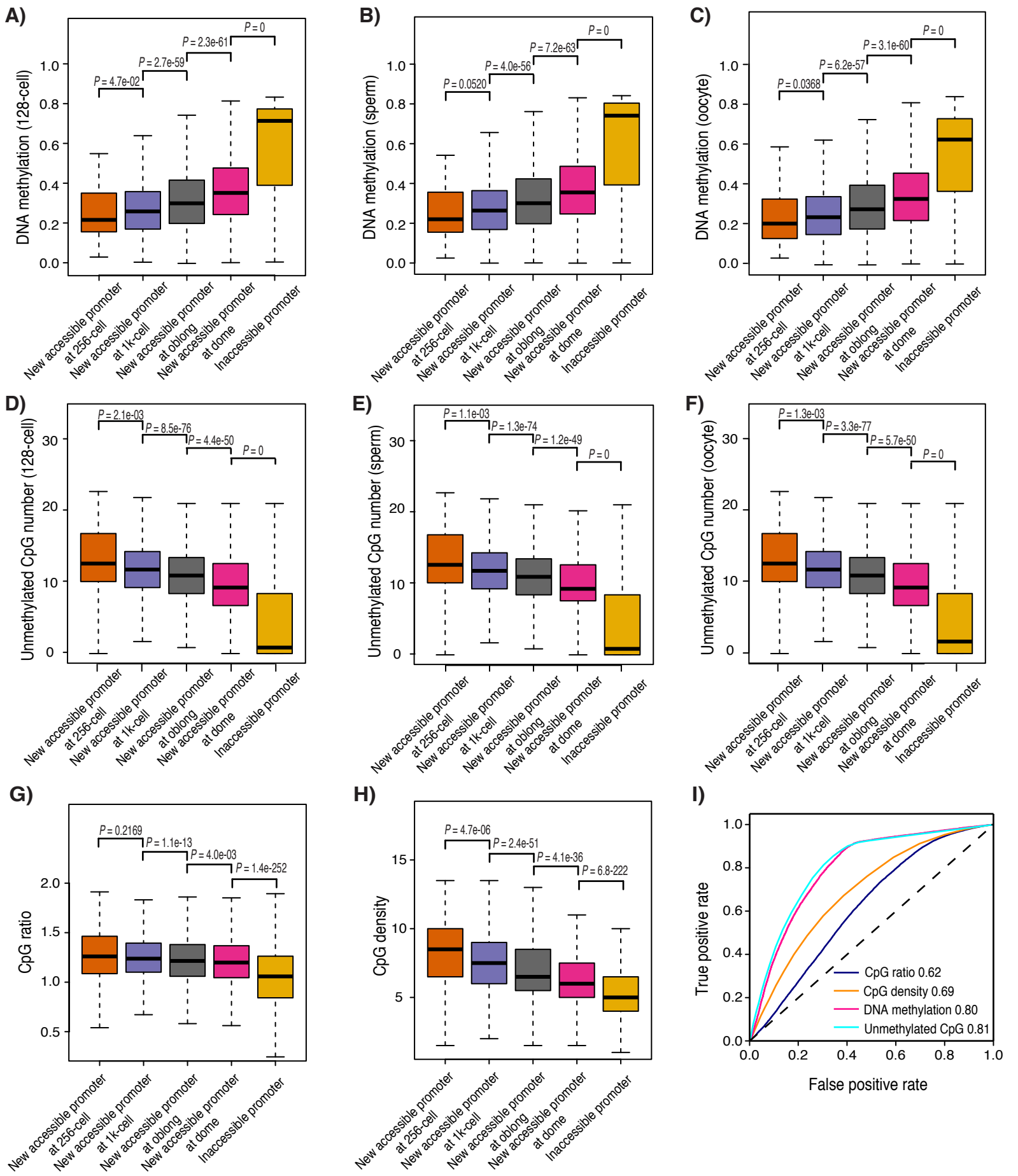


Supplemental_Fig_S4



Supplemental Figure S4. Epigenetic features for newly accessible promoters at each stage. (A-C) The boxplot shows the relationship between newly accessible promoters and DNA methylation levels of 128-cell stage (A), sperm (B) and oocyte (C). Earlier accessible promoters have lower DNA methylation levels. (D-F) The boxplot shows the relationship between newly accessible promoters and the largest unmethylated CpG numbers among 200-bp bins based on DNA methylation pattern in 128-cell stage (D), sperm (E) and oocyte (F). Earlier accessible promoters have a higher number of unmethylated CpGs. (G) The boxplot shows the relationship between newly accessible promoters and local maximum CpG ratio. Earlier accessible promoters have higher CpG ratio. (H) The boxplot shows the relationship between newly accessible promoters and local maximum CpG density (the largest CpG number per 100-bp among 200-bp bins). Earlier accessible promoters have higher CpG density. *p-values* were calculated by Wilcoxon test in A-H. (I) ROC curves show the prediction power of sequence features and epigenetics features on accessible promoters during ZGA. Genes are classified into two groups, based on with or without accessible promoters during ZGA. Epigenetic features show much stronger discriminatory powers to distinguish those two groups (AUC scores: 0.81 for number of unmethylated CpG, aqua; 0.80 for DNA methylation level, deep pink) than DNA sequence features (AUC scores: 0.62 for CpG ratio, navy; 0.69 for CpG density, dark orange).