



Fig.S2 Characterization of super-enhancers.

(A) Distribution of normalized ATAC-seq, H3K27ac and H3K4me1 ChIP-seq signal across all the enhancers ranked for each enhancer feature independently.

(B) Signal density of chromatin accessibility and enhancer marks at the identified super-enhancers (red) and typical-enhancers (blue). Box plots indicated the median (center of box), lower and upper quartiles (bounds of box), minimum and maximum values (bars). Two-tailed *Wilcoxon* rank-sum test; *** $P < 10^{-15}$ versus typical-enhancers.

(C) Landscape of super-enhancers and their target genes in the genome.

(D) Relative expression level of SE-associated genes and TE-associated genes (log-transformed data). Box represents lower quartile, median and upper quartile; whiskers denote the 5th and 95th percentiles. Violin plots denote the density estimates. Two-tailed *Wilcoxon* rank-sum test; *** $P < 10^{-5}$.

(E-F) Biological processes of KEGG terms (E) and GO terms (F) enriched in SE-associated genes.