







Data S1. ESI-MS data and RP-HPLC of modified histones. (A-M) (right) Analytical RP-HPLC chromatograms. (left) ESI-MS and deconvoluted spectra of indicated histones prepared for this study. Kac: lysine acetylation; Kme1: lysine monomethylation; Kme3: lysine trimethylation; Kub: lysine monoubiquinination;TFA = trifluoroacetic acid adduct; H4Kpolyac: N-terminal acetylated H4K5ac/K8ac/K12ac/K16ac/K20ac; (*) expected MS of neutral species.



cBAF complexes- validation experiments

Data S2. Restriction enzyme accessibility assay (REAA) performed using unmodified and selected modified nucleosomes incubated with canonical BAF (cBAF) complexes. cBAF complex (~10 nM) were incubated with nucleosomes (10 nM) in the present of Pstl restriction enzyme. The reactions were triggered by addition of ATP and analyzed at indicated times by native polyacrylamide gel with SYBR gold staining.



Data S3. Restriction enzyme accessibility assay (REAA) performed using unmodified and selected modified nucleosomes incubated with polybromo-associated BAF (PBAF) complexes. PBAF complex (~5 nM) were incubated with nucleosomes (10 nM) in the present of PstI restriction enzyme. The reactions were triggered by addition of ATP and analyzed at indicated times by native polyacrylamide gel with SYBR gold staining.



Data S4. Restriction enzyme accessibility assay (REAA) performed using unmodified and selected modified nucleosomes incubated with non-canonical BAF (ncBAF) complexes. ncBAF complex (~5 nM) were incubated with nucleosomes (10 nM) in the present of PstI restriction enzyme. The reactions were triggered by addition of ATP and analyzed at indicated times by native polyacrylamide gel with SYBR gold staining.