proteasome complex (sensu Eukaryota), GO:0000502 signalosome complex, GO:0008180 RNA processing, GO:0006396 ribosomal large subunit biogenesis and assembly, GO:0042273 nucleoplasm, GO:0005654 transferase activity, transferring phosphorus-containing groups, GO:0016772 nuclear export, GO:0051168 DNA recombination, GO:0006310 nuclear chromatin, GO:0000790 mitotic cell cycle, GO:0000278 endoplasmic reticulum, GO:0005783 plasma membrane, GO:0005886 vacuolar membrane, GO:0005774 nitrogen compound metabolic process, GO:0006807 protein sumoylation, GO:0016925 structural constituent of ribosome, GO:0003735 regulation of protein metabolic process, GO:0051246

Golgi apparatus, GO:0005794

Figure S7: GO analysis of clustered PPI network profile

iPAGE (<a href="http://tavazoielab.princeton.edu/iPAGE/">http://tavazoielab.princeton.edu/iPAGE/</a>) analysis of clustered protein-protein interaction data from BioGRID. Clusters include groups enriched for biological processes such as RNA processing and protein sumoylation, cellular components such as nucleoplasm and proteosomal complex, and molecular functions such as transferase activity. The columns represent protein clusters and correspond to the columns in Figure S8.