Supplementary Information

A dynamic interplay of nucleosome and Msn2 binding regulates kinetics of gene activation and repression following stress

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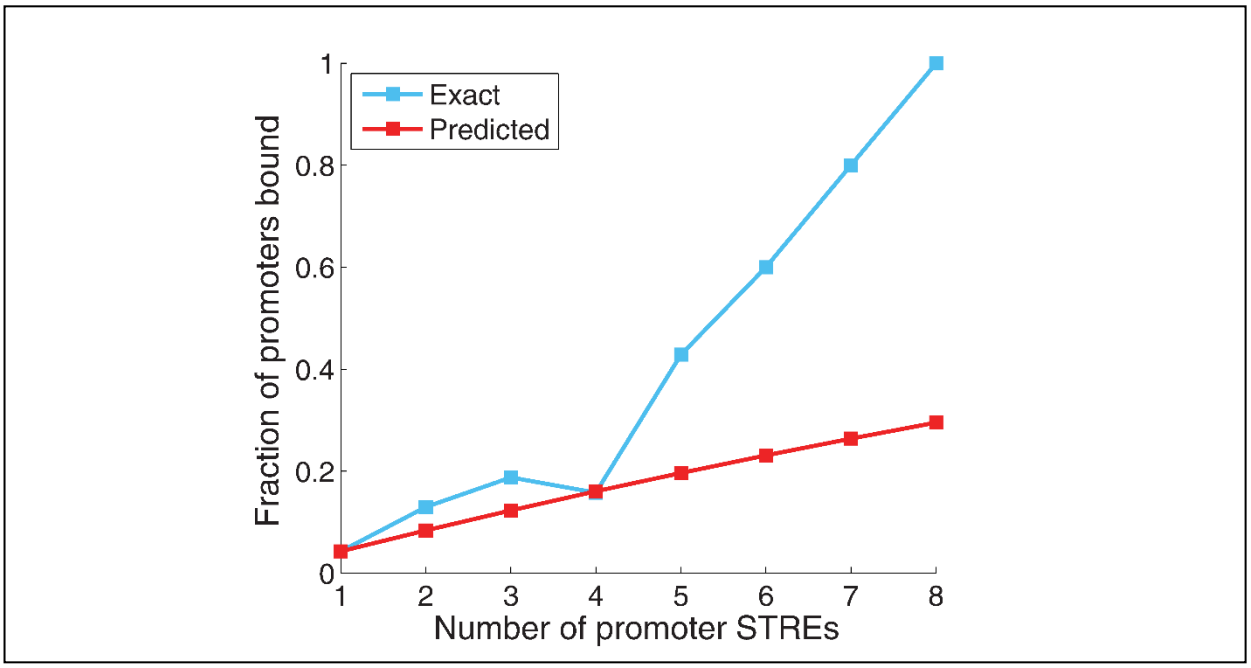

Figure S1. Synergistic binding of Msn2 to promoter STREs. The fraction of promoters to which Msn2 showed significant binding is plotted as a function of the number of STREs within the promoter (blue line). Using the fraction of promoters with a single STRE bound by Msn2 as the probability of Msn2 binding to a single STRE, the expected fraction of promoters bound by Msn2 is plotted as a function of the number of STREs in a promoter, assuming independent binding of Msn2 to each STRE within a promoter (red line).

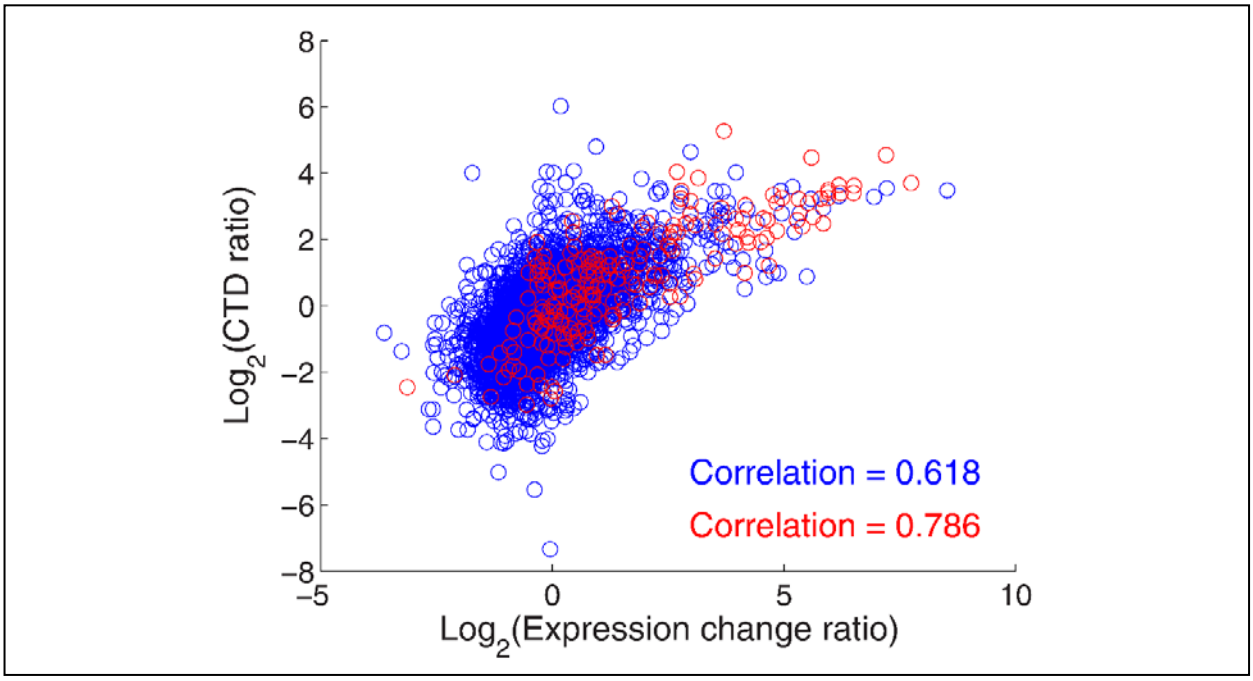

Figure S2. Correlation of CTD occupancy and expression change following nutrient downshift. Correlation plot of the log ratio of CTD integrated over the coding region of all genes (blue) or only those genes bound by Msn2 (red) 20 minutes following a glucose to glycerol nutrient downshift relative to that at time 0, as determined from the CTD ChIP-Seq data, versus the expression level changes of the same genes under the same condition, as obtained by global transcript level determination by two color microarray analysis.

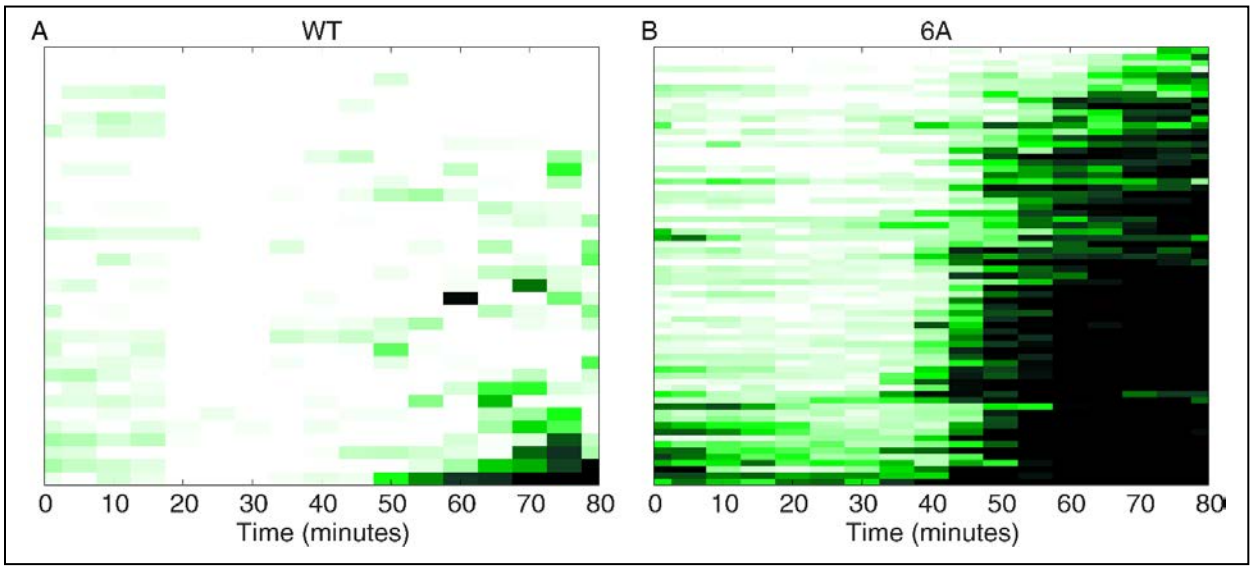

Figure S3. Nuclear localization of Msn2 following estradiol induction of Z_4EV strains. Y4131 (P_{ACT1}-Z_4EV P_{Z4EV}-*MSN2*-GFP, Panel A) or Y4132 (P_{ACT1}-Z_4EV P_{Z4EV}-$MSN2^{6A}$-GFP, Panel B) cells were immobilized in a microfluidic flow cell perfused with SD medium and imaged over time, as described in Petrenko et al. (2013). At time 0, the medium was switched to SD containing 1 μM estradiol. Data are presented as kymographs representing the subcellular localization of GFP-tagged Msn2 in individual cells (y-axis) over time (x-axis) with the intensity of green color indicating the extent of nuclear occupancy by Mns2-GFP. Frames were taken at 5 min intervals over 80 min. Original data are available in Movies S1 and S2.

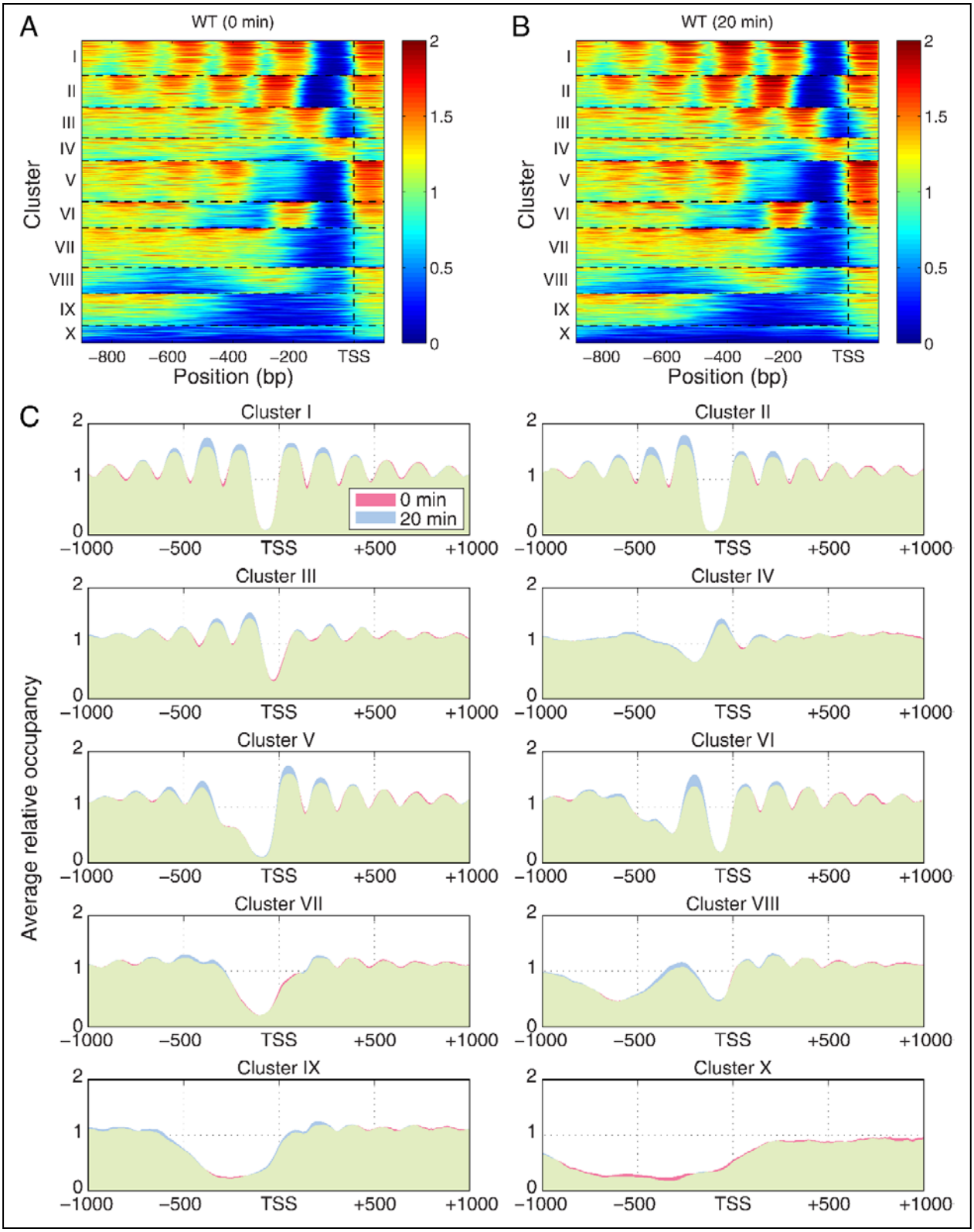

Figure S4. Limited nucleosome repositioning following nutrient downshift. Heatmap of nucleosome occupancy over the region surrounding the transcription start site (TSS) of all ~6000

yeast genes before (A) and 20 minutes after (B) a glucose-to-glycerol nutrient downshift, organized into related groupings by k-means clustering. Genes are represented in the same order in both panels. Panel C provides a direct comparison of the average occupancy in each cluster in the two panels.

Movie S1. Nuclear occupancy of wild type Msn2 following Z_4EV induction. Strain Y4131 (*MAT***a** *leu2*Δ::P_{ACT1}-Z_4EV-NatMX KanMX4-P_{Z4EV}-*MSN2*-GFP) cells were immobilized in a microfluidic flow cell perfused with SD medium, shifted to SD medium + 1 μM estradiol and imaged over time. Frames were taken at 5 min intervals over 80 min.

Movie S2. Nuclear occupancy of Msn2^{6A} following Z_4EV induction. Strain Y4132 (*MAT***a** *leu2*Δ::P_{ACT1}-Z_4EV-NatMX KanMX4-P_{Z4EV}-*MSN2*^{6A}-GFP) cells were immobilized in a microfluidic flow cell perfused with SD medium, shifted to SD medium + 1 μM estradiol and imaged over time. Frames were taken at 5 min intervals over 80 min.