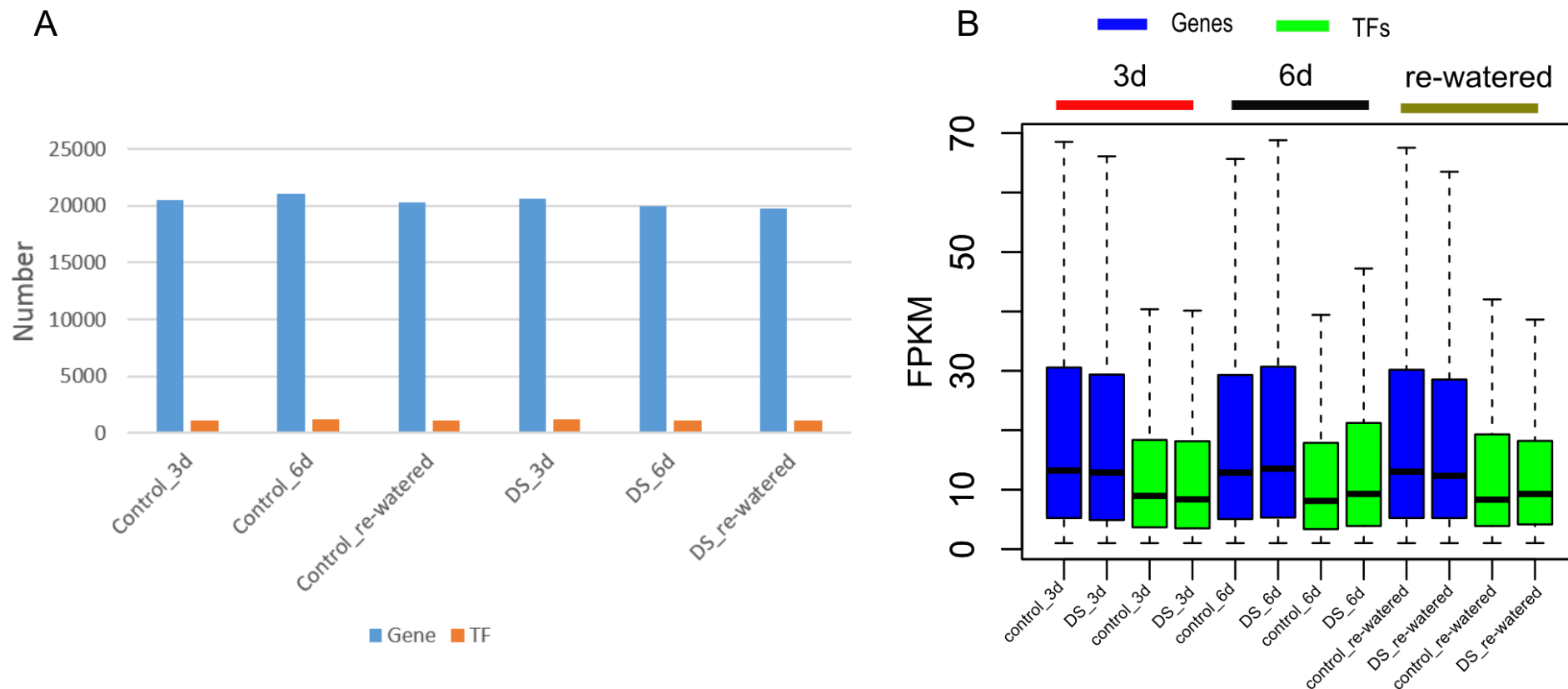
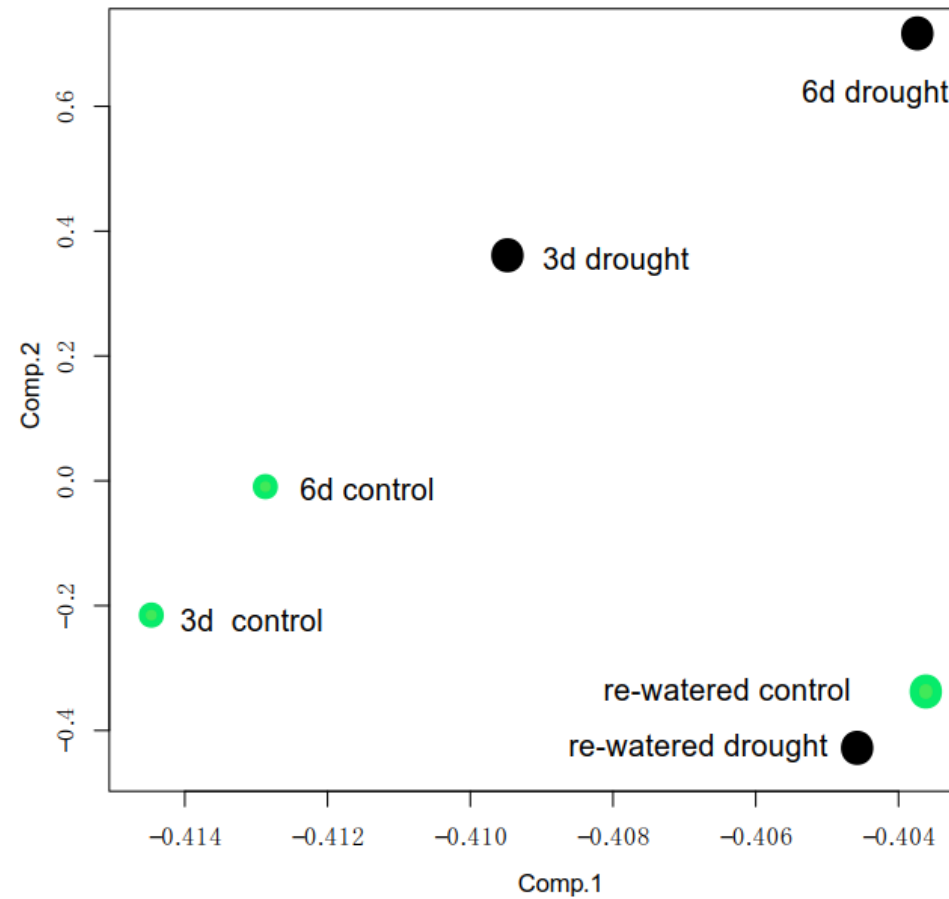


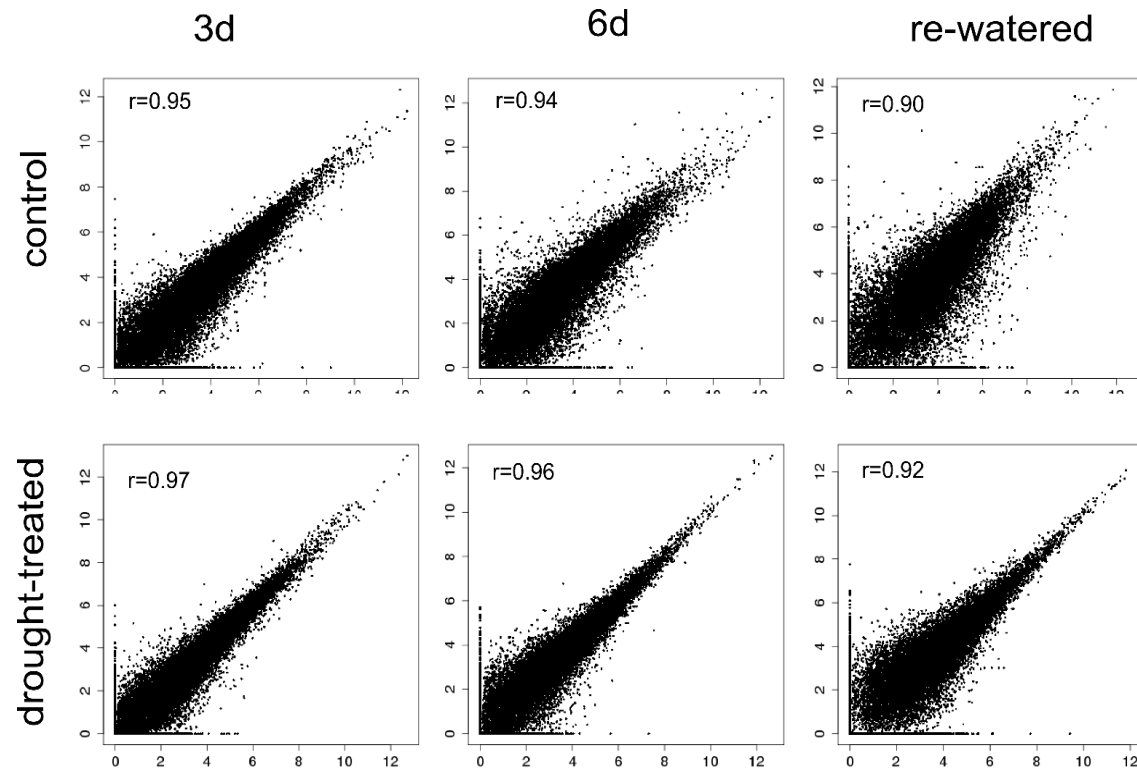
**Figure S1. Elongation rate of leaf during drought treatment stage(3d-6d) and Re-watered stage.** The elongation rate of leaf during drought stage (3d-6d) and re-watered stage for control and drought treatment seedlings were calculated respectively. The X-axis represents two different stages (drought stage from 3d to 6d and re-watered stage from 6d to re-watered). The Y-axis represents the elongation rate of leaf (elongation length of leaf divided by elongation days). Orange line represents drought treatment seedlings and blue line represents control seedlings.



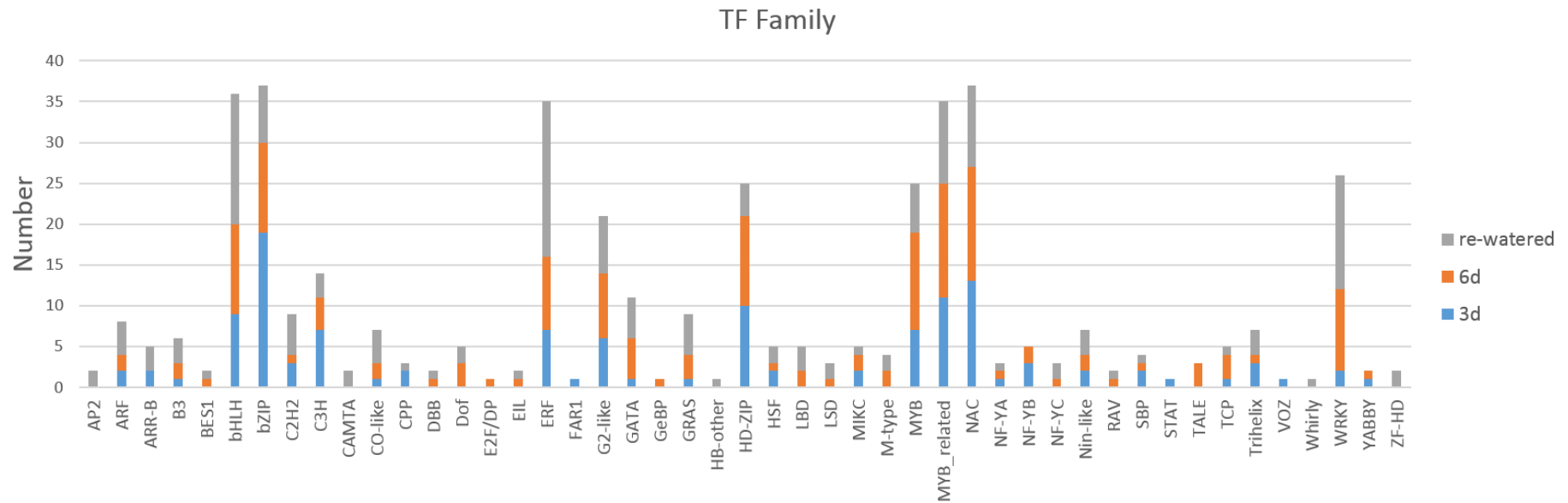
**Figure S2. Global gene expression level.** Number of expressed genes, including those encoding transcription factors (TFs), and their expression levels (median boxplot) after a 3-day or 6-day drought treatment and a 1-day water recovery period according to RNA sequencing data (**A** and **B**)



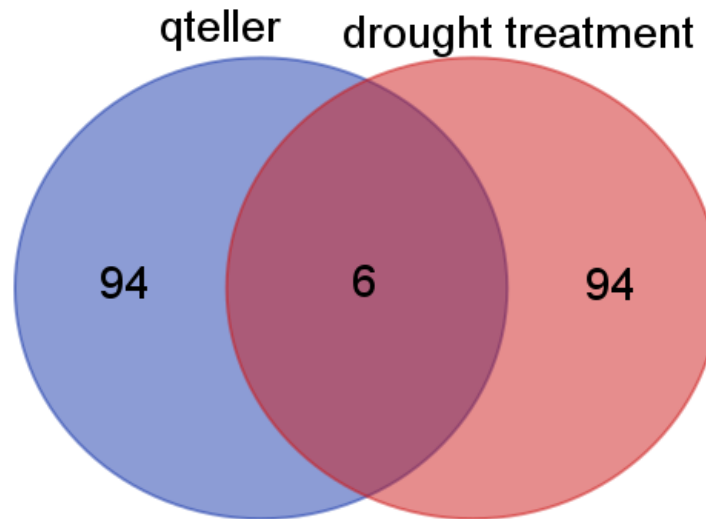
**Figure S3. PCA analysis of six samples in the three time points.** We cluster the six seedling samples in the three time points using R function princomp with expression value(FPKM) as input. Green points show control seedlings and black color show drought treatment seedlings.



**Figure S4. Correlation analysis between two biological replicates under drought treatments and controls.** We calculated the expression level (FPKM) for each replicate. The normalized data of  $\log_2(\text{FPKM} + 1)$  was used to calculate the Pearson Correlation Coefficient (PCC).

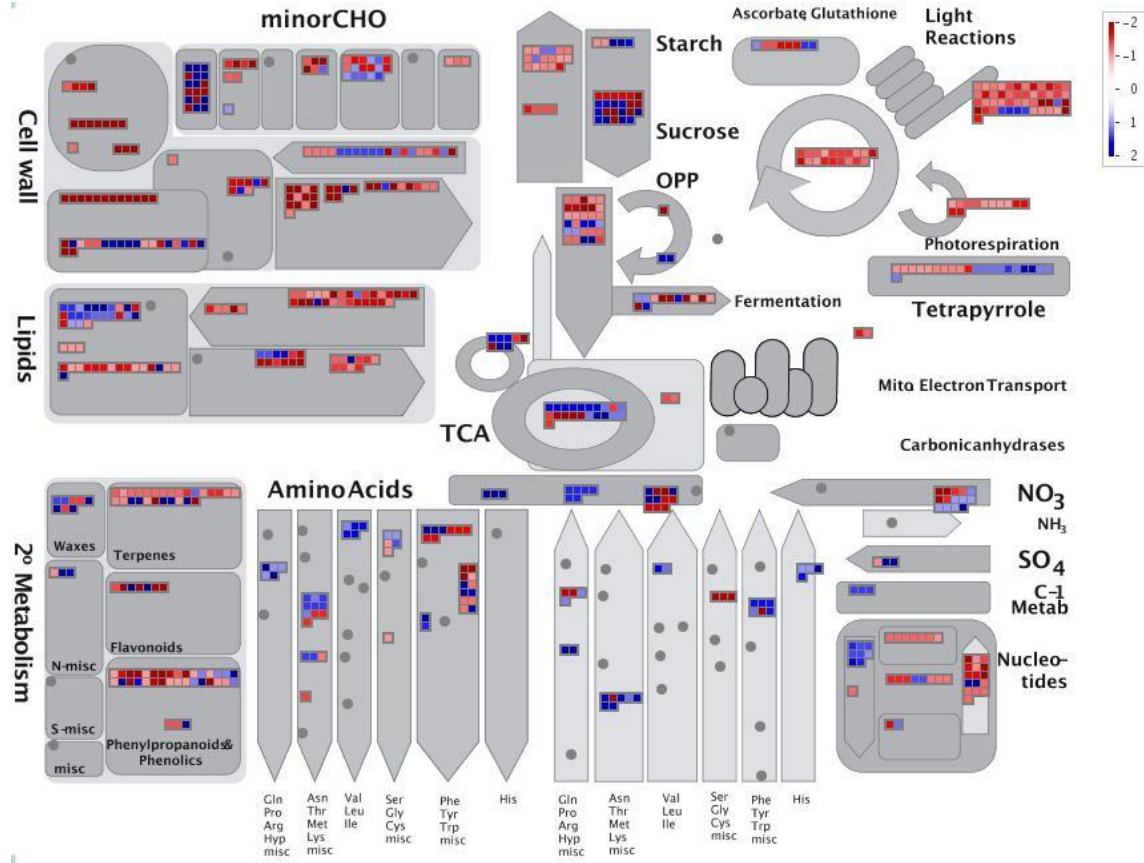


**Figure S5. Number of differentially expressed transcription factor genes in response to drought stress treatments.** The different transcription factor families responding to water deficit and recovery were summarized and compared. The X-axis represents the transcription factor family members. The Y-axis represents the number of differentially expressed family members.

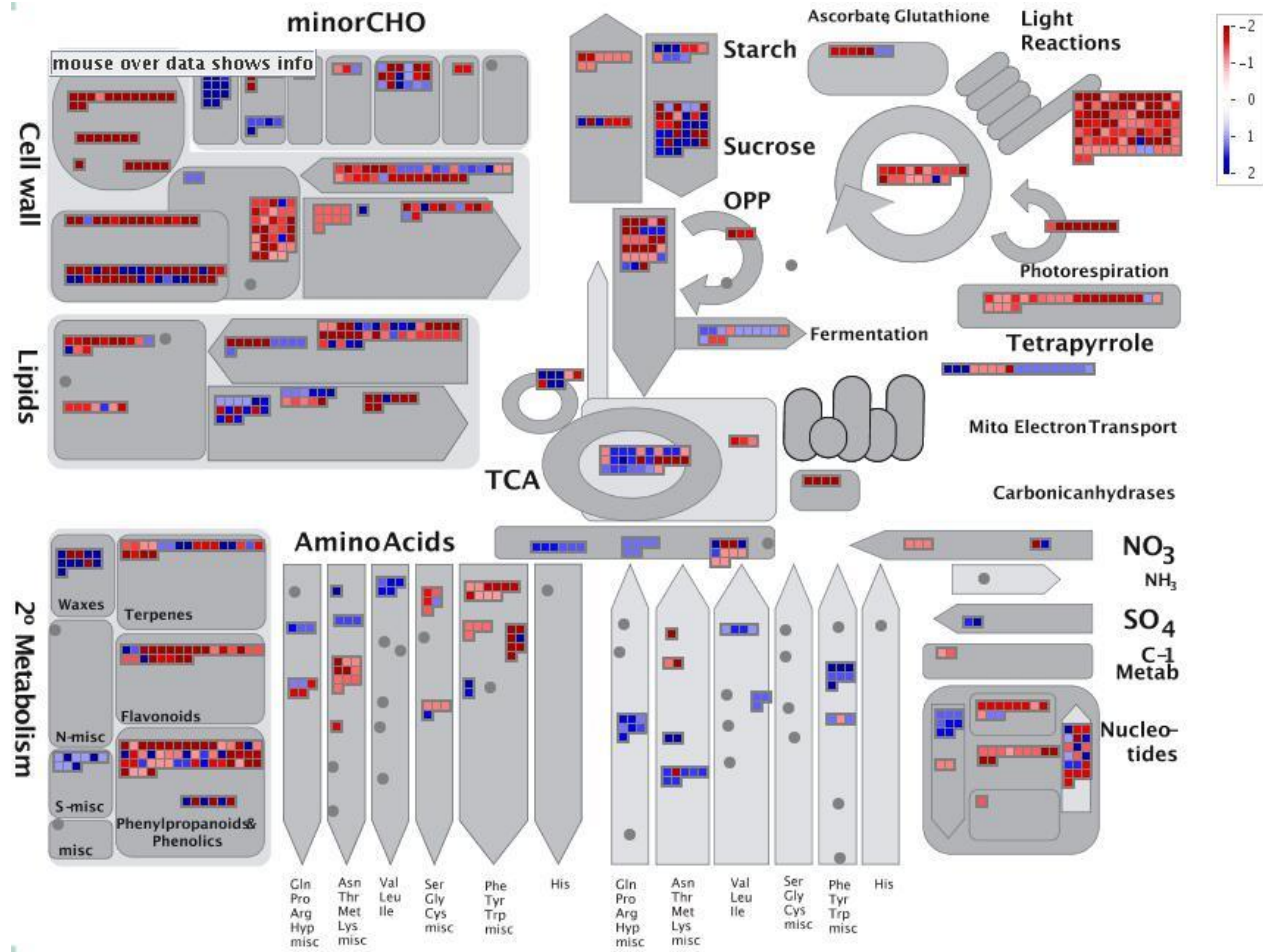


**Figure S6. The identification of Co-expressing genes with *ZmNAC111* Using qTeller data and our drought-treatment data.** We selected the top 100 co-expressing genes with *ZmNAC111* (measure by Pearson correlation coefficient) using public qTeller data and our data, respectively. The overlapped genes were considered as the target genes of *ZmNAC111*.

(A)

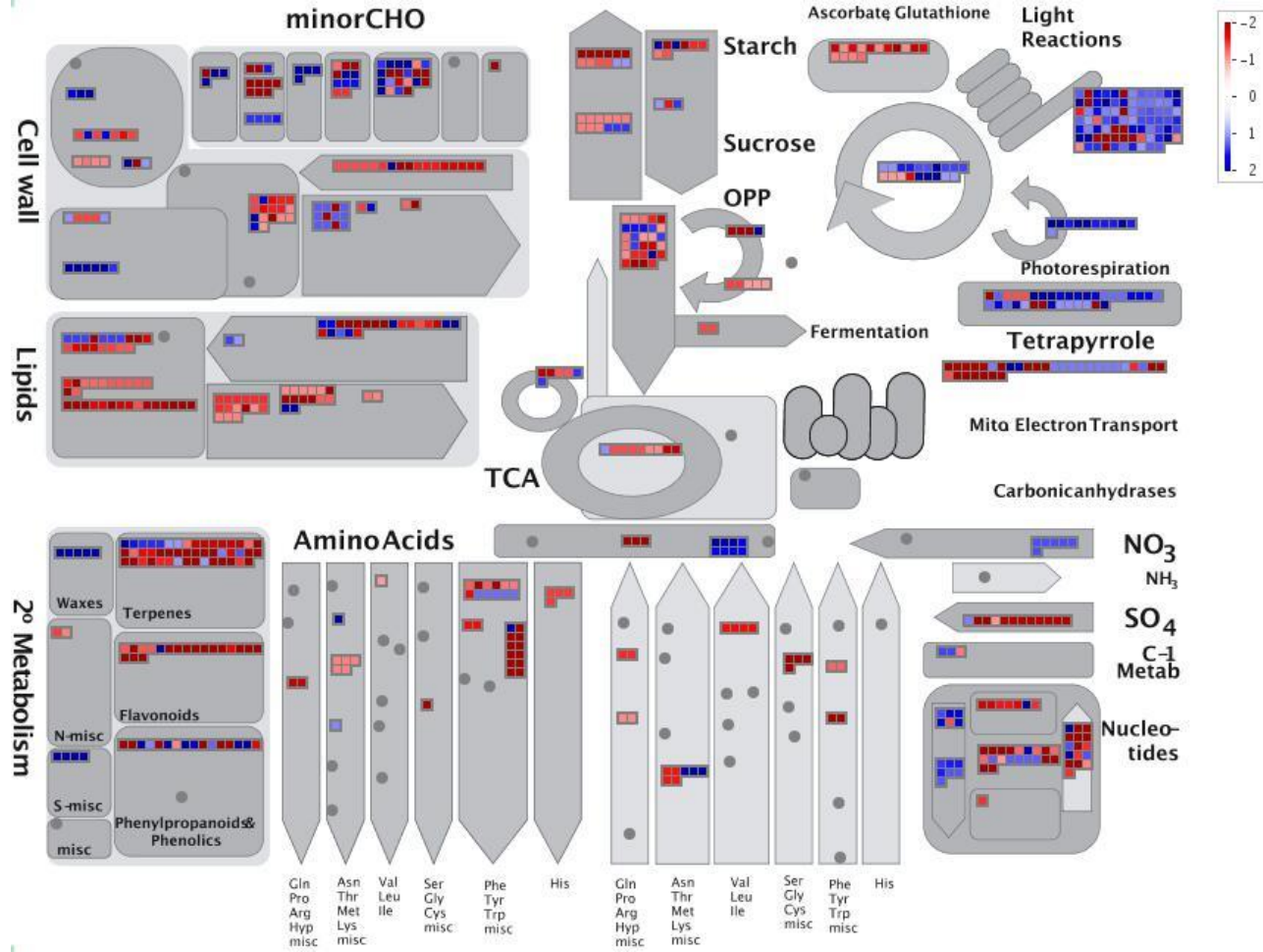


(B)

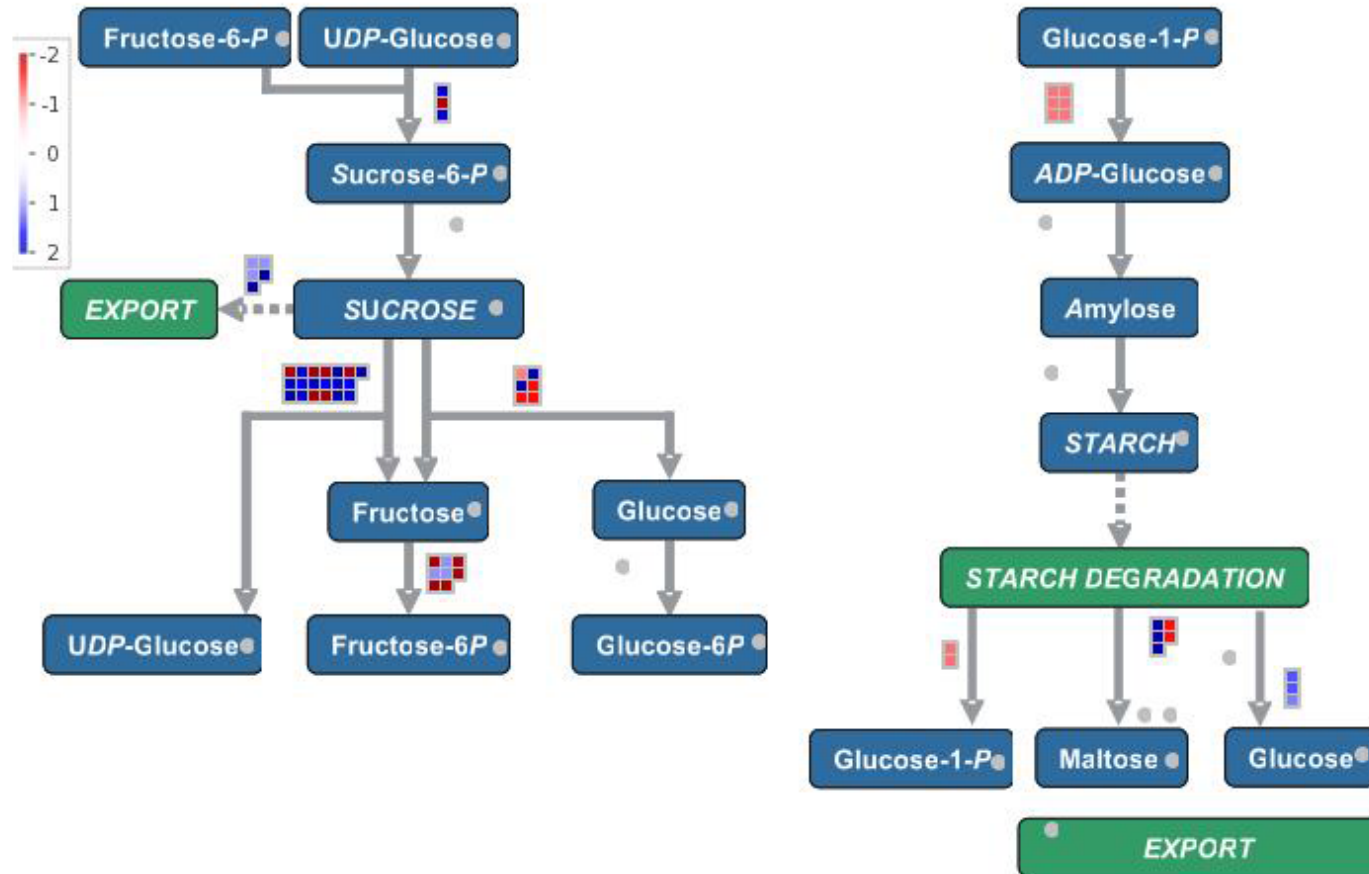




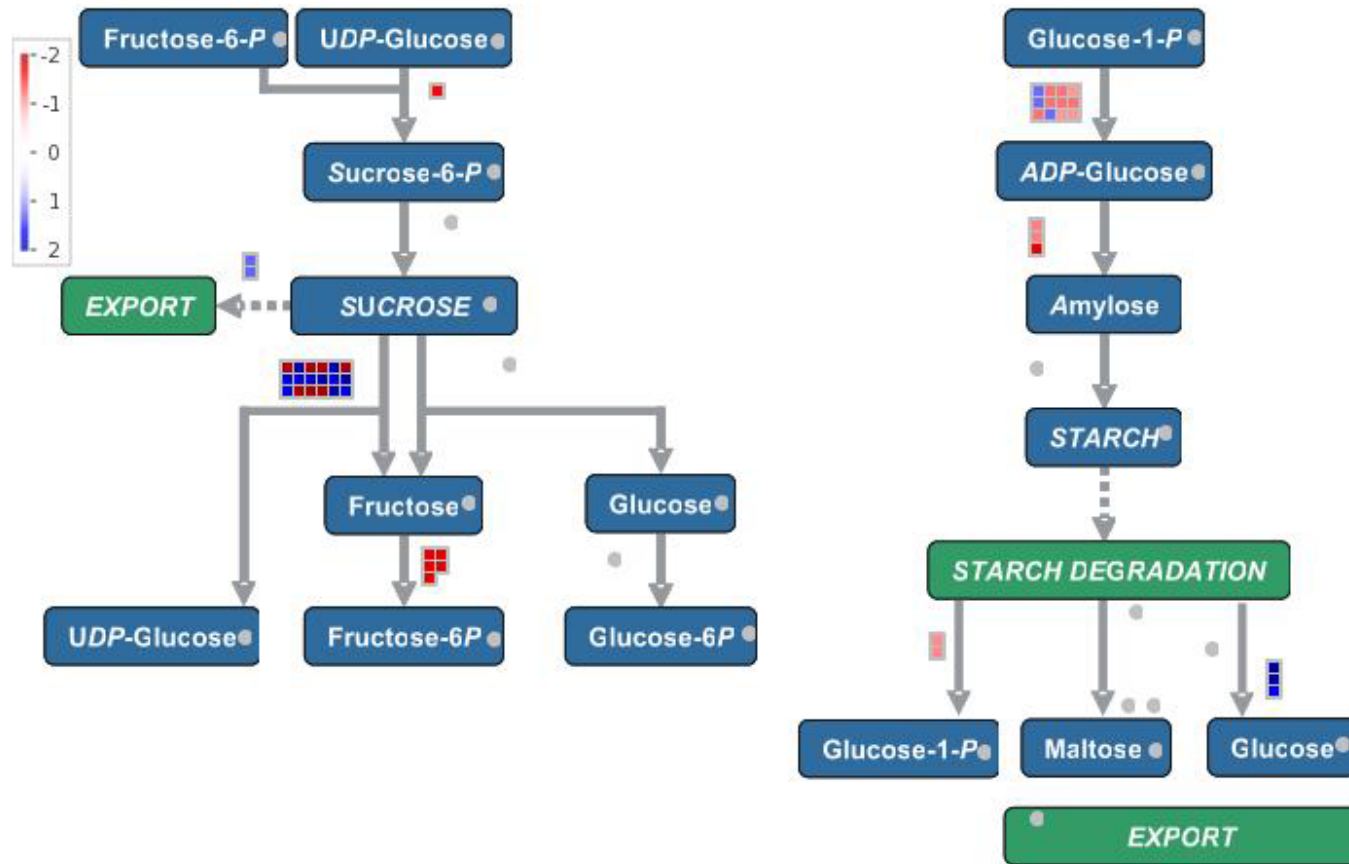
(C)



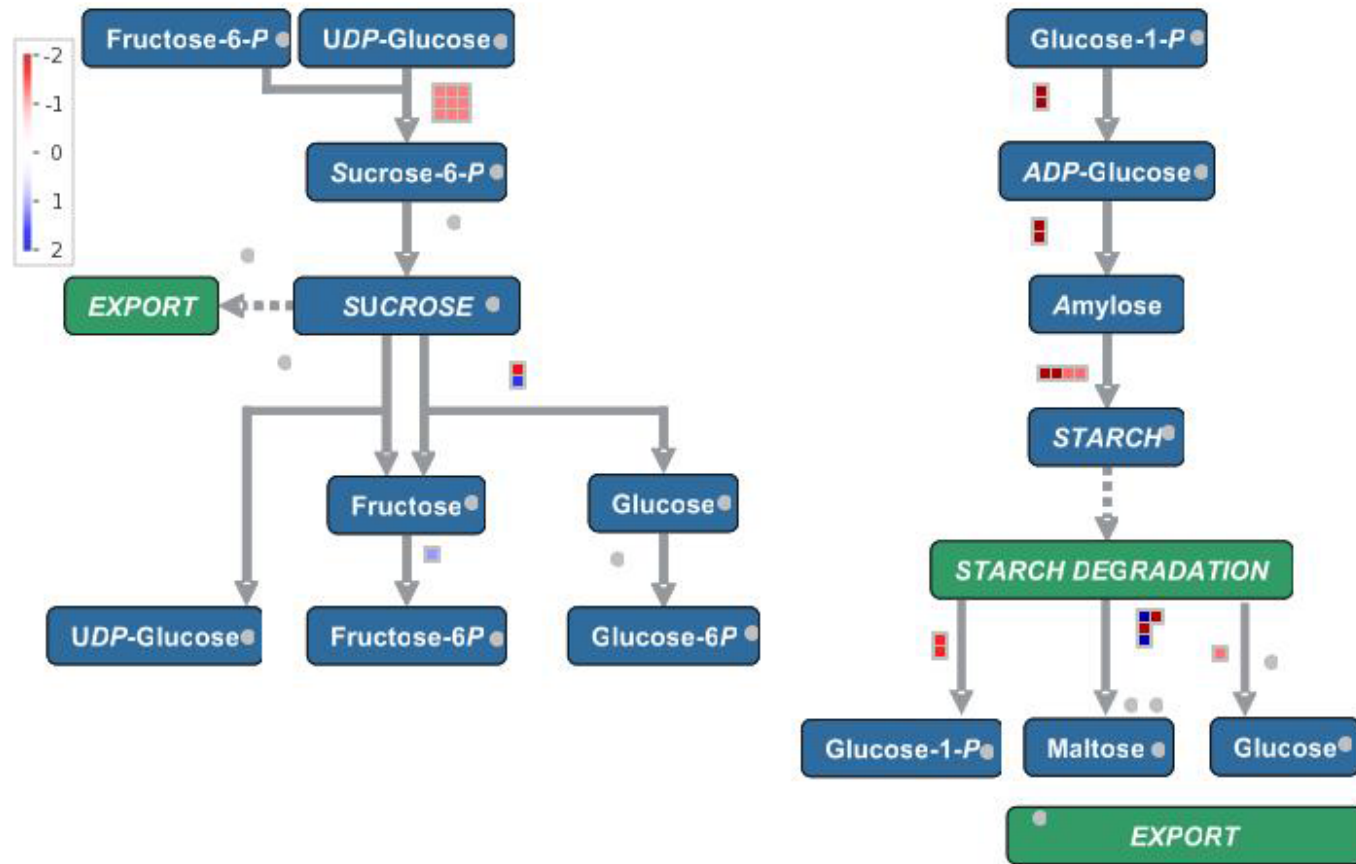
(D)



(E)



(F)



**Figure S7 Overview of different metabolic pathways and carbohydrates affected by the differentially expressed genes in response to drought and water recovery treatments.** Metabolic pathways associated with differentially expressed genes after the 3-day drought treatment (**A**), 6-day drought treatment (**B**), and water recovery period (**C**). Carbohydrate metabolic pathways associated with differentially expressed genes after the 3-day drought treatment (**D**), 6-day drought treatment (**E**), and water recovery period (**F**). In each panel, the expression levels of up- and down-regulated genes are indicated in blue and red, respectively.

	3d	6d	Re_watered	
GRMZM2G113432	-1.11	-2.37	-0.22	cellulose
GRMZM2G173759	-1.57	-1.27	0.51	
GRMZM2G015886	0.00	-2.32	0.00	
GRMZM2G018241	-0.43	-1.01	-0.32	
GRMZM2G025231	-0.51	-1.45	-0.42	
GRMZM2G027723	-0.97	-1.93	-0.57	
GRMZM2G028353	-0.04	-1.00	-0.45	
GRMZM2G074546	-1.15	-2.17	1.39	
GRMZM2G082580	-0.85	-1.97	-0.22	
GRMZM2G109326	0.33	-1.83	1.06	
GRMZM2G110145	-0.43	-1.29	-0.43	
GRMZM2G112336	-0.30	-1.11	-0.67	
GRMZM2G113137	-0.54	-1.03	-0.65	
GRMZM2G115772	-0.59	-1.52	-0.25	
GRMZM2G142898	-0.84	-1.67	0.31	
GRMZM2G424832	-0.42	-1.39	0.01	
GRMZM5G826714	-0.31	-1.00	-0.77	
GRMZM2G177631	-0.74	-1.67	-1.09	
GRMZM2G010142	-0.50	-0.77	-1.49	
GRMZM2G028286	-0.63	-0.54	-1.44	
GRMZM2G039454	-0.26	0.46	-1.06	
GRMZM2G071970	0.00	-0.78	-1.01	
GRMZM2G074792	-0.14	-0.10	-1.32	
GRMZM5G870176	-0.63	0.17	-1.90	
GRMZM2G122431	1.51	1.58	1.70	
GRMZM2G014558	0.48	0.81	3.23	

GRMZM2G445169	0.00	0.60	0.00	expansin
GRMZM2G176595	-2.76	-3.53	0.16	
GRMZM2G082520	-1.73	-5.69	0.67	
GRMZM2G004955	-0.84	-2.45	2.47	
GRMZM2G013002	-0.69	-1.60	1.06	
GRMZM2G013671	1.12	-2.39	0.00	
GRMZM2G021621	-1.15	-1.85	0.91	
GRMZM2G056236	0.19	-3.95	-0.24	
GRMZM2G327266	0.51	-3.94	0.62	
GRMZM2G339122	-0.15	-3.13	0.53	
GRMZM2G361064	-1.26	-3.46	1.57	
GRMZM2G154178	-1.01	-3.42	-0.73	
GRMZM2G026147	0.68	2.67	0.20	
GRMZM2G095968	2.86	2.87	2.38	
GRMZM5G859316	3.98	2.57	1.26	
GRMZM2G021427	-1.21	0.00	2.40	

GRMZM2G004699	-0.85	-1.95	0.01	xyloglu can
GRMZM2G039919	-1.63	-2.02	1.02	
GRMZM2G063566	0.26	-2.25	1.60	
GRMZM2G119783	-1.01	-4.65	0.08	
GRMZM2G364748	1.55	1.31	1.45	
AC210669.3_FG001	2.75	-0.84	-1.93	

**Figure S8 Expression profile of genes involved in cell wall development.** Cellulose, expansin and xyloglucan endotransglucosylase related genes are involved in cell wall development. The fold change value (  $\log_2(\text{MT}/\text{WT})$  ) in the figure is calculated. Green color represent down-regulated genes. Red color represent up-regulated genes.