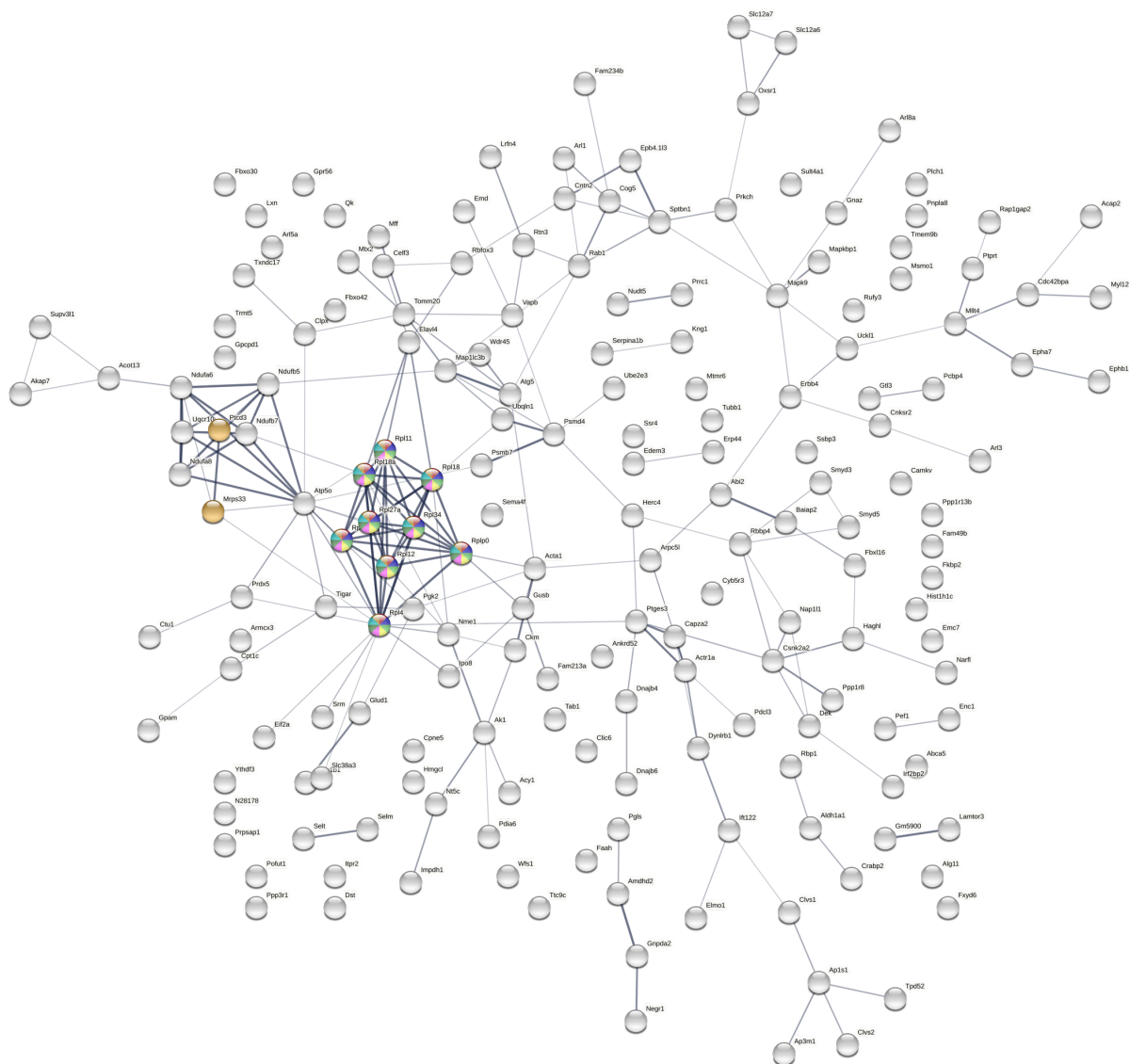


**FIGURE S3**



- **MMU-1799339** SRP-dependent cotranslational protein targeting to membrane  
Strength: 1.09; False Discovery rate: 0.00095
- **MMU-975956** Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)  
Strength: 1.08 ; False Discovery rate: 0.00095
- **MMU-72689** Formation of a pool of free 40S subunits  
Strength: 1.05; False Discovery rate: 0.0010
- **MMU-156827** L13a-mediated translational silencing of Ceruloplasmin expression  
Strength: 1.01; False Discovery rate: 0.0018
- **MMU-72706** GTP hydrolysis and joining of the 60S ribosomal subunit  
Strength: 1.0; False Discovery rate: 0.0018
- **MMU-975957** Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)  
Strength: 0.99; False Discovery rate: 0.0018
- **MMU-6791226** Major pathway of rRNA processing in the nucleolus and cytosol  
Strength: 0.8; False Discovery rate: 0.0254
- **MMU-72766** Translation  
Strength: 0.77; False Discovery rate: 0.0064

Strength:

Log10(observed / expected). This measure describes how large the enrichment effect is. It's the ratio between i) the number of proteins in your network that are annotated with a term and ii) the number of proteins that we expect to be annotated with this term in a random network of the same size.

False Discovery Rate:

This measure describes how significant the enrichment is. Shown are p-values corrected for multiple testing within each category using the Benjamini–Hochberg procedure.