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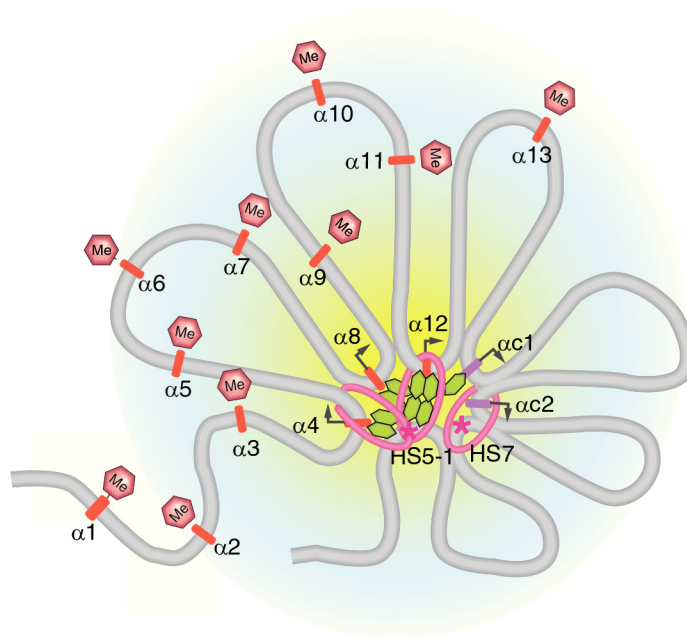


Figure 5. Summary of the epigenetic properties of the *Pcdh- α* cluster. (A) Summary of ChIP-seq (parallel sequencing technologies coupled to chromatin immunoprecipitation) analysis in a human diploid neuroblast cell line (SK-N-SH) that expresses only three variable *Pcdh- α* exons. There are two CTCF binding sites at each active variable exon (CSE and eCBS sequences) and two at the HS5-1 enhancer (HS5-1a and HS5-1b). (B) Summary of the epigenetic properties of active and silenced *Pcdh- α* exons on forming a 3D transcriptional hub, based on chromosome conformation capture (3C) data. Regions outside the central transcriptional hub are thought to be packaged in a repressive chromatin conformation (blue-shaded region), suggested by the DNA methylation of inactive *Pcdh- α* promoter regions. Active genes are thought to be concentrated in a transcriptional hub, aided by double-clamp binding of CTCF between the variable exons and the HS5-1 enhancer and cohesin.