SUPPLEMENTAL TABLE LEGENDS

Table S1. Nucleosome calls. Start and stop positions of all called nucleosomes.

Table S2. Nucleosome metaset. Start and stop sites, dynamic class, and $\log_2$ normalized sequencing counts per nucleosome are listed for nucleosomes in the metaset.

Table S3. Nucleosome positions and changes for loading into an integrated genome browser.

Table S4. Msn2p-bound loci. Start and stop positions, dynamic class, and $\log_2$ average array signal over the identified peak.

Table S5. Gene expression data. Log_2 fold-change in expression is shown for coding and non-coding transcripts, whose start and stop positions and significance of change are also shown

Table S6. Venters comparison. The Bonferroni-corrected p-values are shown for the overlap in genes bound by the denoted factor at either 25C or 37C, and containing an upstream nucleosome from the denoted class. See text for details.

SUPPLEMENTAL FIGURE LEGENDS

Figure S1. Biological reproducibility of dynamic classes of nucleosome repositioning. Of the 9,509 nucleosomes scored as changing in occupancy in the MNase-seq experiment, 4,943 were measured with at least two observations of 1.5X change in an independent time course hybridized to tiled yeast genomic arrays from Nimblegen (unpublished data). Nucleosomes were organized according to the classification of nucleosomes shown in Figure 3, and the mean of each cluster was calculated for the MNase-seq experiment (blue) versus the biological replicate hybridized to tiled arrays (red). The trends in the data were highly reproducible in the biological replicates, although the MNase-seq experiment had a significantly wider dynamic range, as expected for sequencing data. Biological replicates of the 30 min time point that were

hybridized to microarrays were highlight reproducible (R ~ 0.7 for $\log_2$ changes in nucleosome occupancy). Adjacent timepoints in the MNase-seq experiment were also well correlated (R ~0.72 – 0.81).

Figure S2. Associations between dynamic classes of nucleosome loss and chromatin regulators. Genes harboring upstream nucleosomes repositioned with different dynamic patterns were compared to genes whose upstream regions were bound by chromatin regulators at 25C (left) or after a 25C-37C heat shock (right) by Venters *et al*. (67). Blue boxes in the diagram represent significant (Bonferroni-corrected) overlap between genes bound by different regulators (y-axis) and genes harboring upstream nucleosomes in different dynamic classes (x-axis). Enrichments that were significant both before and after heat shock (left) and those for which at least nucleosome class changed significantly in enrichment upon stress (right) are shown. Annotations list the bound protein and the complex(es) it participates with. ATP-dependent chromatin remodelers are highlighted in red, SAGA components in pink, TFII subunits in blue, and transcription factors in green. P-values for all comparisons (including nucleosome loss and gain classes) are available in Table S6.

Figure S1

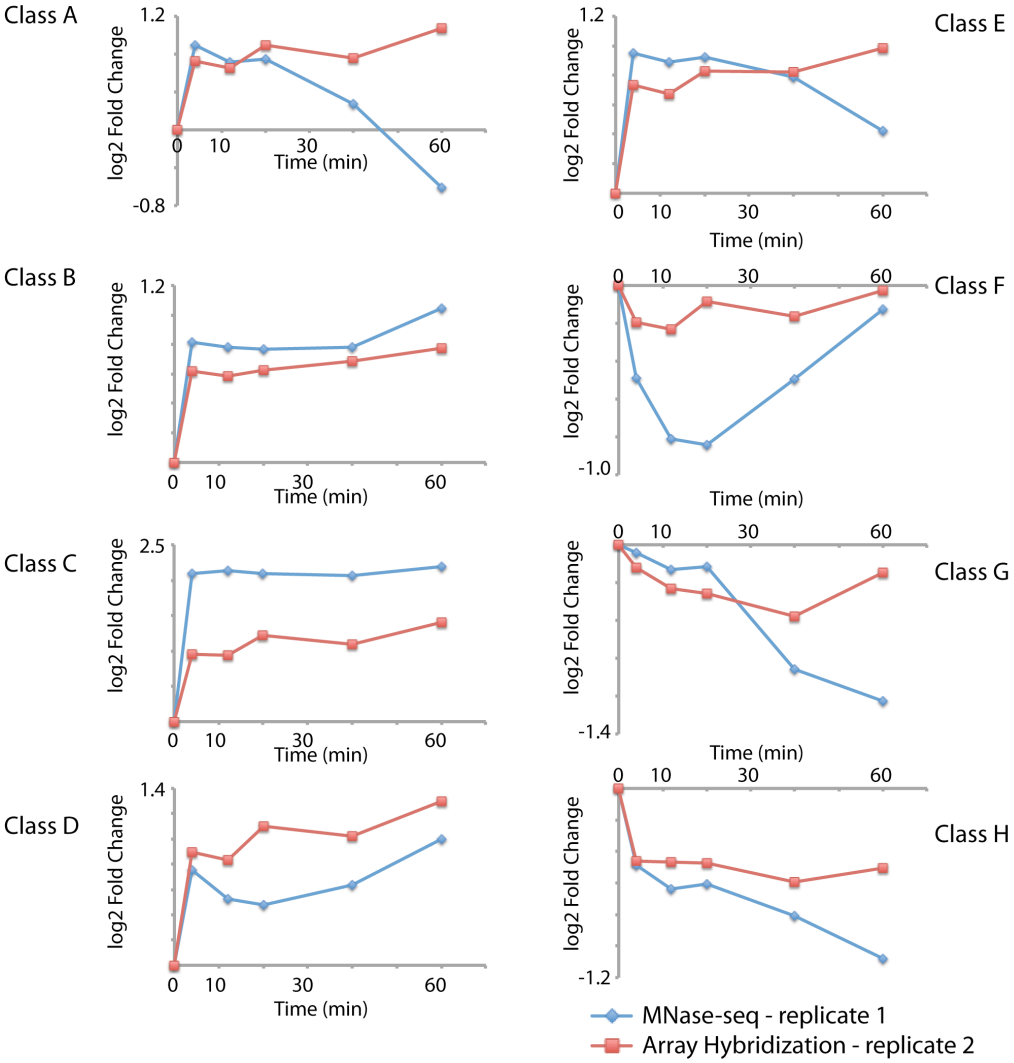
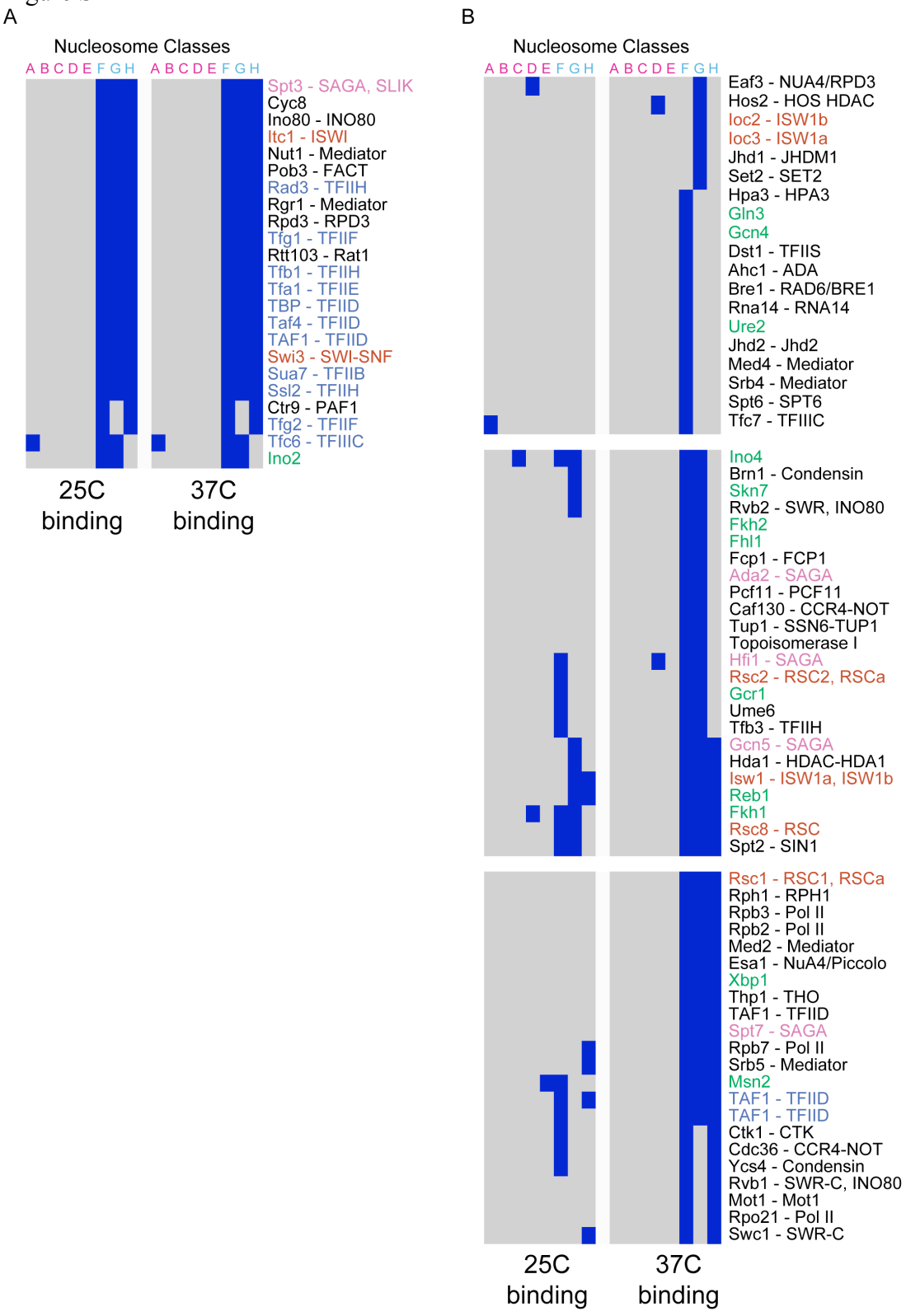

Class A
Class B
Class C
Class D
Class E
Class F
Class G
Class H
log2 Fold Change
Time (min)
1.2
-0.8
2.5
1.4
-1.0
-1.4
-1.2
0
10
30
60
MNase-seq - replicate 1
Array Hybridization - replicate 2

Figure S2


A
Nucleosome Classes
A B C D E F G H
A B C D E F G H
Spt3 - SAGA, SLIK
Cyc8
Ino80 - INO80
Itc1 - ISWI
Nut1 - Mediator
Pob3 - FACT
Rad3 - TFIIH
Rgr1 - Mediator
Rpd3 - RPD3
Tfg1 - TFIIF
Rtt103 - Rat1
Tfb1 - TFIIH
Tfa1 - TFIIE
TBP - TFIID
Taf4 - TFIID
TAF1 - TFIID
Swi3 - SWI-SNF
Sua7 - TFIIB
Ssl2 - TFIIH
Ctr9 - PAF1
Tfg2 - TFIIF
Tfc6 - TFIIIC
Ino2
25C binding
37C binding
B
Nucleosome Classes
A B C D E F G H
A B C D E F G H
Eaf3 - NUA4/RPD3
Hos2 - HOS HDAC
Ioc2 - ISW1b
Ioc3 - ISW1a
Jhd1 - JHDM1
Set2 - SET2
Hpa3 - HPA3
Gln3
Gcn4
Dst1 - TFIIS
Ahc1 - ADA
Bre1 - RAD6/BRE1
Rna14 - RNA14
Ure2
Jhd2 - Jhd2
Med4 - Mediator
Srb4 - Mediator
Spt6 - SPT6
Tfc7 - TFIIIC
Ino4
Brn1 - Condensin
Skn7
Rvb2 - SWR, INO80
Fkh2
Fhl1
Fcp1 - FCP1
Ada2 - SAGA
Pcf11 - PCF11
Caf130 - CCR4-NOT
Tup1 - SSN6-TUP1
Topoisomerase I
Hfi1 - SAGA
Rsc2 - RSC2, RSCa
Gcr1
Ume6
Tfb3 - TFIIH
Gcn5 - SAGA
Hda1 - HDAC-HDA1
Isw1 - ISW1a, ISW1b
Reb1
Fkh1
Rsc8 - RSC
Spt2 - SIN1
Rsc1 - RSC1, RSCa
Rph1 - RPH1
Rpb3 - Pol II
Rpb2 - Pol II
Med2 - Mediator
Esa1 - NuA4/Piccolo
Xbp1
Thp1 - THO
TAF1 - TFIID
Spt7 - SAGA
Rpb7 - Pol II
Srb5 - Mediator
Msn2
TAF1 - TFIID
TAF1 - TFIID
Ctk1 - CTK
Cdc36 - CCR4-NOT
Ycs4 - Condensin
Rvb1 - SWR-C, INO80
Mot1 - Mot1
Rpo21 - Pol II
Swc1 - SWR-C
25C binding
37C binding