

Figure S1. Subcellular localization of proteins with decreased expression. The majority of proteins with decreased expression were distributed in 'cytoplasm' (41.51%), 'nucleus' (27.62%) and 'plasma membrane' (8.58%).

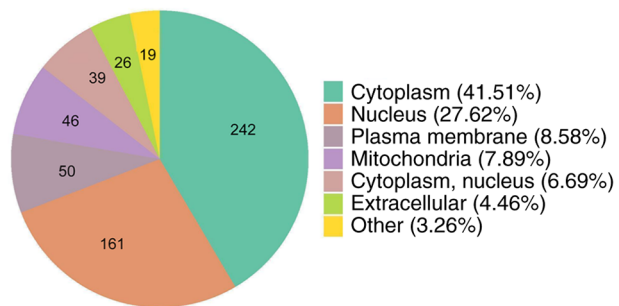


Figure S2. Functional enrichment analysis of proteins with decreased expression. (A) Gene Ontology enrichment analysis of biological process, cellular component and molecular function. (B) Kyoto Encyclopedia of Genes and Genomes pathway enrichment analysis. (C) Protein domain enrichment analysis.

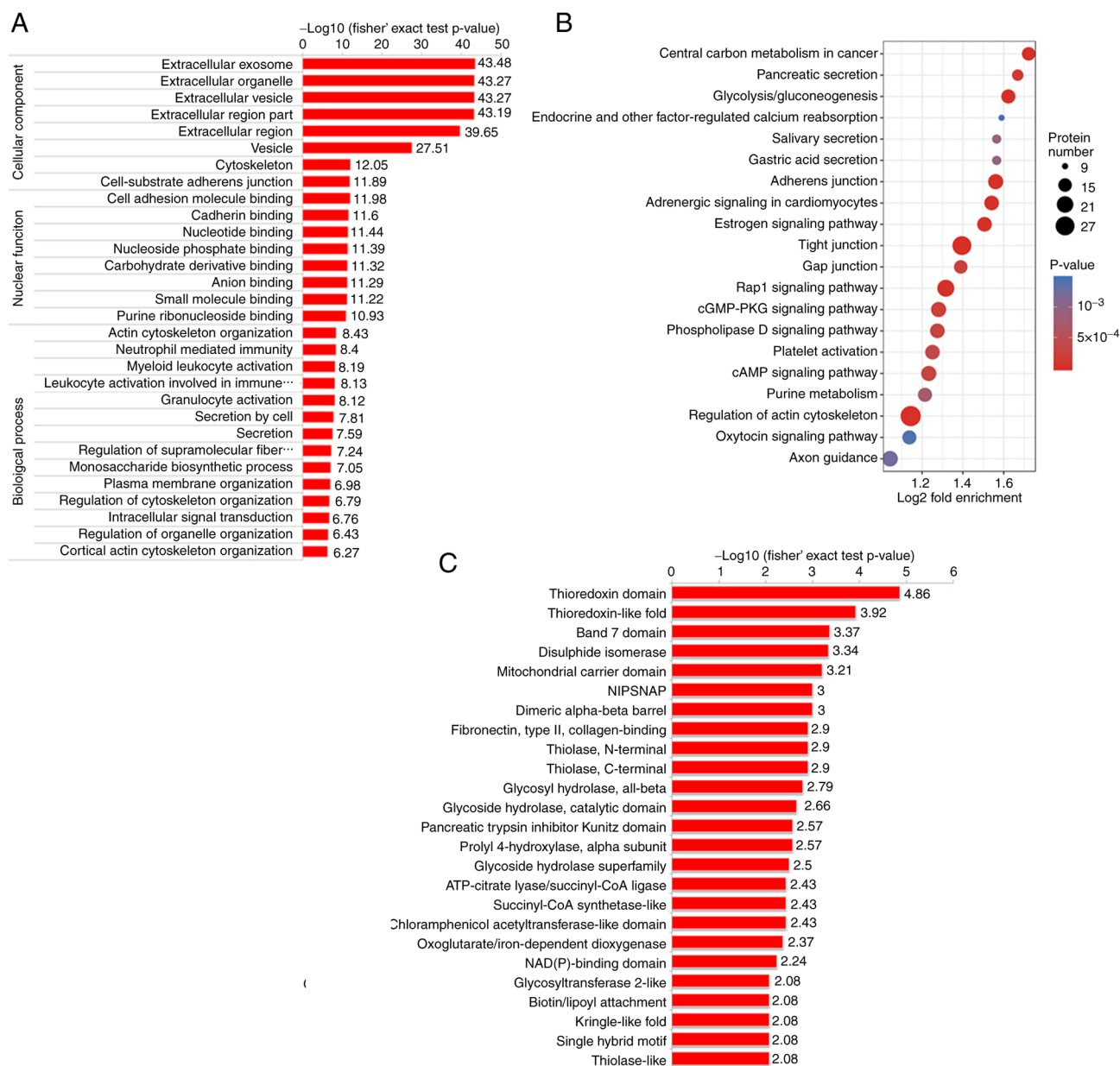


Figure S3. PPI network analysis of proteins with increased expression. Network nodes represent proteins; edges represent protein-protein associations. Line thickness indicates the strength of supporting data. The hub shows proteins with functions in relation to oxidative phosphorylation. PPI, protein-protein interaction.

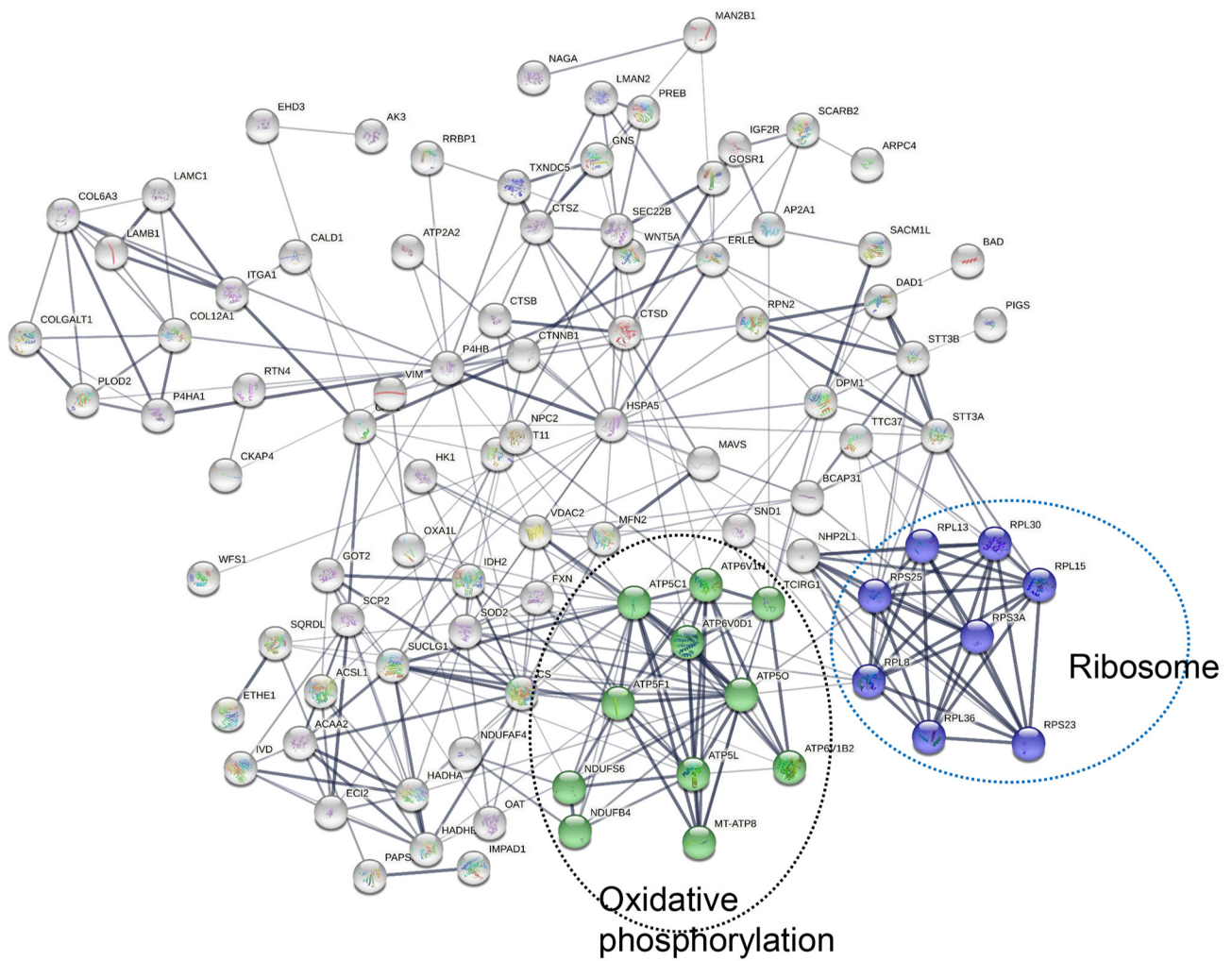


Figure S4. Validation of six selected proteins by PRM. A total of four candidate proteins displayed similar trends with 4D label-free quantitative proteomics analysis. PRM, parallel reaction monitoring; TCIRG1, T cell immune regulator 1.

