Supporting Information

Polybromo-1 (PBRM1) bromodomains variably influence nucleosome interactions and cellular function

Mariesa J. Slaughter[‡§], Erin K. Shanle[¶], Andrew W. McFadden[§], Emily S. Hollis[§], Lindsey E. Suttle[§], Brian D. Strahl[‡§¶], Ian J. Davis[‡§]**

From the [‡]Department of Genetics, Curriculum in Genetics and Molecular Biology, the [§]Lineberger Comprehensive Cancer Center, the [¶]Department of Biochemistry and Biophysics, University of North Carolina, Chapel Hill, North Carolina 27599, and the **Department of Pediatrics, University of North Carolina, Chapel Hill, North Carolina 27514

Supplementary Figures

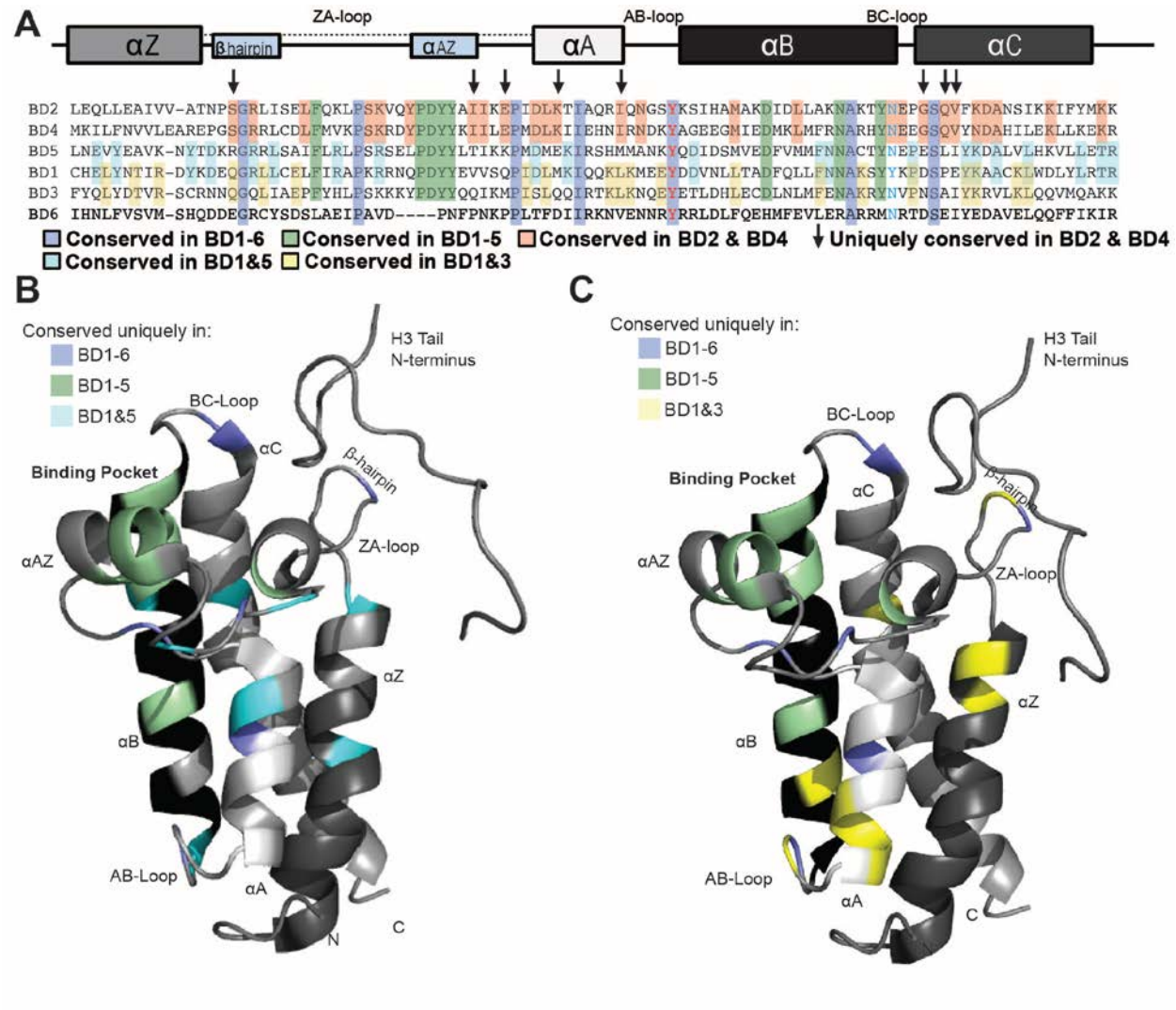

Figure S1. BD1, BD3, and BD5 conserved residues located away from histone interacting region. **(A)** Sequence alignment of PBRM1 bromodomains. Shading and arrows reflect the degree of conservation between bromodomains. Residues commonly mutated in ccRCC are shown with red and blue text. Structural elements of a bromodomain are indicated above the alignments. Conserved residues are overlaid on an NMR-derived secondary structure of PBRM1 BD2 in association with histone H3 tail with residues shared between **(B)** only BD1 and BD5 shaded in blue and **(C)** only shared between BD1 and BD3 in yellow.

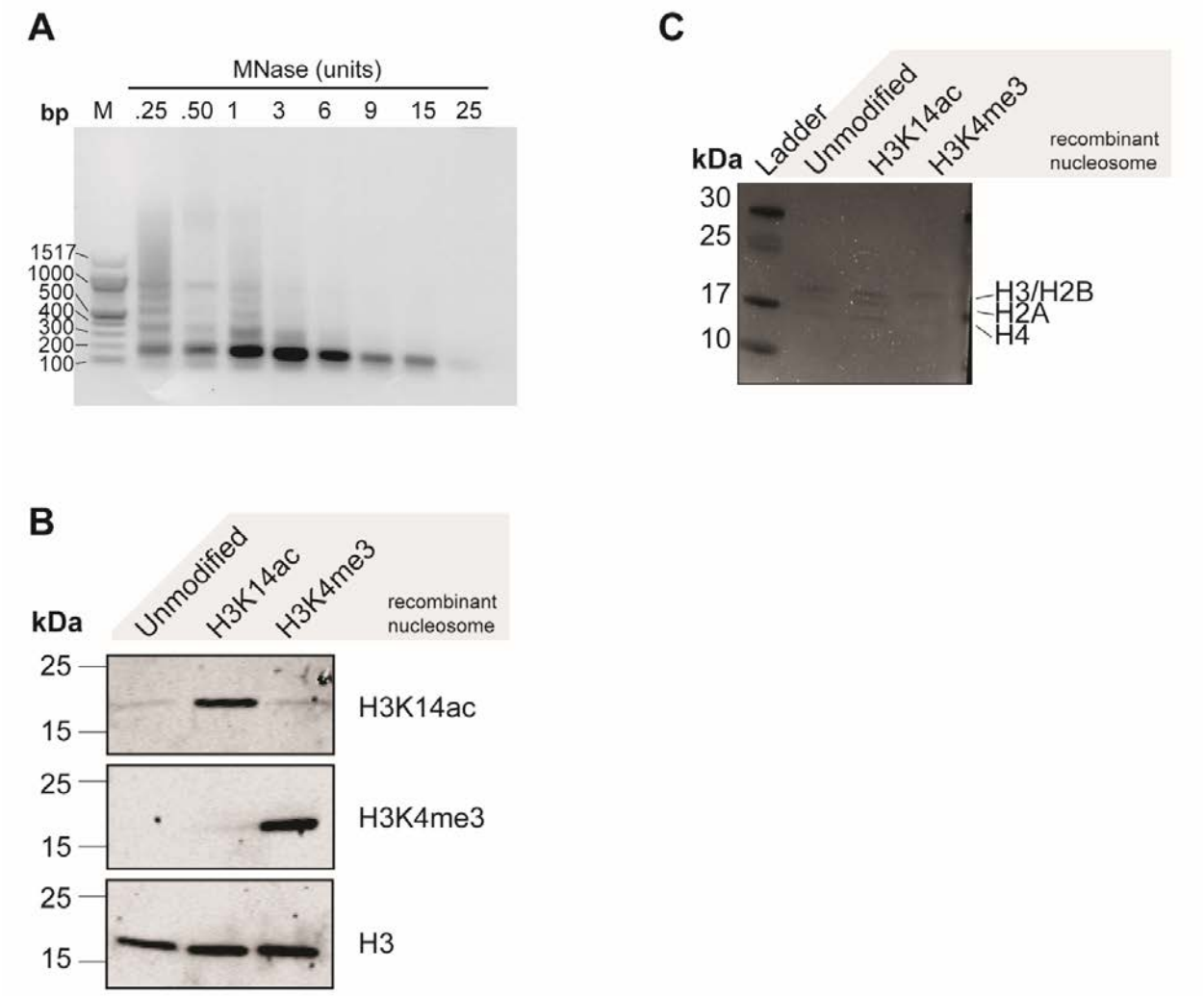

Figure S2. (A) *In nucleo* digestion of HEK293 cells with varying concentrations of MNase. (**B)** Validation of modified recombinant nucleosomes by Western blot. **(C)** Coomassie stained SDS-PAGE gel of recombinant nucleosomes. Presence of all four core histones are indicated.

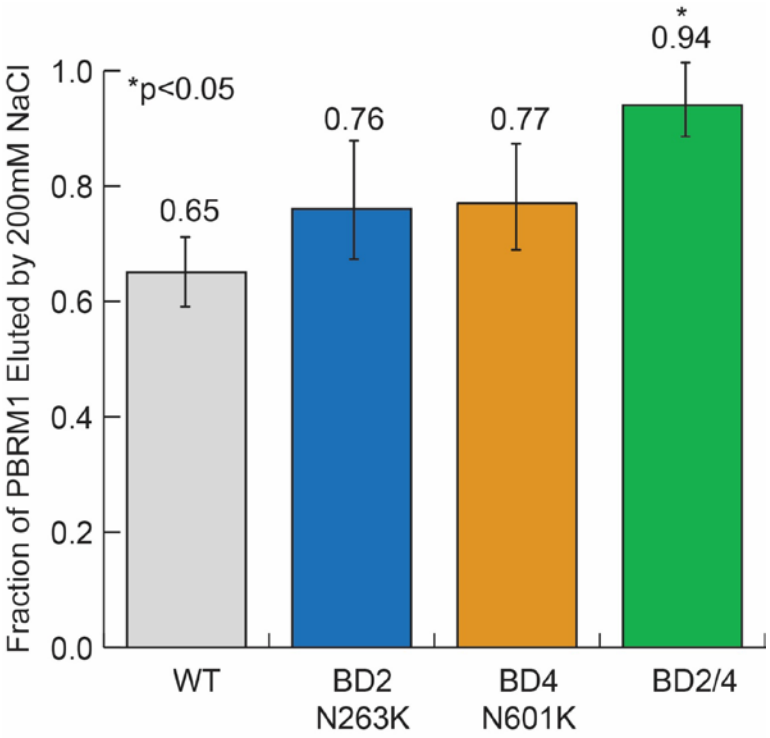

Figure S3. Percent of PBRM1 eluted as calculated by the sum of PBRM1 eluted from 50 mM, 100 mM and 200 mM NaCl plotted over total PBRM1 eluted.