Integrated Transcriptome and Metabolome Analysis Revealed Primary bud Necrosis in 'Summer Black' Grape

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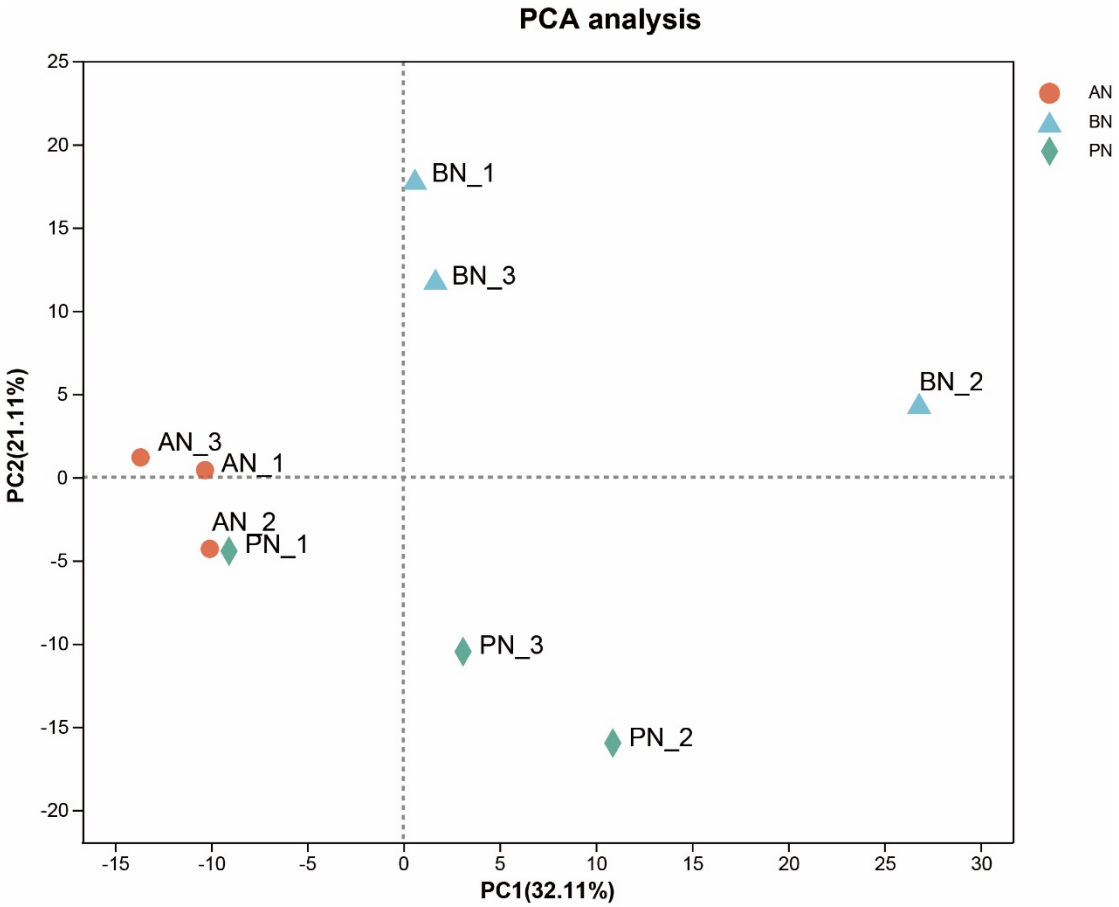
Supplementary Figures



Figures S1. Principal component analysis of transcriptome data.

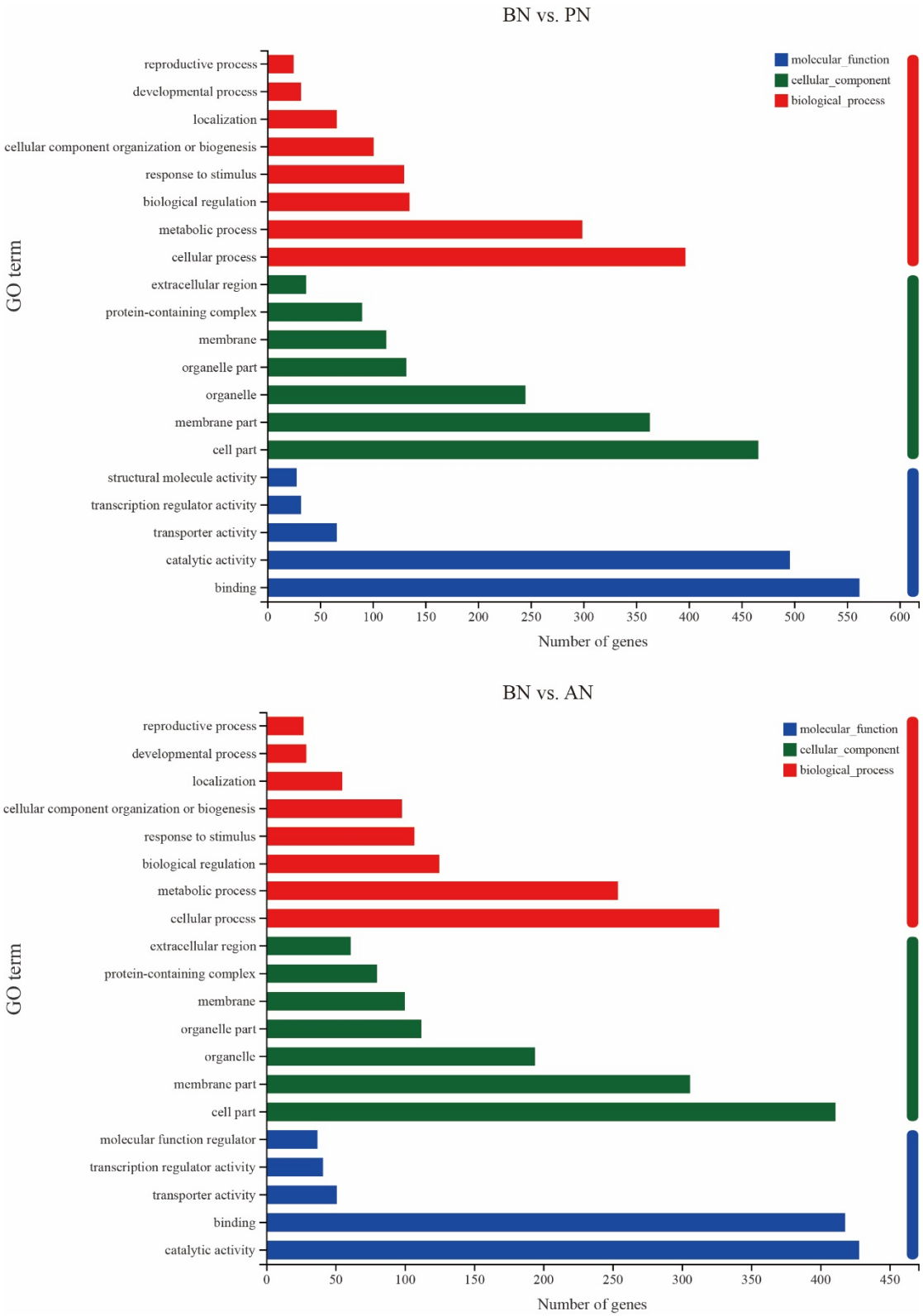


Figure S2. The DEGs gene ontology functional classification

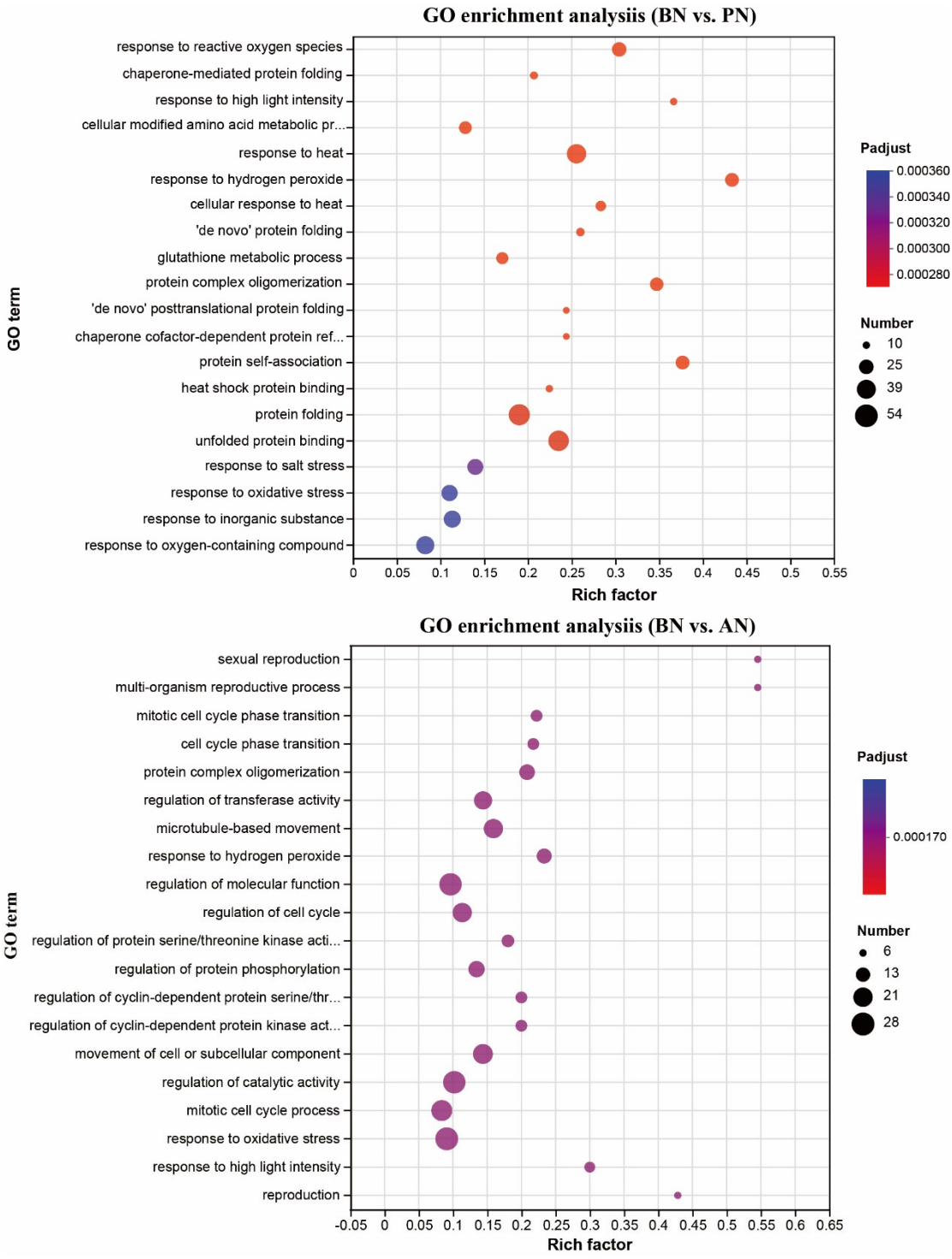


Figure S3. Go enrich analysis of DEGs

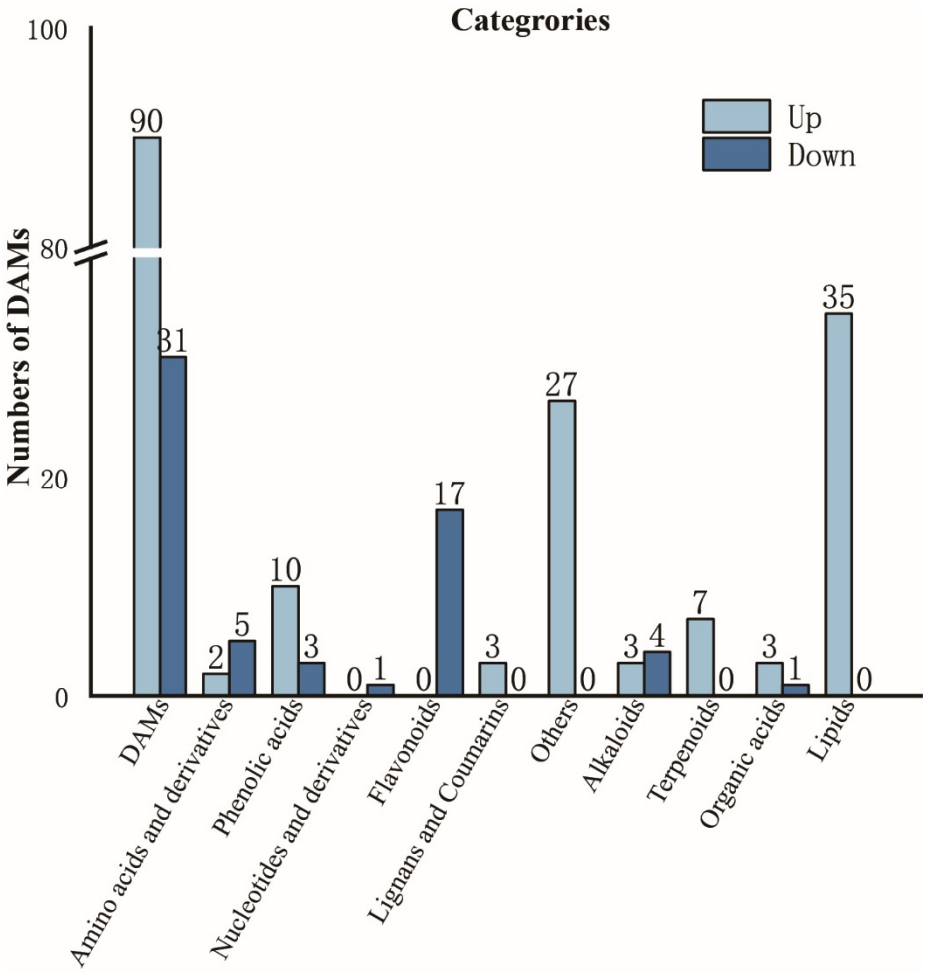


Figure S4. Categories of common DAMs in the comparison of BN vs. PN and BN vs. AN

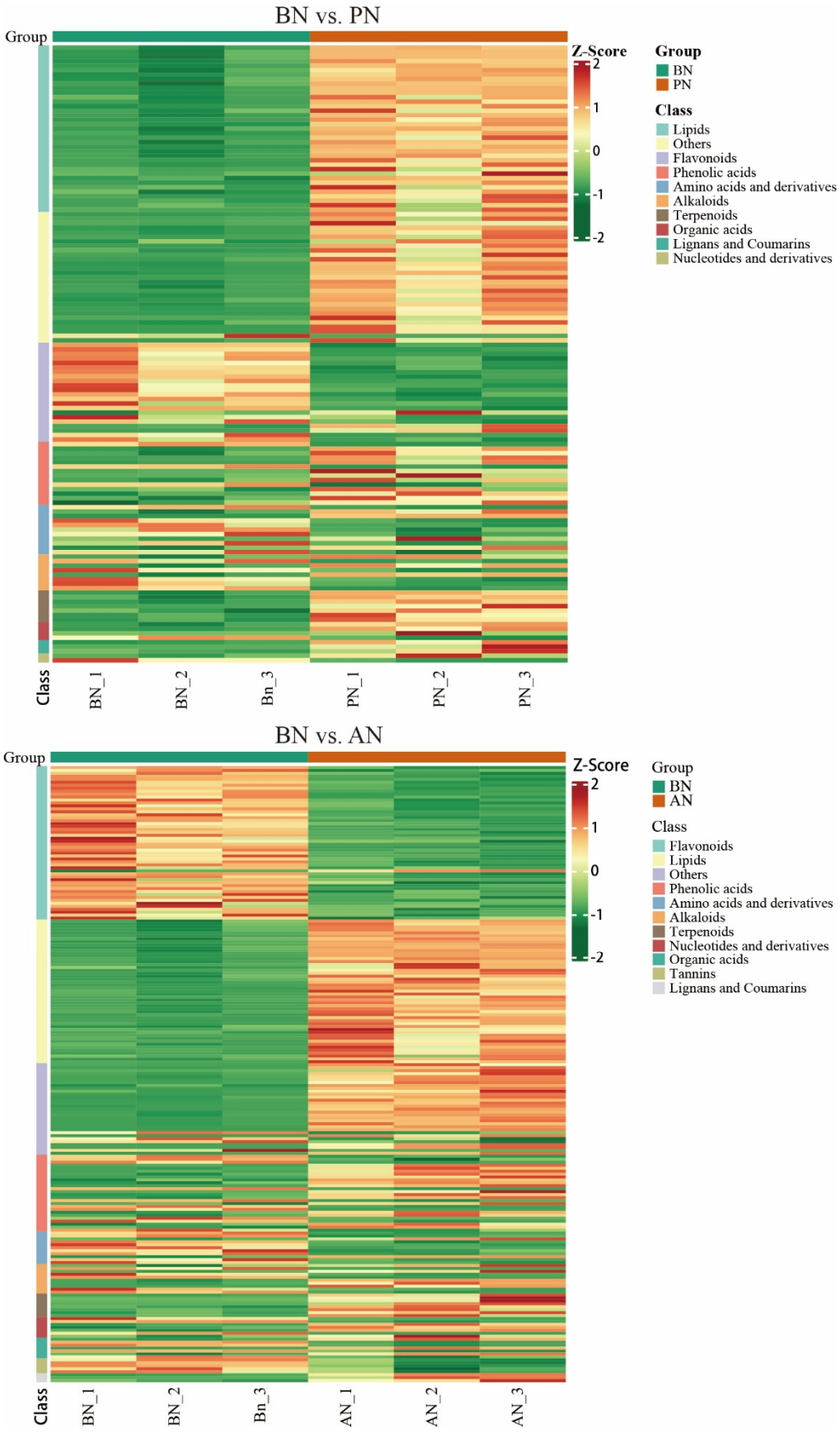


Figure S5. Clustering analysis of DAMs in the comparison of BN vs. PN and BN vs. AN

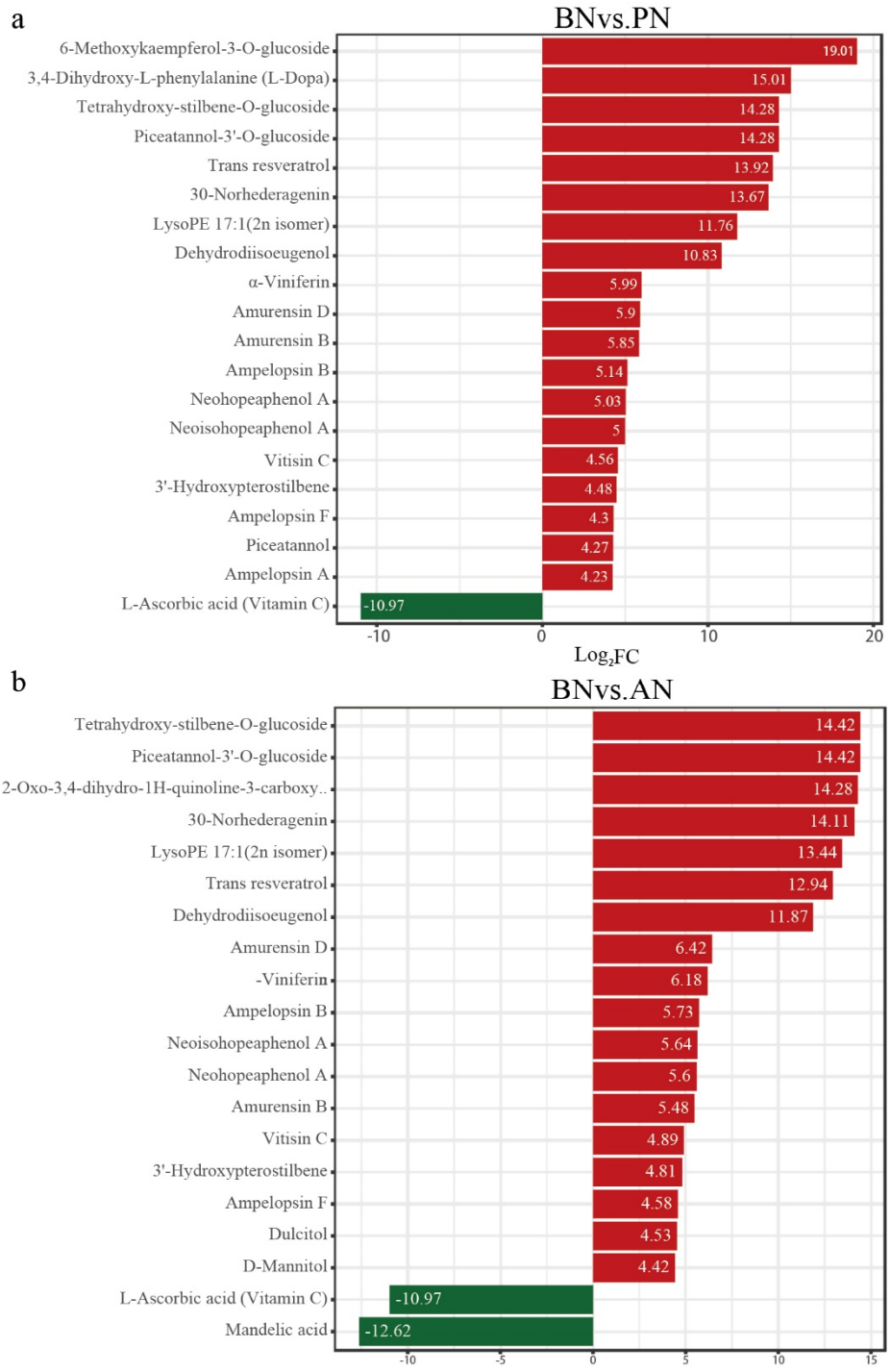


Figure S6. The bar graph of the top 20 differentially expressed metabolites.

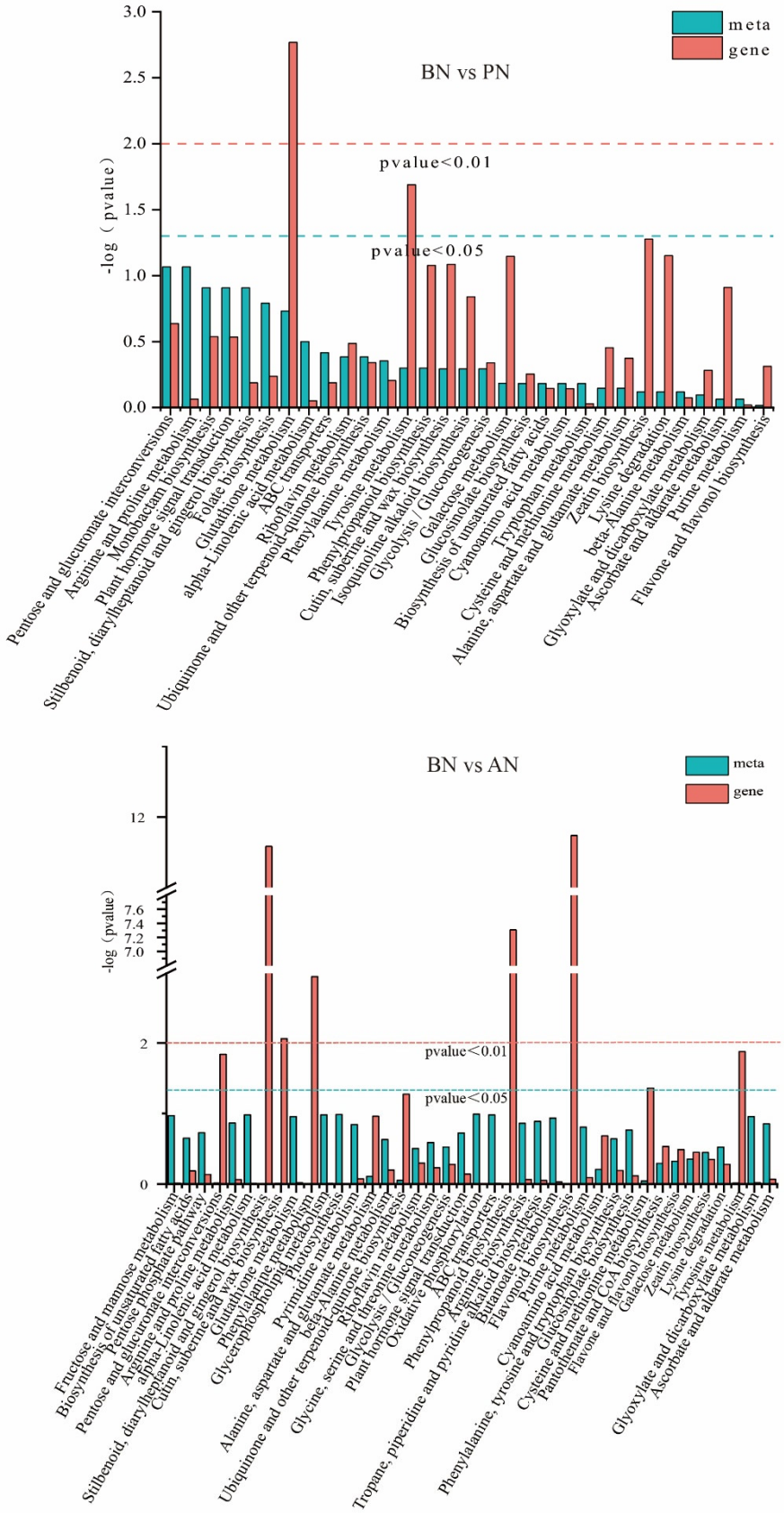


Figure S7. The Co-enriched KEGG pathways of correlation analysis of differentially accumulated metabolites and differentially expressed genes.