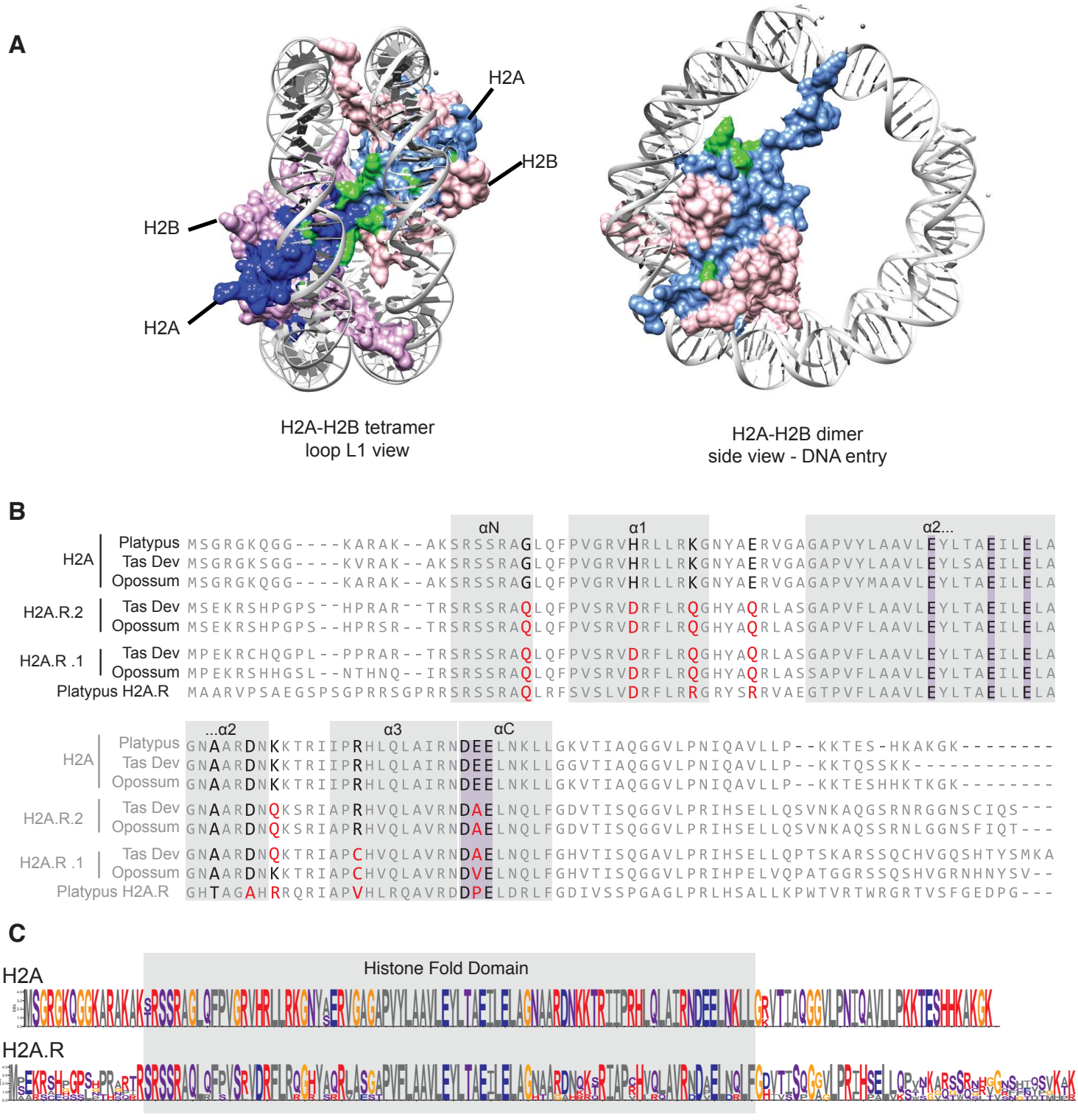

Supplemental Fig S6: Structural modeling of short H2As' discriminative residues and analysis of H2A.R sequences. (A) Left panel, loop L1 view of a H2A-H2B tetramer in the context of the nucleosome crystal structure (see methods). Right panel, H2A-H2B dimer view from the DNA entry site. H2A molecule surfaces are shown in light and dark blue, H2B in pink and purple. DNA is shown in grey. Charge-altering discriminative residues highlighted in Figure 3 are mapped in green onto the H2A structure. (B) A protein alignment of all five sequenced H2A.R variants along with canonical H2A representatives. We highlight the acidic patch residues in purple boxes (note the deviation from the DEE consensus in alphaC). We also highlight in bold red charge-altering residues in H2A.R proteins at the eight positions that distinguish short histone variants from canonical H2A (Figure 3). (C) Protein logos of H2A.R variants and canonical H2A further highlight that they share several features in common to the exclusion of short histone H2A variants.

Supplemental Fig S6
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