

## Supplementary Information for

## The nucleosome core particle remembers its position through DNA replication and

## transcription

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Figs. S1 to S8



**Fig. S1.** Histone H3 was tagged at both endogenous loci *HHT1* and *HHT2* with a 15 amino acid AviTag. Tagged histones are biotinylated by the TetR-BirA protein. Neither individual domain of the split TetR-BirA heterodimer is capable of biotinylation without its reciprocal domain. Arc1 is an endogenously biotinylated protein, and the TetR-BirA fusion proteins did not affect endogenous protein biotinylation.



**Fig. S2**. Cells grown on rich media arrest durably in the presence of alpha factor, suggesting that chromatin-based gene repression at *HML* and mating pathway gene regulation was functionally intact. Strains expressing TetR-BirA(s/213) and H3-Avi had no detectable growth defect.



**Fig. S3.** Only a single off-target locus was biotinylated by TetR-BirA, and it corresponds to a degenerate TetO sequence. **(A)** Tet-BirA targets were identified by comparing biotin pulldown density in YPD to density in YPD + doxycycline for 1kb intervals genome-wide. The only two loci that showed dox-sensitive biotin pulldown corresponded to *gal10-tetO* and to *YEL1*. Using EMBOSS Water, we identified a near perfect match for the *TetO* sequence in the *YEL1* promoter that we speculate was responsible for TetR-BirA recruitment (*5*). **(B)** Biotin density at *YEL1* was ~1.5-fold lower that *gal10-tetO* in cells expressing hypomorphic TetR-BirA-G115S **(C)** Biotin density was ~15-fold lower than at *gal10-tetO* in cells expressing the split TetR-BirA(s/213) pair. In both TetR-BirA-G115S and TetR-BirA(s/213), maximal biotinylation was restricted to a region of ~600bp, however at *YEL1* biotinylation was observed on both sides of the operator. **(D)** Biotinylation at *gal10-TetO* reflected TetR-BirA (anti-V5) ChIP signal at the locus, however biotinylation at *YEL1* occurred without observable TetR-BirA ChIP signal.



**Fig. S4.** Cells were stained with SYBR green to detect genome copy number and track passage through the cell cycle. H3-Avi TetR-BirA(s/213) strains showed efficient arrest in G1 and release after addition of protease to the growth medium.



**Fig. S5.** The observed nucleosome positions after one cell cycle were best explained by the model that nucleosomes do not move during DNA replication. To simulate experimental data, each nucleosome from the arrested culture was modelled as moving +/- binomial(200,0.81), centered on 162bp with probability  $\rho$  after one cell division, and the Euclidean distance was calculated between the observed data and simulated data sets in non-overlapping 10bp bins. The value of  $\rho$  that minimizes the squared error loss corresponds to the most likely model tested, and we found that the loss is minimized for  $\rho = 0$ . The result was robust to bin size between 5bp and 45bp bins.



**Fig. S6.** Cells were stained with SYBR green to detect genome copy number and track passage through the cell-cycle. H3-Avi TetR-BirA(s/213) *mcm2-3A* strains showed efficient G1 arrest and release and their cell cycle timing was similar to that of wild-type cells. Cells encoding *dpb3* $\Delta$  and *mcm2-3A dpb3* $\Delta$  showed relatively slower passage through the cell cycle, and both cultures included a population of cells that were arrested throughout the experiment.



**Fig. S7.** Two biological replicates of replisome mutant strains showed similar patterns of nucleosome inheritance during DNA replication. Plotted data reflects the arrested condition (grey line) and the replicated condition after one cell cycle (red line) detected by streptavidin chromatin precipitation and sequencing. Data from replicate 1 is reproduced from Fig 2,3 for direct comparison between replicates. In each case, biotinylated nucleosome density decreased through DNA replication without detectable local diffusion.



**Fig. S8.** Cells grown in raffinose then switched into either dextrose or galactose were efficiently arrested in G1 by alpha-factor.