**SUPPLEMENTAL METHODS**

***Cell growth***

TAP-tagged strains of *Saccharomyces cerevisiae* for all factors in a BY4741 background were obtained from Open Biosystems. Cultures were grown in 500 ml of yeast peptone dextrose (YPD) media at 25°C to an OD600=0.8. For each heat shock time series, 100 ml (empirically-determined) of hot (100˚C) YPD media was added to swirling cultures growing at 25˚C, such that a final temperature of 37°C was achieved. Incubations were continued at 37˚C for the time indicated in each figure (3, 6, 9, 12, and 15 minutes). Cold formaldehyde (Fisher Scientific, 9.5 ml of 37% that had been freshly diluted into ddH2O at 0˚C) was added to each swirling culture (1% v/v final concentration and 25˚C final temperature). Shorter crosslinking times gave the same results, but were kept at 15 minutes to be consistent with prior studies. When no heat shock was applied (zero time point), 25˚C formaldehyde was added. Incubation was continued at 25˚C for 15 minutes, after which 5.5 ml of 2.5 M glycine was added to a final concentration of 125 mM for 5 minutes. Cells were then harvested by centrifugation at 3000g for 4 minutes at 4 °C. The pellet was washed with ST buffer containing protease inhibitor, flash frozen in liquid nitrogen and stored at -80°C until used. Two or more independent biological replicates were performed for each experiment or time point.

***ChIP-exo***

Antibodies to Pol II CTD S7P (4E12, Cat. # 04-1570), S5P (3E8, Cat. # 04-1572), and S2P (3E10, Cat. # 04-1571) were from Millipore. ChIP-exo experiments were performed essentially as described (Rhee and Pugh 2011). This included an immunoprecipitation from cross-linked sonicated extracts with protein-A coupled magnetic beads followed by DNA polishing, A-tailing, Illumina adaptor ligation (ExA2), and λ and RecJ exonuclease (New England Biolabs) digestion on the beads. After elution, a primer was annealed to EXA2, extended with Phi29 DNA polymerase (New England Biolabs), and then A-tailed. A second Illumina adaptor was then ligated, and the products were PCR-amplified and gel-purified. Sequencing was performed using Illumina HiSeq 2000 and NextSeq500.

***Nucleosomes***

MNase H3-ChIP-seq maps of nucleosomes (Nuc) (0 and 5 minutes of heat shock) are from (Batta et al. 2011).

***PIP-seq***

Formaldehyde cross-linked cells were produced as described above. Cell pellets were resuspended in PBS (phosphate buffer saline) and washed with 1 ml PBS. Collected cells were oxidized in 100 µl of 100 mM KMnO4 (Potassium Permanganate) for 1 min in PBS buffer at room temperature, with mixing (Li et al. 2013). Reactions were stopped by adding 500 µl of PBS buffer containing 0.8 M β-mercaptoethanol and 40 mM EDTA. Cells were washed with PBS and processed to produce sonicated extracts, as described above. Fragmented chromatin was immunoprecipitated, and Phi-29 nick-repaired. Libraries were digested using 10 µl of piperidine and incubated at 90 °C for 30 minutes. Piperidine was then removed by isobutanol followed with ether extraction. Protein-DNA was reverse cross-linked overnight at 65˚C followed by phenol extraction and adaptor ligation library completion.

***Bioinformatics***

Datasets used for individual figure panels are indicated in Supplemental Table S1. For single-end reads from HiSeq, base calls were performed using CASAVA version 1.7 (Illumina), and for paired-end reads from NextSeq, base calls were performed using Bcl2fq version 2.16 (Illumina). ChIP-exo reads were aligned to the sacCer3 genome assembly using BWA (version 0.6.2 for HiSeq single-end reads and version 0.7.9a for NextSeq paired-end reads) with default parameters. Uniquely aligned sequence tags were mapped to the yeast genome (sacCer3) using BWA (Li and Durbin 2009). Tag 5’ ends were shifted in the 3′ direction by 6 bp to reflect the point of crosslinking, and strand information was removed. To normalize datasets, each coordinate-strand was rank-ordered within each dataset by tag count, then averaged across datasets for each rank order (Qiu et al. 2013). The untagged BY4741 negative control was normalized so that it matched background regions (ORFs) for GTFs. DESeq (Anders and Huber 2010) was used to compute the significant changes in TFIIH (Ssl2) ChIP-exo tag counts upon heat shock in the interval -100 bp to +100 bp from annotated TSSs. A significance threshold of p-value (<0.05) was used to define the set of genes that were heat shock induced or heat shock repressed. Biological replicates were treated separately and used to confirm the findings. Only Hsf1 replicates were combined (*n= 3*). Reference +1 nucleosome dyads were from (Zhang et al. 2011); TSS locations were from (Xu et al. 2009). The set of SAGA/TFIID-dominated genes were obtained from (Huisinga and Pugh 2004).

***Hsf1 binding sites***

Hsf1 ChIP-exo strand-separate peaks were called using the GeneTrack algorithm (parameters: *sigma = 5, exclusion zone = 10*) {Albert, 2008 #149}. Strand separate peaks were then paired and merged into one candidate binding site under the requirement they be 0–80 bp 3’ from each other and on opposite strands. MEME analysis (Bailey et al. 2009) was performed on 80-bp sequences centered on the location of the top 500 most-highly occupied binding locations for Hsf1, so as to obtain a position-specific percentage matrix (PSPM) of nucleotide frequency. FIMO was then used to find all instances of Hsf1 motifs within 40 bp of all Hsf1-bound locations, using this PSPM and a motif p-value cutoff of 0.001 (Bailey et al. 2009). The binding locations were centered on the most significant motifs if a motif was present within a 40-bp distance. The candidate locations that were significantly enriched over non-specific antibody control with a q value of <0.05 were selected (q values are adjusted P values from binomial tests for multiple-hypothesis testing). Hsf1-bound sites were attached to the nearest annotated coding gene if it was <500 bp upstream of its TSS.