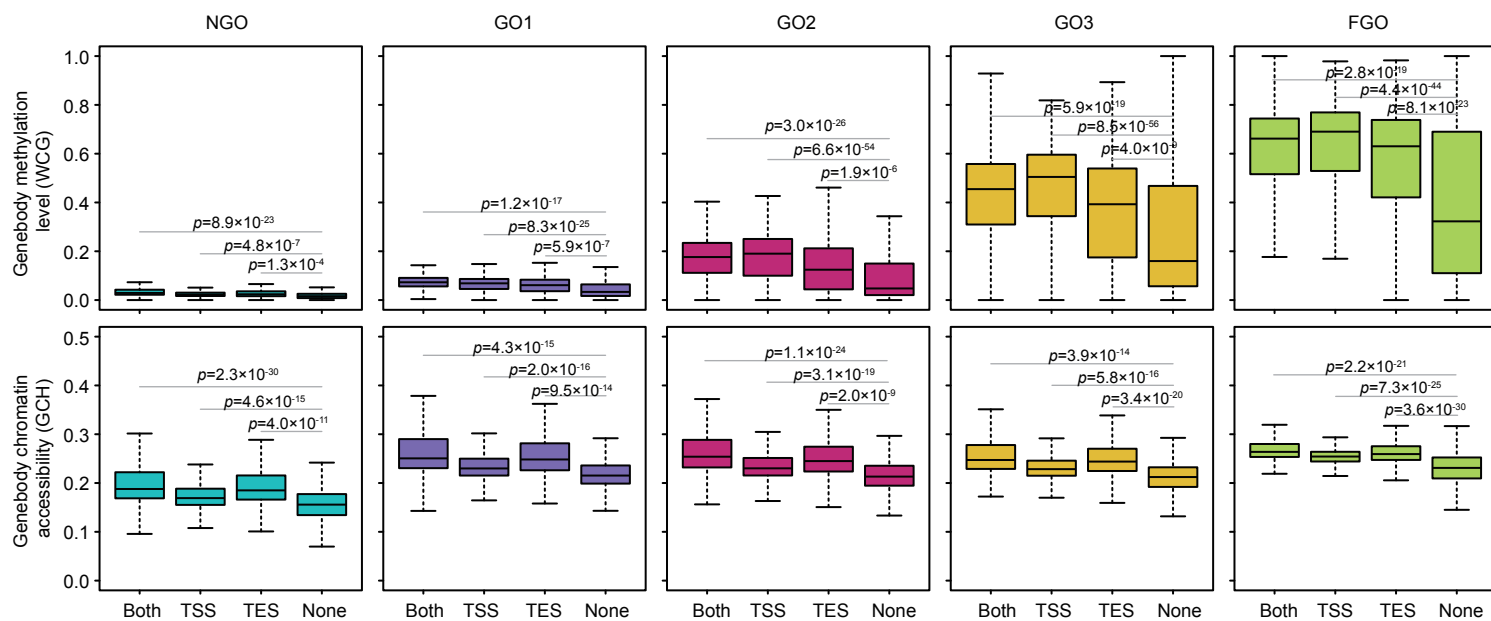
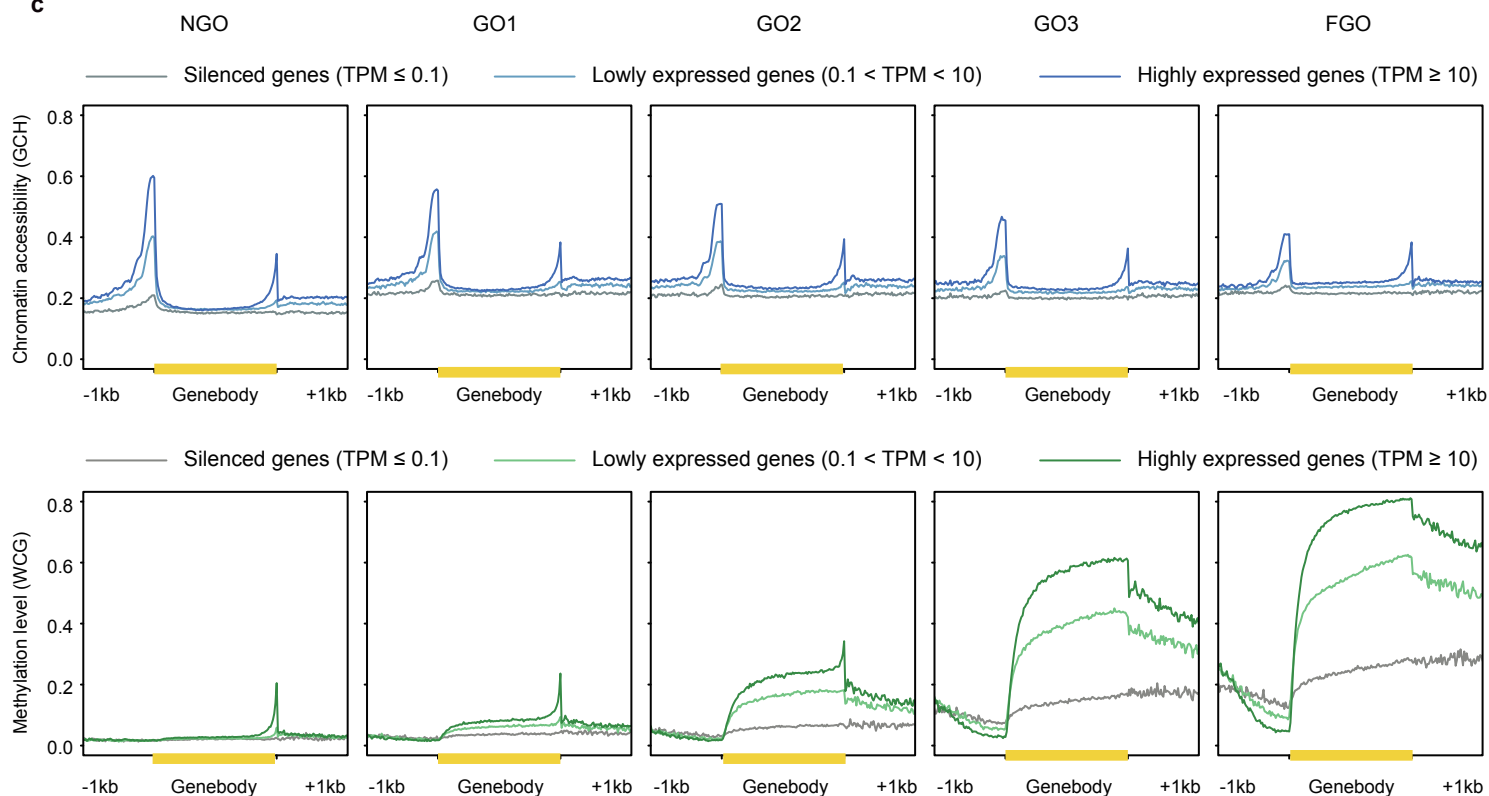


a**b****c**

Supplementary information, Fig. S9 Relationship among chromatin accessibility, *de novo* DNA methylation and gene expression. **(a)** Representative loci showed *de novo* DNA methylation at actively transcribed regions in oocytes. The starting point and direction of red arrows at RefSeq genes panel represented the gene transcriptional starting site and gene transcriptional direction. **(b)** DNA methylation level (upper panel) and chromatin accessibility (lower panel) of gene bodies from genes with both TSS and TES NDRs (Both), genes with only TSS-NDRs (TSS), genes with only TES-NDRs (TES) and genes with no NDR (None) in mouse oocytes. **(c)** The average chromatin accessibility (upper panel) and DNA methylation (lower panel) of RefSeq genes along gene bodies, 1 kb upstream of the TSS and 1 kb downstream of the TES at each stage. Genes were separated into three categories by their expression level. P-values were defined by the two-tailed Student's *t*-test.