

Supplemental Figure Legends

Figure S1. Distribution of the lengths of histone H3K27me3 domains.

(A) CD4⁺ T cells and (B) HeLa cells. Two-thirds of the domains range in length between 5- and 25-kb.

Figure S2. CTCF binding sites are enriched at the H3K27me3 domain boundaries.

(A) and (B) The H3K27me3 domain boundaries were aligned, so as to have high H3K27me3 regions on the left side and low H3K27me3 on the right side and the CTCF binding site density was plotted. CTCF binding sites were more abundant in the H3K27me3 domain boundaries extending up to 5 kb into the domains of (A) CD4⁺ T cells and (B) HeLa cells. *x* axis: Position relative to the H3K27me3 domain boundary. DB: H3K27me3 domain boundary. *y* axis: CTCF binding site density. (C) Number of CTCF binding sites near the H3K27me3 domain boundaries in CD4⁺ T cells and HeLa cells. *x* axis: Distance from H3K27me3 domain boundary. *y* axis: Number of CTCF binding sites.

Figure S3. The positioning and phasing of nucleosomes are similar between the cell type specific CTCF sites and those that are shared among cell types.

(A) Position of nucleosomes at the CD4⁺ T cells specific CTCF binding sites. (B) Position of nucleosomes at the CTCF binding sites shared among CD4⁺ T cells and HeLa cells.