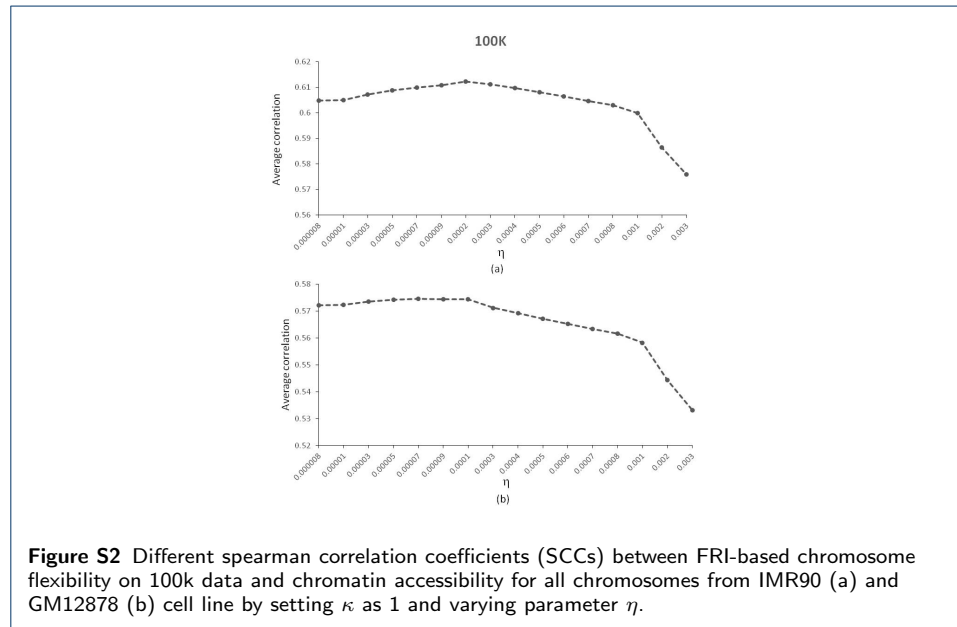
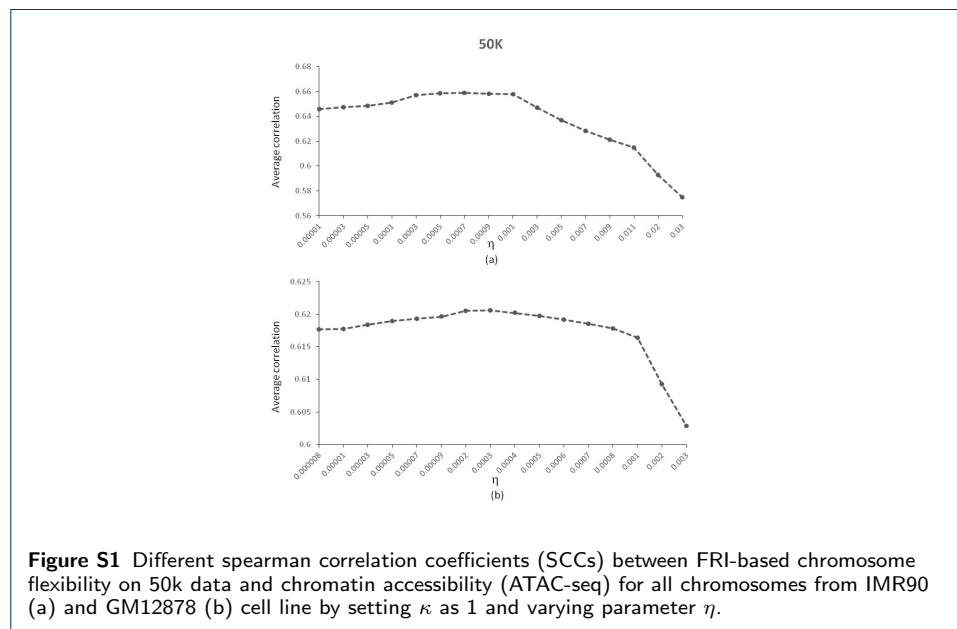


Supplementary document of “Flexibility and rigidity index for chromosome packing, flexibility and dynamics analysis”

1 Supplementary Figures



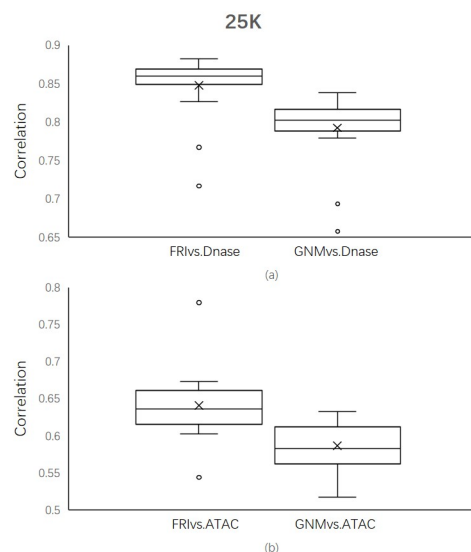


Figure S3 Boxplots of spearman correlation coefficients (SCCs) between chromosome flexibility on 25k data and chromatin accessibility (Dnase-seq (a) and ATAC-seq (b)) for chromosome 4 from GM12878 cell line. In this figure, the chromosome 4 is separated into 20 small regions. Spearman correlation coefficient is calculated for each region. The top and bottom of the boxes represent 75th and 25th percentiles, middle lines in the boxes are the median. Cross nodes represent the mean. Circle nodes represent outliers that are larger than the sum of 75th and 1.5 interquartile range.

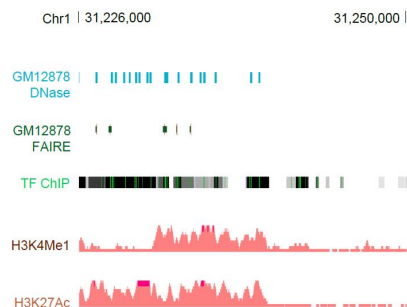


Figure S4 Case study of a region with high FRI-based flexibility. The selected region is from 31,226,000 to 31,250,00 on chromosome 1 from GM12878 cell line. In this region, several strong regulatory signals are identified, including DNase signal, FAIRE signal, transcription factor (TF) binding hot spots, epigenetic marks H3K4me1 and H3K27ac. This figure is generated based on the corresponding tracks from UCSC genome browser.