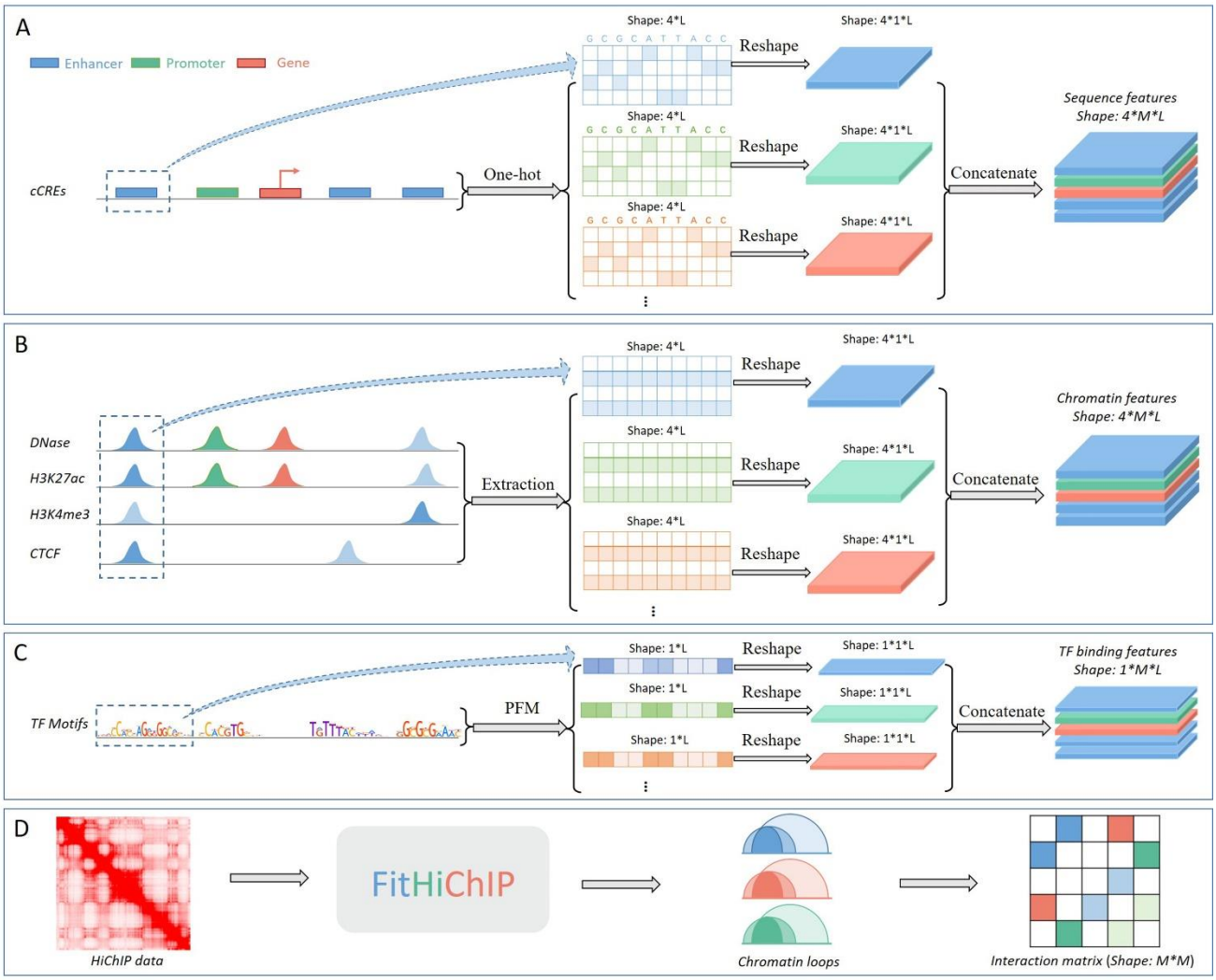

Supplemental Fig S1: Details of data construction. (A) The process of contructing sequence featrues: i) a gene and its surrounding cCREs were extracted, where each sequence was transformed into a matrix of shape 4**L* using the *one-hot* encoding method and then reshaped into a matrix of shape 4*1**L*. Here, 4 means the number of nucleotides [A, C, G, T]; ii) all matrices of shape 4*1**L* were concatenated along with the second dimension to form a matrix of shape 4**M***L*. (B) The process of contructing chromatin features: i) the epigenomic signals of a a gene and its surrounding cCREs were extracted using the *pyBigWig* software and and scaled by the $\log_{10}(1+x)$ function., where each region was assembled into a matrix of shape 4**L* and then reshaped into a matrix of shape 4*1**L*. Here, 4 means the number of epigenomic datasets (DNase, H3K27ac, H3K4me3, and CTCF); ii) all matrices of shape 4*1**L* were concatenated along with the second dimension to form a matrix of shape 4**M***L*. (C) The process of constructing TF binding features: i) a total of *L* TF motifs was used to calculate TF binding scores for each cCRE, resulting in a matrix of shape 1**L*, which was then normalized to a range of 0 to 1 and reshaped into a matrix of shape 1*1**L*; ii) all matrices of shape 1*1**L* were concatenated along with the second dimension to form a matrix of shape 4**M***L*. (D) The process of contructing chromatin loops: i) some significant chromatin loops were identified from H3k27ac HiChIP data by using FitHiChIP; ii) If there exist interactions between cCREs and cCREs, as well as between genes and cCREs in chromatin loops, the normalized counts of chromatin loops were calculated and scaled by the $\log_{10}(1+x)$ function, otherwise 0. As a result, for each gene and its surrounding cCREs, an interaction matrix of shape $M \times M$ was constructed. Note that *L* denotes the length of sequences or the number of TF motifs, *M* is equal to *m*+1 where *m* denotes the number of cCREs.