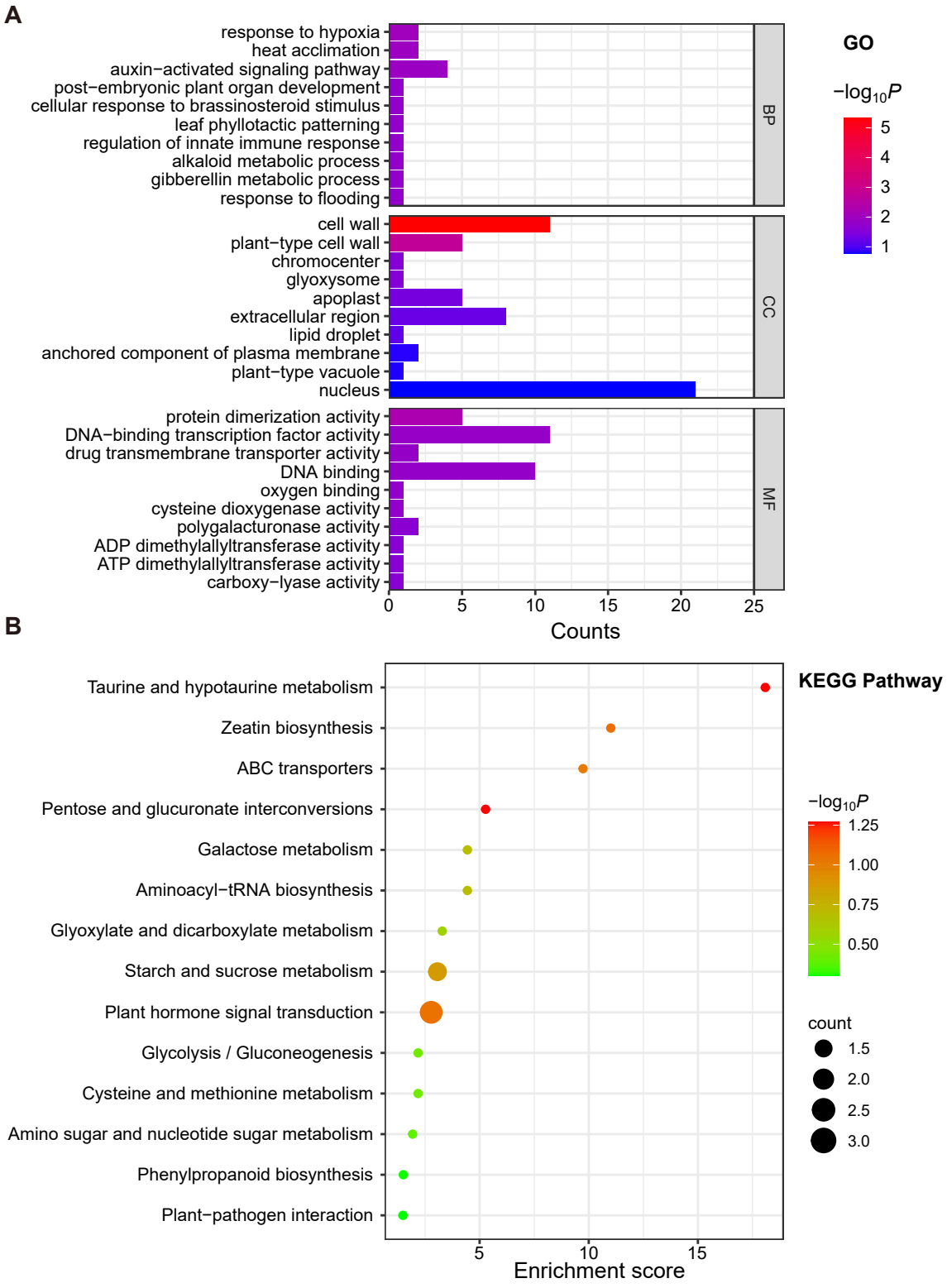


Figure S3 Commonly up-regulated genes in *lon1-2*, *atg5-1* and *lon1-2atg5-1* are enriched with cell wall processes.

(A) A total of 92 genes were commonly upregulated in *lon1-2*, *atg5-1*, and *lon1-2atg5-1*, and were subjected to Enrichment of Gene Ontology (GO). The horizontal bars represent the counts for Biological Processes (BP), Cell Compartments (CC) and Molecular Functions (MF), while the blue-red color bar indicates the range of Log-transformed P values. (B) KEGG pathway enrichment analysis of down-regulated genes in all three mutants. The size of the bubbles corresponds to the number of genes involved, while the green-red color bar indicates the range of Log-transformed P values.