Description of additional supplementary Data files

Supplementary Data 1. Raw data quality control (QC) results across processing steps for Hi-C and HiChIP samples. The fraction of uniquely aligned read pairs was calculated based on the total number of initial reads. Self-circle and dangling-end fractions were calculated based on the total number of aligned read pairs. Intra- and inter-chromosomal contacts were calculated as a fraction of filtered valid interactions.