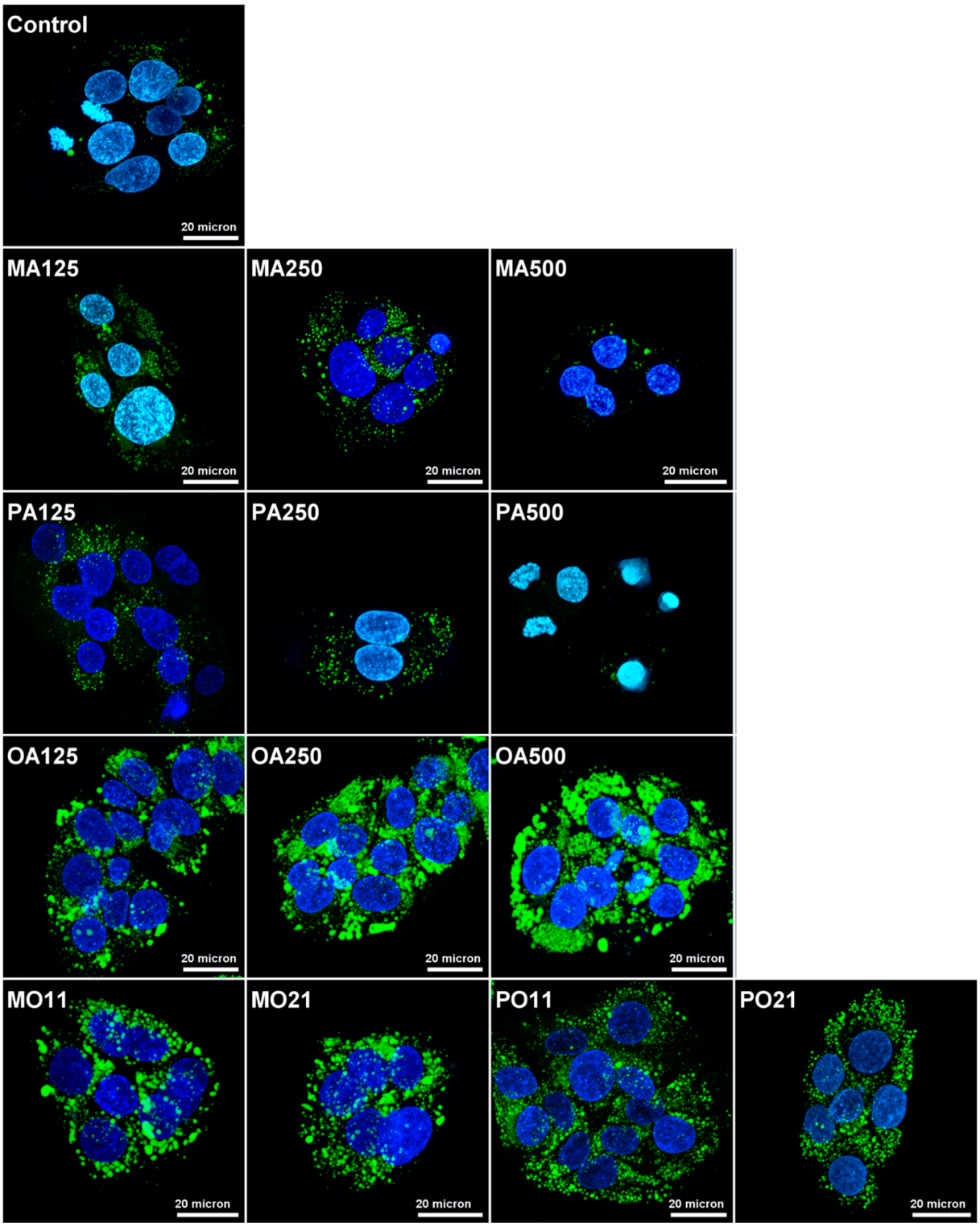
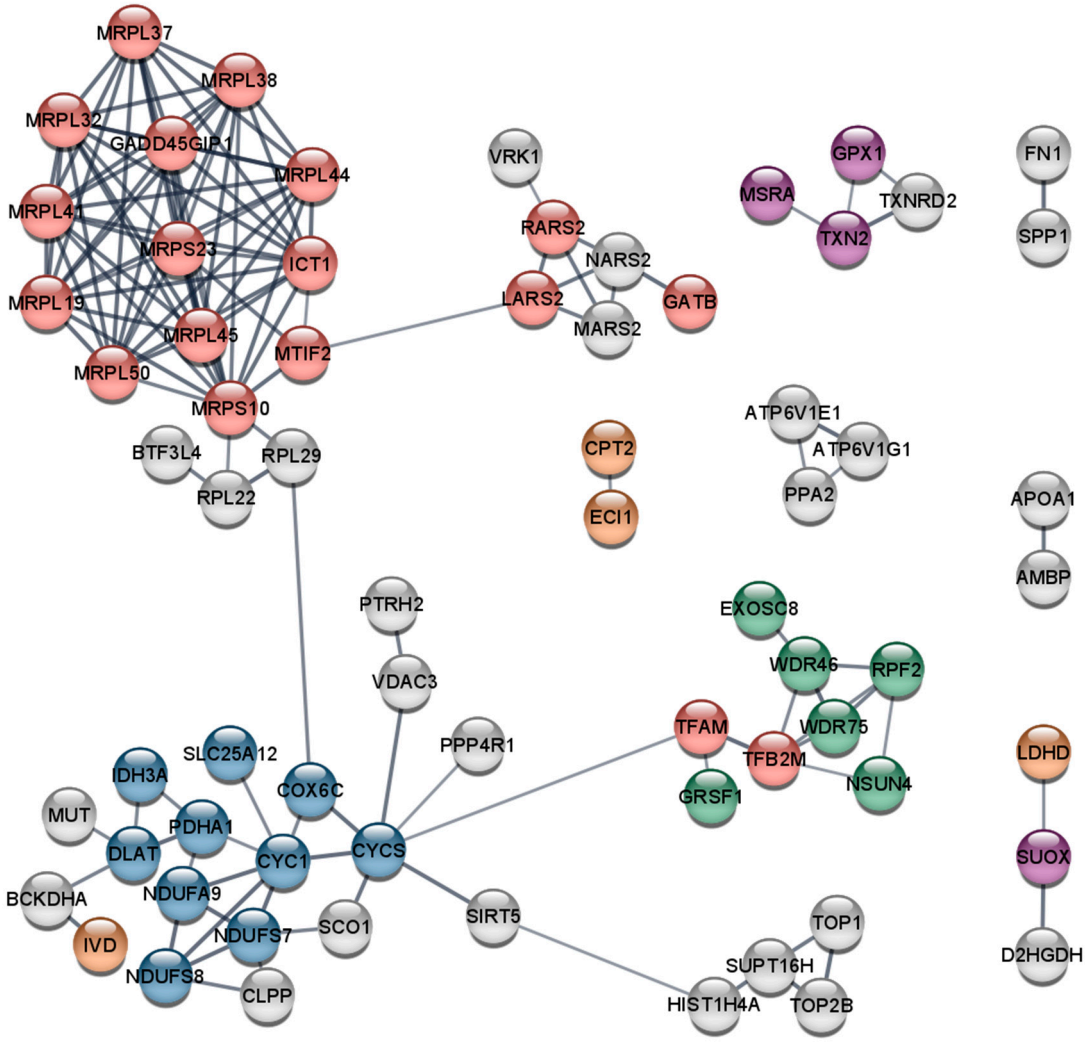


Figure S1: Representative images of HepG2 cells after lipid loading for 24 hours. LDs stained with BODIPY™ 493/503 and nuclei with DAPI (LD= green; nuclei= blue). LD: lipid droplets; MA: myristic acid; PA: palmitic acid; OA: oleic acid; MO: myristic: oleic acid; PO: palmitic: oleic acid; 11: 125µM: 125 µM; 21: 250 µM: 125 µM.



GO-term	strength	FDR
Mitochondrial gene expression	1.33	4.94e-15
Cellular respiration	1.05	4.59e-06
Monocarboxylic acid catabolic process	0.91	0.0317
ncRNA metabolic process	0.69	0.00058
Sulfur compound metabolic process	0.66	0.0237

Figure S2: String analysis of proteins exhibiting a ≥1.5-fold change following MA500 treatment. The minimum required interaction score was set to 0.7 (high confidence) and disconnected nodes were excluded from the display. Nodes were coloured correspondingly to selected GO biological process search results. MA treatment resulted in an upregulation of proteins associated with mitochondrial protein synthesis as well as oxidative phosphorylation. MA500: 500 µM myristic acid for 24 h.

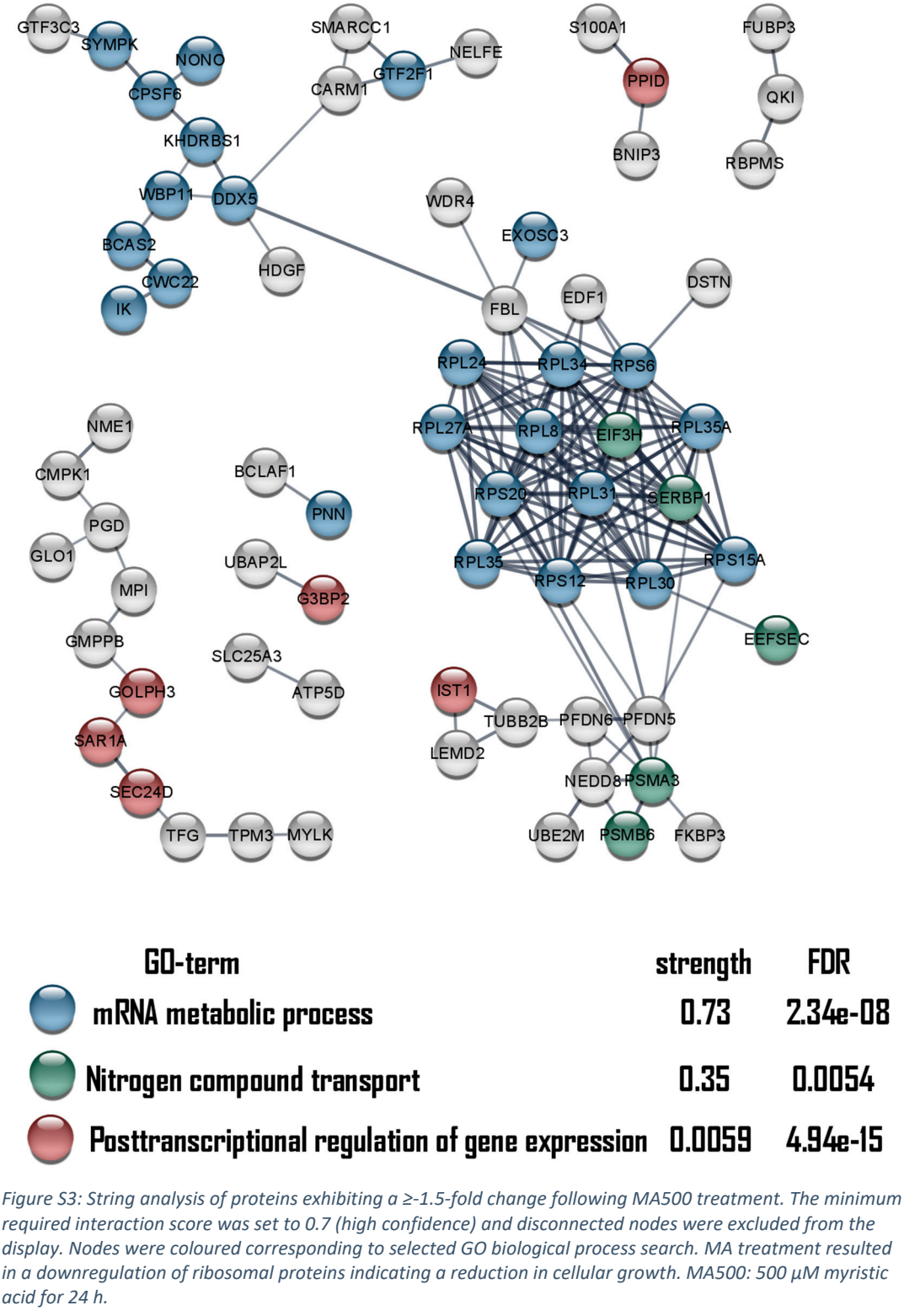


Figure S3: String analysis of proteins exhibiting a ≥-1.5-fold change following MA500 treatment. The minimum required interaction score was set to 0.7 (high confidence) and disconnected nodes were excluded from the display. Nodes were coloured corresponding to selected GO biological process search. MA treatment resulted in a downregulation of ribosomal proteins indicating a reduction in cellular growth. MA500: 500 µM myristic acid for 24 h.

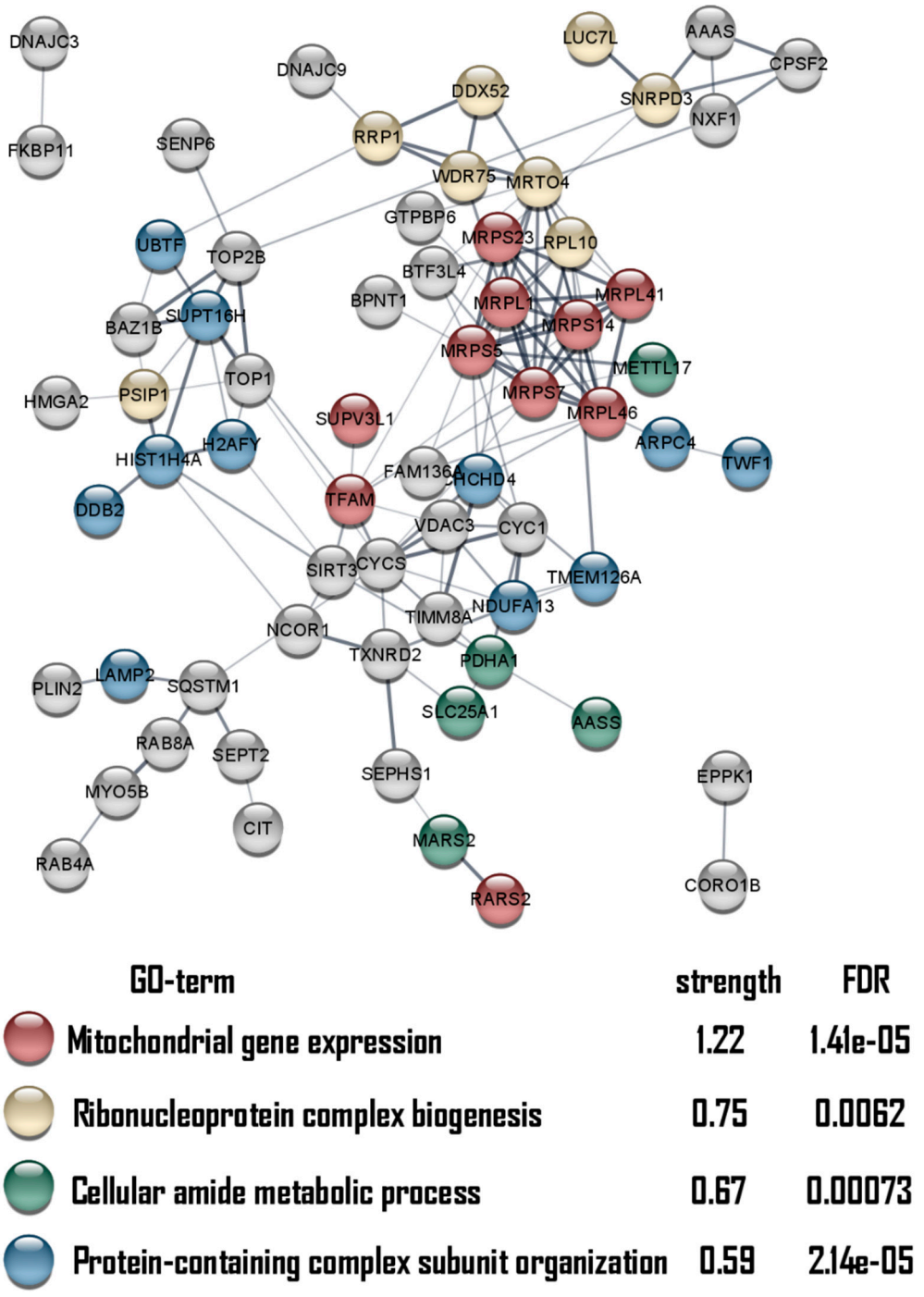


Figure S4: String analysis of proteins exhibiting a ≥1.5-fold change following PA500 treatment. The minimum required interaction score was set to 0.7 (high confidence) and disconnected nodes were excluded from the display. Nodes were coloured correspondingly to selected GO biological process search results. PA treatment resulted in an upregulation of proteins associated with mitochondrial protein synthesis.PA500: 500 µM palmitic acid for 24 h.

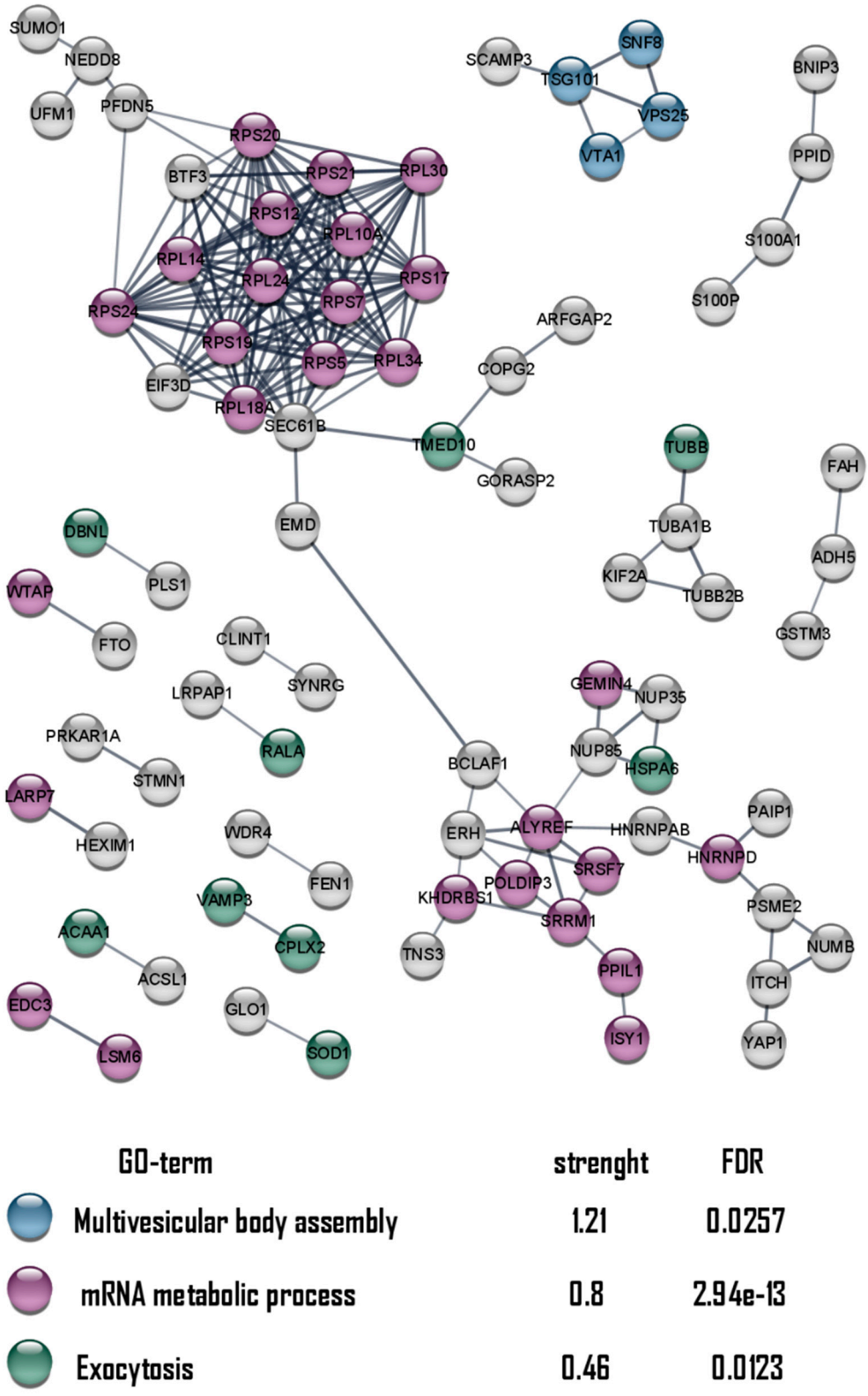


Figure S5: String analysis of proteins exhibiting a ≥-1.5-fold change following PA500 treatment. The minimum required interaction score was set to 0.7 (high confidence) and disconnected nodes were excluded from the display. Nodes were coloured correspondingly to selected GO biological process search. PA treatment resulted in a downregulation of ribosomal proteins indicating a reduction of cellular growth. PA500: 500 µM palmitic acid for 24 h.

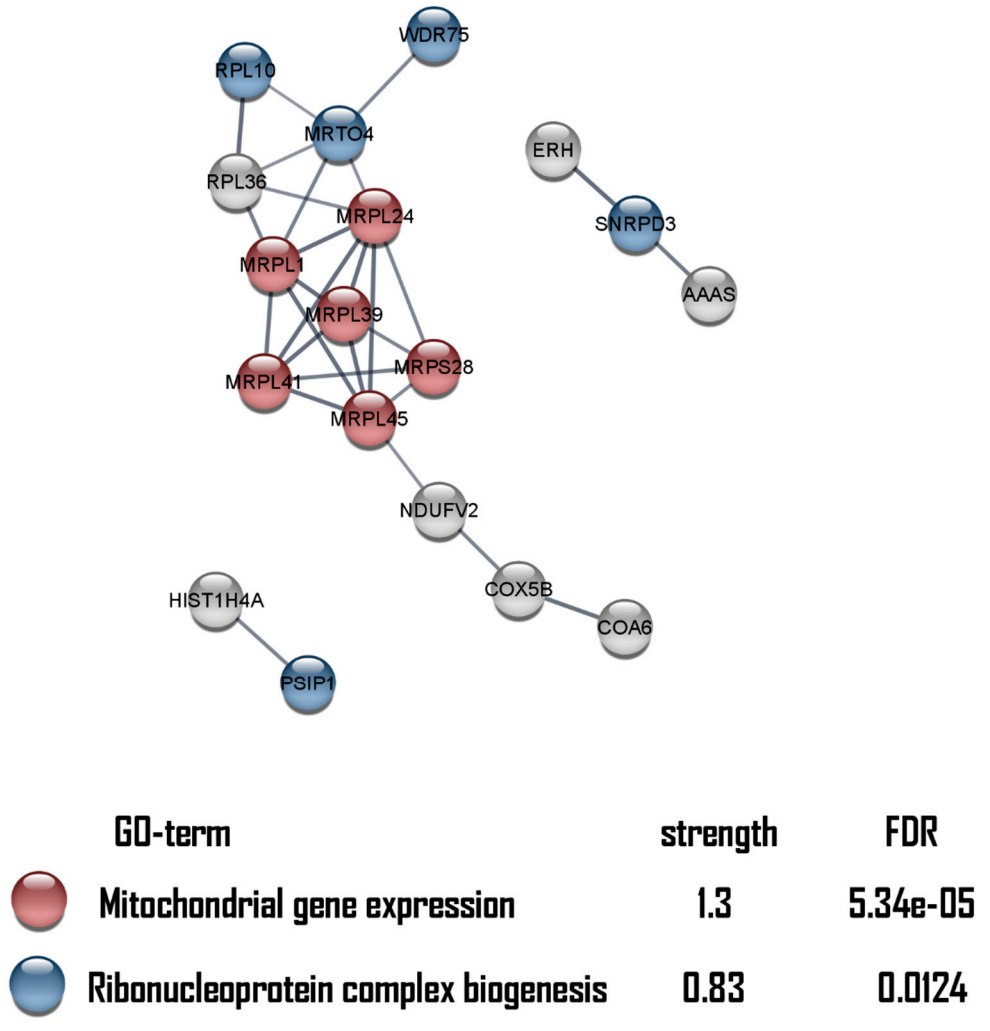


Figure S6: String analysis of proteins exhibiting a ≥1.5-fold change following OA500 treatment. The minimum required interaction score was set to 0.7 (high confidence) and disconnected nodes were excluded from the display. Nodes were coloured correspondingly to selected GO biological process search results. Treatment with OA led to an increase of proteins associated with mitochondrial protein synthesis. OA500: 500 µM oleic acid for 24 h.

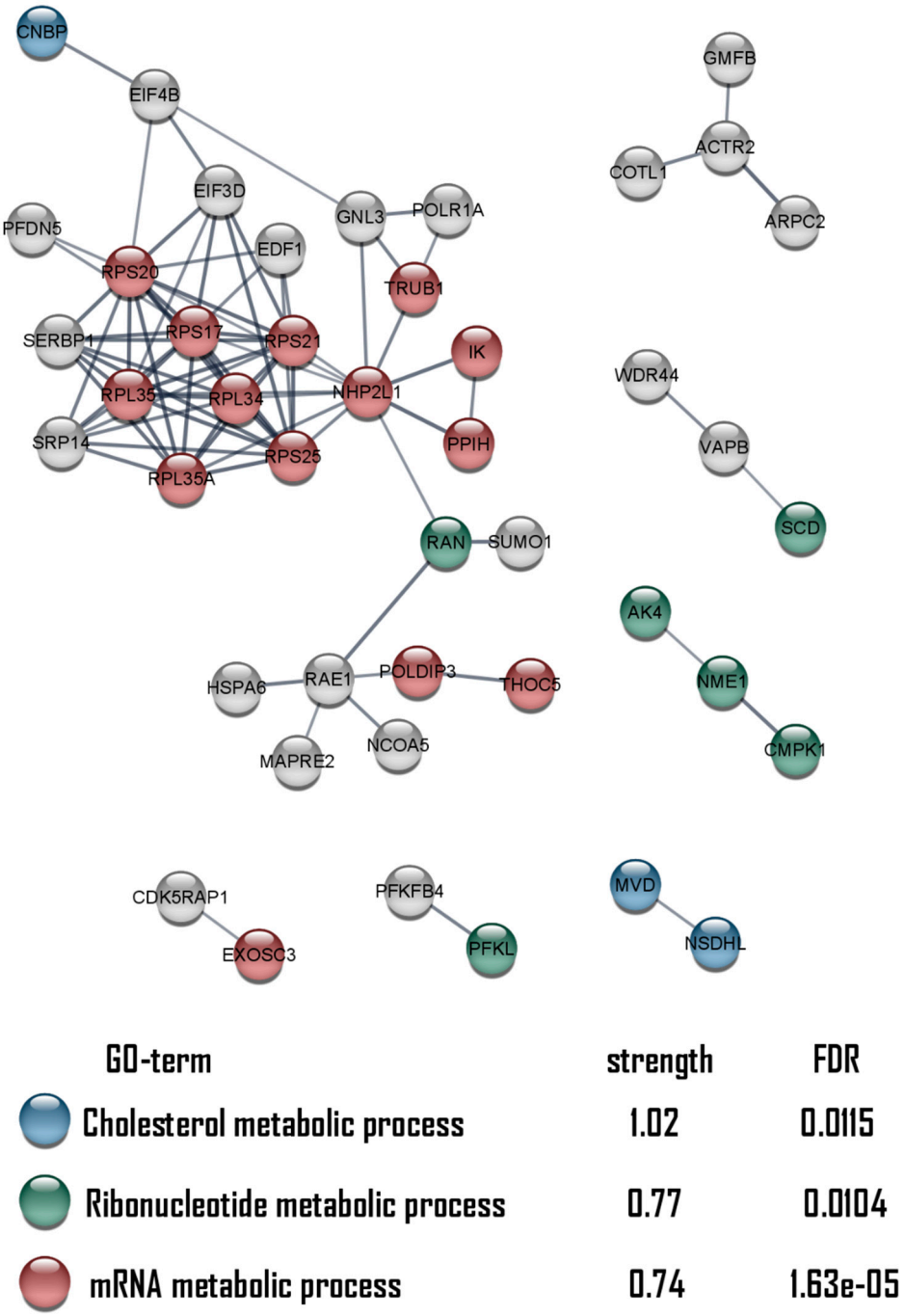


Figure S7: String analysis of proteins exhibiting a ≥-1.5-fold change following OA500 treatment. The minimum required interaction score was set to 0.7 (high confidence) and disconnected nodes were excluded from the display. Nodes were coloured correspondingly to selected GO biological process search results. OA treatment resulted in a downregulation of ribosomal proteins indicating a reduction of cellular growth. OA500: 500 µM oleic acid for 24 h.

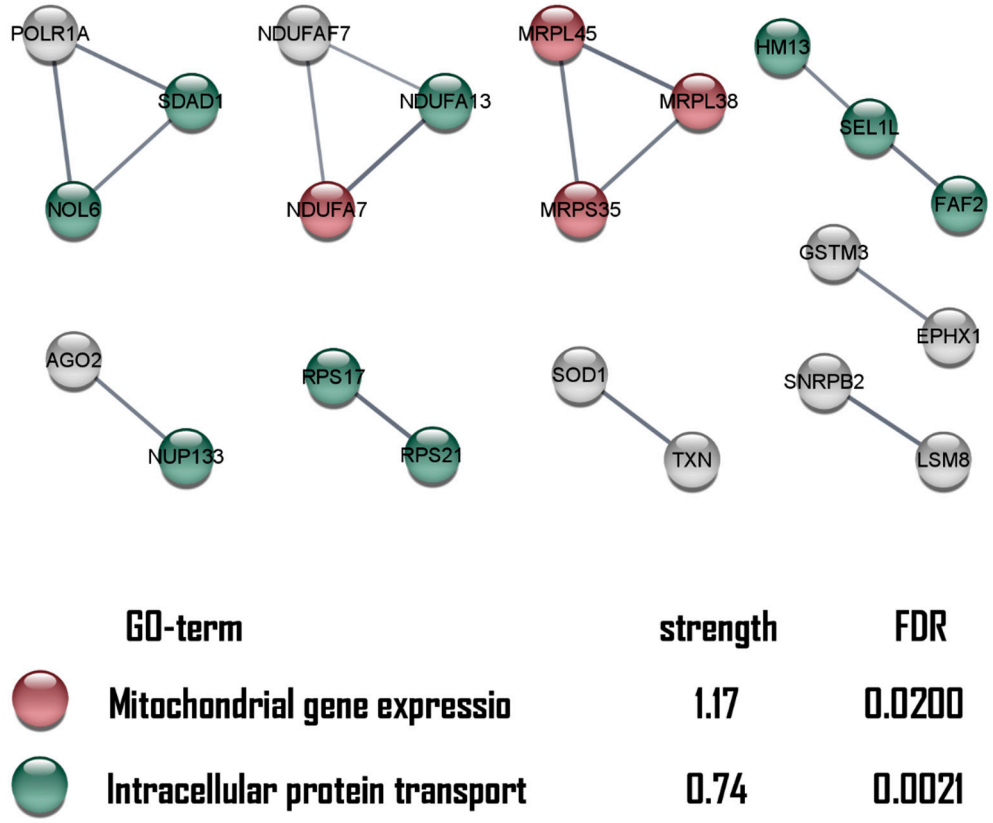


Figure S8: String analysis of proteins exhibiting a ≥1.5-fold change comparing MA250 treatment to MO21. The minimum required interaction score was set to 0.7 (high confidence) and disconnected nodes were excluded from the display. Nodes were coloured correspondingly to selected GO biological process search results. Compared to the prevention treatment, MA250 presented with an upregulation of proteins associated with mitochondrial and cytoplasmatic protein synthesis. MA250: 250 µM myristic acid for 24 h. MO21: 250 µM myristic acid: 125 µM oleic acid for 24 h.

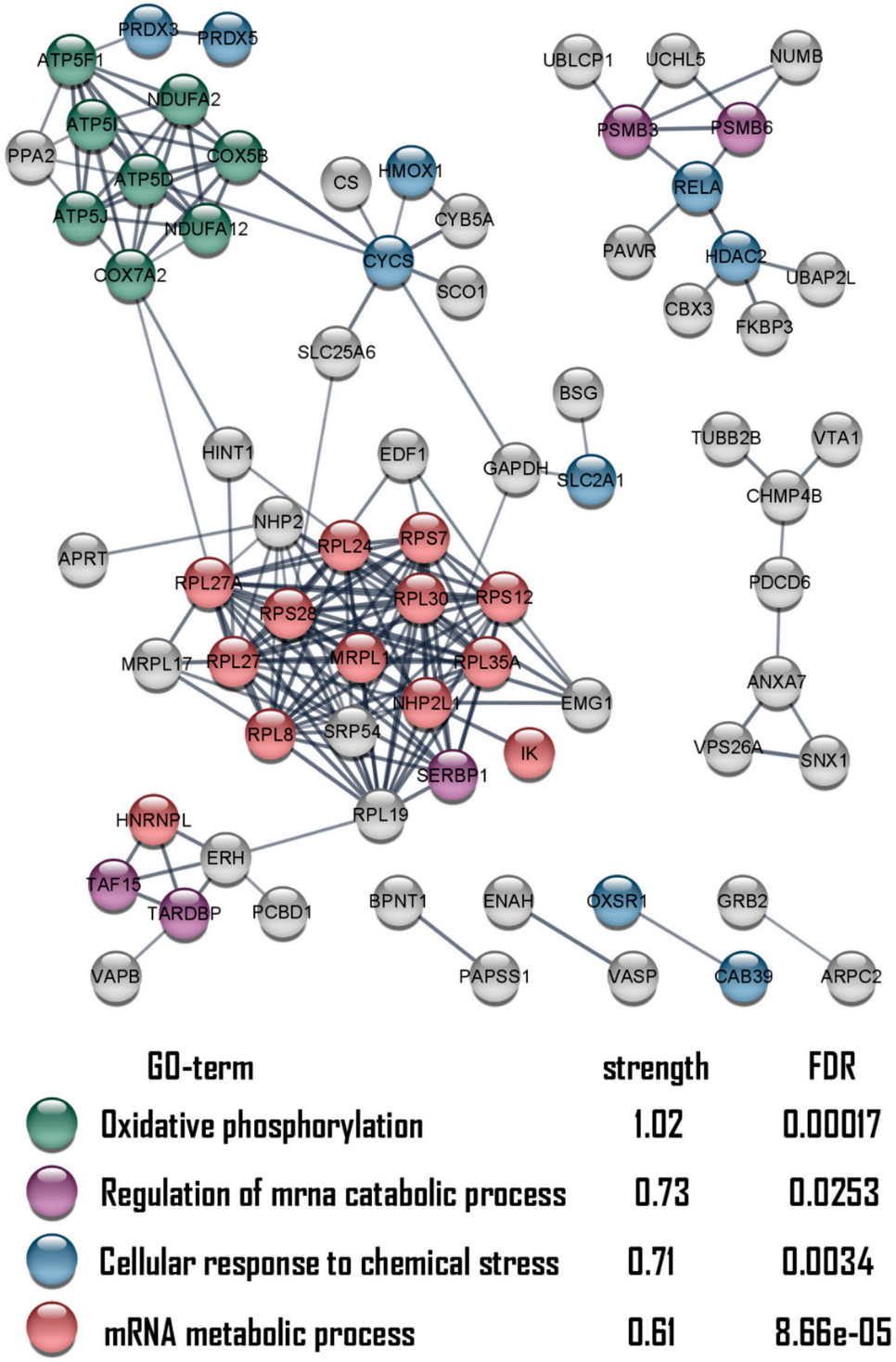


Figure S9: String analysis of proteins exhibiting a ≥-1.5-fold change comparing MA250 treatment to MO21. The minimum required interaction score was set to 0.7 (high confidence) and disconnected nodes were excluded from the display. Nodes were coloured correspondingly to selected GO biological process search results. In the prevention treatment proteins associated with oxidative phosphorylation and ribosomal proteins were found to be more abundant. The overabundance of ribosomal proteins corroborated the increase of proliferation rates back to control levels. MA250: 250 µM myristic acid for 24 h. MO21: 250 µM myristic acid: 125 µM oleic acid for 24 h.

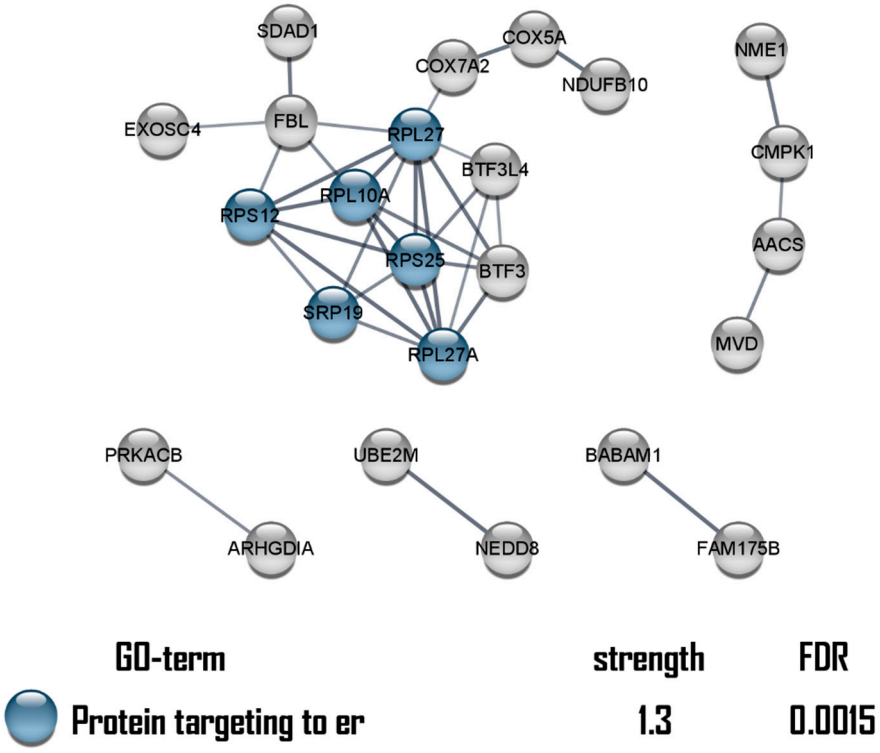


Figure S10: String analysis of proteins exhibiting a ≥1.5-fold change comparing PA250 treatment to PO21. The minimum required interaction score was set to 0.7 (high confidence) and disconnected nodes were excluded from the display. Nodes were coloured correspondingly to selected GO biological process search results. Compared to the prevention treatment, a subset of ribosomal proteins was found to be significantly enriched following PA treatment. PA250: 250 µM palmitic acid for 24 h. PO21: 250 µM palmitic acid: 125 µM oleic acid for 24 h.

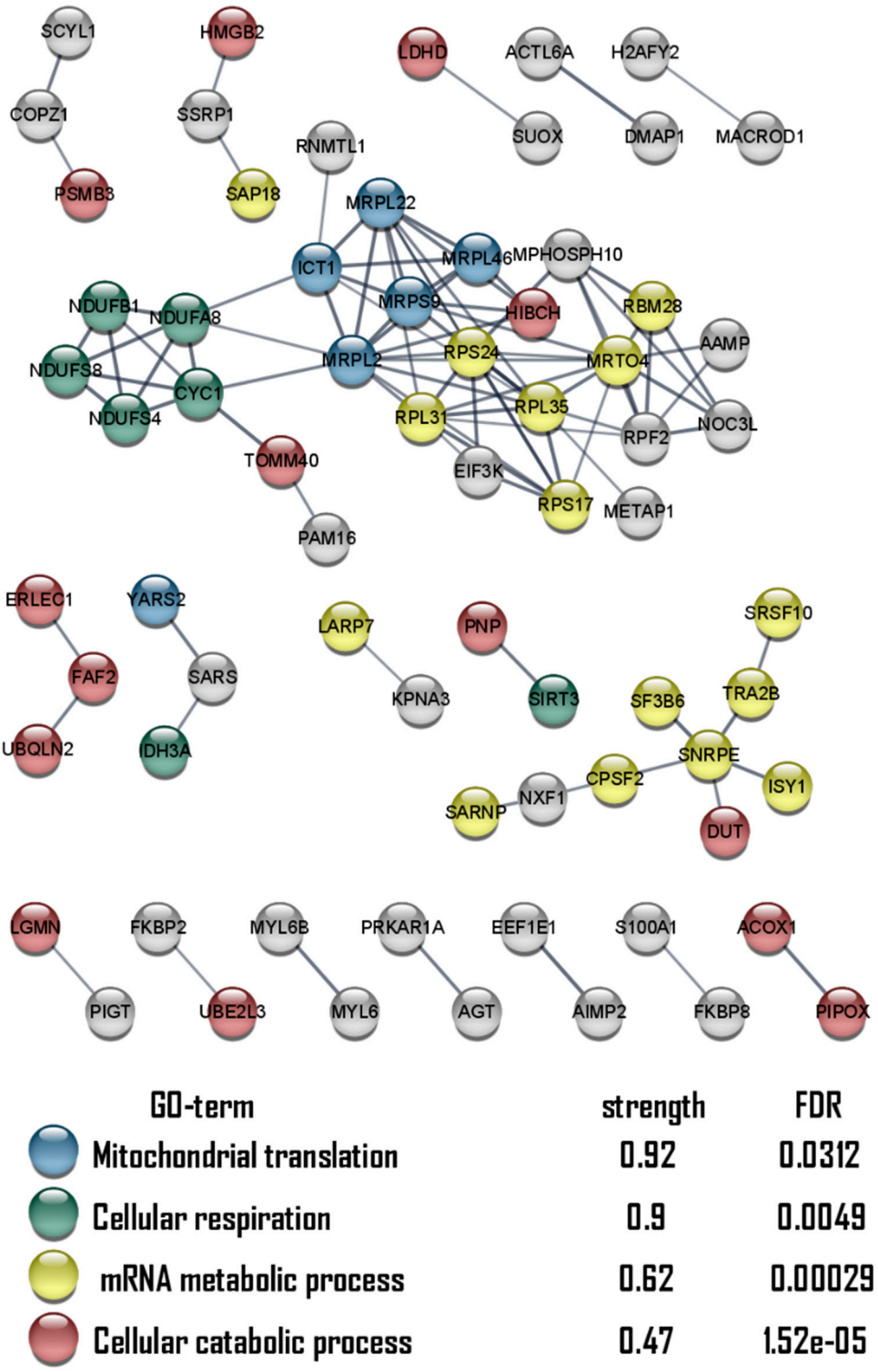


Figure S11: String analysis of proteins exhibiting a ≥-1.5-fold change comparing PA250 treatment to PO21. The minimum required interaction score was set to 0.7 (high confidence) and disconnected nodes were excluded from the display. Nodes were coloured correspondingly to selected GO biological process search results. Proteins associated with mitochondrial protein synthesis and oxidative phosphorylation, as well as a subset of ribosomal proteins was found to be significantly enriched in the prevention treatment. PA250: 250 µM palmitic acid for 24 h. PO21: 250 µM palmitic acid: 125 µM oleic acid for 24 h.