

iScience, Volume 29

## Supplemental information

### Comparative analysis of gene expression and metabolites in female and male *Cannabis sativa* flowers

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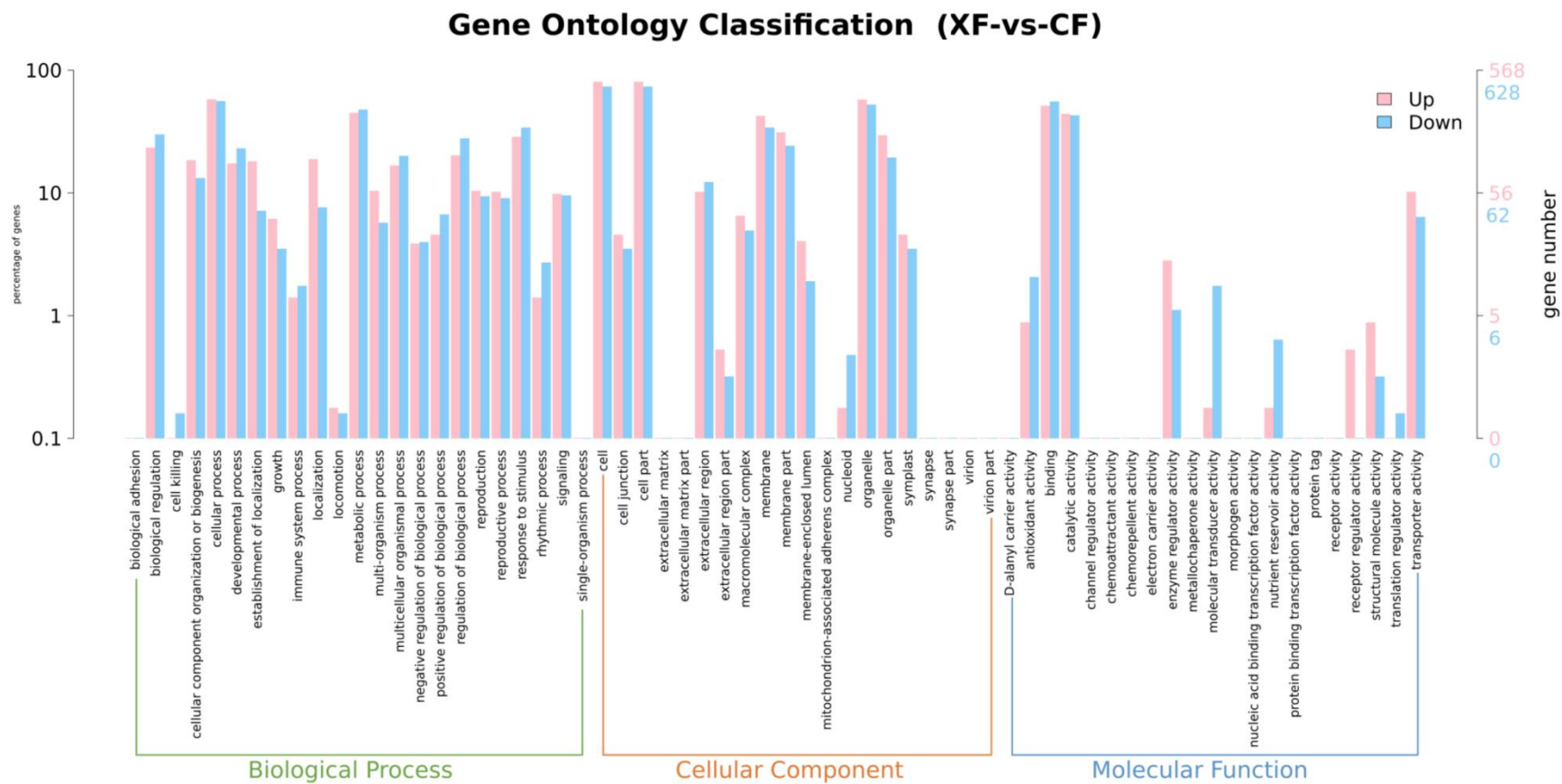


Figure S1 Gene Ontology (GO) functional enrichment analysis of male and female *Cannabis sativa* L. flowers

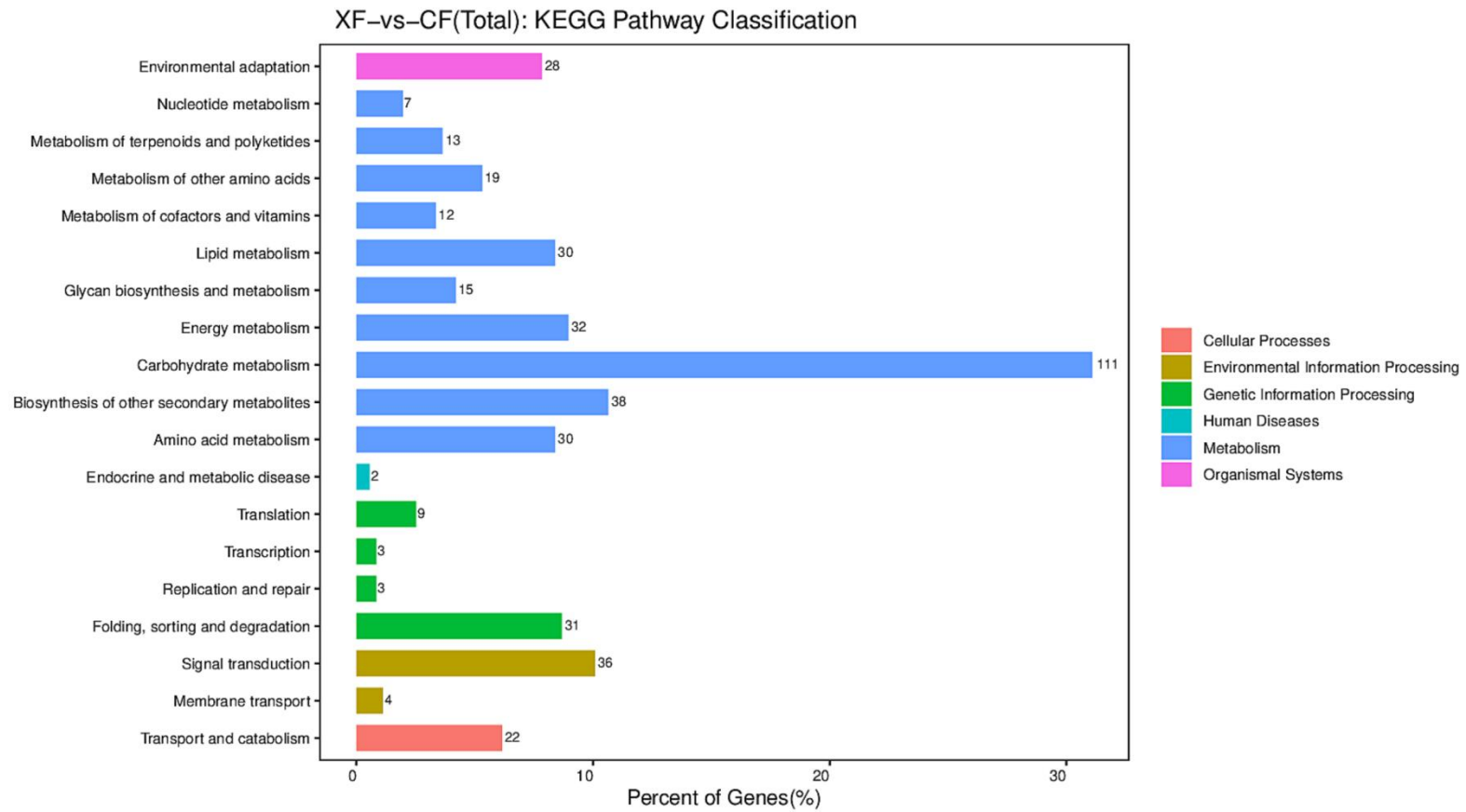


Figure S2 KEGG enrichment analysis of differentially expressed genes (DEGs) of male and female *Cannabis sativa* L. flowers

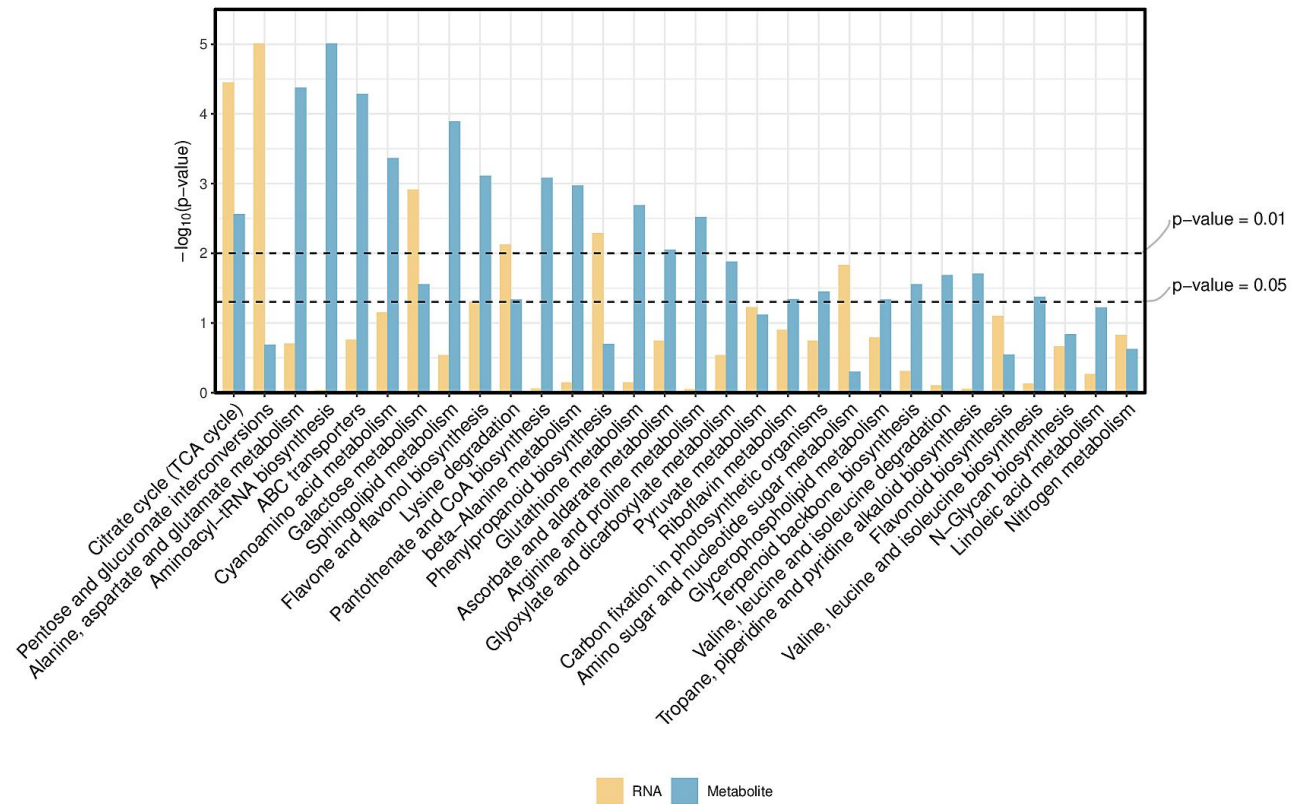


Figure S3 Bar chart of the top 30 KEGG pathways of differentially expressed genes (DEGs) and differentially accumulated metabolites (DAMs) of male and female Cannabis sativa L. flower

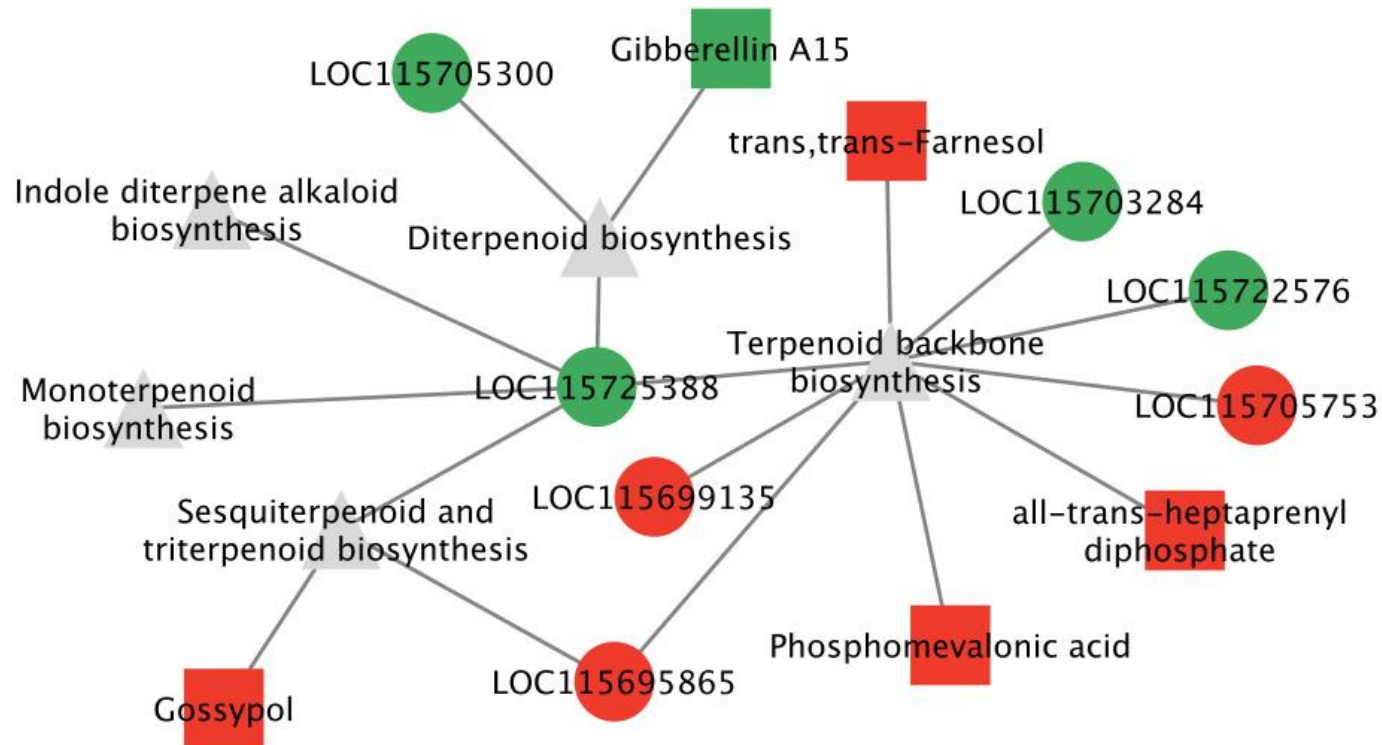


Figure S4 Comprehensive metabolomic and transcriptomic analysis of biosynthetic pathways of phenylpropanes, flavonoids and terpenes. The correlation analysis results of differentially expressed genes (DEGs) and differentially expressed metabolites (DAM) ( $p < 0.05$ ) showed that the red dots and squares represented the up-regulation of DEG and DAM, respectively, and the green dots and squares represented the down-regulation of DEG and DAM, respectively.