Supporting Information

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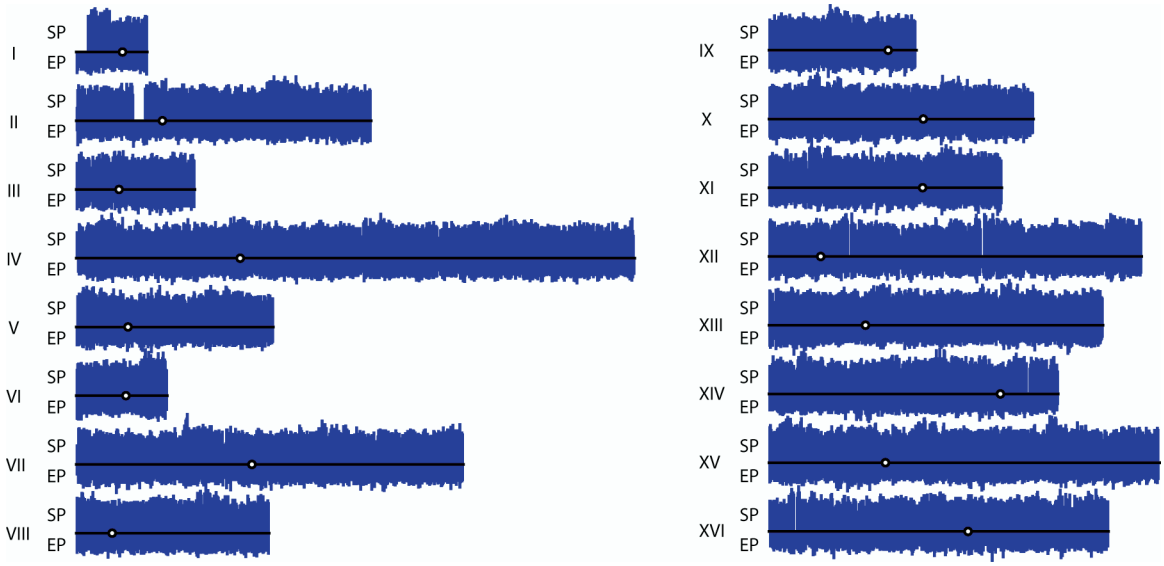

Fig. S1. Genome-wide increase in Hho1p binding to chromatin in stationary phase. ChIP was performed on a yeast strain expressing a unique, *c*-myc tagged Hho1p after growth to 6 d (SP) or 1 h after transfer of the culture to rich growth media (EP). The recovered DNA from the SP and EP samples was labeled and hybridized to a *S. cerevisiae* microarray slide. The microarray data were normalized to the average level of the *DNF1*, *SNZ1*, and *ROX1* genes, determined by quantitative PCR of the recovered ChIP DNA. Shown is the normalized level (median, $n = 4$) of Hho1p binding to each gene on each of the yeast chromosomes, where the height of the line at each gene is proportional to the level of Hho1p binding. The scaling of the EP data is inverse to that of the SP data. Hho1p binding in regions in the genome for which no data were obtained are shown as zero.

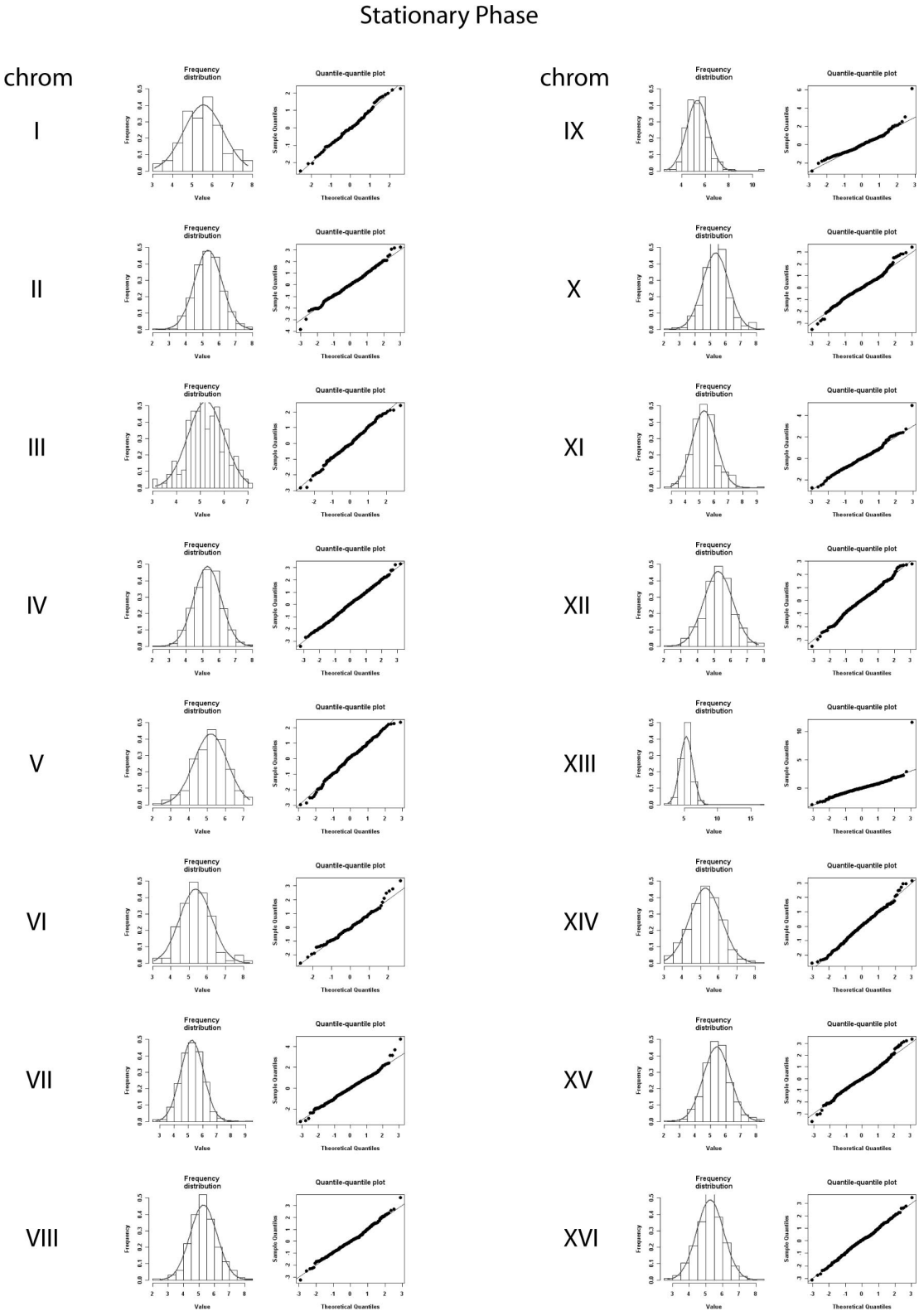

Fig. S2. Binding distribution of Hho1p to the *S. cerevisiae* genome *in vivo*. A Gaussian curve was fitted to the frequency distribution of the Hho1p binding level for genes in each of the yeast chromosomes in stationary phase (Stationary Phase) and 1 h after stationary phase exit (Exponential Phase). A quantile-quantile plot was also constructed for the binding data for each chromosome. Note the absence of outliers in the fitted peaks and the relative linearity of the quantile–quantile plots.

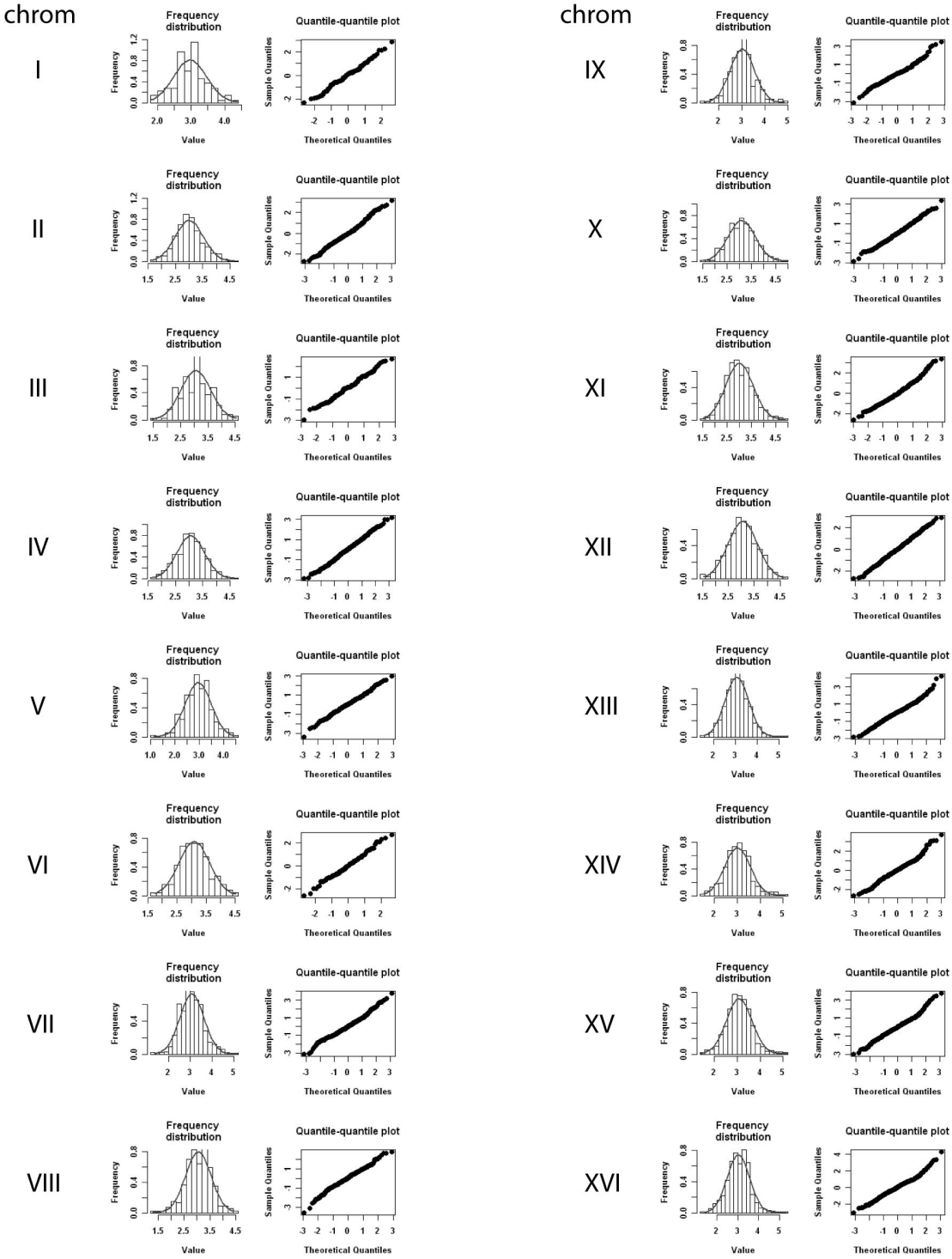

Fig. S2. Continued.

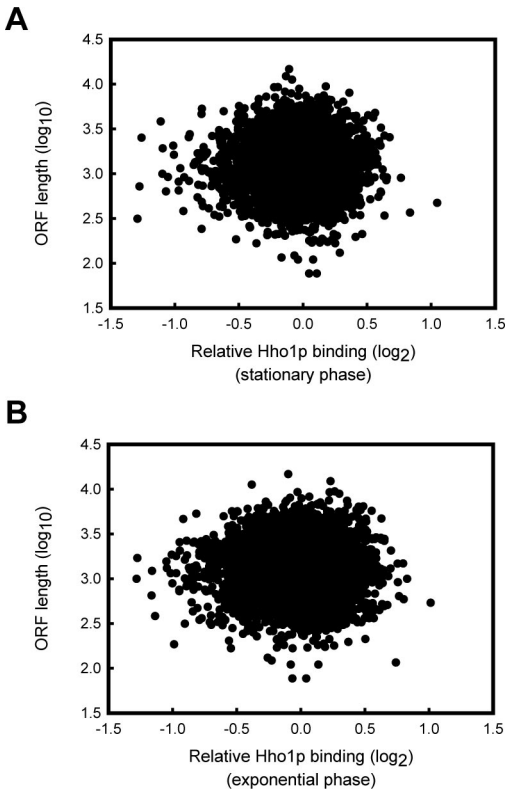

Fig. S3. No correlation between Hho1p binding and ORF length. A plot of the relative binding of Hho1p, expressed as $\log_2$ relative to the population average is shown for every gene versus the ORF length of that gene in stationary phase (*A*) and 1 h after exiting stationary phase (*B*).

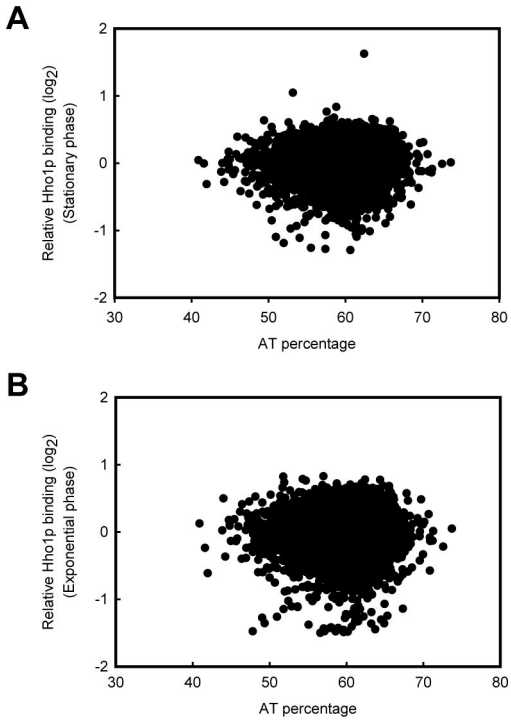

Fig. S4. Hho1p in not enriched at AT-rich regions of the *S. cerevisiae* genome *in vivo*. A plot of the AT composition versus the relative binding of Hho1p to every gene, expressed as $\log_2$ relative to the population average, is shown in stationary (*A*) and 1 h after exiting stationary phase (*B*).

Table S1. Nucleotide sequences of oligonucleotide primers used in this study

Primer	Nucleotide sequence
25S rDNA F	aggacgtcatagagggtgagaatc
25S rDNA R	ttgacttacgtcgcagtcctcagt
CUP1 F	ctagtaacaaggctaagatatcag
CUP1 R	gtaagccgatcccattaccgacat
MFA-1 F	caaacgagtgtgtaattaccc
MFA-1 R	ccctctcattaattcatttctggc
HHO1 F	cacccaagaaatccactacca
HHO1 R	aggtcaatgaagaaggcgaa
SNZ1 F	cagttaattatcacgatgactggag
SNZ1 R	atacctgttcaaagaaatcaccacc
ROX3 F	tggcttctagagtggacgaaa
ROX3 F	tccagcctccttcttttcat

Regions in the indicated gene coding sequences were amplified by PCR with the following forward (F) and reverse (R) primer pairs.