

Supplementary data (Denecker et al.)

Supplementary Data S1: Excel spreadsheet in which sample description are summarized. LogFC (Fold Change) values calculated for each gene after inter-channel (Cy3 and Cy5) normalization with MAnGO software are presented here, as well as statistical parameters calculated with LIMMA software to select differentially expressed genes (iron responsive genes).

Supplementary Data S2: Excel spreadsheet with all information regarding the “iron responsive genes” and “iHKG” identified in this study. Iron responsive genes are a list of genes for which a differential of expression was observed in a least one condition (C1, C2, C3 or C4). Statistics for differential expression are shown here. They were calculated with LIMMA methodology (logFC and adjusted p-values). iHKG are a sub-class of iron responsive genes, for which particular de-regulations were observed (see main text). Gene names, gene descriptions (CGD and GRYC databases, see Methods), functional information and orthologs in *S. cerevisiae* are also indicated in this data file.

Supplementary Data S3: Excel spreadsheet with all information regarding the data mining of GO terms to define a limited number of general functions. Levels of each GO term in the hierarchical organization of all terms were calculated with the OntologyIndex methodology (see Methods). These levels were used to cluster the GO terms into Meta-GO (level 4, see Main text). The 171 Meta-GO identified in this study are listed here with their final classification into the General Functions (F1, F2, F3, F4, F5 and Others).

Supplementary Data S4: Detailed results for functional enrichment analyses with GO terms. The tool GOterm Finder available in CGD was used, with default parameters, and querying “Cellular Component”, “Molecular Function” and “Biological Process” categories.

Supplementary Data S5: PDF file summarizing the in vitro models with transcriptomic analysis to study the impact of iron availability on *C. glabrata*, deficient or overload conditions at different temperatures.

Supplementary Data S6: List of orthologous genes in *S. cerevisiae* and *C. albicans* yeast species for the iHKG (Type I and Type II) identified in this study.