Dependence of the Linker Histone and Chromatin Condensation on the Nucleosome Environment

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Supplementary material

a) Distances between beads 1 and 11

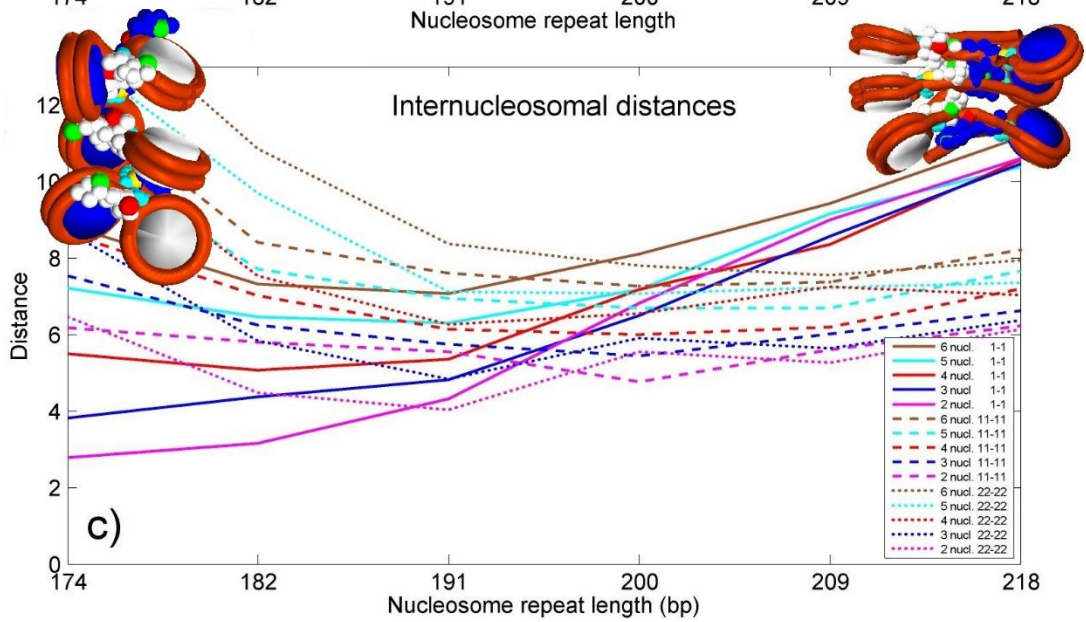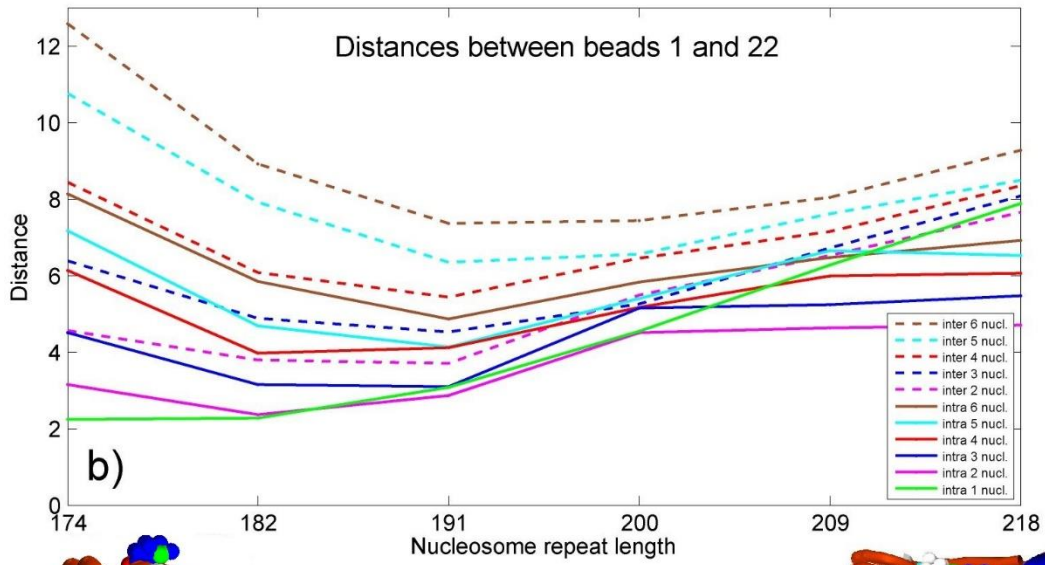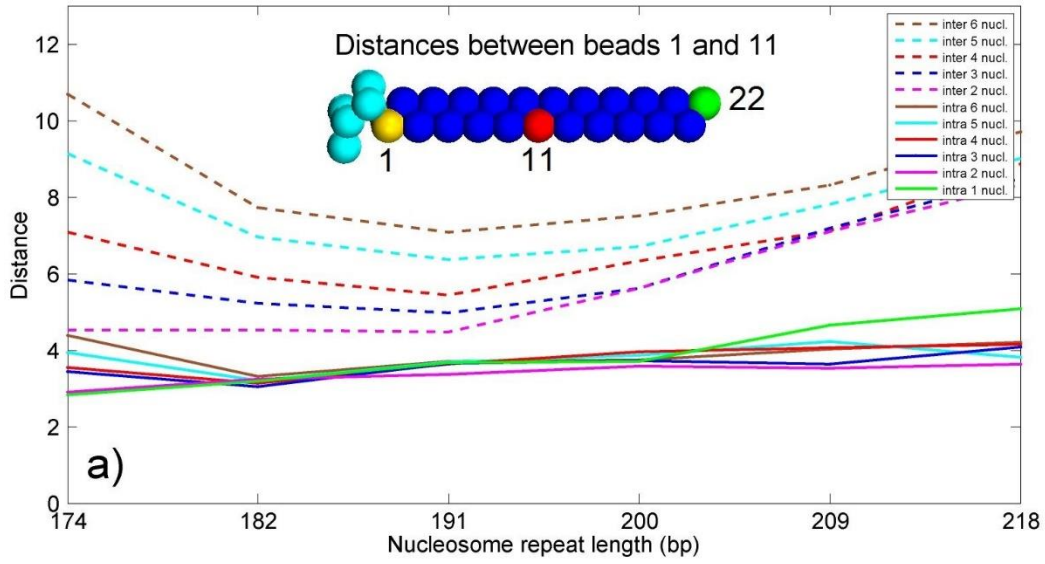b) Distances between beads 1 and 22

c) Internucleosomal distances

Figure S1. Inter and intra bead distances within the linker histone C-terminal domain (CTD). a) Distances between beads 1 and 11 (half LH length distance) within LH (intra – full lines) and between neighboring LHs (inter – dashed lines). b) Distances between beads 1 and 22 (full LH length) within single LH (intra – full lines) and between neighboring LHs (inter – dashed lines). c) Internucleodistancesome distances between beads 1-1 (full lines), 11-11 (dashed lines) and 22-22 (dotted lines).
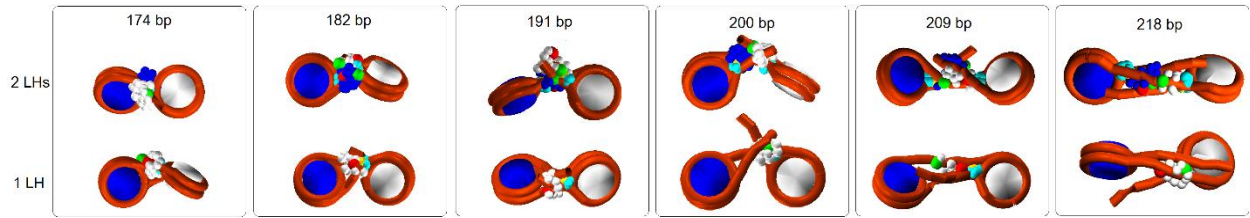
Figure S2. Dinucleosome configurations with fully saturated 2-core arrays (upper images) and subsaturated 2-core arrays with 1 LH per dinucleosome (lower images). LHs are colored identically to their histone core, blue and white.
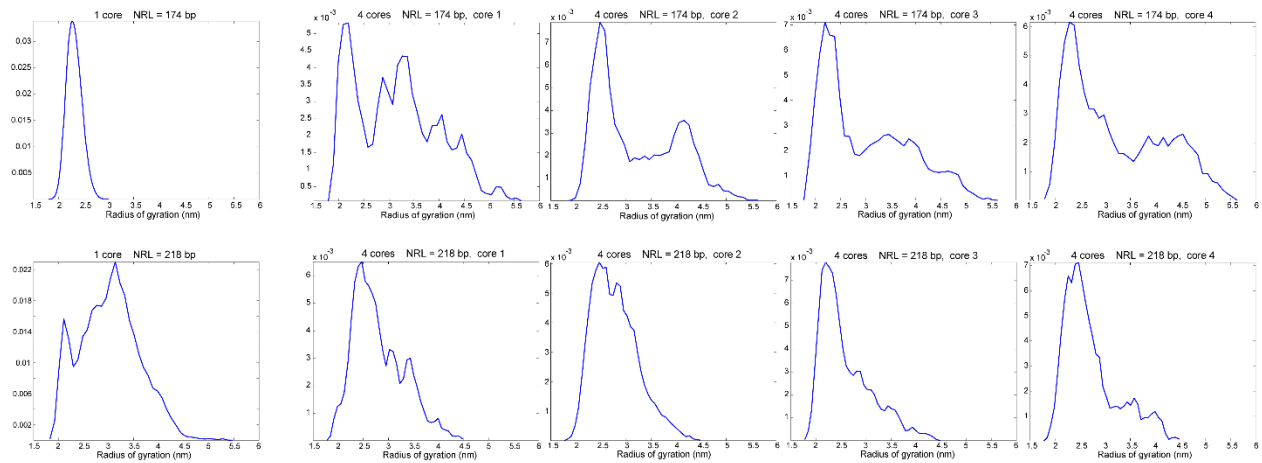
Figure S3. Linker histone radii of gyration histograms for mononucleosomes and 4-nucleosome arrays, for shortest (174 bp) and longest (218 bp) NRLs, extracted from all trajectories, using the last 10 million steps per trajectory. The sum under each curve is normalized to 1.