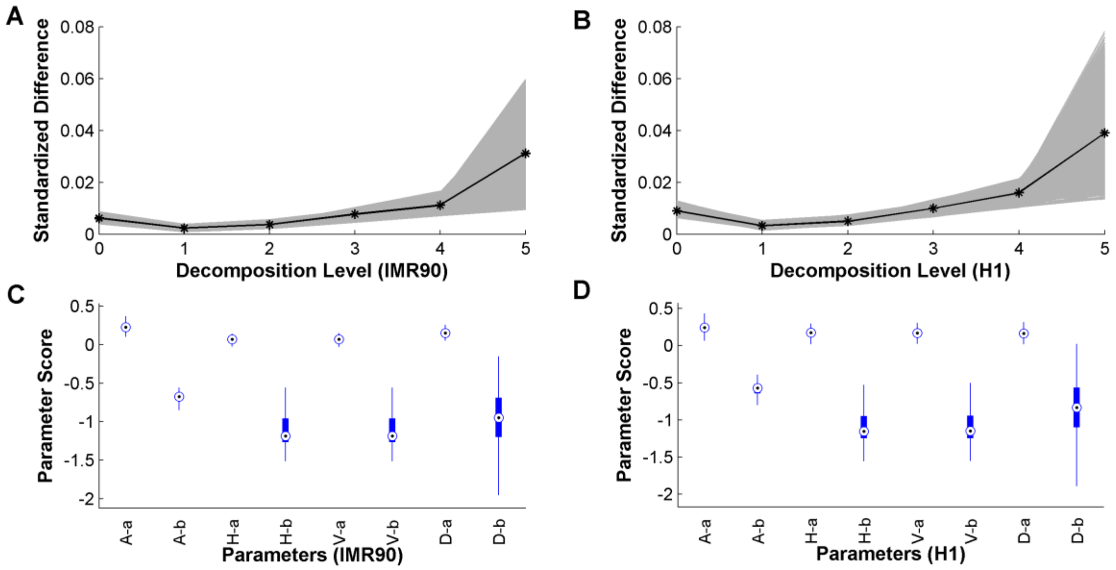
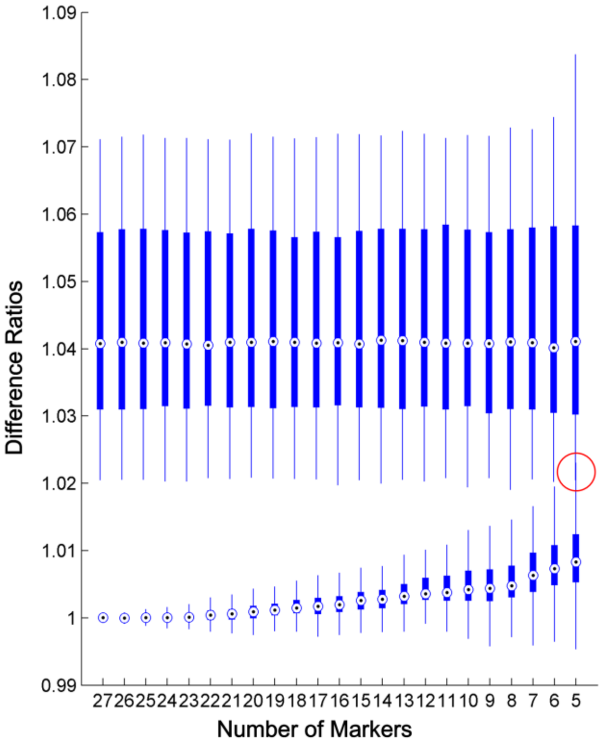
Supplementary Data File 2 includes Figure S1-S9

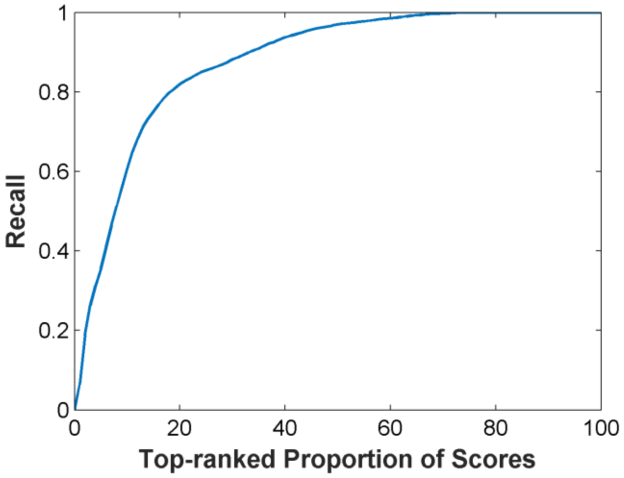
Supplementary Figure S1. The statistical analyses of trained parameters on IMR90 and H1 cell type. (**A**) The level one decomposition can obtain the minimal standardized difference between our constructed matrices and corresponding Hi-C matrices (IMR90). The standardized differences of predicted interaction matrices and Hi-C interaction matrices were shown for different decomposition levels. For each level, the standardized differences were calculated for 1000 chromosomal regions with size of 20Mb. The black solid line shows the averaged value of each decomposition level. (**B**) The decomposition level analysis of H1 cell type that were processed as in (A). (**C**) Boxplots of 8 parameters that used in nonlinear transformations of 4 coefficient matrices obtained from level one wavelet decomposition (IMR90). A-α and A-β are the parameters of the approximation coefficients matrix A. H-α and H-β are the parameters of the horizontal details coefficients matrix H. V-α and V-β are the parameters of the vertical details coefficients matrix V. D-α and D-β are the parameters of the diagonal details coefficients matrix D. The dot circle shows the median of 1000 runs. (**D**) The statistical analysis of 8 parameters of H1 cell type.



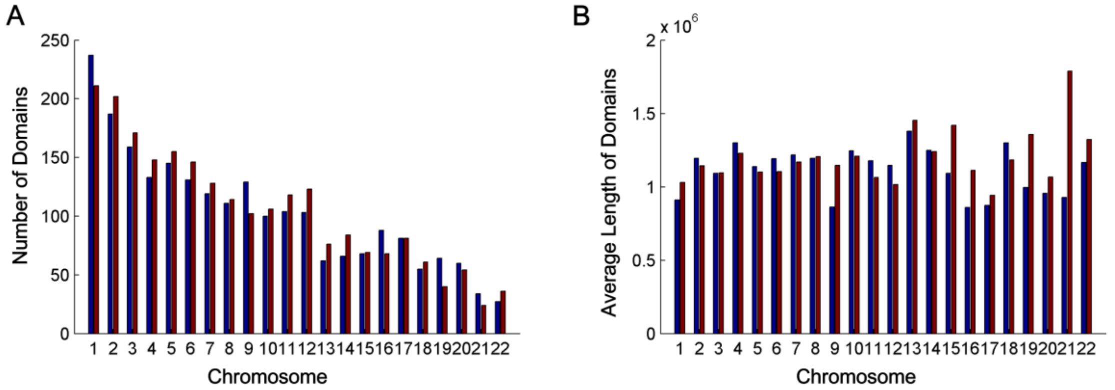
Supplementary Figure S2. The testing of different modification combinations (IMR90 cell). For a subset of 28 modifications, CITD was used to predict the interaction matrix and calculated the standardized difference by comparing with the related Hi-C matrix. The comparative ratio was calculated by the standardized difference of this subset dividing the standardized difference of total 28 modifications. The above part in the figure shows the comparative ratio of the permuted matrixes. For each of combinations, the boxplot shows results of 1000 repeats. The dot circle shows the median and the red circle highlights the overlapped region.



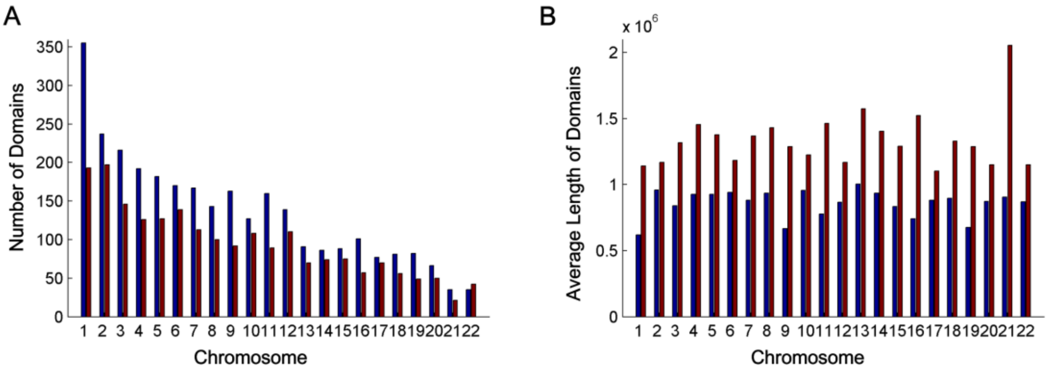
Supplementary Figure S3. Comparison with PreSTIGE[1] predicted enhancer-promoter interactions of H1 cell. The recall of PreSTIGE predicted enhancer-promoter interactions in the top-ranked proportion of CITD prediction scores.



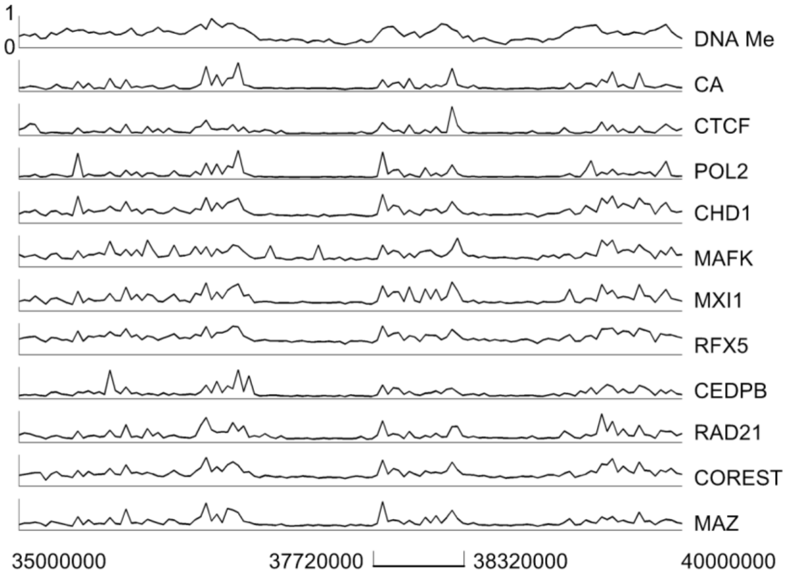
Supplementary Figure S4. The comparative and statistical analysis of topological domains (IMR90 cell). (**A**) The number distributions of 2,263 IMR90-TAD domains (blue) and 2,317 domains from CITD (red). (**B**) The average length distributions of 2,263 IMR90-TAD domains (blue) and 2,317 domains from CITD (red).



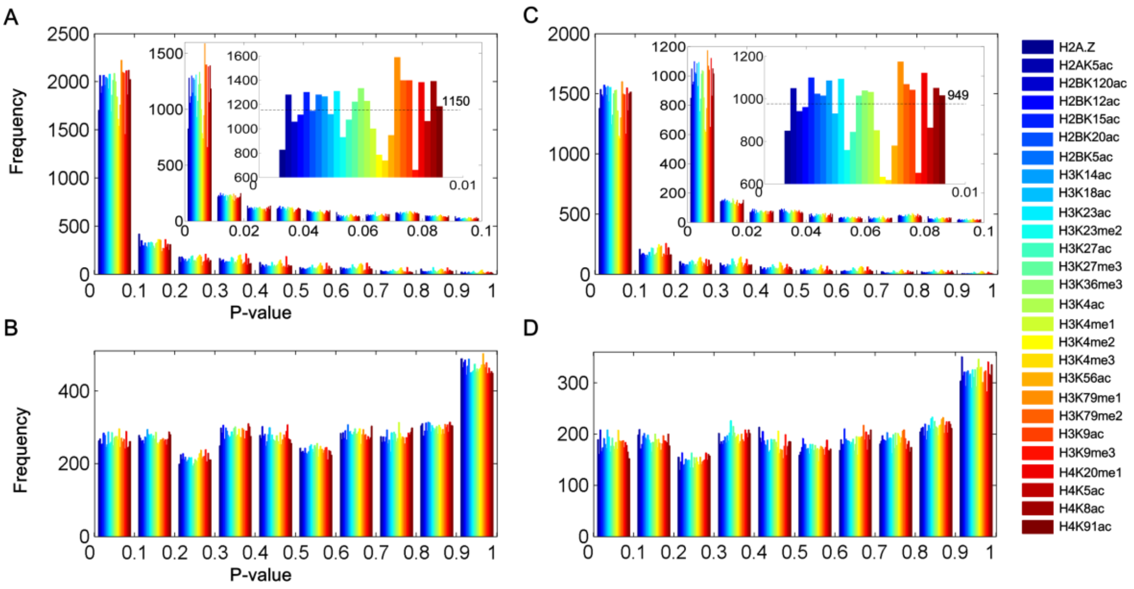
Supplementary Figure S5. The comparative and statistical analysis of topological domains (H1 cell). (**A**) The number distributions of 2,993 H1-TAD domains (blue) and 2,104 domains from CITD (red). (**B**) The average length distributions of 2,993 H1-TAD domains (blue) and 2,104 domains from CITD (red).



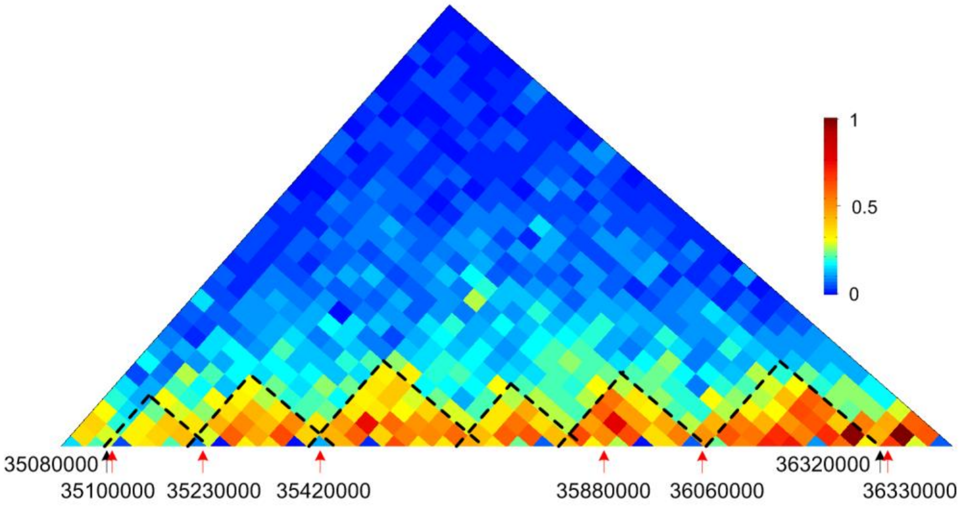
Supplementary Figure S6. The signals of DNA methylation (DNA Me), chromatin accessibility (CA) and 10 transcriptional factors. The region is from 35000000 to 40000000 on chr1 of IMR90. The signals were normalized (ranged from 0 to 1) by the maximal value of this region.



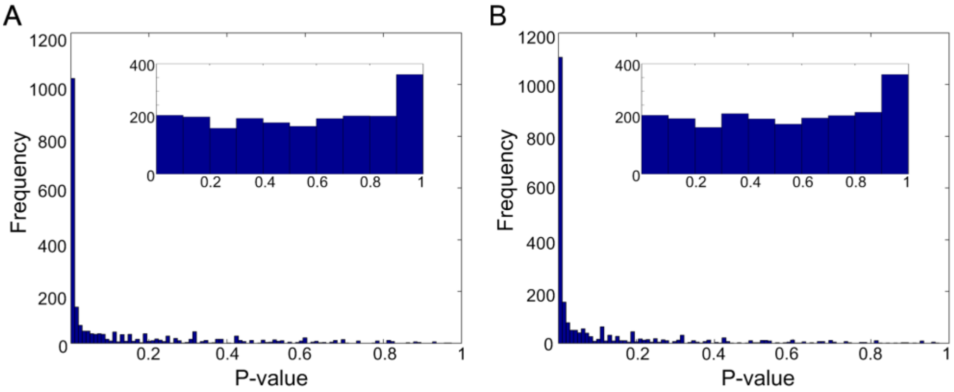
Supplementary Figure S7. Histone modifications are differently distributed between neighbouring topological domains of H1 cell. (**A**) The P-value distribution of 28 histone modifications between neighbouring H1-TAD domain pairs (K-S test). The zoom-in figures shows the distribution of P-values ranged from 0 to 0.1 or 0.01 respectively. The dot line indicates the average number of neighbouring domain pairs with P-values less than 0.01 for 28 modifications. (**B**) The P-value distribution of 28 histone modifications for randomly selected domain pairs with the same length distribution of H1-TAD domains. (**C**) The P-value distribution of 28 histone modifications between neighbouring domains predicted by CITD (K-S test). (**D**) The P-value distribution of 28 histone modifications for randomly selected domain pairs with the same length distribution of CITD predicted domains.



Supplementary Figure S8. A case study of predicted domains with 10kb bin size (IMR90 cell). Hierarchically predicted domains within a big IMR90-TAD domain (35080000-36320000). The heatmap shows the corresponding submatrix that extracted from Hi-C interaction matrix. The red arrows show the boundaries of 5 sub-domains that predicted by CITD with 10kb bin size. Near 6 boundaries, the changes of interactions achieved from Hi-C interaction matrices can be observed (black dot lines).



Supplementary Figure S9. Statistical tests of CTCF signal distributions among neighbouring topological domains (IMR90 cell). (**A**) The P-value distribution of CTCF signals for neighbouring IMR90-TAD domain pairs (K-S test). The inserted figure shows P-value distribution of randomly selected domain pairs with the same length distribution of 2,263 IMR90-TAD domains. (**B**) The p-value distribution of CTCF signals for neighbouring topological domains predicted by CITD (K-S test). The inserted figure shows P-value distribution of randomly selected domain pairs with the same length distribution of CITD predicted 2,317 domains.



Reference:

[1] He, B., Chen, C., Teng, L. and Tan, K. (2014) Global view of enhancer-promoter interactome in human cells. *Proceedings of the National Academy of Sciences of the United States of America*, **111**, E2191-2199