

# Metabolomic Profiling Reveals Synchronized Accumulation of Biomass and Bioactive Flavonoids During In Vitro Development of *Anoectochilus roxburghii*

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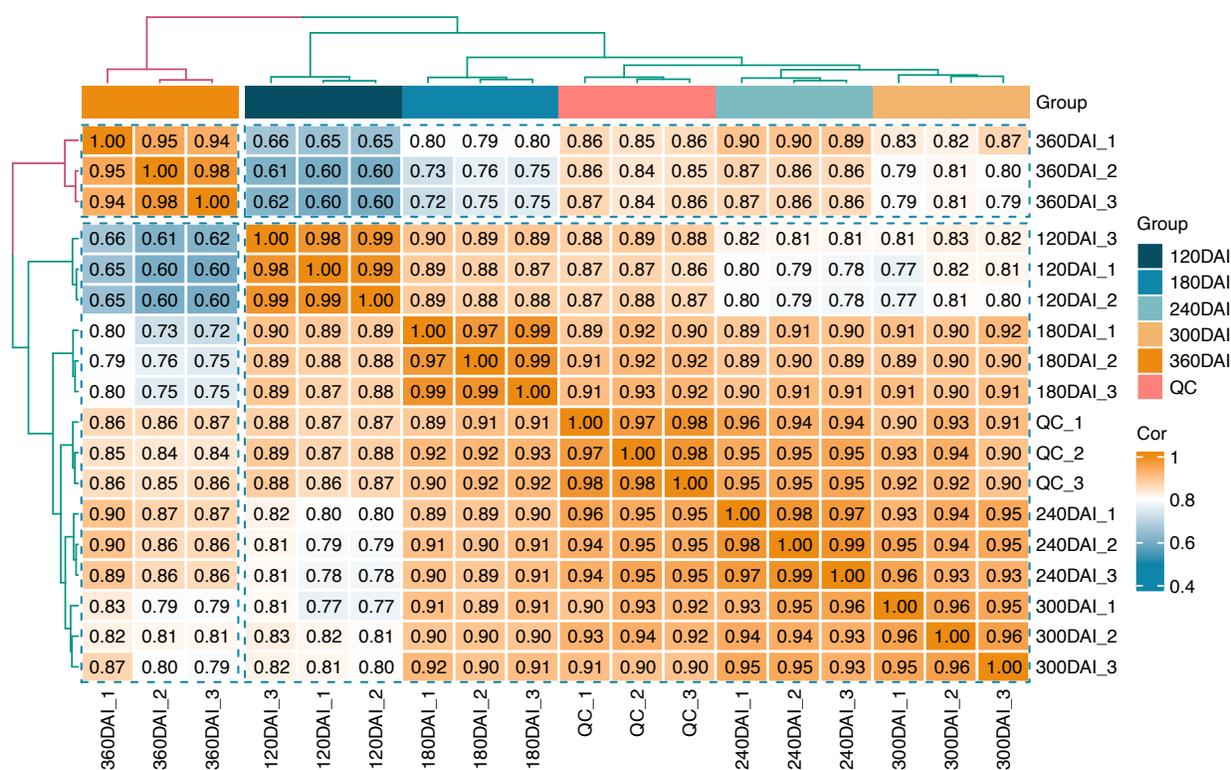
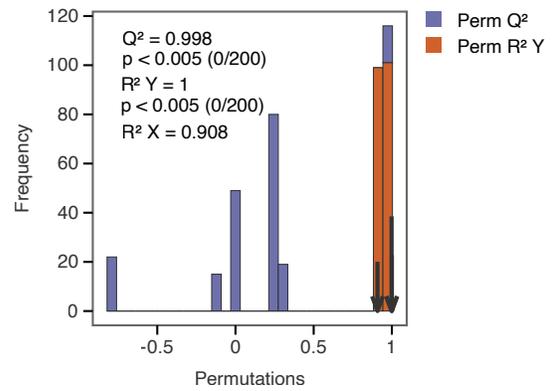
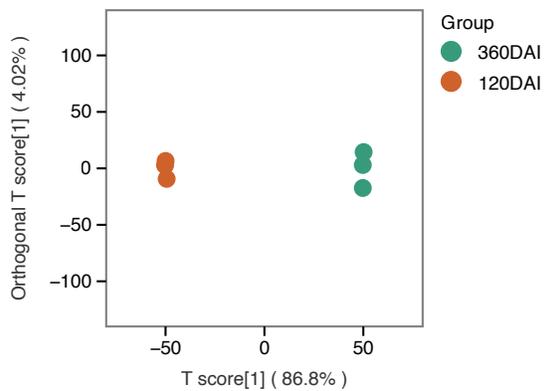
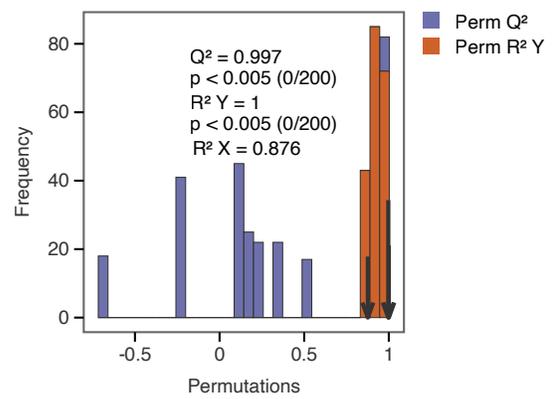
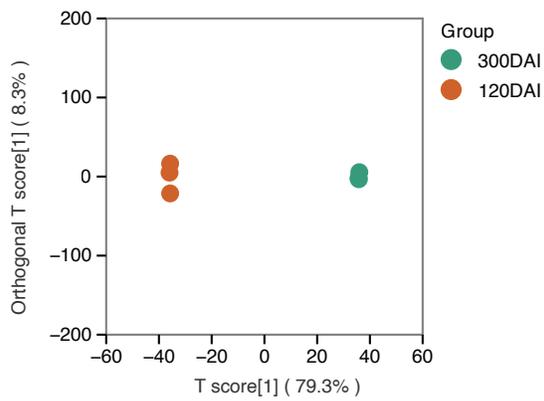
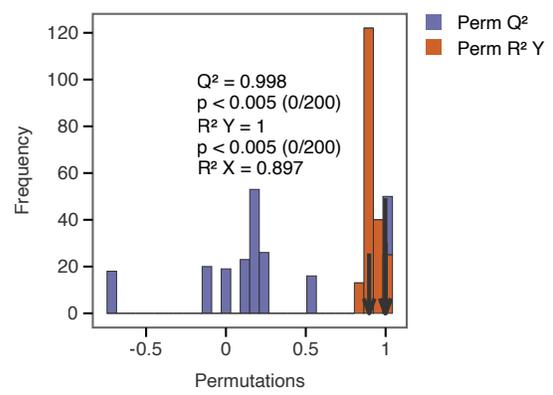
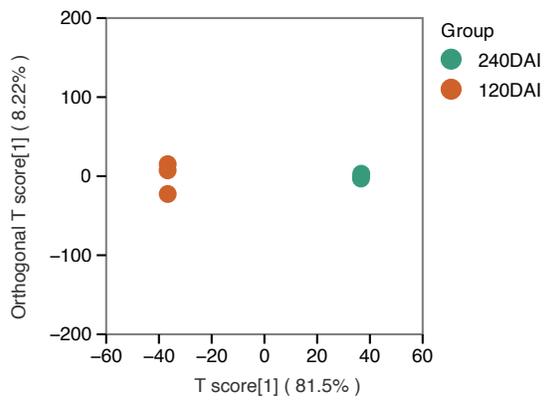
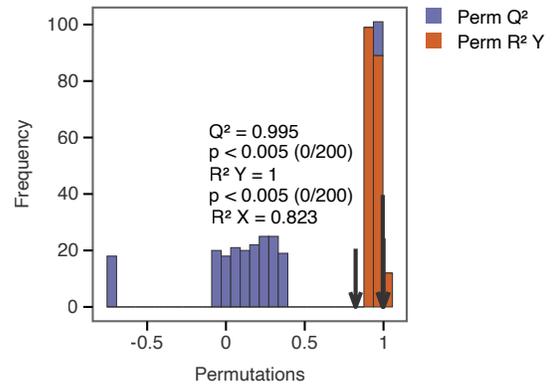
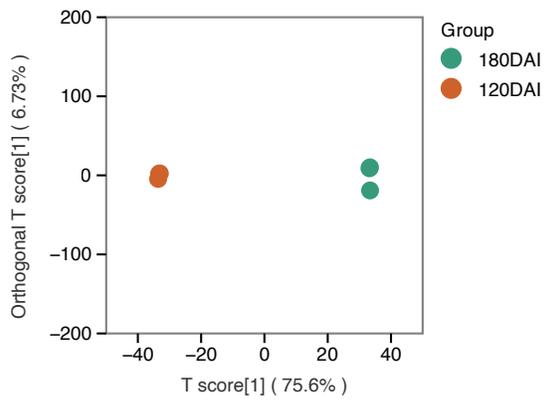
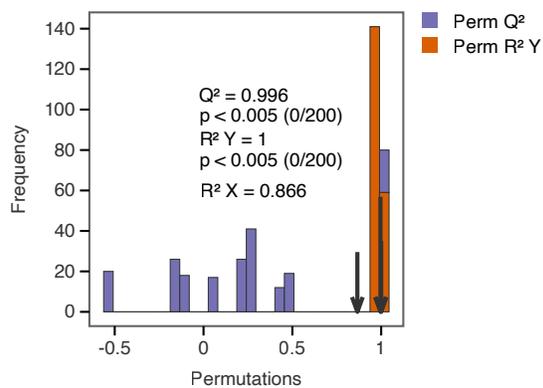
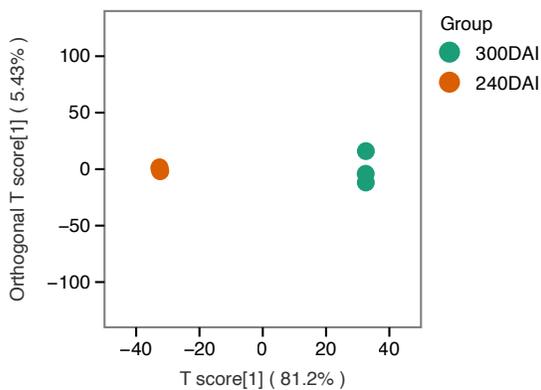
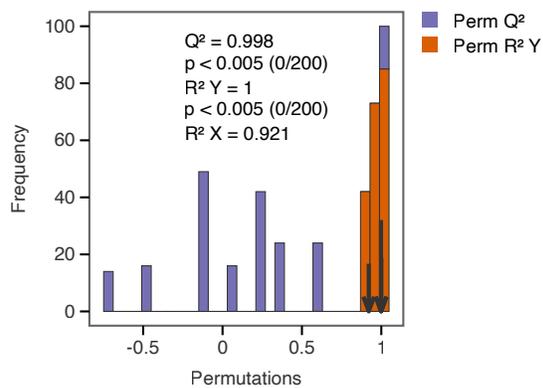
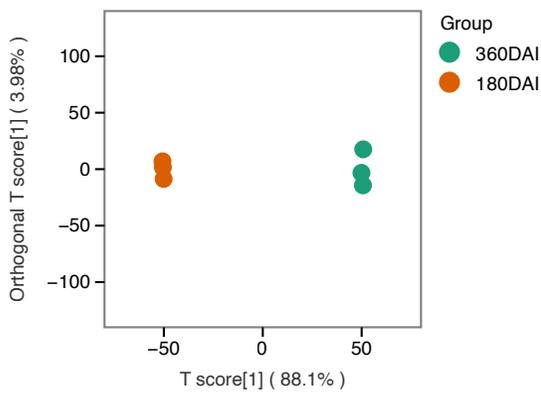
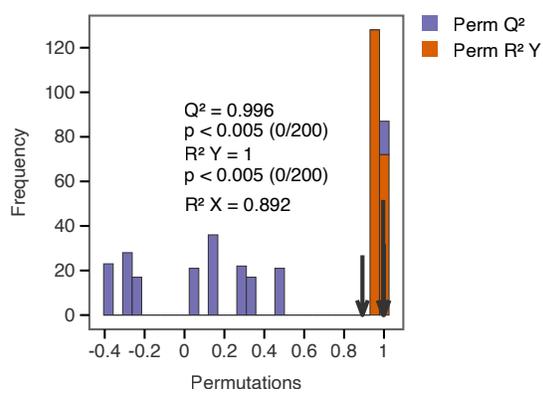
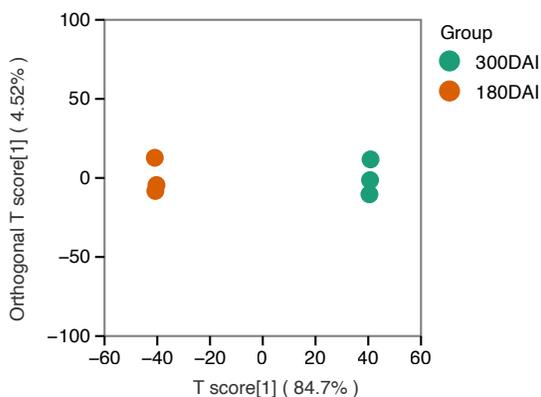
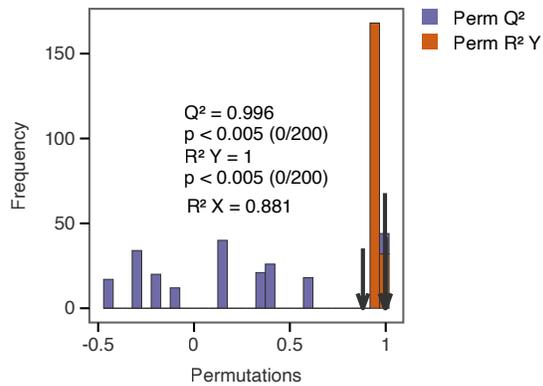
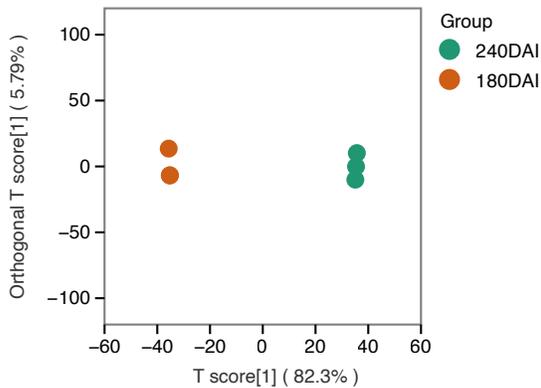


Figure S1: Pearson correlation analysis of samples across different stages.





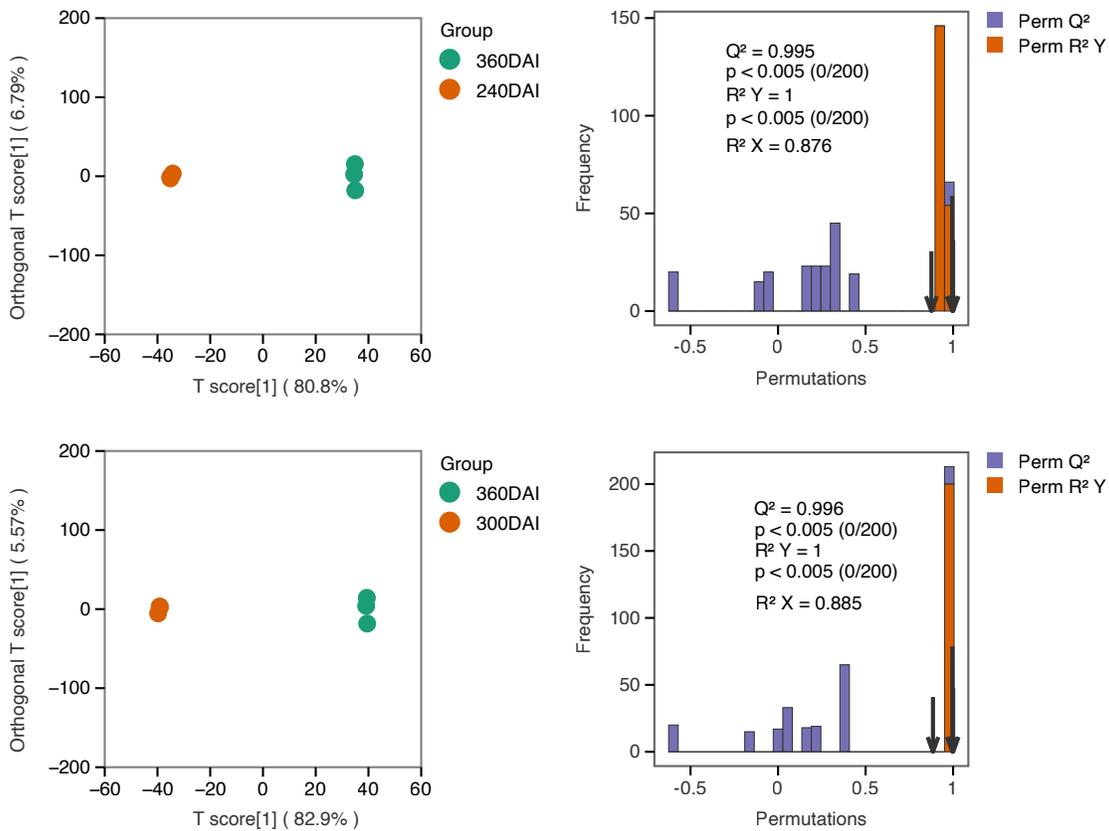


Figure S2: The score plots of OPLS-DA pairwise comparisons of differential metabolites and corresponding model validation.  $R^2 X$  and  $R^2 Y$  represent the explanatory power of the model for the X and Y matrices, respectively, while  $Q^2$  reflects the model's predictive ability. The closer these three indicators are to 1, the more stable and reliable the model is. A  $Q^2$  value greater than 0.5 indicates a valid model, and a  $Q^2$  value greater than 0.9 indicates an excellent model.

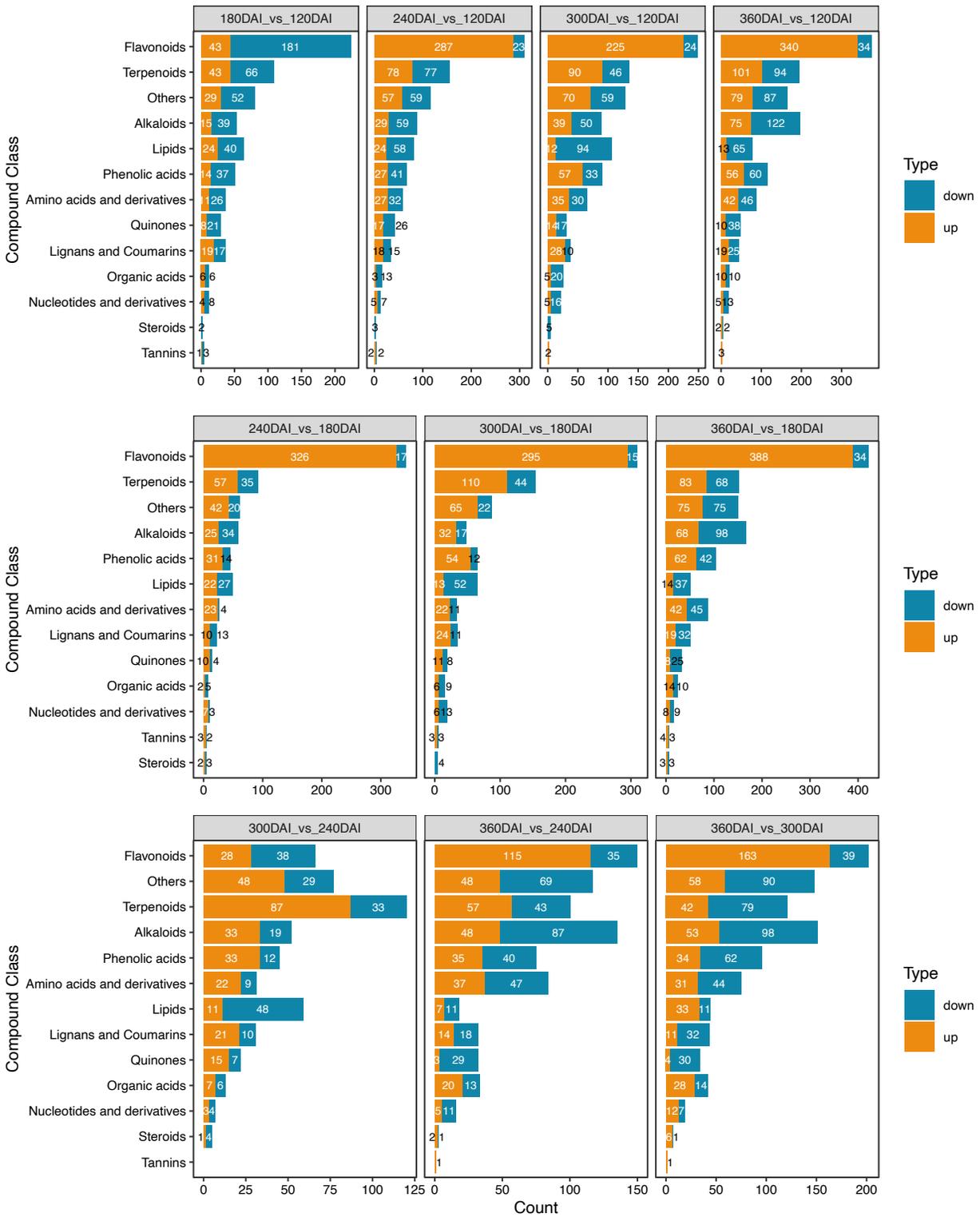


Figure S3: Statistical classification of DAMs across multiple comparison groups.

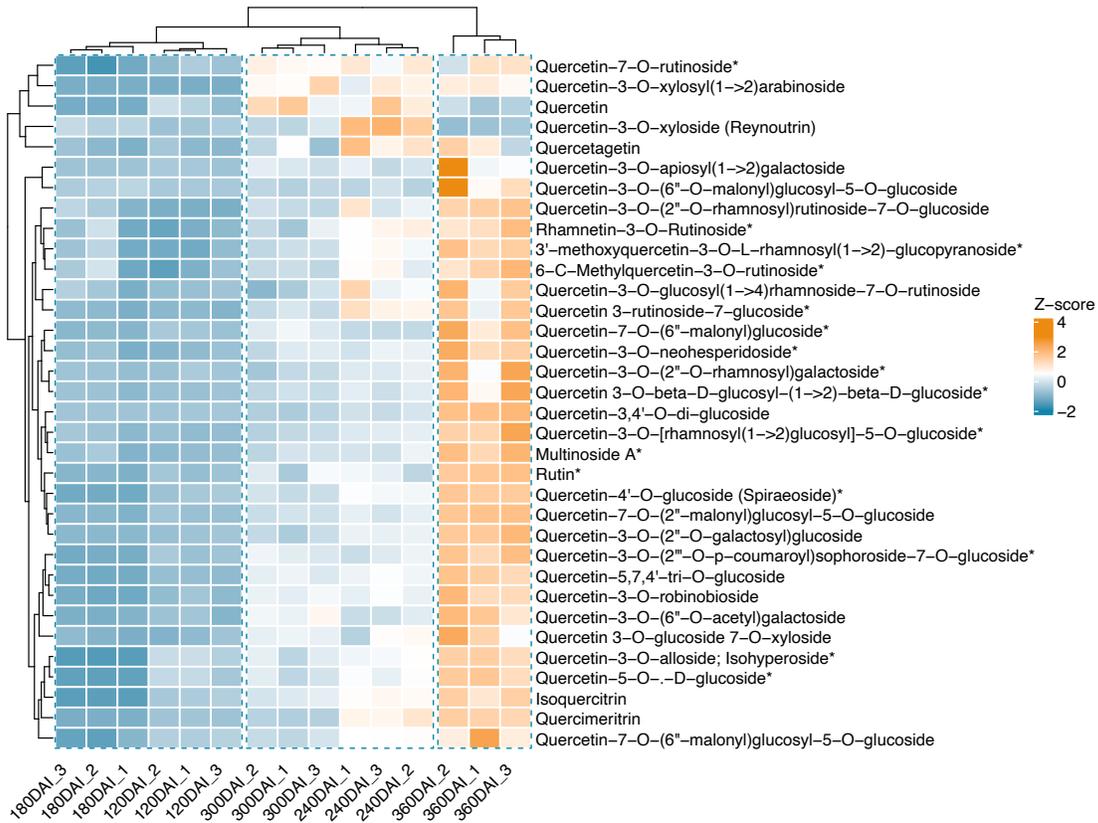


Figure S4: DAMs enriched in biosynthesis of quercetin aglycones I and II pathways across five stages. The color scale represents the Z-score normalized expression values by row. Columns are sorted by the average of the columns.

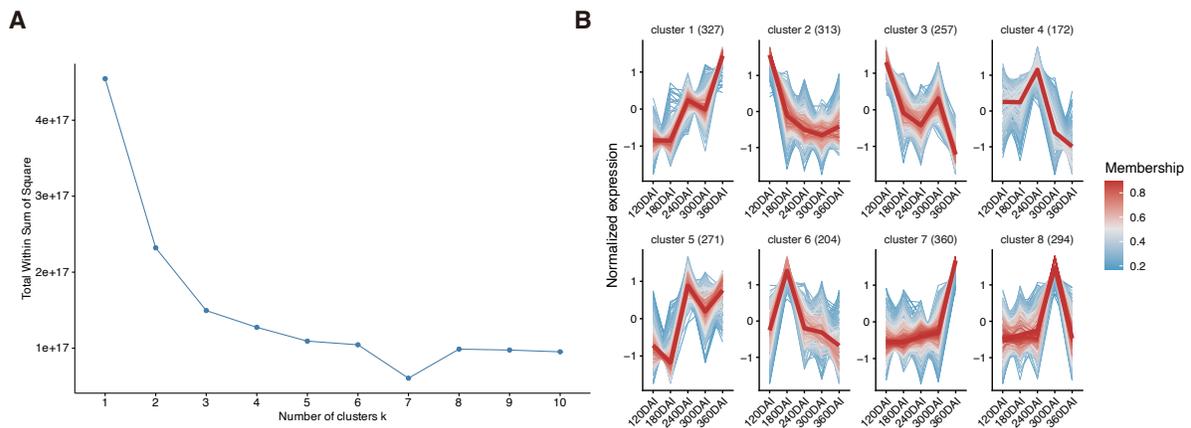


Figure S5: Mfuzz clustering Analysis. (A) The total within sum square value for different cluster numbers. (B) Mfuzz clustering and expression trend analysis of metabolites. This figure illustrates the grouping of metabolites based on their temporal accumulation patterns across five stages (120 DAI to 360 DAI).

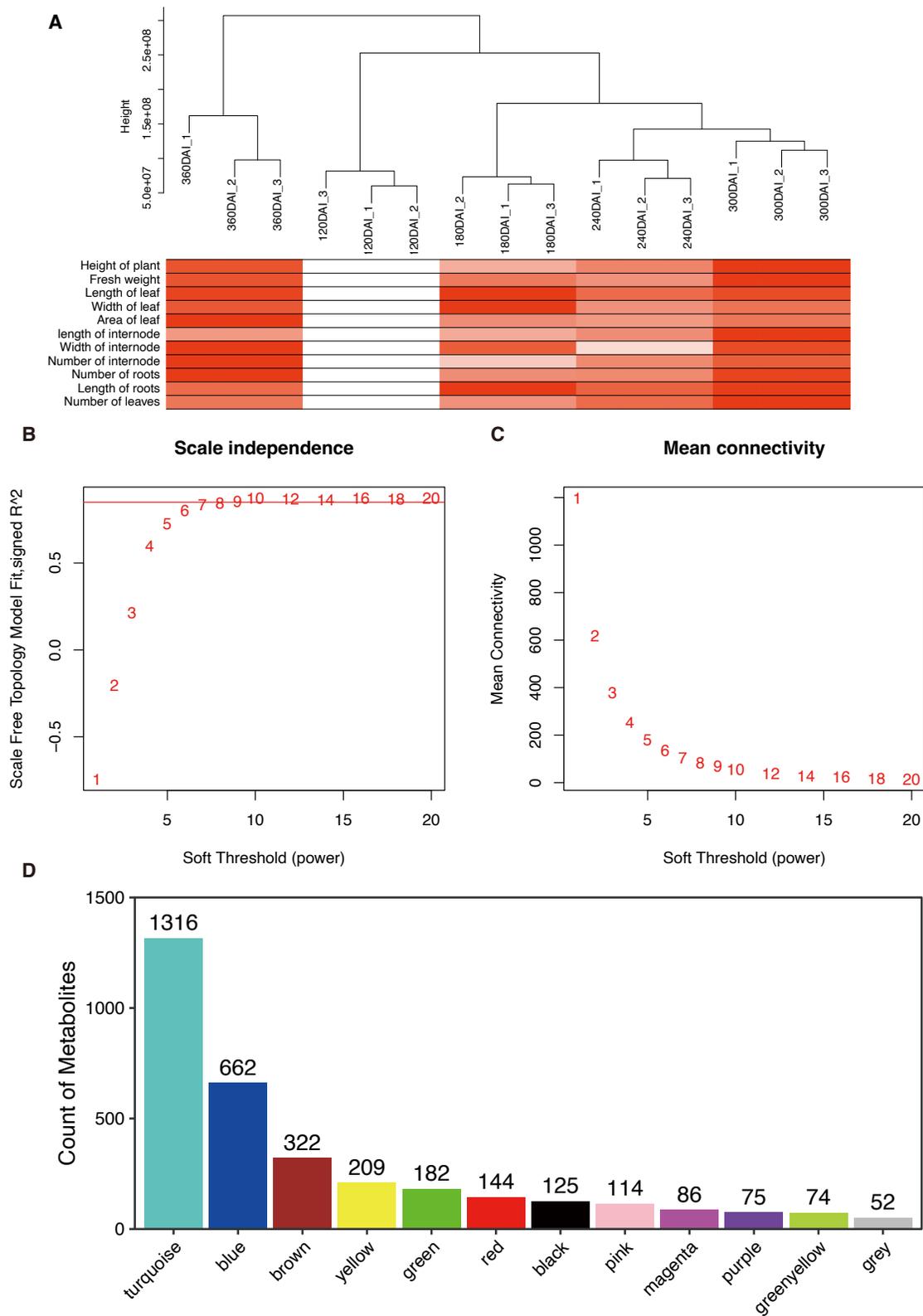


Figure S6: WGCNA analysis of all metabolites. (A) Clustering dendrogram of samples and heatmap of phenotypic traits. The color intensity in the heatmap represents the standardized values of each trait. (B) Scale independence of soft threshold. (C) Mean connectivity of soft threshold. (D) The count of metabolites of different modules.

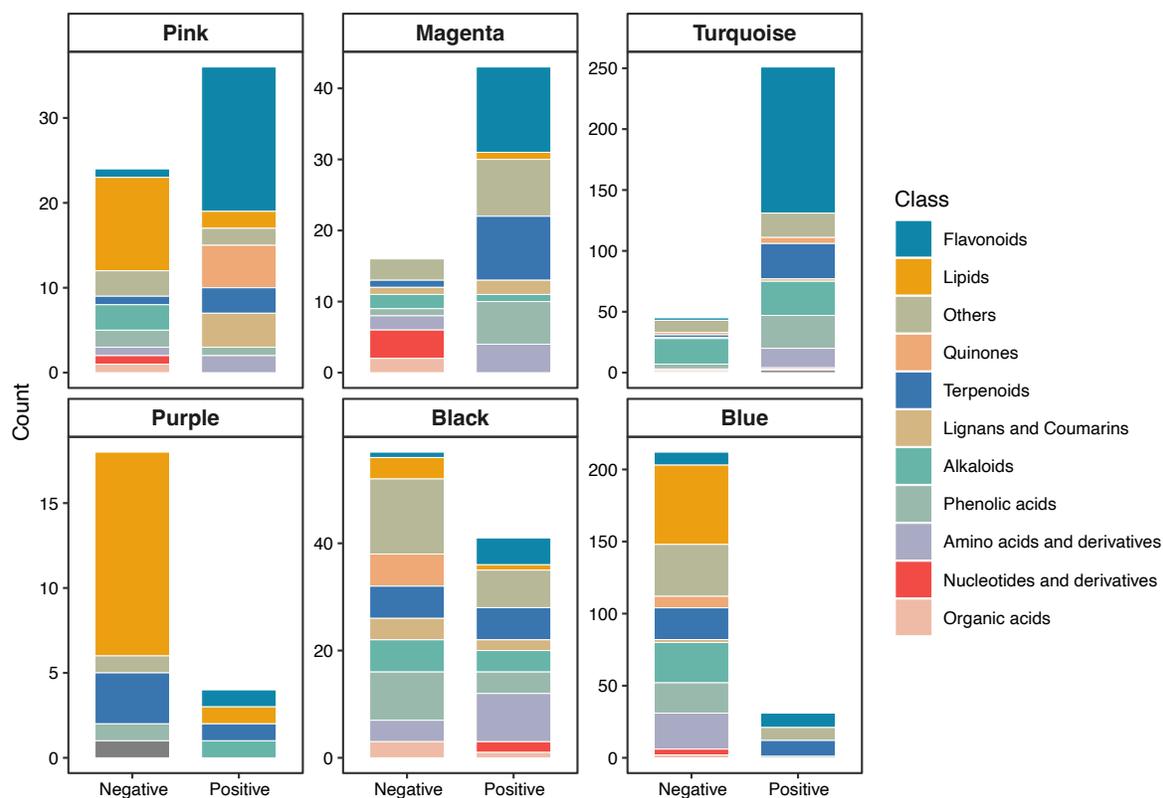


Figure S7: Classification of metabolites within specific correlation modules. Positive/Negative shows the count of metabolite classes that are positively or negatively correlated with the module's eigengene or associated trait.

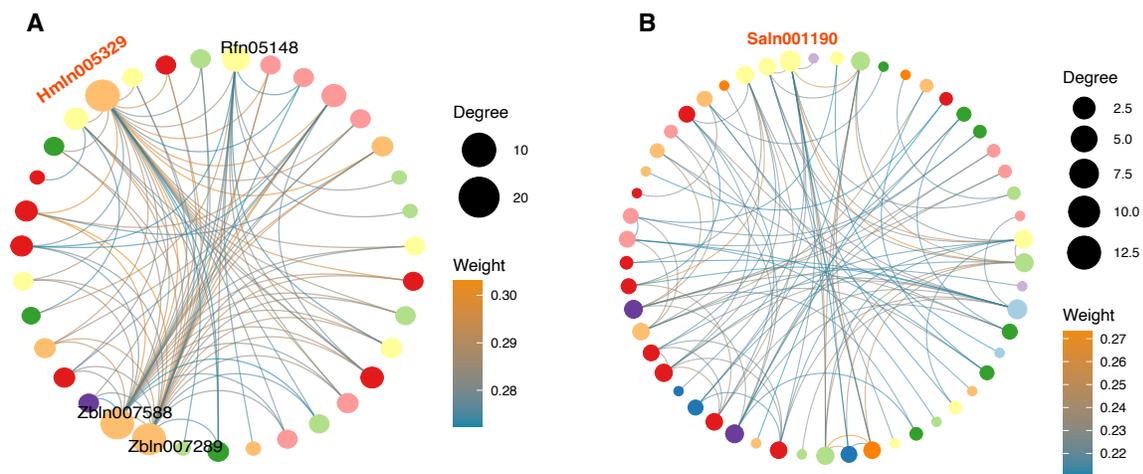
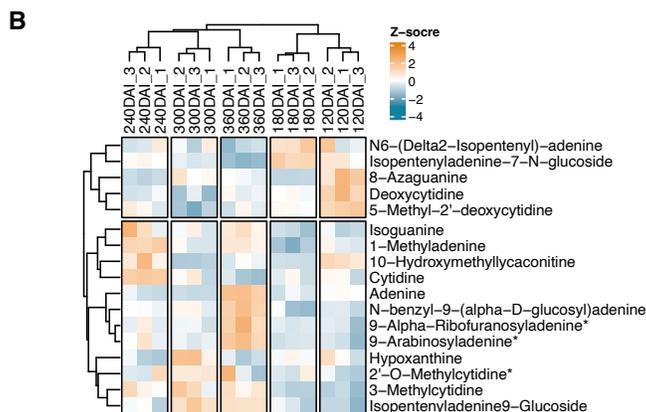
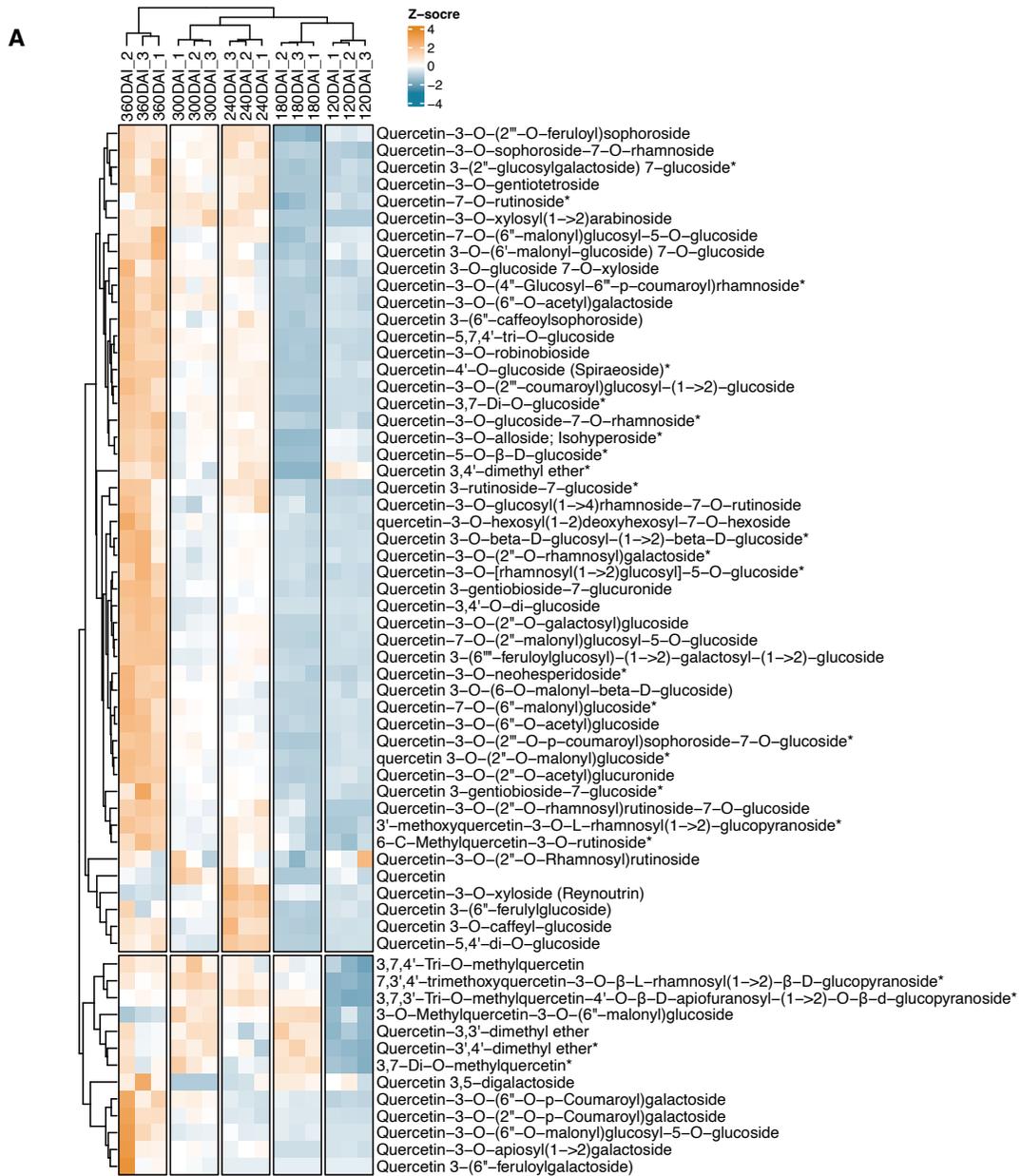
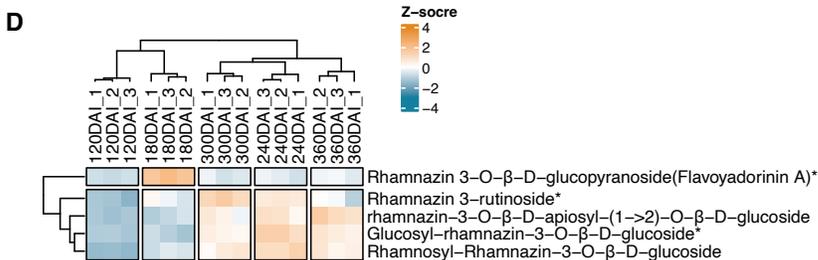
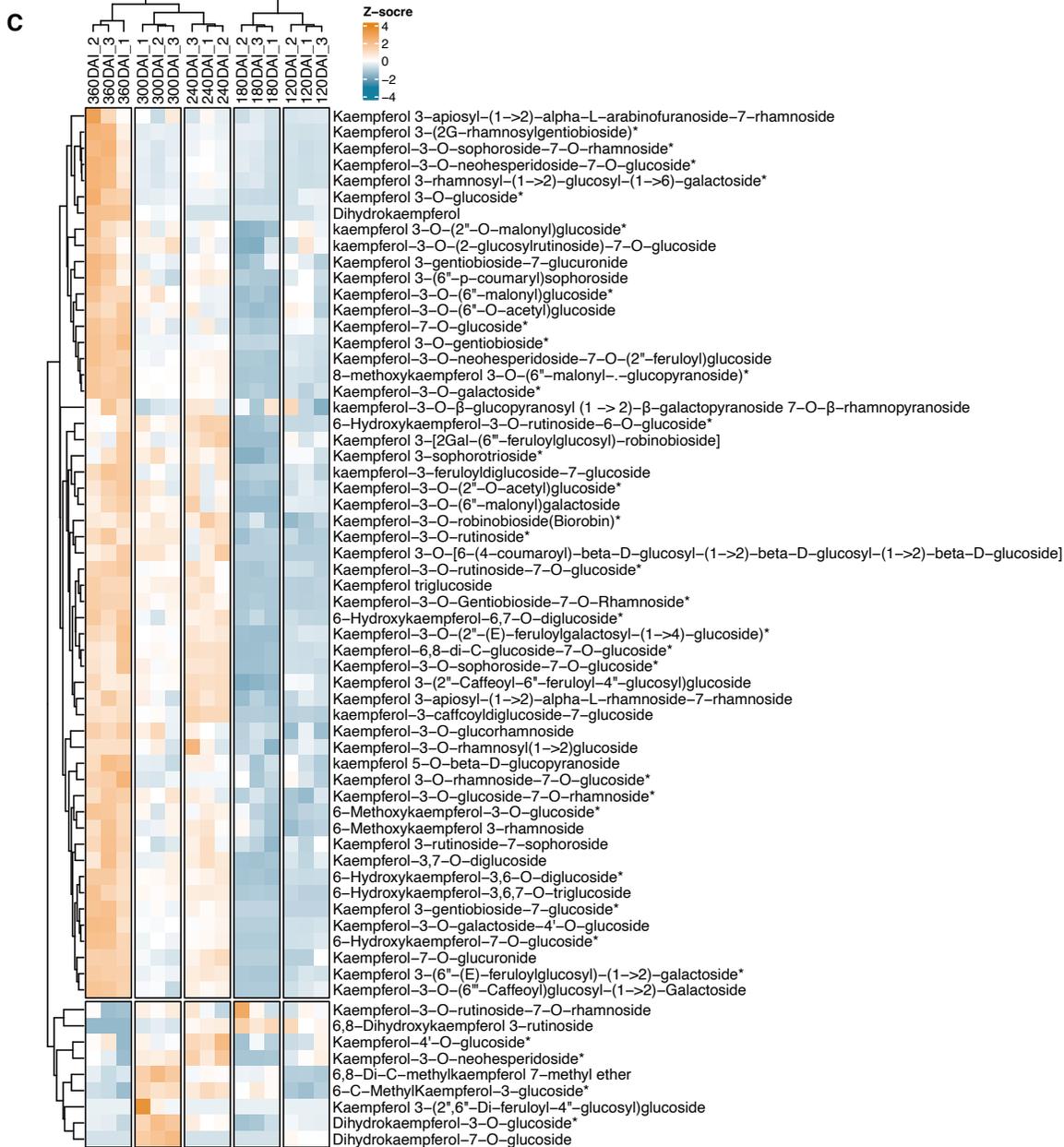


Figure S8: (A) Turquoise and (B) purple modules





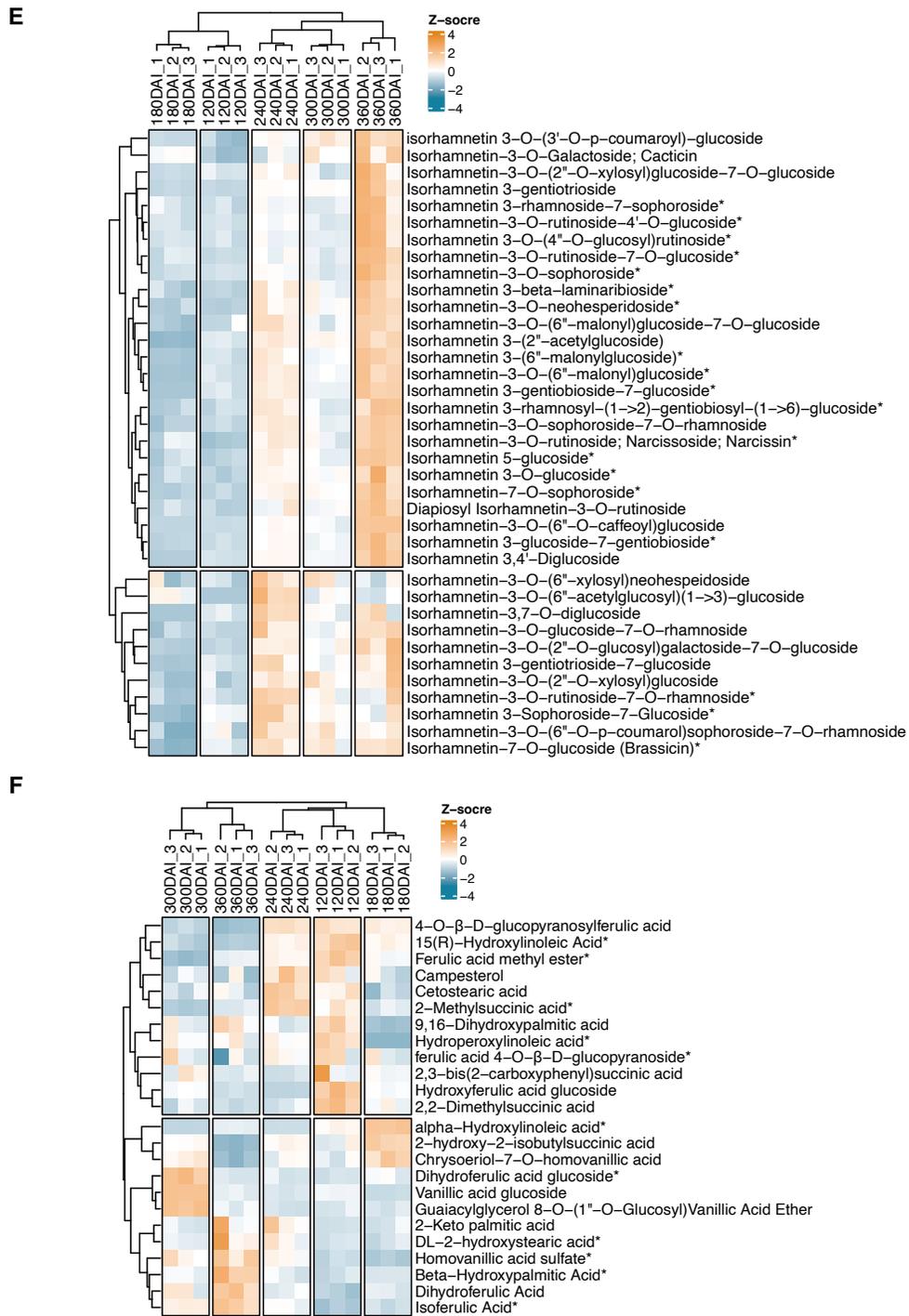


Figure S9: Heatmap of flavonoid glycosides, organic acids and volatile compounds, and steroids based on Z-score normalization across five stages. (A) Quercetin, (B) steroids, (C) kaempferol, (D) rhamnazin, (E) isorhamnetin, and (F) organic acids and volatile compounds.