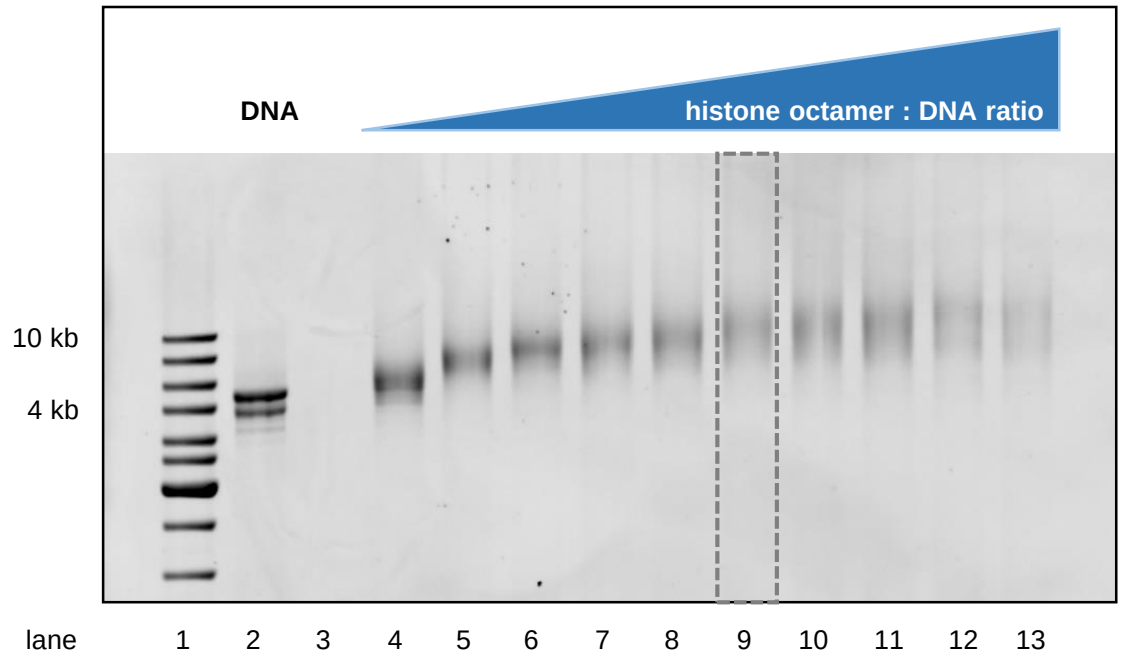
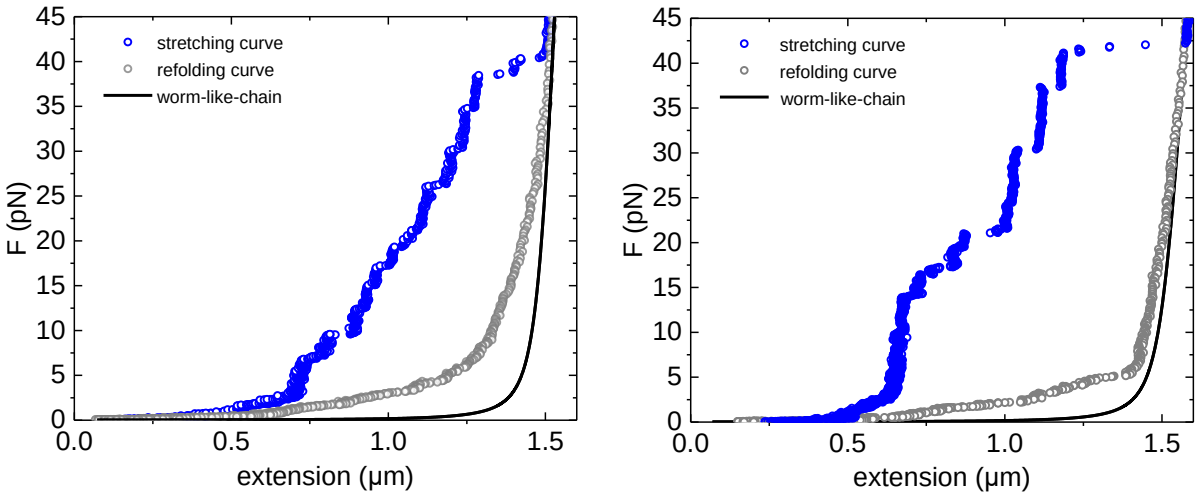


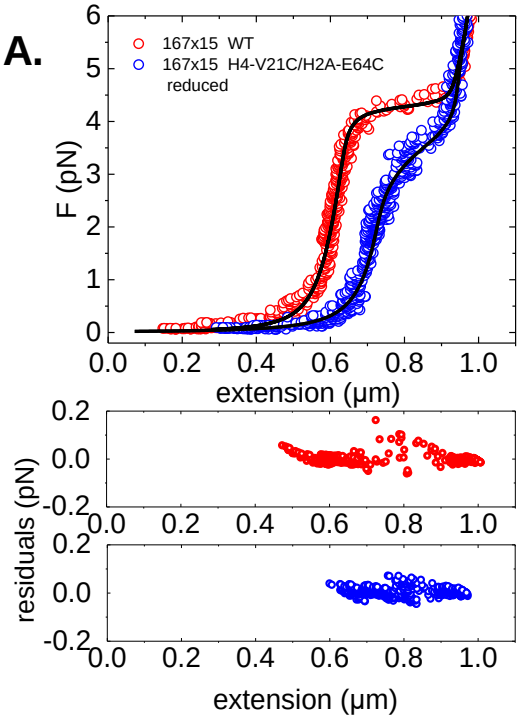
Supplementary Figure 1

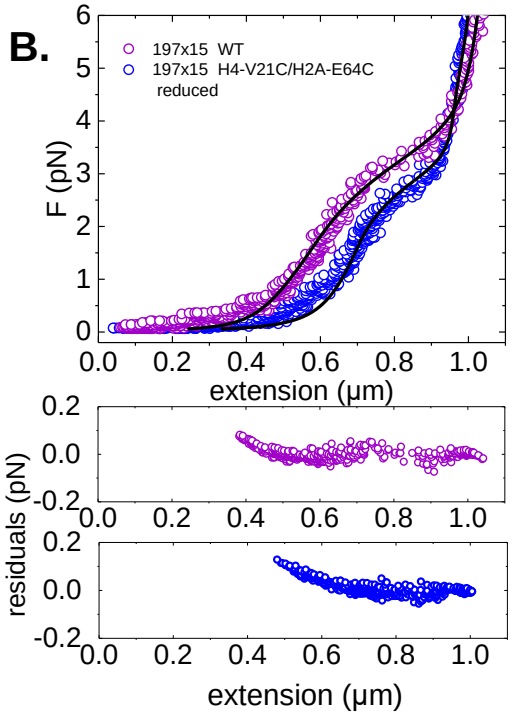
Band shift assay (0.7 percent agarose gel run in 0.2 x TB) depicts the assembly of DNA with histone octamers into a nucleosomal array. The best stoichiometry of protein versus DNA was determined experimentally by titration of the octamer:DNA ratio. With the increasing histone concentration, the chromatin fiber becomes more saturated and migrates slower through the agarose gel. Band-shift reaches a plateau at the saturation level, after which nucleosomes reconstitute on the DNA handles. For our experiments, we used the reconstitutions corresponding to lane 9.



Supplementary Figure 2

Force-extension curves of cross-linked chromatin fibers with depicted hysteresis between a stretching curve (blue) and a refolding curve (grey). Hysteresis is only observed at forces higher than 10 pN.



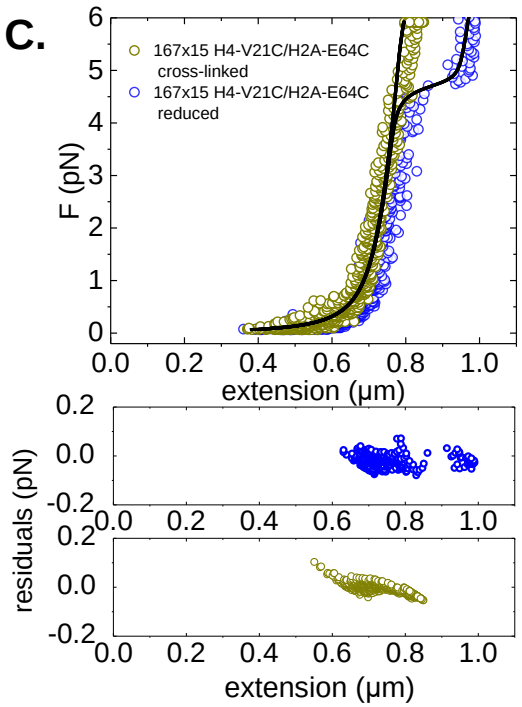


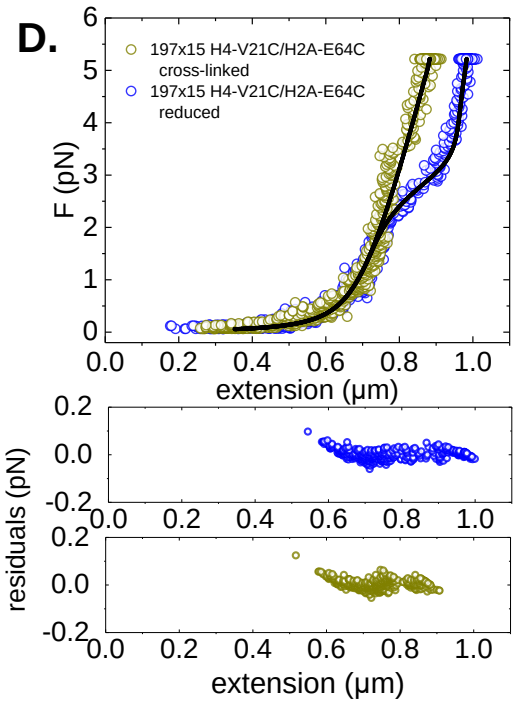
	WT	Cys
k [pN/nm]	1.1	1.1
dG [k_BT]	19.3	16.1
N ($N_{tetrasomes}$)	19 (5)	19/10

	WT	Cys
k [pN/nm]	0.19	0.24
dG [k_BT]	16.5	16.5
N ($N_{tetrasomes}$)	23 (8)	24 (15)

Supplementary Figure 3

Overview of the force - extension curves presented in Fig. 4 A, B along with the residuals of the fit by the statistical mechanics model (above 0.5 pN) and fitted parameters (Meng, H., Andresen, K., and van Noort, J. (2015) Quantitative analysis of single-molecule force spectroscopy on folded chromatin fibers. *Nucleic Acids Research*. **43**, 3578–3590).





	Cys_DTT	Cys
k [pN/nm]	1.1	1.1
dG [k_BT]	21.4	-
N ($N_{tetrasomes}$)	19(10)	

	Cys_DTT	Cys
k [pN/nm]	0.24	0.24
dG [k_BT]	16.5	-
N ($N_{tetrasomes}$)	24(15)	

Supplementary Figure 4

Overview of the force - extension curves presented in Fig. 4 C, D along with the residuals of the fit by the statistical mechanics model (above 0.5 pN) and fitted parameters (Meng, H., Andresen, K., and van Noort, J. (2015) Quantitative analysis of single-molecule force spectroscopy on folded chromatin fibers. *Nucleic Acids Research*. **43**, 3578–3590).