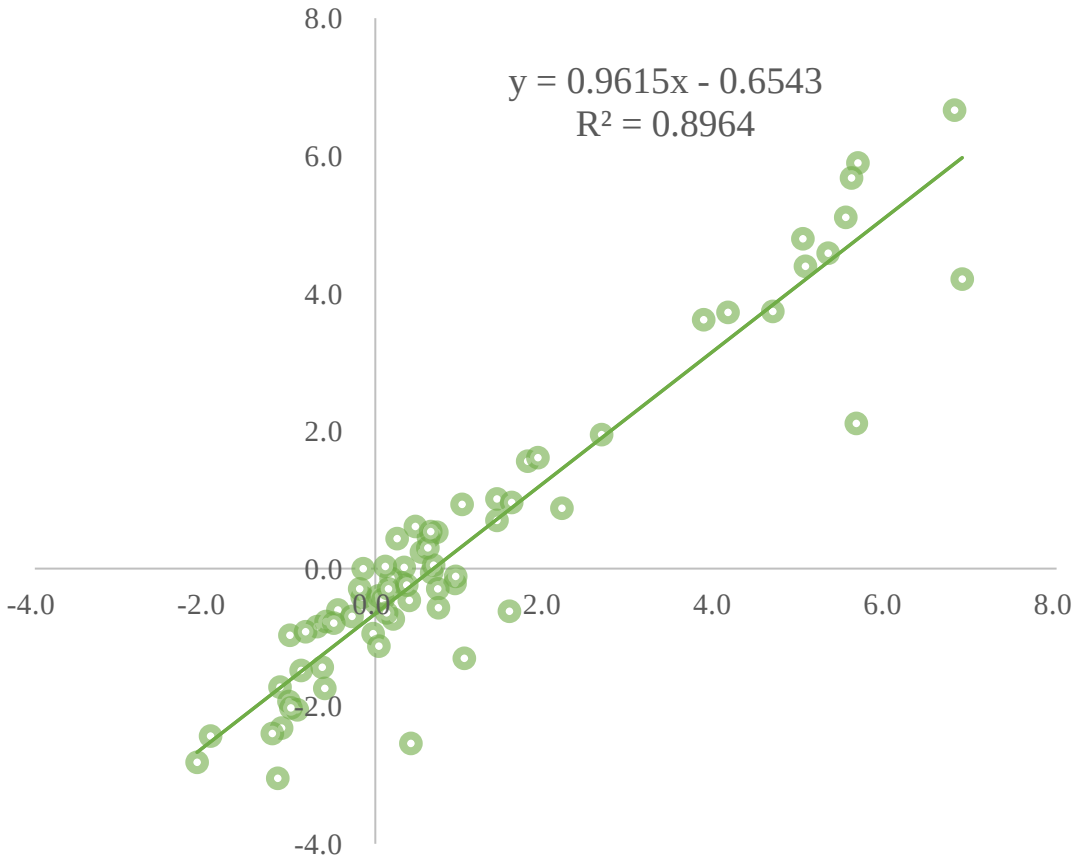
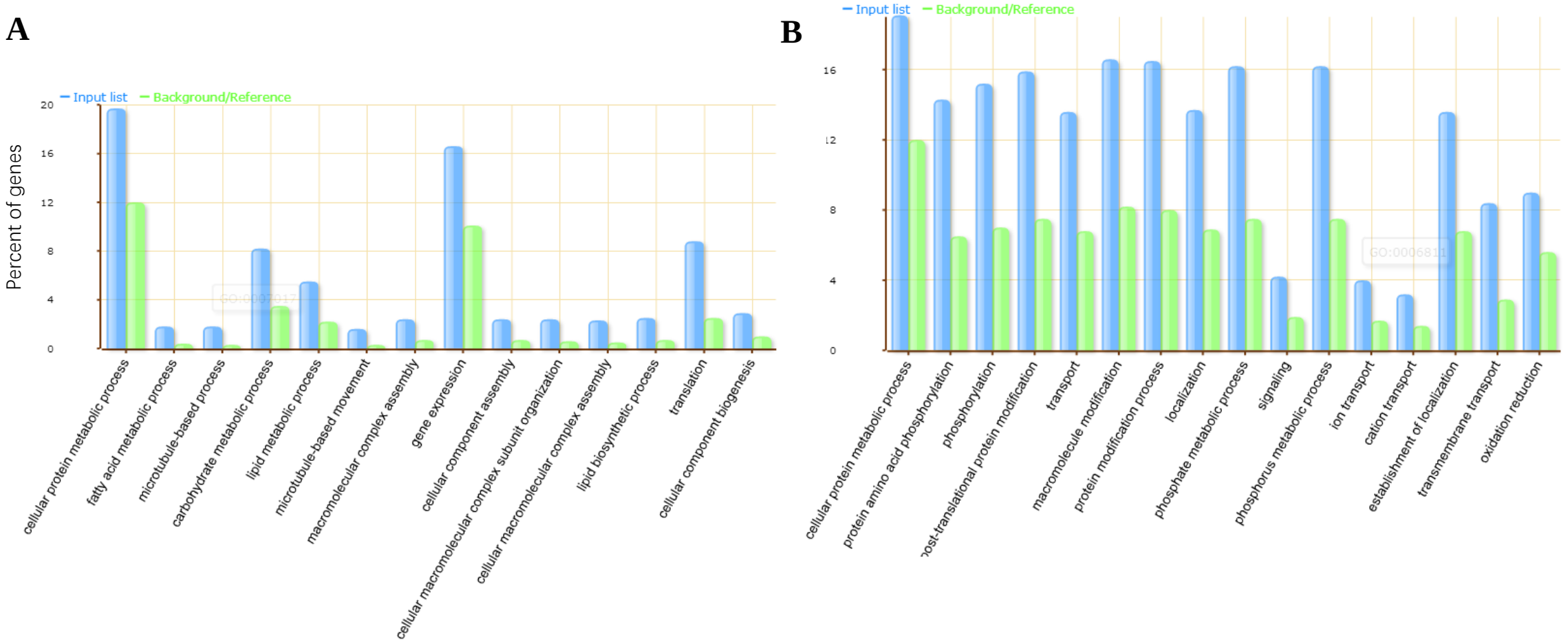
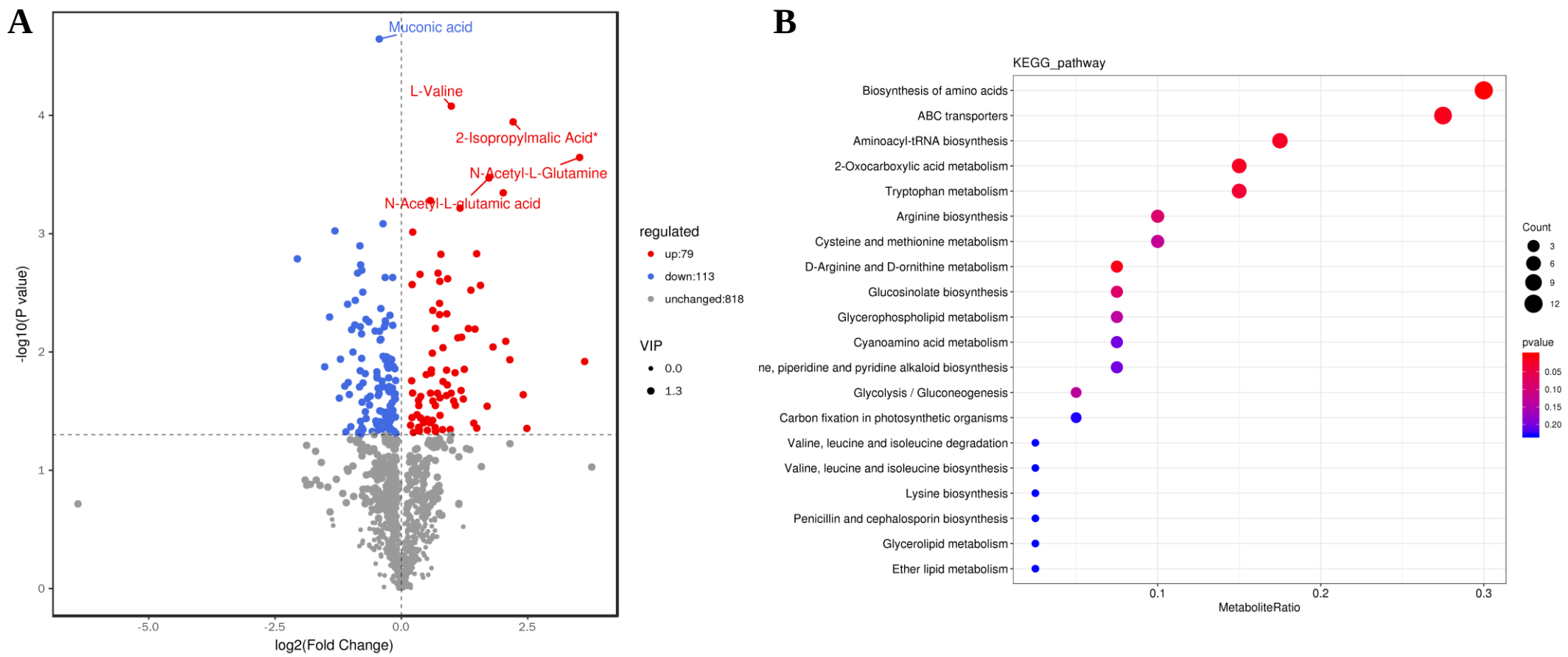


Supplementary Figure S1. Validation of the expression of 24 differentially expressed genes by a quantitative real-time (qRT)-PCR analysis. The genes and the corresponding qRT-PCR primers are listed in Supplementary Table 1.



Supplementary Figure S2. Results of a GO enrichment analysis of the differentially expressed genes in the C18 seedlings revealed by the comparison between the allantoin treatment and the control treatment. Functional enrichment of the up-regulated genes (**A**) and down-regulated genes (**B**).



Supplementary Figure S3. Differentially abundant metabolites (DAMs) in the C18 seedlings revealed by the comparison between the allantoin treatment and the control treatment. Volcano diagram of the DAMs (**A**). Enriched KEGG pathways among the DAMs (**B**).