

**Supplementary Table S3.** Functional enrichment of significantly upregulated 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 Process	GO:0044282	Small molecule catabolic process	19	61	0.55	0.4	0.0153
GO Process	GO:0046395	Carboxylic acid catabolic process	17	53	0.56	0.4	0.0166
GO Component	GO:0005739	Mitochondrion	43	218	0.35	0.52	0.00064
KEGG Pathways	map01100	Metabolic pathways	96	776	0.15	0.33	0.01
KEGG Pathways	map00280	Valine, leucine and isoleucine degradation	14	47	0.53	0.41	0.0141
KEGG Pathways	map01212	Fatty acid metabolism	11	35	0.55	0.35	0.0305
KEGG Pathways	map01110	Biosynthesis of secondary metabolites	44	307	0.21	0.28	0.0363
Reactome Pathways	MAP-1268020	Mitochondrial protein import	11	20	0.79	0.55	0.0047
Reactome Pathways	MAP-1430728	Metabolism	67	494	0.19	0.27	0.0391
Reactome Pathways	MAP-9609507	Protein localization	17	47	0.61	0.52	0.0041