

Fig. S3. Boxplots showing the distribution of ChIP signal for each quartile of genes, based on expression level. The fourth quartile refers to the most highly expressed genes. Top and bottom of each box represents the 75th and 25th percentiles of ChIP signal, respectively; center line represents the median. Vertical lines extend beyond the box up to 1.5-times the difference between the 75th and 25th percentiles. Hatchmarks represent outliers. For each expression level quartile, the distribution of ChIP signal is statistically significantly different from that of the other quartiles ($P < 10^{-15}$, independent two-group Mann-Whitney U test).

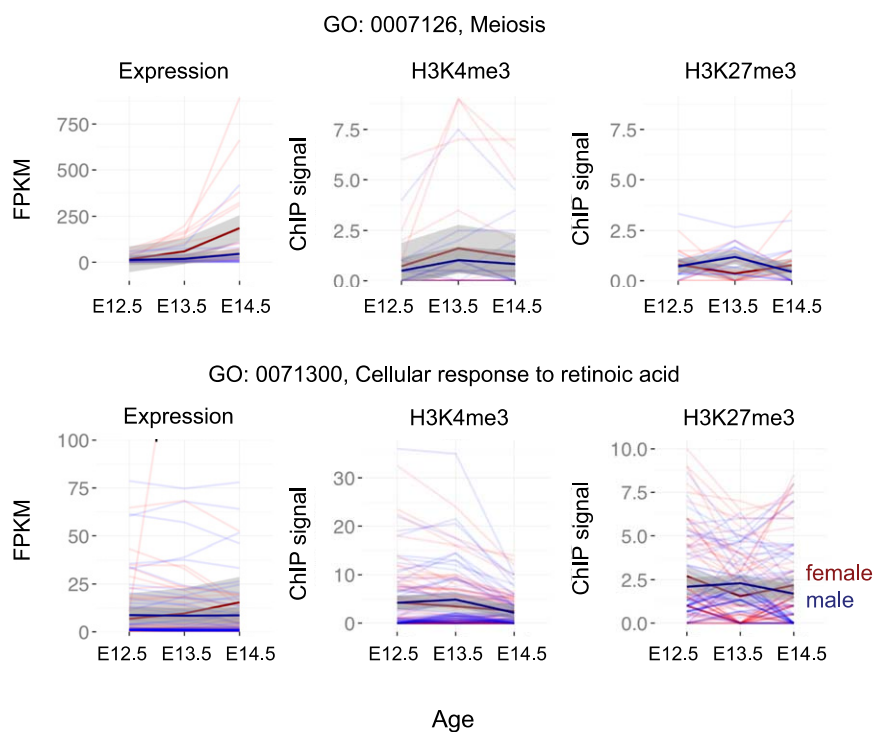


Fig. S4. Expression, K4 signal, and K27 signal across fetal time points for genes with significantly changed expression in the “meiosis” GO category, and for all genes in the “cellular response to RA” (RA, retinoic acid) GO category. Faint lines represent individual genes, and dark lines represent the mean. Red, female; blue, male.

Table S1. Log₂ fold-change values for differentially expressed genes ($P < 0.05$) in fetal germ cells (index for Fig. S1)

[Table S1 \(DOCX\)](#)