Figure S2

Mapping of coarse-grained polymers to physical parameters. Shown are results for a chain length of $N = 256$ using different looping probabilities. Experimental data shows results from FISH measurements on human chromosome 1 and 11. The chain is mapped to chromosome 11 by assuming one bead to comprise a 400kb-stretch of chromatin. Consistent with the experimental data, this is set equal to 480 nm. Different symbols indicate different looping lifetimes (▲: $\tau = 0.01\tau_{int}$; ◇: $\tau = \tau_{int}$; ●: $\tau = 100\tau_{int}$, see Materials & Methods). **A.** This panel shows the mean square distance in relation to genomic separation of model and experimental data to assess the quality of the mapping. **B.** The potential of mean force between two model chromosomes in relation to physical distance r between the centers of mass. The effective potential strongly increases with increasing looping number at a separation of about 2-3 μm, i.e. the size range of the assumed chromosome territories.