Fig. S1

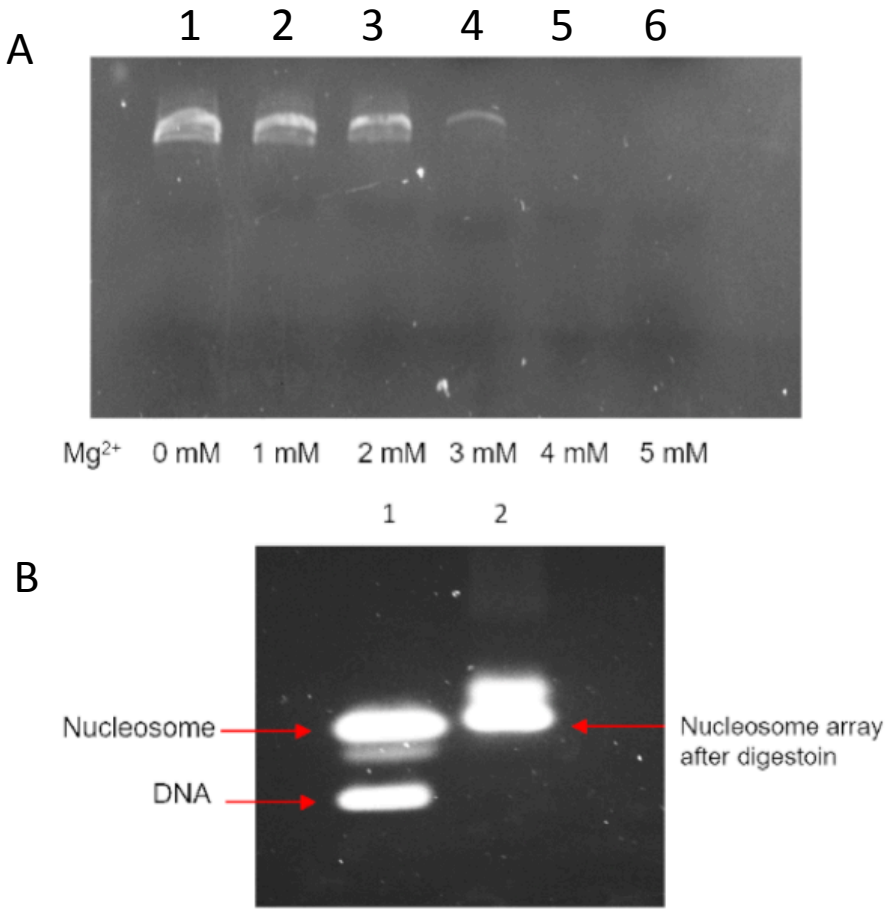

Fig. S1. Saturation of reconstituted arrays. A. Self-association of reconstituted arrays. Arrays (10 µl) were incubated in the presence of increasing concentrations of MgCl2 in 10 mM Tris, pH 8.0, 0.1 mM EDTA buffer and then pelleted for 2 minutes in a microfuge. The amount of array remaining in 5 µl of the supernatant was determined on a 0.8 % agarose gel containing 0.2% SDS. B. reconstituted nucleosome arrays were digested with EcoR I. Lane 1, mononucleosome reconstitution control. Lane 2, product of the peak fraction of nucleosomal array digestion.

Fig S2

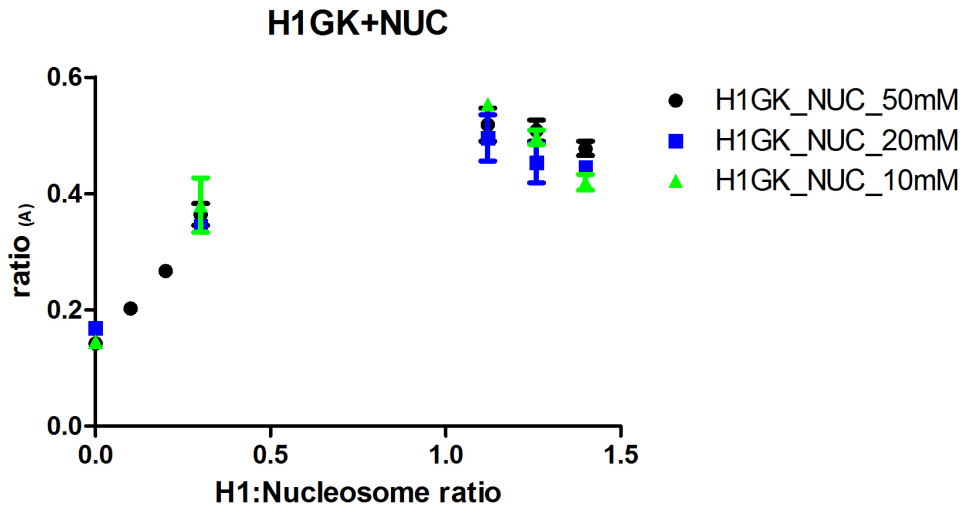

Fig. S2. Identical FRET response is obtained from Cy3/Cy5 labeled H1 G101C/K195 bound to 30-N-30 mononucleosomes in 10, 20 and 50 mM NaCl. Shown is RatioA response for H1: nucleosome ratios from 0 to 1.4 in TE buffer containing the indicated NaCl concentrations.

Fig. S3.

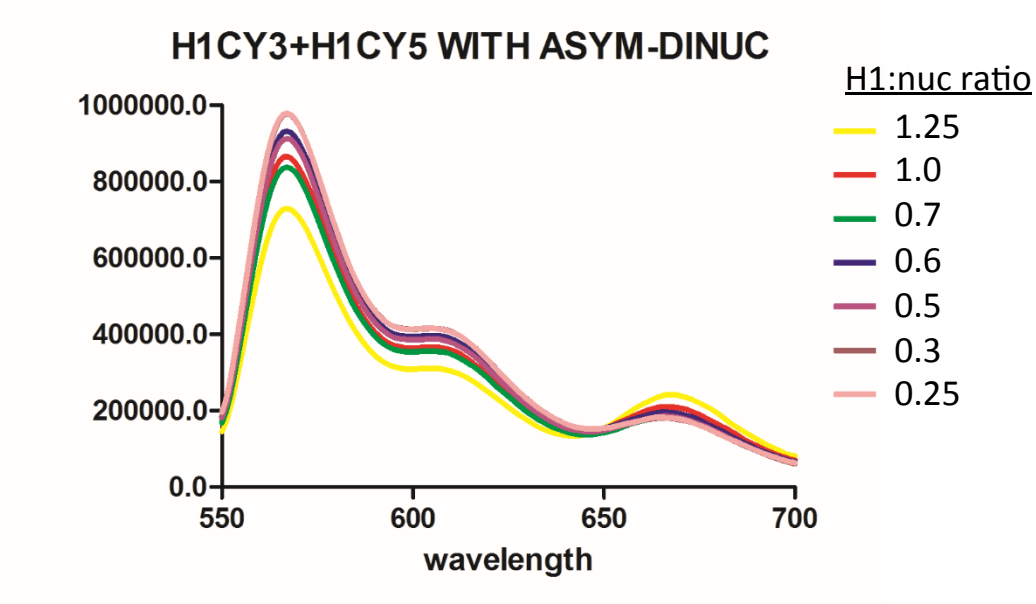

Fig. S3. No inter-molecular FRET is observed when Cy3-labeled and Cy5 labeled H1 G101C/K195C are bound to an asymmetric dinucleosome. A. An increasing amount of a 50/50 mix of Cy3-labeled and Cy5-labeled H1 G101C/K195C was incubated with asymmetric dinucleosomes (25-N-50-N-0) and the FRET response determined. Ratios range from 0.25 to 1.25 H1s per nucleosome. Shown are emission spectra with excitation at 515 nm.

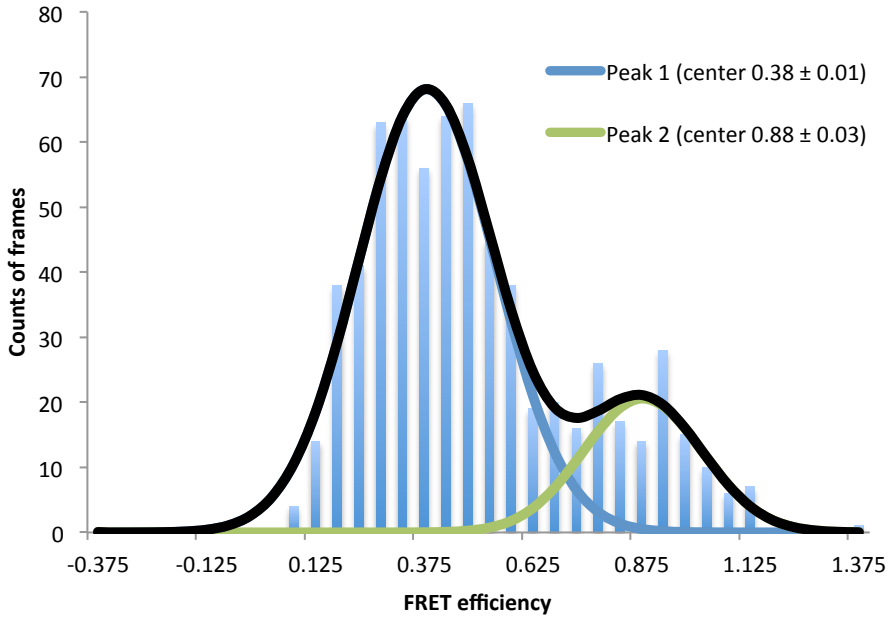

Fig. S4. Histogram combining all smFRET counts without pre-evaluation. Single molecule FRET efficiency histogram reveals two H1 CTD conformations without pre-evaluating the average FRET of each H1. This histogram is the sum of the two histograms shown in figure 8. This histogram is fit well with two gaussian distributions whose peak positions remain the same within error as those shown in figure 8.