

Supplementary Material to “Mapping of QTL for total spikelet number per spike on chromosome 2D in wheat using a high-density genetic map”

Table S1 - SNPs and candidate genes significantly associated with Total spikelet number per spike (TSS) QTL.

QTL	Marker interval	Chr_arm_ENS EMBL ^a	Locus (cM) ^b	Candidate genes name ^c	Annonation	Gene ID	Gene Ontology(GO) ^d			KEGG Pathway ^e
							Biological process	Molecular function	Cellular component	
QTSS.sic au-2D.1	AX948141 33- AX110571 866	2DS	10.45- 11.72	TRIAE_CS42_2DS_TGACv 1_177910_AA0587020	Arabidopsis thaliana (thale cress) gene RPPL1	AT3G144 70	\	[GO:0043531]ADP binding	\	\
				TRIAE_CS42_2DS_TGACv 1_177910_AA0586990	Arabidopsis thaliana (thale cress) gene CKR6	AT4G388 30	GO:0042742defense response to bacterium	\	\	\
QTSS.sic au-2D.2	gpw4473- wPt740855	2DS	32.64- 33.67	TRIAE_CS42_2DS_TGACv 1_177373_AA0574990	Arabidopsis thaliana (thale cress) gene LECRK42	AT3G538 10	[GO:0009555]pollen development	\	\	\
				TRIAE_CS42_2DS_TGACv 1_177544_AA0579700	Arabidopsis thaliana (thale cress) gene AtRLP7	AT1G478 90	\	[GO:0016301]kinase activity	\	\
				TRIAE_CS42_2DS_TGACv 1_179152_AA0604760	Arabidopsis thaliana (thale cress) gene SDR2A	AT3G516 80	\	[GO:0016491]oxidore ductase activity	\	\
				TRIAE_CS42_2DS_TGACv 1_177581_AA0580490	Arabidopsis thaliana (thale cress) gene AT2G13980	AT2G139 80	\	[GO:0003676]nucleic acid binding	\	\

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							Biological process	Molecular function	Cellular component	
				orf173	Arabidopsis thaliana (thale cress) gene	AT2G07689	[GO:0006120]mitochondrial electron transport, NADH to ubiquinone	\	\	\
				atp1	Arabidopsis thaliana (thale cress) gene ATP1	ATMG01190	\	\	\	[ath00190] Oxidative phosphorylation
				TRIAE_CS42_2DS_TGACv1_178525_AA0597050	Arabidopsis thaliana (thale cress) gene PME53	AT5G19730	\	[GO:0045330]aspartyl esterase activity	\	[ath00040] Pentose and glucuronate interconversions
				TRIAE_CS42_2DS_TGACv1_178525_AA0597060	Arabidopsis thaliana (thale cress) gene BDG3	AT4G24140	\	[GO:0016787]hydrolase activity	\	\
				TRIAE_CS42_2DS_TGACv1_178369_AA0594670	Arabidopsis thaliana (thale cress) gene AT5G33406	AT5G33406	\	[GO:0046983]protein dimerization activity	\	\
				TRIAE_CS42_2DS_TGACv1_178820_AA0601350	Arabidopsis thaliana (thale cress) gene SCPL40	AT3G63470	\	[GO:0004185]serine-type carboxypeptidase activity	\	\
				TRIAE_CS42_2DS_TGACv1_177420_AA0576610	Arabidopsis thaliana (thale cress) gene TMKL1	AT3G24660	[GO:0007169]transmembrane receptor protein tyrosine kinase signaling pathway	\	\	\
				TRIAE_CS42_2DS_TGACv1_177420_AA0576620	Arabidopsis thaliana (thale cress)	AT4G29780	\	\	\	\

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							Biological process	Molecular function	Cellular component	
				gene AT4G29780 TRIAE_CS42_2DS_TGACv 1_177420_AA0576640	Arabidopsis thaliana (thale cress)	AT5G01740	\	\	\	\
				gene AT5G01740 TRIAE_CS42_2DS_TGACv 1_177268_AA0571460	Arabidopsis thaliana (thale cress)	AT3G08840	\	\	\	\
				gene AT3G08840 TRIAE_CS42_2DS_TGACv 1_177172_AA0567770	Arabidopsis thaliana (thale cress)	AT1G68580	\	[GO:0003682]chromatin binding	\	\
				gene AT1G68580 TRIAE_CS42_2DS_TGACv 1_177172_AA0567780	Arabidopsis thaliana (thale cress)	AT2G34930	[GO:0050832]defense response to fungus	\	\	\
				gene AT2G34930 TRIAE_CS42_2DS_TGACv 1_177172_AA0567810	Arabidopsis thaliana (thale cress) gene ACR2	AT5G25320	\	[GO:0016597]amino acid binding	\	\
				gene PME21 TRIAE_CS42_2DS_TGACv 1_177172_AA0567820	Arabidopsis thaliana (thale cress) gene PME21	AT3G05610	\	[GO:0045330]aspartyl esterase activity	\	[ath00040] Pentose and glucuronate interconversions
				TRIAE_CS42_2DS_TGACv 1_180706_AA0611240	Arabidopsis thaliana	AT4G16120	[GO:0010215]cellulose microfibril organization	\	\	\

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							Biological process	Molecular function	Cellular component	
QTSS.sic au-2D.3	AX110089 401- AX944997 21	2DS	53.70- 53.99	TRIAE_CS42_2DS_TGACv 1_178226_AA0592980	(thale cress) gene COBL7 Arabidopsis thaliana	AT3G569 \	[GO:0016308]1- phosphatidylinositol- 4-phosphate 5-kinase activity	\	\	
				TRIAE_CS42_2DS_TGACv 1_179035_AA0603780	(thale cress) gene PIP5K4 Arabidopsis thaliana	AT4G231 \				
					(thale cress) gene CRK8					

a, chromosome location in hexaploid wheat from Blast program of Ensemblplant

b, genetic distance in RIL

c, identified genes in the QTL interval from Blast program of Ensemblplant

d, the best blast GO Annotate results from Annotate program of KOBAS 3.0

e, the best blast KEGG Pathway Identify results from Identify program of KOBAS 3.0