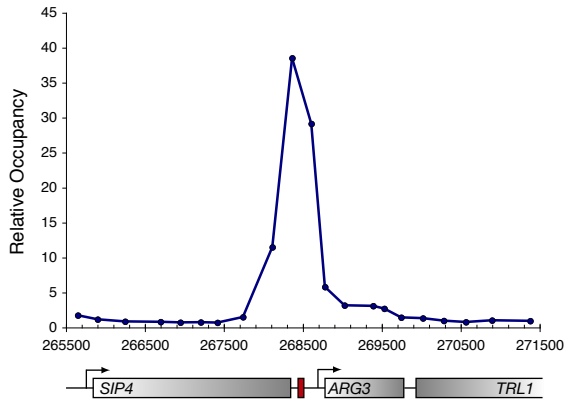
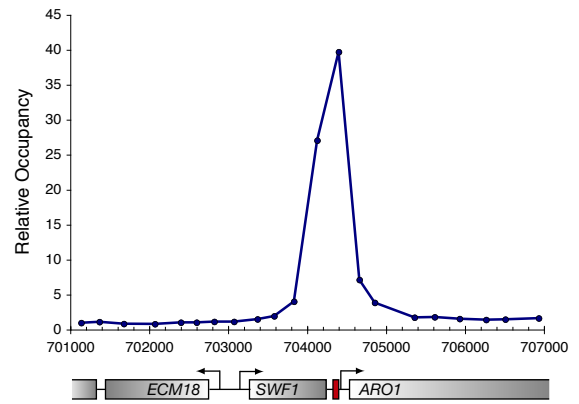


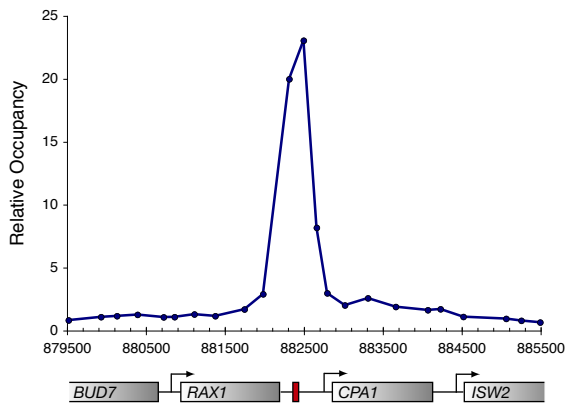
A



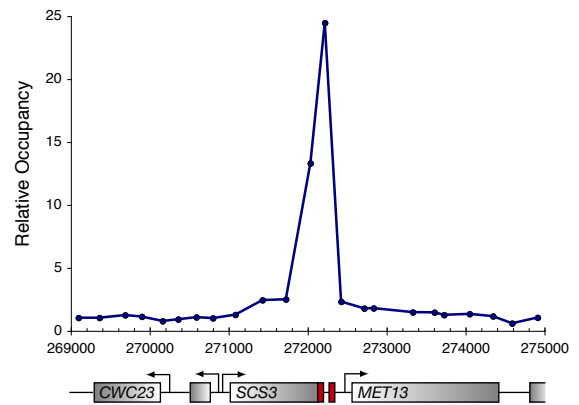
B



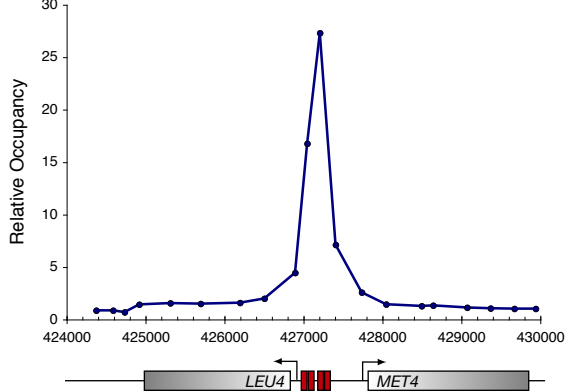
C



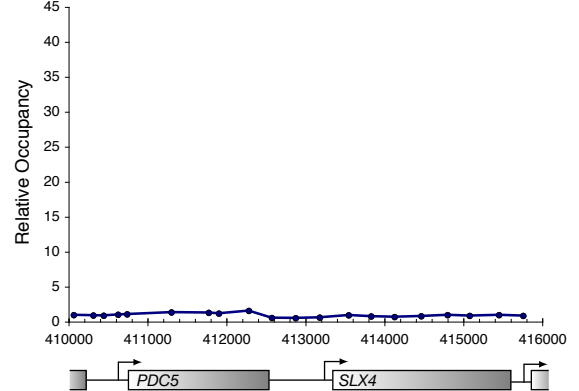
D



E



F



Supplemental Figure 1. Positive and negative examples of Gcn4 binding.

A. Occupancy of the *ARG3* promoter by Gcn4. The genomic positions of probe regions are arrayed along the x-axis with the ratio of enrichment of Gcn4 for probes along the y-axis. ORFs are depicted as gray rectangles, and arrows indicate the direction of transcription. Red boxes represent sequence matches to the Gcn4 binding specificity within promoter regions.

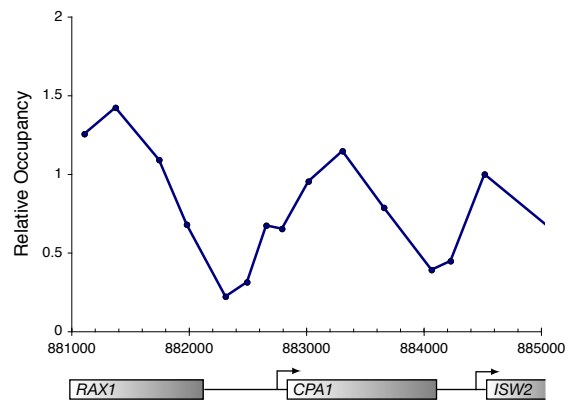
B. Occupancy of the *ARO1* promoter by Gcn4 as in A.

C. Occupancy of the *CPA1* promoter by Gcn4 as in A.

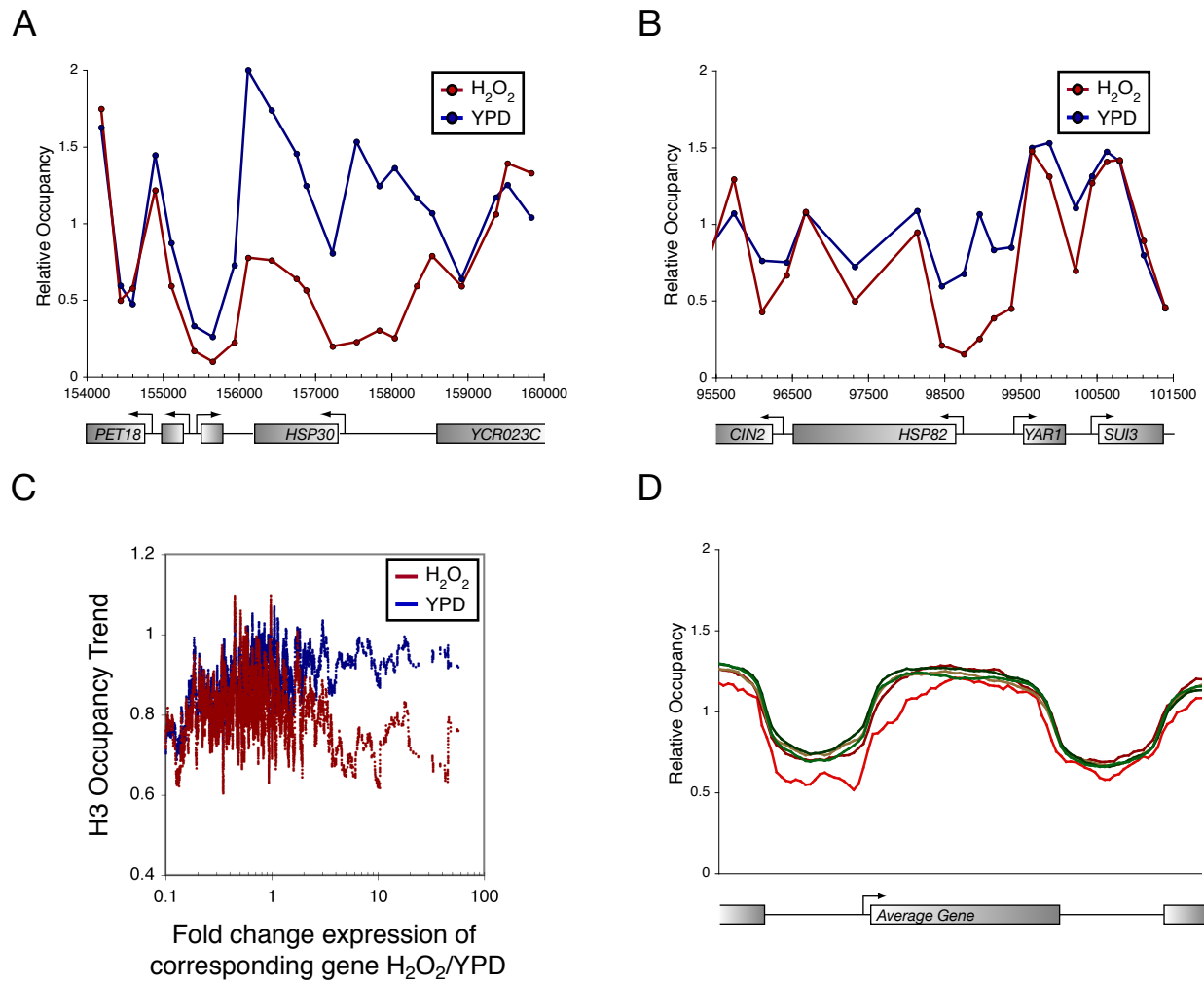
D. Occupancy of the *MET13* promoter by Gcn4 as in A.

E. Occupancy of the *LEU4/MET4* promoter by Gcn4 as in A.

F. Occupancy of the *PDC5* and *SLX4* promoter by Gcn4 as in A (negative control).

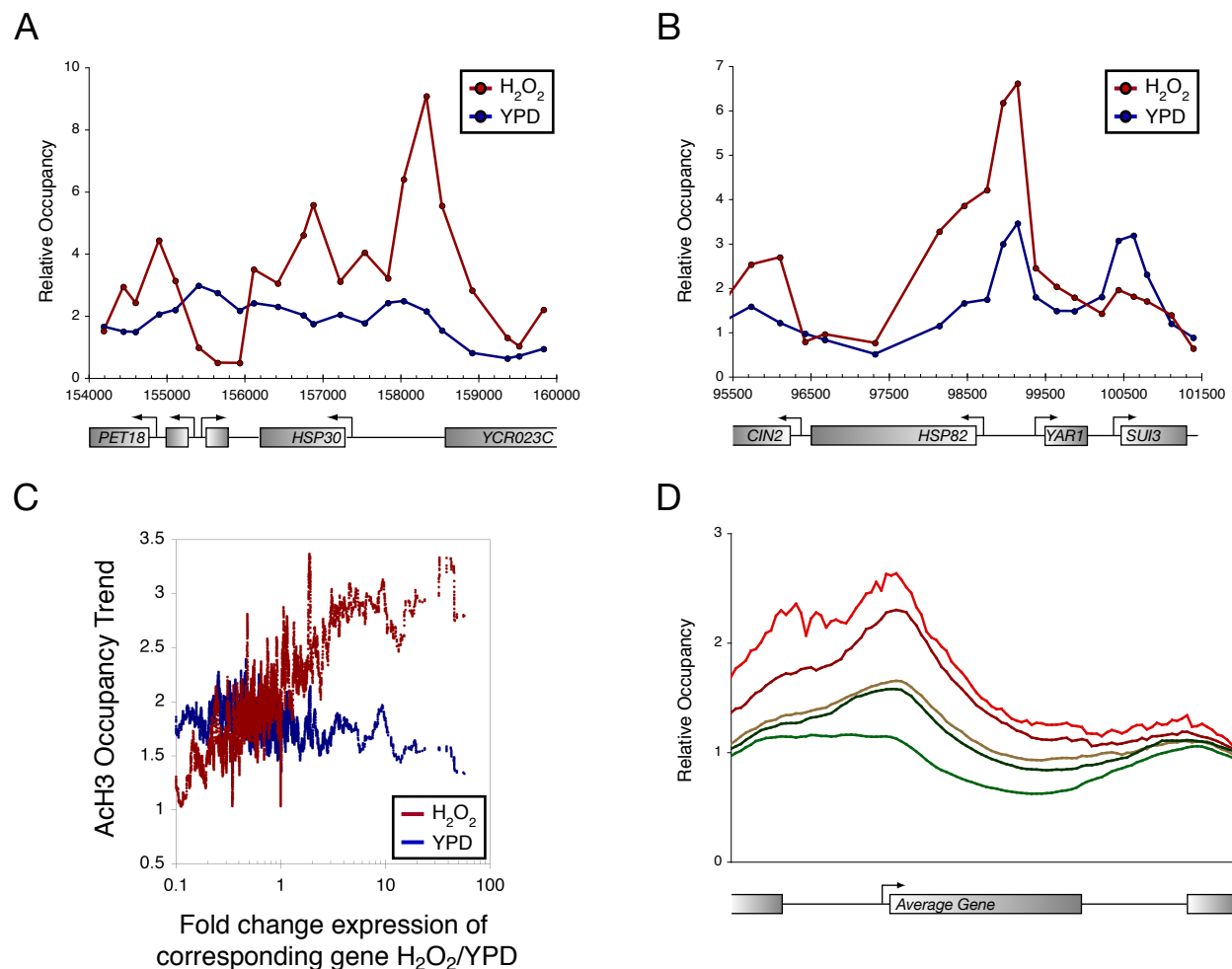


Supplemental Figure 2. Histone H3 occupancy at the *CPA1* locus after normalization to a no-antibody control.



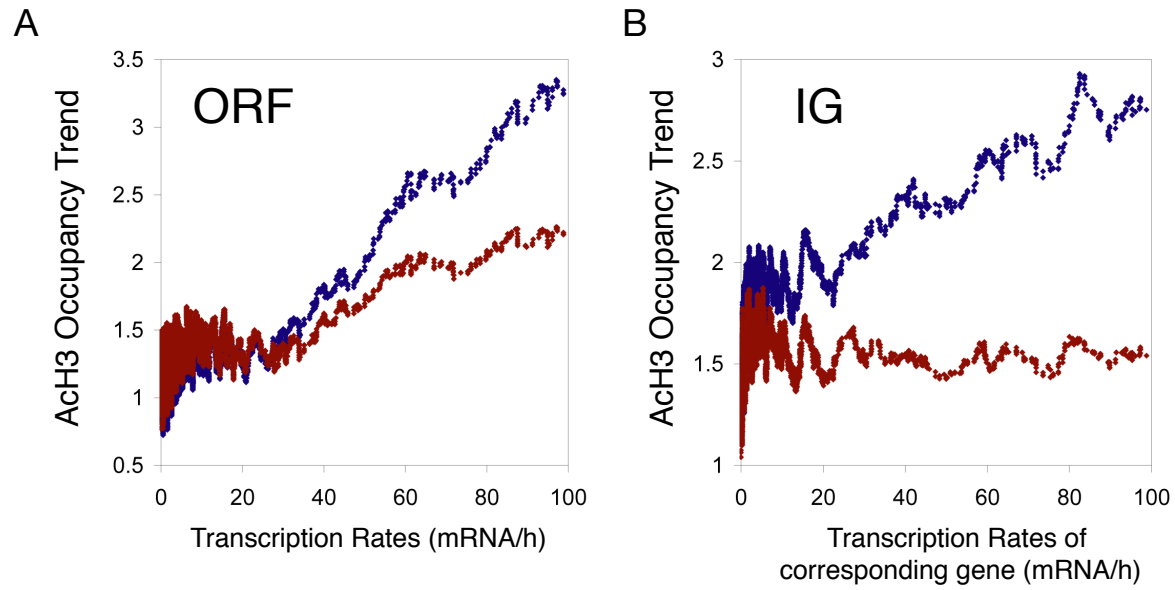
Supplemental Figure 3. Changes in nucleosome occupancy in response to changes in environmental conditions.

- A. Changes in nucleosome occupancy at the *HSP30* locus in response to hyperoxia (red), YPD (blue).
- B. Changes in nucleosome occupancy at the *HSP82* locus in response to hyperoxia (red), YPD (blue).
- C. A sliding window (size=100) of H3 enrichment as a function of hyperoxia-induced changes in gene expression as determined in (Causton et al., 2001), hyperoxia (red), YPD (blue).
- D. A composite profile of H3 occupancy for sets of genes according to changes in transcriptional activity, genes induced more than 10 fold in bright red, induced 10 to 2 fold - dark red, induced up to 2 fold - gold, repressed up to 2 fold - dark green, repressed more than 2 fold - bright green.



Supplemental Figure 4. Changes in acetylation of Histone H3 lysine 14 (H3K14ac) in response to changes in environmental conditions.

- A. Changes in nucleosome acetylation at the *HSP30* locus in response to hyperoxia (red), YPD (blue).
- B. Changes in nucleosome acetylation at the *HSP82* locus in response to hyperoxia (red), YPD (blue).
- C. A sliding window (size=100) of H3 acetylation as a function of hyperoxia-induced changes in gene expression as determined in (Causton et al., 2001), hyperoxia (red), YPD (blue).
- D. A composite profile of nucleosome acetylation for sets of genes according to changes in transcriptional activity, genes induced more than 10 fold in bright red, induced 10 to 2 fold - dark red, induced up to 2 fold - gold, repressed up to 2 fold - dark green, repressed more than 2 fold - bright green.

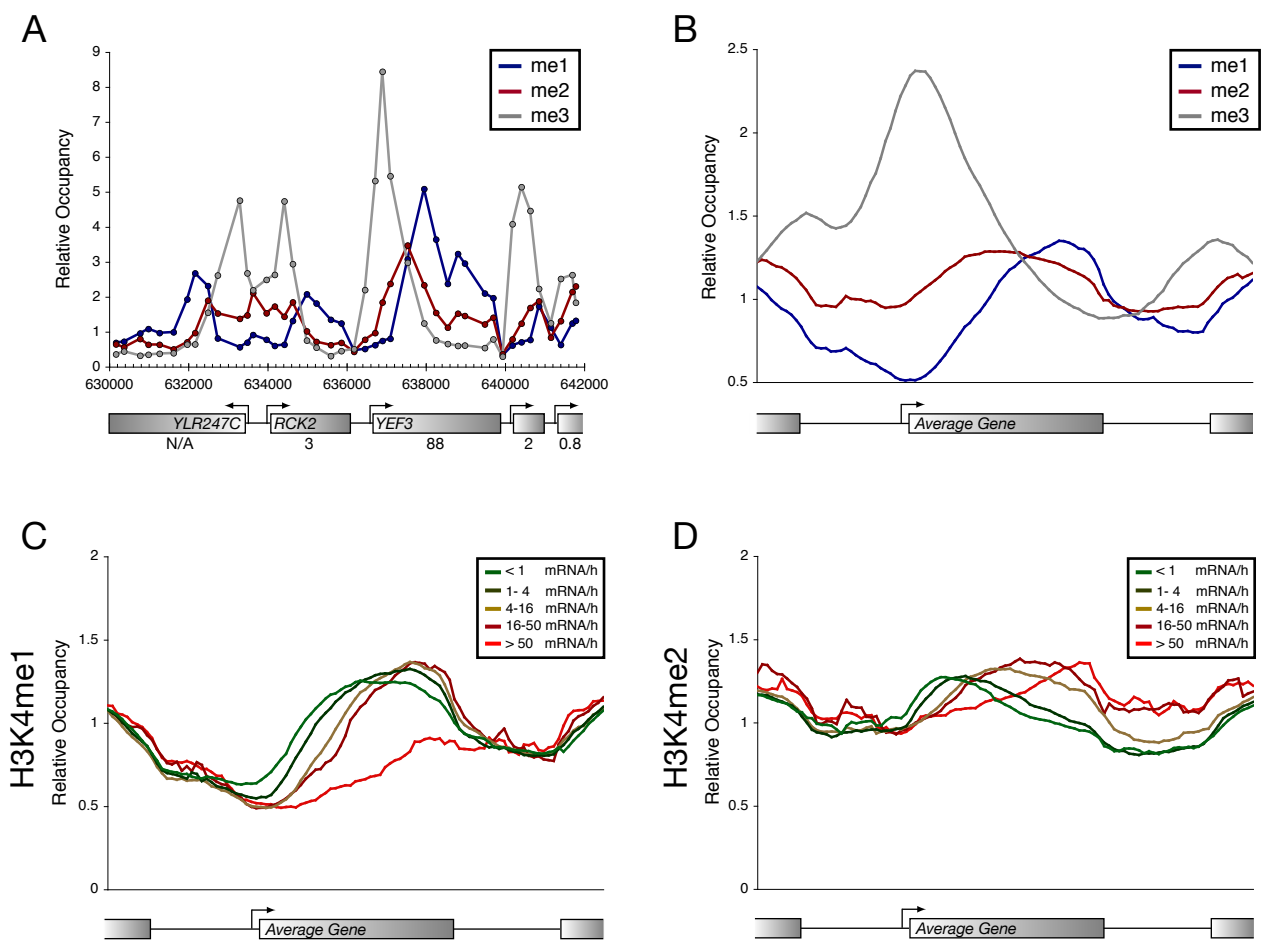


Supplemental Figure 5. Correlation of Histone H3 acetylation at lysine 14 (H3K14ac) with transcriptional activity.

A. A sliding window of H3 acetylation (size=100) within ORFs compared to transcriptional activity in mRNA/hr (Holstege et al. 1998).

Red line - H3K14ac vs WCE, blue line - H3K14ac vs H3.

B. A sliding window of H3 acetylation (size=100) within intergenic regions compared to the transcriptional activity of downstream genes in mRNA/hr (Holstege et al. 1998). Red line - H3K14ac vs WCE, blue line - H3K14ac vs H3.



Supplemental Figure 6. Differential profiles of methylated H3K4.

A. Profiles of mono- (blue), di- (red) and tri-methylated (grey) H3K4 are shown at a portion of Chromosome XII.

B. Composite profiles of mono- (blue), di- (red) and trimethylated (grey) H3K4 at the average gene.

C. Composite profiles of monomethylated H3K4 according to transcriptional activity.

D. Composite profiles of dimethylated H3K4 according to transcriptional activity.