



Supplemental Fig S4. Occupancy and ChIP-exo patterning around RpoN motifs. Some panels are identical to Fig. 4A, D, E except that acute heat shock data were added.

A) Shown are distribution of RpoN around the ATG start codons of RpoN-bound TU. Data are sorted based on RpoN occupancy ± 500 bp from the ATG start of each gene. Transcription units (rows, N=50 TUs) are aligned by their ATG start codons (5'-3', left to right) and sorted by RpoD occupancy (summed -80 to +80 bp from TU ATG start) at 30°C. Sense and antisense tags were shifted in the 3' direction by 6 bp (to adjust for the headroom of lambda exonuclease) and merged. Data files have an x-axis bin size of 2 bp.

B) Shown are occupancy heatmaps of indicated protein targets distributed around the RpoN motif reference point defined in Fig. 4C. Both are shown on linear y-axis scales that are arbitrary for each target and condition, and thus not comparable between each target and condition. Relative peak heights are comparable within a dataset.

C) Shown are composite plots of panel B, where the antisense/opposite strand data are inverted (N=166). Both are shown on linear y-axis scales that are arbitrary for each target and condition, and thus not comparable between each target and condition. Relative peak heights are comparable within a dataset. Data files have an x-axis bin size of 2 bp and smoothed with a 3 bp moving average. Composites are also shown from ± 300 bp and ± 1000 bp from the reference motif.