S1: Significant SNPs obtained through GWAS†

Loc	num_snp	gene_num	peakPOS	Chr	Bin	PVE (%)	P(-log10)
21YS	1	2	242858336	2	2.24	17.74	5.98
	1	0	180296831	8	8.18	6.34	5.08
22YS	3	3	126528998	10	10.12	14.88	5.64
19BS	1	0	135828991	6	6.13	3.24	5.15
19DH	1	0	120370778	5	5.12	8.83	5.05
	5	2	177304649	7	7.17	6.40	6.03
21JH	1	31	76395713	1	1.07	9.09	5.16
	1		83163645	1	1.08	21.01	6.40
	1		198129347	1	1.19	7.02	6.01
	1		199106836	1	1.19	6.14	5.89
	1		199222030	1	1.19	8.42	6.64
	1		199314176	1	1.19	6.49	5.63
	1		199335283	1	1.19	4.73	5.18
	3		201355723	1	1.20	5.57	5.70
	1		254646097	1	1.25	14.18	6.05
	2		257676626	1	1.25	5.69	5.58
	1		306464753	1	1.30	8.58	5.56
	1		42354101	2	2.04	5.88	5.65
	1		104677372	2	2.10	9.92	5.79
	1		192141542	2	2.19	12.01	5.79
	1		195713294	2	2.19	6.56	5.36
	1		214756894	2	2.21	12.53	6.10
	3		215468689	2	2.21	14.31	6.12
	1		24283034	3	3.02	13.44	5.29
	1		135283055	4	4.13	6.70	6.13
	1		187159704	4	4.18	9.96	6.37
	4		46725146	5	5.04	10.57	8.39
	2		138554600	5	5.13	8.40	5.42
	1		150393177	5	5.15	10.64	5.98
	1		30305673	6	6.03	8.89	6.31
	1		71741394	6	6.07	7.79	5.82
	2		71920788	6	6.07	6.33	6.24
	1		76471294	6	6.07	8.70	5.98
	2		84033777	8	8.08	9.61	8.61
	1		146316294	8	8.14	5.61	5.95
	1		68447065	10	10.06	11.15	5.00
SUM	53	38					

†Loc: Refers to the Environment or Location where the association was detected.
 Chr: Indicates the Chromosome on which the significant SNP is located.
 PVE: Represents the Proportion of Phenotypic Variance Explained by the associated SNP.
 P: Represents the p-value.

Table S2: Summary of Genetic Linkage Groups of two RIL populations†

population	Chr	Marker number	Length (cM)	inter marker	Max-gap
Sub-pop3	lg01	180	169	0.94	5.95
	lg02	93	117.35	1.26	9.08
	lg03	117	109.28	0.93	10.05
	lg04	131	118.91	0.91	4.72
	lg05	85	78.41	0.92	9.56
	lg06	91	162.62	1.79	17.5
	lg07	96	121.87	1.27	12.12
	lg08	84	58.93	0.7	5.54
	lg09	66	76.24	1.16	13.78
	lg10	38	33.23	0.87	4.33
	Total	981	1045.83	1.07	17.5
Sub-pop4	lg01	144	148.39	1.03	17.75
	lg02	78	76.86	0.99	8.47
	lg03	89	83.28	0.94	11.78
	lg04	109	151.08	1.39	28.89
	lg05	80	64.76	0.81	6.6
	lg06	61	95.89	1.57	12.68
	lg07	80	63.94	0.8	8.47
	lg08	54	53.92	1	9.26
	lg09	56	41.88	0.75	6.24
	lg10	70	48.27	0.69	3.56
	Total	821	828.27	1.01	28.89

†lg1,lg2,...lg10 represent chromosome 1,2, ...10, respectively. Marker-number: indicates the number of SNP markers. Length: The total genetic distance of each chromosome (cM); Average_length: average genetic distance (cM). Max-gap: refers to the maximum allowable gap or distance between adjacent genetic markers (usually microsatellites or SNPs) along a chromosome.