

Figure S1. GO functional enrichment analysis of DEGs. **(a)** GO enrichment analysis of DEGs in D_0h vs D_4h. **(b)** GO enrichment analysis of DEGs in D_0h vs D_8h. The ordinate indicates the GO term, and the abscissa indicates the number of enrichment. Select the Top ten terms with the largest number were selected for display from MF (molecular_function), BP (biological_process) and CC (cellular_component), respectively.

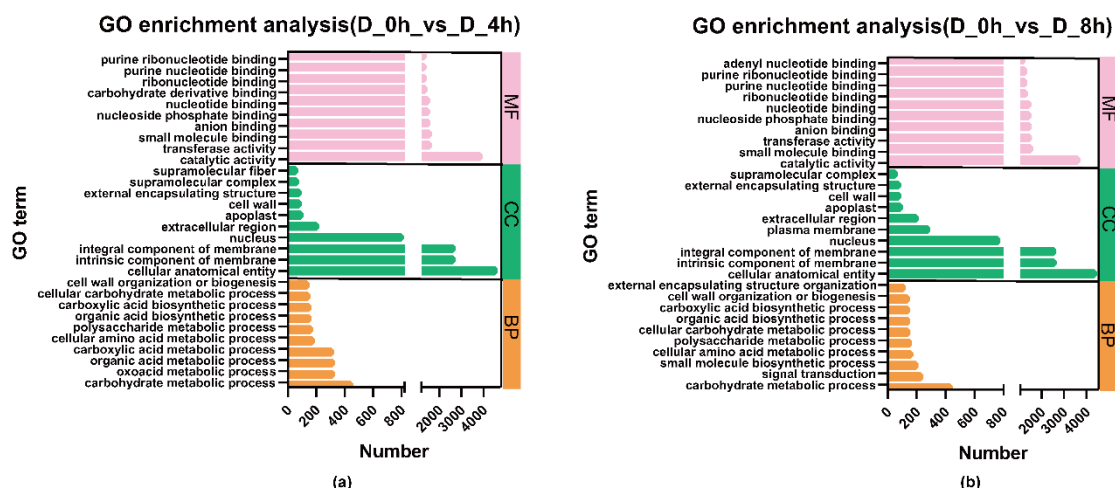


Figure S2. Selected unigenes with gene family in *Arabidopsis*. Phylogenetic tree was generated using the neighbor-joining method by MEGA11 software. The numerals next to the branch nodes indicate bootstrap values from 1000 replications. **(a)** The phylogenetic tree includes TF annotated as DREB (TRINITY_DN14213_c0_g1) and the *Arabidopsis* DREB gene family. *Arabidopsis* DREB gene family was downloaded from the *Arabidopsis* database. **(b)** Phylogenetic analysis of selected unigene (TRINITY_DN14213_c0_g1) and *Arabidopsis* DREB A-1 subfamily including AT1G12610.1, AT1G63030.1, AT5G51990.1, AT4G25490.1, AT4G25470.1, AT4G25480.1. **(c)** Phylogenetic analysis of 9 PYL/PYR/RCAR both annotated in drought and ABA transcriptome with the *Arabidopsis* PYL/PYR/RCAR family. AtPYLs were downloaded from the *Arabidopsis* database. AtPYL1 (AT5G46790), AtPYL2 (AT2G26040), AtPYL3 (AT1G73000), AtPYL4 (AT2G38310), AtPYL5 (AT5G05440), AtPYL6 (AT2G40330), AtPYL7 (AT4G01026), AtPYL8 (AT5G53160), AtPYL9 (AT1G01360), AtPYL10 (AT4G27920), AtPYL11 (AT5G45860), AtPYL12 (AT5G45870), AtPYL13 (AT4G18620), AtPYR1/RCAR11 (AT4G17870).

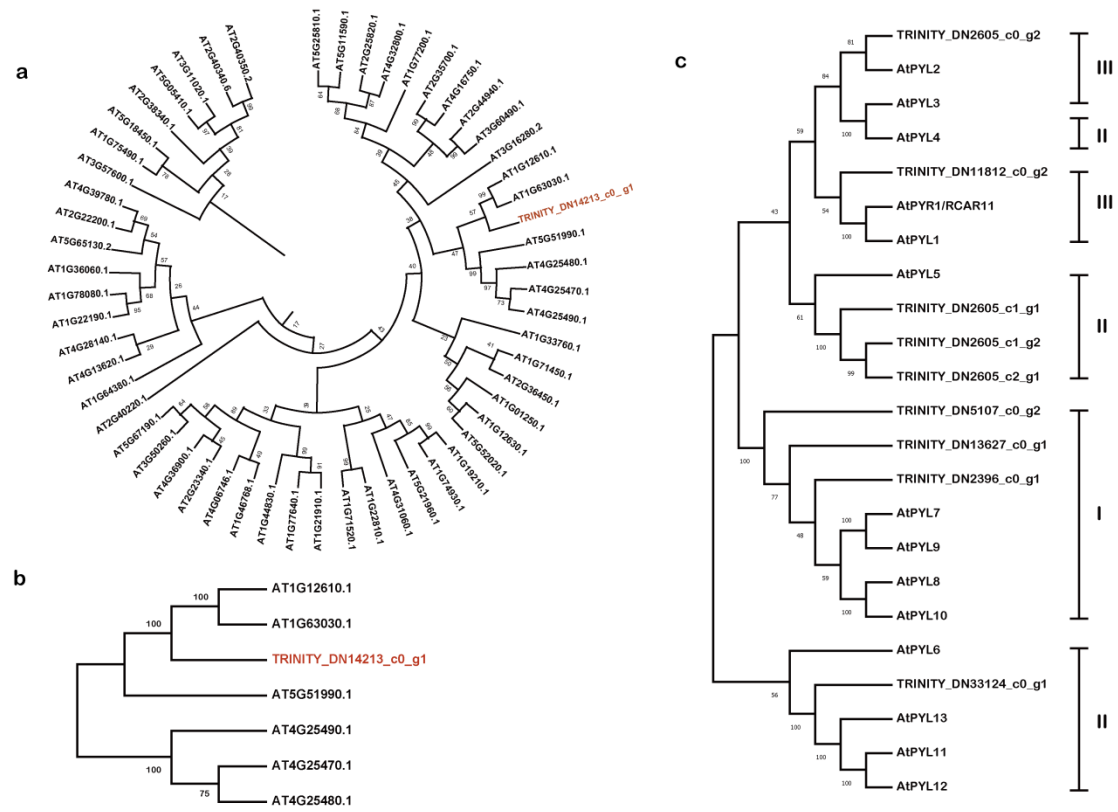


Figure S3. Physiological state of *S. miltiorrhiza* plants at 0h, 2h, 4h, 8h of drought treatment.

