

Figure S1. Principal component analysis of the 12 RNA-Seq samples.

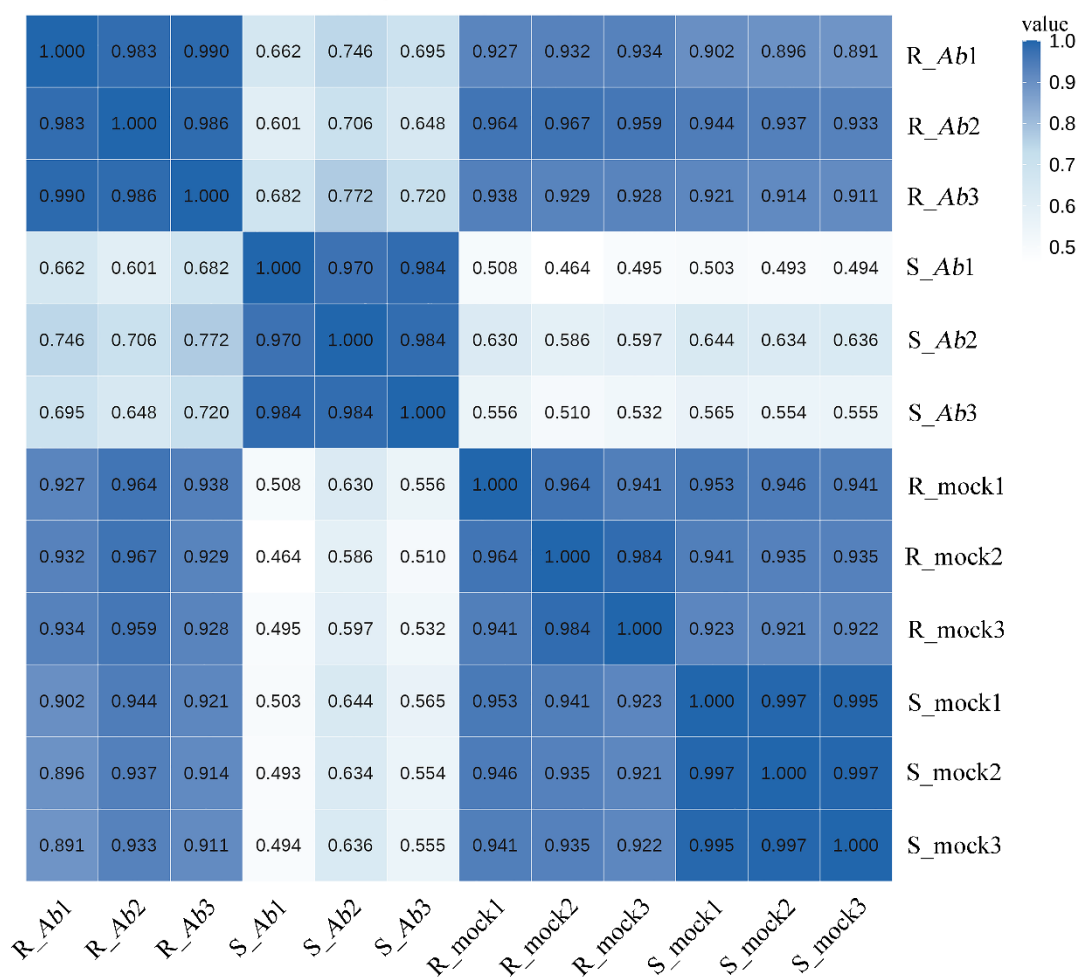


Figure S2. Pearson correlation analysis of the 12 RNA-Seq samples.

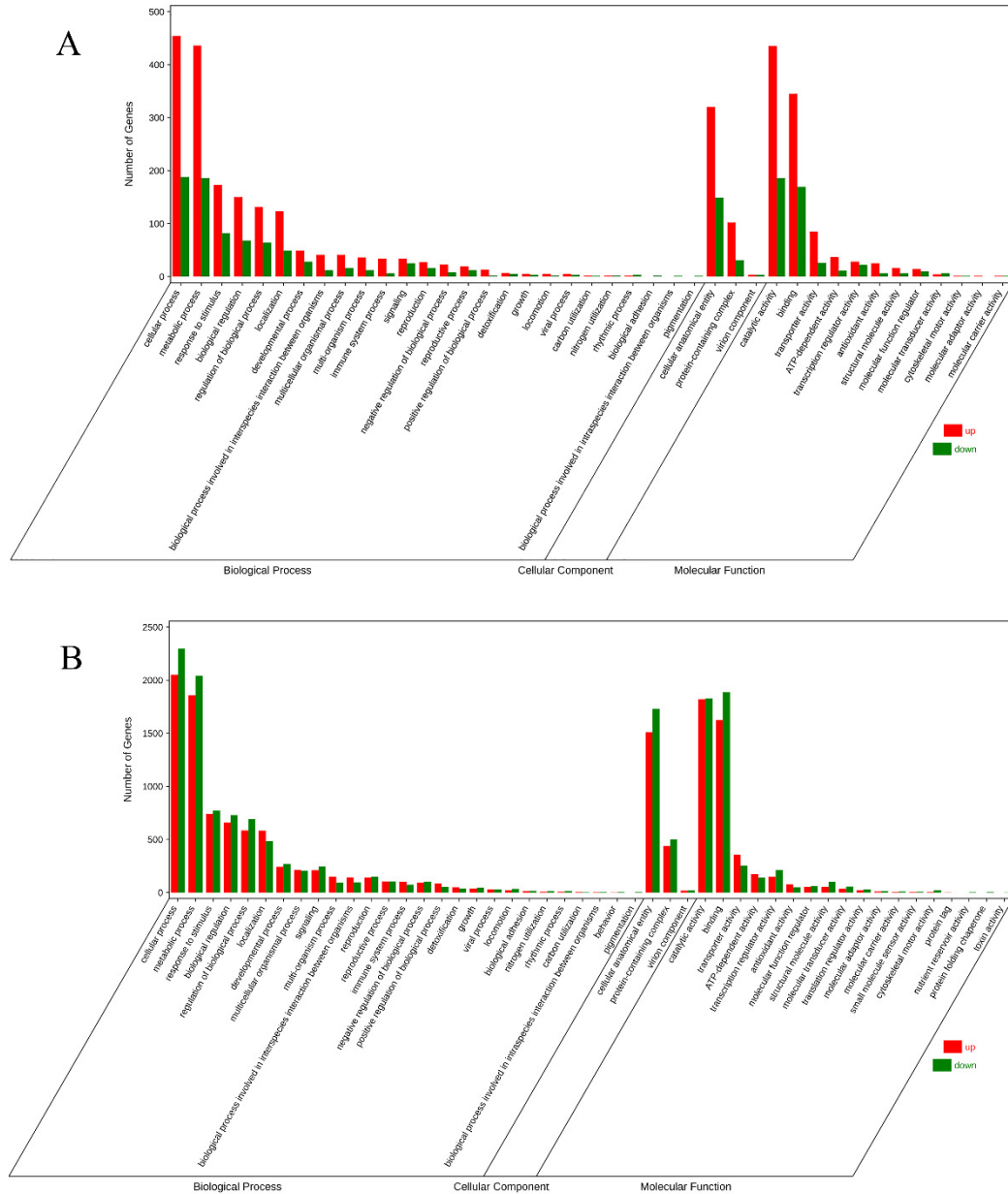


Figure S3. GO enrichment analysis of DEGs in Bo257 (R_mock vs. R_Ab) and Bo190 (S_mock vs. S_Ab) after Ab infection. A, GO enrichment analysis of DEGs in Bo257 (R_mock vs. R_Ab). B, GO enrichment analysis of DEGs in Bo190 (S_mock vs. S_Ab). The y-axis represents the total number of DEGs annotated to each GO process. The x-axis represents three ontologies, including biological processes, molecular functions, and cellular components. The red and green sections represent up-regulated and down-regulated DEGs, respectively.

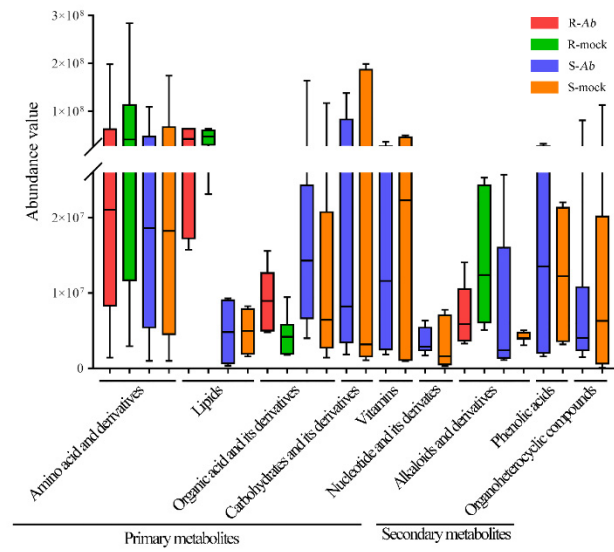


Figure S4. Comparison of the metabolite abundance value in Bo257 (R_mock vs. R_Ab) and Bo190 (S_mock vs. S_Ab) after Ab infection.