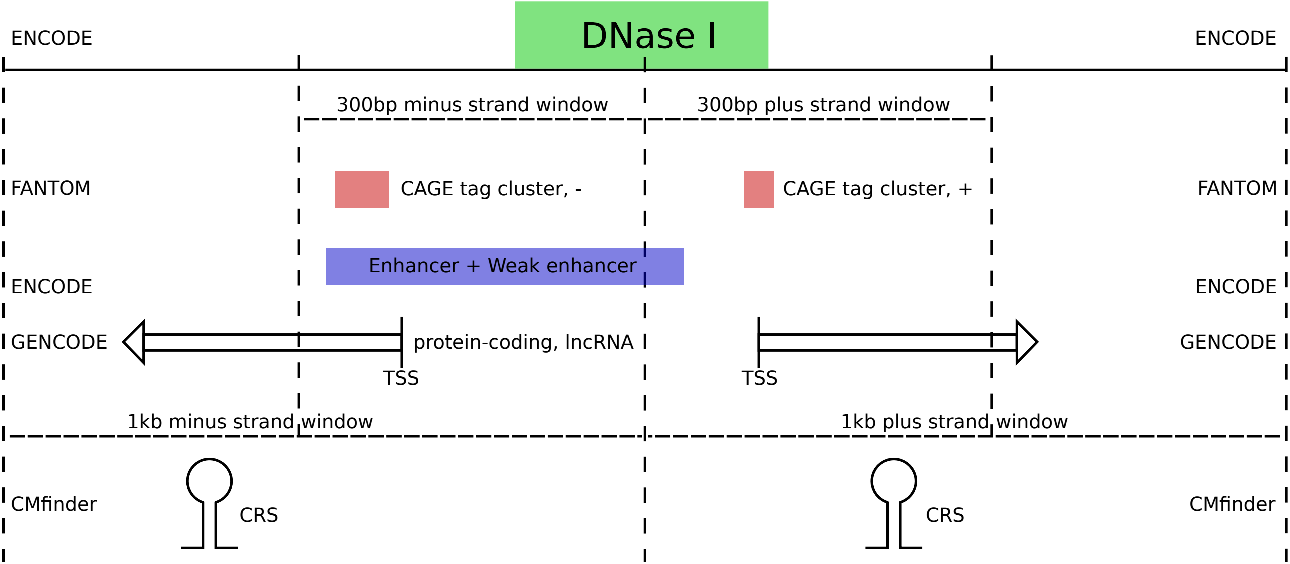

Supplemental Figure S11. Schematic illustration of the characterization of structured regulatory regions. We used the following data to define regulatory regions: DNase I Hypersensitivity Peak Clusters from ENCODE (95 cell types), CAGE expression of robust (expression>10TPM) peaks (maximal length of 200bp) from FANTOM5 Phase 2.0, ENCODE chromatin segmentation states and GENCODE v25 gene/TSS annotation of mRNAs and lncRNAs. For the detailed definition of regulatory regions in this study see the Methods section "Definition of gene regulatory regions" and Supplemental Methods.