

Supplementary Table S2. Functional enrichment of significantly downregulated proteins ($\log_2FC < -0.58$). Gene Ontology (GO), KEGG (Kyoto Encyclopaedia of Genes and Genomes) pathway, annotated keyword (UniProt), and reactome pathway enrichment analyses were performed against the background list of all expressed proteins using the ‘Analysis’ tab in the STRING-DB v12.0 (Szklarczyk et al., 2023), with default settings and an FDR threshold of < 0.05 .

Category	Term ID	Term description	Observed gene count	Background gene count	Strength	Signal	FDR
GO Function	GO:0016491	Oxidoreductase activity	49	281	0.37	0.65	1.60E-05
GO Function	GO:0016614	Oxidoreductase activity, acting on CH-OH group of donors	17	64	0.56	0.48	0.0057
GO Function	GO:0016616	Oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	16	56	0.59	0.49	0.0057
KEGG Pathways	map00010	Glycolysis / Gluconeogenesis	20	75	0.56	0.64	0.00038
KEGG Pathways	map00051	Fructose and mannose metabolism	10	18	0.88	0.77	0.00045
KEGG Pathways	map01100	Metabolic pathways	85	776	0.17	0.42	0.00058
KEGG Pathways	map00620	Pyruvate metabolism	12	50	0.51	0.37	0.022
KEGG Pathways	map01110	Biosynthesis of secondary metabolites	38	307	0.22	0.29	0.0303
KEGG Pathways	map00030	Pentose phosphate pathway	7	21	0.66	0.35	0.0364
KEGG Pathways	map01200	Carbon metabolism	20	127	0.33	0.3	0.0364
UniProt Annotated Keywords	KW-0812	Transmembrane	61	364	0.36	0.75	1.33E-07
UniProt Annotated Keywords	KW-1133	Transmembrane helix	60	359	0.36	0.74	1.33E-07
UniProt Annotated Keywords	KW-0472	Membrane	62	413	0.31	0.65	1.69E-06