

## Supplementary Figure S2: KEGG Pathway Enrichment of DEGs Across Tissue and Developmental Stage Comparisons

### Description

This supplementary figure includes 10 charts presenting the KEGG pathway enrichment results for differentially expressed genes (DEGs) across pairwise comparisons of *Cannabis sativa* tissues and developmental stages. Each chart illustrates the enriched metabolic and regulatory pathways, providing insights into tissue-specific and developmental-stage-specific functional differentiation.

### Sample Groups and Pairwise Comparisons

The analyzed samples consist of four biological replicates per group, representing different tissues and developmental stages. Each group is denoted by a letter, with comparisons between groups summarized as follows:

**1:** A vs. B (Flowering leaves vs. Fruiting leaves) **2:** A vs. C (Flowering leaves vs. Vegetative leaves) **3:** B vs. C (Fruiting leaves vs. Vegetative leaves) **4:** E vs. F (Early fruiting leaves vs. Late fruiting leaves) **5:** H vs. I (Fruiting stems vs. Flowering stems) **6:** H vs. J (Fruiting stems vs. Seedling whole plant) **7:** I vs. J (Flowering stems vs. Seedling whole plant) **8:** K vs. L (Fruiting roots vs. Vegetative roots) **9:** K vs. M (Fruiting roots vs. Flowering roots) **10:** L vs. M (Vegetative roots vs. Flowering roots)

### Figure Details

- **X-axis:**  $-\log_{10}(\text{Q-value})$ , indicating the statistical significance of enrichment (lower Q-values represent higher significance).
- **Y-axis:** KEGG pathway names, ordered by Q-value.
- **Dot Size:** Number of DEGs associated with each pathway.
- **Dot Color:** Represents the Rich Factor (ratio of DEGs to the total number of genes in the pathway), with higher values indicating stronger enrichment.

These charts reveal tissue- and stage-specific metabolic differentiation in *Cannabis sativa*. For example:

- **Leaf samples (e.g., A, B, C)** are predominantly enriched for secondary metabolic pathways, such as terpenoid backbone biosynthesis and phenylpropanoid biosynthesis, reflecting their primary role in metabolite production.
- **Root samples (e.g., K, L, M)** exhibit enrichment in primary metabolic pathways, such as nitrogen metabolism and amino acid biosynthesis, indicating their foundational roles in nutrient absorption and environmental adaptation.
- **Seedling stage (J)** is enriched for pathways related to rapid growth and signaling, including MAPK signaling and circadian rhythm regulation, consistent with the developmental demands of this stage.



















