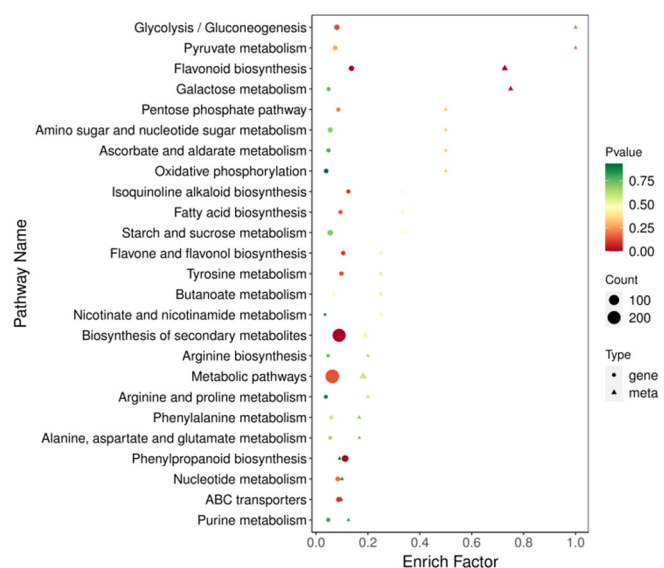
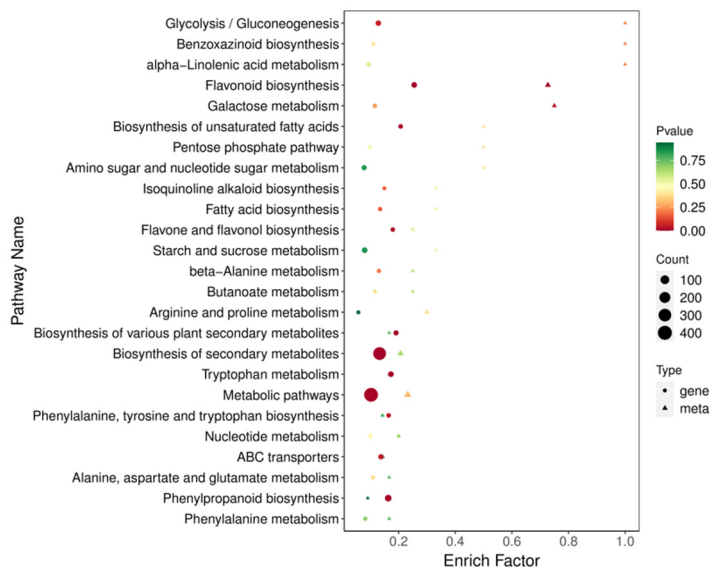


24-meta and 12-trans



48-meta and 24-trans



72-meta and 48-trans

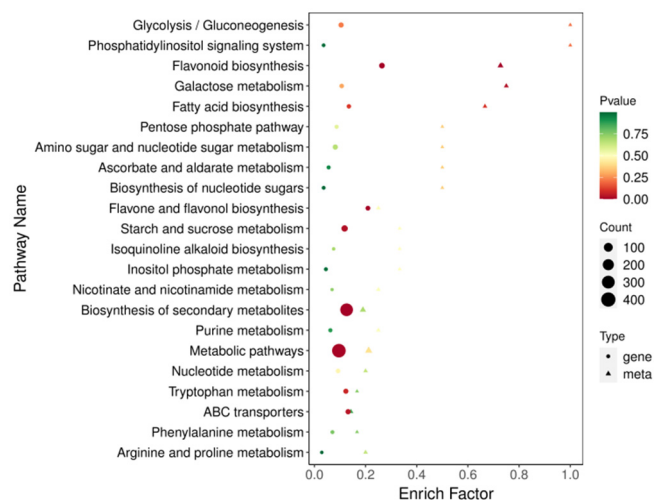


Figure S6. Statistics of Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways co-enriched by transcriptome and metabolome data. Hierarchical cluster analysis (HCA) of all differentially expressed genes and differentially accumulated metabolites between the SBPH-infested (meta24-trans12, meta48-trans24 and meta72-trans48) and uninfested (meta0-trans0) groups. p -value ≤ 0.05 and the absolute value of Log2 FC (fold-change) ≥ 1.0 were used as the threshold for significant difference.