

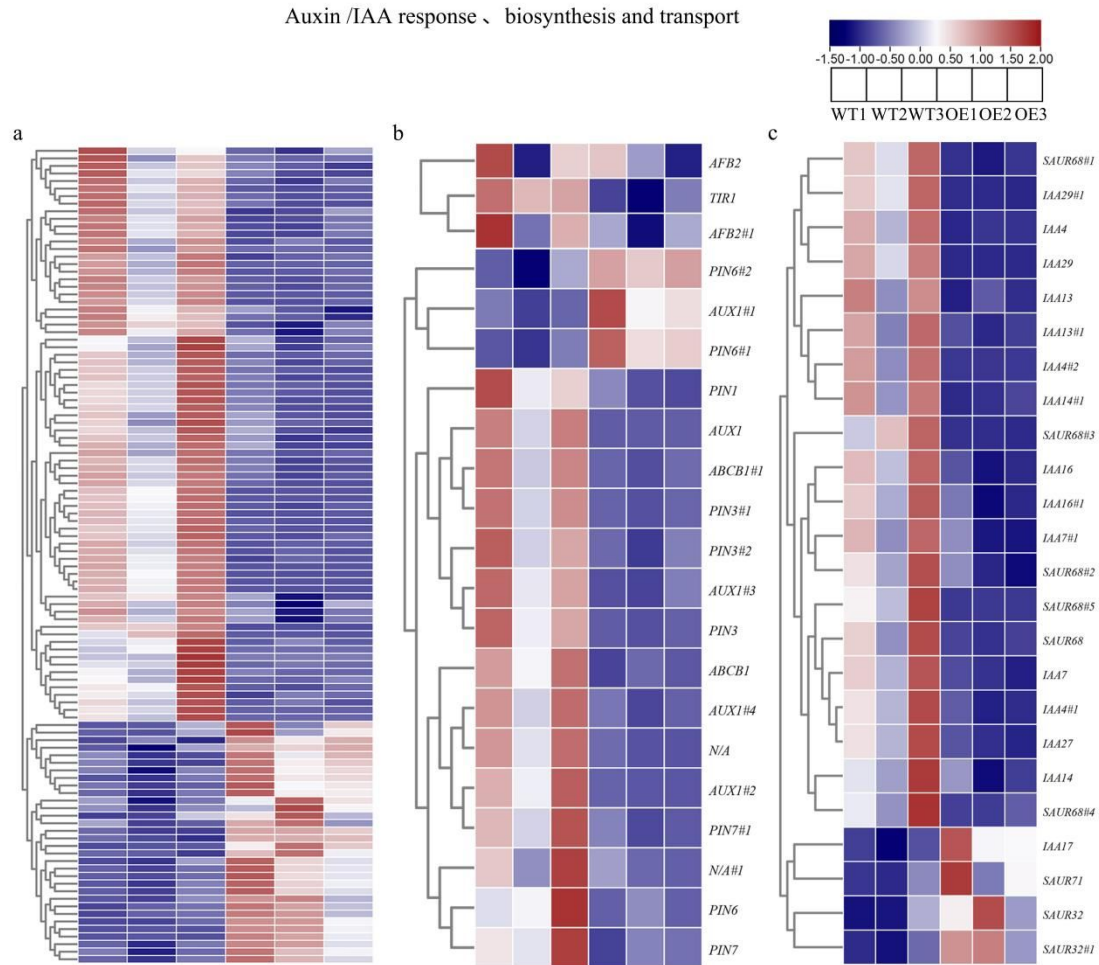


Fig. S16. Overexpression of *Flfbp* reshapes the transcript profile of auxin-related genes in *N. benthamiana*. *N. benthamiana* plants were inoculated with WT or *Flfbp*^{OE} strains, and samples were collected at 10 days post-inoculation. Transcript levels of auxin-responsive and auxin transport-related genes were analyzed by RNA-seq. (a) Heatmap of auxin-responsive genes. (b) Heatmap of auxin transport-related genes. (c) Heatmap of another set of auxin-responsive genes. Genes were clustered based on their expression patterns across treatments. Color scale: blue, down-regulated; red, up-regulated; white, median expression level. Compared with WT, infection by *Flfbp*^{OE} resulted in down-regulation of most auxin-related genes, indicating that overexpression of *Flfbp1* can reshape the auxin signaling network in *N. benthamiana*. Each treatment contained three biological replicates with consistent trends.