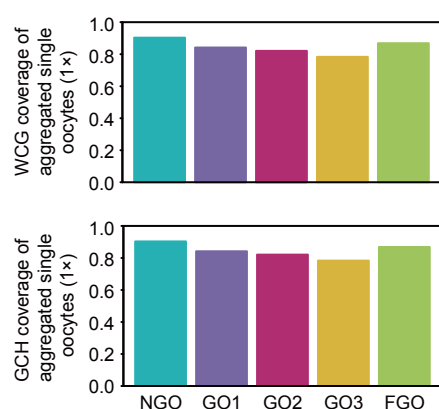
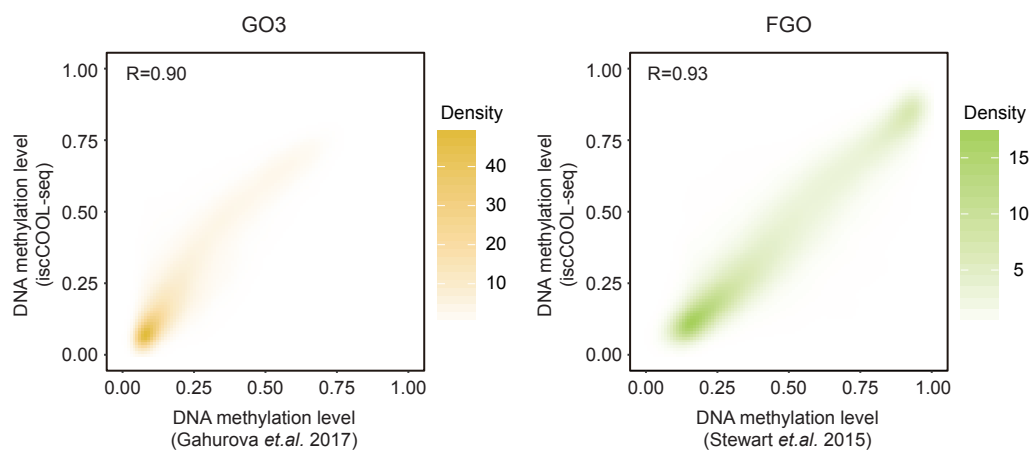
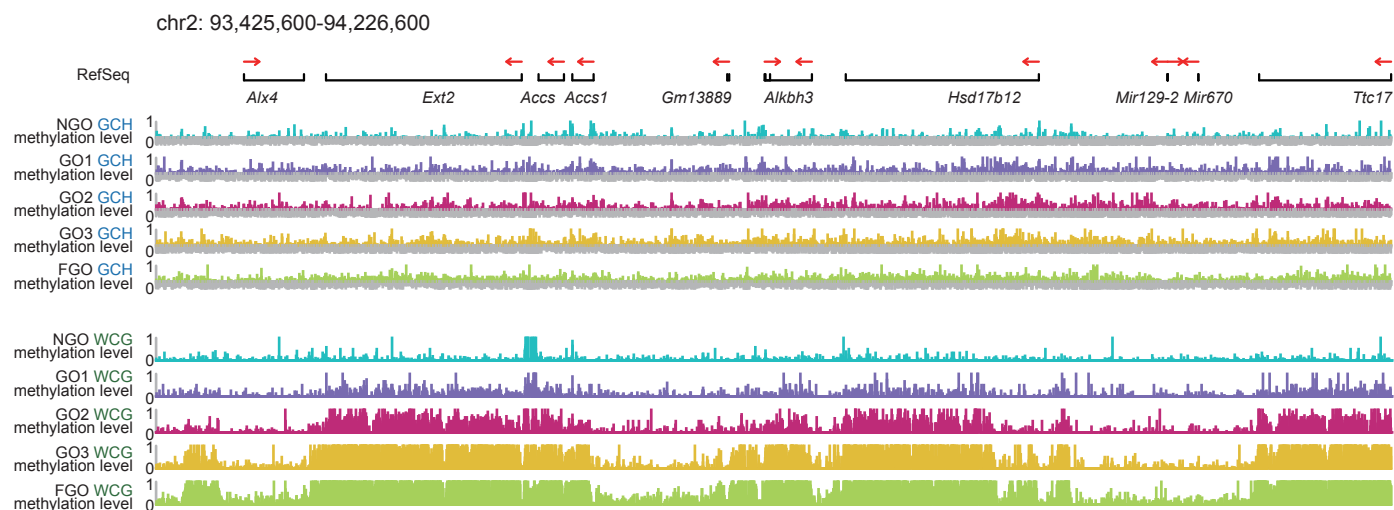


a**b****c**

Supplementary information, Fig. S2 Data quality of single-cell multi-omic profiling of growing mouse oocytes. **(a)** The genome-wide coverage ($1\times$) of WCGs and GCHs in aggregated single mouse oocytes by iscCOOL-seq. **(b)** Spearman's correlation of DNA methylation in the GO3 and FGO stages between the iscCOOL-seq method and the traditional PBAT method. **(c)** Representative loci showed chromatin accessibility (GCH methylation level) and DNA methylation (WCG methylation level) in growing mouse oocytes. The starting point and direction of red arrows at RefSeq genes panel represented the gene transcriptional starting site and gene transcriptional direction.