



Supplemental Fig S3. Occupancy and ChIP-exo patterning around RpoH motifs. Some panels are identical to Fig. 3A, B, E, F for heat shock genes except that acute heat shock (42°C for 6 min) data were added.

A) Shown are distributions of RpoH around the ATG start codons of previously defined heat shock genes (Nonaka et al. 2006; Gama-Castro et al. 2016). Data are sorted based on RpoH occupancy ± 120 bp from the ATG start of each gene. Transcription units (rows, $N=120$ 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 composite plots of RpoH (from Fig. 3B), RpoD, RpoN, and RpoA occupancy of the top-most RpoH-bound TUs from panel A ($N=46$). AU denotes arbitrary linear units. Datafiles have an x-axis bin size of 2 bp. The MglB data are the same in both panels. To compare y-axis magnitudes between same-target samples from 30°C and 42°C, gene-averaged y-axis values were empirically scaled (i.e., one scaling factor per dataset) to achieve similar y-axis minima values in the x-axis window (i.e., to achieve similar average local background). This assumes that the minima are background.

C) Occupancy heatmap of indicated protein targets distributed around the RpoH motif reference point in Fig. 3D. Blue indicates exonuclease stop sites on the sense/motif strand (sequence tag Read_1 5' ends); red is the same on the antisense/opposite strand. Top panels show a zoom in of the relevant section of the bottom panels. Data are sorted based on RpoH occupancy ± 50 bp from the reference point.

D) Shown are composite plots of panel C, where the antisense/opposite strand data are inverted ($N=52$). 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.