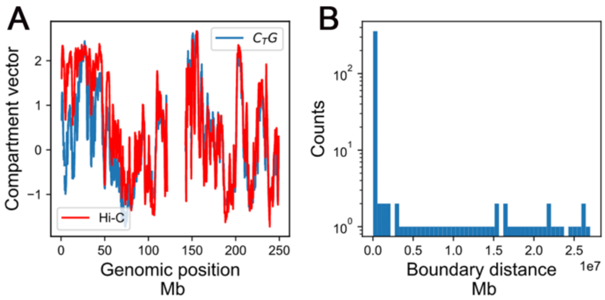

Supplemental Fig S6. (A)The compartment vector derived from C_TG distance matrix (blue) and Hi-C contact matrix (red) by performing PCA. The correlation coefficient reaches 0.890. (B) The genomic distance between TAD boundaries found in CTG distance matrix and those found in Hi-C contact matrix. We used KMeans to find TADs in C_TG distance matrix, compared with the TADs found by HiCExplore, the boundaries generated from two methods are very close.