

Figure S1. Oxidative phosphorylation pathways of the KEGG pathway annotation analysis of the differentially expressed proteins. The parts marked in red are proteins annotated to a node (enzyme) on the pathway. Arrows indicate the mode of action. Small circles represent small molecules in the pathway.

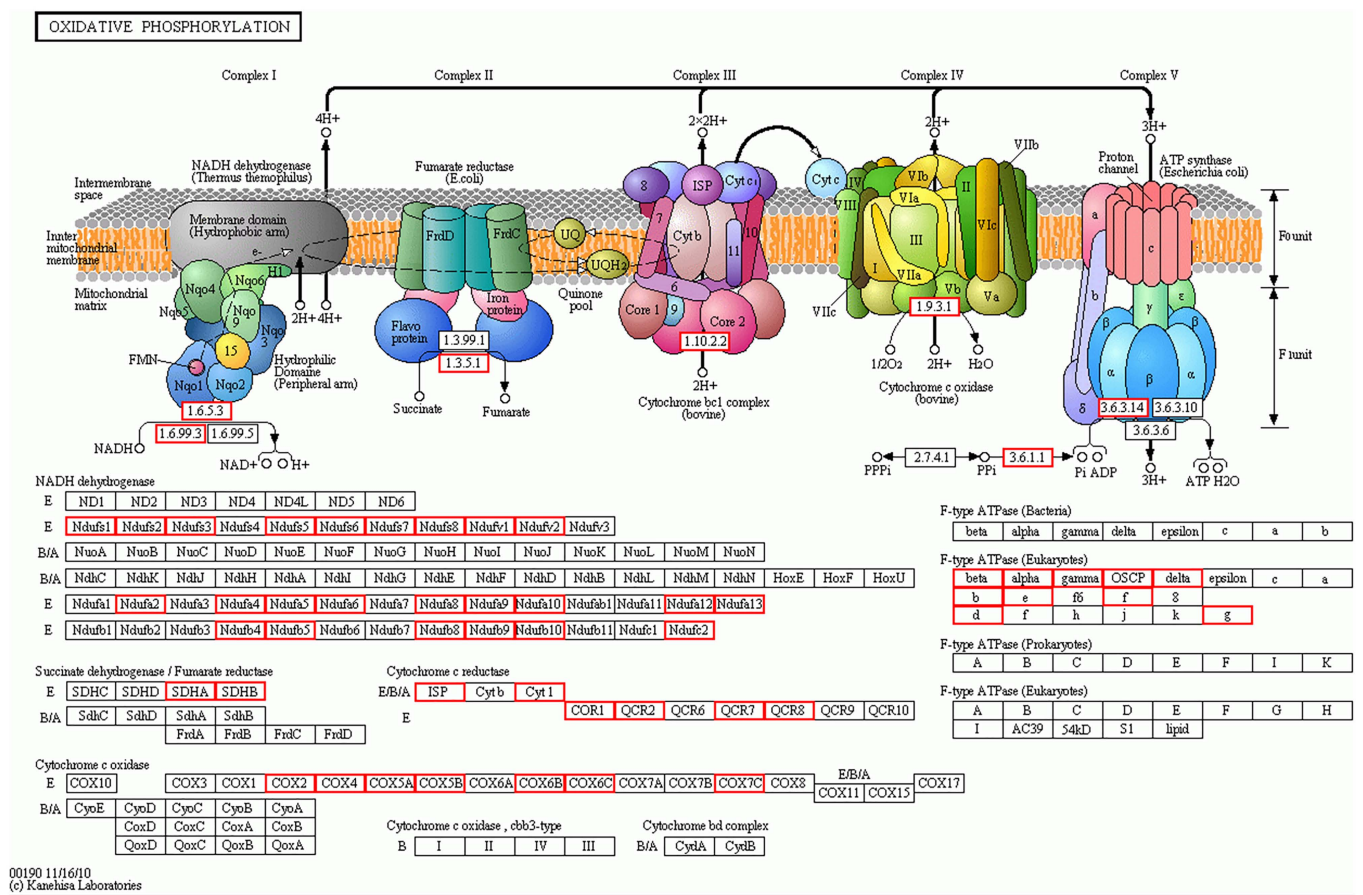


Figure S2. Cellular compartment enrichment analysis. Differentially expressed proteins were mainly located in the mitochondrion, mitochondrial matrix, mitochondrial intermembrane, mitochondrial intermembrane space, mitochondrial inner membrane, mitochondrial outer membrane and mitochondrial respiratory chain complex I.

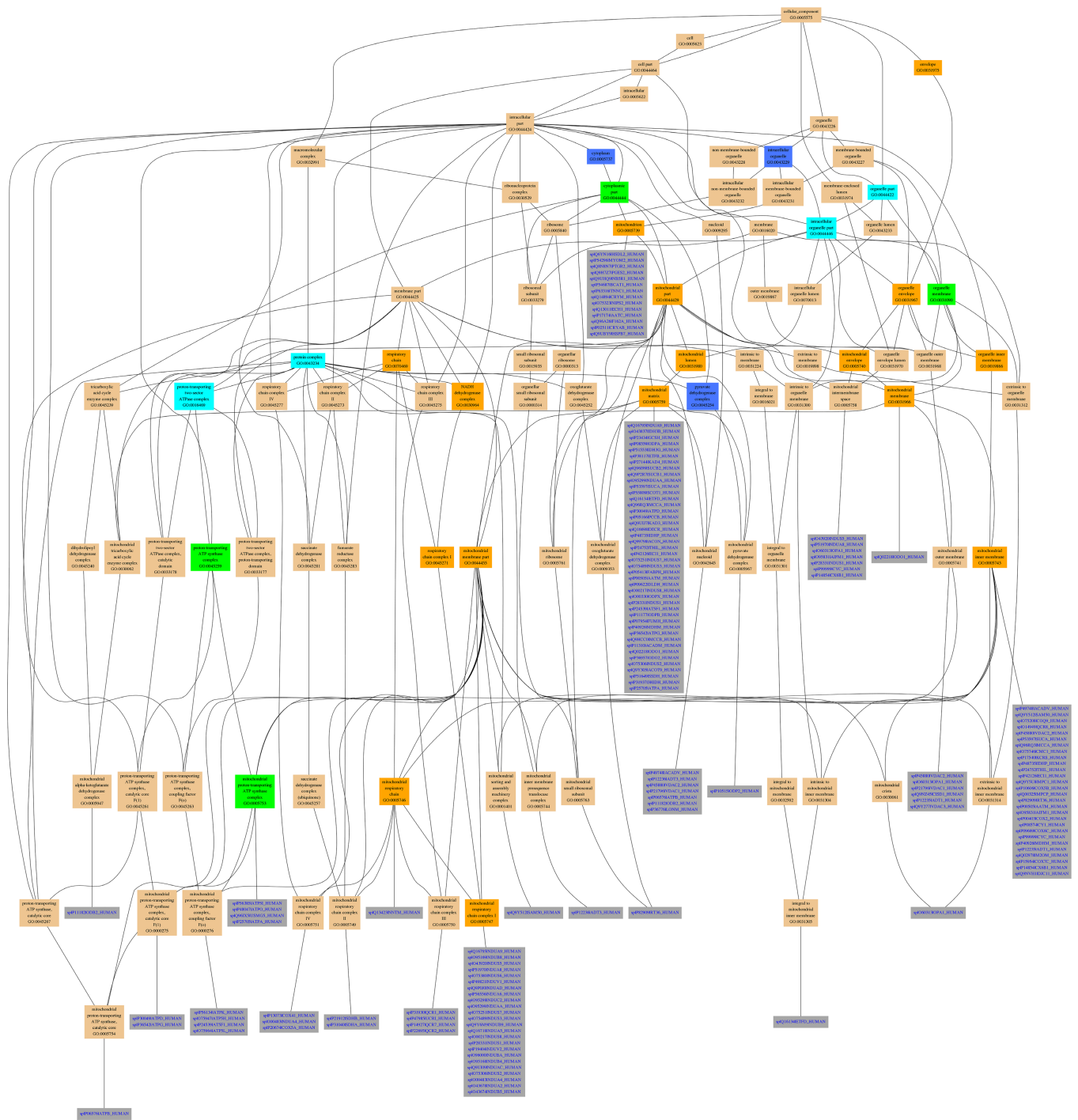
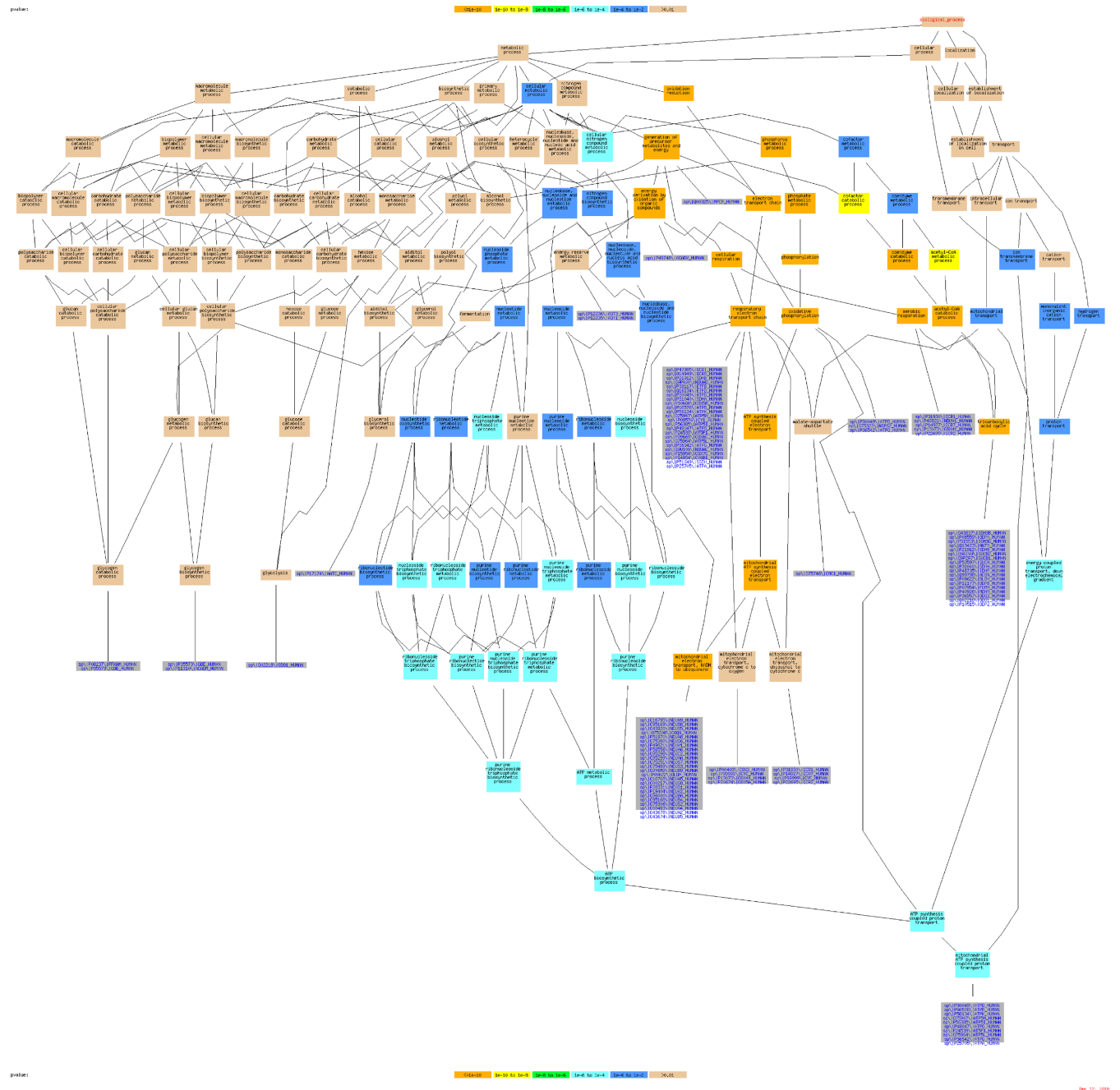


Figure S3. Biological process enrichment analysis. Respiratory electron transport chain, tricarboxylic acid cycle, mitochondrial electron transport NADH to ubiquinone and mitochondrial ATP synthase coupled proton transport are included.



[illegible]