K=725,785 ± 66,540; S=2.515 ± 0.092 kb; c =110.515 ± 2.028 kb

Additional data 3. Fitting the circular polymer model to mouse gene-rich loci.
The circular polymer model (Eq.1 & 2b) was fitted to 3C-qPCR data obtained at
gene-rich loci. The best fit curve is shown in red; best fit parameters are as follows:
R^2=0.50 with K=725,785 ± 66,540; S=2.515 ± 0.092 kb; c=110.515 ± 2.028 kb. The
black curve depicts the best fit obtained with the linear polymer model (Eq. 1 & 2a)
(R^2 = 0.18).