Supplemetary figures
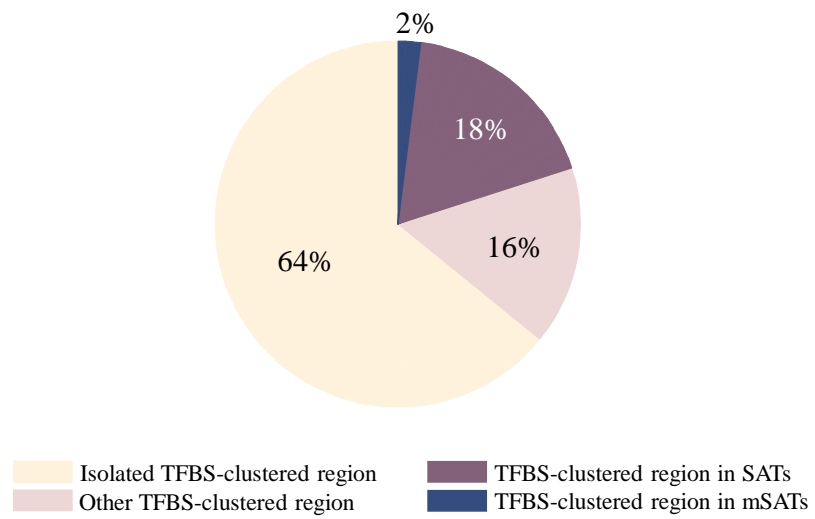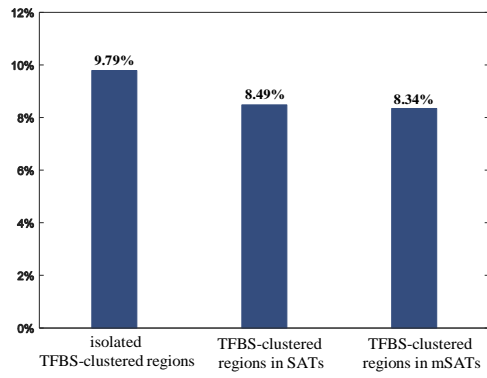

Figure S1
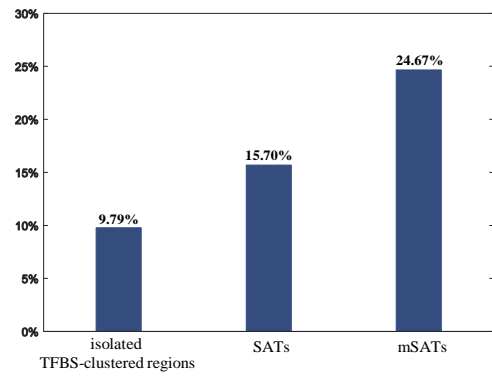the proportion of different types of TFBS-clustered regions in H1 cell line.

Figure S2

(A) Proportions of TFBS-clustered regions in different regulatory models located in promoter domain in IMR90 cell line.

(B) Proportion of different type of regulatory models located in promoter domain in IMR90 cell line.
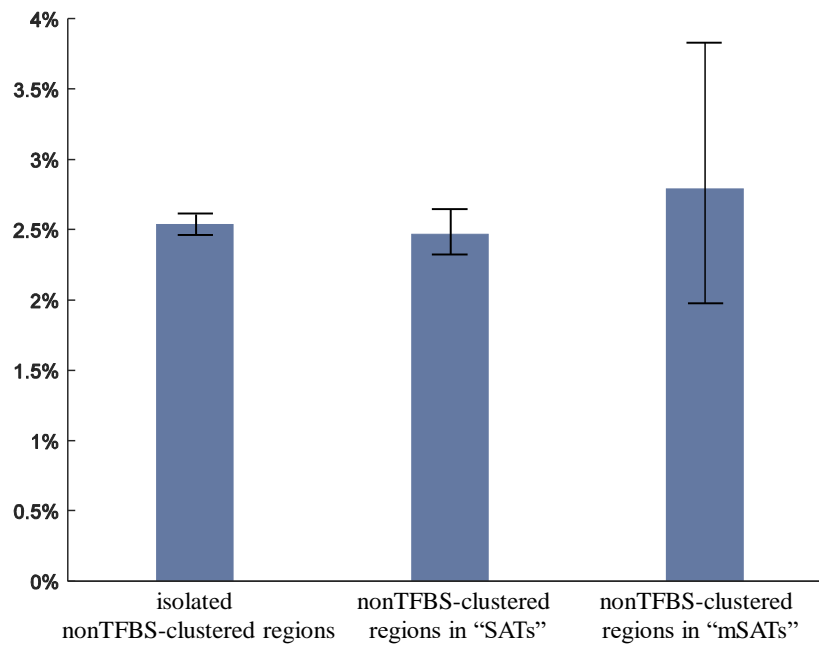
Figure S3

Average proportions of nonTFBS-clustered regions in different regulatory models located in promoter domain in IMR90 cell line. NonTFBS-clustered regions were generated using "bedtools shuffle" command, which samples a set of regions with random position and the same size distribution as that of TFBS-clustered regions in H1 cell line. This test was repeated for 10,000 times. Each colored bar shows the average proportion of each type of nonTFBS-clustered regions and each pair of parallel horizontal lines shows the 95th percentile of the proportion of each type of nonTFBS-clustered regions.
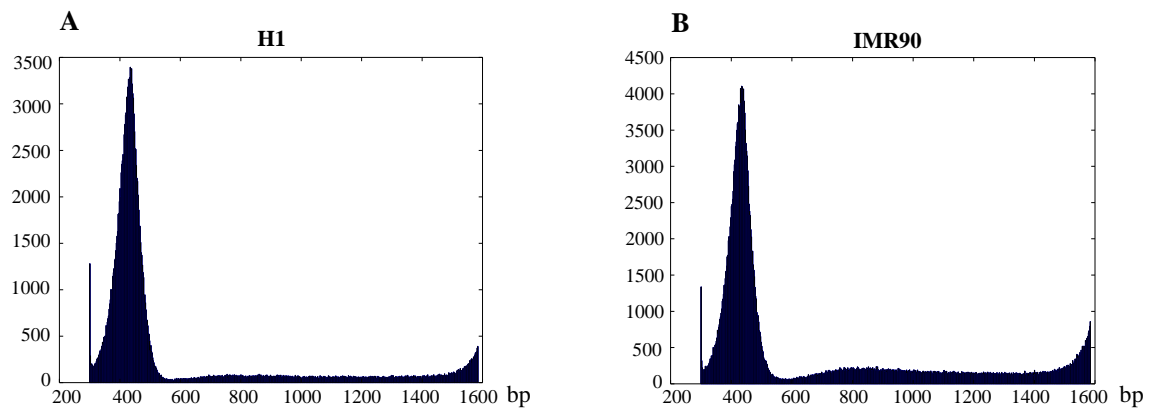
Figure S4

(A) The length distribution of the TFBS-clustered regions in H1 cell line.

(B) The length distribution of the TFBS-clustered regions in IMR90 cell line.