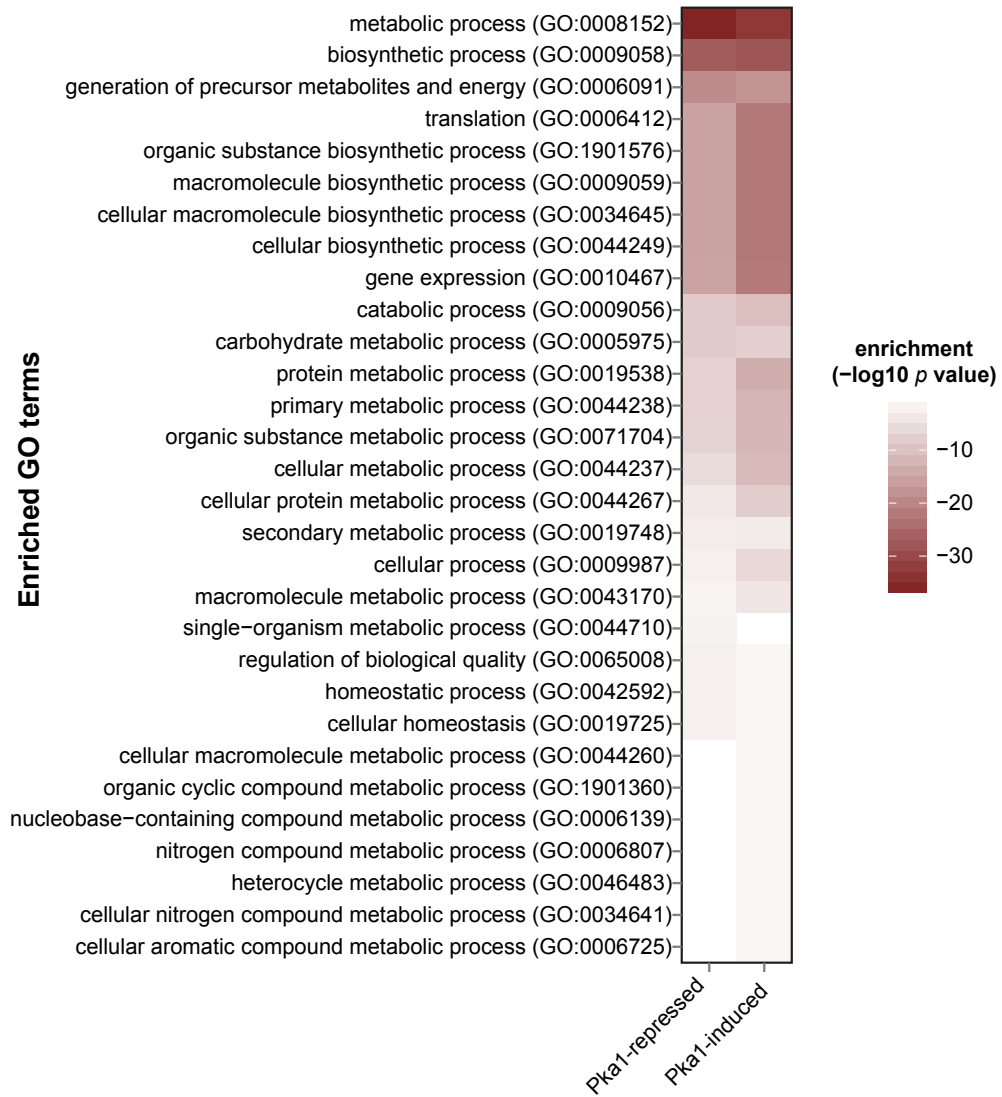
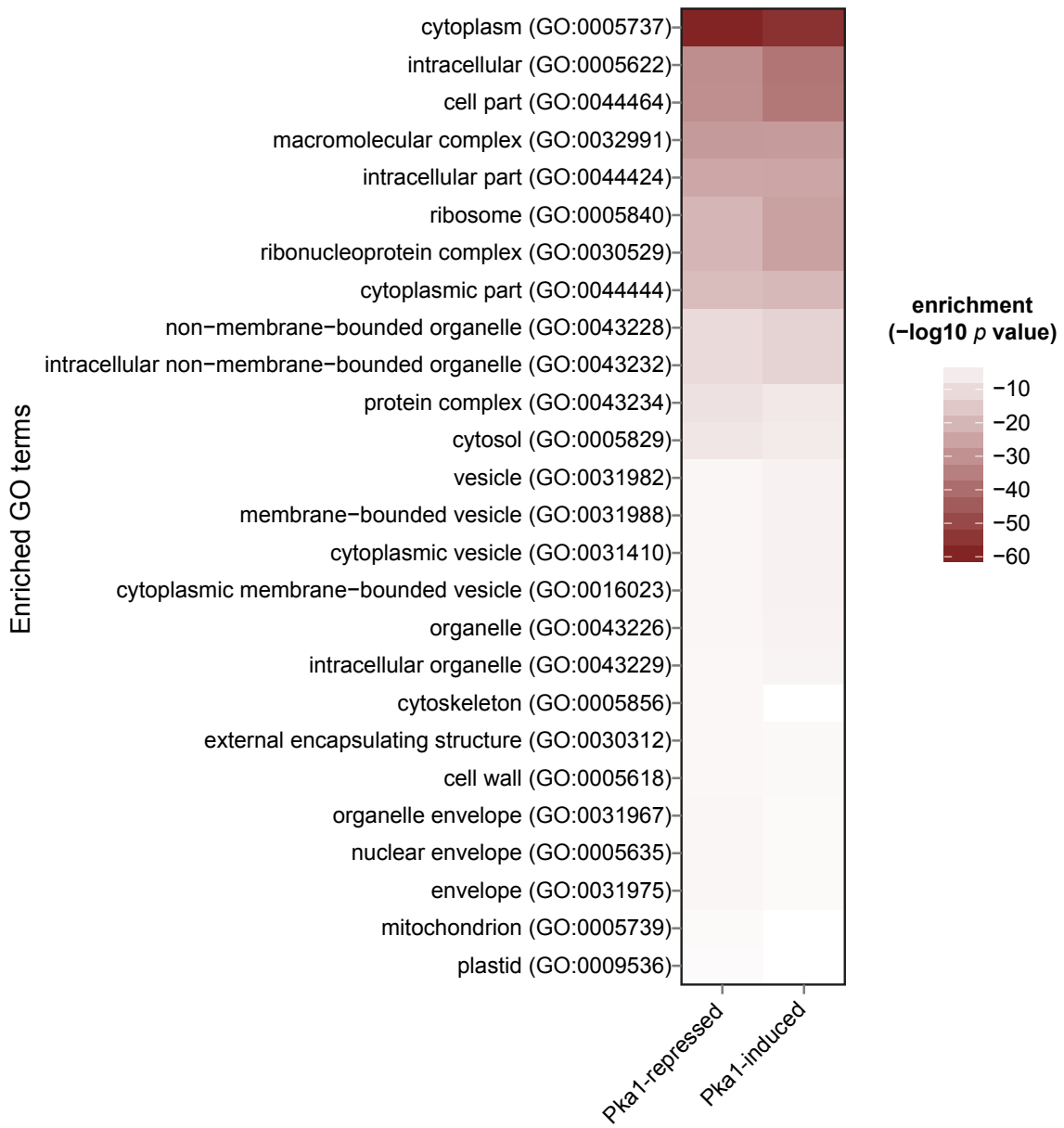


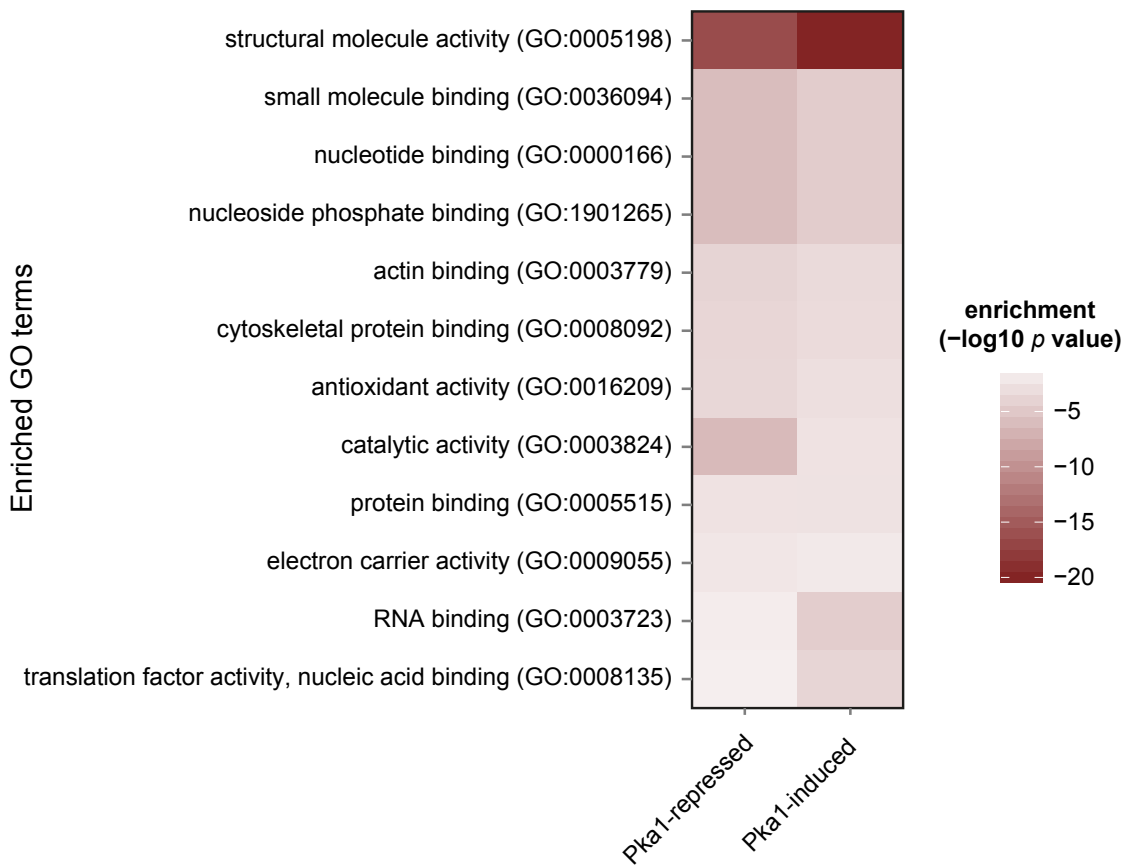
A



B



C



D

GO category ^a	<i>p</i> -value ^b
Translation	3.49e ⁻¹⁵
Macromolecule biosynthetic process	3.49e ⁻¹³
Cellular macromolecule biosynthetic process	3.49e ⁻¹³
Cellular biosynthetic process	3.49e ⁻¹³
Organic substance biosynthetic process	3.49e ⁻¹³
Gene expression	6.85e ⁻¹³
Biosynthetic process	3.56e ⁻¹¹
Metabolic process	3.87e ⁻⁹
Generation of precursor metabolites and energy	5.50e ⁻⁷
Protein metabolic process	1.06e ⁻⁵
Cellular protein metabolic process	6.35e ⁻⁵
Cellular metabolic process	3.60e ⁻⁴
Primary metabolic process	9.32e ⁻³
Macromolecule metabolic process	9.63e ⁻³
Organic substance metabolic process	1.24e ⁻²
Cellular macromolecule metabolic process	4.32e ⁻²

Figure S1. Enrichment of genes represented in the proteome analysis grown upon modulation of *PKA1* expression compared to all genes present in the genome. The enrichment was based on GO terms associated with biological processes (A), cellular components (B), and molecular functions (C). Additionally, enrichment of Pka1-regulated genes was performed based on biological classification represented in the proteome analysis (D). Strains were grown under Pka1-repressed (glucose-containing medium) or Pka1-induced (galactose-containing medium) conditions. Statistical analysis of the dataset was performed using the Benjamini and Hochberg false discovery rate multiple testing correction ($p\text{-value} < 0.05$).