



FIGURE S4.—Heme and ergosterol depletion induces a subset of the Hog1-dependent hypoxic genes. Genes identified in Figure 5A as regulated by Hog1 that also contain consensus Upc2 binding sites in their promoters, were analyzed for their fold-induction when heme or ergosterol biosynthetic genes are repressed. The data shown here were obtained from a previous study that employed microarrays to monitor expression of all yeast genes 12 hours after turning off individual essential genes (Mnaimneh S, Davierwala AP, Haynes J, Moffat J, Peng WT, et al. Cell 118: 31-44 (2004)). Fold-induction was determined by comparing the expression of each gene to a wild-type strain grown under the same conditions. The bar labeled “average of all genes” represents the average induction of all ~6300 genes for that particular essential gene shutoff, and the standard deviation. The symbol labeled “*PAUs*” represents the average expression of all 24 *PAU* genes.