

Supplementary Table 7. Details of GWAS for grain length, grain width and thousand-grain weight trait performed using SUPER

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 adjust ed 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	NA	<i>Unknown function (OsR498G0612839600.01)</i>
7~25105073	Chr7	2.5E+07	2.15E-07	0.003919	NA	NA	NA	NA	NA	NA	Upstream	<i>Leaf and flower related protein (LOC_Os07g41900)</i>
3~16733441	Chr3	1.7E+07	2.86E-07	0.003919	NA	NA	NA	NA	NA	NA	Intergenic	<i>GS3 (Os03g0407400)</i>
12~25514661	Chr12	2.6E+07	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	3.5E+07	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	2E+07	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	0.0020	5.69E-08	0.0020783	NA	NA
11~24534050	Chr11	2.5E+07	NA	NA	2.35E-10	1.29E-05	NA	NA	NA	NA	3' UTR	<i>Receptor-like protein kinase precursor (LOC_Os11g40970)</i>
5~5371686	Chr5	5371686	NA	NA	3.36E-08	0.0007	NA	NA	NA	NA	Downstream	<i>GW5 (LOC_Os05g09520)</i>
5~5390763	Chr5	5390763	NA	NA	NA	NA	0.00000007	0.348	NA	NA	Downstream	<i>GW5 (LOC_Os05g09520)</i>
IG2~18885542	IG2	1.9E+07	NA	NA	1.93E-07	0.001756	NA	NA	NA	NA	NA	<i>LOC_Os10g31770</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		
11~23154487	Chr11	2.30E+07	NA	NA	4.38E-06	0.0342	NA	NA	NA	NA	Synonymous	NA
5~991259	Chr5	991259	NA	NA	5.25E-06	0.0359	NA	NA	NA	NA	5' UTR	NA
11~25783593	Chr11	2.60E+07	NA	NA	8.95E-06	0.0544	NA	NA	NA	NA	Intergenic	NA
Adm~7425964	Adm	7425964	NA	NA	1.44E-05	0.0789	NA	NA	NA	NA	NA	NA
2~18141348	Chr2	1.80E+07	NA	NA	2.03E-05	0.1011	NA	NA	NA	NA	Intergenic	NA
9~5770786	Chr9	5770786	NA	NA	2.25E-05	0.1027	NA	NA	NA	NA	Intergenic	NA
11~27490883	Chr11	2.70E+07	NA	NA	2.65E-05	0.1116	NA	NA	NA	NA	Downstream	NA
3~25711563	Chr3	2.60E+07	NA	NA	5.30E-05	0.2073	NA	NA	NA	NA	Intergenic	NA
5~5390763	Chr5	5390763	NA	NA	NA	NA	7E-08	0.348	7.60E-08	0.002	Downstream	<i>GW5 (LOC_Os05g09520)</i>
4~4486000	Chr4	4486000	NA	NA	NA	NA	7.98E-06	0.145	7.99E-06	0.145	Missense	<i>LRR family protein encoding gene (LOC_Os04g08390)</i>
10~21588761	Chr10	2.20E+07	NA	NA	NA	NA	4.14E-05	0.454	4.14E-05	0.454	Intergenic	NA
11~2611306	Chr11	2611306	NA	NA	NA	NA	0.00004	0.454	4.15E-05	0.454	Upstream	NA
8~17187746	Chr8	1.70E+07	NA	NA	NA	NA	5.82E-05	0.501	5.82E-05	0.501	Upstream	NA
5~4222429	Chr5	4222429	NA	NA	NA	NA	6.41E-05	0.501	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.