

Supplementary Figure 2

Loop size distribution and specific contact probabilities for $N = 128$. **Upper-most figure:** Shown is the size distribution $P(\ell)$ of functional chromatin loops of model polymers with $N = 128$ beads. Model polymers were fully equilibrated and the loop size distribution was determined for various looping probabilities p (for reasons of comparison the average number of loops per conformation is displayed by a color code) and lifetimes τ of the functional loops. Looping lifetimes are chosen relative to the relaxation time (cf. Materials & Methods in the manuscript). Increasing the loop number results in a markedly smaller exponent, leading to a high probability for large loops. **Bottom-most figure:** The contact probability $p_c(l)$ for two specific sites with genomic separation (contour length) l to be co-localized. Shown are the results for equilibrated model polymers with $N = 128$ beads and various looping probabilities p . The contact probability decreases as a power-law $l^{-\beta}$ with a biphasic behaviour, the exponent changing at about $l \approx 15\%$ of the chromosome length. The grey line represents the self-avoiding walk. Again, the co-localization probability is strongly increasing due to diffusion-based looping.

