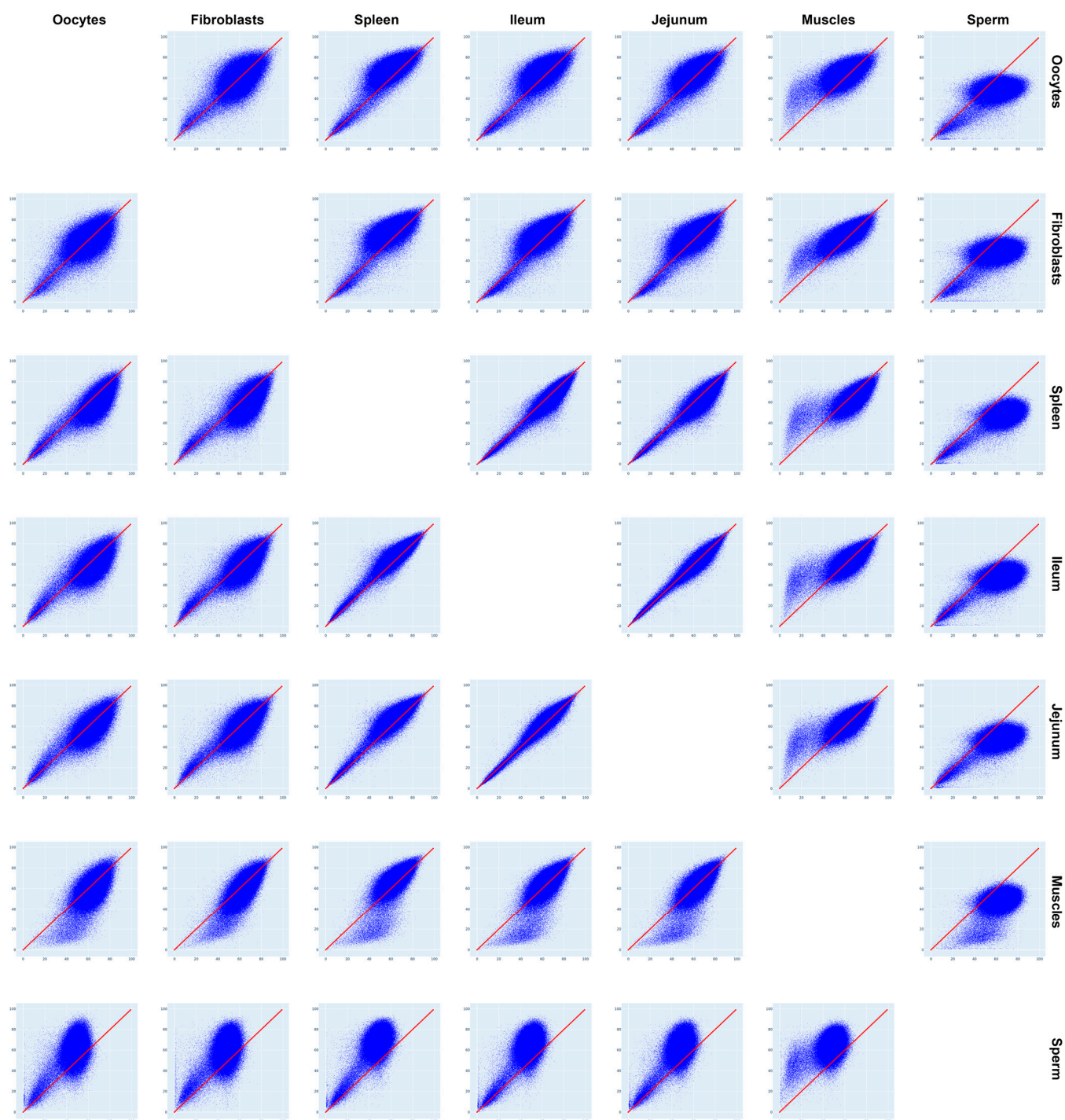
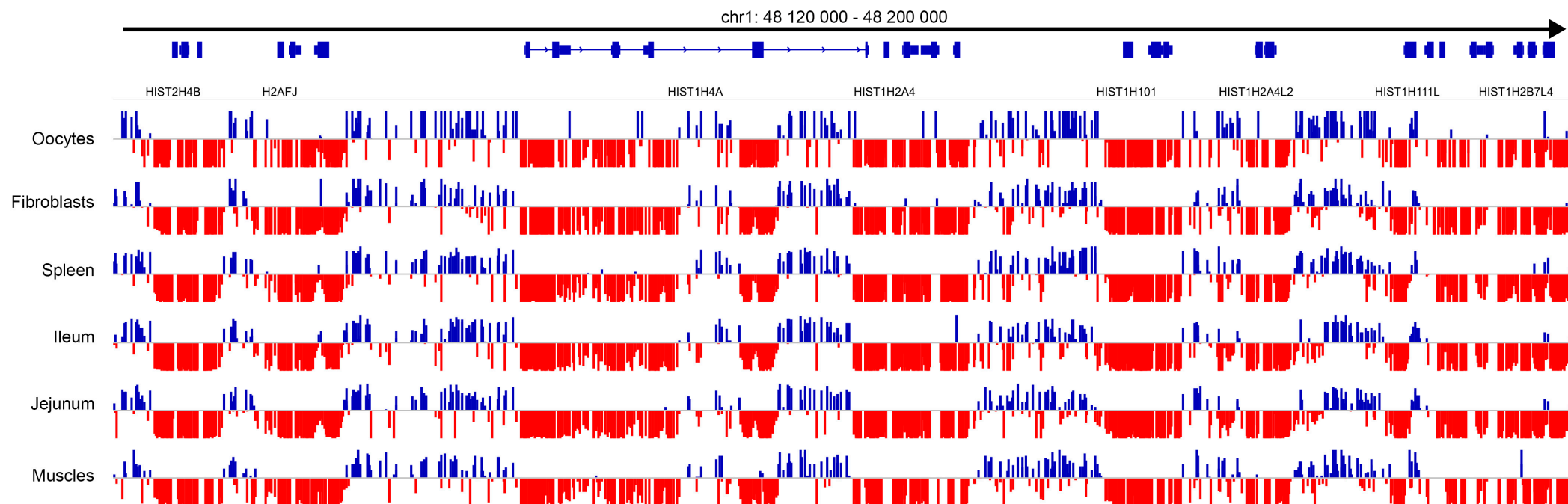


# Single-cell DNA methylation analysis of chicken lampbrush chromosomes

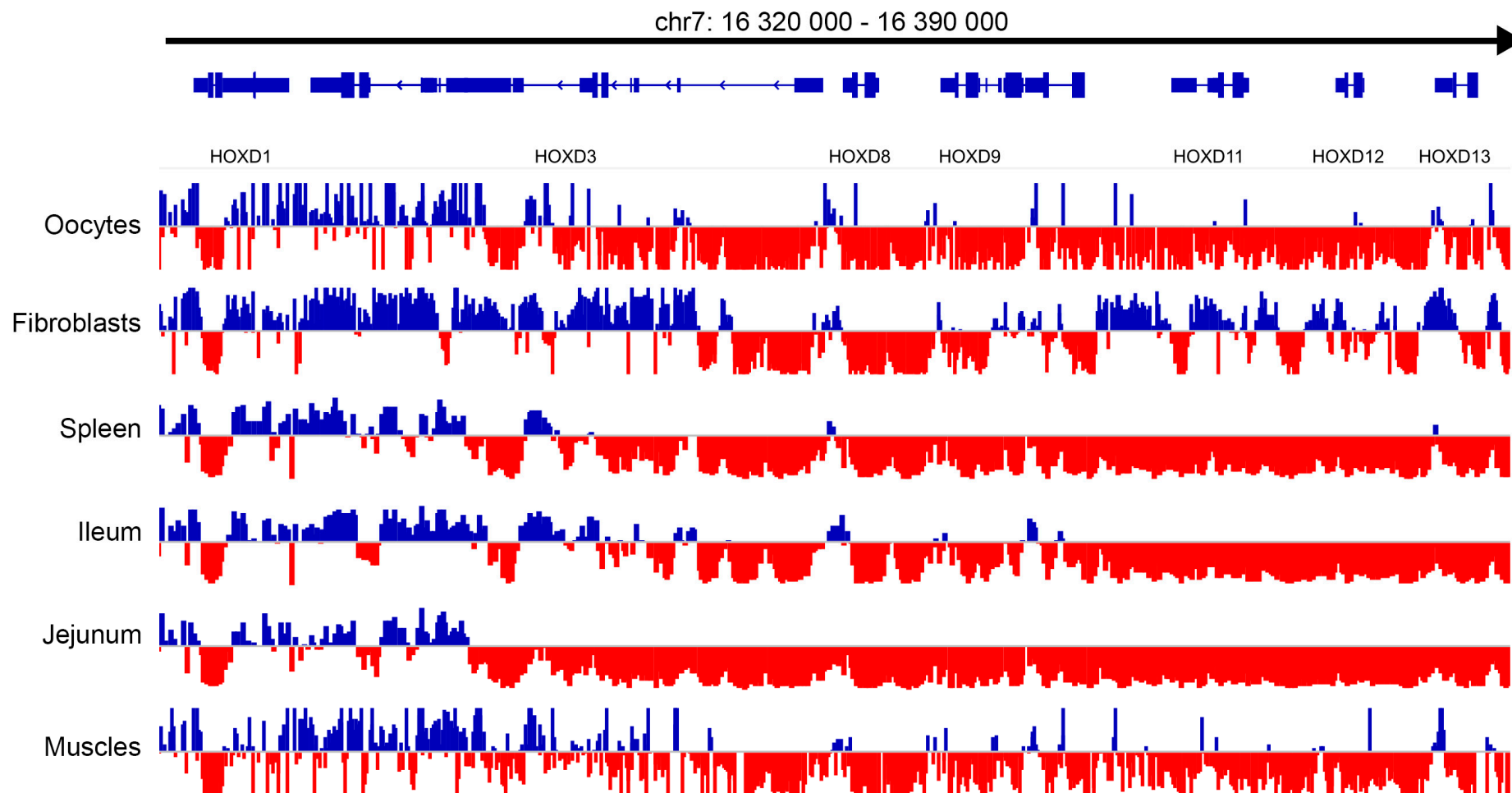
## Supplementary figures



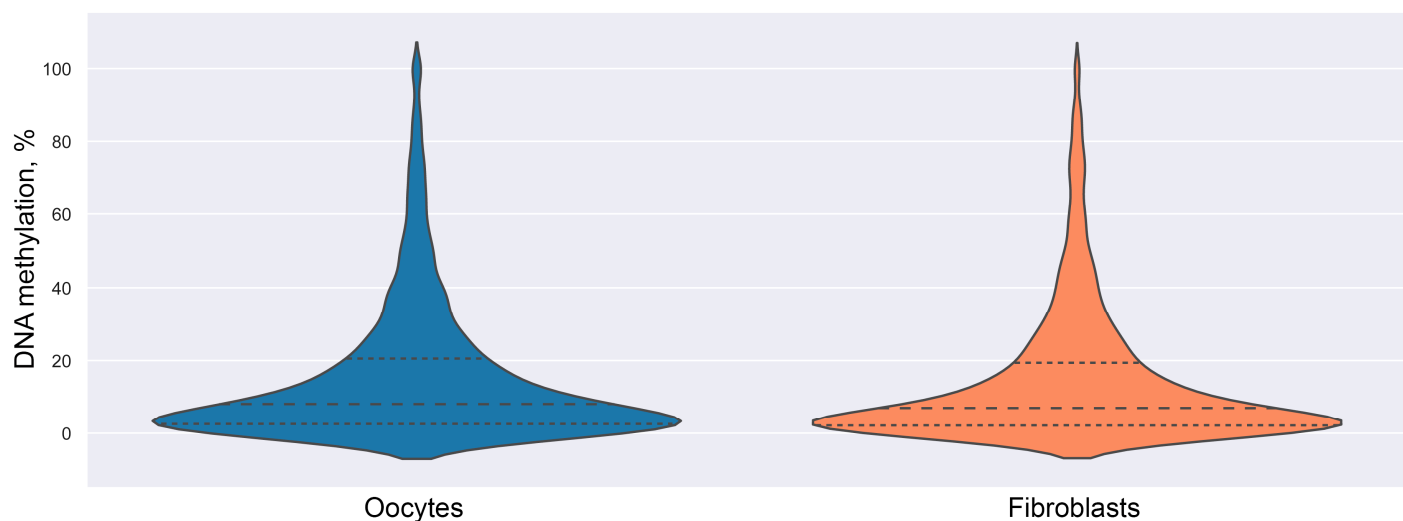
**Figure S1.** Pairwise methylation comparison of 5 kb genomic regions between different cell types. X and Y axes represent methylation levels in different cell types, each dot represents one 5 kb genomic bin.



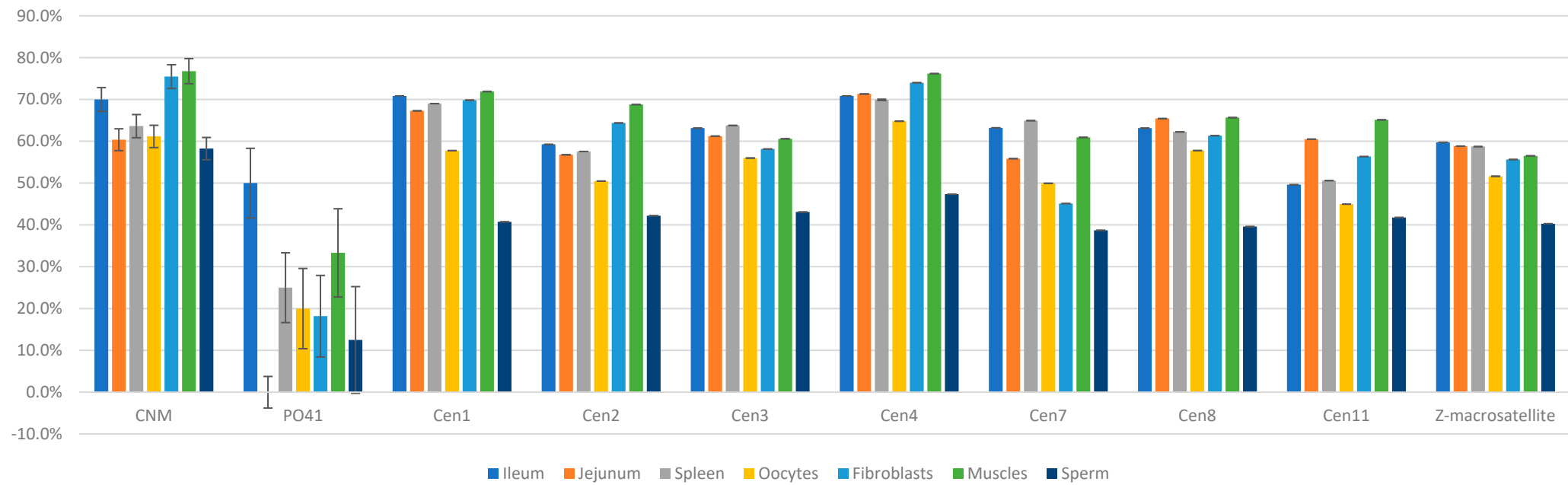
**Figure S2.** DNA methylation status of histone genes cluster in oocytes and other cell types.



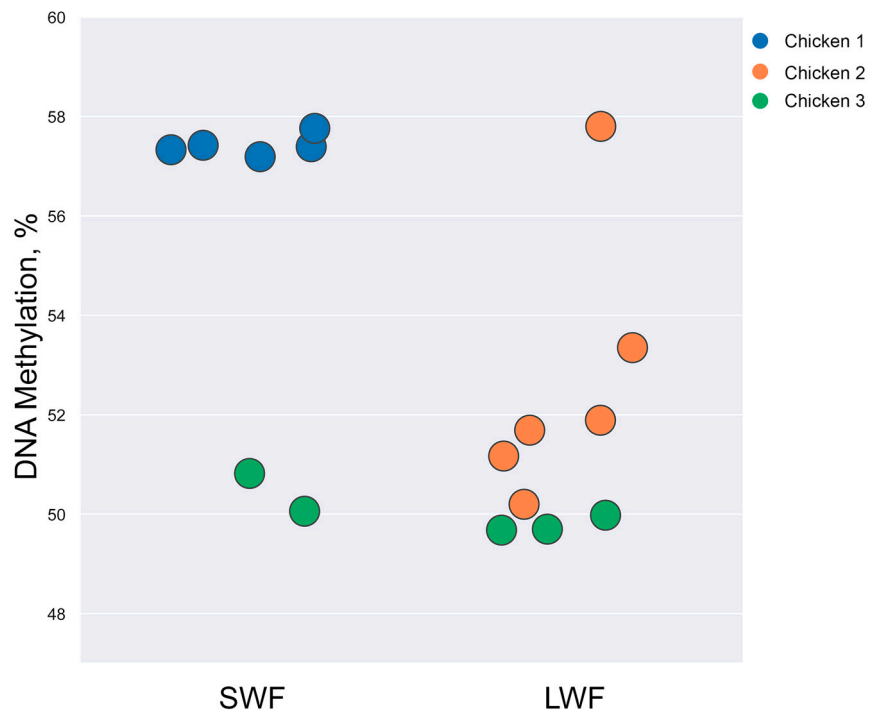
**Figure S3.** DNA methylation status of HoxD genes cluster in oocytes and other cell types.



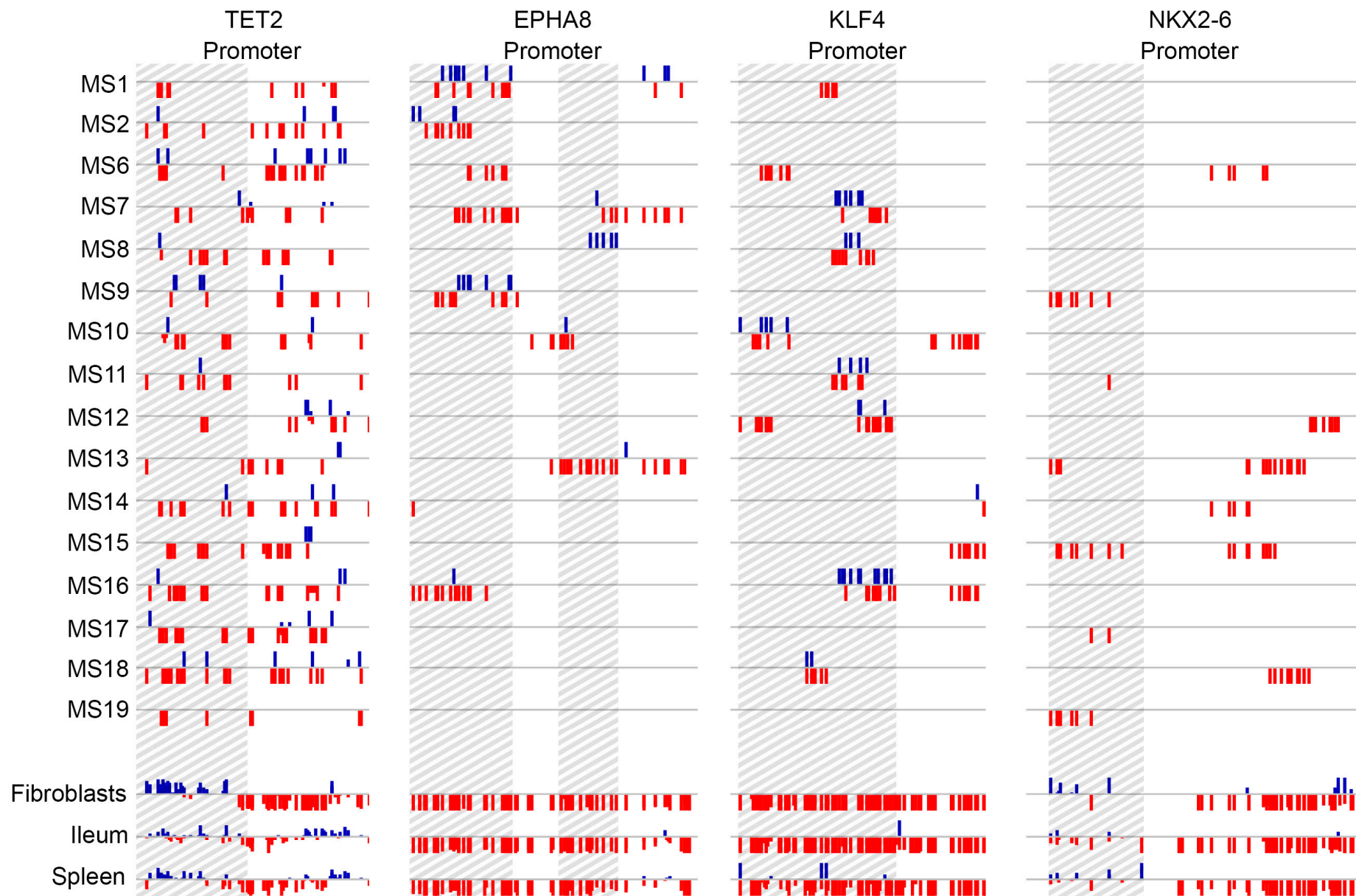
**Figure S4.** DNA methylation in CTCF binding sites – comparison between fibroblasts and diplotene oocytes. CTCF sites coordinates are taken from HD3 cell line ChIP-seq data (GSM1253766).



**Figure S5.** DNA methylation of avian-specific repeated elements across different chicken cell types.



**Figure S6.** DNA methylation of chicken oocytes from different stages and animals. Data shows no significant difference in methylation between SWF and LWF stages ( $p=0.11$ ).



**Figure S7.** Examples of differentially methylated regions within promoters identified using HMM, single-cell samples are shown. Differentially methylated regions are highlighted.