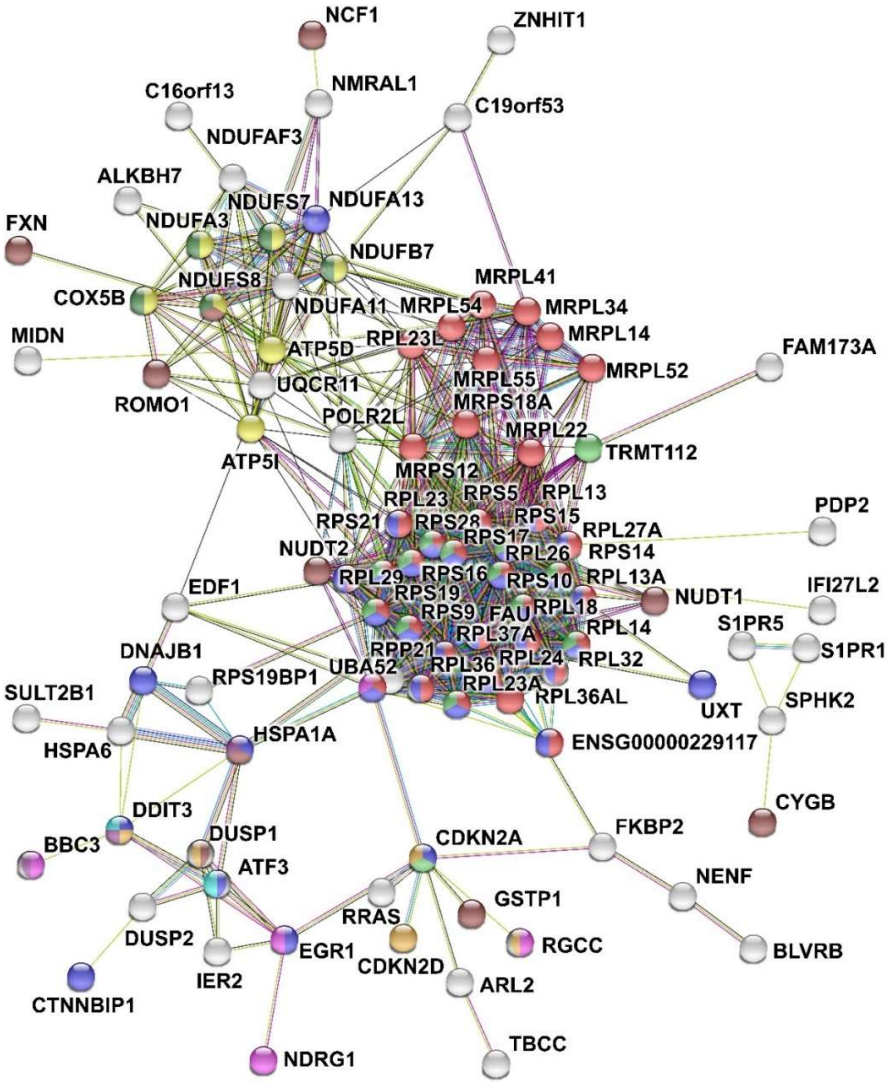
Supplementary Figure 1



Upregulated genes

Network Stats
number of nodes: 135
number of edges: 691
average node degree: 10.2
avg. local clustering coefficient: 0.516
expected number of edges: 176
PPI enrichment P value: < 1.0E-16

GO-term	description	FDR
GO:0043604	Amide biosynthetic process	5.71E-27
GO:0010629	Negative regulation of gene expression	6.39E-10
GO:0042254	Ribosome biogenesis	7.97E-09
GO:0006119	Oxidative phosphorylation	0.00022
GO:0006979	Response to oxidative stress	0.00033
GO:0071456	Cellular response to hypoxia	0.0014
GO:0042775	Mitochondrial ATP synthesis coupled electron transport	0.0047
GO:0007050	Cell cycle arrest	0.0106
GO:1902235	Regulation of ER stress-induced apoptosis	0.0233
GO:0036499	PERK-mediated unfolded protein response	0.0482