

# DNA methylation regulates discrimination of enhancers from promoters through a H3K4me1-H3K4me3 seesaw mechanism

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## Supplementary material captions

**Fig. S1 Correlation of chromatin marks and gene transcription regulators with DNA methylation in distal putative enhancers.** The distal putative enhancers (that are located outside gene coding regions, and have a distance of minimum 3 kb with the nearest TSS) are split into **(a)** DNA hypermethylated (DNA methylation  $> 0.5$ ) and **(b)** DNA hypomethylated (DNA methylation  $\leq 0.5$ ) groups. In each DNA methylation group, distal enhancers are classified based on their genomic location (rows). For each class, Spearman's rank correlations between DNA methylation of ESCs and 9 different chromatin marks, the repressive histone 3 (H3), the gene transcription marker RNA polymerase 2 (Pol2), the enhancer marker histone acetyltransferase P300, and insulator marker CCCTC-binding factor are presented in columns. Red, white and blue colors show positive, null and negative correlations, respectively.

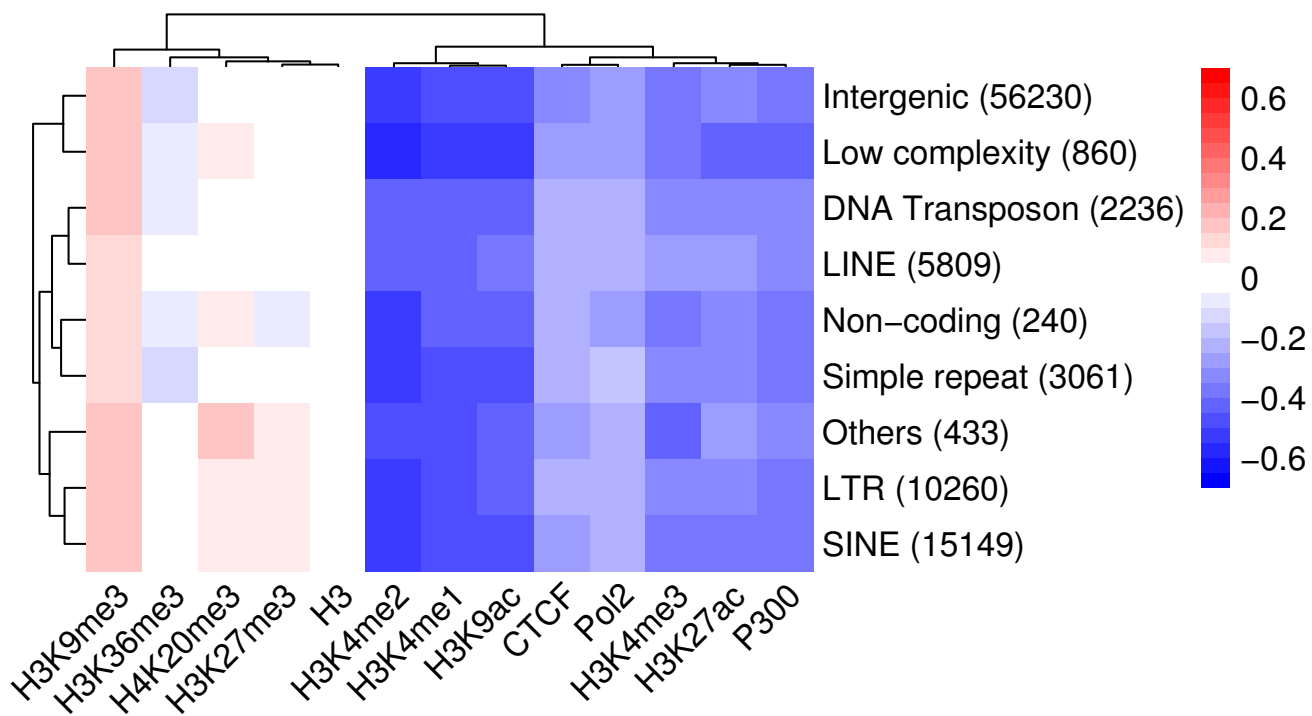
**Fig. S2 Correlation of chromatin marks and gene transcription regulators with DNA methylation in 200 bp windows.** The putative enhancers and promoter are split into **(a)** DNA hypermethylated (DNA methylation  $> 0.5$ ) and **(b)** DNA hypomethylated (DNA methylation  $\leq 0.5$ ) groups. The DNA methylation and enrichment of chromatin marks are measured within a 200 bp window ( $\pm 100$  bp) around the TSS or putative enhancer location.

**Fig. S3 Correlation of chromatin marks and gene transcription regulators with DNA methylation in 400 bp windows.** The putative enhancers and promoter are split into **(a)** DNA hypermethylated (DNA methylation  $> 0.5$ ) and **(b)** DNA hypomethylated (DNA methylation  $\leq 0.5$ ) groups. The DNA methylation and enrichment of chromatin marks are measured within a 400 bp window ( $\pm 200$  bp) around the TSS or putative enhancer location.

**Fig S4. Proximal and distal H3K27me3 and H3K4me3 cell-type specific peaks in WT and *Dnmt1* KO MEF cells.**

Figure S1

**a**



**b**

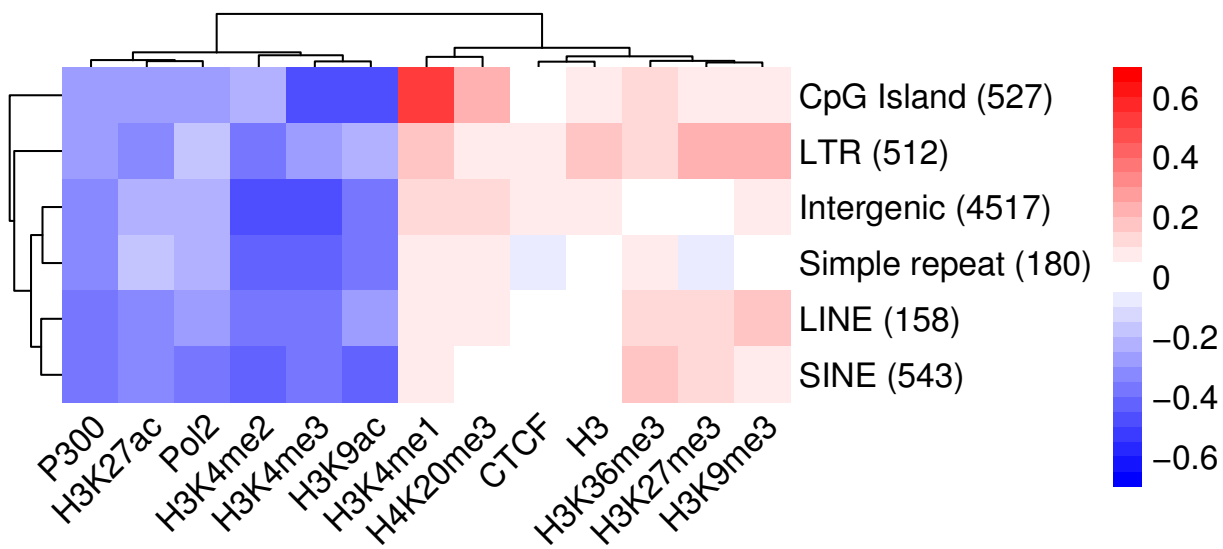
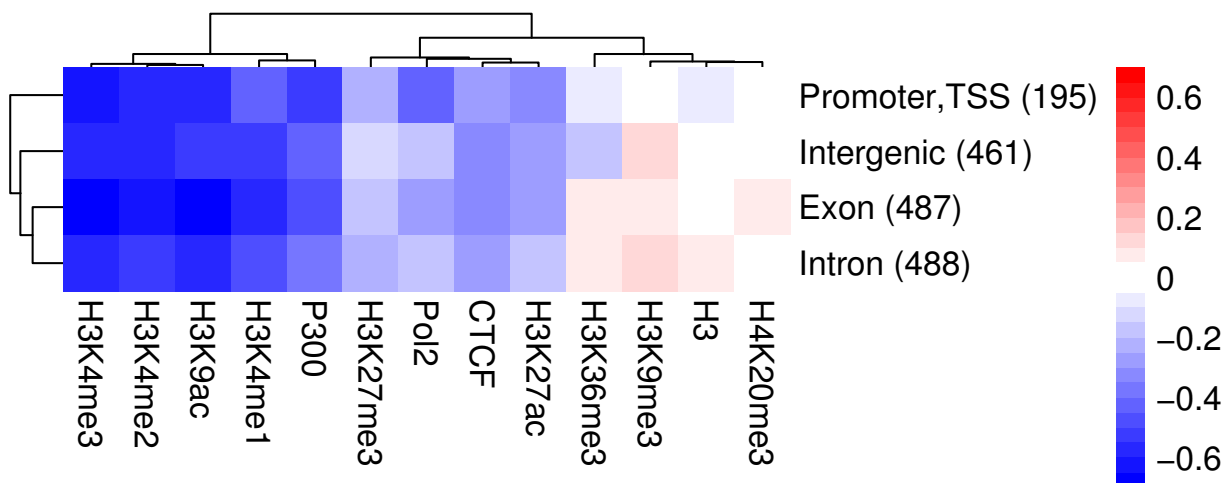


Figure S2

**a**

Hypermethylated (DNA Methylation > 50%)



**b**

Hypomethylated (DNA Methylation ≤ 50%)

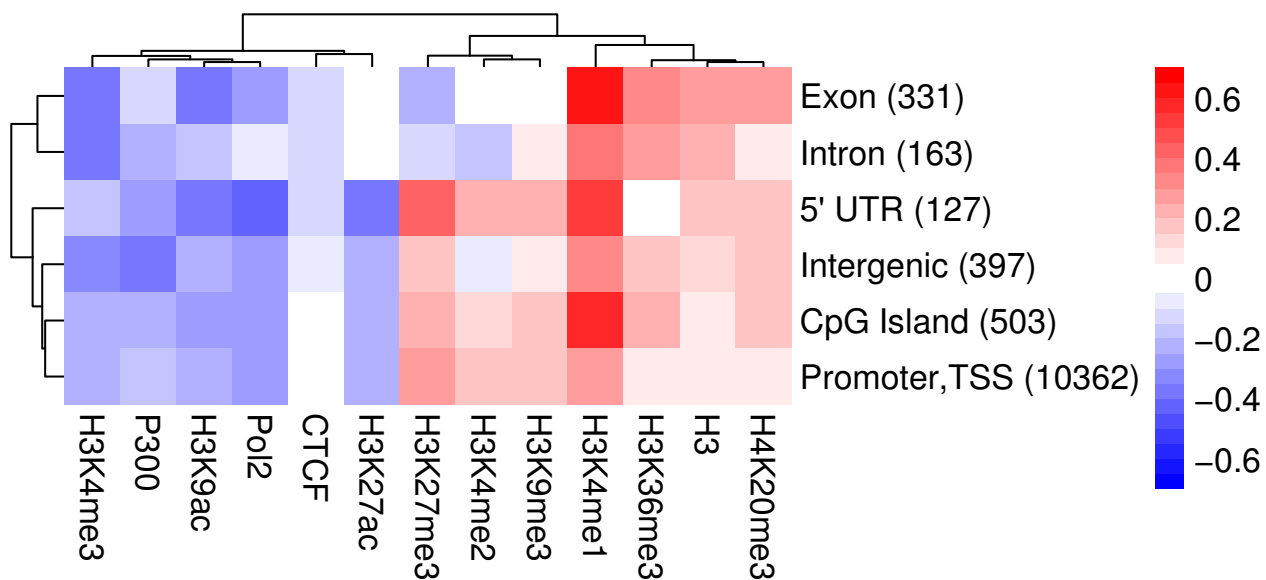
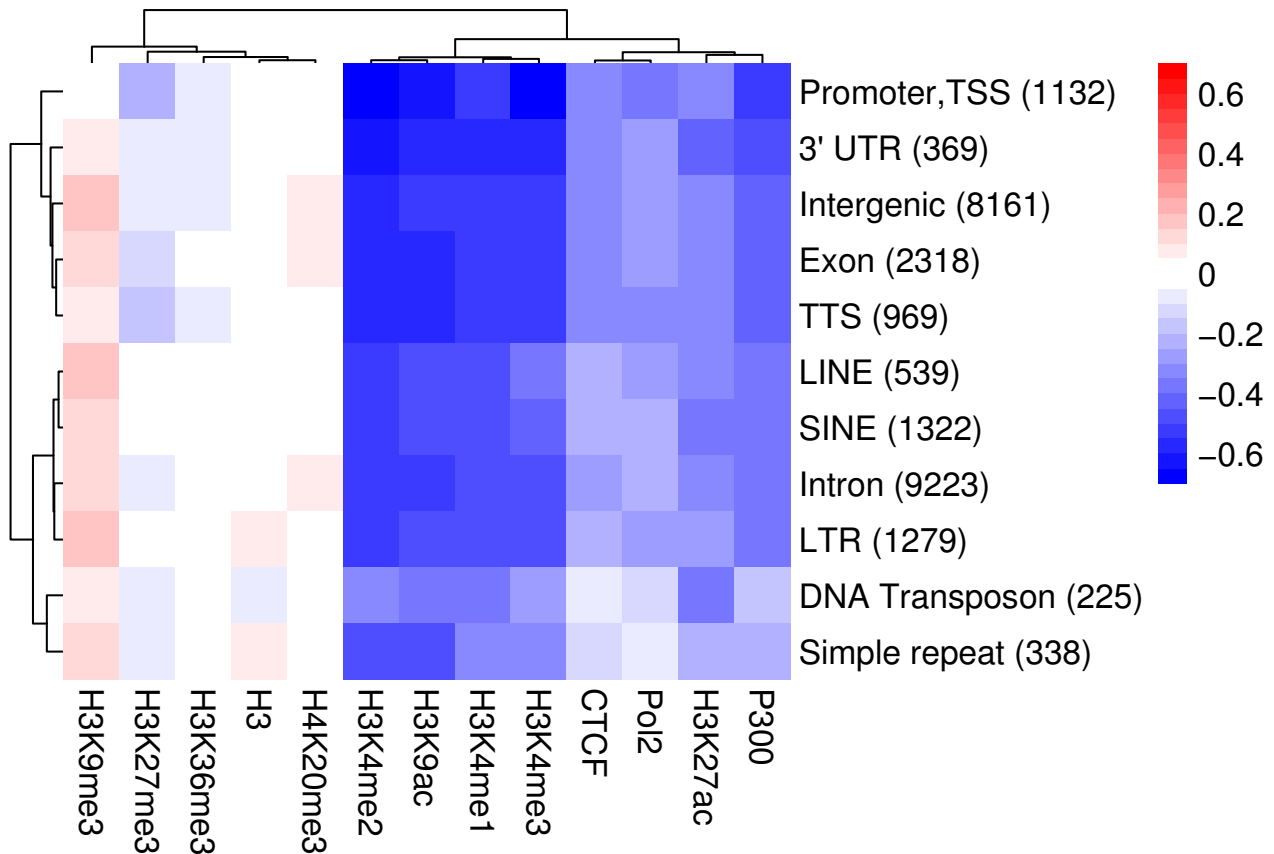


Figure S3

**a**

Hypermethylated (DNA Methylation > 50%)



**b**

Hypomethylated (DNA Methylation  $\leq$  50%)

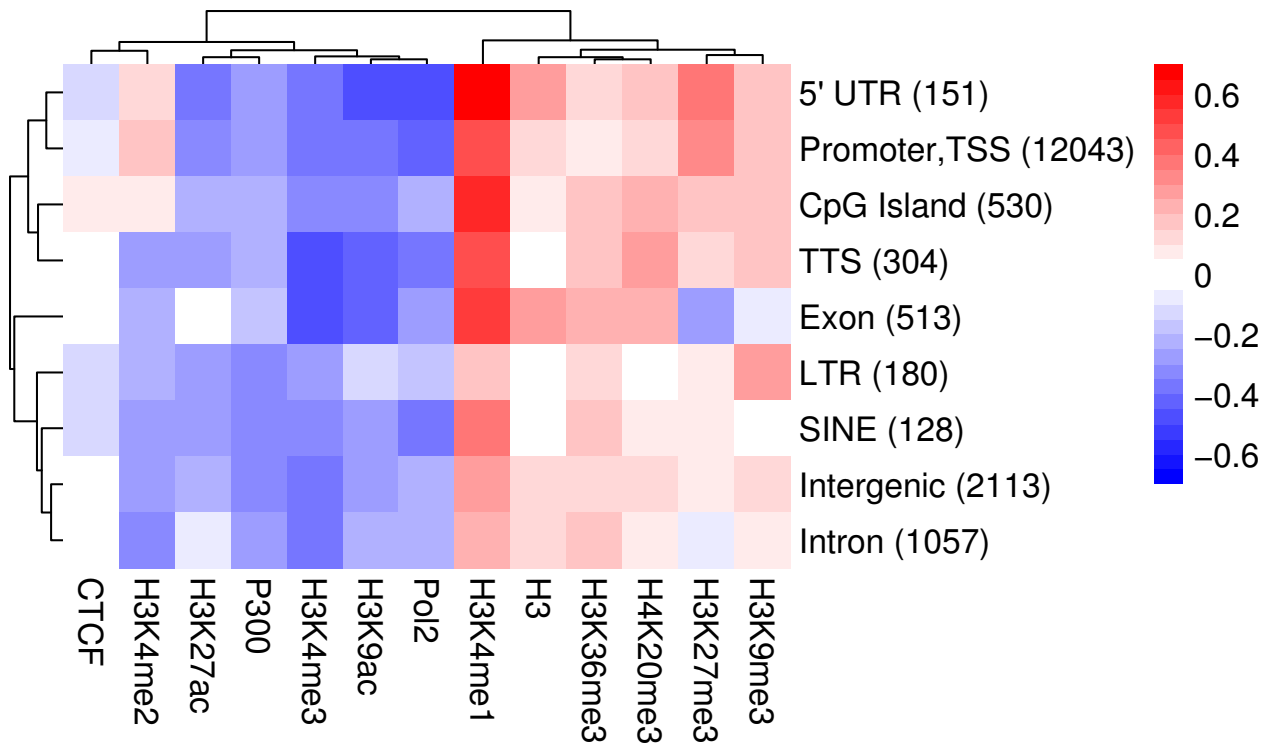


Figure S4

