Supplementary Figure 1:

Each matrix represents the pairwise Pearson correlation between all genes associated with the cytoplasmic ribosomal proteins (RP), ribosomal RNA processing (rRNA), mitochondrial ribosomal proteins (MRP) and stress response (STR) in *S. cerevisiae* (left column) and *C. albicans* (right column) using a color-code (legend).
The gene sets were identified in *S. cerevisiae* using the Iterative Signature Algorithm. For *C. albicans* we used the orthologues of these genes (see Methods). To distinguish those orthologues that are also co-expressed in *C. albicans*, the 'raw' gene sets were further processed using the Signature algorithm. White lines demarcate the part of the original set that was retained after application of the signature algorithm (upper left). For MRP this procedure also reduces the original *S. cerevisiae* gene sets.
Full and processed sets of genes are listed in Supp. Tables 1 and 2, respectively.