

Supplementary Figure S1: GO Classification of DEGs Across Tissue and Developmental Stage Comparisons

Description

This supplementary figure includes 10 bar charts presenting the Gene Ontology (GO) classification results for differentially expressed genes (DEGs) across pairwise comparisons of *Cannabis sativa* tissues and developmental stages. Each chart illustrates the distribution of DEGs across three main GO categories: biological processes (BP), cellular components (CC), and molecular functions (MF). These results provide insights into the functional differentiation of genes among tissues and stages, highlighting their roles in metabolic and developmental processes.

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:** Number of DEGs annotated to each GO term.
- **Y-axis:** GO term names grouped into biological processes (red), cellular components (blue), and molecular functions (green).
- **Color and Size:** Dot size indicates the number of genes associated with the term, and color represents the enrichment factor.

These charts highlight tissue- and stage-specific functional differentiation in *Cannabis sativa*.

- **Leaf samples (e.g., A, B, C)** are enriched for genes related to secondary metabolism, reflecting their role in metabolite biosynthesis.
- **Root samples (e.g., K, L, M)** show a predominance of genes involved in primary metabolism and environmental adaptation.
- **Seedling stage (J)** exhibits gene functions associated with cellular growth and signal transduction.



















