

## SI Text

### Figure Legends

**Figure S1.** Expression and purification of H2A COOH-terminal deletion and chimeric proteins and hydroxyl radical footprinting of nucleosomes. **(A)** Alignment of human H2A.1 and H2A.Bbd proteins. Domain structure of histone H2A is represented in the form of cartoon drawing below the sequence. H2A docking domain is represented as punctuated line below the sequence. **(B)** 18% SDS PAGE of different histones and H2A COOH-truncated mutant proteins. All the proteins were bacterially expressed in denaturing condition and purified from inclusion bodies using SP-sepharose medium. **(C)** Characterization of conventional, variant and mutant nucleosomes by  $\bullet\text{OH}$  footprinting. The gel shows  $\bullet\text{OH}$  radical cleavage profile of the indicated nucleosomes reconstituted on 205 bp 3'-labeled 601 DNA fragment. Note the higher background (smaller contrast) observed in the cleavage pattern of H2A.Bbd, ddBbd and d79 nucleosomes.

**Figure S2.** One pot restriction accessibility assay of conventional and H2A.Bbd nucleosomes. Both types of nucleosomes were digested with *Hae* III and samples were processed and percentage of *Hae* III cleavage was quantified as described for Figure 2. Cleavage efficiency of conventional (triangles) and H2A.Bbd (Squares) nucleosomes are presented.

**Figure S3.** Scans of hydroxyl radical cleavage profile (See Figure 4B) for H2A, H2A.Bbd and H2A.ddBbd containing dinucleosomes in absence or presence of linker histone H1.

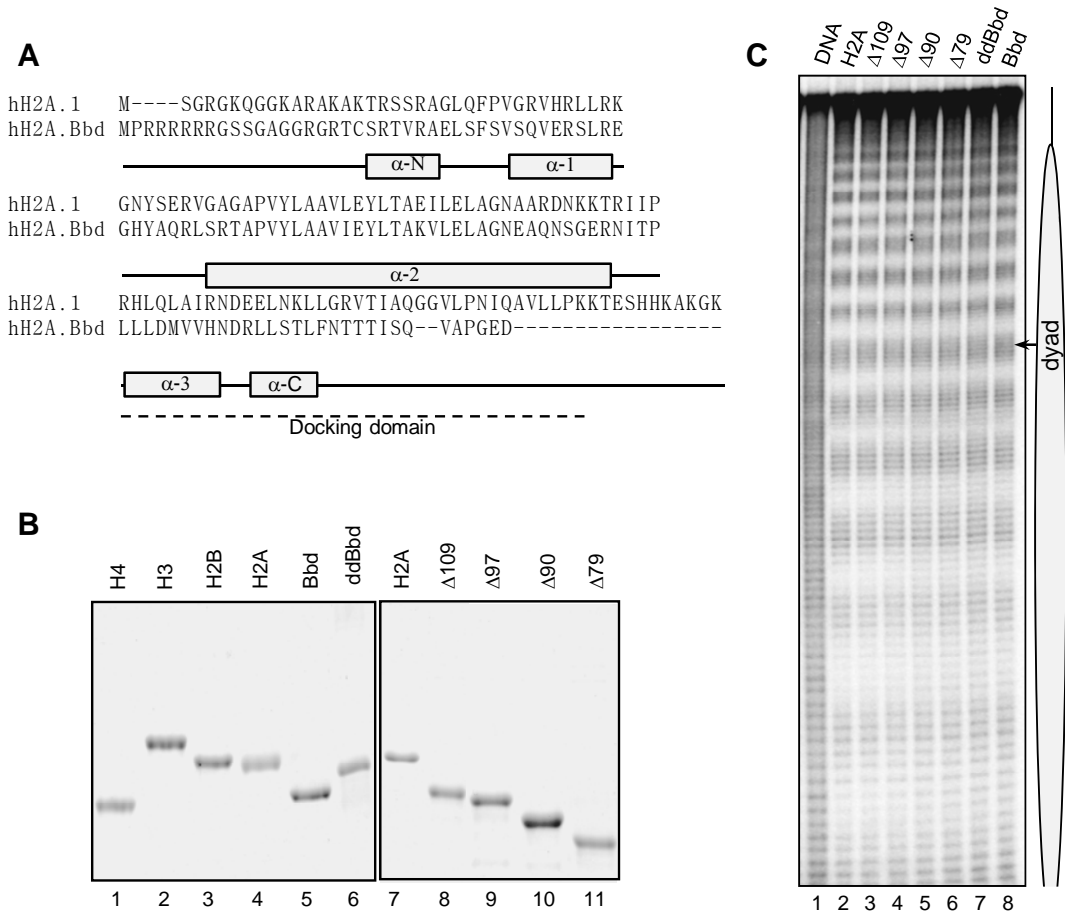


Figure S1

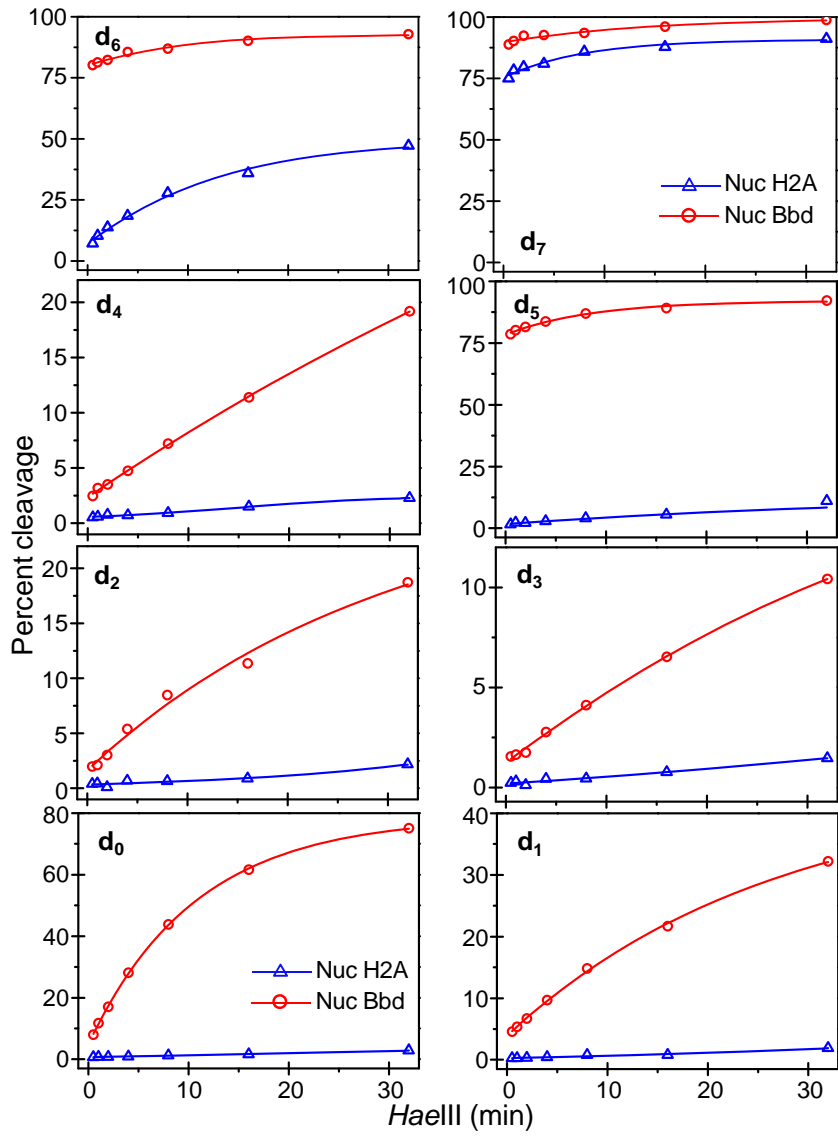


Figure S2

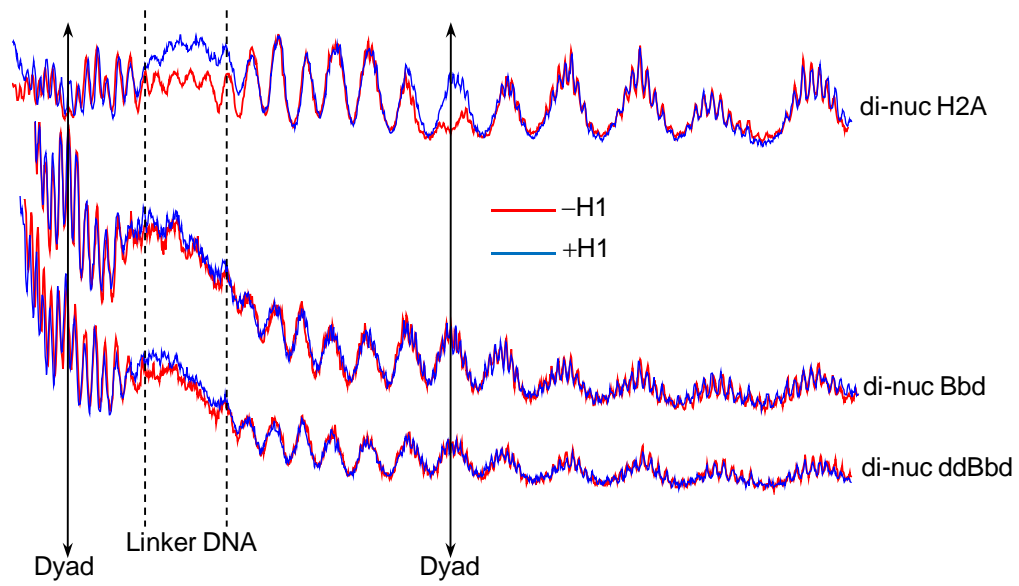


Figure S3