Nucleosome architecture throughout the cell cycle

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Supplementary Figures & Dataset Captions

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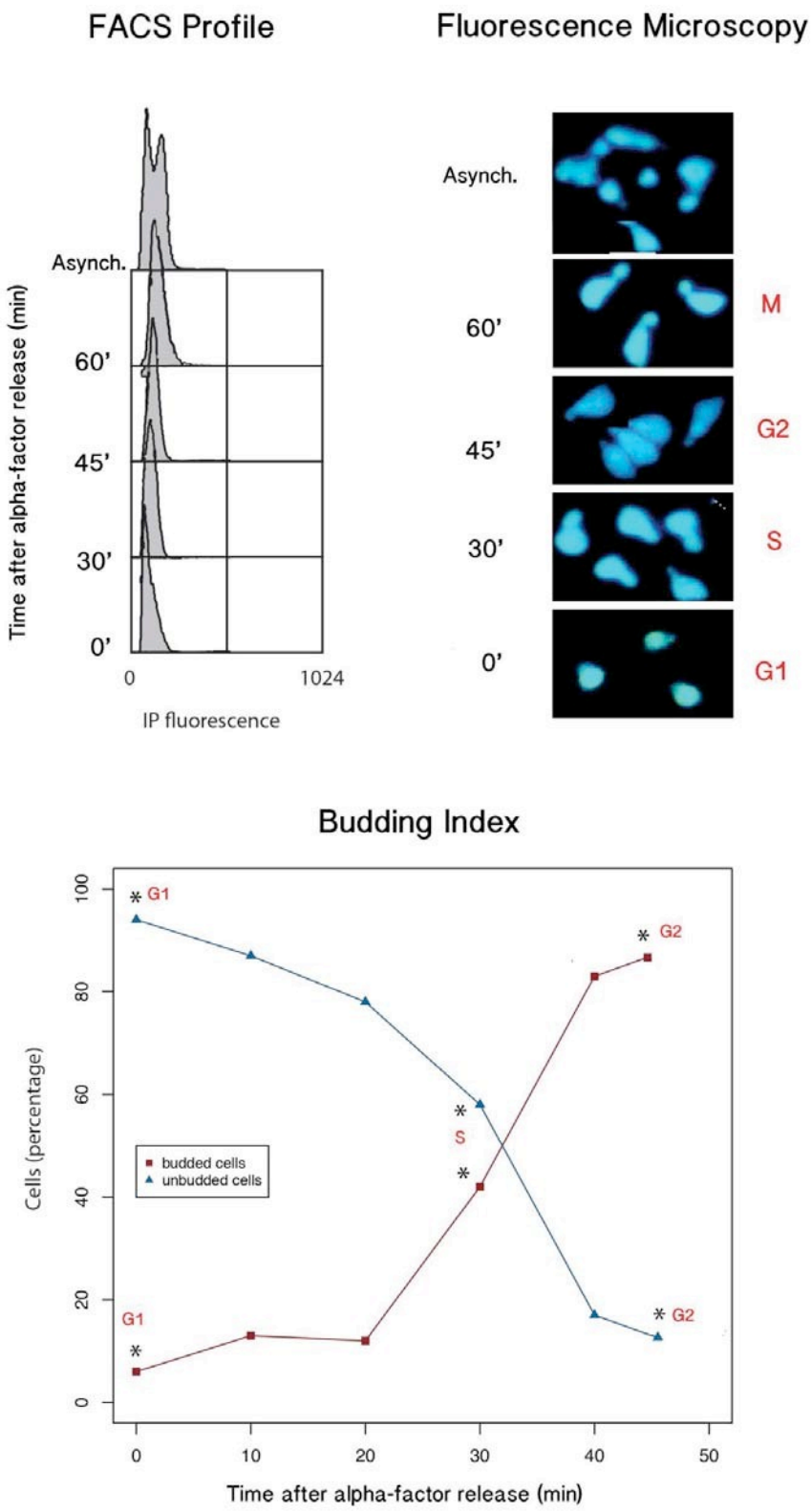
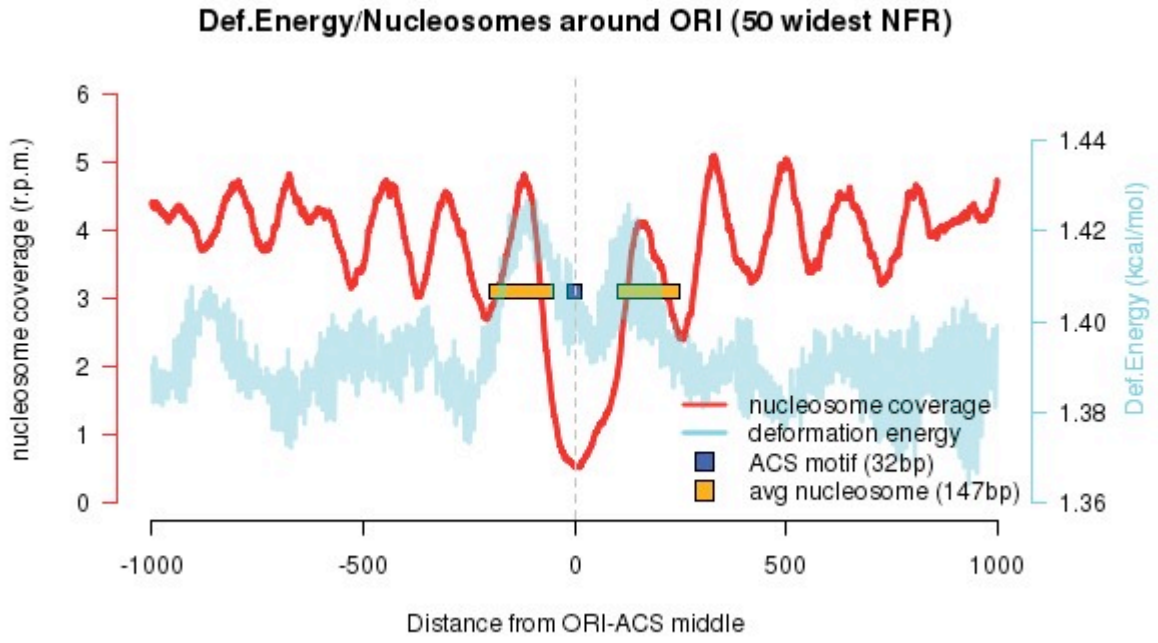
SUP FIGURE S1



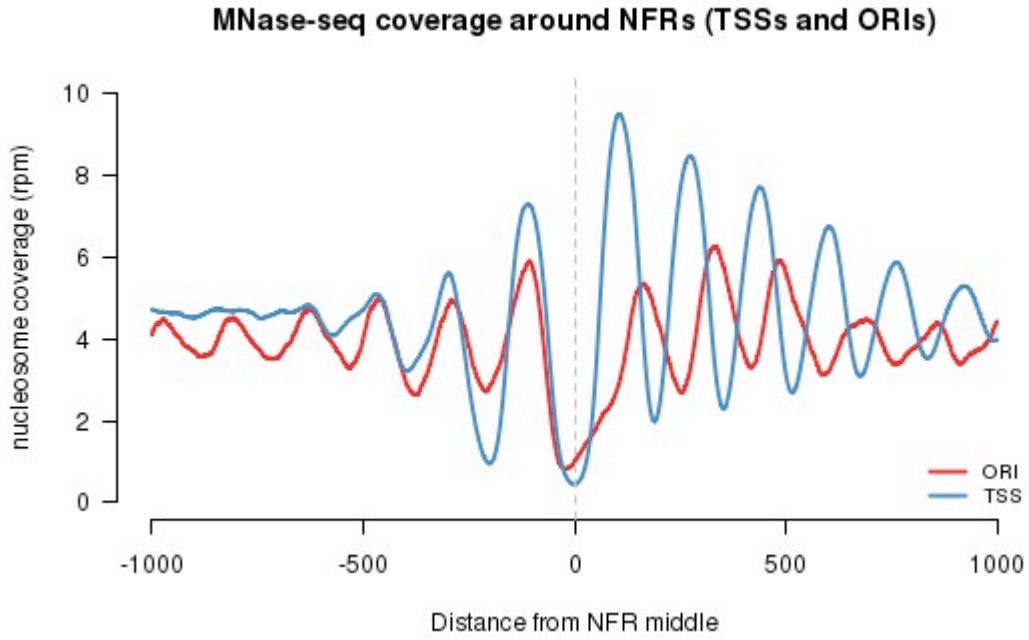
Supplementary Figure S1 – Monitoring cell cycle progress of BY4741 cells, by flow cytometry (top left), fluorescence microscopy (top right) and budding index (bottom).

SUP FIGURE S2

a)

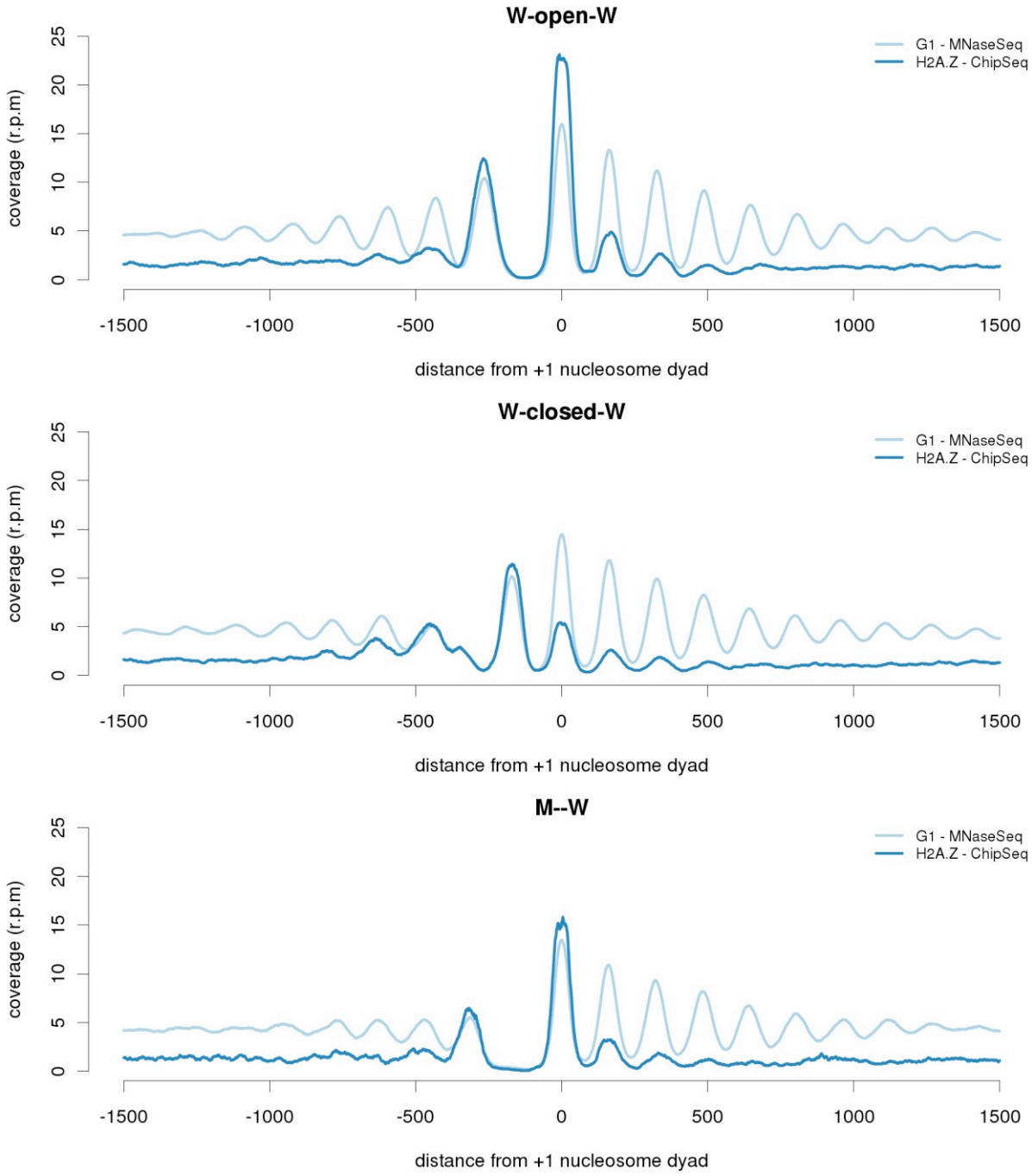


b)



Supplementary Figure S2 – Properties of the NFRs at ORIs. **a)** The deformation energy (blue) and coverage maps (red) were calculated and averaged across the widest NFRs at ORIs (top 50). ORI-NFRs are signaled by specific physical properties of the underlying DNA sequence (higher deformation energy shown in blue), in a similar manner to TSS-NFRs (Flores et al, 2014) **b)** Distribution of average nucleosome coverage profiles at TSSs (blue) and ORIs (red). Average nucleosome positioning at TSSs are directional and asymmetrical, meanwhile symmetry is more prevalent in the ORIs.

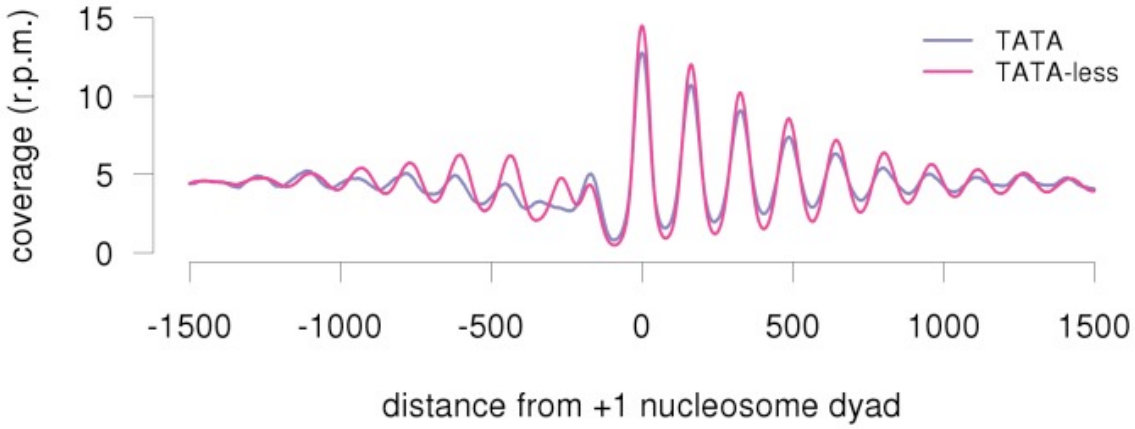
SUP FIGURE S3



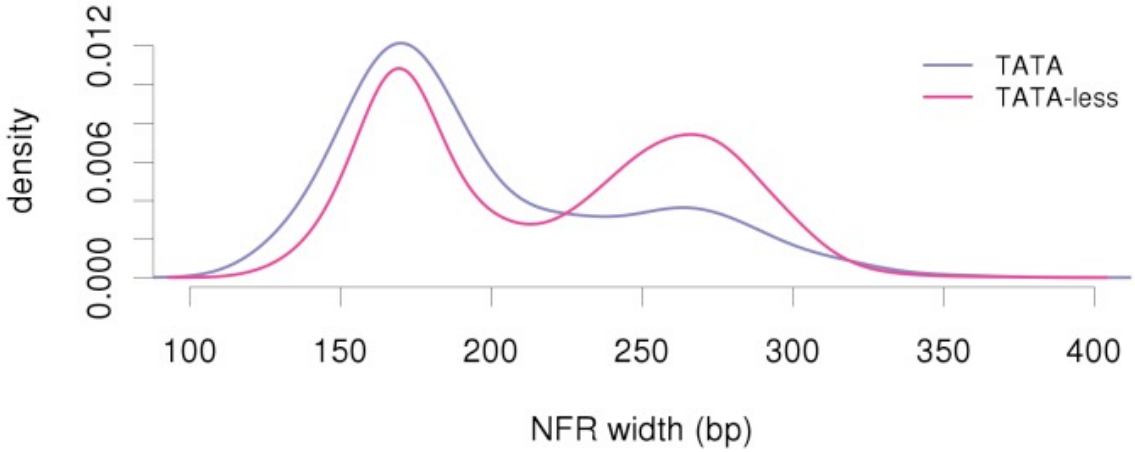
Supplementary Figure S3 – H2A.Z histone variant enrichment in gene clusters. H2A.Z coverage (Albert, 2007) is compared with G1 nucleosome coverage maps in a) open, b) closed and c) missing -1 nucleosome families with flanking well positioned nucleosomes.

SUP FIGURE S4

a)

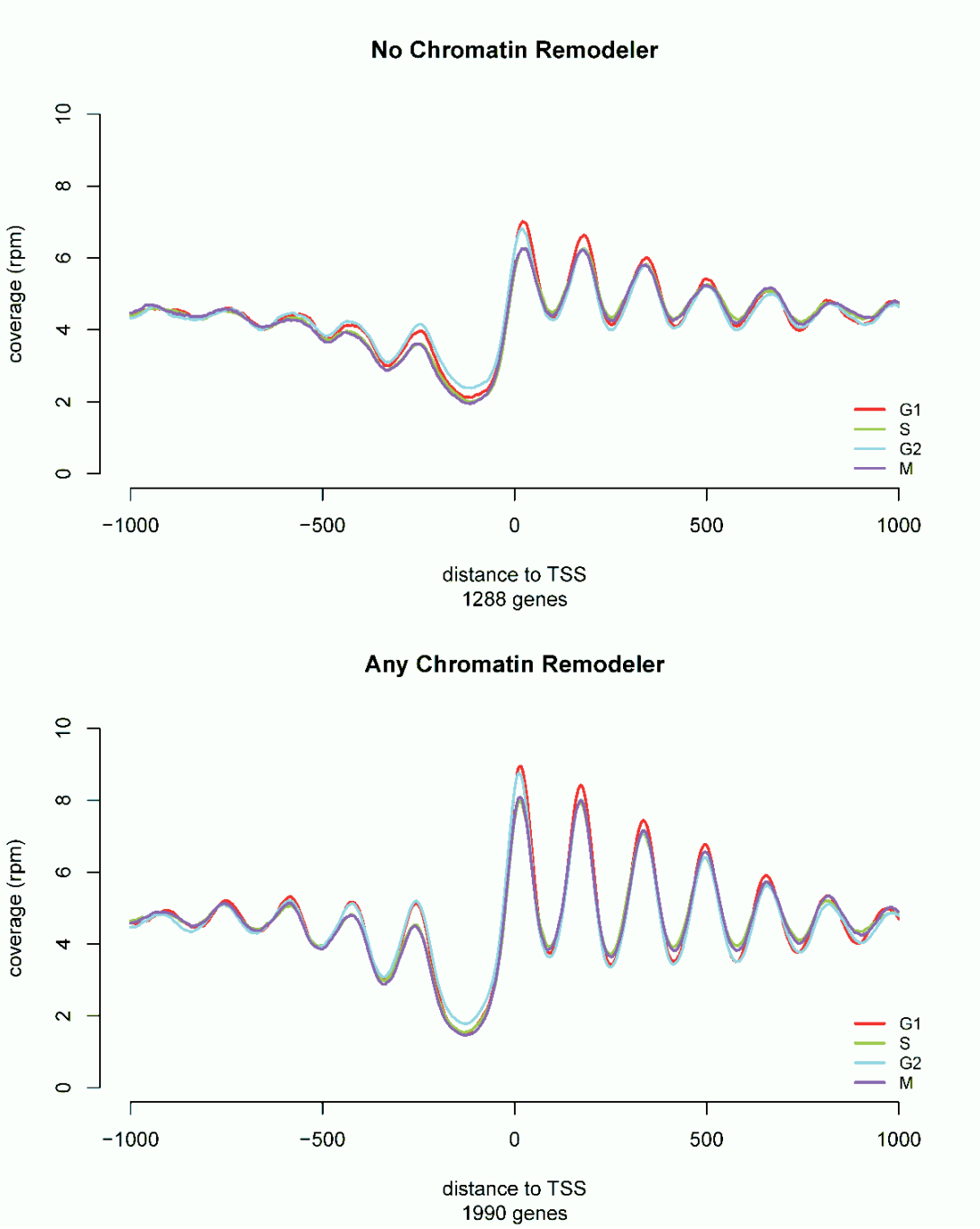


b)



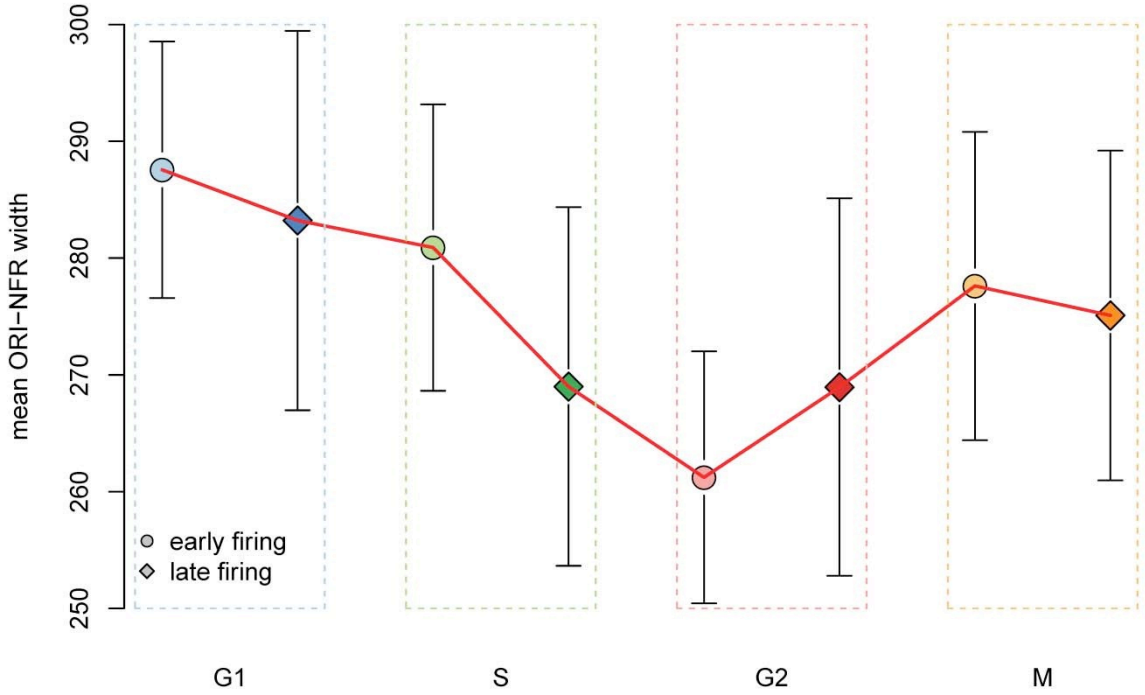
Supplementary Figure S4 – Nucleosome coverage in TATA and TATA-less promoters. Nucleosome coverage maps of TATA-box regulated genes (pink) are compared with TATA-less genes (purple). **a)** Average coverage taking the dyad of the +1 nucleosome as reference does not display any difference in the gene body. **b)** NFR distribution in TATA and TATA-less promoters.

SUP FIGURE S5



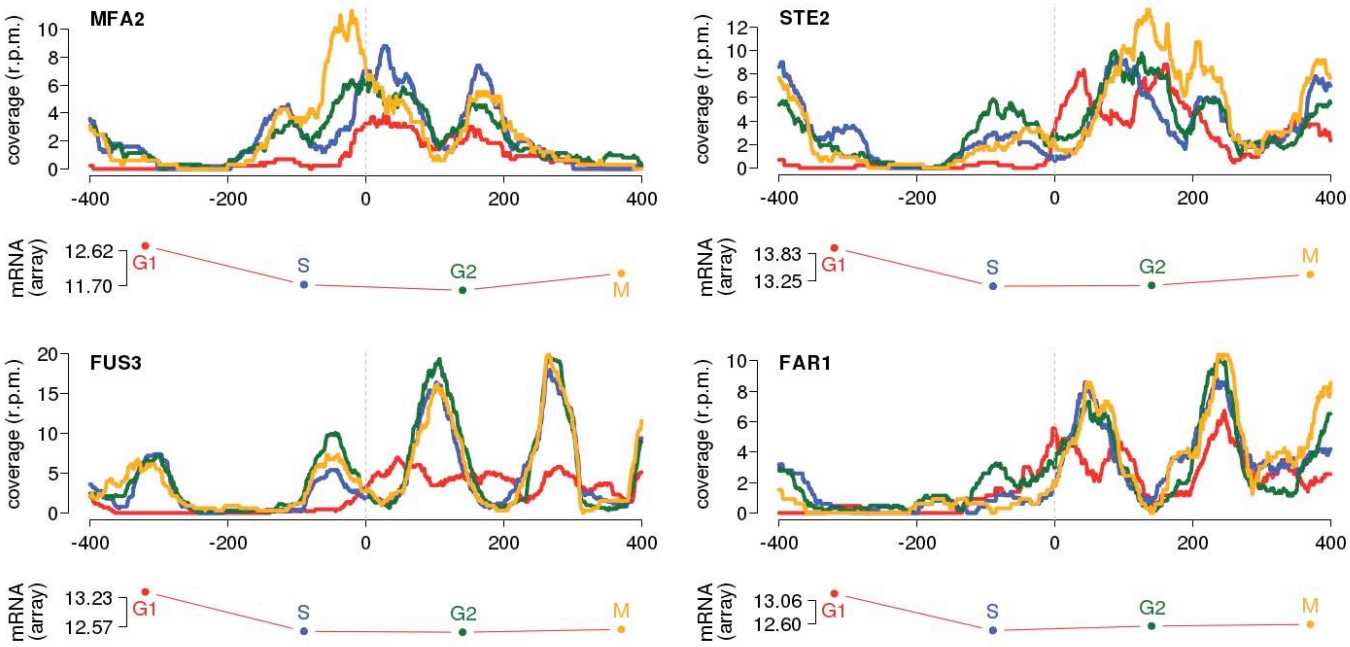
Supplementary Figure S5. Effect of chromatin remodelers in nucleosome architecture. Average nucleosome coverage at TSSs for genes not bound by any chromatin remodelers (top) and bound by any chromatin remodeler (bottom). The genes regulated by remodelers display a better phasing of nucleosome arrays.

SUP FIGURE S6



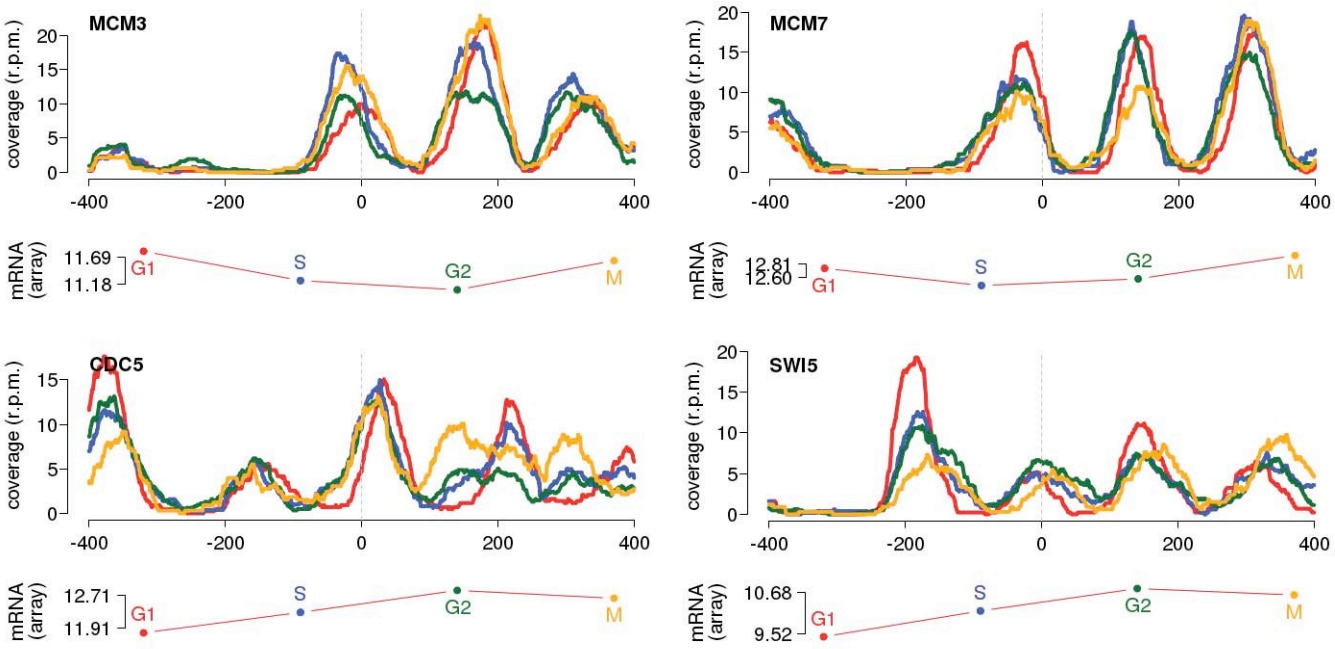
Supplementary Figure S6 – Nucleosome free region at ORIs along cell cycle. Average width of ORI-NFRs changes during cell cycle, both in early and late firing ORIs. Error bars signal the 95% confidence interval, which is wide due to the low number of observations (N=100 in both groups)

SUP FIGURE S7



Supplementary Figure S7 – Nucleosome architecture and expression plasticity of genes involved in alpha-factor pheromone mating and its desensitization response. Up to bottom and left to right): MFA2, STE2, FUS3 and FAR1. Gene expression levels are indicated as log2 values of the hybridization ratios from the Affymetrix GeneChip Yeast Genome 2.0 arrays.

SUP FIGURE S8



Supplementary Figure S8 – Nucleosome architecture and expression plasticity of genes involved in cell cycle progression. Up to bottom and left to right): MCM3, MCM7, CDC5 and SWI5. Gene expression levels are indicated as log2 values of the hybridization ratios from the Affymetrix GeneChip Yeast Genome 2.0 arrays.

Dataset captions

Dataset 1. Nucleosome architecture dynamics around TSS during cell cycle

Dataset 2. GO-term enrichment analysis for different gene clusters

Dataset 3. GO-term enrichment analysis for combinations of mobile genes with high expression fold-change (>1.2)