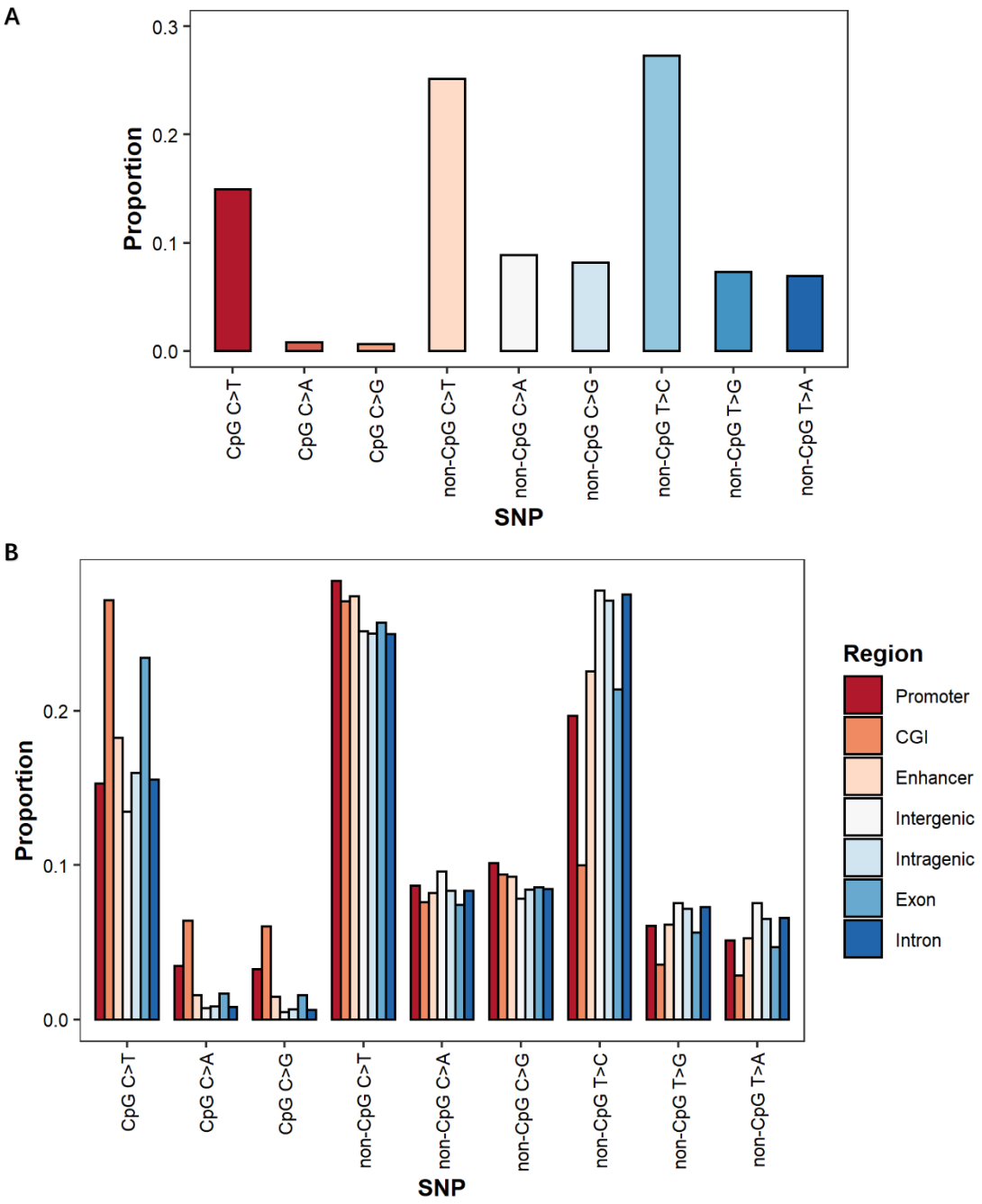


Figure S1. Distribution of all SNPs for each type of mutation in the human genome.

CpG M>N is an M>N mutation at a CpG site, and non-CpG M>N is an M>N mutation at a non-CpG site. (A) The proportion of all SNPs for each type of mutation in the human genome. (B) The proportion of SNPs for each type of mutation in different genomic regions in the human genome.

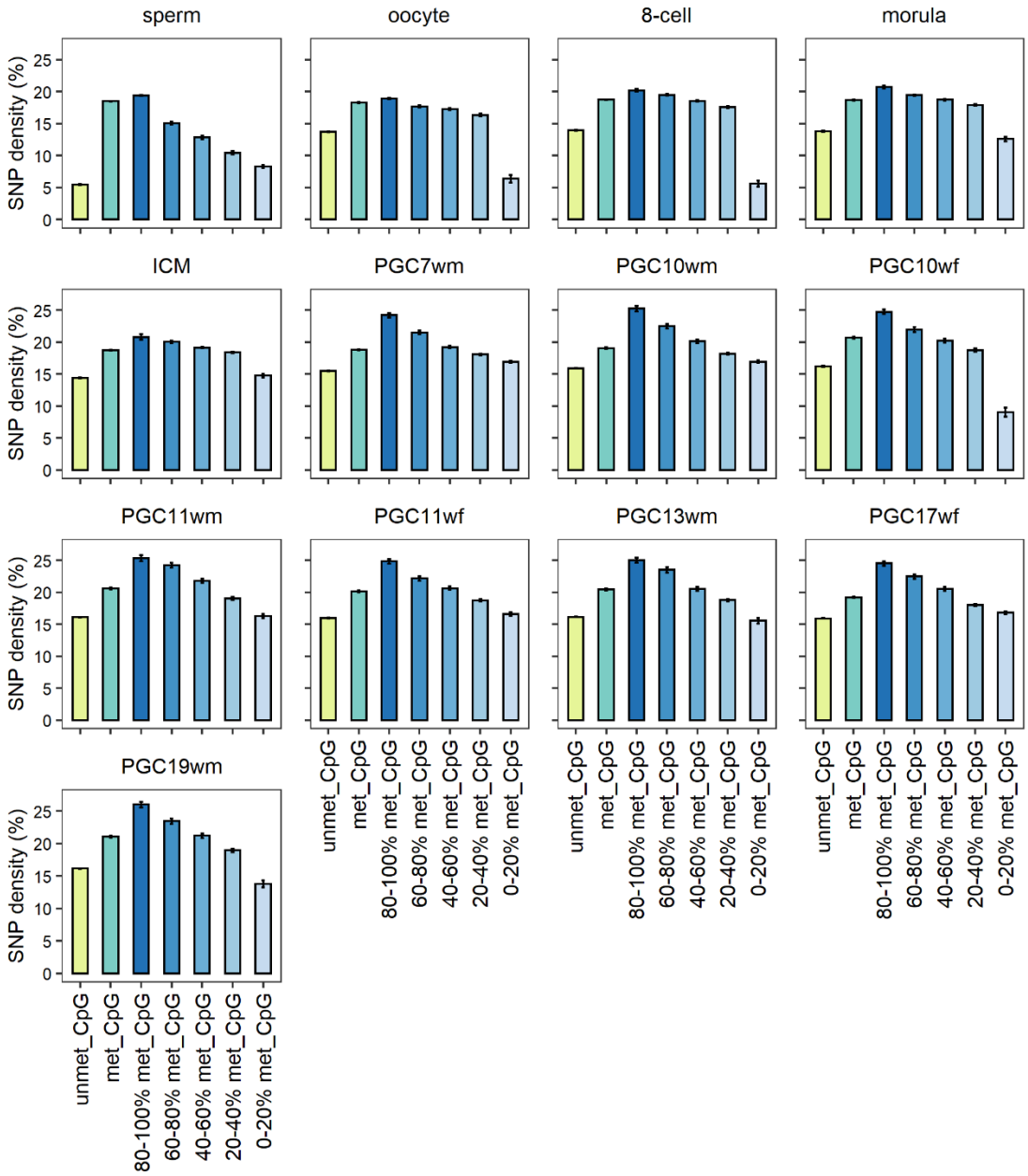


Figure S2. The mutation rates for all CpG sites, unmethylated CpG sites and methylated CpG sites during developmental stages.

The single-site methylated CpG levels are further classified into five different DNA methylation level categories (80-100%, 60-80%, 40-60%, 20-40%, and 0-20%). The Y-axis shows the mutation rate computed by the SNP density at CpG sites.

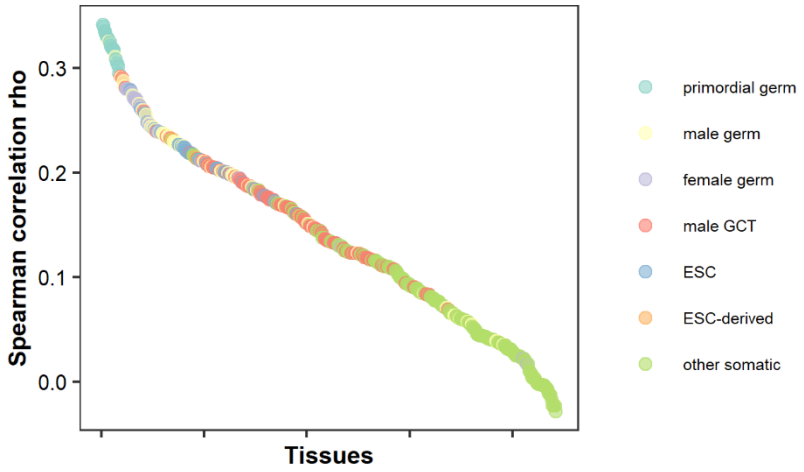
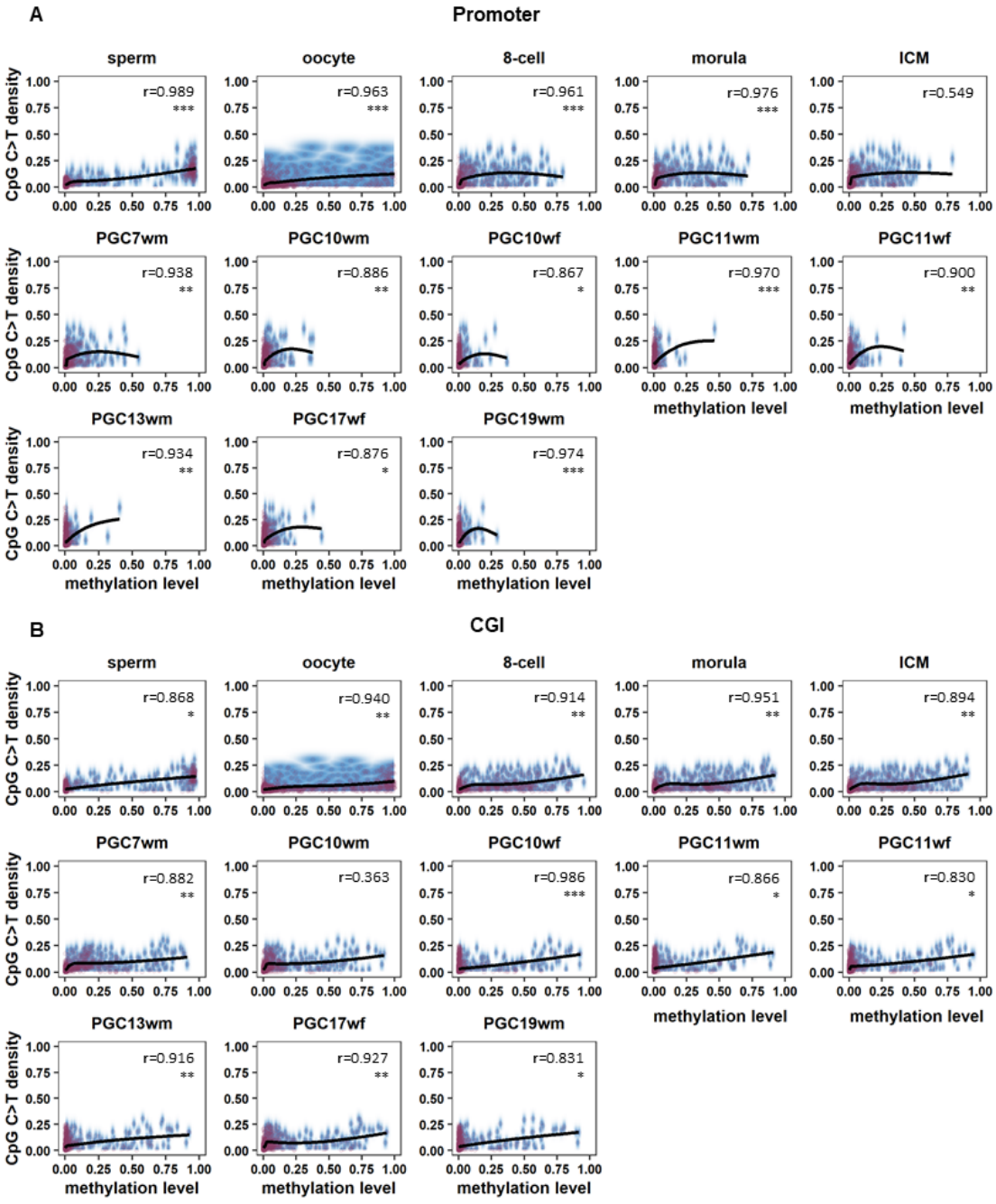
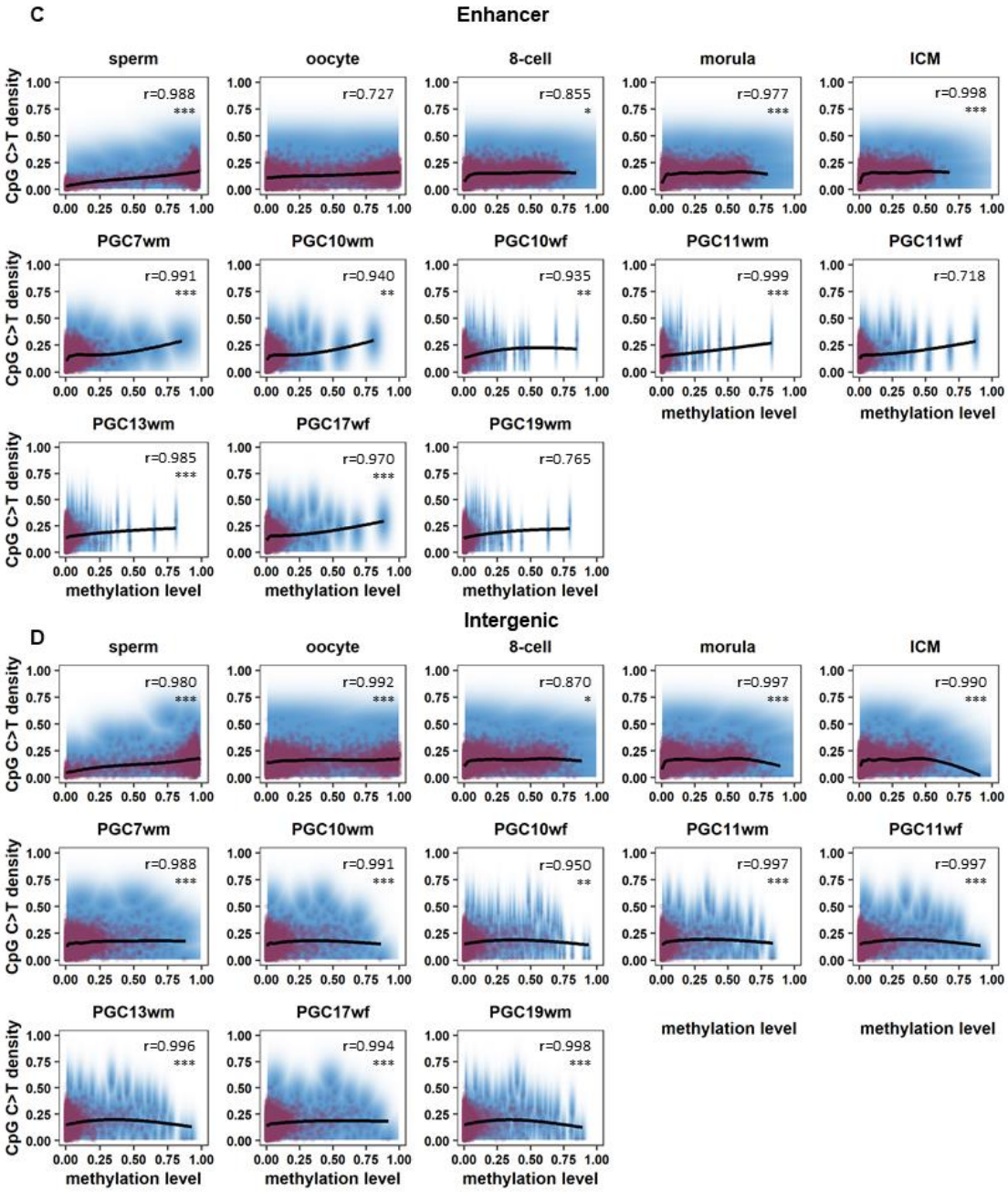
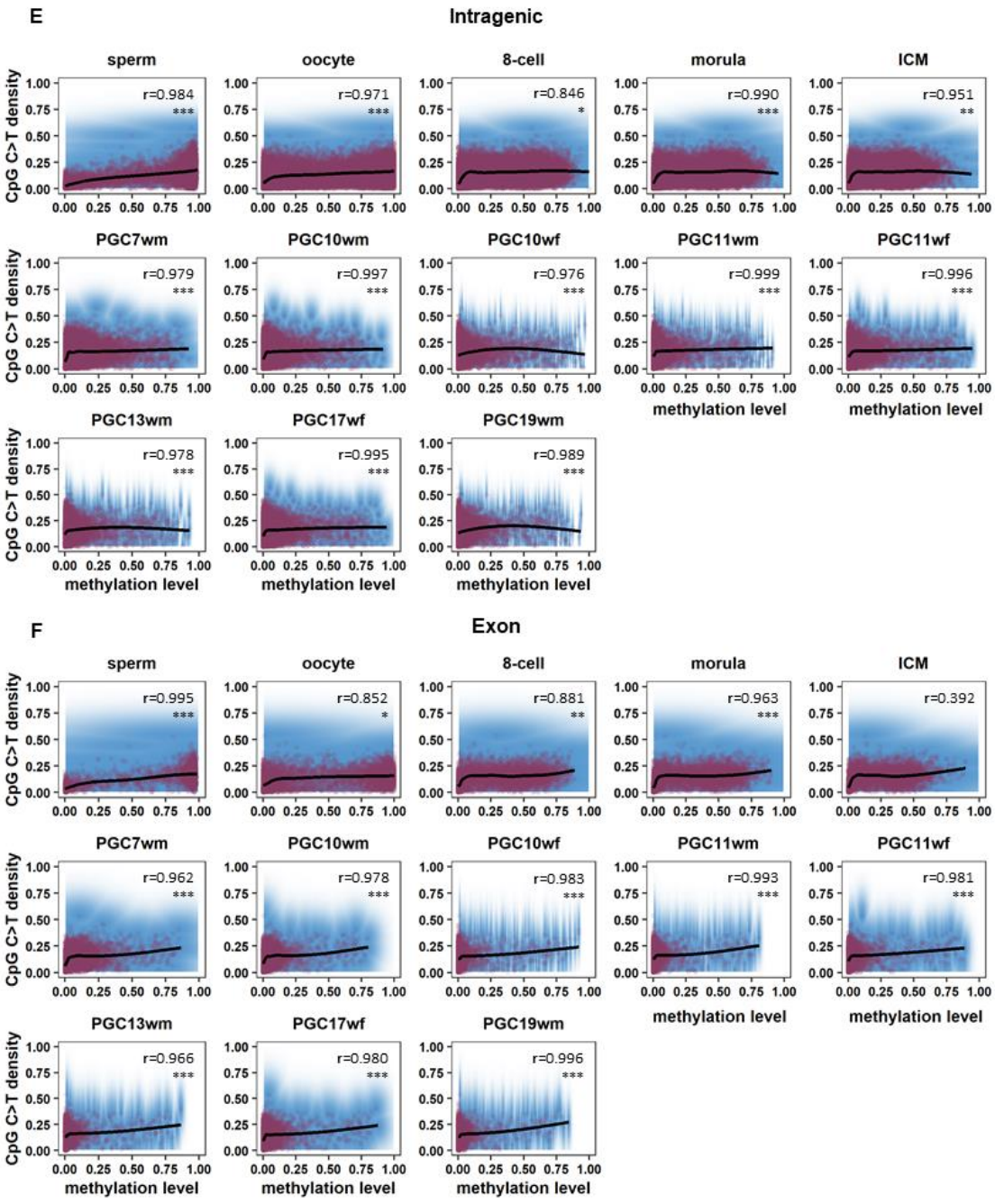


Figure S3. Spearman correlations between gene expression and the $CpG_{O/E}$ ratio in the promoter regions with high tissue differentiation.

Each of the 442 tissue samples is represented by a single dot. The color indicates a specific tissue type. ESC: embryonic stem cells. GCT: germ cell tumors. Dots are ordered from left to right by the correlation (rho value).


A
Promoter
sperm
r=0.989
***
oocyte
r=0.963
***
8-cell
r=0.961
***
morula
r=0.976
***
ICM
r=0.549
PGC7wm
r=0.938
**
PGC10wm
r=0.886
**
PGC10wf
r=0.867
*
PGC11wm
r=0.970
***
PGC11wf
r=0.900
**
PGC13wm
r=0.934
**
PGC17wf
r=0.876
*
PGC19wm
r=0.974
***
CpG C>T density
methylation level
B
CGI
sperm
r=0.868
*
oocyte
r=0.940
**
8-cell
r=0.914
**
morula
r=0.951
**
ICM
r=0.894
**
PGC7wm
r=0.882
**
PGC10wm
r=0.363
PGC10wf
r=0.986
***
PGC11wm
r=0.866
*
PGC11wf
r=0.830
*
PGC13wm
r=0.916
**
PGC17wf
r=0.927
**
PGC19wm
r=0.831
*
CpG C>T density
methylation level


C
Enhancer
sperm
oocyte
8-cell
morula
ICM
r=0.988
***
r=0.727
r=0.855
*
r=0.977
***
r=0.998
***
PGC7wm
PGC10wm
PGC10wf
PGC11wm
PGC11wf
r=0.991
***
r=0.940
**
r=0.935
**
r=0.999
***
r=0.718
PGC13wm
PGC17wf
PGC19wm
r=0.985
***
r=0.970
***
r=0.765
CpG C>T density
methylation level
D
Intergenic
r=0.980
***
r=0.992
***
r=0.870
*
r=0.997
***
r=0.990
***
r=0.988
***
r=0.991
***
r=0.950
**
r=0.997
***
r=0.997
***
r=0.996
***
r=0.994
***
r=0.998
***


E
Intragenic
sperm
r=0.984
***
oocyte
r=0.971
***
8-cell
r=0.846
*
morula
r=0.990
***
ICM
r=0.951
**
PGC7wm
r=0.979
***
PGC10wm
r=0.997
***
PGC10wf
r=0.976
***
PGC11wm
r=0.999
***
PGC11wf
r=0.996
***
PGC13wm
r=0.978
***
PGC17wf
r=0.995
***
PGC19wm
r=0.989
***
CpG C>T density
methylation level
F
Exon
sperm
r=0.995
***
oocyte
r=0.852
*
8-cell
r=0.881
**
morula
r=0.963
***
ICM
r=0.392
PGC7wm
r=0.962
***
PGC10wm
r=0.978
***
PGC10wf
r=0.983
***
PGC11wm
r=0.993
***
PGC11wf
r=0.981
***
PGC13wm
r=0.966
***
PGC17wf
r=0.980
***
PGC19wm
r=0.996
***
CpG C>T density
methylation level

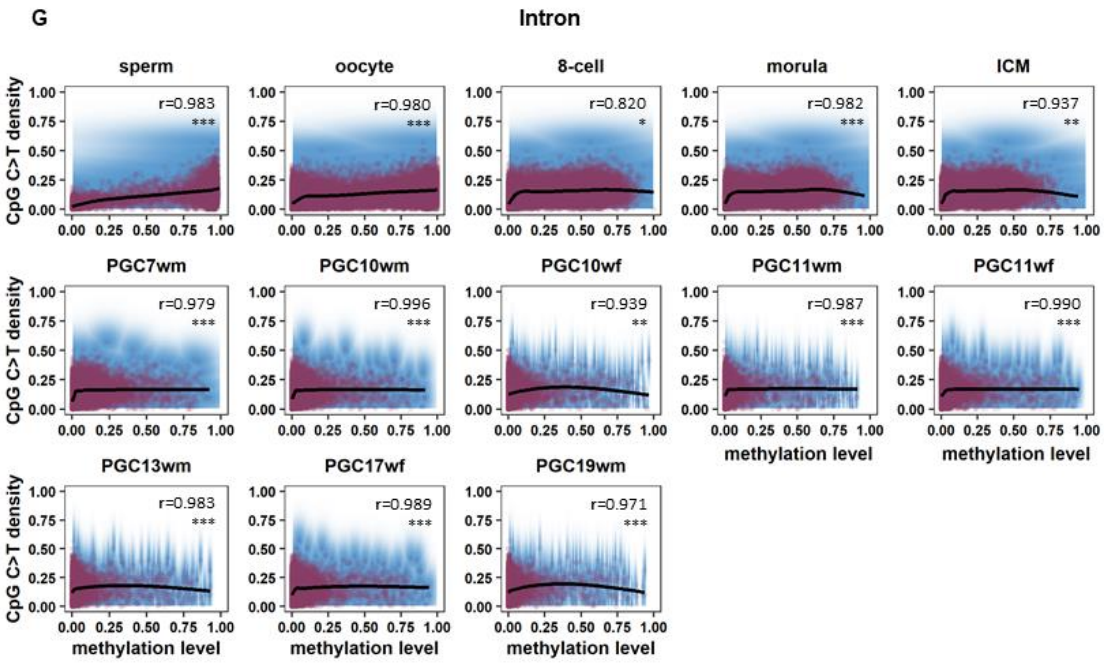


Figure S4. Distribution of methylation level and CpG C>T density of 1-kb windows in different genomic regions during germline development.

(A)-(G) stands for different genomic regions, including promoter, CGI, enhancer, intergenic, intragenic, exon and intron. The X-axis is the methylation level of 1-kb window. The Y-axis is the mutation rate computed by the C>T density at CpG sites. Each purple dot represents a 1-kb window. The blue shadow is calculated by kernel density.

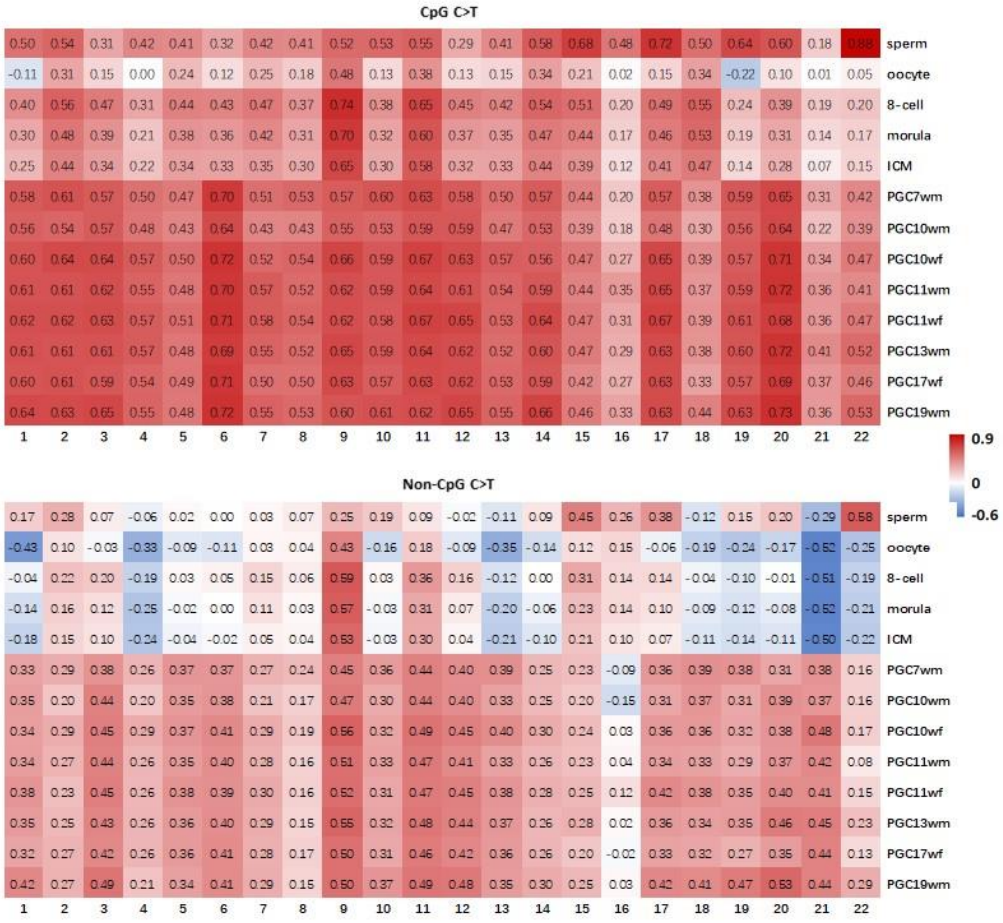


Figure S5. Heatmap of Spearman correlation between methylation and C>T mutation rates on CpG and Non-CpG sites in different chromosomes during germline development

The window size was 1Mb. The numbers on X-axis refer to the chromosome number.