

Supplemental Table 8. Details of GWAS for grain length, grain width and thousand-grain weight trait performed using FarmCPU

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	1.07E-11	5.87E-07	NA	NA	NA	NA	NA	NA	NA	<i>WD repeat-containing protein 12 (LOC_Os07g40930)</i>
JG10~4245875	JG10	4245875	3.38E-08	0.000925	NA	NA	NA	NA	NA	NA	Upstream	<i>Unknown function (OsR498G0612839600.01)</i>
7~25105073	Chr7	25105073	2.15E-07	0.003919	NA	NA	NA	NA	NA	NA	Upstream	<i>LFR (LOC_Os07g41900)</i>
3~16733441	Chr3	16733441	2.86E-07	0.003919	NA	NA	NA	NA	NA	NA	Intergenic	<i>GS3(LOC_Os03g0407400)</i>
12~25514661	Chr12	25514661	8.68E-07	0.007971	NA	NA	NA	NA	NA	NA	Intergenic	<i>IQ calmodulin-binding motif family protein (LOC_Os12g41160)</i>
1~34538998	Chr1	34538998	8.74E-07	0.007971	NA	NA	NA	NA	NA	NA	Intergenic	<i>qGRL1.1/OsGAMYB (LOC_Os01g59660)</i>
11~6484221	Chr11	6484221	3.51E-06	0.027446	NA	NA	NA	NA	NA	NA	Upstream	NA
10~20357189	Chr10	20357189	8.13E-06	0.055605	NA	NA	NA	NA	NA	NA	Intergenic	NA
JG10~6243872	JG10	6243872	2.46E-05	0.149332	NA	NA	5.69E-08	0.002	5.69E-08	0.002078	NA	<i>OsCML28 (LOC_Os12g12730)</i> <i>CAMK-like-46 (LOC_Os12g12860)</i>
1~34538998	Chr1	34538998	8.74E-07	0.007971	NA	NA	NA	NA	NA	NA	Intergenic	<i>qGRL1.1/OsGAMYB (LOC_Os01g59660)</i>
11~24534050	Chr11	24534050	NA	NA	2.35E-10	1.29E-05	NA	NA	NA	NA	3' UTR	<i>Receptor-like protein kinase precursor (LOC_Os11g40970)</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		
5~5371686	Chr5	5371686	NA	NA	3.36E-08	0.0007	NA	NA	NA	NA	Downstream	<i>GW5 (LOC_Os05g09520)</i>
11~23154487	Chr11	23154487	NA	NA	4.38E-06	0.0342	NA	NA	NA	NA	Synonymous	NA
5~991259	Chr5	991259	NA	NA	5.25E-06	0.0358	NA	NA	NA	NA	5' UTR	NA
11~25783593	Chr11	25783593	NA	NA	8.95E-06	0.0544	NA	NA	NA	NA	Intergenic	NA
Adm~7425964	Chr13	7425964	NA	NA	1.44E-05	0.07894	NA	NA	NA	NA	NA	NA
5~5390763	Chr5	5390763	NA	NA	NA	NA	0.000000076	0.002	7.60E-08	0.002	Downstream	<i>GW5 (LOC_Os05g09520)</i>
4~4486000	Chr4	4486000	NA	NA	NA	NA	7.99E-06	0.146	7.99E-06	0.1456	Missense	<i>LRR family protein encoding gene (LOC_Os04g08390)</i>
10~21588761	Chr10	21588761	NA	NA	NA	NA	4.14E-05	0.45	4.14E-05	0.45409	Intergenic	NA
11~2611306	Chr11	2611306	NA	NA	NA	NA	4.149E-05	0.93	4.15E-05	0.45409	Upstream	NA
8~17187746	Chr8	17187746	NA	NA	NA	NA	5.82E-05	0.501	5.82E-05	0.50151	Upstream	NA
5~4222429	Chr5	4222429	NA	NA	NA	NA	6.42E-05	0.502	6.42E-05	0.50151	Intergenic	NA
9~8180057	Chr9	8180057	NA	NA	NA	NA	7.90E-05	0.540	7.90E-05	0.5404	Downstream	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.