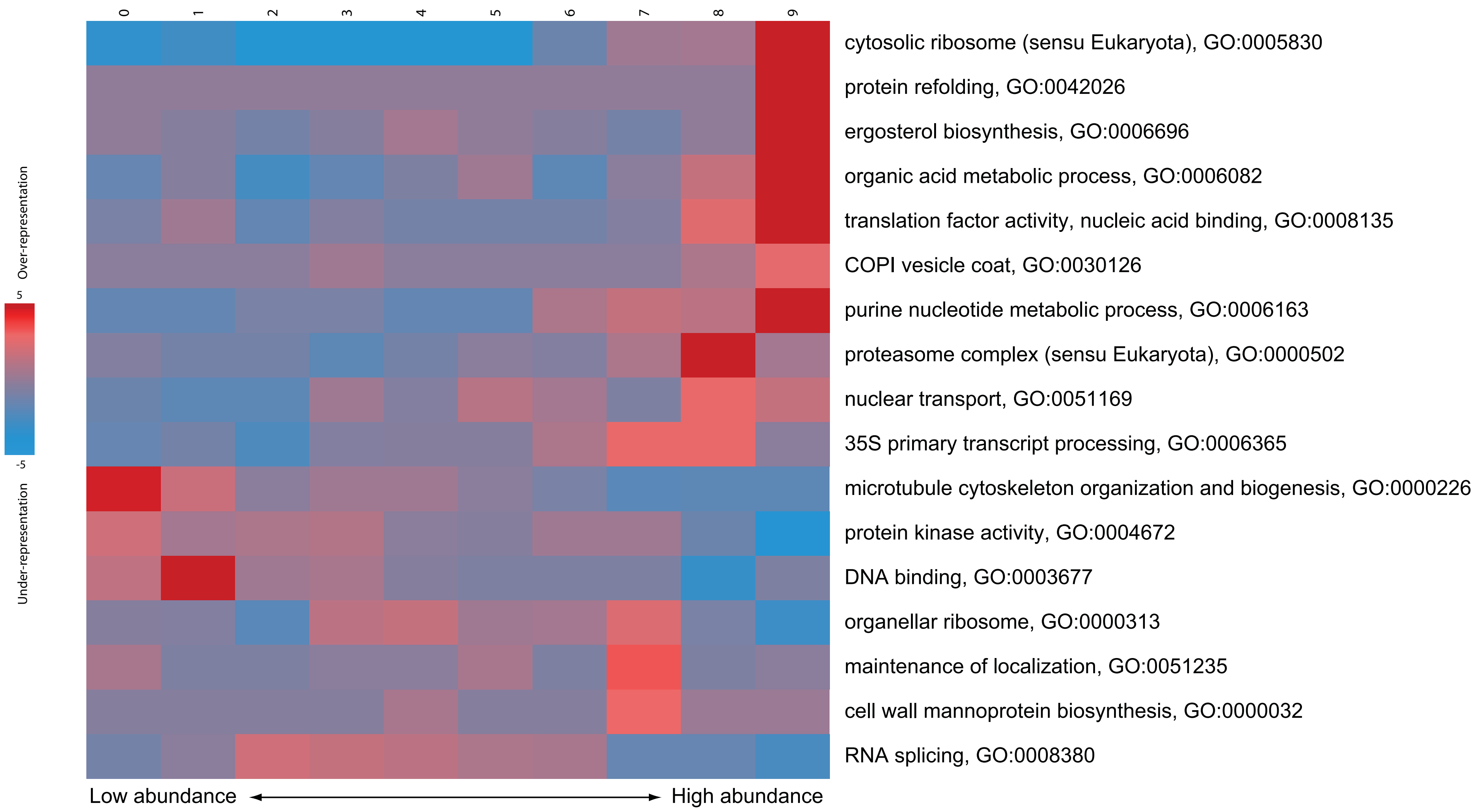

Figure S5: GO analysis of protein abundance profile

iPAGE (http://tavazoielab.princeton.edu/iPAGE/) analysis of continuous *S. cerevisiae* protein abundance data. Protein abundance measurements from ~3,800 TAP-tagged yeast proteins were binned into ten classes, with low-abundance proteins on the left and high-abundance proteins on the right. Columns representing protein behavior classes correspond to columns in Figure S6. Low-abundance proteins are enriched for microtubule-associated proteins, DNA binding proteins, and protein kinases, whereas high-abundance proteins are enriched for constitutively active processes such as ribosomal proteins, nucleotide metabolism and protein-folding proteins. Intermediate-abundance proteins seem to be enriched for RNA splicing proteins.