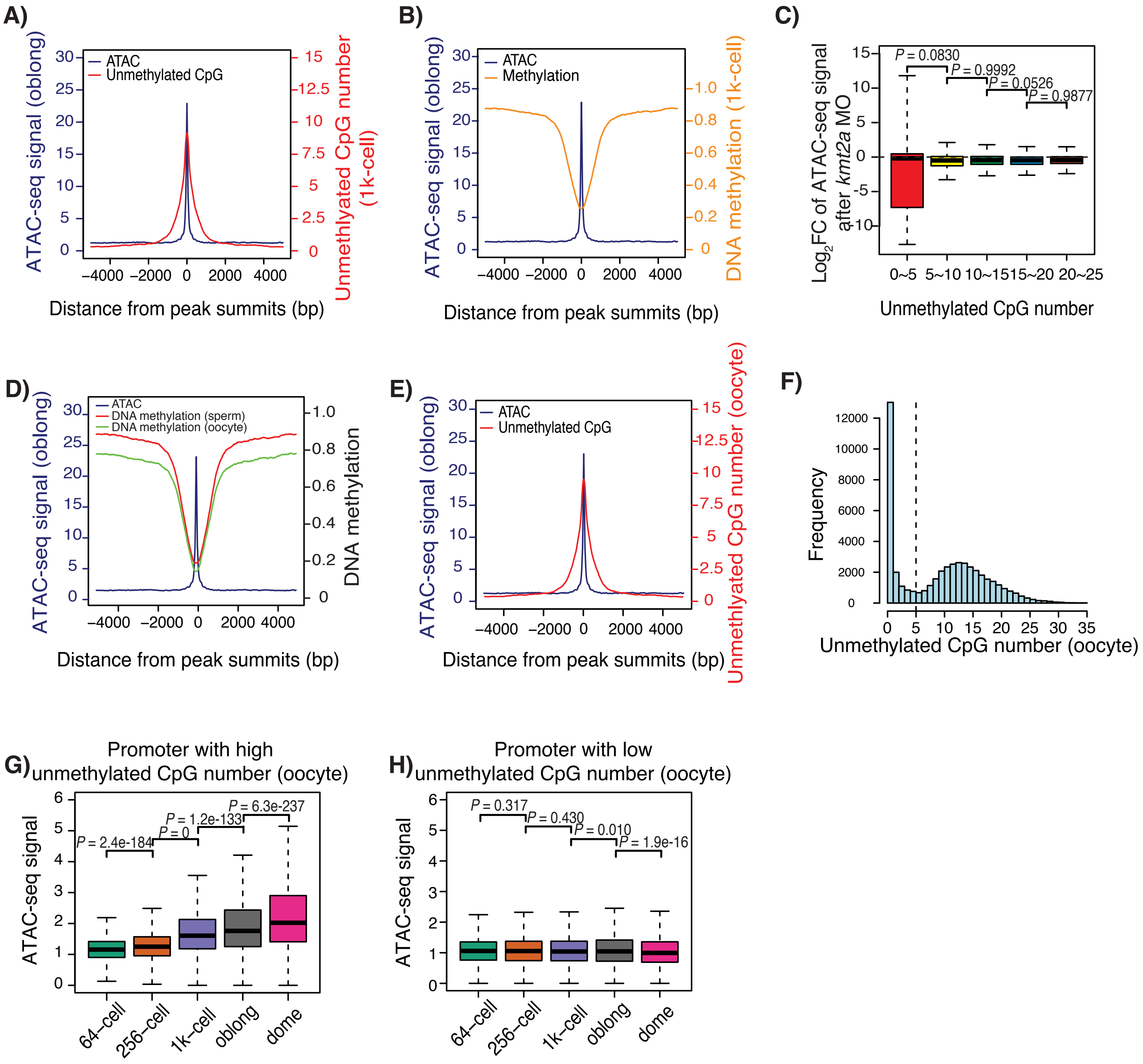
Supplemental_Fig_S6



Supplemental Figure S6. Unmethylated CpGs prime the emergence of accessible promoters. (A) The summit of the ATAC-seq signals (oblong) overlaps with the highest number of unmethylated CpG (1k-cell stage) at promoter regions. (B) The summit of the ATAC-seq signals (oblong) overlaps with the lowest DNA methylation level (1k-cell stage) at promoter regions. (C) The boxplot shows the $\log_2$-transformed fold change in the ATAC-seq signals at the 200 bp bins with largest numbers of unmethylated CpGs at each accessible promoter upon knockdown of *kmt2a*. The accessible promoters were grouped based on the locally largest numbers of unmethylated CpGs. *p-values* were calculated by Wilcoxon test. (D) The summit of the ATAC-seq signals overlaps with the lowest DNA methylation level (sperm and oocyte) at the promoters. (E) The summit of ATAC-seq signals overlaps with the highest number of unmethylated CpGs in the oocyte at the promoters. (F) All promoters are divided into two groups according to the locally largest numbers of unmethylated CpGs in oocyte (cut-off 5). (G) The boxplot shows the ATAC-seq signal during ZGA at the promoters with a high locally largest number of unmethylated CpGs in oocyte. *p-values* were calculated by Wilcoxon test. (H) The boxplot shows the ATAC-seq signal during ZGA at the promoters with a low locally largest number of unmethylated CpGs in oocyte. *p-values* were calculated by Wilcoxon test. The ATAC-seq peaks in A-E are newly emerged ones in 1k-cell or oblong stages.