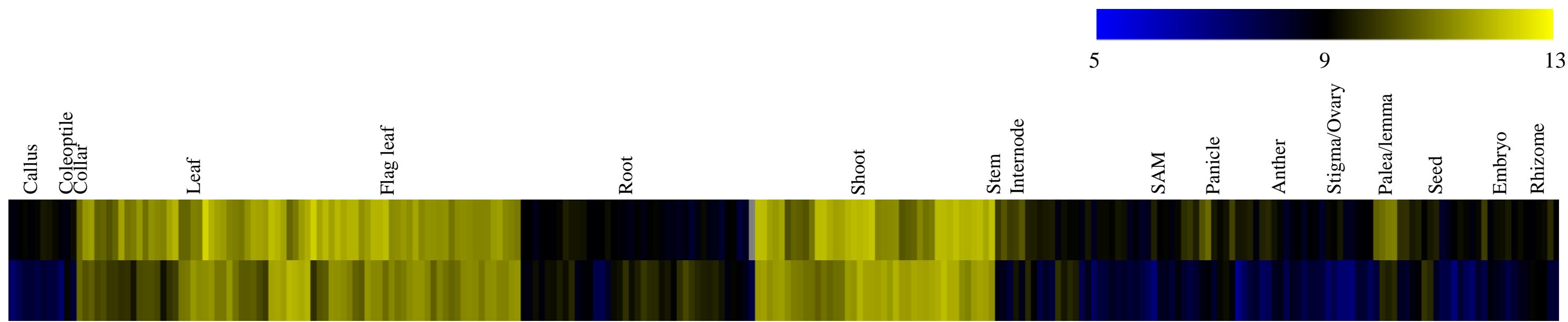
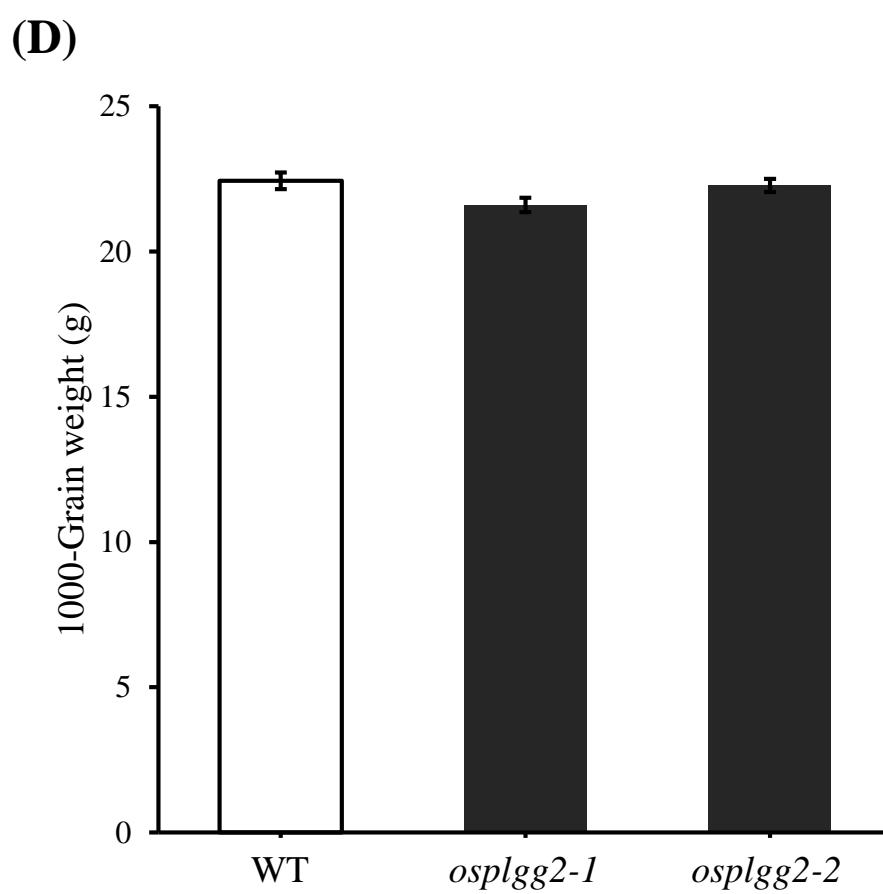
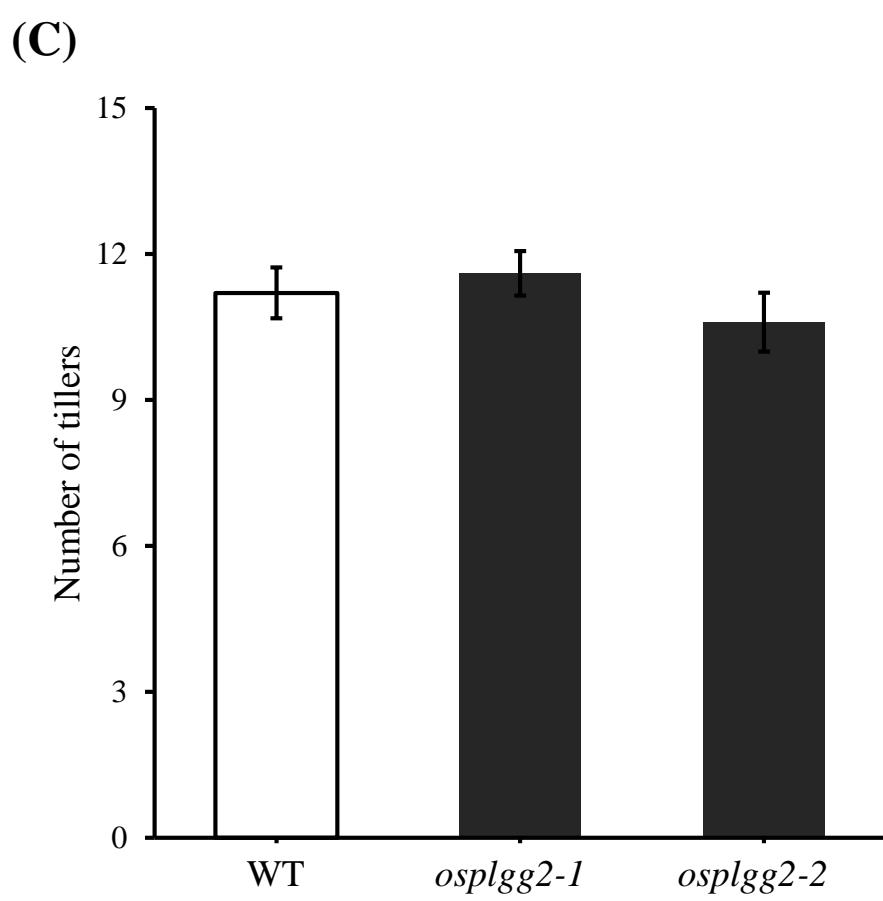
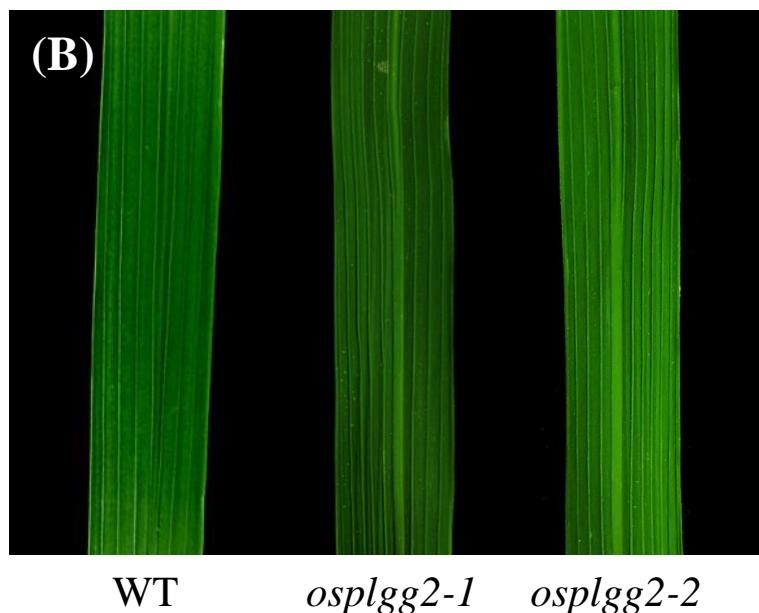


AtPLGG1	MATL—LATP FSPLASSPARNRLSCSK RFGSKNGK LNSDGAQKLNL SKFRKPDGQRF	58
OsPLGG1	MAATSSSSPCM ASLRSSHRCRLSPSATATSPPRRLRTLPPRRCRRNPSSSSSRQAAA	60
OsPLGG2		0
AtPLGG1	LQMGSS—KEMNFERKLSVQAMDGAGT-----GNTST SRNVIA SHLLVSLGI LAADYF	112
OsPLGG1	ISMAPANPRHRL AP HAAAAAGGGGGGAGATSPSGLPSL—VG AHLLVSLGI VLASDKF	119
OsPLGG2	--MAVDDLNNHHLIA-----VGVGEEAATAHGLRTLVRNMAQLVVSLGI LVAADKL	49
	*. . . : * . : ::*****:*****:***: :	
AtPLGG1	LKQAFVAAS KFPSALFGMFC FSVLM FDSVVPAAANGLMNFFEP AFLF QRWLPLFYV	172
OsPLGG1	LKQAFAAAS KFPSALFGMFCVFSVLVLD AFAPALAKGFMDFFEPATLF QRWLPLFYV	179
OsPLGG2	VEQAFAAAS KFPSALFAMFCVFALLF---LPPSLANGFMAFFDPATVF HRWLPLFFV	106
	::****,*****:****,***:***:, . . *: *: *: *: *: *: *: ***:*****:*	
AtPLGG1	PSLVVLPLSVRD PAASGVK CY VAGGWLASLCVAGYTA AVRKMVKT TEMTEAEPMAKP	232
OsPLGG1	PSLVVLPLAVRDVPAASGLK FLI FGGGWFASLMVAGYTALT VRK VQTQL PAEPM SKP	239
OsPLGG2	PSLVVLPLAVRDVSPASALK LF TFGGWFASLVVAGYTALS VRR VKTQL PAEPM KRP	166
	*****:***: **, :** * ***:*** *****:***:***: ***: ***: *	
AtPLGG1	SPFSTLELWSWSG FVVSFVGALFYPNSLGT SARTSLPFLSSTV LGY VGSQLPSS IKK	292
OsPLGG1	SPFATLEFWAWGAVFVASFAVAYVNPTALGTTARTCLPFLLA STV LGY VGSG PSGVKK	299
OsPLGG2	SPFGPLEFWAWAAVFVASFAVAYVSPTALGTTATTCLPFLLA STV FGY LGSR LPSGVKK	226
	, **:, :**,**, * . *, :***:*, * , ****:***:***:***: ***: ***: **	
AtPLGG1	VFHP ICCALS A VLA ALA FG YAS GSG LD PVL GN YLT KVA SD PG AGD LMGFLGSV LSFA	352
OsPLGG1	VLHP ICCALS ADL AA AYGYL SRSGV DAVLG DYLTKAPS NPGAGD VLMGFLGSV ISFA	359
OsPLGG2	VLHP ICCALS ADL AA VAYGYL SRSGV DAVLG DYLTESPS NPGAGD LMGFLGSV ISFA	286
	*:*****:***:***:***: * *: *: ***:***: *:*****:*****:***	
AtPLGG1	FSMF KQRKL VKR HAAE FTS VSTVFSLYSTA LVGR LVGLEPSLTV S LP RC TVAL AL	412
OsPLGG1	FSMF KQRKL VKR HAAE FTS A ASTFSLYSTA LGRV GLEPSLTI LP RC TVAL AL	419
OsPLGG2	FSMF NQRKL VRR HAAE FTS AVASTFSLYSTA LGRV VELEP LT IS LP RC TVAL AL	346
	*****:*****:*****: : : ,*****:***:***: ***: ***:*****:*****	
AtPLGG1	S VSLFEGTNSSL TAA VV VTGL GANF VQVLDKLRLR DP ARG ATASSA HGL GTAA L	472
OsPLGG1	S IVSFFEGVNSSL TAA VV VL TGL GANF VQAAMDKLGLNDP ARG GTASSA HGL GTAA L	479
OsPLGG2	RV VSLFEGVNTS VTA A VV VL TGL GANFA QAVMDKLRLKDP ARG GTASSA HGL GTAA V	406
	:***:***, *:***:*****:*****:***, . . :***:*, ****:***, *****:*****:	
AtPLGG1	SAKEPEALPFCA AYALTG FGSLLCSVPAVRQSLLAVVG-----	512
OsPLGG1	SAKEPEALPFCA AYGLTG FGS L CSVP AVRQSLVF AG-----	519
OsPLGG2	SAKEPEALPFCA AYALTGVV ASLFCSL PAIRHSL VF AGDASAS QTQHFSY	458
	*****:*****:***:,,***:***:***:***: :,,*	

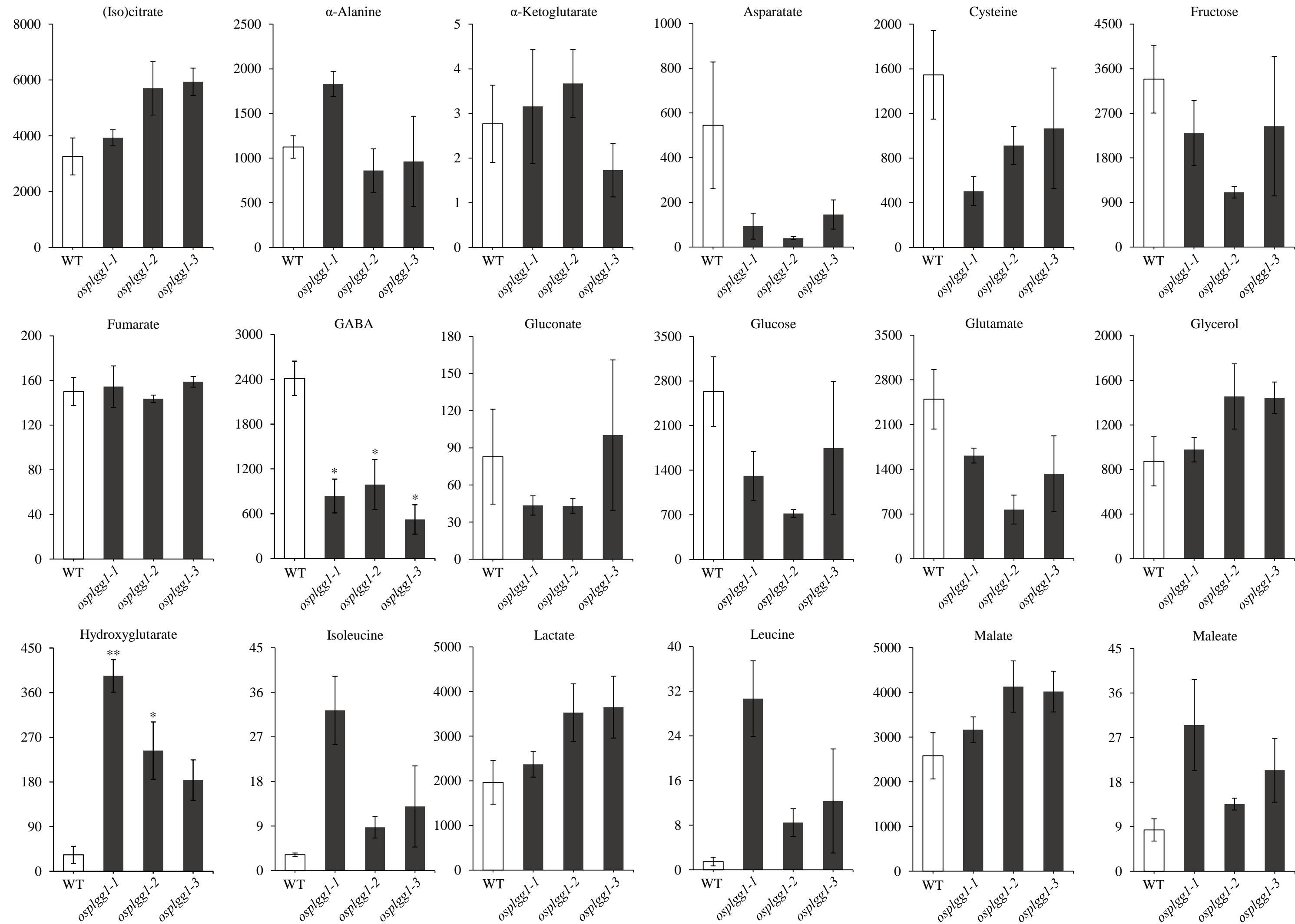
Supplemental Figure S1. Protein sequence alignment of AtPLGG1 and rice candidates. Protein sequences of two rice homologs, OsPLGG1 (LOC_Os01g32830) and OsPLGG2 (LOC_Os10g42780), were aligned with that of AtPLGG1 (At01g32080). Green color indicates a predicted chloroplast targeting peptide.

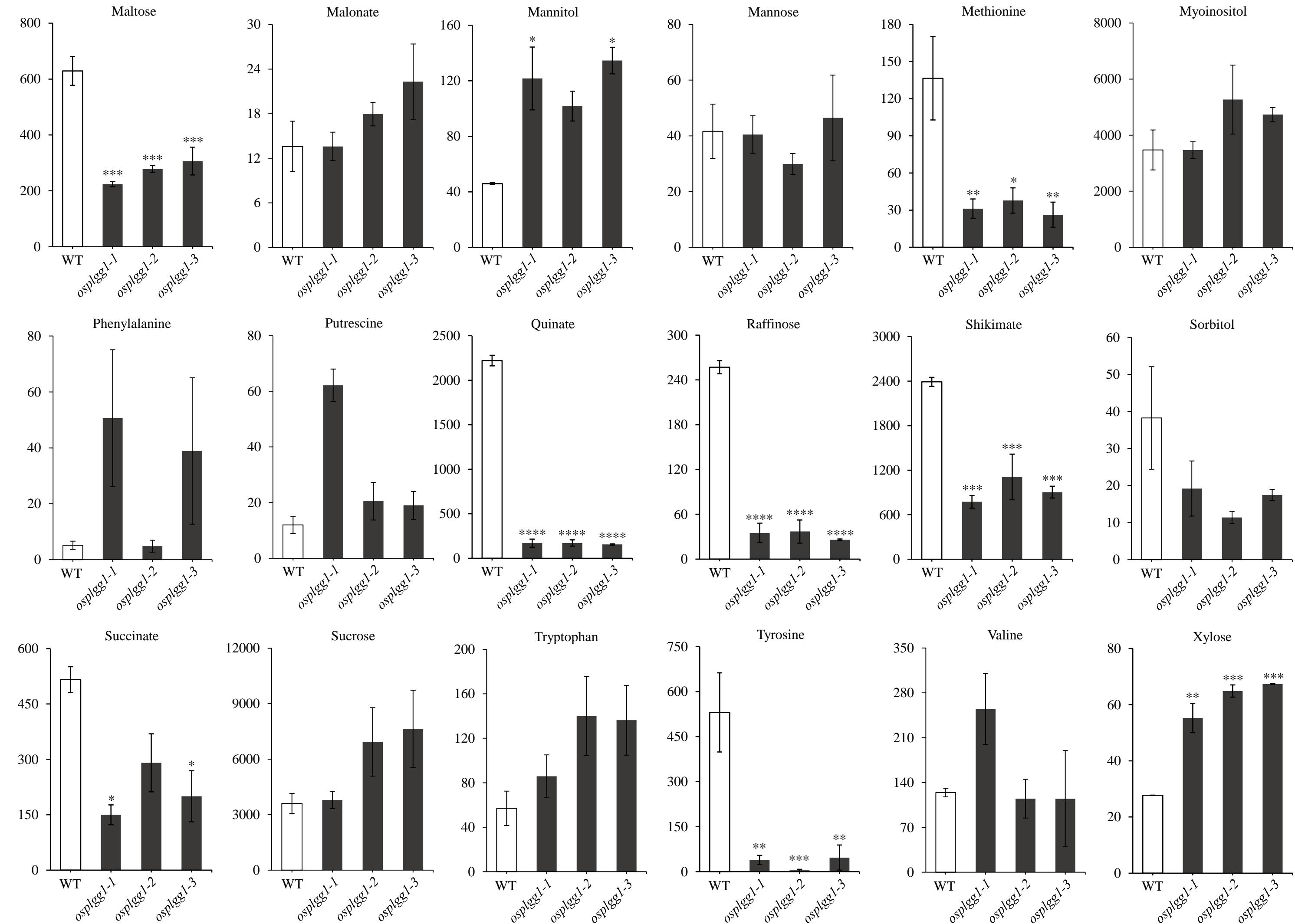


Supplemental Figure S2. Heat map expression analysis of OsPLGG1 (top) and OsPLGG2 (bottom) using Affymetrix rice microarray data downloaded from NCBI GEO.



Supplemental Figure S3. Phenotypic analysis of *osplgg2* mutants. **(A, B)** Mature plants **(A)** and leaf blades **(B)** of WT, *osplgg2-1* and *osplgg2-2* mutant plants grown for three months in the paddy field. Bar = 10 cm. **(C, D)** Number of tillers **(C)** and 1000-grain weight **(D)** of WT, *osplgg2-1* and *osplgg2-2* plants. The experiment consisted of five independent plants per each line. Error bars indicate SEM. P > 0.05 according to Student's *t*-tests.





Supplemental Figure S4. Relative abundances of metabolites which are not intermediates of photorespiration in leaves of one-month-old WT and *osplgg1* mutant plants grown in the paddy field. The relative metabolite levels were normalized to an internal standard (ribitol) and the fresh weight of the samples. Three independent biological replicates were used in the experiment, each having three technical replicates. Error bars indicate SEM. Student's *t*-test was used to show statistical differences. *P < 0.05; **P < 0.01; ***P < 0.001; ****<0.0001.