

Supplemental Data

Genome-wide Map of Nucleosome

Acetylation and Methylation in Yeast

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Table S1. Known Targets of Gcn4 Binding

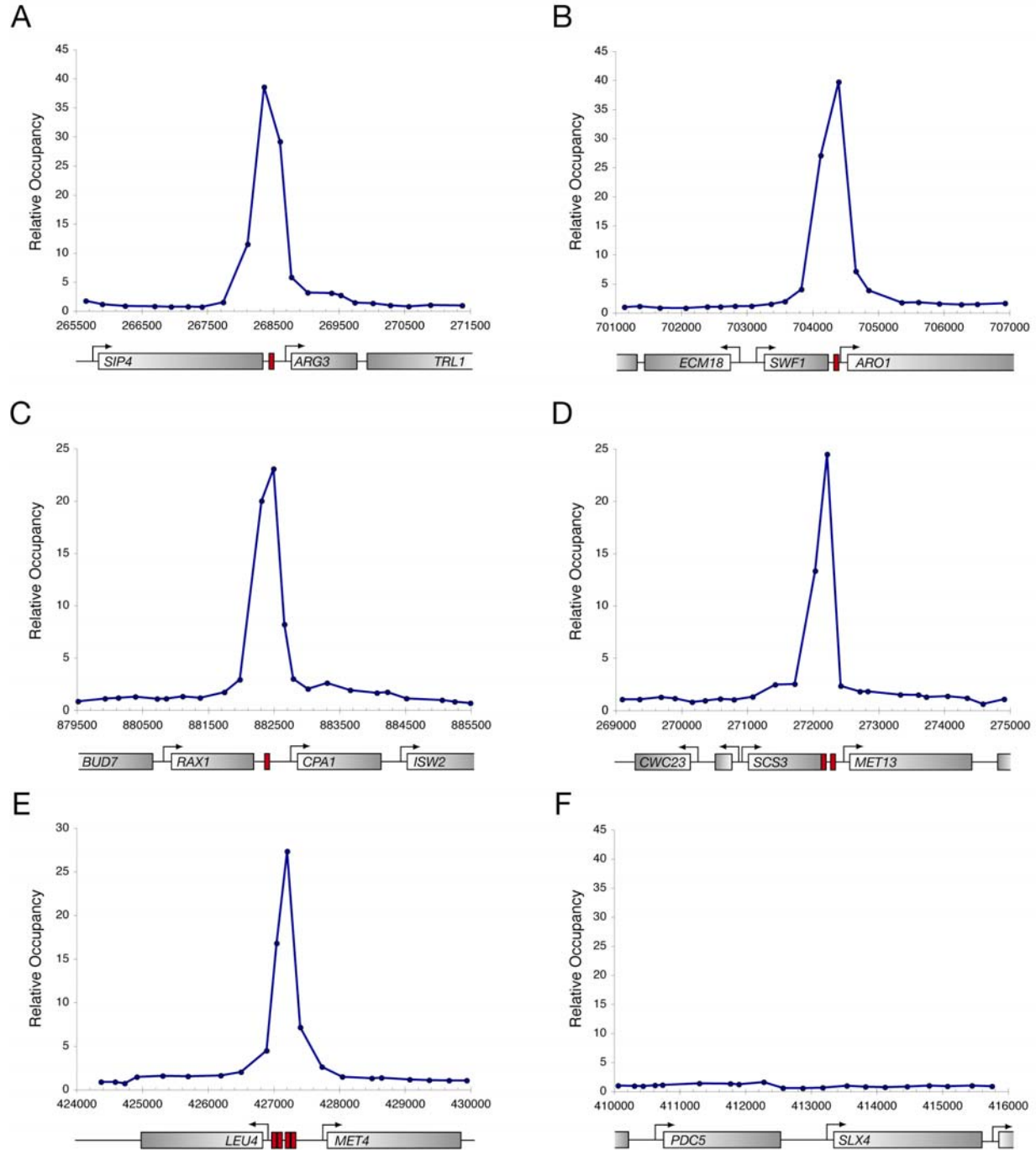
Gene Promoter	p Value	Gene Promoter	p Value
<i>ADE3</i>	3.80E-07	<i>LYS14</i>	6.81E-10
<i>ADH5</i>	4.86E-06	<i>LYS2</i>	1.06E-08
<i>ALD5</i>	3.30E-12	<i>MAS2/THR1</i>	7.78E-04
<i>APG13</i>	8.59E-04	<i>MET13</i>	1.51E-11
<i>ARG1</i>	6.44E-15	<i>MET22</i>	5.75E-06
<i>ARG2/YJL072C</i>	4.55E-05	<i>NCE103</i>	3.43E-08
<i>ARG3</i>	4.77E-15	<i>ODC2</i>	3.29E-12
<i>ARG4</i>	5.22E-15	<i>ORT1</i>	4.28E-10
<i>ARG5</i>	7.06E-14	<i>PHO8</i>	1.65E-12
<i>ARG8</i>	1.72E-14	<i>PYC2</i>	9.03E-08
<i>ARO1</i>	5.97E-14	<i>RIM101</i>	2.17E-04
<i>ARO4</i>	1.78E-10	<i>SFT2</i>	2.16E-08
<i>ARO8</i>	1.73E-05	<i>SNO1/SNZ1</i>	2.42E-04
<i>ATR1</i>	5.78E-04	<i>STB4</i>	3.66E-02
<i>BAP2</i>	1.92E-10	<i>STR3</i>	3.32E-13
<i>BNA1</i>	7.04E-13	<i>TEA1</i>	5.51E-14
<i>CPA1</i>	1.84E-14	<i>THR4</i>	4.32E-04
<i>CPA2/YJR110W</i>	2.22E-15	<i>TRP2</i>	5.64E-07
<i>CPT1/YNL129W</i>	4.13E-04	<i>TRP4</i>	1.13E-07
<i>DBF20</i>	1.07E-03	<i>UGA3</i>	8.45E-14
<i>DED81</i>	1.34E-10	<i>YBR043C</i>	2.70E-12
<i>ECM40</i>	1.71E-14	<i>YBR147W</i>	5.89E-06
<i>ESBP6/YNL124W</i>	8.02E-11	<i>YDL054C</i>	9.37E-04
<i>FOL2</i>	3.01E-09	<i>YDR341C</i>	9.74E-06
<i>GAT1</i>	4.65E-13	<i>YGL059W</i>	4.66E-05
<i>HIS1</i>	2.28E-14	<i>YGL117W</i>	5.73E-09
<i>HIS3/PET56</i>	5.85E-07	<i>YGL186C</i>	5.85E-03
<i>HIS7</i>	6.84E-06	<i>YHR122W</i>	5.63E-02
<i>HOM3</i>	7.88E-15	<i>YHR162W</i>	3.38E-12
<i>HRB1</i>	2.13E-11	<i>YIL056W</i>	1.23E-12
<i>HSP78</i>	3.25E-08	<i>YJL200C</i>	4.70E-09
<i>ICY2</i>	1.20E-13	<i>YLR152C</i>	2.61E-09
<i>IDP1</i>	8.75E-07	<i>YMC1</i>	1.30E-06
<i>ILV1</i>	1.03E-02	<i>YMC2</i>	4.26E-07
<i>ILV3</i>	4.04E-09	<i>YML076C</i>	8.04E-04
<i>ISU1</i>	2.63E-10	<i>YMR135C</i>	2.62E-14
<i>LEU3</i>	2.26E-08	<i>YOL119C</i>	4.25E-04
<i>LEU4</i>	2.13E-14	<i>YPL264C</i>	2.63E-06
<i>LYS1</i>	2.03E-09		

Genes were selected as targets of Gcn4 regulation because they met the following criteria: they displayed a Gcn4-dependent change in expression upon amino acid starvation (Natarajan et al., *MCB*, 2001), they contained within their promoters a phylogenetically conserved match to a Gcn4 binding site motif, and there was prior evidence for in vitro Gcn4 binding to their promoters. Slashes denote a shared promoter. p value is the lowest for any probe within the corresponding promoter region for Gcn4 binding on the current array platform.

Table S2. Correlation of Transcriptional Activity and Nucleosome Occupancy or Modification

Specificity	Correlation
iH3	-0.2915071
iH4	-0.2753623
iH3K9ac	0.3375921
iH3K14ac	0.28140397
iH4K5acK8acK12acK16ac	0.07933304
iH3K4me	-0.0005931
iH3K4me2	0.00558487
iH3K4me3	0.18052056
iH3K36me3	0.32378278
iH3K79me3	-0.0194656
oH3	-0.2304769
oH4	-0.2621408
oH3K9ac	0.29472382
oH3K14ac	0.37440913
oH4K5acK8acK12acK16ac	0.10454317
oH3K4me	-0.0657816
oH3K4me2	0.09084053
oH3K4me3	0.40914098
oH3K36me3	0.40710237
oH3K79me3	0.0474006

The prefix “i” denotes correlation with intergenic probes; the prefix “o” denotes correlation with ORF probes. “Correlation” is the correlation coefficient between ratio enrichment and transcriptional activity in mRNA/hr (Holstege et al.).



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.

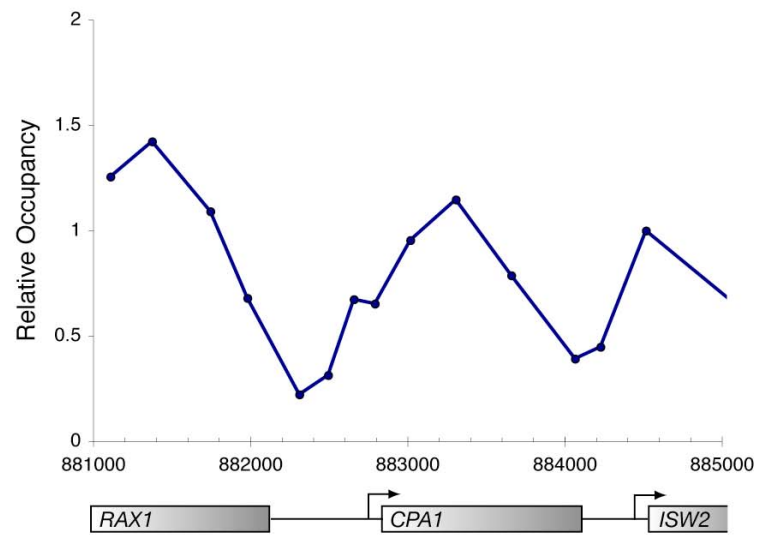
B. Occupancy of the *ARO1* promoter by Gcn4 as in A.

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

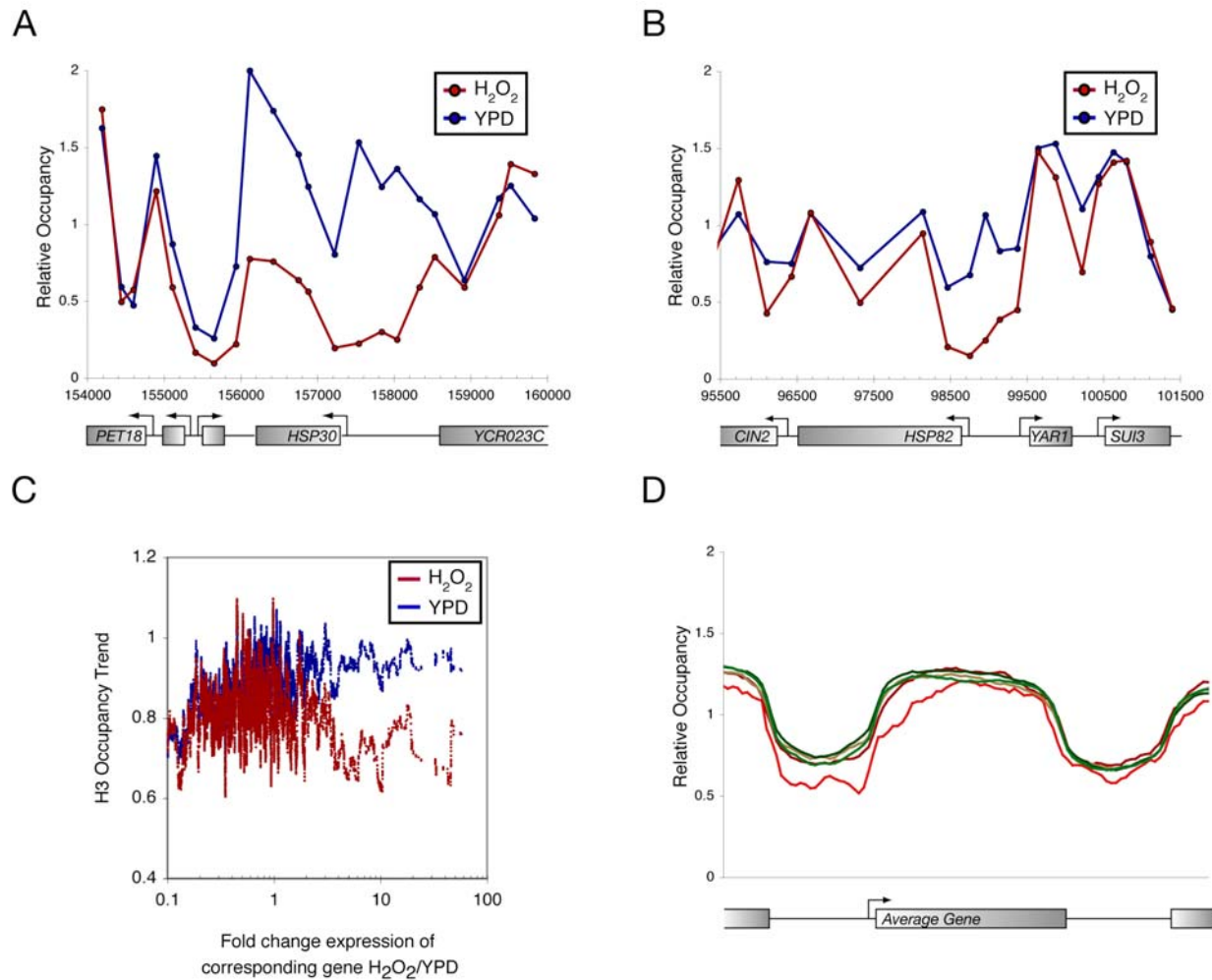
D. Occupancy of the *MET13* promoter by Gcn4 as in A.

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.



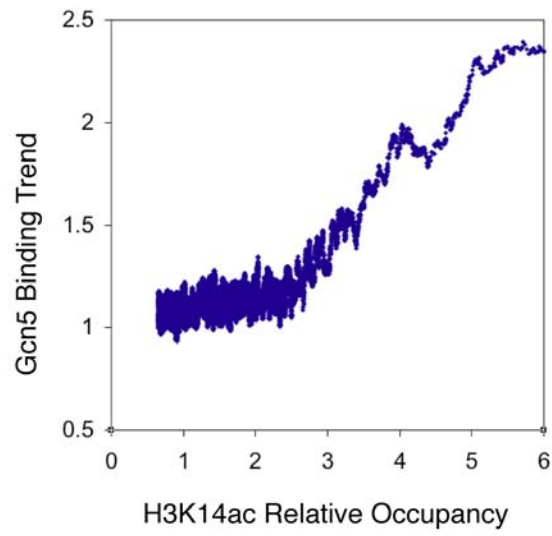
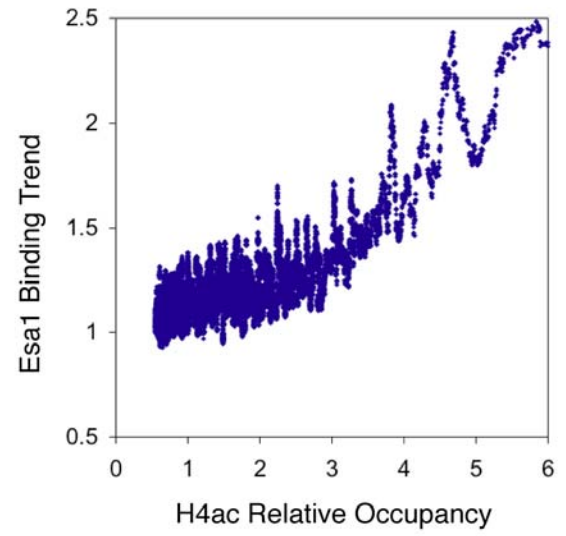
Supplemental Figure 3. Changes in nucleosome occupancy in response to changes in environmental conditions.

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).

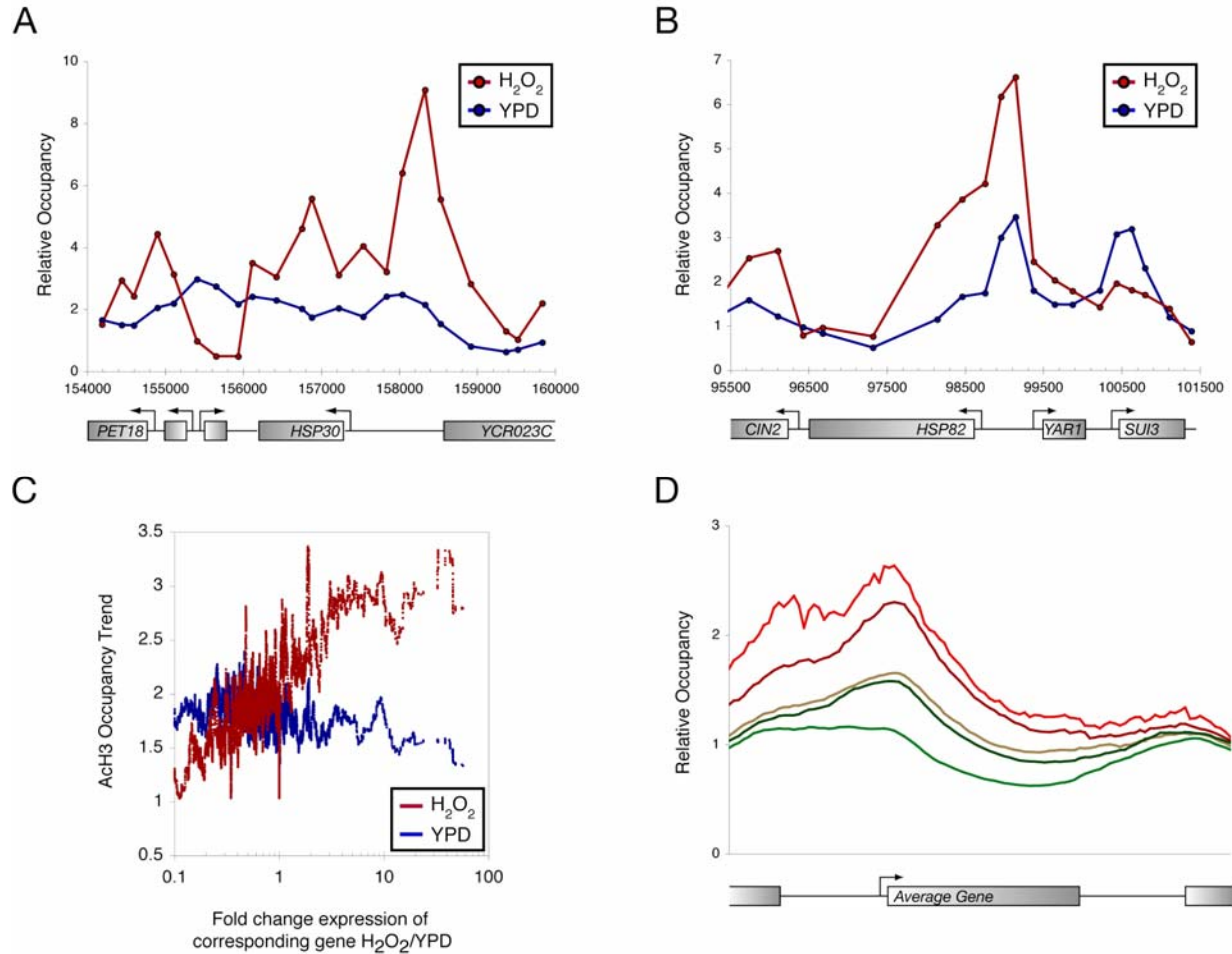
D. A composite profile of H3 occupancy for sets of genes according to changes in transcriptional activity, genes induced more than 10 fold in bright red, induced 10 to 2 fold - dark red, induced up to 2 fold - gold, repressed up to 2 fold - dark green, repressed more than 2 fold - bright green.

A**B**

Supplemental Figure 4. Correlation of Histones H3 and H4 acetylation with Gcn5 and Esa1 occupancy.

A. A sliding window of Gcn5 occupancy (size=100) was compared to histone H3 acetylation at lysine 14 (H3K14ac).

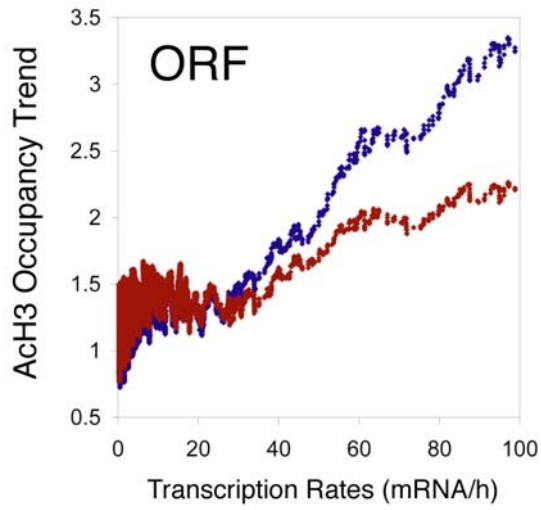
B. A sliding window of Esa1 occupancy (size=100) was compared to histone H4 acetylation (H4ac)



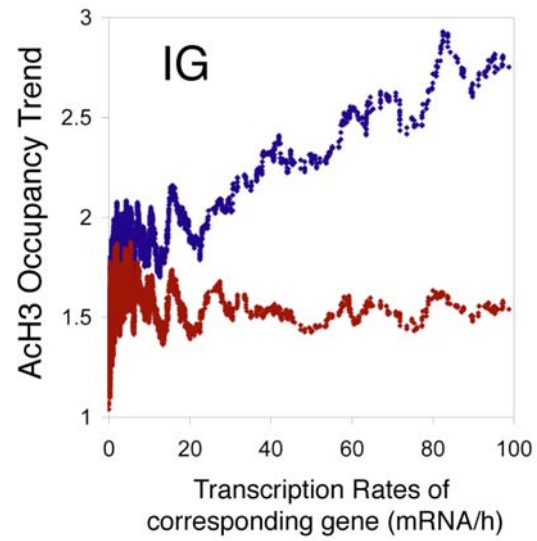
Supplemental Figure 5. Changes in acetylation of Histone H3 lysine 14 (H3K14ac) in response to changes in environmental conditions.

- 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. Similar, though less pronounced, effects were observed for H4ac (data not shown).

A



B

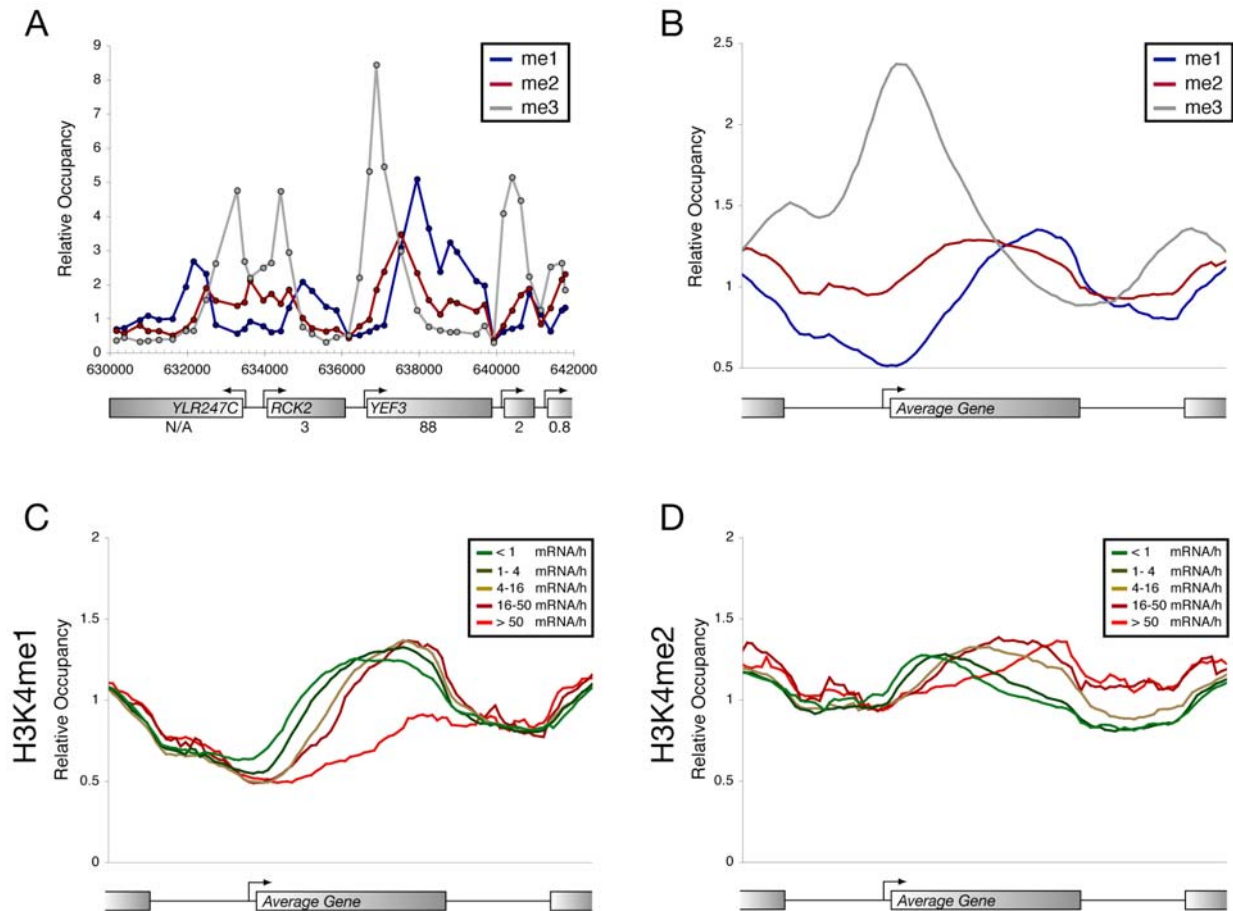


Supplemental Figure 6. Correlation of Histone H3 acetylation at lysine 14 (H3K14ac) with transcriptional activity.

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.



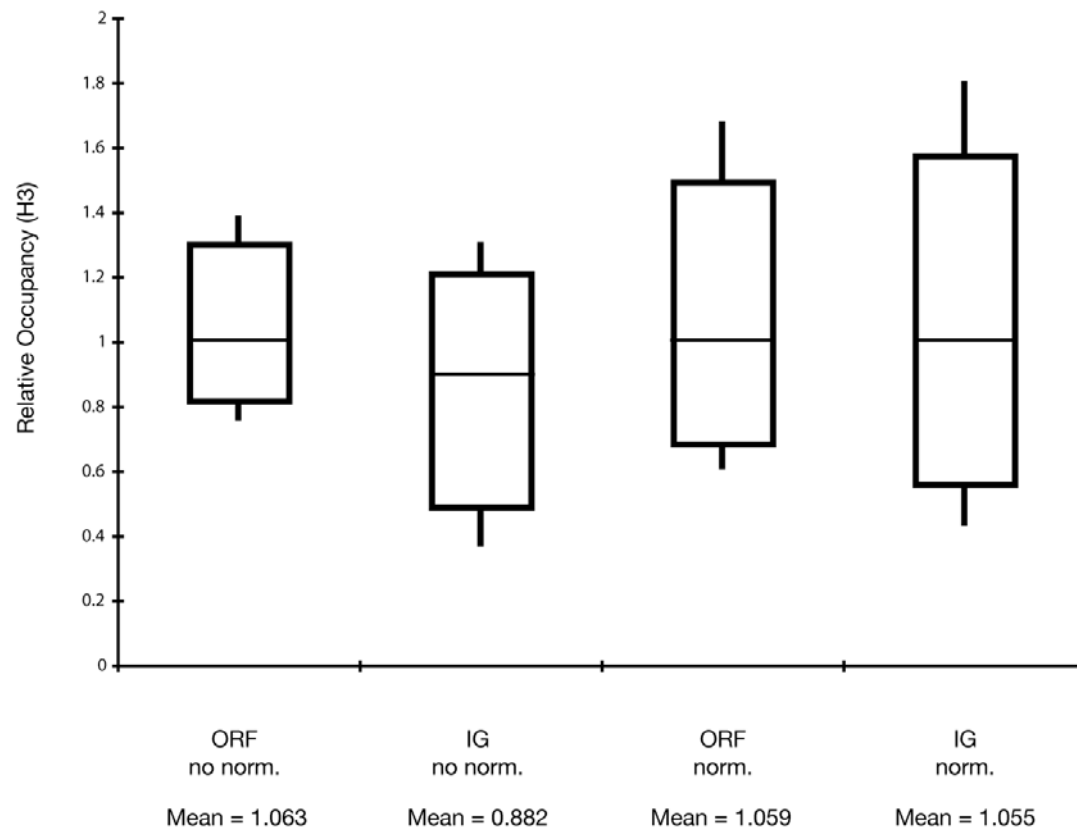
Supplemental Figure 7. Differential profiles of methylated H3K4.

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.



Supplemental Figure 8. Distributions of median H3 enrichment at ORF nad intergenic regions before and after normalization to control experiments. Boxes represent the 10th to the 90th percentiles, vertical lines extend to the 5th and 95th percentiles, and horizontal bars represent the mean of the entire sample. We used a two-sampled T-test to determine the likelihood of obtaining different values for the mean enrichment by chance in both the original and controlled experiments. Assuming unequal variance between the two regions, we found a likelihood estimate of $<10^{-16}$ using non-normalized H3 data. Corrected using the IgG data, this value increases to 0.45, suggesting the differences between the two data sets is insignificant.