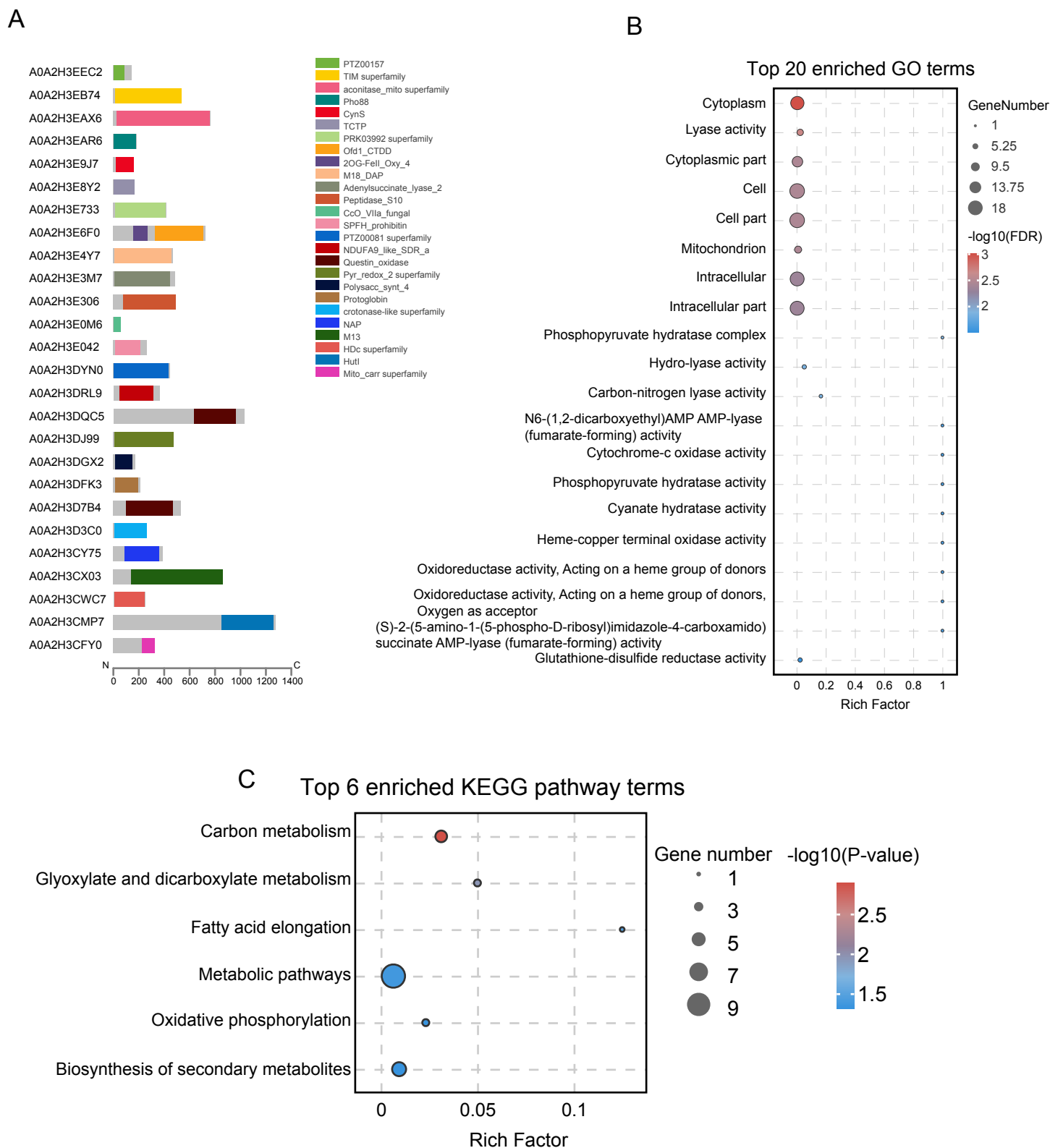




Supplementary figure 10. Protein domain architecture and GO/KEGG enrichment of the 26 significantly upregulated *A. gallica* proteins identified by LC-MS/MS as potential interactors of the GFP protein. (A) 26 protein domain architecture with different colors represent distinct protein domains (see legend on the right), and the horizontal axis indicates protein sequence length (amino acids) from the N-terminus to the C-terminus. (B) Gene Ontology (GO) enrichment analysis showing the top 20 enriched GO terms for the genes encoding the 26 candidate proteins. Dot size represents the number of genes assigned to each term (Gene number), dot color indicates statistical significance ($-\log_{10}(\text{FDR})$), and the horizontal axis shows the Rich Factor. (C) KEGG pathway enrichment analysis showing the top 6 enriched pathways for the same gene set. Dot size represents gene number, dot color indicates $-\log_{10}(\text{P-value})$, and the horizontal axis shows the rich factor.