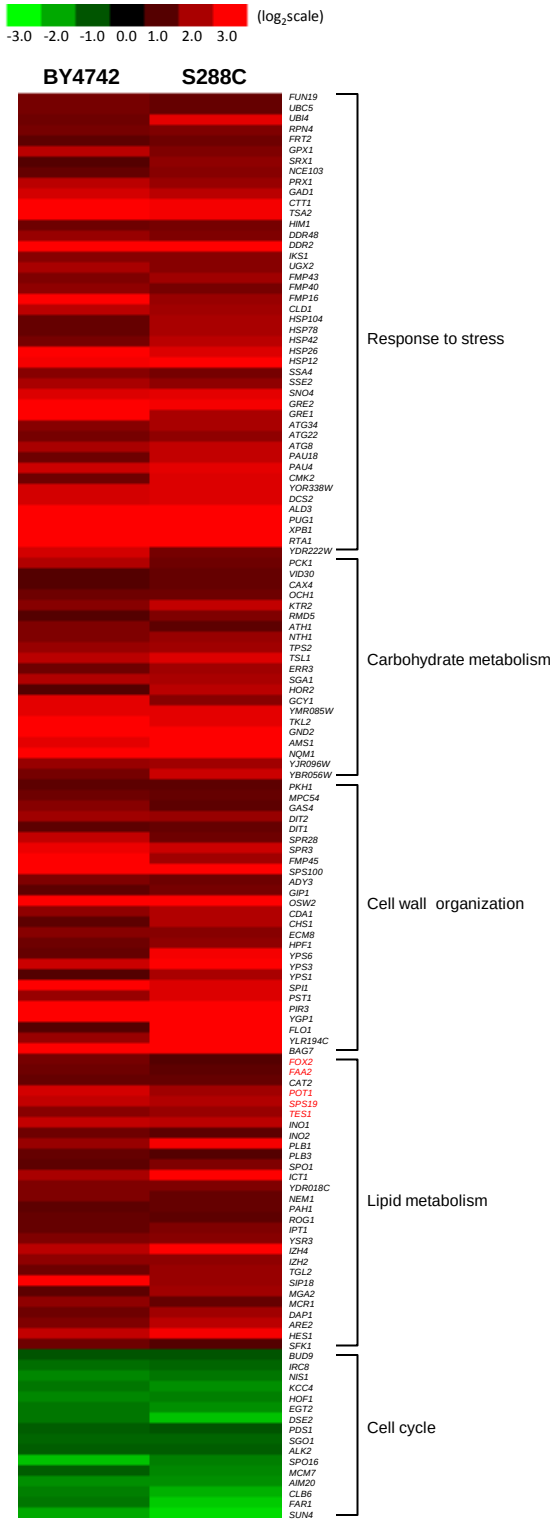
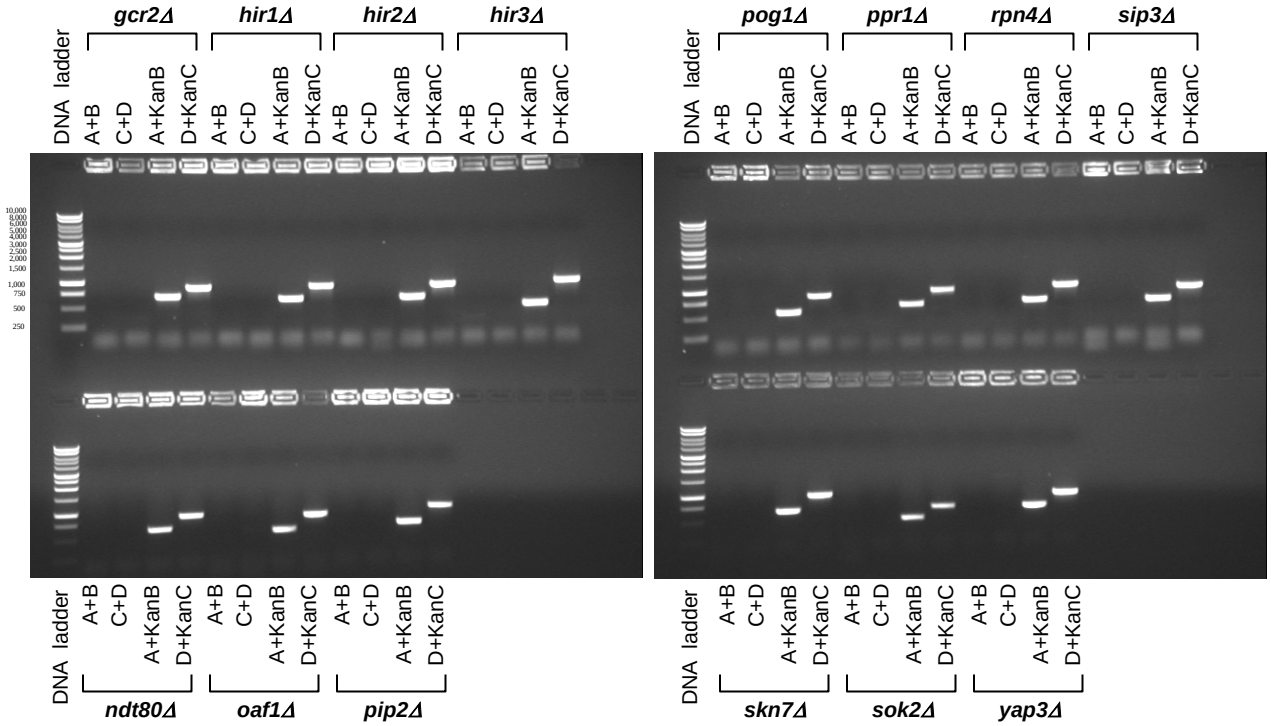
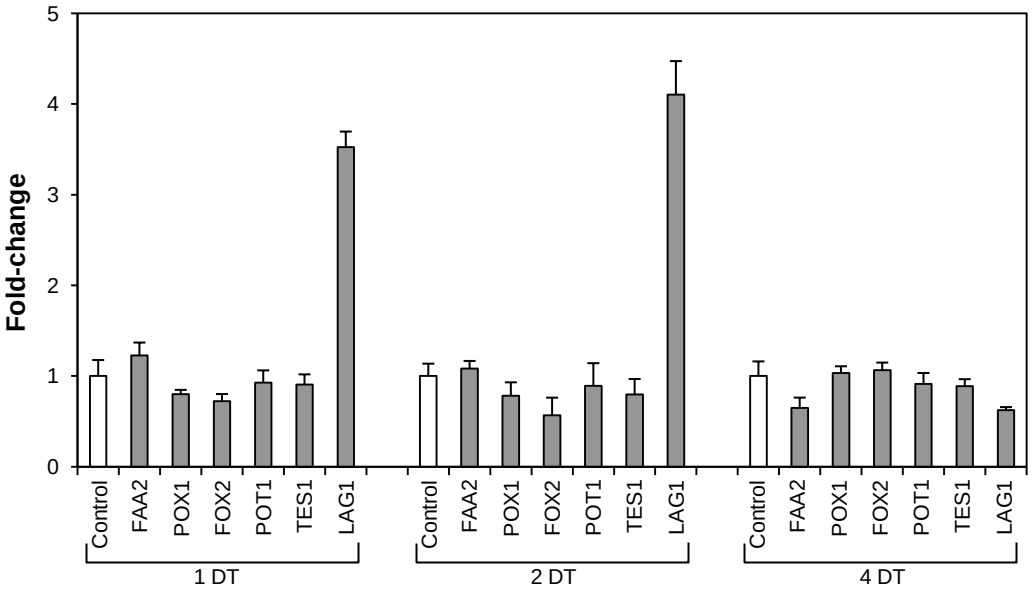


Supplemental Figure S1. Comparison of gene expression responses to 6-NDA between *S. cerevisiae* BY4742 and S288C strains. Triplicate cultures of strain BY4742 were treated with either 6-NDA at the IC_{50} concentration (1.4 μg/ml) or 0.25% DMSO. Media conditions, inoculum size, and treatment times were similar to those used for the S288C strain (see "Materials and Methods"). Microarray experiments and data analysis were also performed as described for the S288C strain. Differentially expressed genes (p-value ≤0.001; fold-change ≥2.0) identified are listed in Supplemental Table S3. Genes that were similarly up- or down-regulated in the S288C strain are also listed in Table S3. To further highlight the similarities between the two profiles, a sub-set of the commonly responding genes in the two strains were distributed into GO functional categories (based on Table 1) and visualized using Java Tree View software. Fatty acid β-oxidation genes are highlighted in red text.



Supplemental Figure S2. PCR confirmation of 14 transcription factor mutant strains. Deletion mutant strains (described in Figure 3) were streaked for single colonies on YPD + G418 plates. Colony PCR was performed by denaturation at 95°C for 5 min, followed by 35 cycles of denaturation at 95°C for 30 sec, annealing at 55°C for 30 sec, and extension at 72°C for 1 min. Platinum Taq DNA Polymerase (Invitrogen Corporation), a hot-start enzyme, was utilized in all reactions to increase specificity and sensitivity. Each deletion mutant was confirmed using the “A,” “B,” “C,” “D,” “KanB,” and “KanC” primers as described on the Saccharomyces Genome Deletion Project website (http://www-sequence.stanford.edu/group/yeast_deletion_project/deletions3.html). The "A" and "D" primers are located upstream and downstream of the coding region respectively, while the "B" and "C" primers are located within the coding region. The "KanB" and "KanC" primers are located in the KanMX4 gene used to replace the target gene in each deletion strain. PCR products are obtained in the “A”/ “KanB” and “D”/ “KanC” primer combinations, while the “A”/ “B” and “C”/ “D” primer combinations result in no PCR products.



Supplemental Figure S3. Quantitative real-time RT-PCR analysis of fatty acid β-oxidation genes in 6-NDA-exposed *C. albicans* cells. Triplicate cultures of *C. albicans* SC5314 cells were treated with either 0.25% DMSO or 6-NDA at the IC_{50} concentration for one doubling (1DT), two doubling (2DT), and four doubling (4DT) times. Further experimental details can be found in the "Supplemental Methods" section. The genes analyzed consisted of five genes involved in fatty acid β-oxidation (*FAA2*, *POX1*, *FOX2*, *POT1*, and *TES1*), and one gene involved in sphingolipid biosynthesis (*LAG1*) as a positive control, which was induced by 5.3-fold in the one doubling microarray experiment (see Table 2 and Supplemental Table S4). Assays were performed in triplicate with SYBR® Green I dye using the 7300 Real-Time PCR System. Data were normalized to an internal control (18S rRNA) and the $\Delta\Delta C_T$ method was used to obtain the relative expression level for each gene. Error bars represent standard deviations. Control indicates DMSO-treated samples.