Supplementary Information

ACF catalyses chromatosome movements in chromatin fibres

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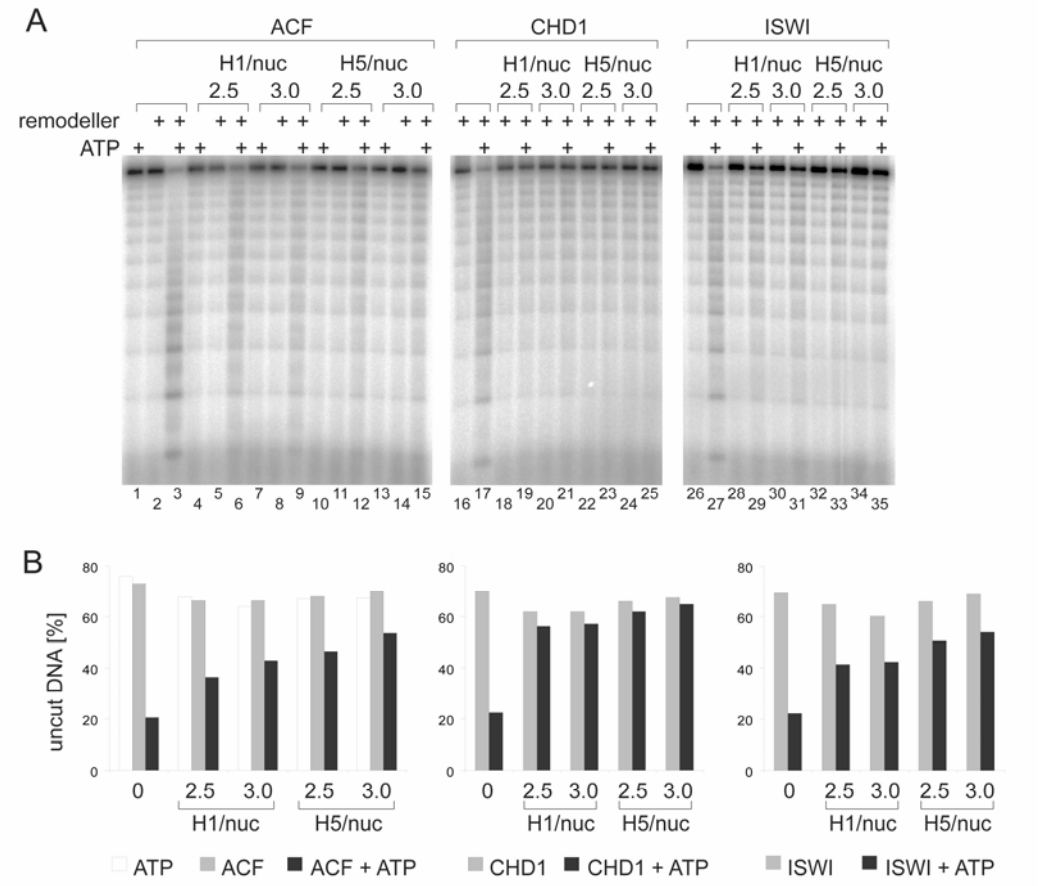
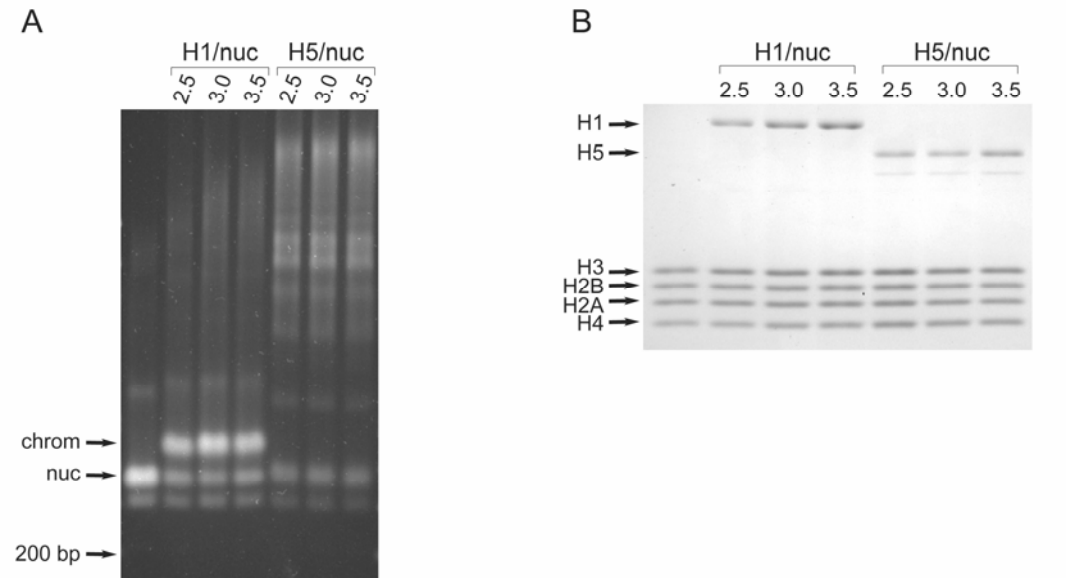


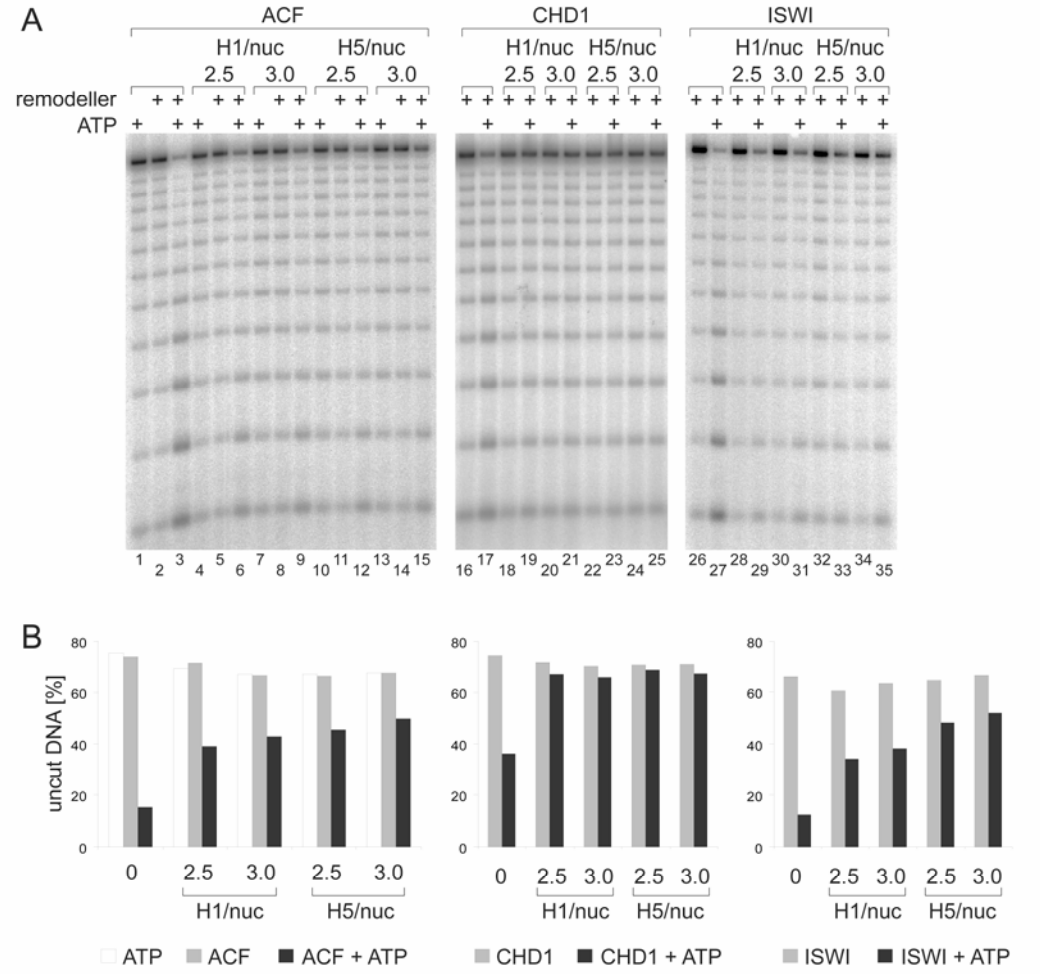
Supplementary figure 1: Comparison of the effect of linker histones on the remodelling activities of ACF, CHD1 and ISWI - amounts of remodellers normalised on their remodelling activity in absence of linker histones

12mer nucleosome or chromatosome arrays were assembled on end-labeled tandem repeats of the 601 positioning sequence using different molar ratios of linker histones H1 or H5 per positioning sequence (H1/nuc or H5/nuc). To monitor ATP-dependent changes in nucleosomal DNA accessibility, arrays were incubated with ACF, CHD1 or ISWI, with or without ATP and with the endonuclease AluI which cuts on the 601 positioning sequence. Proteins were removed, the DNA was analysed on agarose gel (A) and the percentage of uncut DNA was quantified by phosphoimager (B).

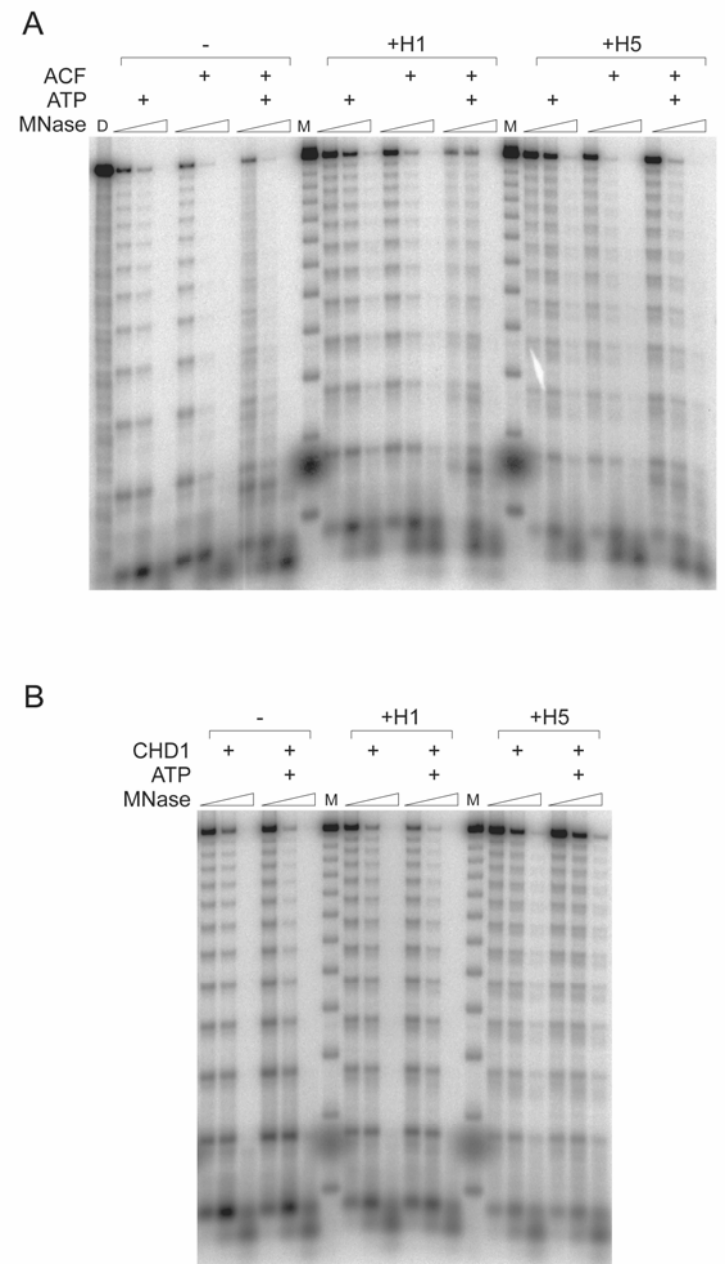


Supplementary figure 2: Quality controls of nucleosome and chromatosome arrays assembled with recombinant histone octamers

Nucleosome and chromatosome arrays assembled on 12mer repeats of the 601 nucleosome positioning sequence (Huynh et al. 2005) with different molar ratios of linker histones H1 or H5 per postioning sequence (H1/nuc and H5/nuc). Arrays were purified by $MgCl_2$-precipitation. (A) To monitor the occupancy of positioning sequences by histone octamers and linker histones, 6 pmol arrays were digested to nucleosomes and chromatosomes by the endonucleases AvaI. Unbound positioning sequences (200 bp), nucleosomes (nuc) and chromatosomes (chrom) were separated on native agarose gel. (B) 15% polyacrylamide gel of 60 pmol arrays purified by $MgCl_2$-precipitation to examine the stoichiometry of core and linker histones.



Supplementary figure 3: Chromatin remodelling assay with nucleosome and chromatosome arrays assembled with recombinant histone octamers, analysed by the endonuclease AluI cutting on the 147 bp nucleosome positioning sequence.
(A) End-labelled arrays assembled with different molar ratios of linker histones H1 or H5 per positioning sequence (H1/nuc or H5/nuc) were incubated with or without ATP and ACF, CHD1 or ISWI. AluI was added together with the remodelling enzyme. The DNA was purified and resolved on agarose gel and evaluated by phosphoimager. (B) Quantification of (A).



Supplementary figure 4: Chromatin remodelling assay with nucleosome and chromatosome arrays assembled with recombinant histone octamers, analysed by partial MNase digestion. End-labelled nucleosome arrays and H1 or H5 chromatosome arrays were incubated with or without ATP and ACF (A) or CHD1 (B). After 1 hr, reactions were partially digested by MNase (3 time points). DNA was purified and analysed on agarose gel. Nucleosome arrays digested by AluI served as a marker (M). As a control, free 12mer 601 repeats were digested by limiting amounts of MNase (A, lane1).