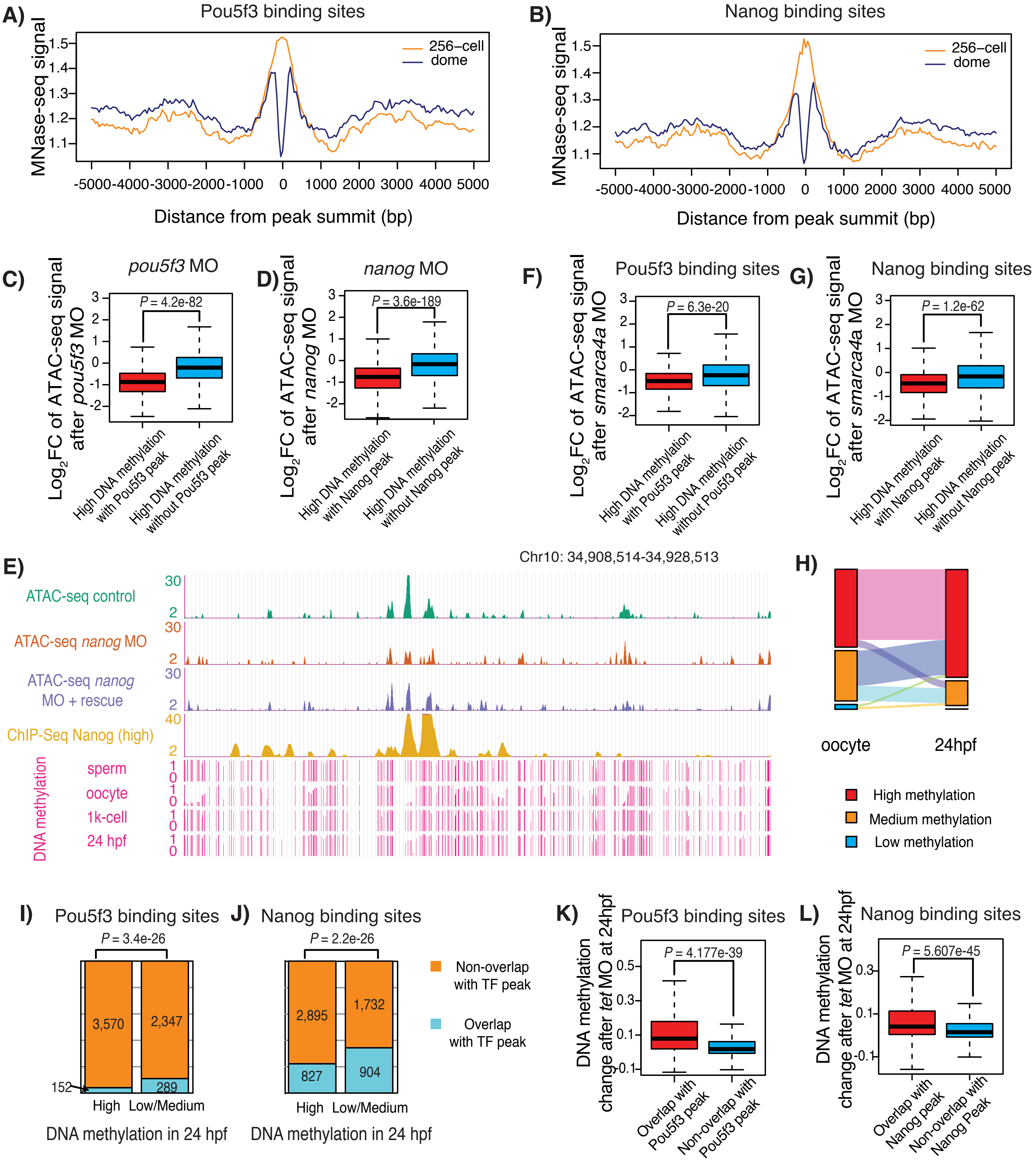
Supplemental_Fig_S7



Supplemental Figure S7. Transcription factors modulate accessible distal regions with high methylation levels. (A) The average MNase-seq signals of 256-cell (dark orange) and dome (navy) stage show the formation of a clear nucleosome depletion pattern during ZGA at the Pou5f3 binding sites. (B) The average MNase-seq signals of 256-cell (dark orange) and dome (navy) stage show the formation of a clear nucleosome depletion pattern during ZGA at the Nanog binding sites. (C) The boxplot shows the $\log_2$-transformed fold change of the ATAC-seq signals at the hypermethylated regions with or without Pou5f3 binding upon knockdown of *pou5f3*. *p-values* were calculated by Wilcoxon test. (D) The boxplot shows the $\log_2$-transformed fold change of the ATAC-seq signals at the hypermethylated regions with or without Nanog binding upon knockdown of *nanog*. *p-values* were calculated by Wilcoxon test. (E) The genome browser view shows the ATAC-seq signals at a representative region as an example of decreasing accessibility at highly methylated distal regions upon knockdown of *nanog* and the partial recovery after co-injections with MO and the *nanog* mRNA. DNA methylation levels at sperm, oocyte, 1k-cell stage and 24 hpf stage are also shown. (F) The boxplot shows the $\log_2$-transformed fold change of the ATAC-seq signals at the hypermethylated regions with or without Pou5f3 binding upon knockdown of *smarca4a*. *p-values* were calculated by Wilcoxon test. (G) The boxplot shows the $\log_2$-transformed fold change of the ATAC-seq signals at the hypermethylated regions with or without Nanog binding upon knockdown of *smarca4a*. *p-values* were calculated by Wilcoxon test. (H) The alluvial plot shows the oocyte-like DNA medium or low methylation level at the distal regions at 24 hpf. (I) The bar plot shows that the demethylated DNA distal regions at 24 hpf are significantly enriched at the binding sites of Pou5f3. *p-values* were calculated by Chi-squared test. (J) The bar plot shows that the DNA demethylated distal regions at 24 hpf are significantly enriched at the binding sites of Nanog. *p-values* were calculated by Chi-squared test. (K) The boxplot shows the DNA methylation level at the distal accessible regions with or without Pou5f3 binding at 24 hpf upon knockdown of *tet*. *p-values* were calculated by Wilcoxon test. (L) The boxplot shows the DNA methylation level at the distal accessible regions with or without Nanog binding at 24 hpf upon knockdown of *tet*. *p-values* were calculated by Wilcoxon test.