

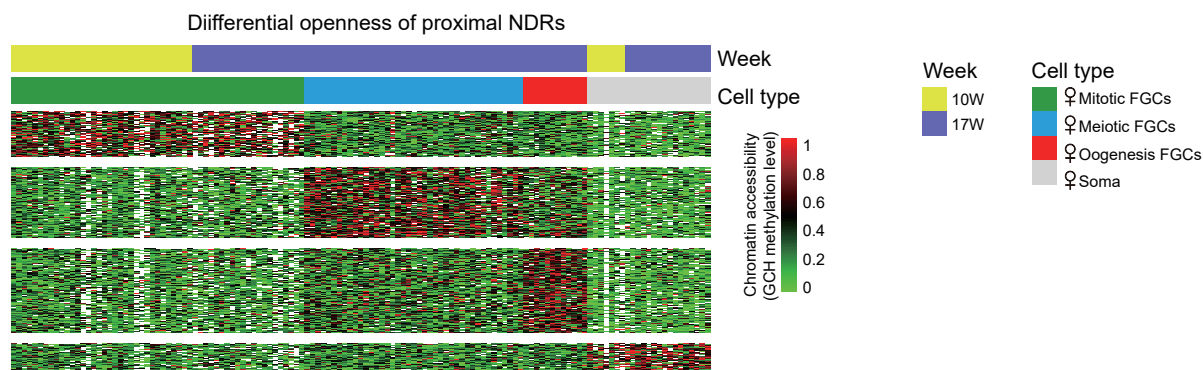
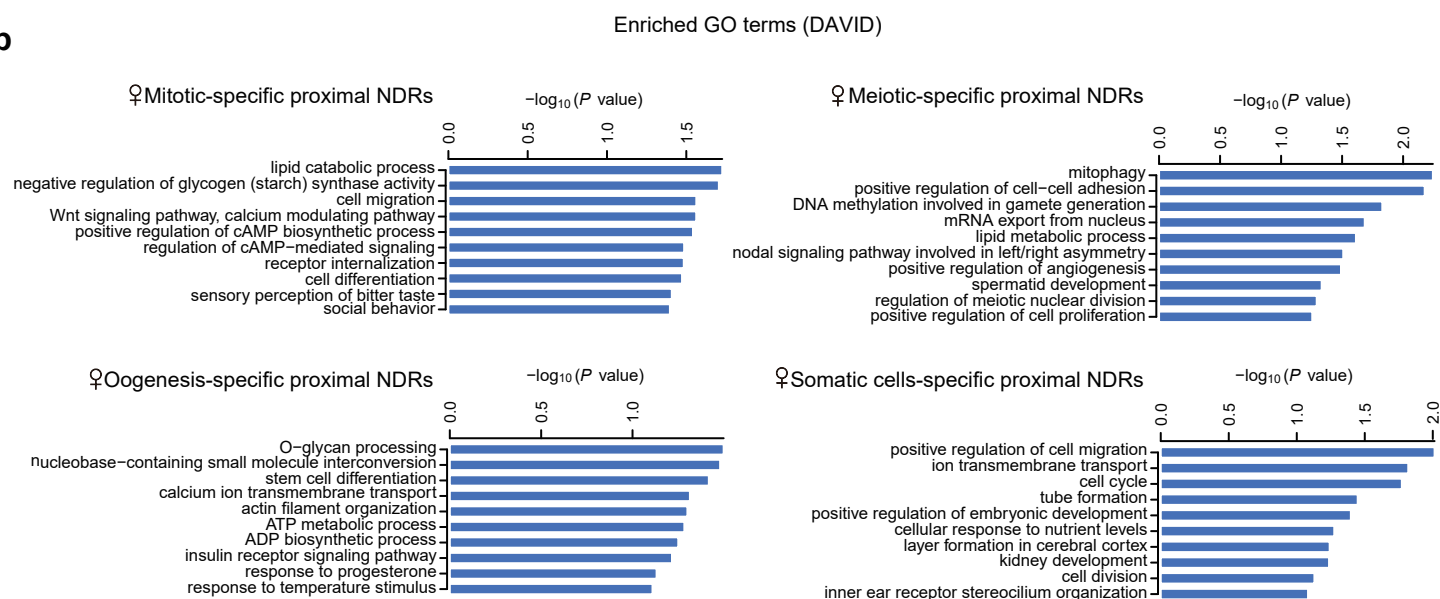
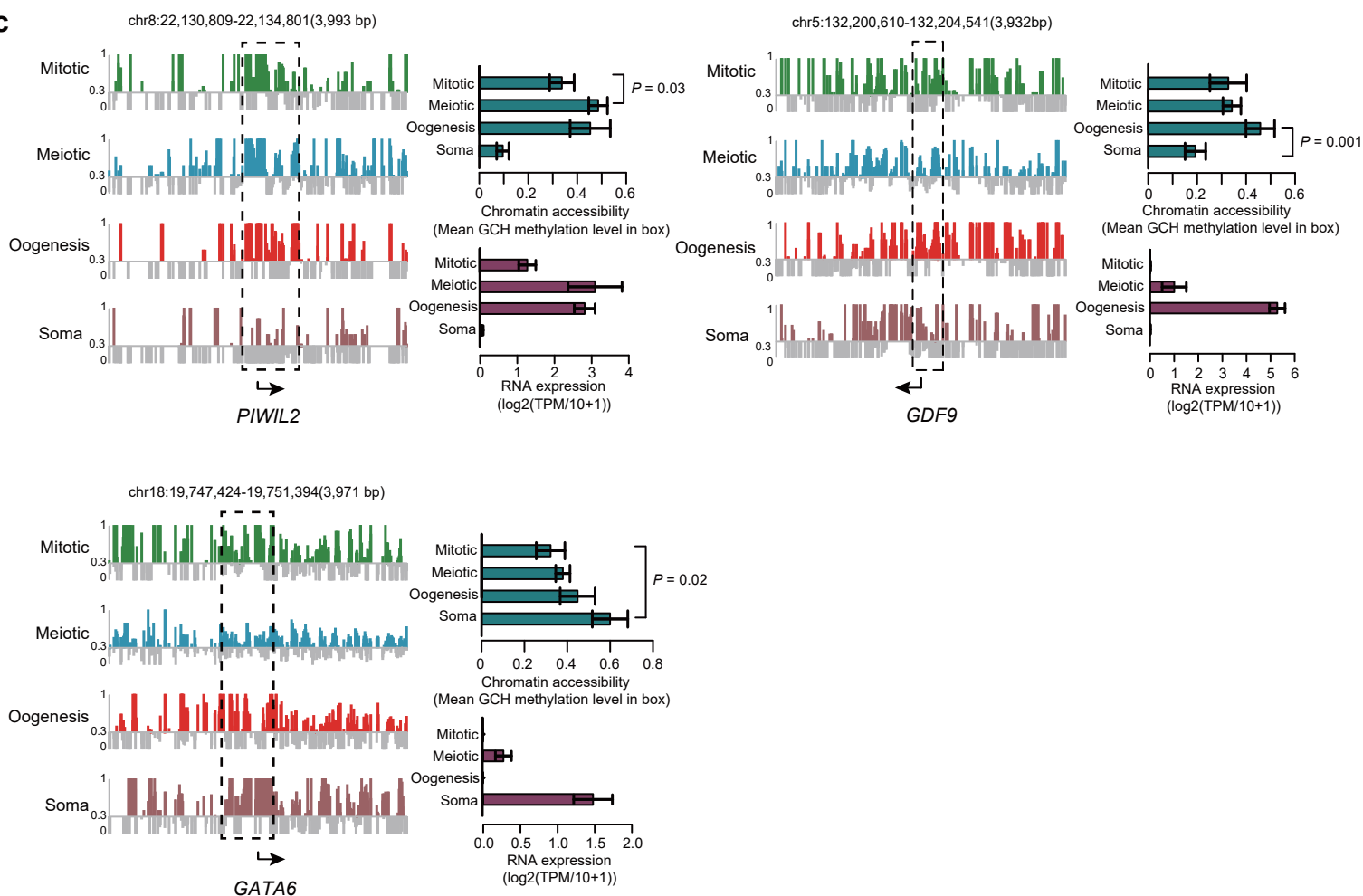
a**b****c**

Fig. S5: The differential openness of proximal NDRs in female FGCs and gonadal somatic cells.

a Heatmap showing 857 differentially open proximal NDRs among female 10- and 17-week FGCs at sequential phases and somatic cells during development.

b GO analysis of the corresponding genes associated with differentially open proximal NDRs in each cell types.

c The chromatin accessibility around the TSSs of *PIWIL2*, *GDF9* and *GATA6* in the female 17-week FGCs and the somatic cells are shown at a single-base resolution. The cytosines with their methylation level less than 0.3 were shown in gray, and only the cytosines with their methylation level greater than 0.3 were shown in green /blue /red /brown based on the cell types. The representative differentially open regions between cell types are highlight in dashed rectangles. The mean chromatin accessibility of representative regions and RNA expression levels of genes (estimated from female 18-week embryos in our previous study) are shown in the right panel¹¹. The direction of the black arrow under each panel represents the direction of transcription. The bar plot and histogram represent means, while the error bars represent s.e.m. values. Statistical significance analysis for the differences of GCH levels between two cell types were performed and the *P* values with Student's t-test were shown here.