

Supplementary Table 9. Details of GWAS for grain length, grain width and thousand-grain weight trait performed using BLINK

SNP-ID	Chr/Pseudo- chr+	Physical position (bp)	Grain length		Grain width		Length-to-width ratio		Thousand-grain weight		Structural annotation*	Candidate genes
			P-value	FDR adjusted P-values	P-value	FDR adjusted P-values	P- value	FDR adjusted P-values	P-value	FDR adjusted P-values		
JG10~6950498	JG10	6950498	3.25E-10	1.78E-05	NA	NA	NA	NA	NA	NA	NA	<i>WD repeat-containing protein 12 (LOC_Os07g40930)</i>
3~3775429	Chr 3	3775429	5.46E-08	1.49E-03	NA	NA	NA	NA	NA	NA	Upstream	<i>PGL1 (LOC_Os03g07510)</i>
4~1881177	Chr 4	1881177	5.73E-06	0.104	NA	NA	NA	NA	NA	NA	Intergenic	NA
JG10~4325684	JG10	4325684	4.47E-05	0.499	NA	NA	NA	NA	NA	NA	NA	NA
AUSG6~24889549	AUSG6	24889549	4.57E-05	0.499	NA	NA	NA	NA	NA	NA	NA	NA
JG10~2239066	JG10	2239066	5.86E-05	0.534	NA	NA	NA	NA	NA	NA	NA	NA
6~2735663	Chr 6	2735663	7.72E-05	0.603	NA	NA	NA	NA	NA	NA	Downstream	NA
JG10~4882245	JG10	4882245	8.86E-05	0.606	NA	NA	NA	NA	NA	NA	NA	NA
2~35350740	Chr2	35350740	NA	NA	2.11E-05	0.661	NA	NA	NA	NA	Intergenic	NA
IG2~35461875	Chr17	35461875	NA	NA	2.44E-05	0.661	NA	NA	NA	NA	NA	NA
2~24960784	Chr2	24960784	NA	NA	6.21E-05	0.661	NA	NA	NA	NA	Upstream	NA
2~35350740	Chr2	35350740	NA	NA	2.11E-05	0.661	NA	NA	NA	NA	Intergenic	NA
IG5~14354843	IG5	14354843	NA	NA	NA	NA	NA	NA	1.69E-10	9.26E-06	NA	<i>GW5 (LOC_Os05g09520)</i>
12~7132122	Chr12	7132122	NA	NA	NA	NA	NA	NA	7.51E-09	0.0002	Intergenic	<i>OsCML28 (LOC_Os12g12730); CAMK-like-46 encoding gene (LOC_Os12g12860)</i>
10~6148264	Chr10	6148264	NA	NA	NA	NA	NA	NA	9.08E-08	0.00145	Synonymous	<i>Ubiquitin conjugating enzyme encoding gene (LOC_Os10g11260)</i>

SNP-ID	Chr/Pseudo- chr +	Physical position (bp)	Grain length		Grain width		Length-to-width ratio		Thousand-grain weight		Structural annotation*	Candidate genes
			P-value	FDR adjusted P-values	P-value	FDR adjusted P-values	P-value	FDR adjusted P-values	P-value	FDR adjusted P-values		
IG5~13672041	IG5	13672041	NA	NA	NA	NA	NA	NA	1.06E-07	0.0014	NA	NA
9~12332184	Chr 9	12332184	NA	NA	NA	NA	NA	NA	7.39E-07	0.008	Intergenic	NA
5~5390763	Chr5	5390763	NA	NA	NA	NA	NA	NA	9.78E-07	0.0089	Downstream	GW5 (LOC_Os05g09520)
IG5~16943583	IG5	16943583	NA	NA	NA	NA	NA	NA	2.23E-05	0.1524	NA	NA
6~24535560	Chr6	24535560	NA	NA	NA	NA	NA	NA	3.36E-05	0.2042	Intergenic	NA
3~7225647	Chr3	7225647	NA	NA	NA	NA	NA	NA	4.14E-05	0.2268	Intergenic	NA
6~23900256	Chr6	23900256	NA	NA	NA	NA	NA	NA	5.42E-05	0.2497	Upstream	NA
10~19634914	Chr10	19634914	NA	NA	NA	NA	NA	NA	5.48E-05	0.249795 563	Intergenic	NA
IG3~5847364	IG3	5847364	NA	NA	NA	NA	NA	NA	6.52E-05	0.274304 155	NA	NA
IG5~12291400	IG5	12291400	NA	NA	NA	NA	NA	NA	8.49E-05	0.323929 122	NA	NA
2~25991206	2	25991206	NA	NA	NA	NA	2E-07	0.01095	NA	NA	Intergenic	NA
7~23605893	7	23605893	NA	NA	NA	NA	1.9E-06	0.05168	NA	NA	Upstream	NA
unaln_IG1~478378 73	16	47837873	NA	NA	NA	NA	3.8E-06	0.06959	NA	NA	NA	NA
unaln_AROG11~1 1935468	14	11935468	NA	NA	NA	NA	7.9E-06	0.10769	NA	NA	NA	NA
unaln_IG5~143548 43	20	14354843	NA	NA	NA	NA	3E-05	0.32688	NA	NA	NA	NA

Chr: Chromosome; Pseudo-chr: Pseudo-chromosome; 5' UTR/3' UTR: five prime untranslated region/ three prime untranslated region defined as per MSU7.0 annotation; Upstream: SNPs located >2 kb upstream from transcription start site of a gene; Downstream: SNPs located >2 kb downstream from transcription stop site of a gene; IG: Indica Group; JG: Japonica Group; Adm: Admixture *Structural annotation performed using MSU 7.0; #Rice Annotation Project locus ID; The loci detected from pseudo-chromosomes are highlighted in red.