

**Supplementary Table 5.** Details of GWAS for grain length, grain width and thousand-grain weight trait performed using CMLM

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_Os07g4093)</i>
JG10~4245875	JG10	4245875	3.38E-08	0.001	NA	NA	NA	NA	NA	NA	NA	Unknown function (OsR498G0612839600)
7~25105073	Chr7	25105073	2.15E-07	0.004	NA	NA	NA	NA	NA	NA	Upstream	<i>Leaf and flower related protein (LOC_Os07g41900)</i>
3~16733441	Chr3	16733441	2.86E-07	0.004	NA	NA	NA	NA	NA	NA	Intergenic	<i>GS3 (Os03g0407400)#</i>
12~25514661	Chr12	25514661	8.68E-07	0.008	NA	NA	NA	NA	NA	NA	Intergenic	<i>IQ calmodulin-binding motif family protein (LOC_Os12g41160)</i>
1~34538998	Chr1	34538998	8.74E-07	0.008	NA	NA	NA	NA	NA	NA	Intergenic	<i>qGRL1.1/OsGAMYB (LOC_Os01g59660)</i>
11~6484221	Chr11	6484221	3.51E-06	0.027	NA	NA	NA	NA	NA	NA	Upstream	NA
10~20357189	Chr10	20357189	8.13E-06	0.055	NA	NA	NA	NA	NA	NA		NA
JG10~6243872	JG10	6243872	2.46E-05	0.149	NA	NA	NA	NA	5.69E-08	0.0020	NA	NA
11~24534050	Chr11	24534050	NA	NA	2.35E-10	1.29E-05	NA	NA	NA	NA	3' UTR	<i>Receptor-like protein kinase (LOC_Os11g4097)</i>
5~5371686	Chr5	5371686	NA	NA	3.36E-08	0.00078	NA	NA	NA	NA	Downstream	<i>GW5 (LOC_Os05g0952)</i>
11~25612932	Chr11	25612932	NA	NA	5.73E-08	0.00078	NA	NA	NA	NA	Intergenic	NA
5~2422324	Chr5	2422324	NA	NA	1.01E-07	0.001	NA	NA	NA	NA	3' UTR	NA
IG2~18885542	IG2	18885542	NA	NA	1.93E-07	0.001	NA	NA	NA	NA	NA	<i>LOC_Os10g31770</i>
11~23154487	Chr11	23154487	NA	NA	4.38E-06	0.034	NA	NA	NA	NA	Synonymous	NA
5~991259	Chr5	991259	NA	NA	5.25E-06	0.035	NA	NA	NA	NA	5' UTR	NA

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		
11~25783593	Chr11	25783593	NA	NA	8.95E-06	0.054	NA	NA	NA	NA	Intergenic	NA
Adm~7425964	Adm	7425964	NA	NA	1.44E-05	0.078	NA	NA	NA	NA	NA	NA
9~5770786	Chr9	5770786	NA	NA	2.25E-05	0.102	NA	NA	NA	NA	Intergenic	NA
11~27490883	Chr11	27490883	NA	NA	2.65E-05	0.111	NA	NA	NA	NA	Downstream	NA
3~25711563	Chr3	25711563	NA	NA	5.30E-05	0.207	NA	NA	NA	NA	Intergenic	NA
5~5390763	Chr5	5390763	NA	NA	NA	NA	2.30E-05	0.7946	7.60E-08	0.00207	Downstream	GW5 (LOC_Os05g09520)
10~21588761	Chr10	21588761	NA	NA	NA	NA	NA	NA	4.14E-05	0.454	Intergenic	NA
11~2611306	Chr11	2611306	NA	NA	NA	NA	NA	NA	4.15E-05	0.454	Upstream	NA
8~17187746	Chr8	17187746	NA	NA	NA	NA	NA	NA	5.82E-05	0.501	Upstream	NA
IG5~14354843	IG5	14354843	2.90E-05	NA	NA	NA	2.90E-05	0.7946	NA	NA	NA	
IG5~14354791	IG5	14354791	5.26E-05	NA	NA	NA	5.26E-05	0.9610	NA	NA	NA	
5~4222429	Chr5	4222429	NA	NA	NA	NA	NA	NA	6.42E-05	0.501	Intergenic	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.