**List of Supplementary Material**

Supplementary Figure 1

**Gene-gene correlation matrices of genes used in the study**

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.

Supplementary Figure 2

**Single sequence appearance**

Shown is the RGE appearance frequency as in Fig. 3, but allowing only for single sequence appearances per gene. Multiple motif appearances in the 50bp window are counted as single.

Supplementary Figure 3

**Dependence of correlation coefficients on experimental conditions**

To verify that the observed correlations are robust wit respect to the exact choice of the experimental conditions, we evaluated average correlation coefficients between the modules rRNA and RP, STR and MRP over subsets of 200 randomly chosen conditions. Shown are the coefficients for 200 different random subsets.

Supplementary Figure 4

**Evolution through mutations in trans-acting regulatory proteins or in cis-acting DNA elements**

The regulation of a common transcription factor could diverge between the species. Alternatively, modifications of the individual *cis*-regulatory elements of each downstream gene could change their regulation, potentially co-opting or losing regulation by a transcription factor.

Supplementary Figure 5

**The AATTTT sequence in *C. albicans* *MRPL10* and *MRPL37* promoters also acts as a rapid growth element.**

Mitochondrial ribosomal protein genes *MRPL10* and *MRPL37* were fused upstream of YFP inserted at the NOP1 locus as was done for the *MRP7* (Fig. 2A, Methods). The AATTTT sequence induce higher levels of transcription during log phase than during stationary phase and replacement of AATTTT with a GC-rich

(GGCGTT) or an AT-rich (ATATAT) sequence reduces expression of the YFP reporter. For *MRPL37*, two isolates of the AT-rich (ATATAT) mutant promoter were tested. For *MRPL10* in stationary phase, levels of detection were too low to quantify during an exposure time that detected expression of the protein in log phase or in the loading control (Histone H4). Overexposure revealed low levels of expression in wild-type and both mutant promoter strains (data not shown).

Supplementary Table 1
Full sets of *S. cerevisiae* genes and their *C. albicans* orthologues used in the study

Supplementary Table 2
Refined sets of genes (after filtering genes listed in Suppl. Tab. 1 with Signature Algorithm)

Supplementary Table 3
List of *S. cerevisiae* expression data references

Supplementary Table 4
List of *C. albicans* expression data references