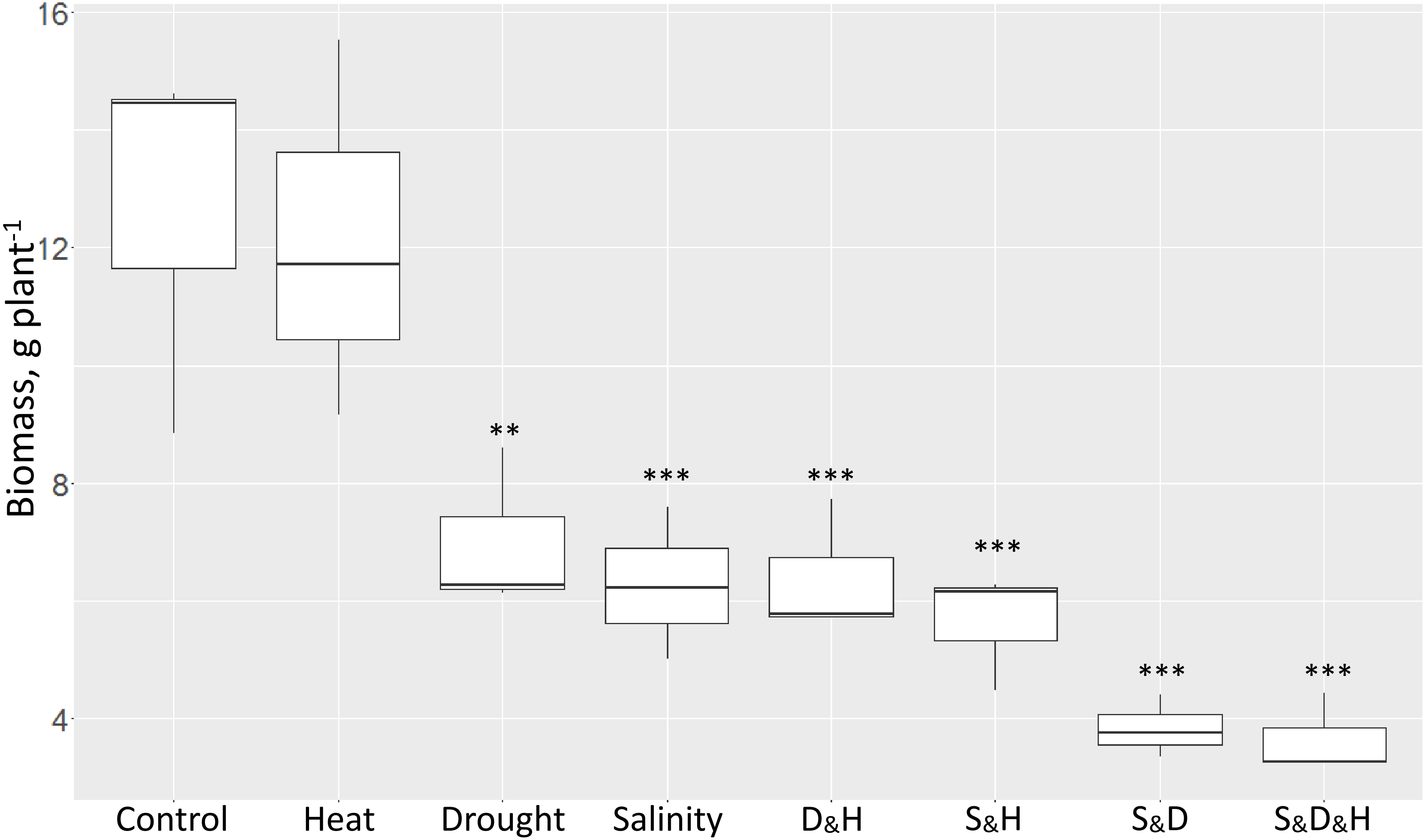
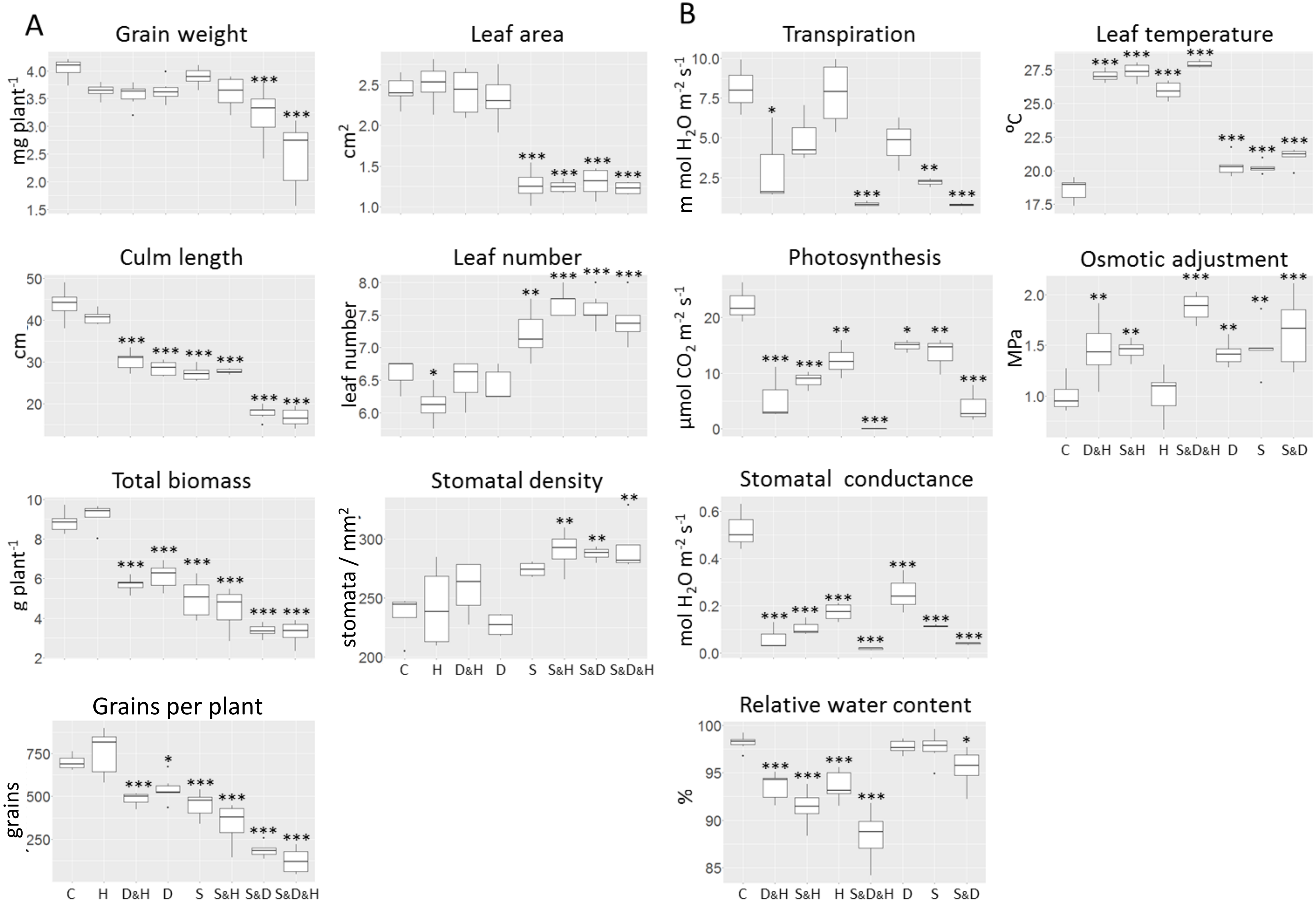
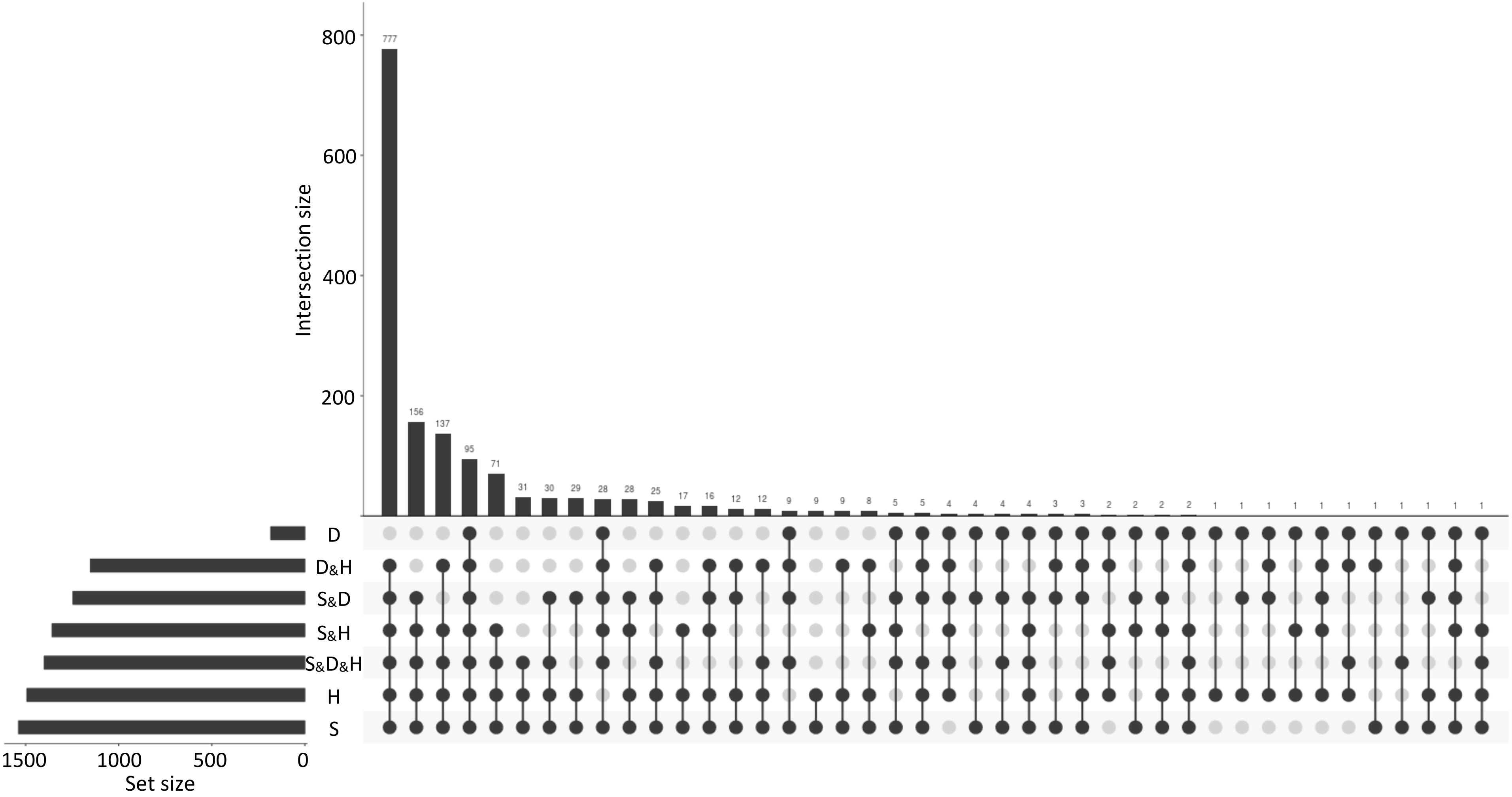


Supplemental Figure S1. Box plots of average plant biomass among three independent assays. Statistical analysis was performed with one-way ANOVA followed by Dunnet's test ($P \leq 0.05$). Values are mean ± SE. Significant differences are denoted with asterisks (**, $P \leq 0.01$ and ***, $P \leq 0.001$). The perpendicular line within each box represents the median value and the ends of the box represent the 3rd and 1st quartile, respectively. $D_{\&}H$, combination of drought and heat; $S_{\&}H$, combination of salinity and heat; $S_{\&}D$, combination of salinity and drought; $S_{\&}D_{\&}H$, combination of salinity, drought and heat.

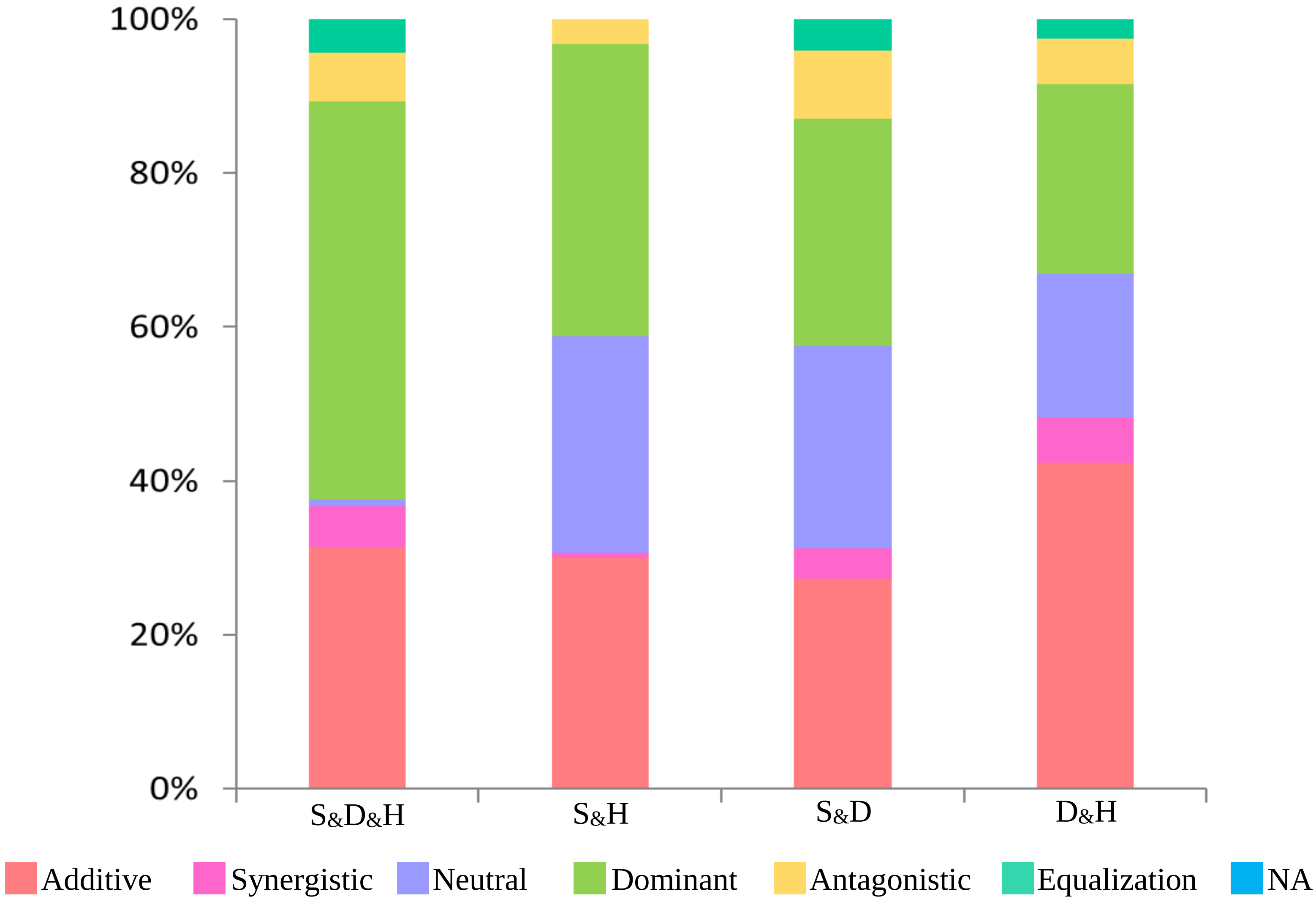


Supplemental Figure S2. Morpho-physiological measurements. (**A**) Morphological and yield parameters and (**B**) physiological parameters under control and stress treatments. Statistical analysis was performed with one-way ANOVA followed by Dunnet's test ($P \leq 0.05$). Values are mean ± SE. Significant differences are denoted with asterisks (*, $P \leq 0.05$; **, $P \leq 0.01$ and ***, $P \leq 0.001$). C, control; H, heat; $D_{\&}H$, combination of drought and heat; D, drought; S, salinity; $S_{\&}H$, combination of salinity and heat; $S_{\&}D$, combination of salinity and drought; $S_{\&}D_{\&}H$, combination of salinity, drought and heat.

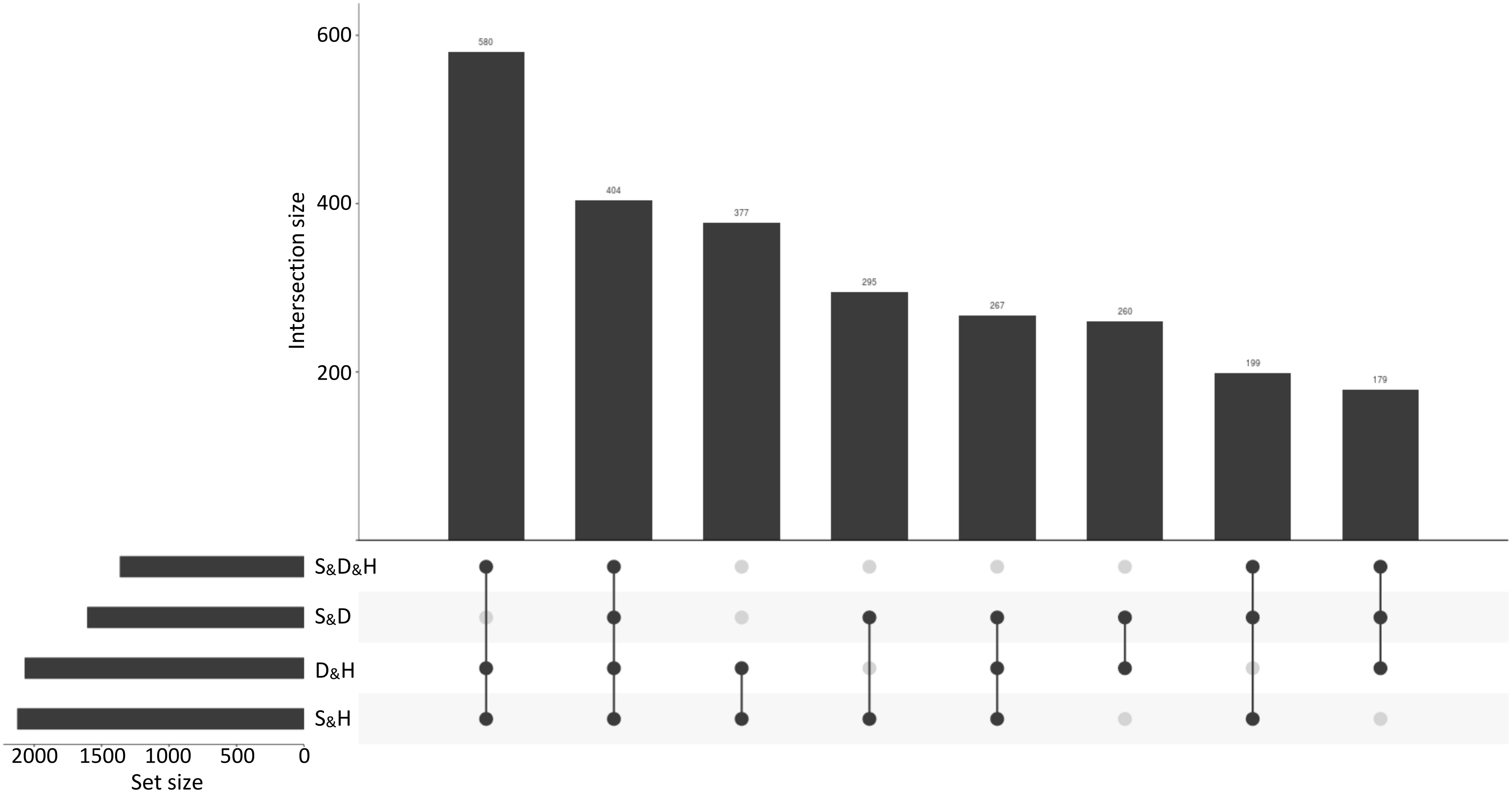
Supplemental Figure S3. Effects of single and combined stresses on plant shoots 17 days after anthesis.



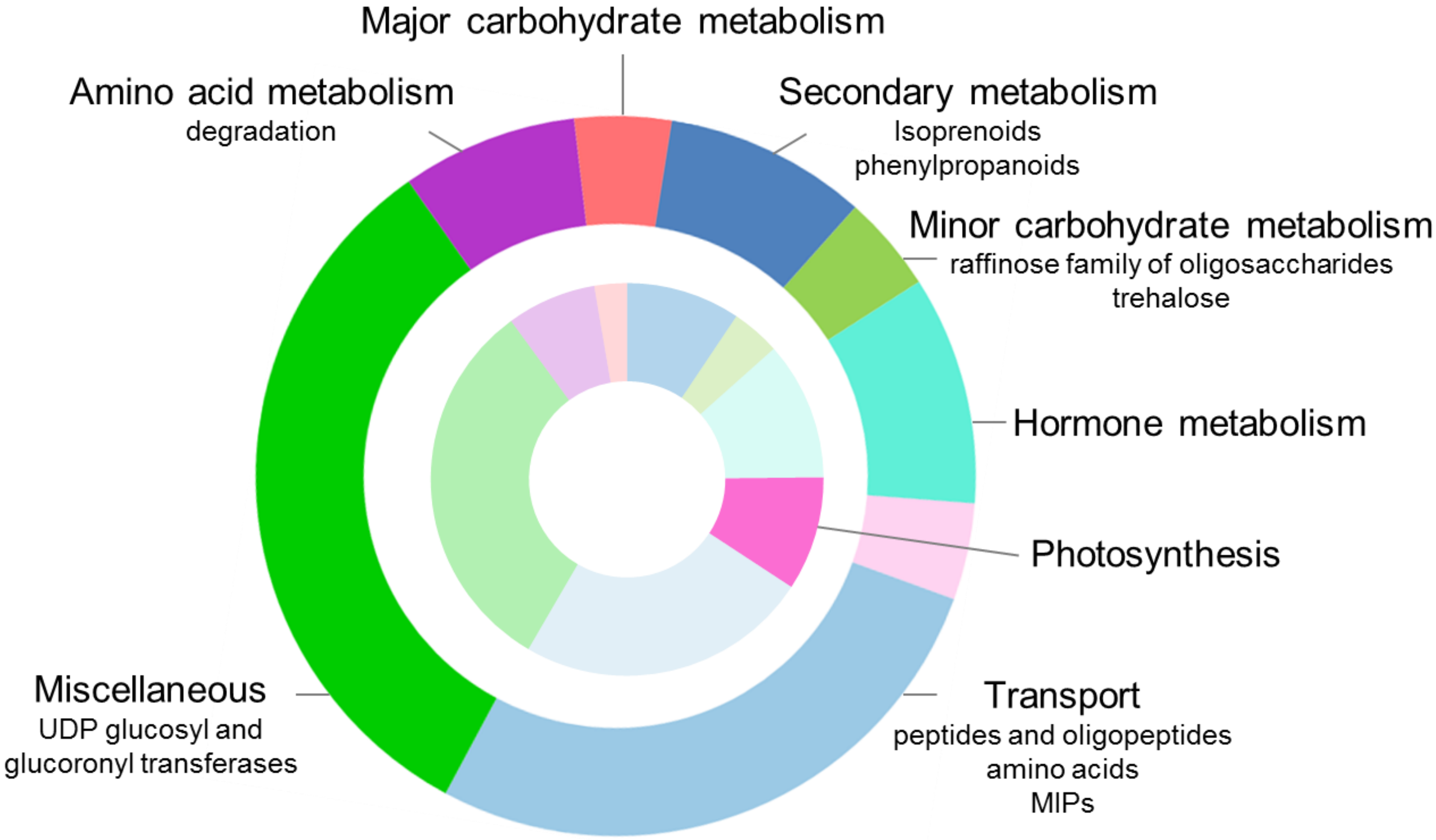
Supplemental Figure S4. Intersections among 1,550 common stress differentially expressed genes across single and combined stresses. Number above bars indicates the number of genes within each intersection. Conditions are as follows: salinity (S), drought (D), heat (H), salinity and drought ($S_{\&}D$), salinity and heat ($S_{\&}H$), drought and heat ($D_{\&}H$), salinity, drought and heat ($S_{\&}D_{\&}H$).



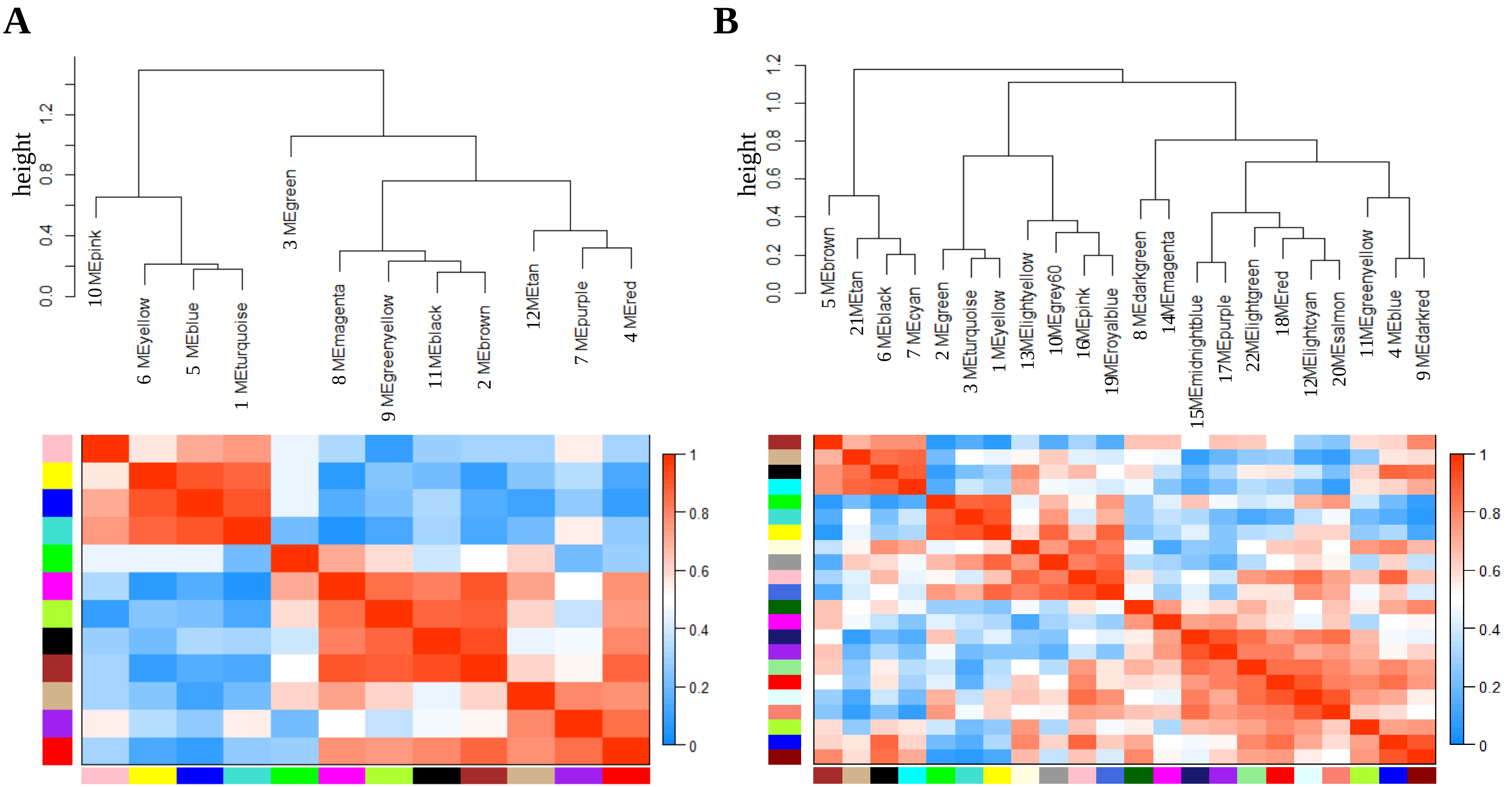
Supplemental Figure S5. Response mode partitions of common stress differentially expressed genes among the transcriptional patterns of triple and double stress combinations. $S_{\&}D_{\&}H$, combination of salinity, drought and heat; $S_{\&}H$, combination of salinity and heat; $S_{\&}D$, combination of salinity and drought; $D_{\&}H$, combination of drought and heat.



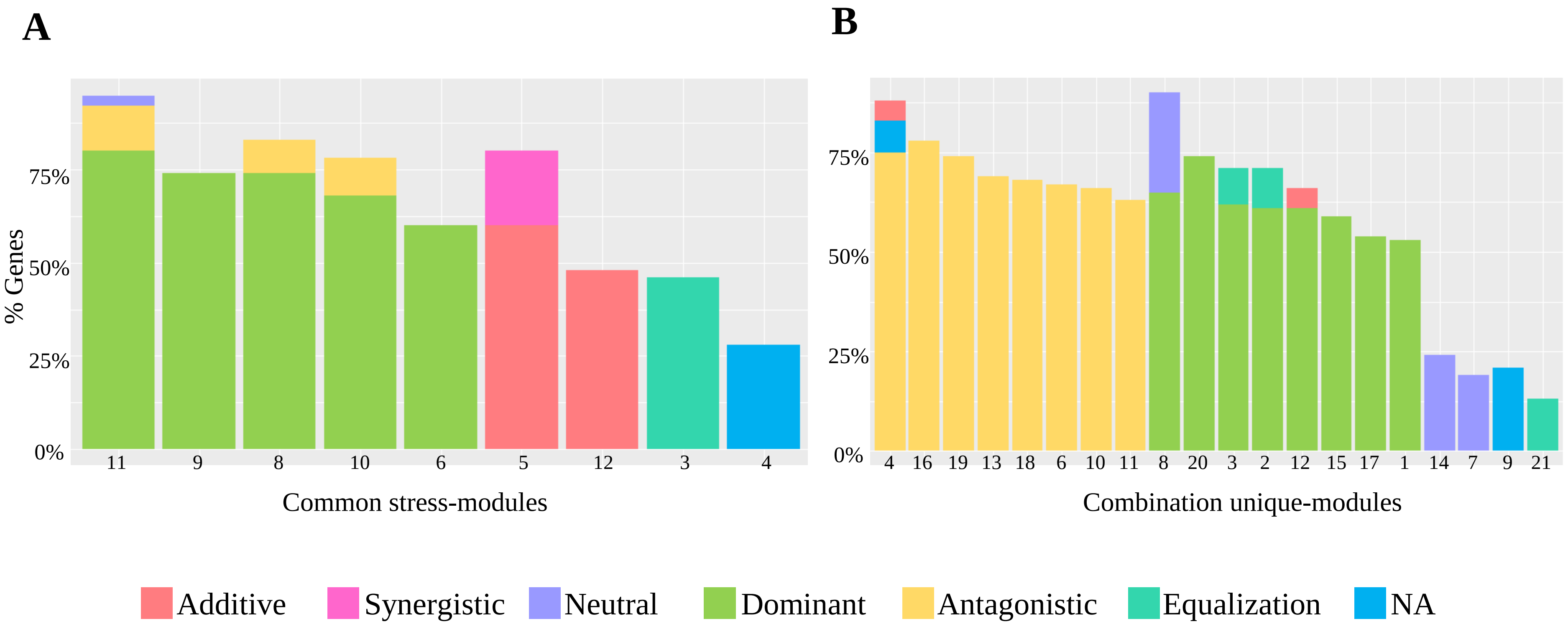
Supplemental Figure S6. Intersections among 2,561 stress combination unique differentially expressed genes across combined stresses. Number above bars indicates the number of genes within each intersection. Conditions are as follows: salinity, drought and heat ($S_{\&}D_{\&}H$), salinity and drought ($S_{\&}D$), drought and heat ($D_{\&}H$), salinity and heat ($S_{\&}H$).



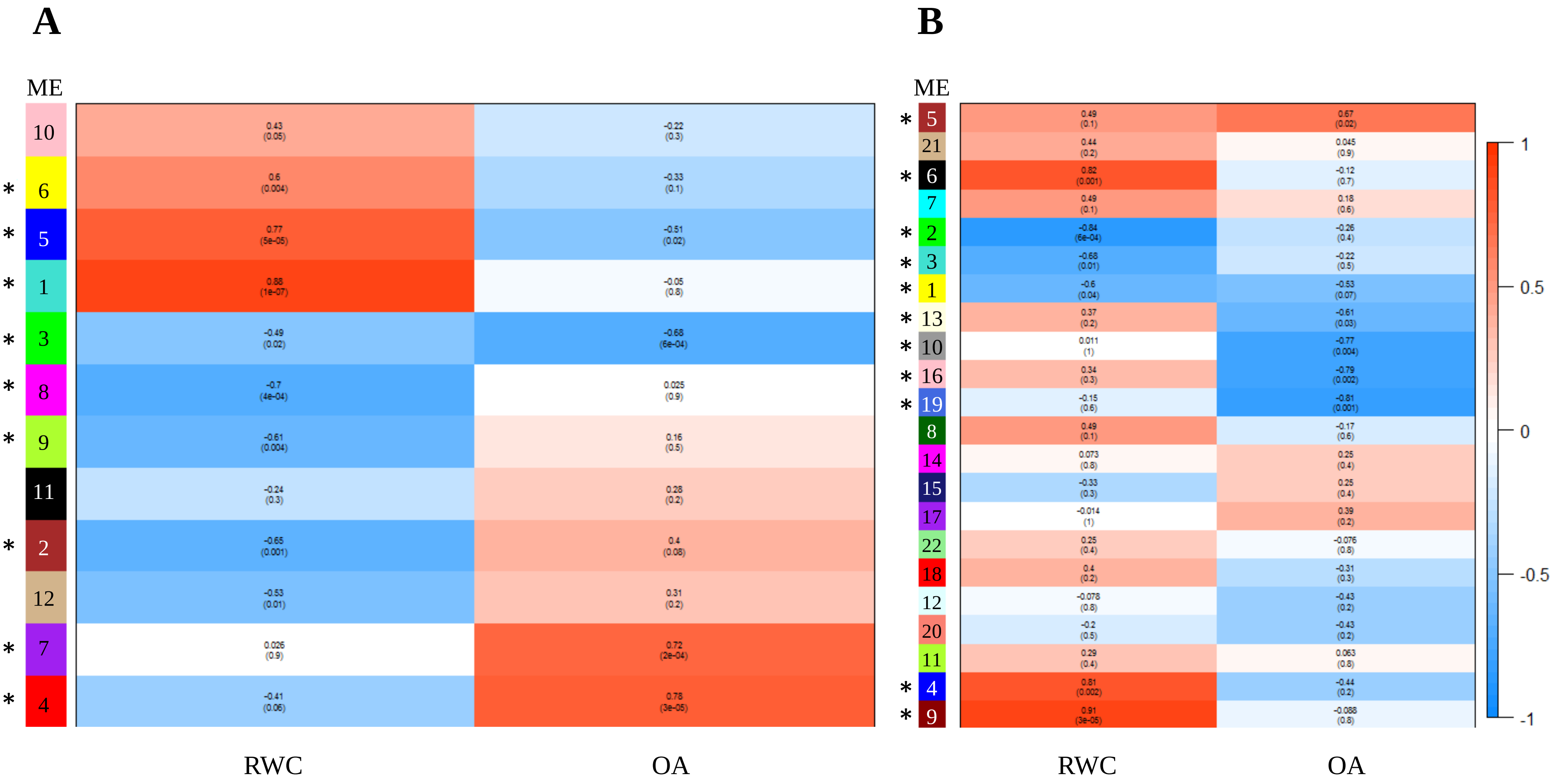
Supplemental Figure S7. Enriched biological pathways found among common stress- (outer) and combination unique-DEGs (inner).



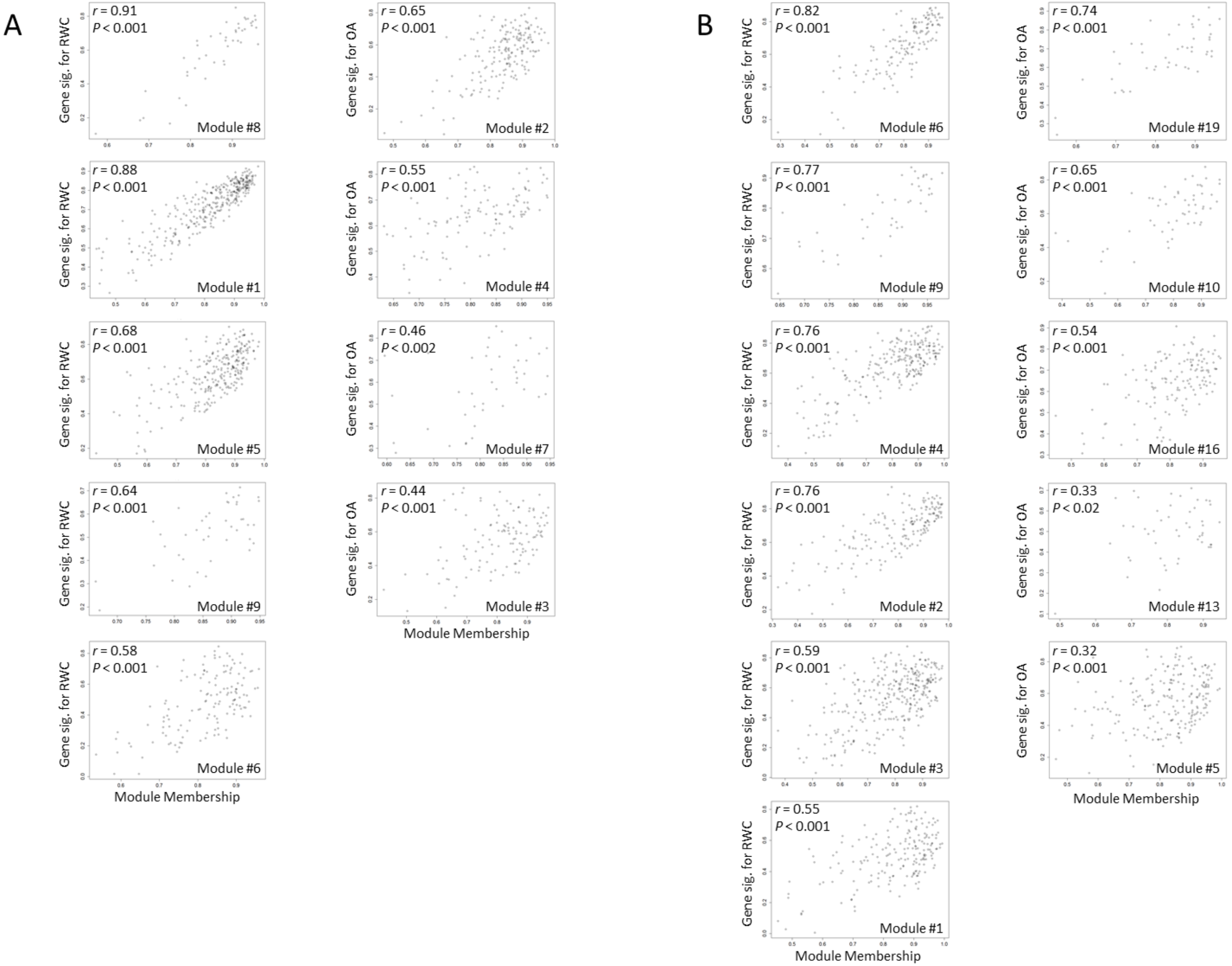
Supplemental Figure S8. Relationships among eigengenes of (**A**) common stress-modules (**B**) and stress combination unique-modules. The upper panel shows an hierarchical clustering dendrogram of module eigengenes (ME). Each module is indicated by numbers and colors. ME with low merging height are highly related. The lower panel shows a heat-map of eigengenes adjacency, in which red and blue color indicates high and low correlation among module eigengenes, respectively.



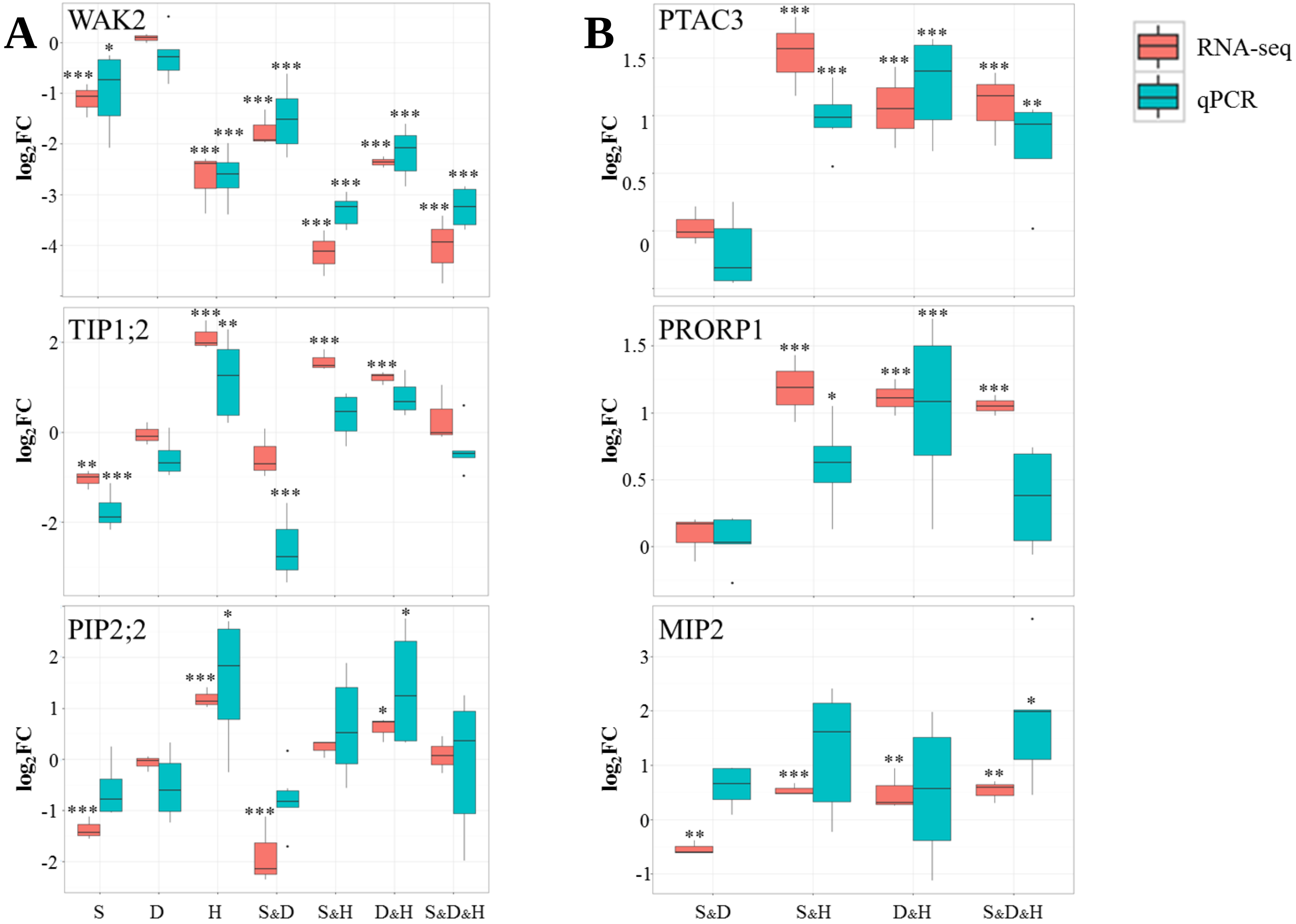
Supplemental Figure S9. Enriched response modes among (**A**) common stress-modules and (**B**) stress combination unique-modules detected by co-expression network analysis.



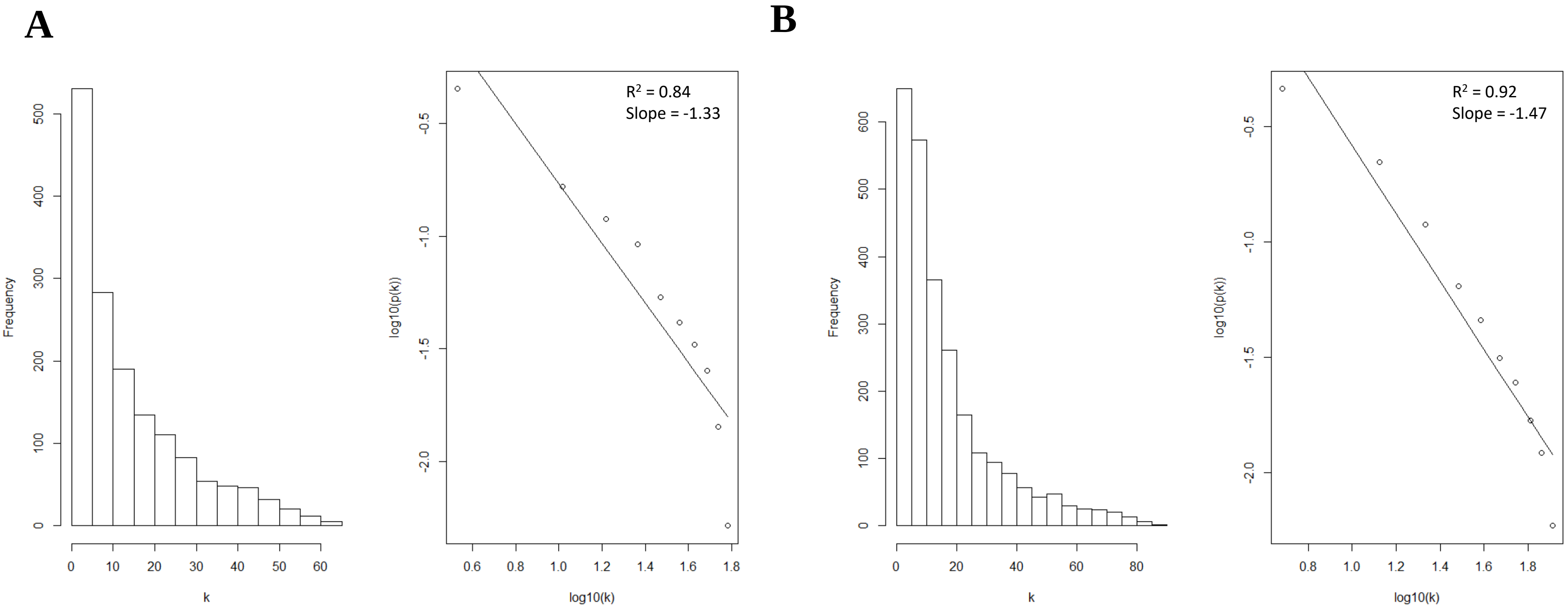
Supplemental Figure S10. Module-trait relationships among (**A**) common stress-modules and (**B**) stress combination unique-modules. Correlation between module eigengene (ME), which is defined as the first principal component of a given module and best represents module expression pattern, and leaf relative water content (RWC) or osmotic adjustment (OA). Red and blue colors indicate high and low correlation coefficient, respectively. Numbers in parenthesis indicate correlation coefficient. *P* values and asterisks indicate significant correlation ($r \geq |0.6|$, $P \leq 0.05$) between ME and leaf RWC or OA.



Supplemental Figure S11. Correlation between module membership *versus* gene significance among (**A**) common stress-modules and (**B**) stress combination unique-modules that were significantly correlated with leaf relative water content (RWC) or osmotic adjustment (OA). Module membership, which is the correlation of ME and gene expression profile, allows to quantify the similarity of all genes to each module. Gene significance is defined as the correlation of gene expression profile with the physiological traits. High correlation indicates that central genes, within these modules, may also be highly associated with RWC or OA.



Supplemental Figure S12. Relative expression of selected (**A**) common stress differentially expressed genes (DEGs) and (**B**) stress combination unique-DEGs based on RNA-seq analysis (red) and qPCR validation (blue). Wall-associated kinase 2-like (WAK2, BRADI3G49170); Tonoplast intrinsic protein 1;2 (TIP1;2, BRADI2G62520); Plasma membrane intrinsic protein 2;2 (PIP2;2, BRADI5G15970); Plastid transcriptionally active 3 (PTAC3, BRADI3G28060); Proteinaceous RNase P1 (PRORP1, BRADI5G27596); MAG2-interacting protein 2 (MIP2, BRADI4G33310). Statistical analysis was performed with one-way ANOVA followed by Dunnet's test ($P \leq 0.05$). Values are mean ± SE (n = 3 and 6 for RNA-seq analysis and qPCR validation, respectively). Significant differences are denoted with asterisks (*, $P \leq 0.05$; **, $P \leq 0.01$ and ***, $P \leq 0.001$). The perpendicular line within each box represents the median value and the ends of the box represent the 3rd and 1st quartile, respectively. Conditions are as follows: salinity (S), drought (D), heat (H), salinity and drought ($S_{\&}D$), salinity and heat ($S_{\&}H$), drought and heat ($D_{\&}H$), salinity, drought and heat ($S_{\&}D_{\&}H$).



Supplemental Figure S13. Evaluation of scale free topology of co-expression networks that were constructed based on (**A**) common stress differentially expressed genes (DEGs) and (**B**) stress combination unique-DEGs. The left panel displays a histogram of network connectivities using a soft thresholding power of 14 and 13, for networks of common stress-DEGs and stress combination unique-DEGs, respectively. The right panel displays a log-log plot of the same histogram. The high R^2 value indicates approximate scale free topology.