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Supplemental Information

Chromatin Compaction Leads to a Preference for Peripheral Heterochromatin

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Supplemental materials for chromosomal condensation leads to a preference for peripheral heterochromatin

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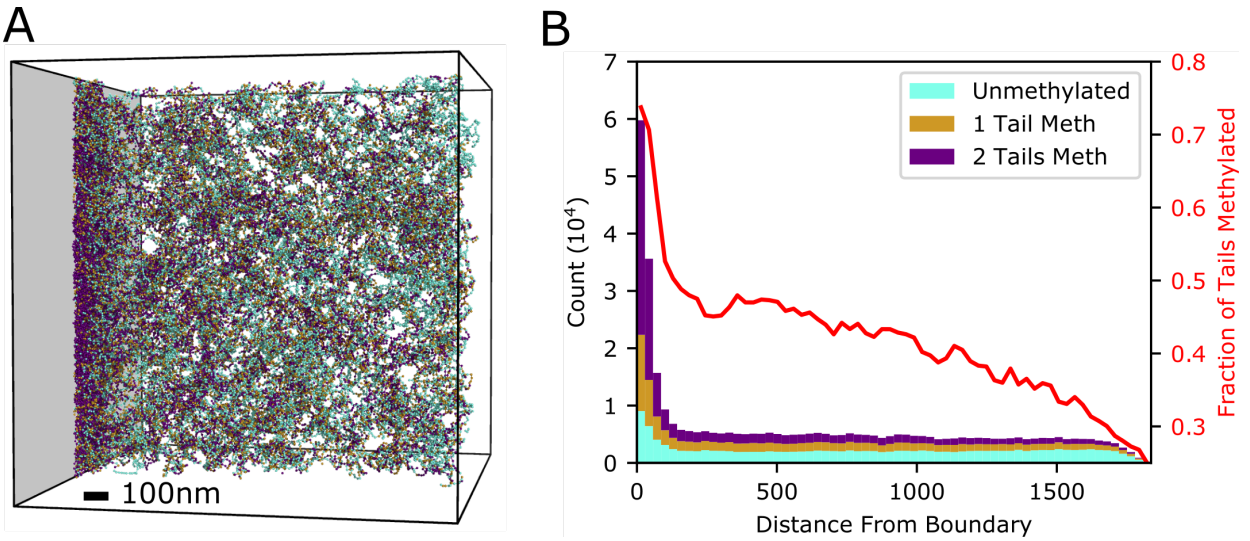

Figure S1: **A**: Simulation slice without the action of Loop Extrusion Factors (LEFs). Each bead represents a nucleosome with neither (cyan), one (tan), or both (purple) of its histone 3 tails trimethylated. **B** Composition histogram (left y axis) with colors corresponding the methylation type. Red curve (right y axis) shows fraction methylated. As in the case without LEFs, a chromatin dense, H3K9me3 rich, peripheral heterochromatin phase forms along the boundary.

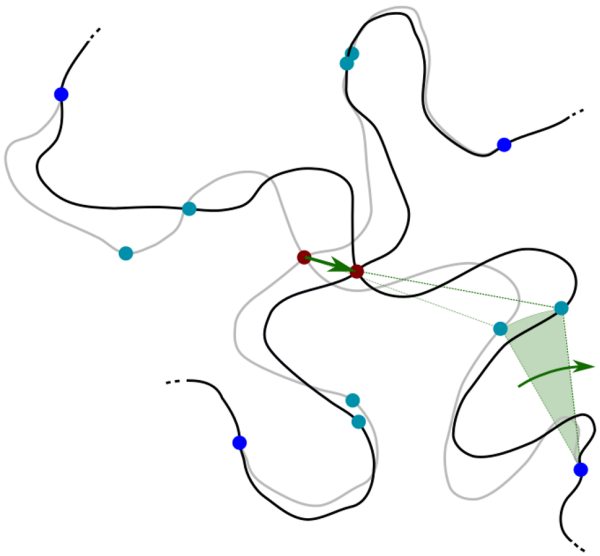

Figure S2: The "spider" move allows two or more semiflexable polymers that are bound to each other (red point) to move by bending but not stretching each polymer. Light grey shows polymer configuration prior to move. The red point is translated and the polymers are bent to accommodate. If a second bound point (not pictured) connecting to a third polymer is within a leg, than it also is translated by the same amount as the red point and the "legs" protruding from it are likewise bent. This is applied recursively so that an arbitrary network of polymers can be deformed.

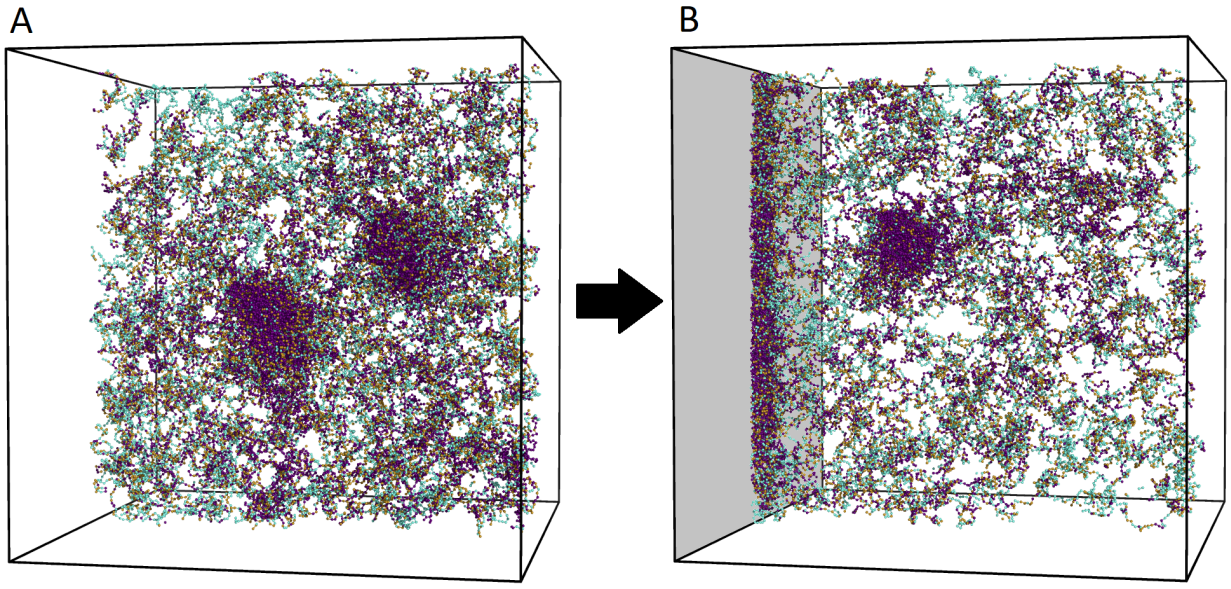

Figure S3: **A**: Simulation slice with the interaction with the boundary turned off. **B**: After turning the boundary interaction on, heterochromatin forms along the boundary. Each bead represents a nucleosome with neither (cyan), one (tan), or both (purple) of its histone 3 tails trimethylated.

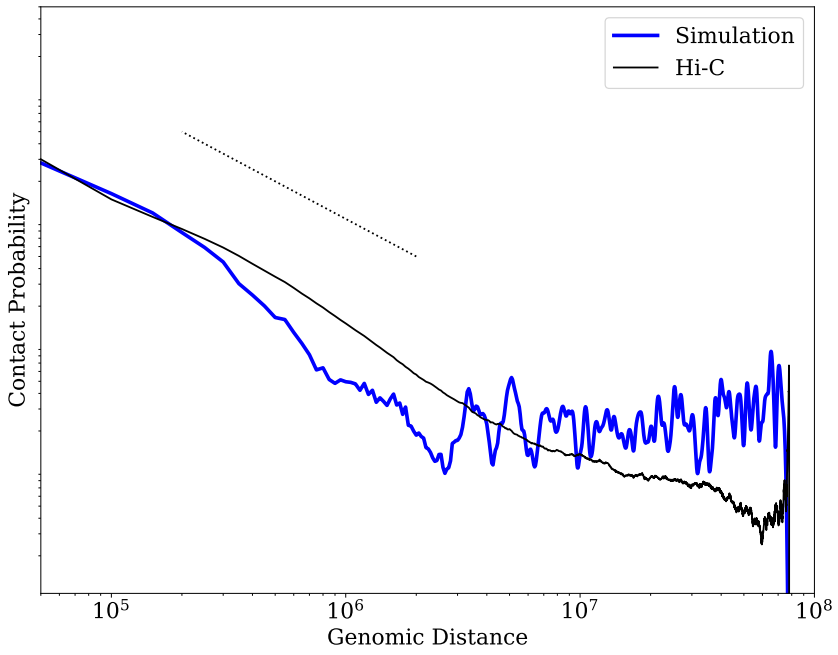

Figure S4: The blue curve shows the contact probability vs. genomic distance in bp for a simulation of chromosome 18 with a general attraction to the cube boundary. The black curve shows a comparison to Hi-C (GEO accession no, GSM 733664). The dotted line shows a power law of -1. The relative vertical position between the curves is arbitrary.

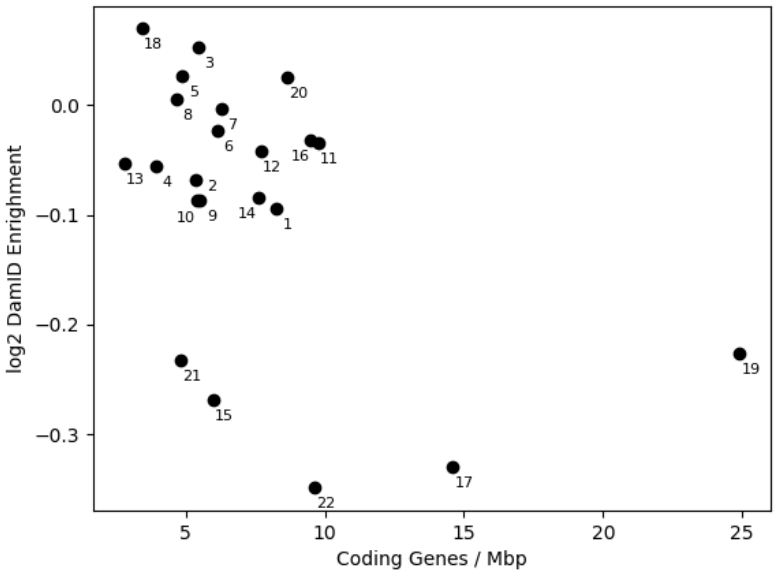

Figure S5: There is an anti-correlation between the number of coding genes per magabace (Ensembl release 98 [2]) and the average log2 DamID Enrichment for Lamin B [1] as in the main text Figure 7. Person r=-0.579, p=0.024.

References

[1] Lars Guelen, Ludo Pagie, Emilie Brasset, Wouter Meuleman, Marius B. Faza, Wendy Talhout, Bert H. Eussen, Annelies de Klein, Lodewyk Wessels, Wouter de Laat, and Bas van Steensel. Domain organization of human chromosomes revealed by mapping of nuclear lamina interactions. *Nature*, 453(7197):948–951, June 2008.

[2] Sarah E. Hunt, William McLaren, Laurent Gil, Anja Thormann, Helen Schuilenburg, Dan Sheppard, Andrew Parton, Irina M. Armean, Stephen J. Trevanion, Paul Flicek, and Fiona Cunningham. Ensembl variation resources. *Database (Oxford)*, 2018, January 2018.