

Figure S1. (A) Venn diagram of the detected metabolites in ‘Gaogai-1’ buds and leaves. (B) Categories’ statistics of differentially accumulated metabolites during the leaf development.

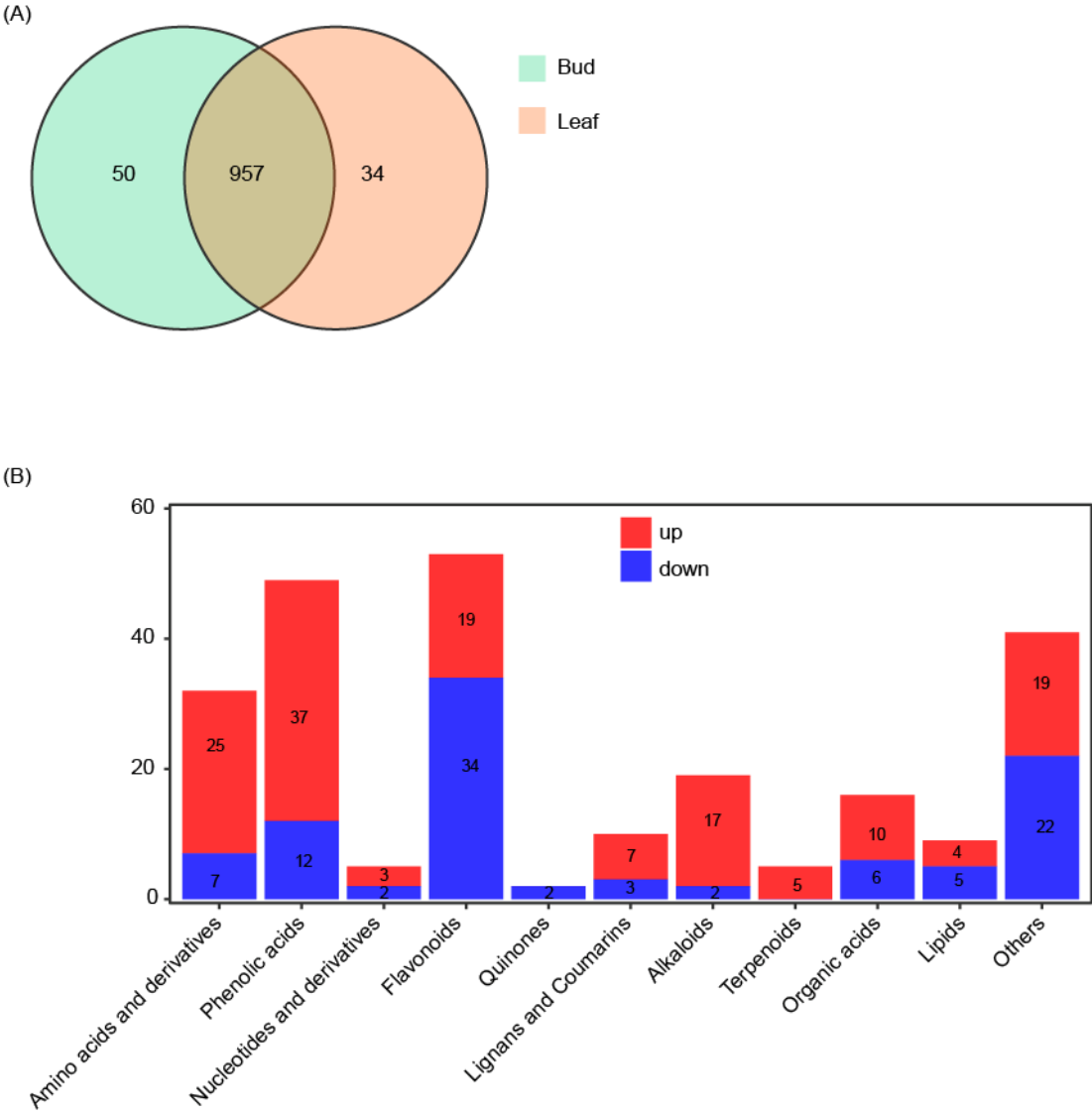


Figure S2. Relative content of glucose (A), fructose (B) and galactose (C) in the second and fourth pairs of leaves, which were determined by MetWare. Total starch content of the second to fourth pairs of leaves (C), which was determined in our lab.

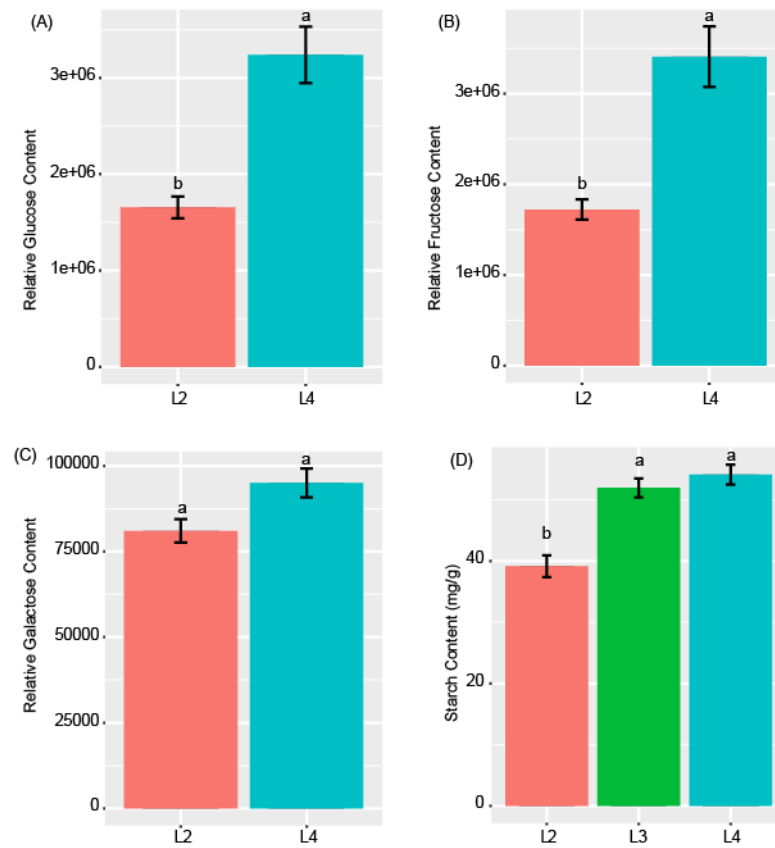


Figure S3. Diagram showing the gene ontology categories of the differentially expressed genes during the ‘Gaogai-1’ leaf development.

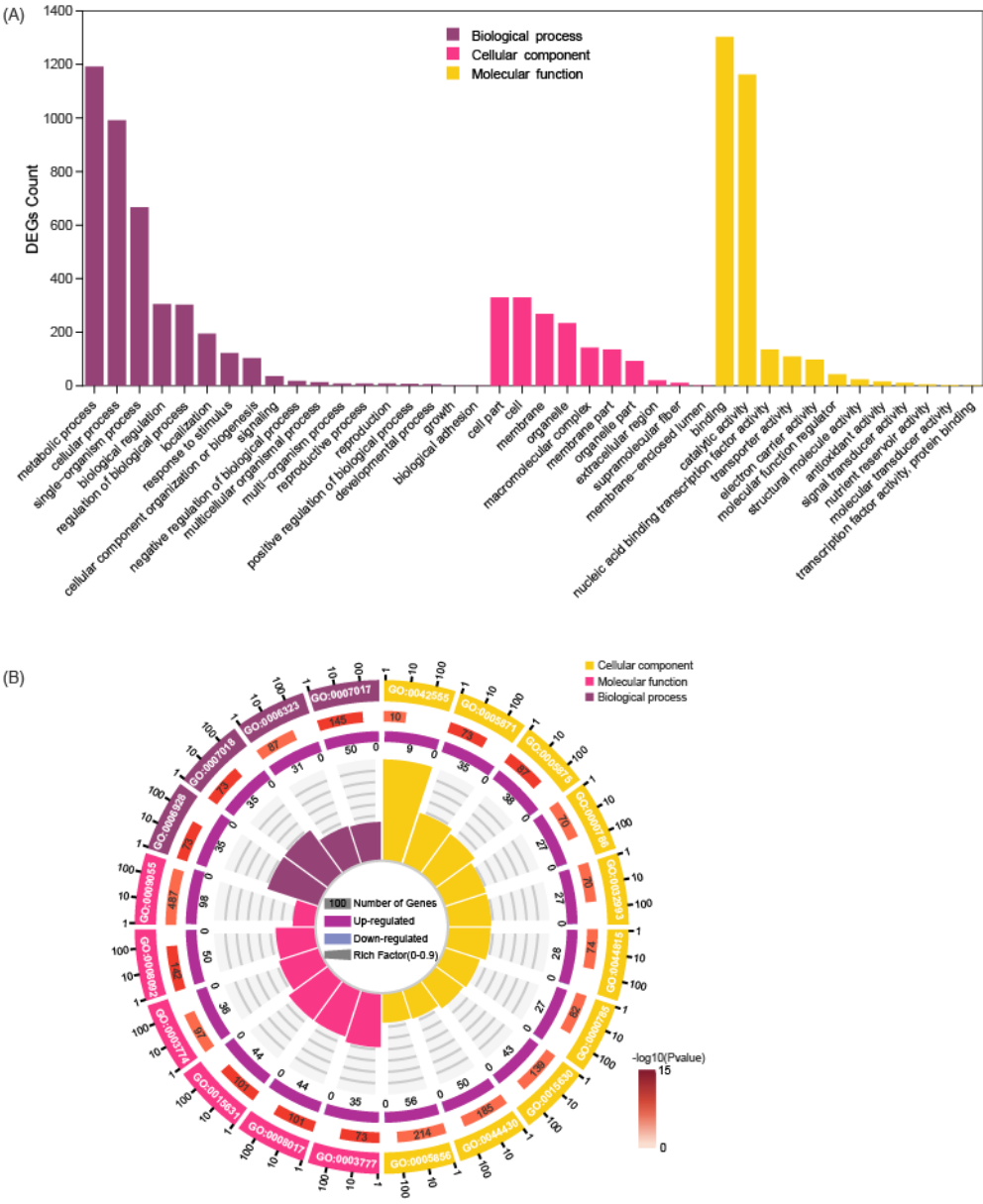


Figure S4. Four clusters representing 3689 DEGs with distinct stage-specific expression patterns. These clusters were further grouped into two superclusters (Cluster 1+3 and Cluster 2+4). Heatmap of transcript accumulation patterns (relative expression) of these genes generated by RNA-seq was shown.

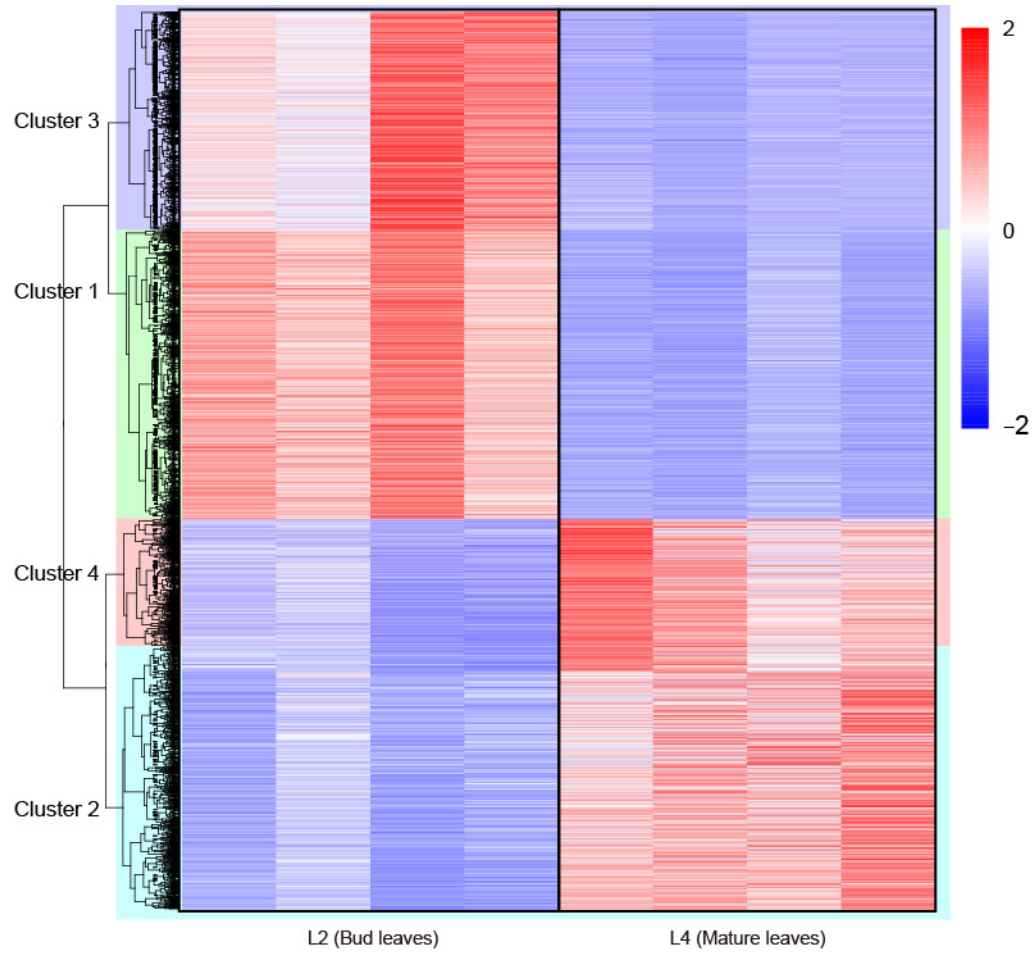


Figure S5. Correlation analysis of qRT-PCR and RNA-seq results.

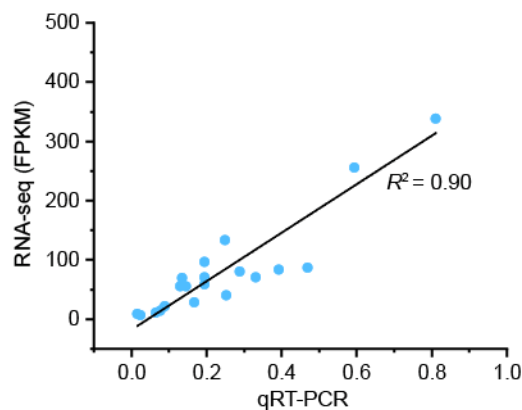


Figure S6. Potential interacting networks between the differentially expressed structural genes and transcription factors. Pearson correlation coefficient (PCC) values were calculated, and a PCC value over 0.9 was used to determine potential interactions. (A), (B), and (C) represent pathways of carbohydrate, amino acid, and phenylpropanoid metabolism, respectively.

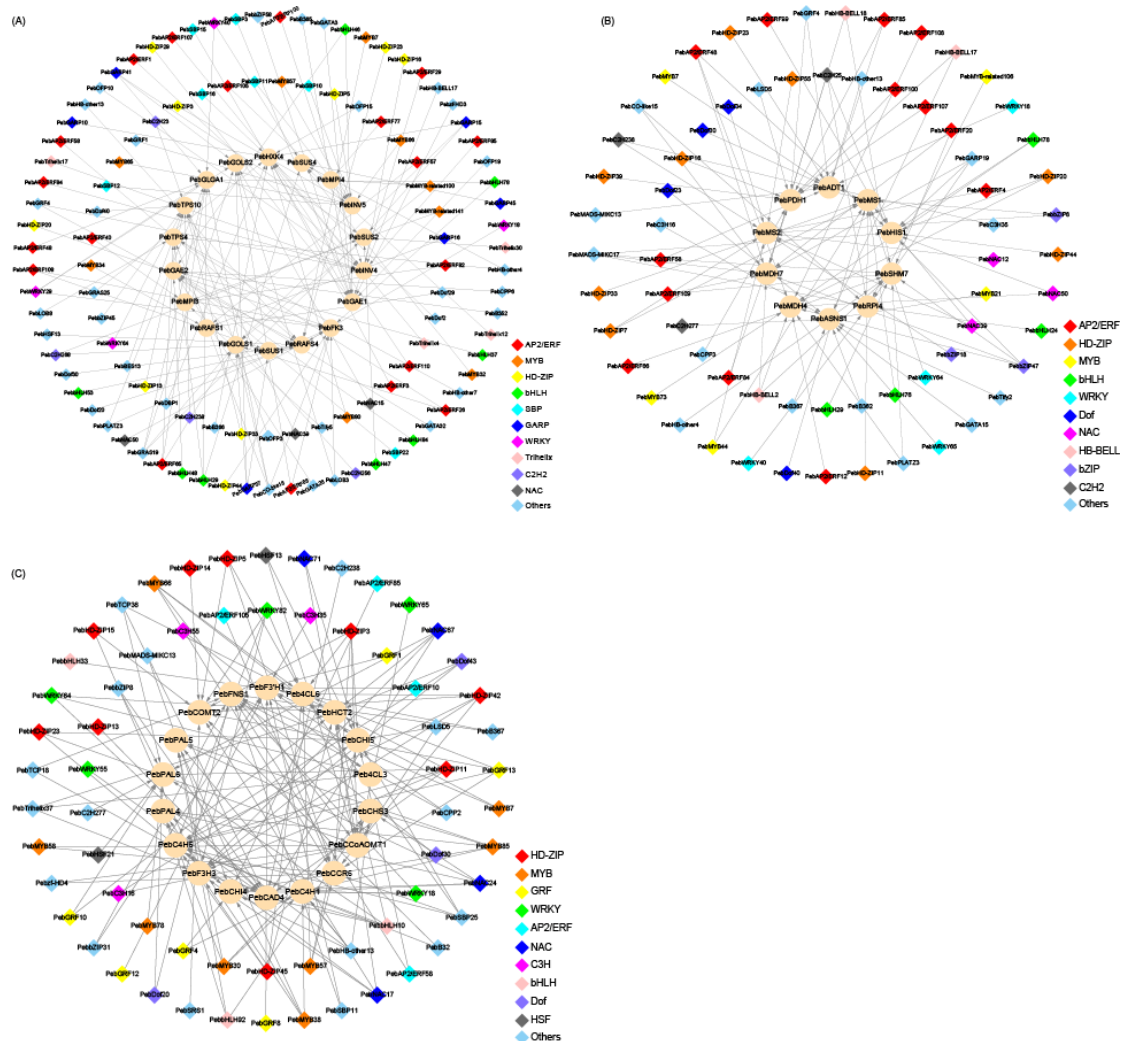


Figure S7. Heatmap of transcript accumulation patterns (relative expression) of Ca^{2+} -ATPases and Ca^{2+} permeable channels genes generated by RNA-seq. Scaled \log_2 expression values (FPKM) are shown in the heatmap legend. ANN: Annexin; PMCA: Ca^{2+} -ATPase; CNGC: Cyclic nucleotide-gated ion channel; GLR: Glutamate receptor; MCA: Mid1-complementing activity; OSCA: Hyperosmolarity-gate calcium-permeable channel; TPC: Two pore calcium channel.

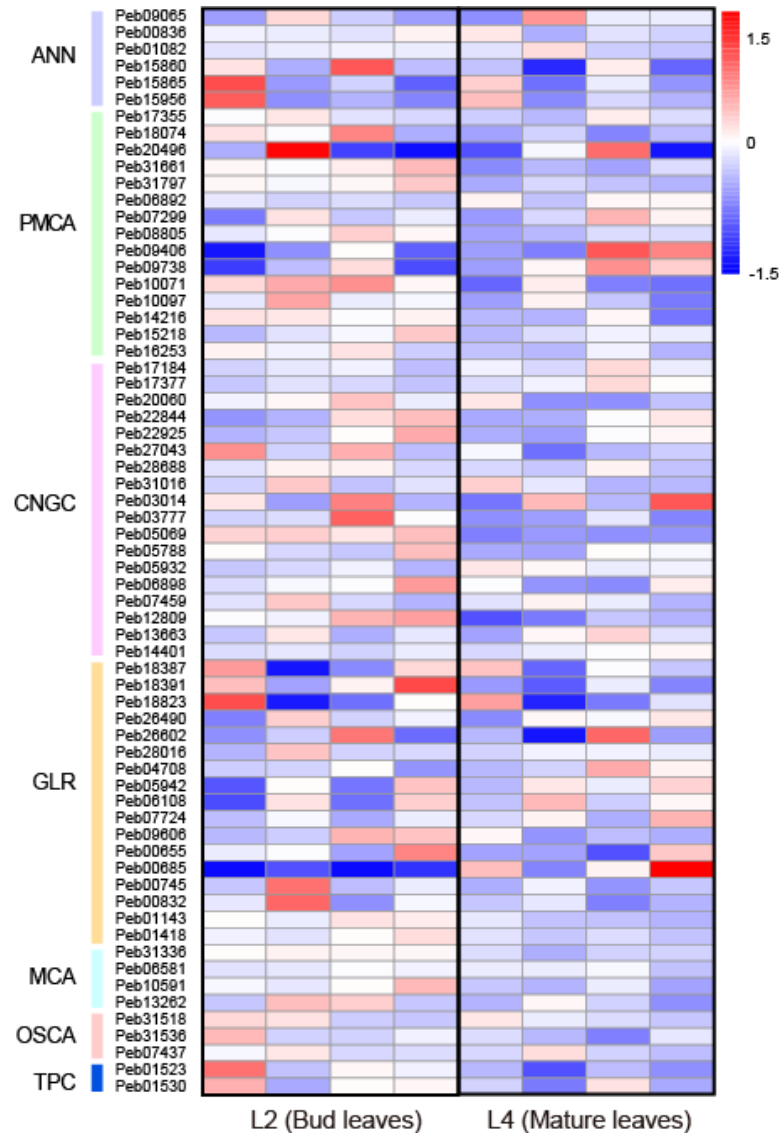


Figure S8. Simplified model of biosynthesis pathways of *L*-Dopa and salicylic acid in ‘Gaogai-1’ and the heatmap of metabolite accumulation and related gene expression patterns at different developmental stages. The differentially expressed genes and differentially accumulated metabolites are marked with asterisks.

