

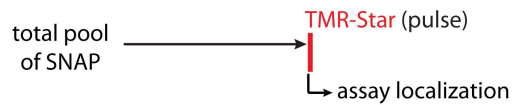
Supplemental figure legends

Figure S1 (related to Figure 1). Direct pulse labeling of SNAP-tagged histones. (A) Outline of SNAP-based pulse labeling experiment to visualize the total pool of SNAP protein. (B) Results of A for indicated histone-SNAP fusion proteins. (C) Centromeric enrichment can be observed in cells expressing low levels of H4-YFP.

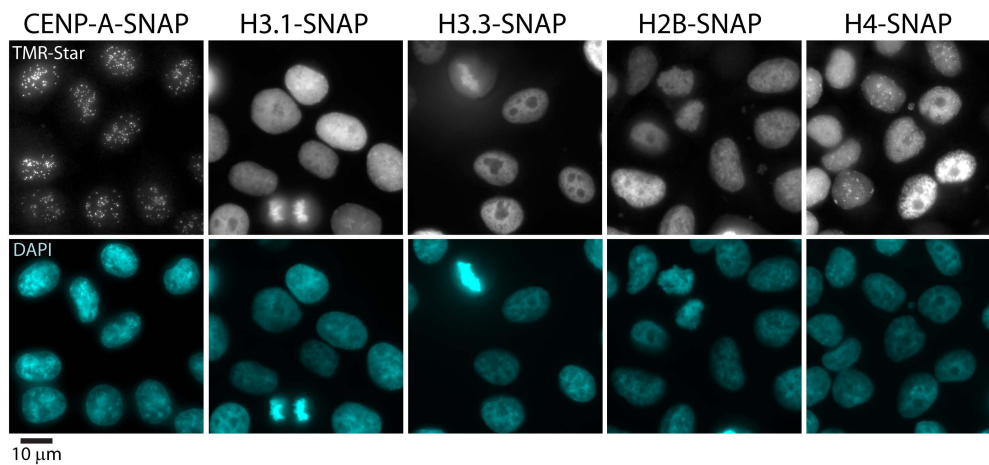
Figure S2 (related to Figure 2). Quench-chase-pulse experiments reveal distinct assembly modes for H4 during the cell cycle. (A-E) Outlines and results for synchronized quench-chase-pulse experiments, analyzing H4-SNAP assembly for indicated portions of the cell cycle. (F) As in E, except that nocodazole was added to arrest cells upon mitotic entry.

Figure S3 (related to Figures 3 and 4). Stable retention at centromeres is restricted to CENP-A, H4, and H3^{CATD}. (A) Indicated cell lines were treated as in Figure 3A and imaged at indicated time points. Enlargements show rescaled images of centromeric signal. (B) Results of experiment as in Figure 3A for SNAP-tagged H3.1, H3.3, and H2B. Saturated enlargements of boxed cells are shown. No preferential retention at centromeres is observed for these histones.

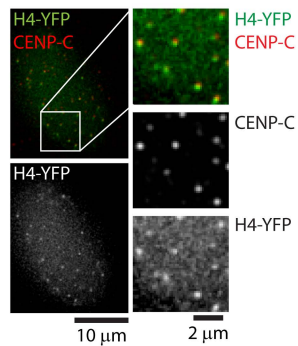
A



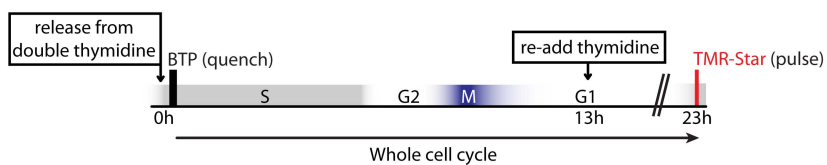
B



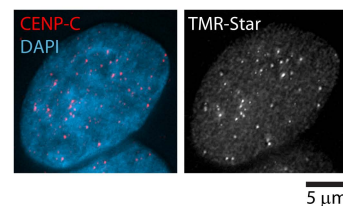
C



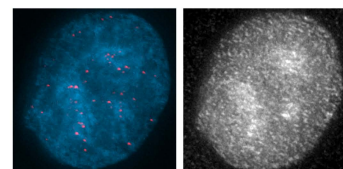
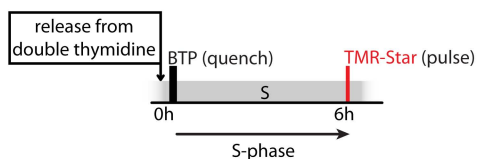
A



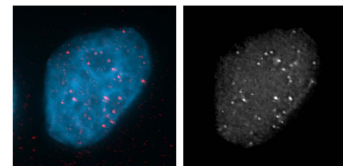
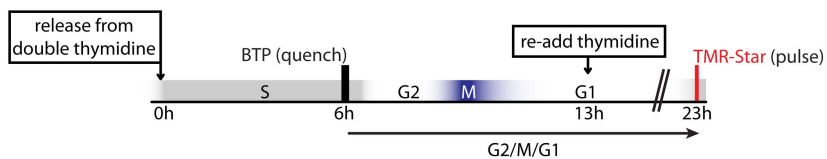
H4-SNAP



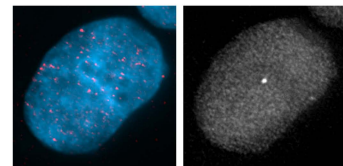
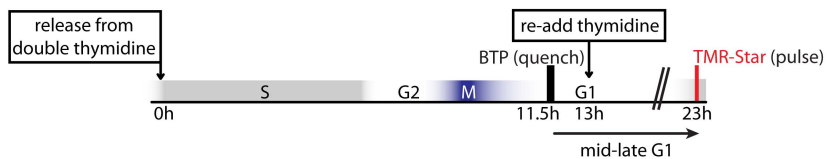
B



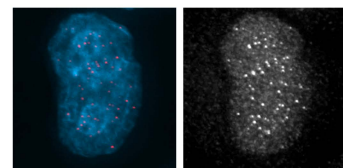
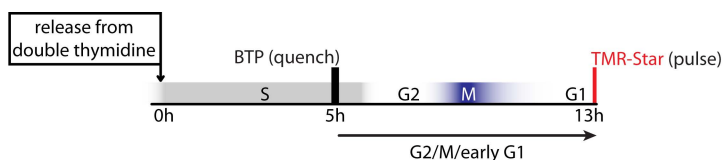
C



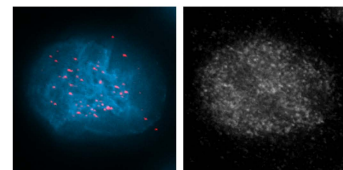
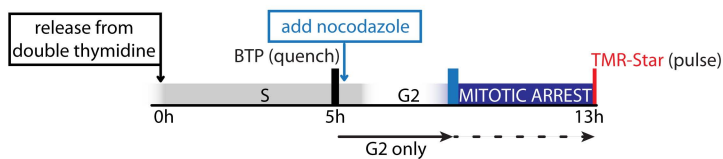
D



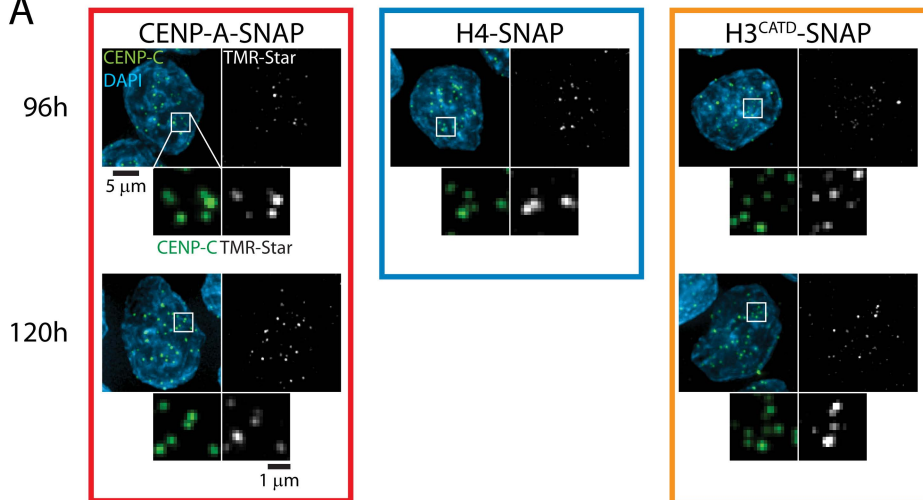
E



F



A



B

