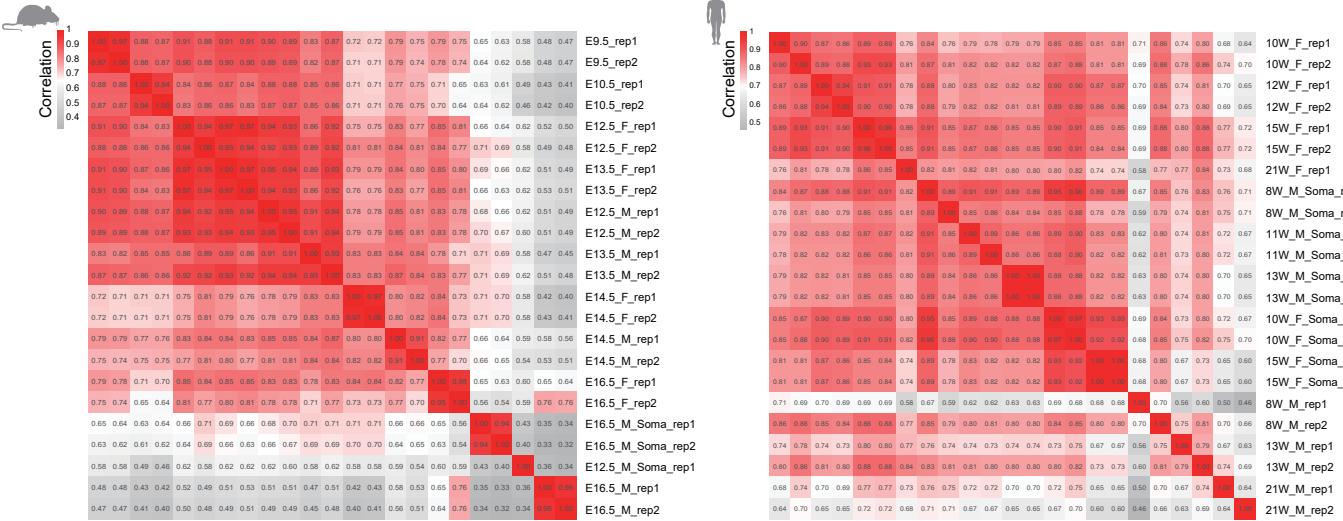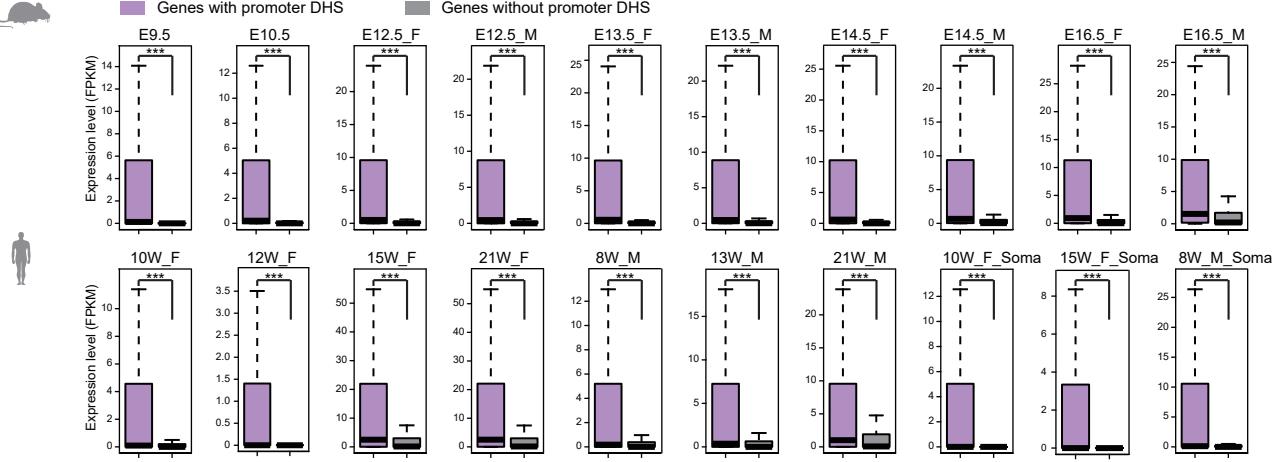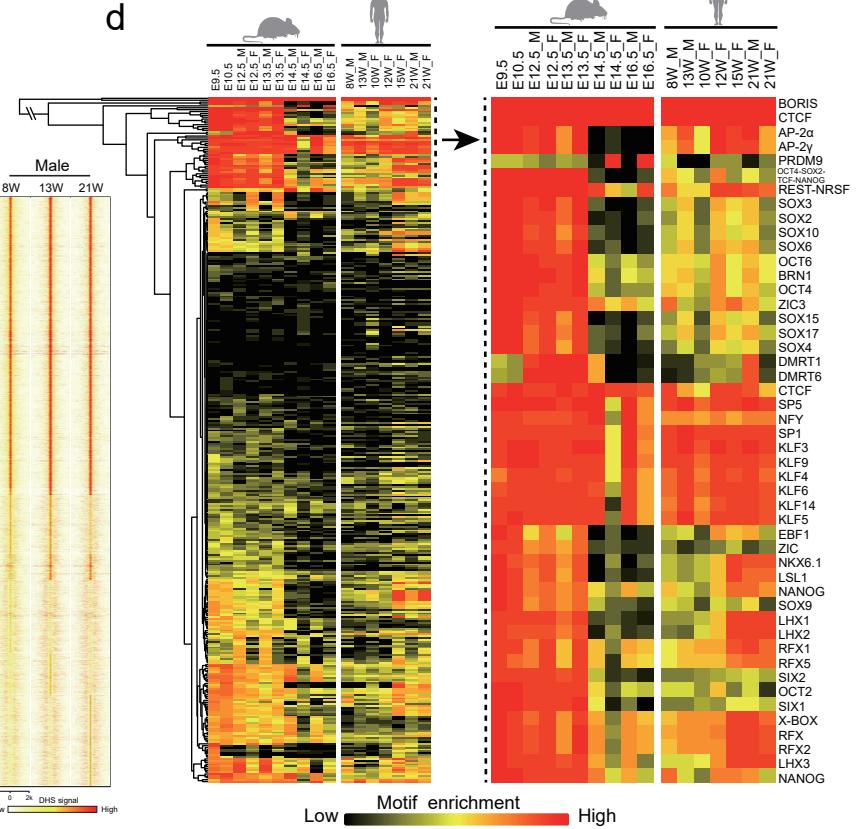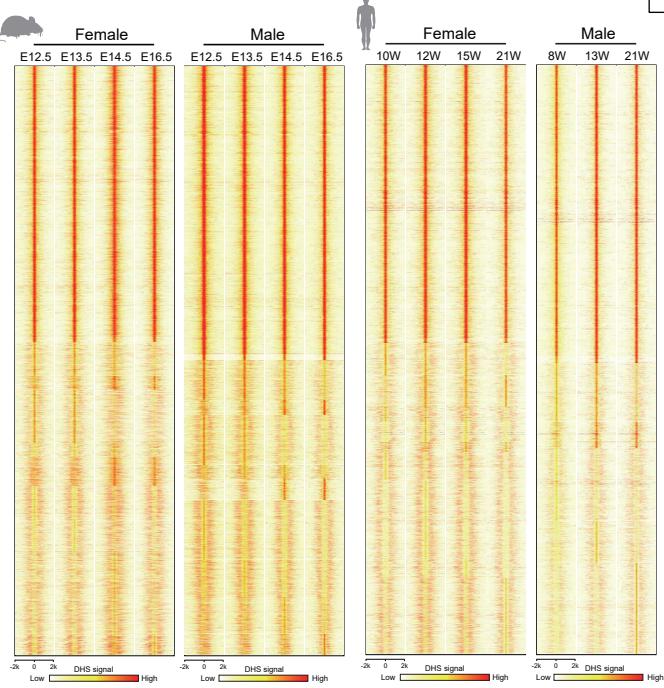**Fig. S2** See next page for caption.

Fig. S2 Profiling and annotation of accessible chromatin in mouse and human DNase-seq samples.
a Pearson correlation matrices of DNase signals in mouse and human PGCs and gonadal somatic cells generated by our low-input DNase-seq method. **b** Box plots showing the expression levels of genes with or without promoter DHSs in mouse and human PGCs and gonadal somatic cells. The difference between the two groups are statistically significant by Wilcoxon rank sum test (******* denotes p < 0.001). **c** Heat maps displaying the dynamic changes of promoter DHSs in mouse and human PGCs across multiple developmental stages. **d** Left panel: TF motif enrichment data set (n=363), annotated TF motifs are hierarchically clustered by enrichment patterns. Right panel: representative enriched TF motifs selected from the enrichment data set (n=48).