

SUPPORTING MATERIAL

Nonspecific protein-DNA binding is widespread in the yeast genome

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Supporting Figure Legend

Figure S1. This figure is analogous to **Figure 1** in the main text, except for the way of how the highest and the lowest average TF occupancy genes are selected in TSS and UAS regions. Here, the experimentally measured average TF occupancy is defined in the following way. First, for each TF the genes are ordered according to their occupancy score for this TF, and 20% of the highest and the lowest occupancy genes are selected for each TF (1). Second, each gene receives a score of how many times it was selected in the highest or the lowest occupancy group. Finally, 10% of the genes with the highest and the lowest scores are selected. Each of these two groups contains 496 genes. **A.** Average free energy of nonspecific TF-DNA binding per bp, $\langle \Delta f \rangle = \langle \Delta F \rangle / M$, computed within the interval (-400,400) for the two groups of genes selected according to the experimentally measured average TF occupancy, as defined above, in the TSS region: 10% highest TF occupancy in the TSS region (red) and 10% lowest TF occupancy in the TSS region (blue). Each group contains 496 genes. Horizontal bar, marked 'TSS', on the x -axis, shows the corresponding region where the TF occupancy was measured. **B.** Similar to **(A)**, but the two groups of genes are selected according to the experimentally measured average TF occupancy in the UAS region. Horizontal bar, marked 'UAS', on the x -axis, shows the corresponding region where the TF occupancy was measured. The p -values were computed in the following way. First, we selected 10^5 pairs of groups of randomly chosen 496 genes. Second, for each of these pairs of random groups we computed the free energy of nonspecific binding, as described above. Third, within each region of interest (TSS or UAS), we computed the difference between the minima of the average free energy of nonspecific binding, $\langle \Delta f \rangle_{\min}$, for the corresponding pairs of groups. Finally, we computed the probability that this difference is equal or larger than the actual value of the difference.

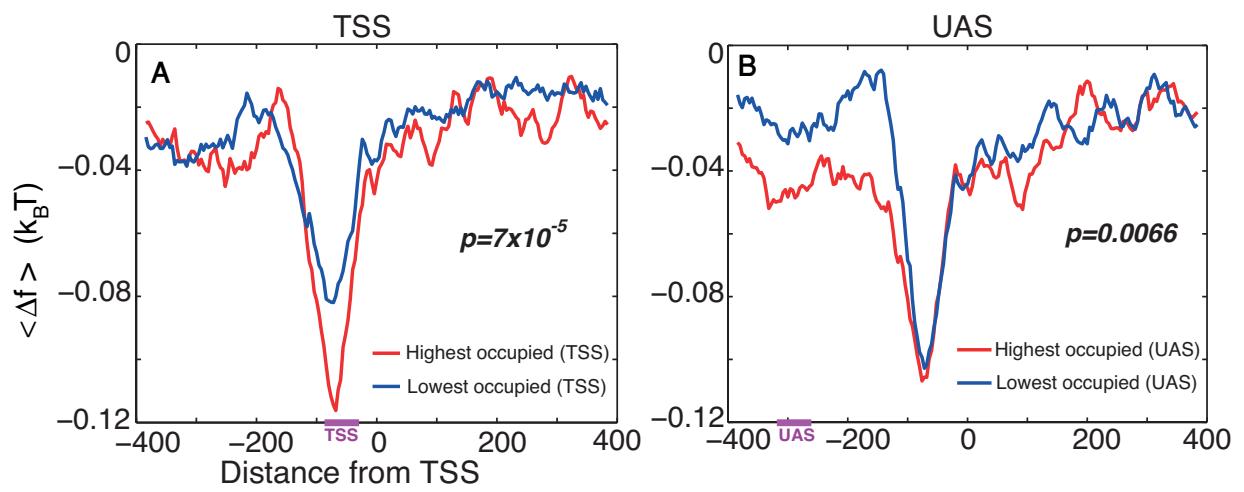


Figure S1.

1. Venters, B. J., S. Wachi, T. N. Mavrich, B. E. Andersen, P. Jena, A. J. Sinnamon, P. Jain, N. S. Rolleri, C. Jiang, C. Hemeryck-Walsh, and B. F. Pugh. 2011. A comprehensive genomic binding map of gene and chromatin regulatory proteins in *Saccharomyces*. *Mol Cell* 41:480-492.