

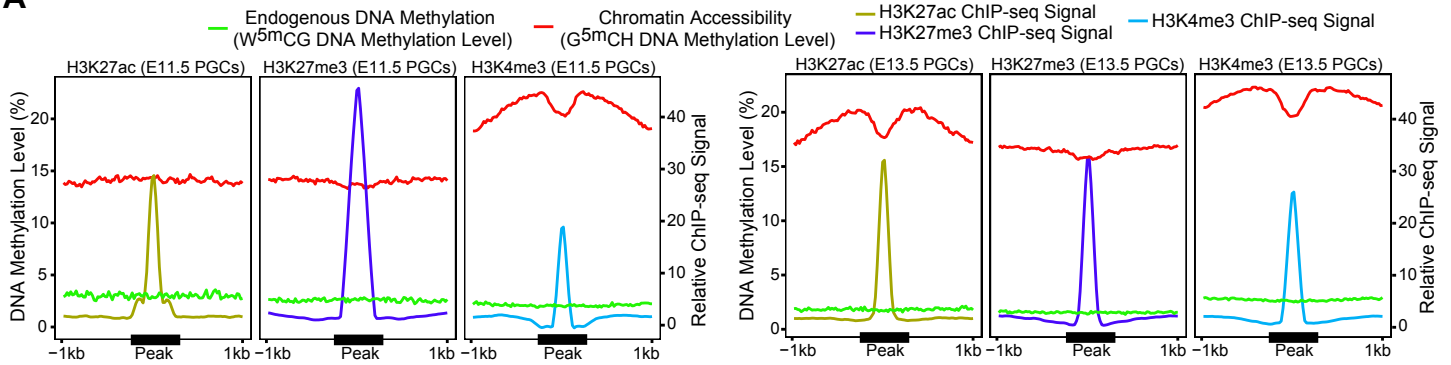
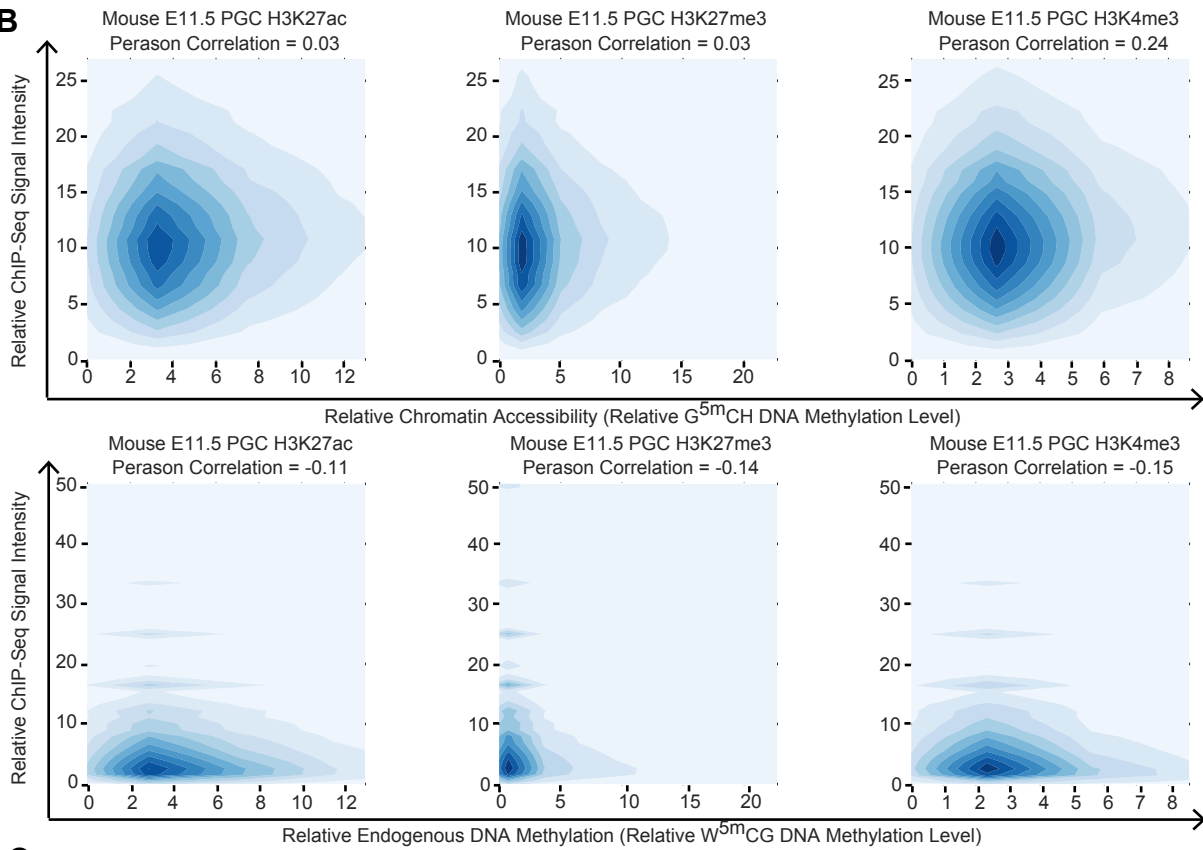
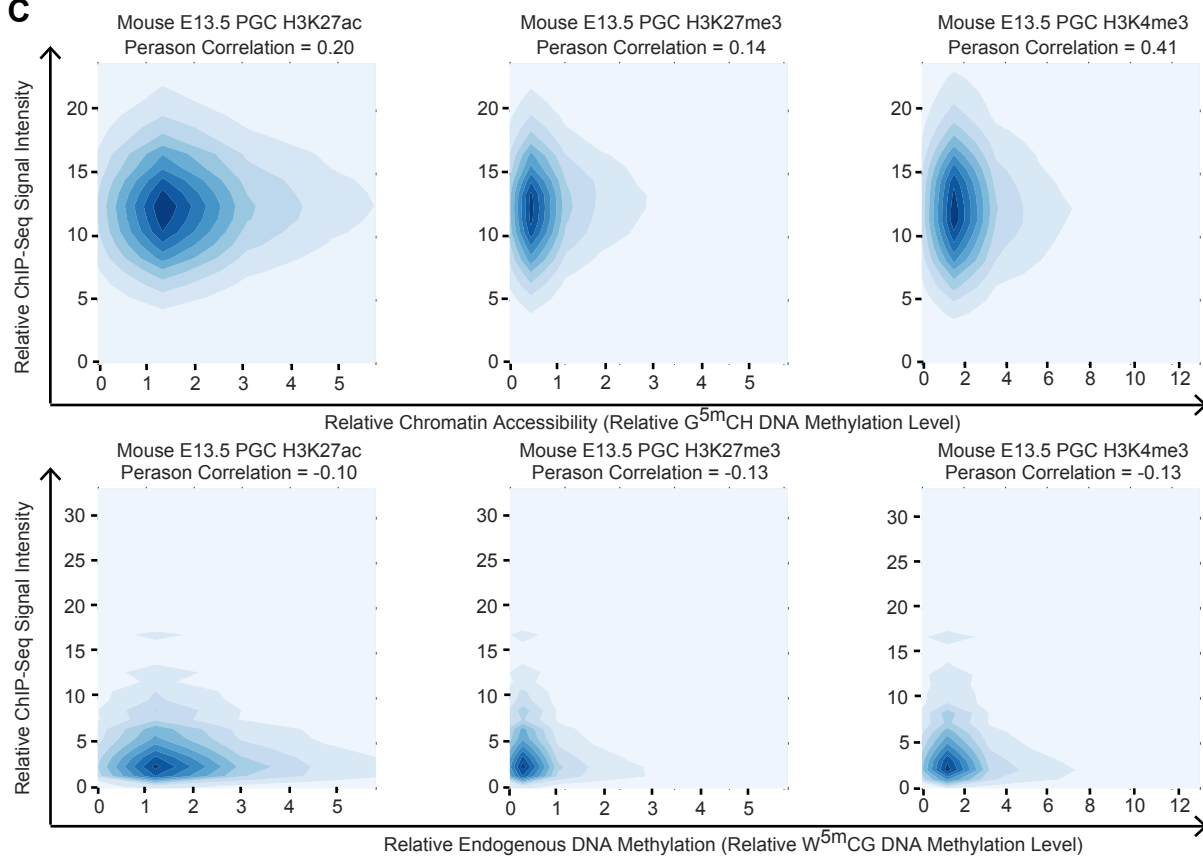
Figure S9**A****B****C**

Figure S9 The relationships between the histone modifications and the chromatin accessibilities in mouse PGCs.

(A) The chromatin accessibility and endogenous DNA methylation level on the ChIP-seq peak and the flanking regions in mouse E11.5 and E13.5 PGCs. (B-C) The contour charts showing the person correlations between ChIP-seq signal of histone marks and the chromatin accessibility or endogenous DNA methylation in each consecutive 1kb bins in mouse E11.5 (panel B) and E13.5 (panel C) PGCs.