

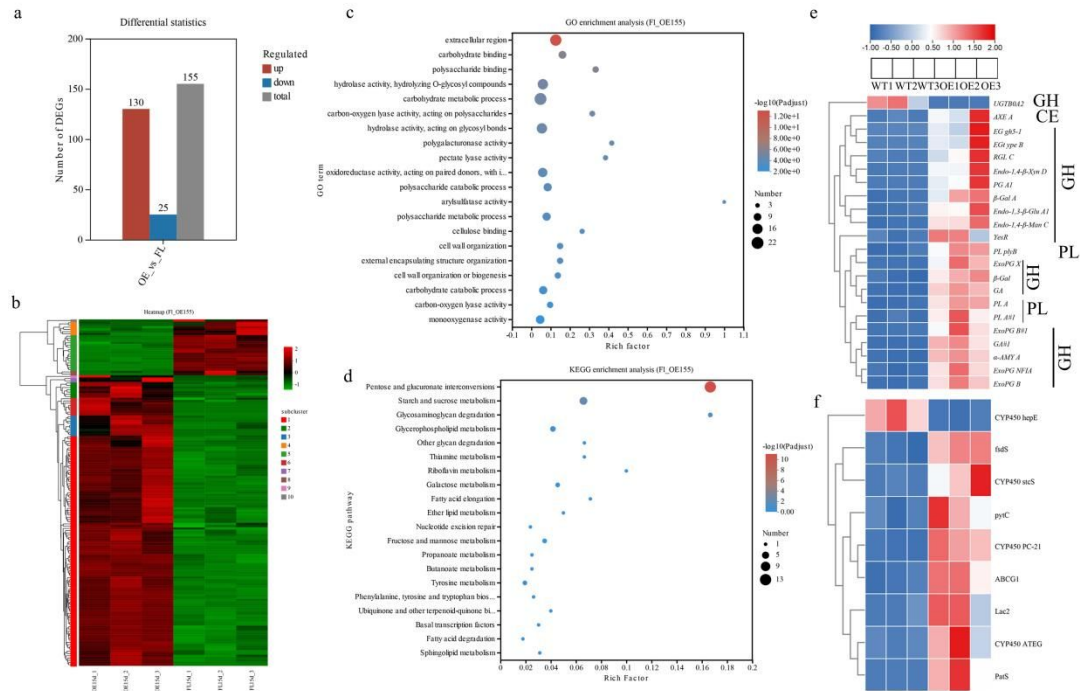


Fig. S7. Transcriptome differential analysis of WT and *Flfbp1*^{OE} of *F. lateritium* Fl617. (a) Statistics of differentially expressed genes (DEGs) between WT and *Flfbp1*^{OE} strains. A total of 155 DEGs were identified, comprising 130 upregulated and 25 downregulated genes. (b) Heatmap of DEGs between WT and *Flfbp1*^{OE} strains. (c) Gene Ontology (GO) enrichment analysis of DEGs. (d) Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analysis of DEGs. (e) Heatmap of expression profiles of cell wall-degrading enzyme-related genes in WT and *Flfbp1*^{OE} strains. (f) Heatmap of expression profiles of secondary metabolism-related genes in WT and *Flfbp1*^{OE} strains. Data are based on triplicate biological RNA-seq replicates (FDR < 0.05). KEGG (Kyoto Encyclopedia of Genes and Genomes) pathway enrichment analysis was performed to annotate the functions of differentially expressed genes, using the KEGG database (<https://www.kegg.jp/>). The enrichment significance was calculated based on the hypergeometric distribution, and pathways with Padj < 0.05 were considered significantly enriched. The results were visualized as a bubble plot.