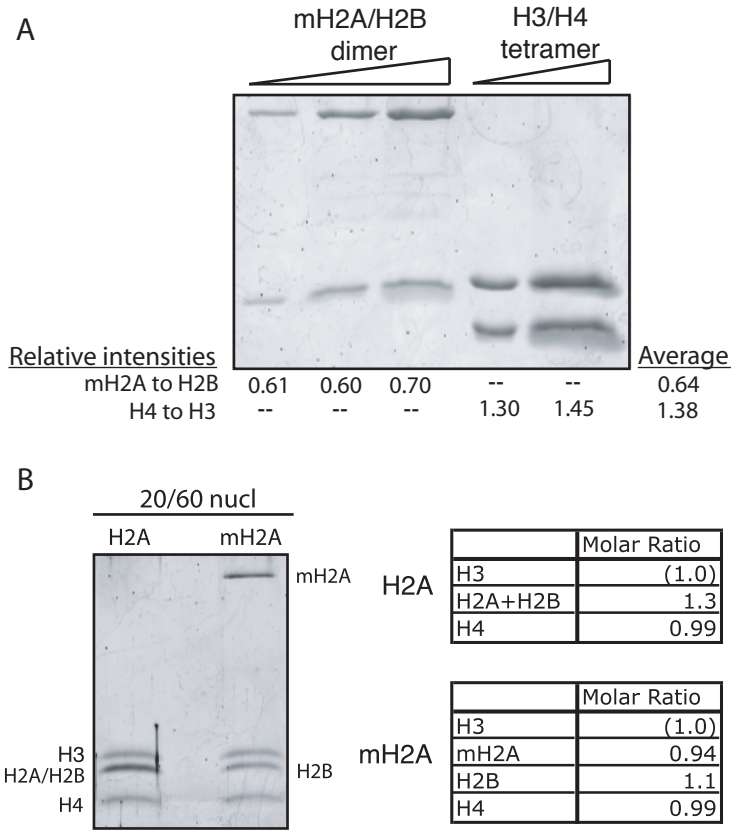
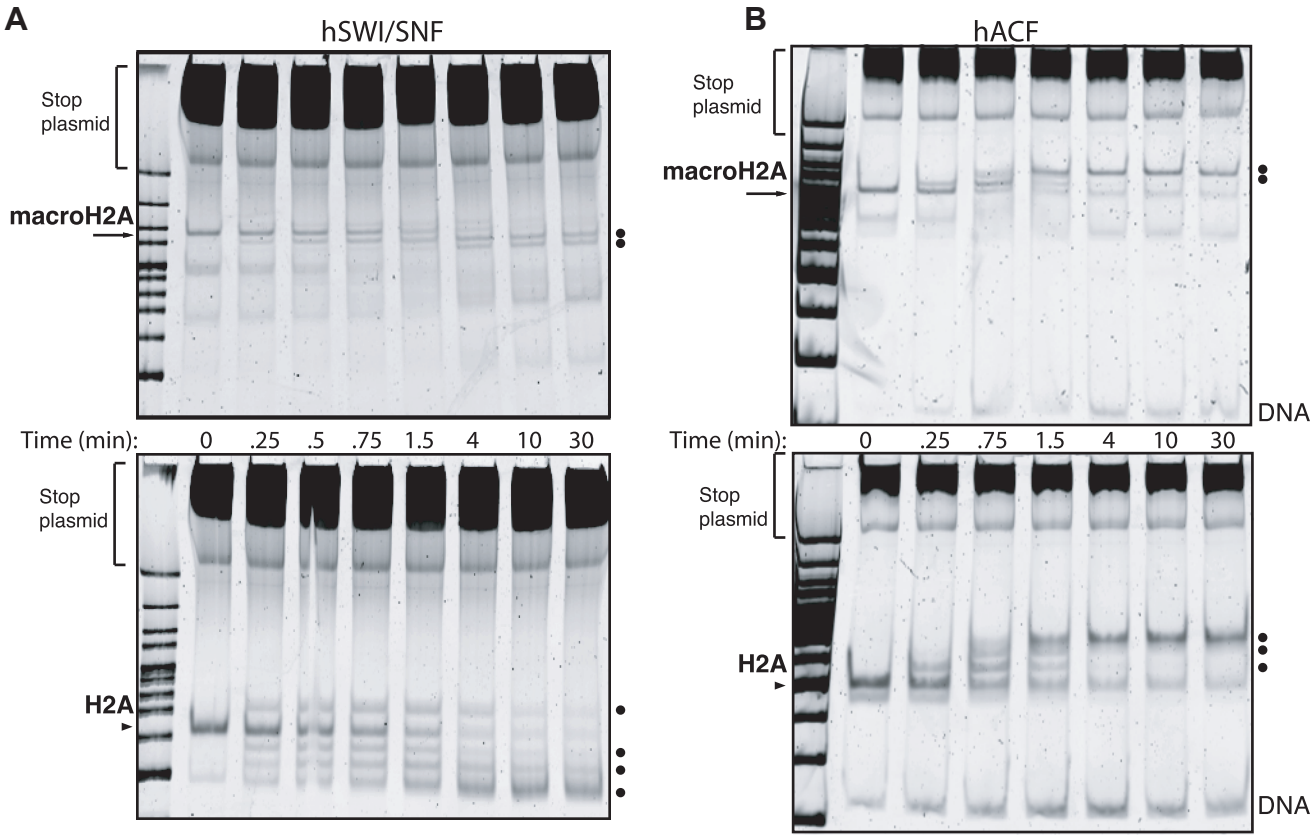
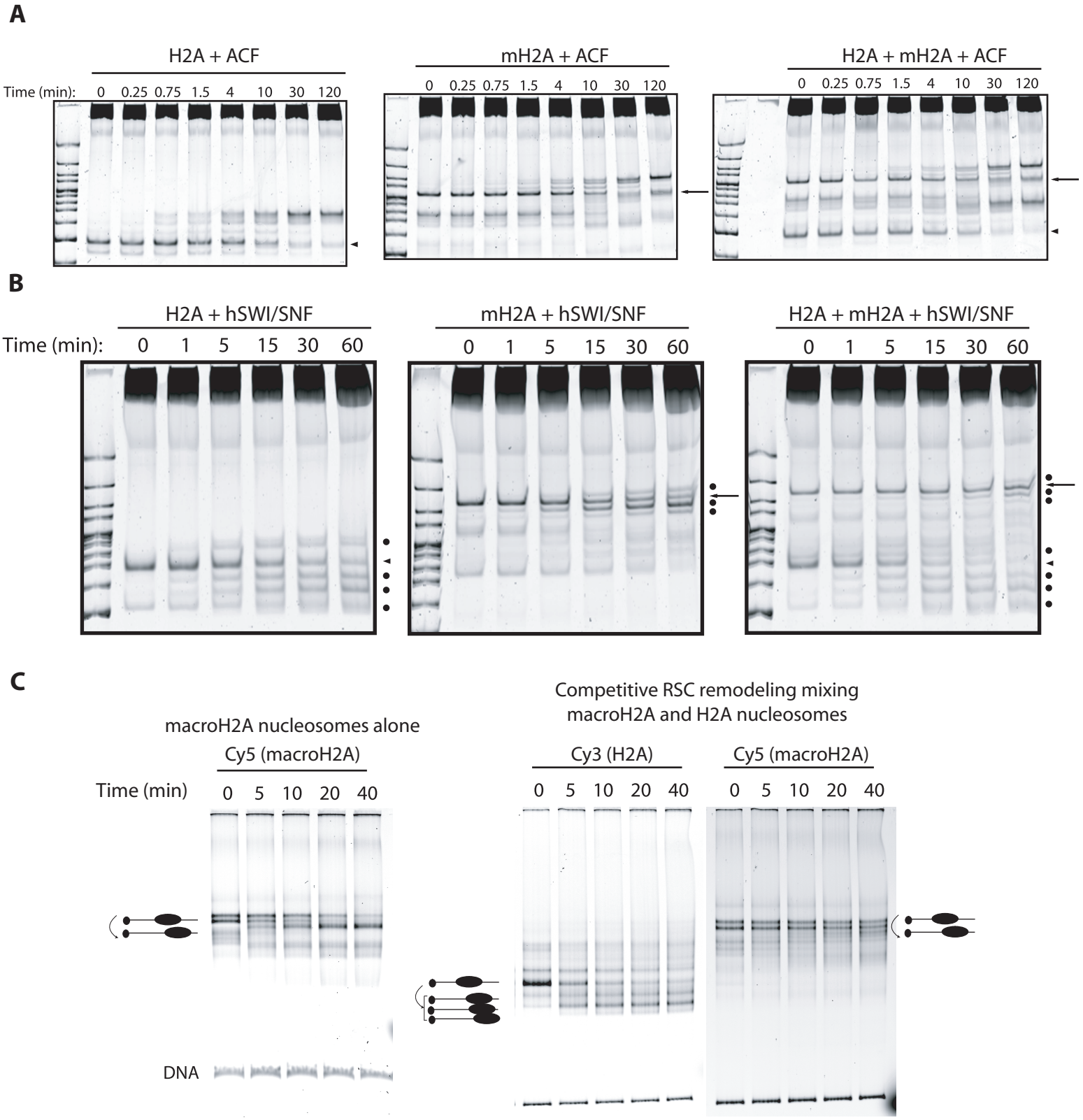


Supplementary Figure 1. Nucleosome assembly by dimer and tetramer produces stoichiometric nucleosomes. (A) Relative staining efficiencies of different histones for SYPRO red. Increasing amounts of individually purified macroH2A/H2B dimer and H3/H4 tetramer were run on SDS gels and stained with SYPRO red. The resulting band intensities were quantified and compensated for molecular weight, and the resulting ratios calculated. (B) Histone stoichiometry of H2A and macroH2A (mH2A) nucleosomes shown for the 20/60 nucleosomes. Molar ratios were obtained by quantifying individual bands and normalizing for molecular weight and for differences in efficiency of SYPRO red staining as measured in (A).



Supplementary Figure 2. Complete gels for single-turnover remodeling assays. (A) Native gel shift assay showing remodeling of 20/60 H2A nucleosomes and macroH2A nucleosomes by hSWI/SNF. The left-most lane on each gel contains a DNA ladder. (B) Native gels showing products of ACF upshift of 0/80 nucleosomes. Long arrows mark positions of initial, unremodeled macroH2A nucleosomes, while arrowheads mark initial positions of H2A nucleosomes. Circles mark repositioned nucleosomes.



Supplementary figure 3. Complete gels for multiple turnover and competitive conditions. (A) 160 nM of either H2A (left) or macroH2A (center) nucleosomes were mixed with 5 nM hACF. 80 nM each of H2A and macroH2A nucleosomes were were mixed with 5 nM hACF. Arrowhead mark unremodeled H2A nucleosomes; arrows mark unremodeled macroH2A nucleosomes. (B) Reactions of 12 nM hSWI/SNF and 60 nM of either H2A (left) or macroH2A nucleosomes (center). For competitive assays, 30 nM each of H2A and macroH2A nucleosomes were mixed together with 12 nM hSWI/SNF (right). Arrows mark initial nucleosome position; circles mark repositioned nucleosomes. (C) 0.1 μM of Cy5-labeled macroH2A nucleosomes were mixed with 2 nM RSC complex (left). For competition, 0.1 μM each of Cy3-DNA labeled H2A and Cy5-labeled macroH2A nucleosomes were mixed with 2 nM RSC. Curved arrows show shift of initial nucleosomes to repositioned products as previously mapped.