Figure S1 Full macromorphology scans (stem segments).

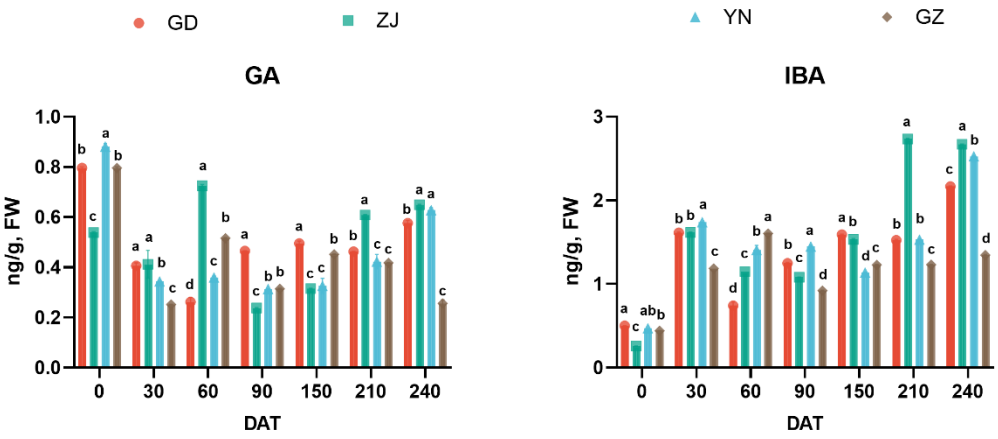

Figure S2 Endogenous concentrations of indole-3-butyric acid (IBA) and gibberellic acid (GA_3) in stems of four accessions (n=3). Data were analyzed by two-way ANOVA with accession and DAT as factors; simple main effects of accession were evaluated at each DAT by Tukey's multiple-comparisons test (adjusted $P < 0.05$).

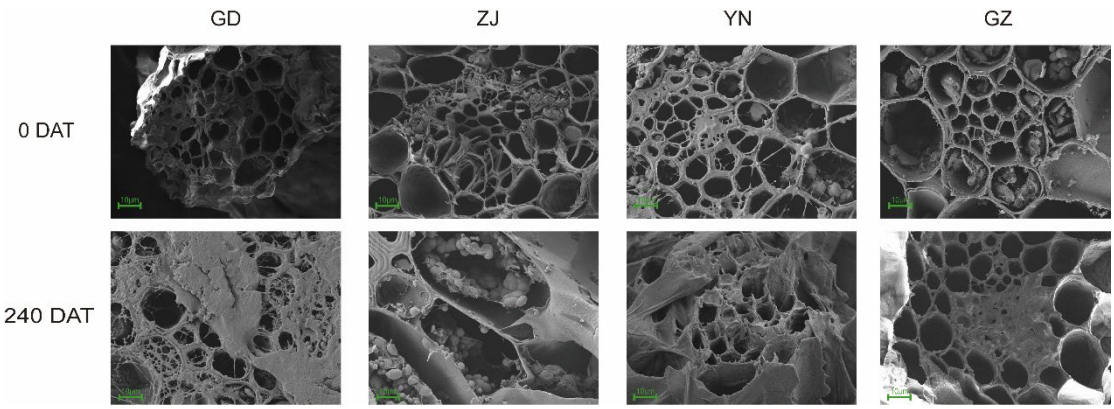

Figure S3 SEM images of stem fracture surfaces at 0 and 240 DAT for each accession; scale bars as indicated.

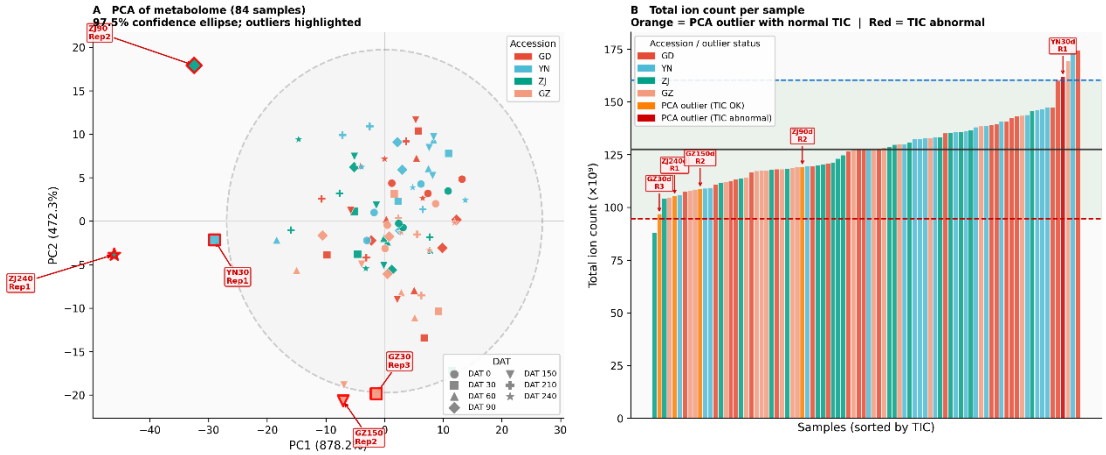

Figure S4 Metabolome PCA diagnostics and outlier checks.

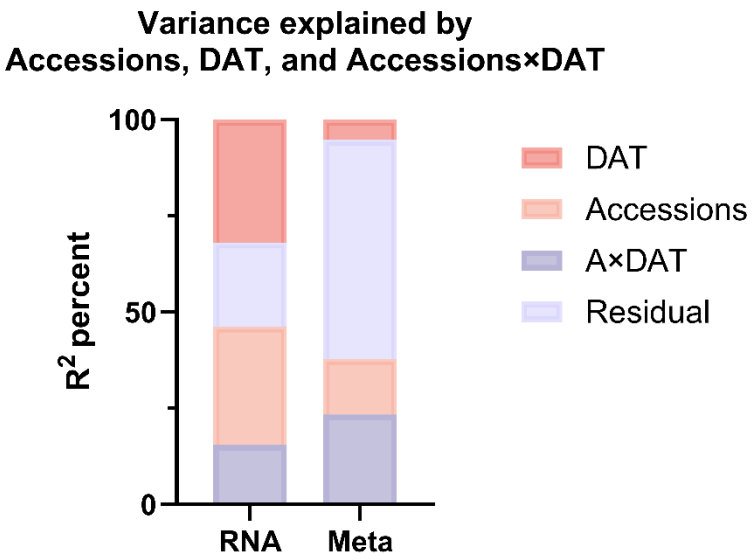

Figure S5 Variance partitioning of transcriptomic and metabolomic variation attributed to accession identity and developmental stage.

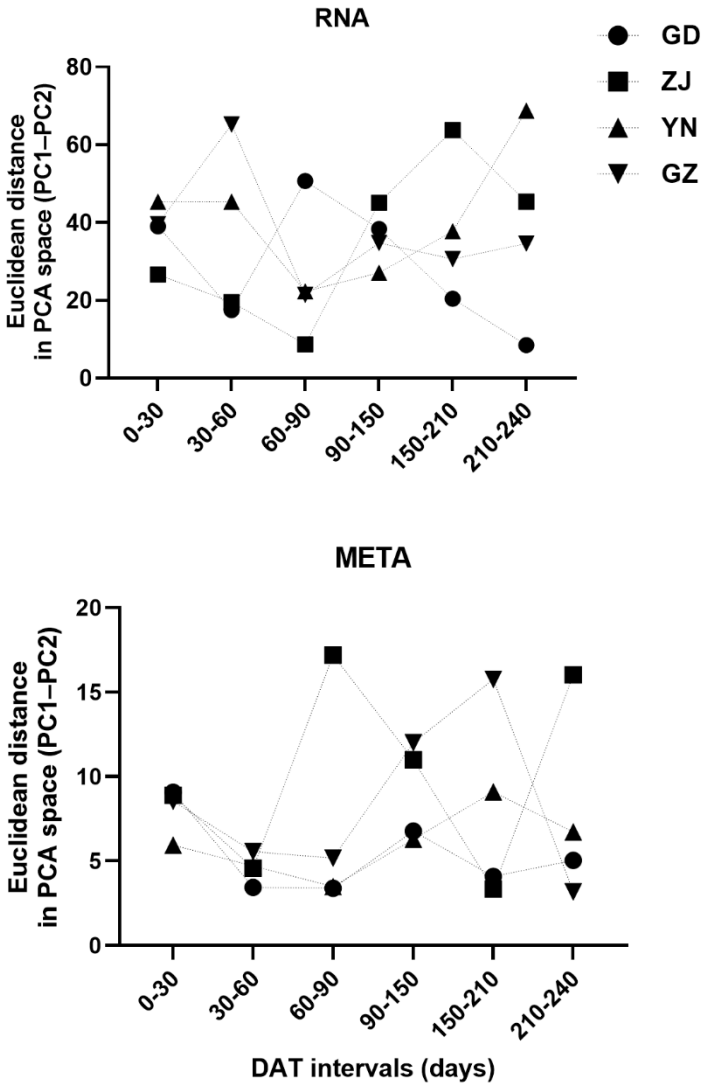

Figure S6 Stepwise PCA distances between adjacent developmental phases for transcriptomic (left) and metabolomic (right) datasets. Distances were calculated as Euclidean distances between phase centroids in PCA space and interpreted within each omics layer independently. Lines connect adjacent DAT intervals (0–30, 30–60, 60–90, 90–150, 150–210, 210–240 days).

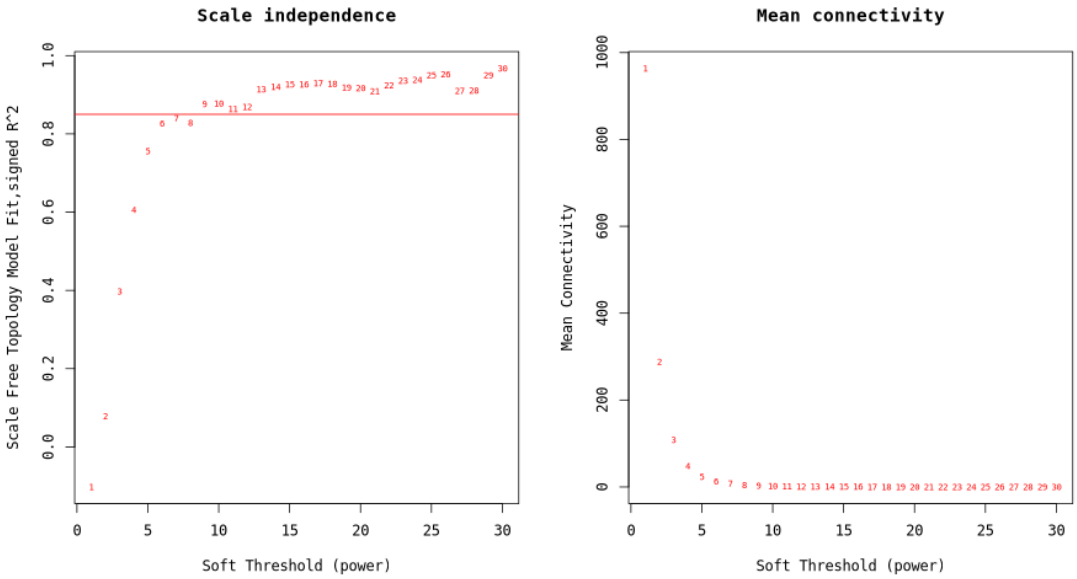

Figure S7 Soft-thresholding power selection for WGCNA network construction. Scale-free topology fit index (R^2, signed; left) and mean network connectivity (right) as functions of soft-thresholding power β (range 1–30). Numbers on each data point indicate the corresponding β value. The horizontal dashed line (left panel) marks R^2 = 0.85; β = 9 was selected as the lowest power at which R^2 exceeded this threshold, indicating adequate approximation of a scale-free network topology while maintaining sufficient mean connectivity for downstream module detection.

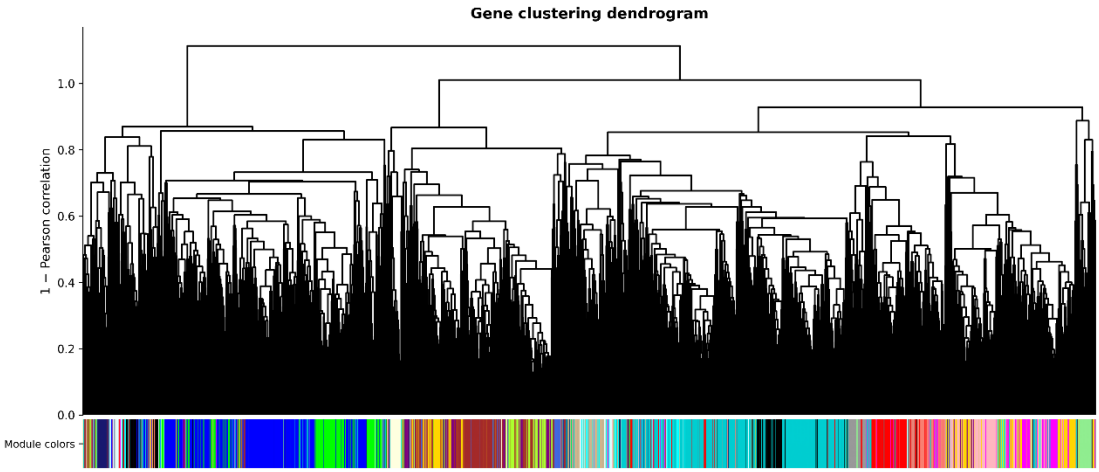

Figure S8 Gene clustering dendrogram based on topological overlap matrix (TOM)-derived dissimilarity (1 − Pearson correlation of $\log_2$-transformed FPKM values), with the corresponding module color assignments shown below. Genes are ordered according to hierarchical clustering (average linkage). Each color represents one co-expression module; grey indicates genes not assigned to any module. A total of 5,000 high-variance genes selected from 22,566 expressed genes were input into the WGCNA pipeline and partitioned into 20 co-expression modules (3,450 assigned genes) plus a grey module comprising 1,550 unassigned genes (31.0%). Soft-thresholding power $\beta = 9$ was selected on the basis of scale-free topology fit ($R^2 \geq 0.85$; Supplementary Figure S7).

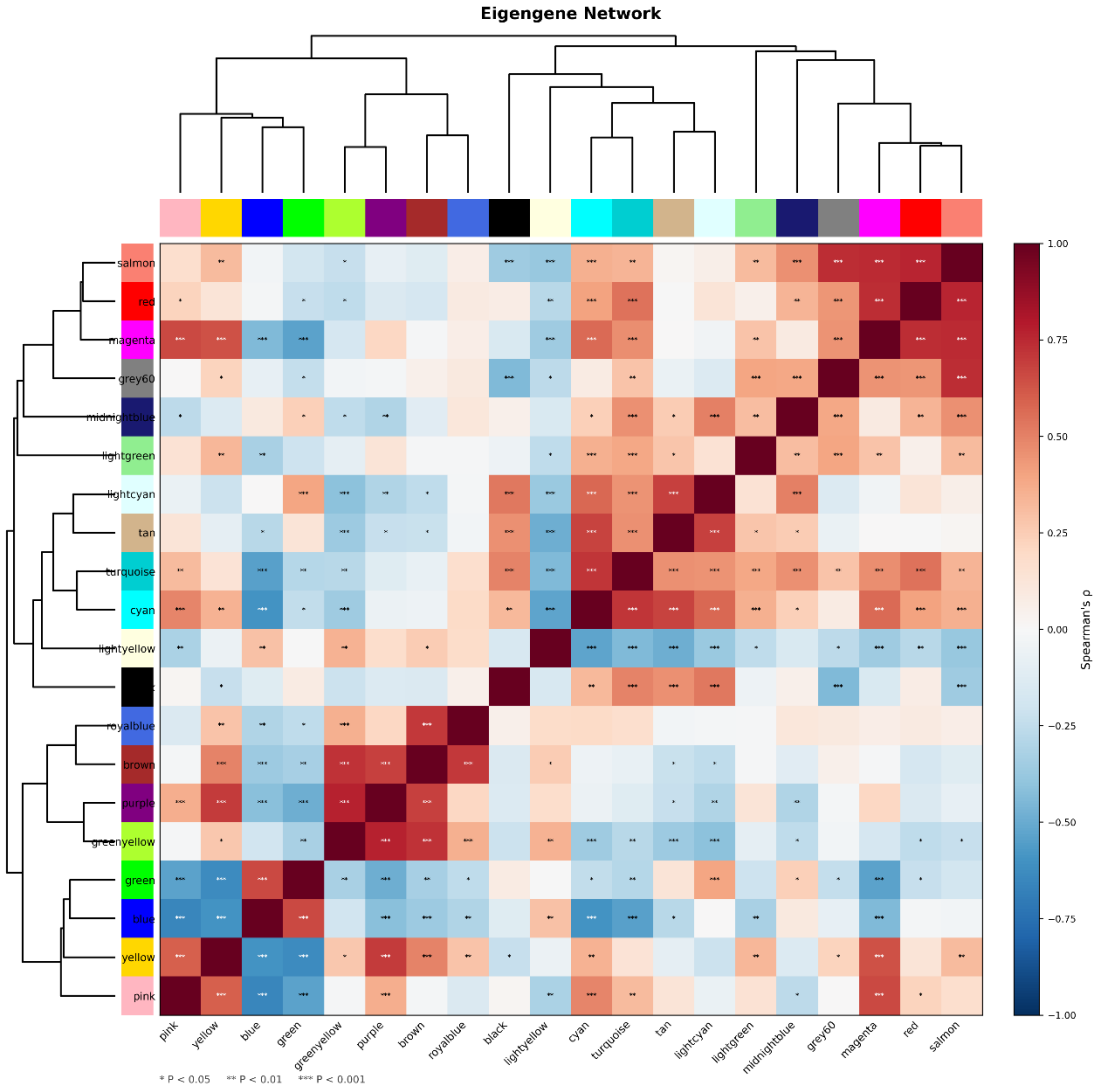

Figure S9 Eigengene network heatmap showing pairwise Spearman correlations among module eigengenes across all 84 samples. Modules are hierarchically clustered by eigengene similarity ($1 - |\rho|$, average linkage). Color scale indicates Spearman's ρ (red, positive; blue, negative). Asterisks indicate statistical significance (*P < 0.05; **P < 0.01; ***P < 0.001).