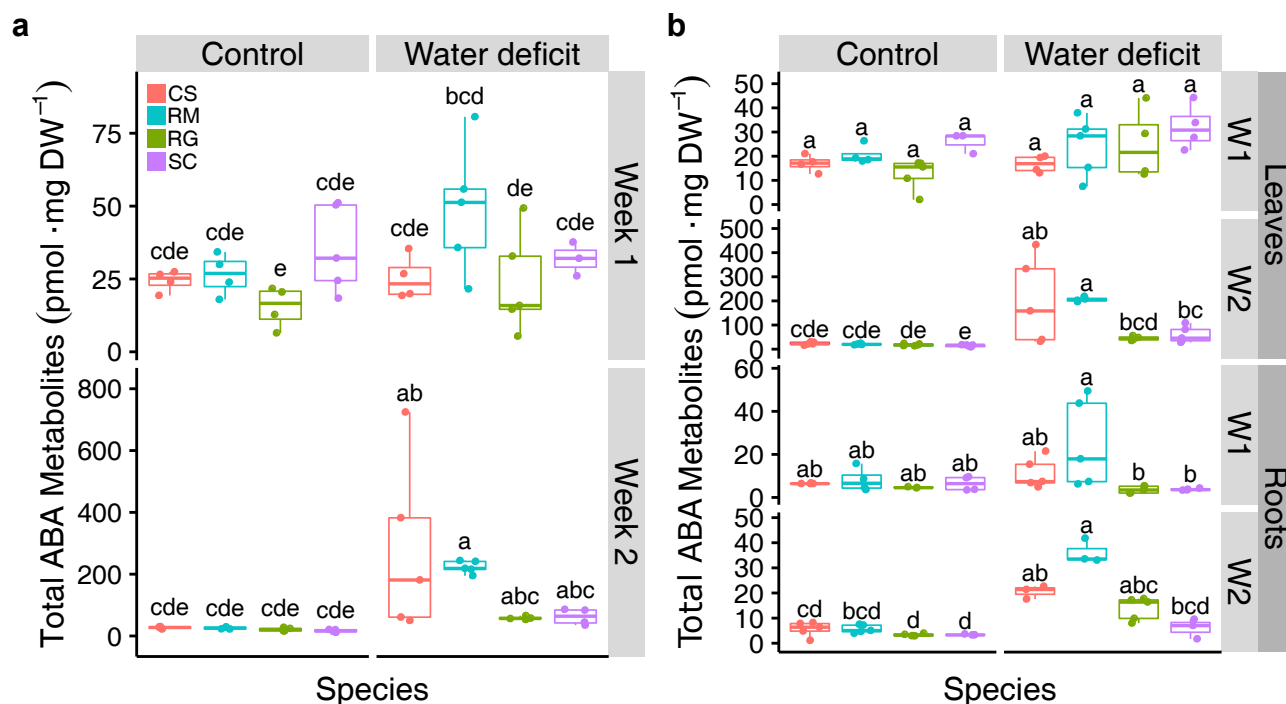
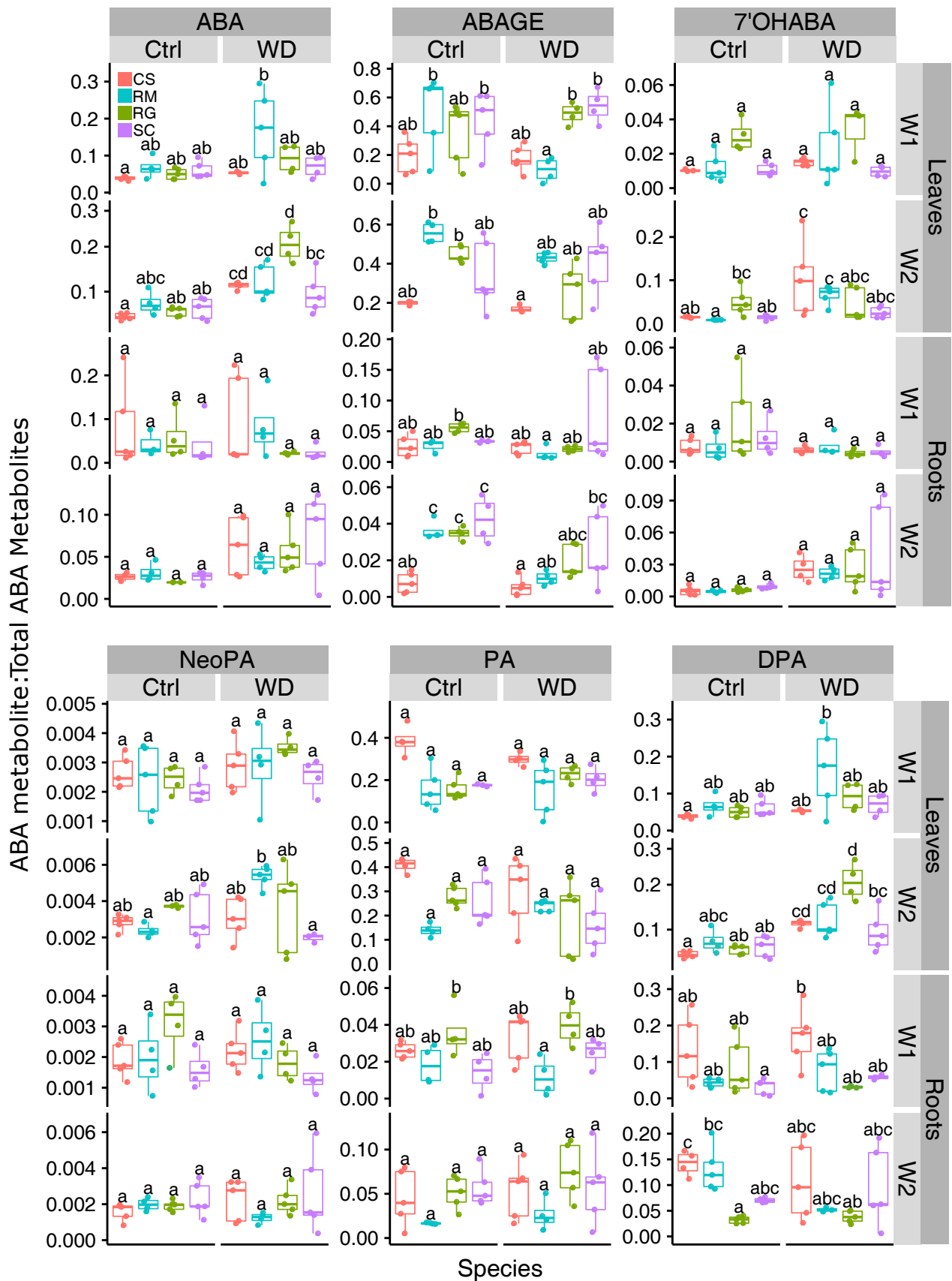


SUPPLEMENTARY FIGURES

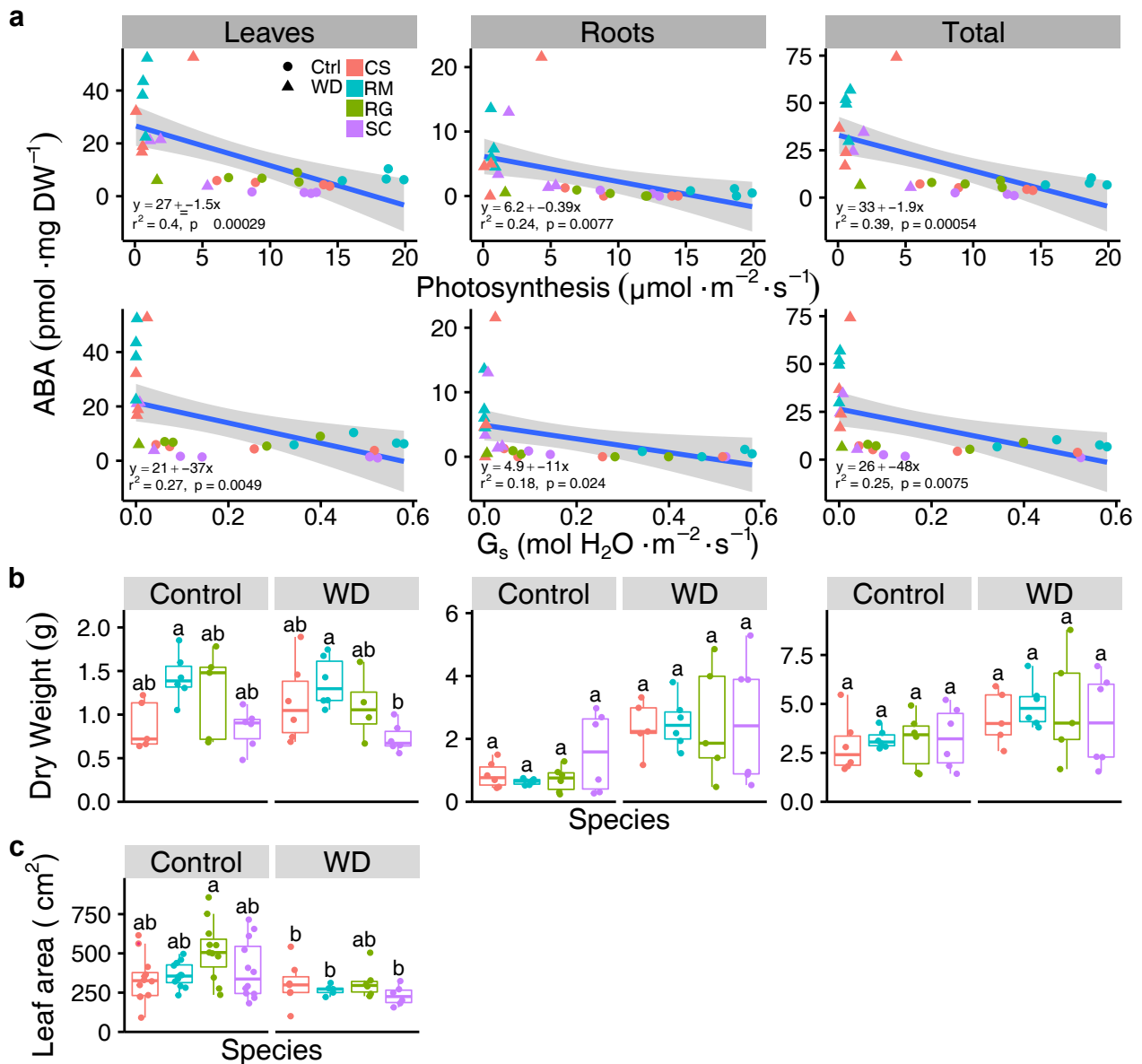
Toups, H., Cochetel, N., Deluc, L., & Cramer, G. (2022). Abscisic acid metabolism pathways differ between grapevine species, leaves, and roots during water deficit. *OENO One*, 56(4). Retrieved from <https://oeno-one.eu/article/view/5483>



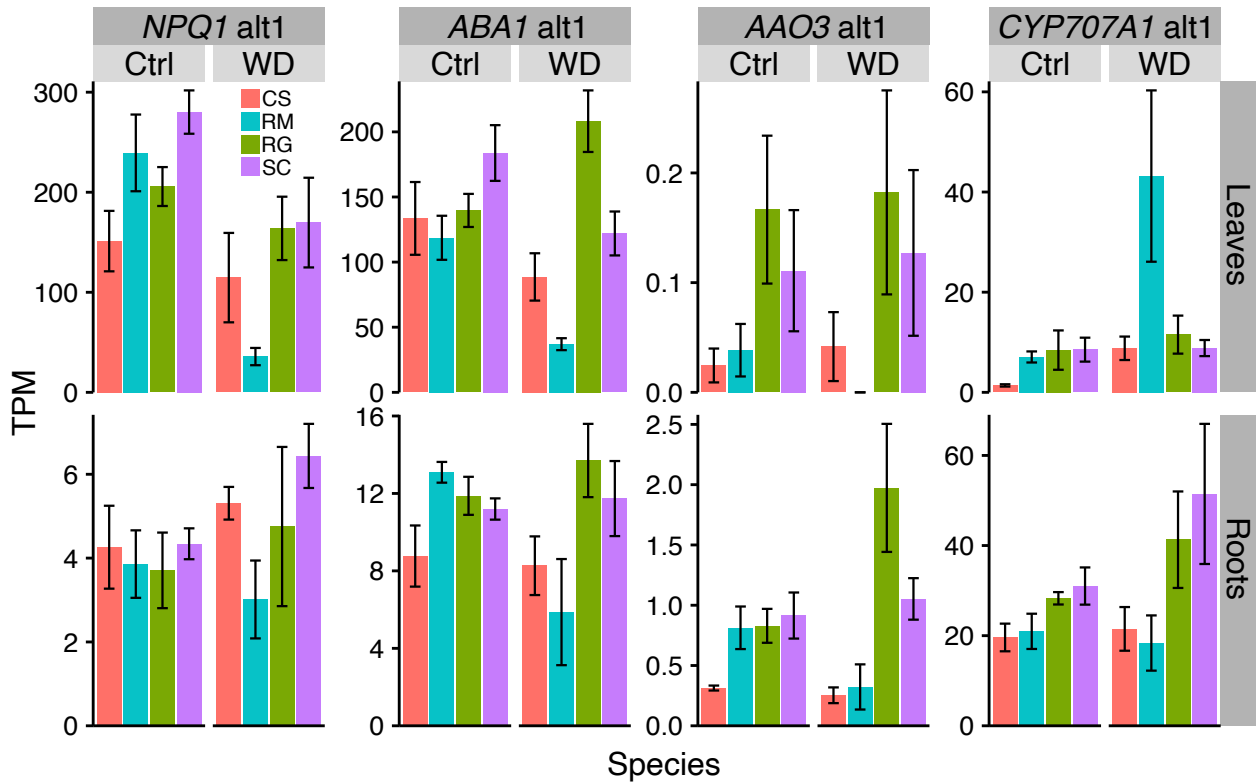
**Supplementary Figure 1: Summed total whole plant ABA metabolite concentration and summed total whole plant ABA metabolite concentration per organ after one- and two-weeks of moderate WD. a)** Combined ABA, ABA-GE, 7’OH ABA, NeoPA, PA, and DPA concentrations from both leaves and roots (Total ABA Metabolites (pmol·mg DW<sup>-1</sup>)) referred to as summed total of whole plant ABA metabolites after one- (top) and two-weeks (bottom) of Control (left) or WD (right) treatment. Three-way ANOVA Tukey’s HSD ( $p \leq 0.05$ ). **b)** Combined ABA, ABA-GE, 7’OH ABA, NeoPA, PA, and DPA concentrations (Total ABA Metabolites (pmol·mg DW<sup>-1</sup>)) for leaves (top) and roots (bottom) after one- (top) and two-weeks (bottom) of Control (left) or WD (right) treatment. Two-way ANOVA Tukey’s HSD ( $p \leq 0.05$ ) letters per organ per week. Pink, blue, green, and purple correspond to CS, RM, RG, and SC respectively. Each point represents an individual measurement.  $n =$  three-five individual vines.



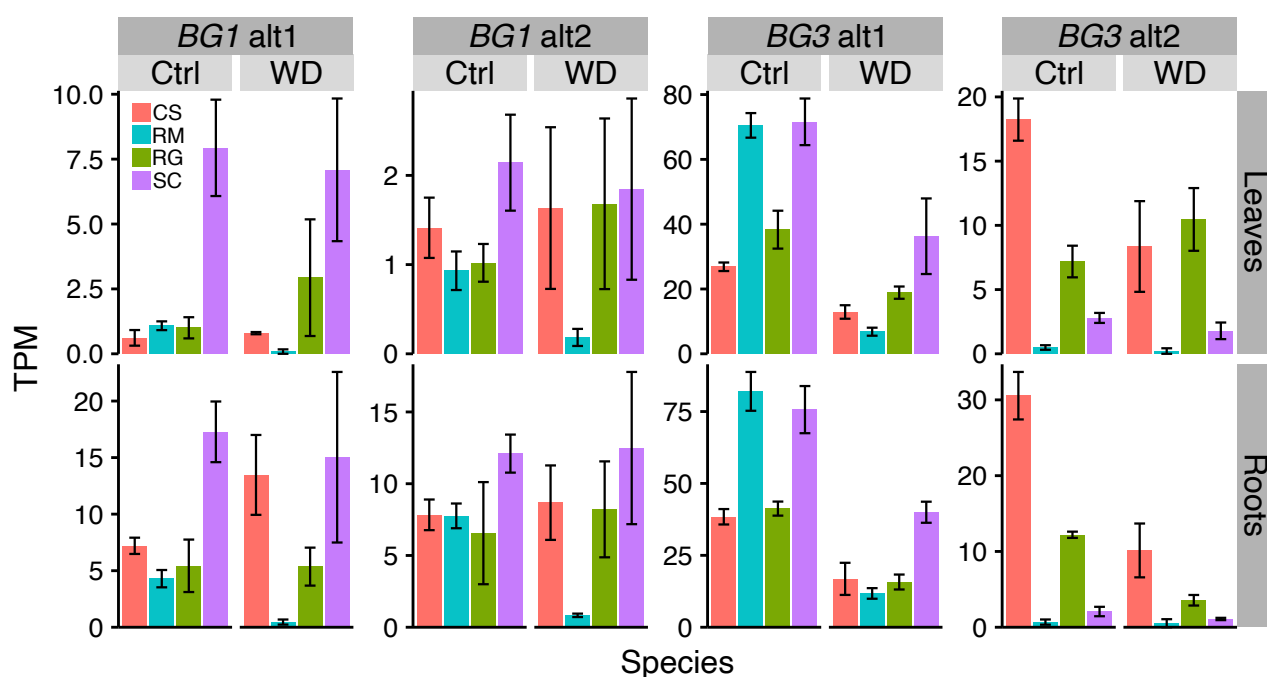
**Supplementary Figure 2: ABA metabolite distribution relative to total whole plant ABA metabolites per organ after one- and two-weeks of moderate WD.** ABA, ABAGE, 7'OH ABA (left to right top), NeoPA, PA, and DPA (left to right bottom) ratio relative to summed total of whole plant ABA metabolites in leaves (top) and roots (bottom) after one- and two-weeks of Control (Ctrl) or WD treatment. Two-way ANOVA Tukey's HSD ( $p \leq 0.05$ ) letters for each metabolite per organ per week. Pink, blue, green, and purple correspond to CS, RM, RG, and SC respectively. Each point represents an individual measurement.  $n =$  three-five individual vines.



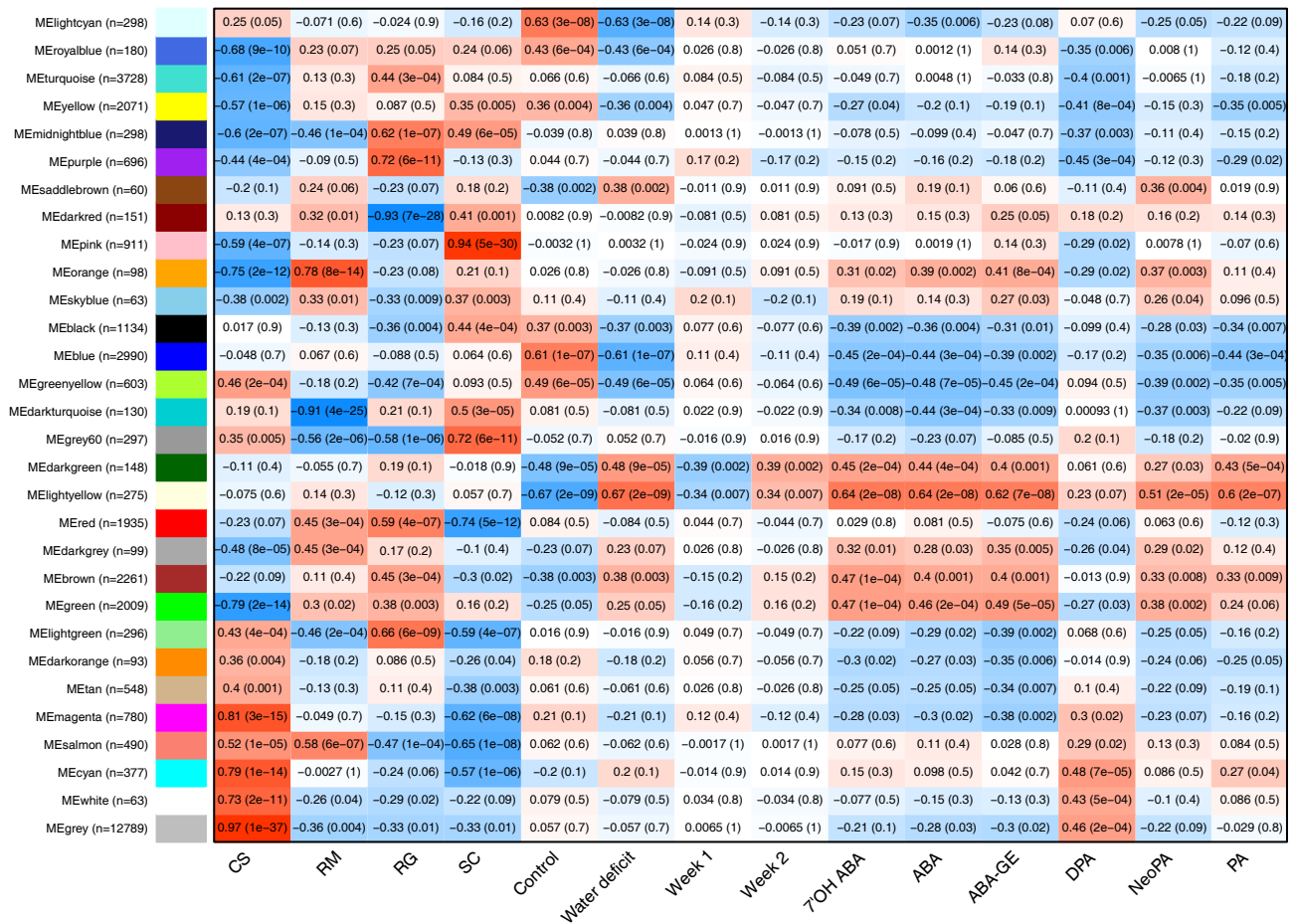
**Supplementary Figure 3: ABA concentrations related to photosynthesis (Ps) and stomatal conductance (Gs) for the severe WD experiment. a)** ABA concentration ( $\text{pmol} \cdot \text{mg DW}^{-1}$ ) in leaves (left), roots (middle), and total (combined leaves and roots (right)) related to Ps ( $\mu\text{mol} \cdot \text{m}^{-2} \cdot \text{s}^{-1}$ ) (top) and Gs ( $\text{mol H}_2\text{O} \cdot \text{m}^{-2} \cdot \text{s}^{-1}$ ) (bottom) for the severe WD experiment. WD treated samples are shown as triangles and control (Ctrl) treated samples are represented by circles. Linear regression was performed per organ for each correlation; resulting equation,  $r^2$ , and p-value are shown. **b)** Dry weight (g) of in leaves (left), roots (middle), and total (combined leaves and roots (right)) for the severe WD experiment. Control (Ctrl) samples on the left and WD samples on the right. **c)** Leaf area ( $\text{cm}^2$ ) of the four species for the severe WD experiment. Control (Ctrl) samples on the left and WD samples on the right. Two-way ANOVA Tukey's HSD ( $p \leq 0.05$ ) letters per organ for **b)** and **c)**. Pink, blue, green, and purple correspond to CS, RM, RG, and SC, respectively. Each point represents an individual vine.  $n \geq 1$  individual vines per organ x treatment combination.



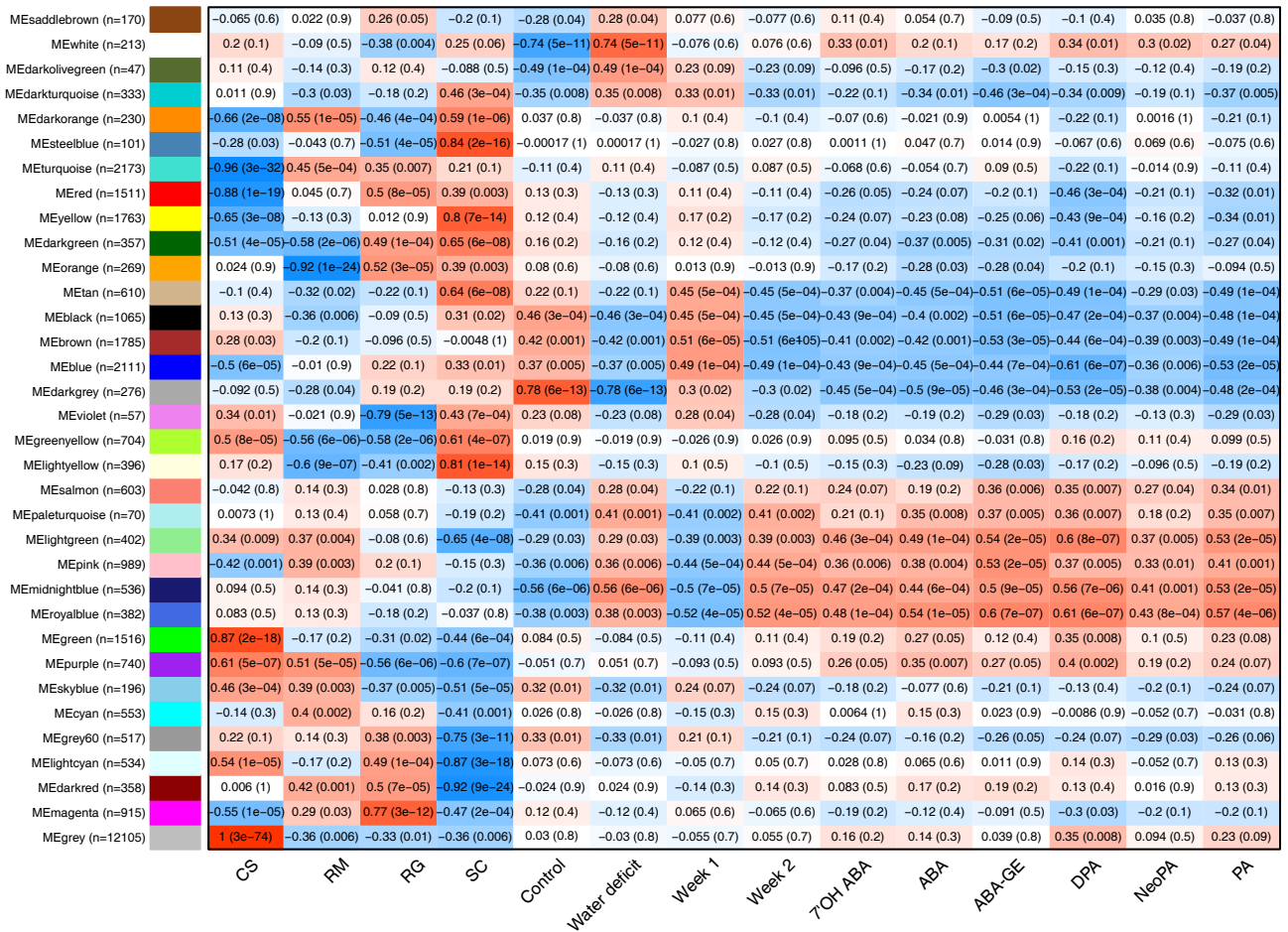
**Supplementary Figure 4: Differentially expressed ABA metabolism genes in RM WD W2 leaves and roots.** *NPQ1 alt1*, *ABA1 alt1*, *AAO3 alt1*, and *CYP707A1 alt1* (left to right) expression represented as TPM after two-weeks of Control (Ctrl) (left) or WD (right) treatment in leaves (top) and roots (bottom). Pink, blue, green, and purple correspond to CS, RM, RG, and SC respectively. Mean  $\pm$  SE, n = three-five individual vines.



**Supplementary Figure 5: *BG1* and *BG3* transcript abundance after one- and two-weeks of moderate WD.** *BG1* alt1 and alt2 and *BG3* alt1 and alt2 (left to right) expression represented as TPM after two-weeks of Control (Ctrl) (left) or WD (right) treatment in leaves (top) and roots (bottom). Pink, blue, green, and purple correspond to CS, RM, RG, and SC respectively. Mean  $\pm$  SE, n = three-five individual vines.



**Supplementary Figure 6: WGCNA of the leaves.** Heatmap representation of the association of modules and experimental conditions for the leaf samples. Experimental conditions, species, and ABA-related metabolites are listed in columns and modules in rows. Module eigengene Pearson's correlation coefficient and p-value (in parenthesis) are listed for each module per each experimental condition. Cell colors range from high positive correlation (red) to negative correlation (blue). The number of genes in each module is represented by n in parenthesis after the module name.



**Supplementary Figure 7: WGCNA of the roots.** Heatmap representation of the association of modules and experimental conditions for the root samples. Experimental conditions, species, and ABA-related metabolites are listed in columns and modules in rows. Module eigengene Pearson's correlation coefficient and p-value (in parenthesis) are listed for each module per each experimental condition. Cell colors range from high positive correlation (red) to negative correlation (blue). The number of genes in each module is represented by n in parenthesis after the module name.