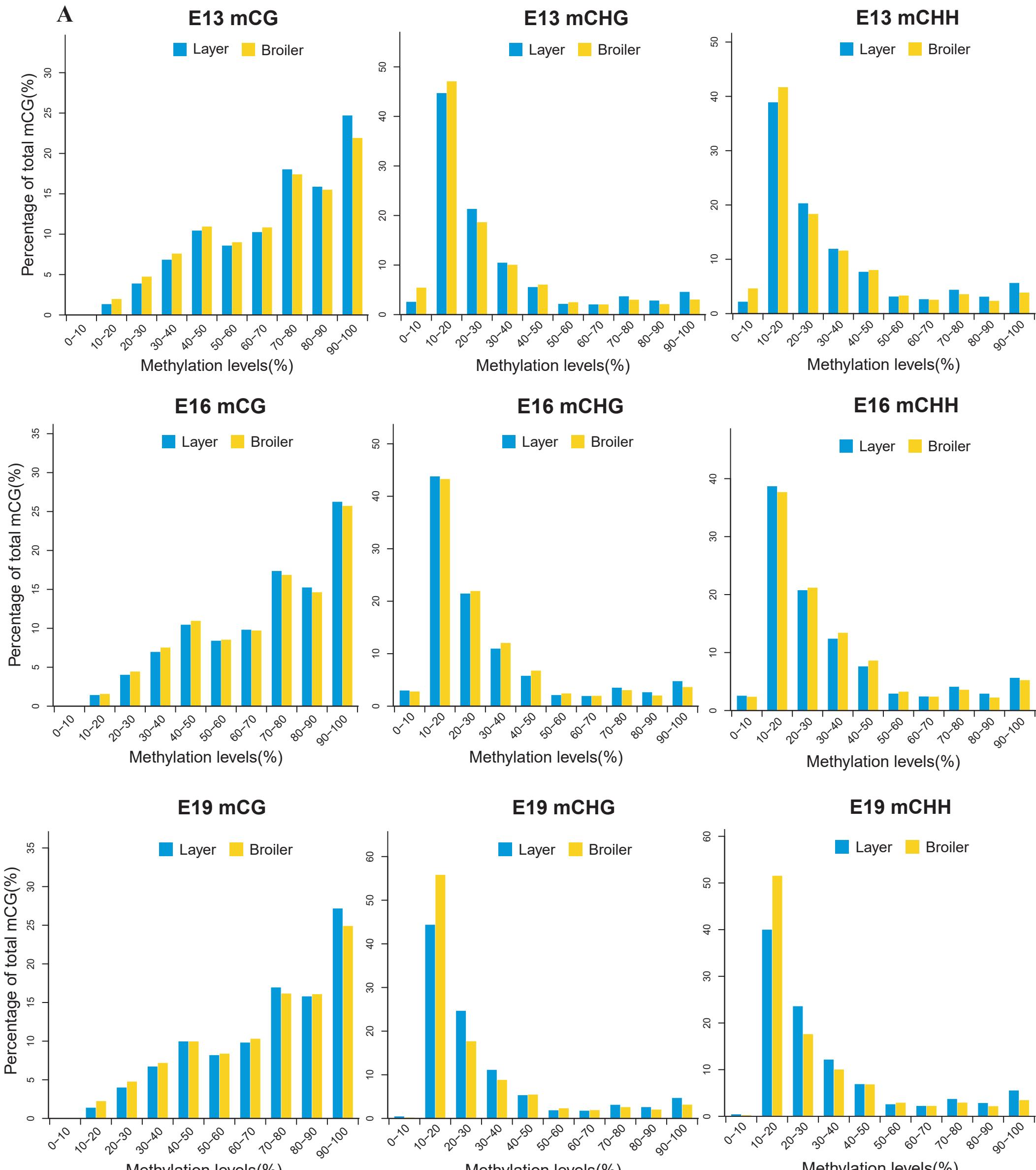


Supplementary Figure 1. Genome-wide profiles of DNA methylation among different sample groups. **(A)** Distribution of CpG methylation level at different time points in CG, CHG and CHH contexts, respectively. **(B)** Numbers of CGIs in different genomic regions at 4 time points. **(C)** Numbers of CGIs in different genomic regions at 4 time points. The numbers were adjusted by the lengths of genomic regions they belong to.

Supplementary Figure 2. Comparative measurement of methylation levels of genes and different types of lncRNAs in three contexts. **(A-B)** Methylation level of various regions of genes in layers and broilers in CHG and CHH contexts. **(C-D)** Measurement of methylation levels of different types of lncRNAs for 4 time points. * $P<0.05$, ** $P<0.01$ for comparison between two chicken lines. The red star means the methylation level of layers is significantly higher than broilers whereas the green star represents an opposite result.

Supplementary Figure 3. Methylation levels of various types of TEs at different time points. **(A-B)** Comparative measurement of methylation levels of SINE, LINE, LTR, DNA and Satellite regions between two chicken lines in different contexts. **(C)** Comparison of methylation levels of genes or TEs between layers and broilers in three contexts. **(D-F)** Methylation of upstream, body and downstream regions of different types of TEs in three contexts at E10, E13 and E16 using 20 bins across the whole genome.

Fig S1**B**

Numbers of CGIs in Developmental Stages

C

Numbers of CGIs in Developmental Stages

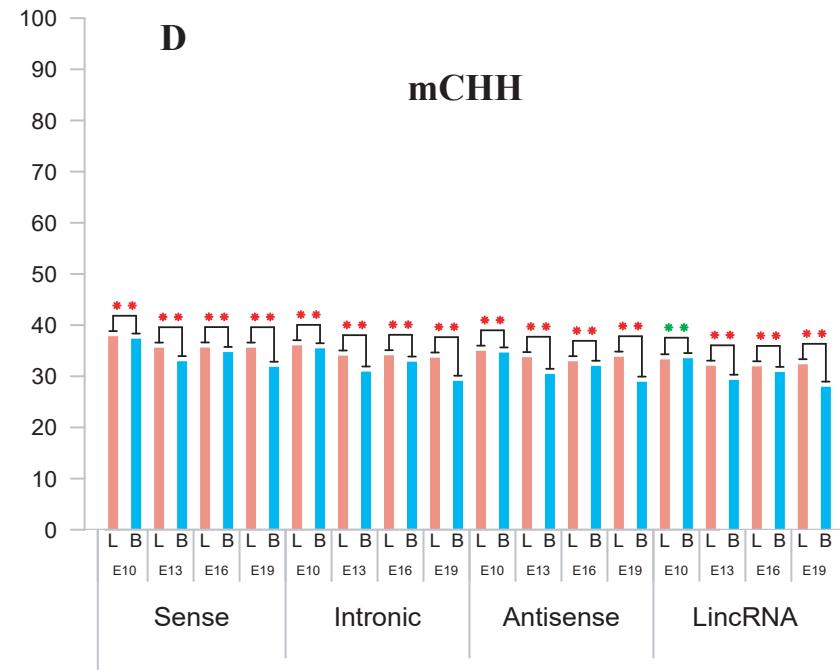
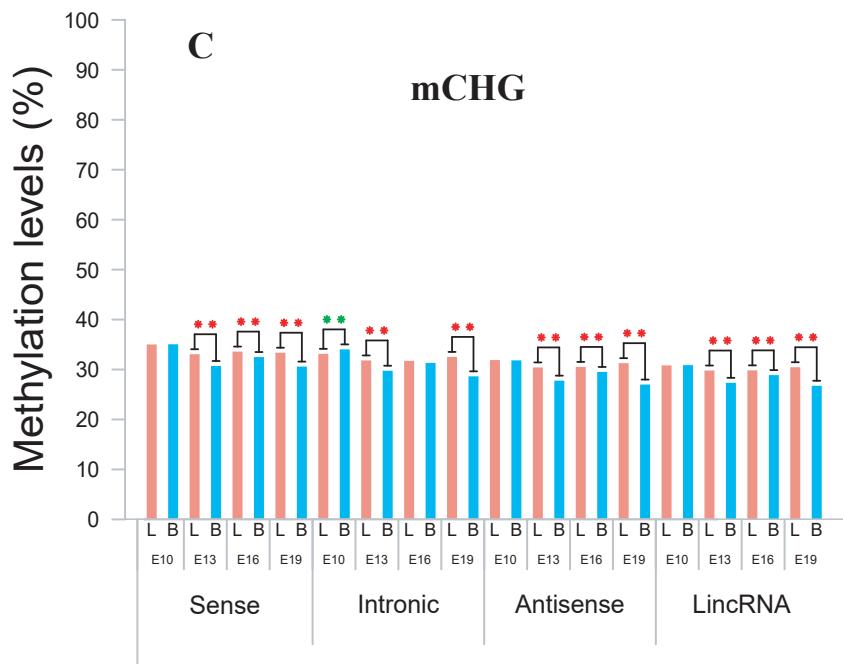
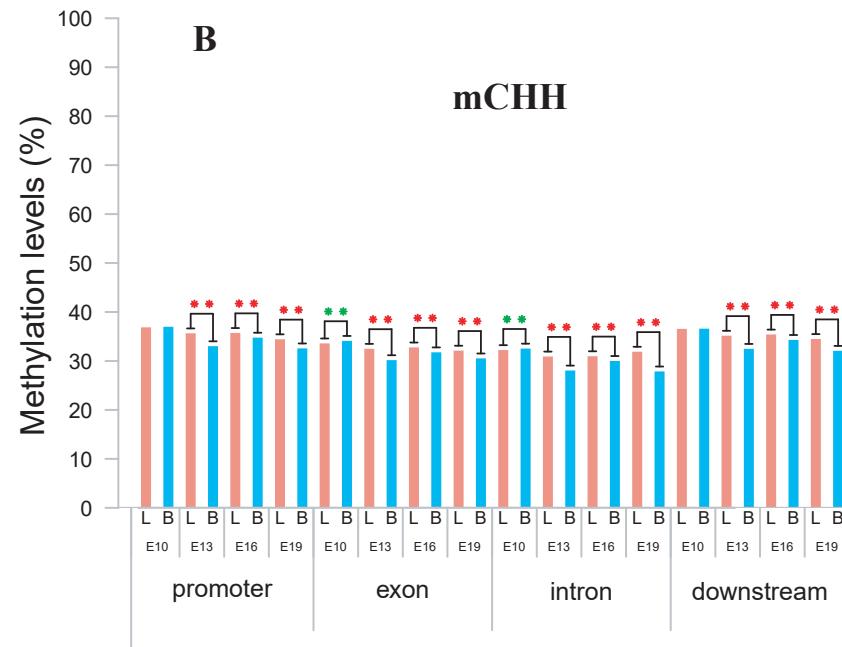
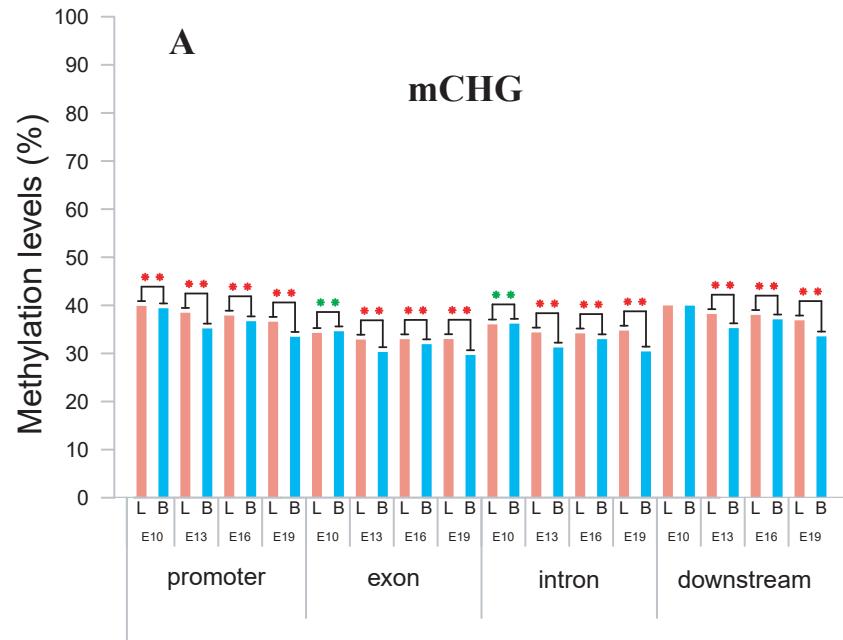
Fig S2

Fig S3

