SUPPLEMENTARY FIGURES:

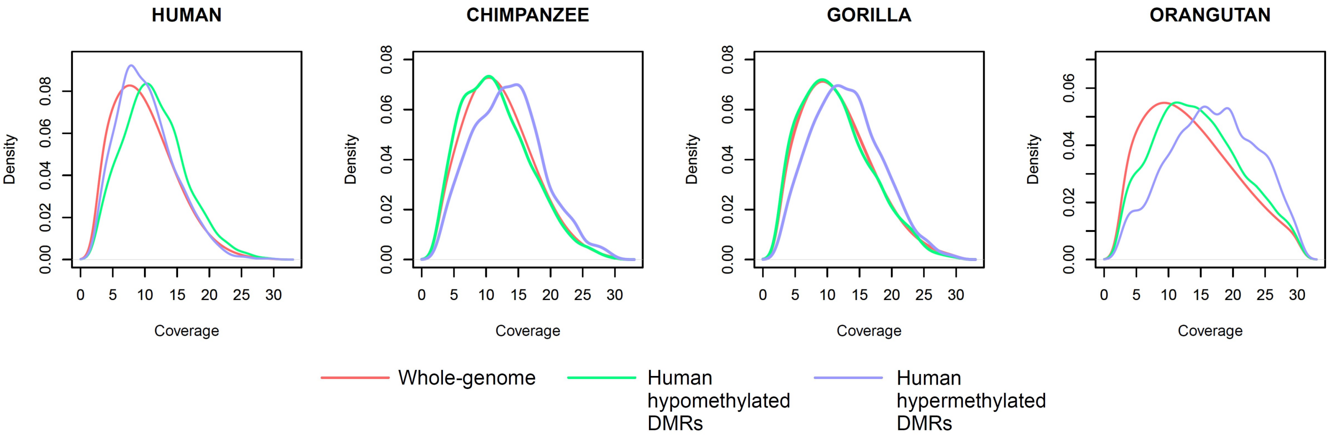

Figure S1: Coverage distribution within human hypo- and hypermethylated DMRs and across the whole genome in the different samples.

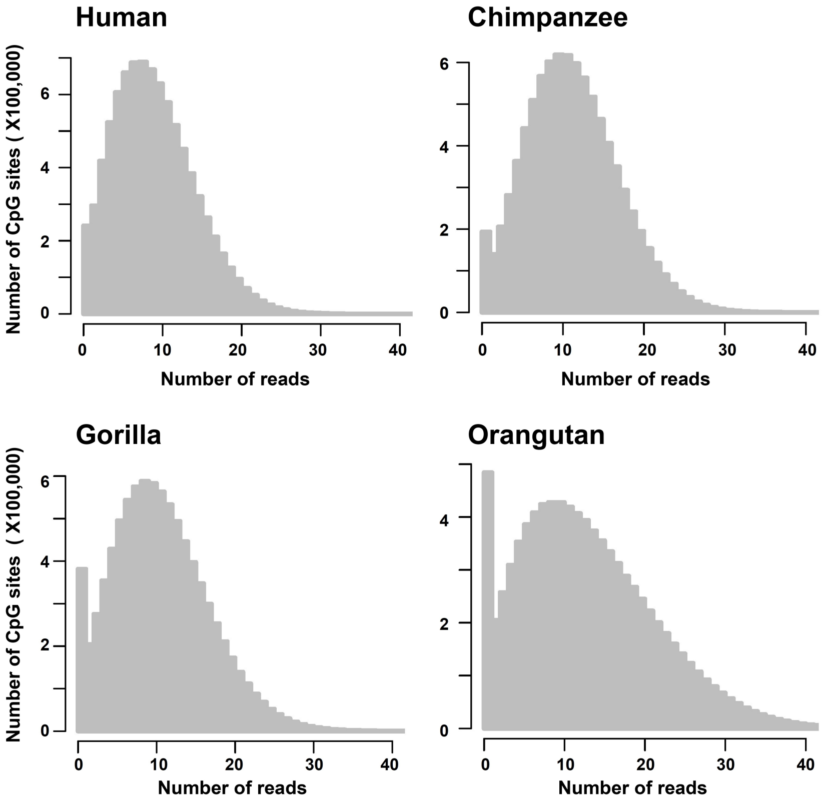

Figure S2: Read coverage across samples.

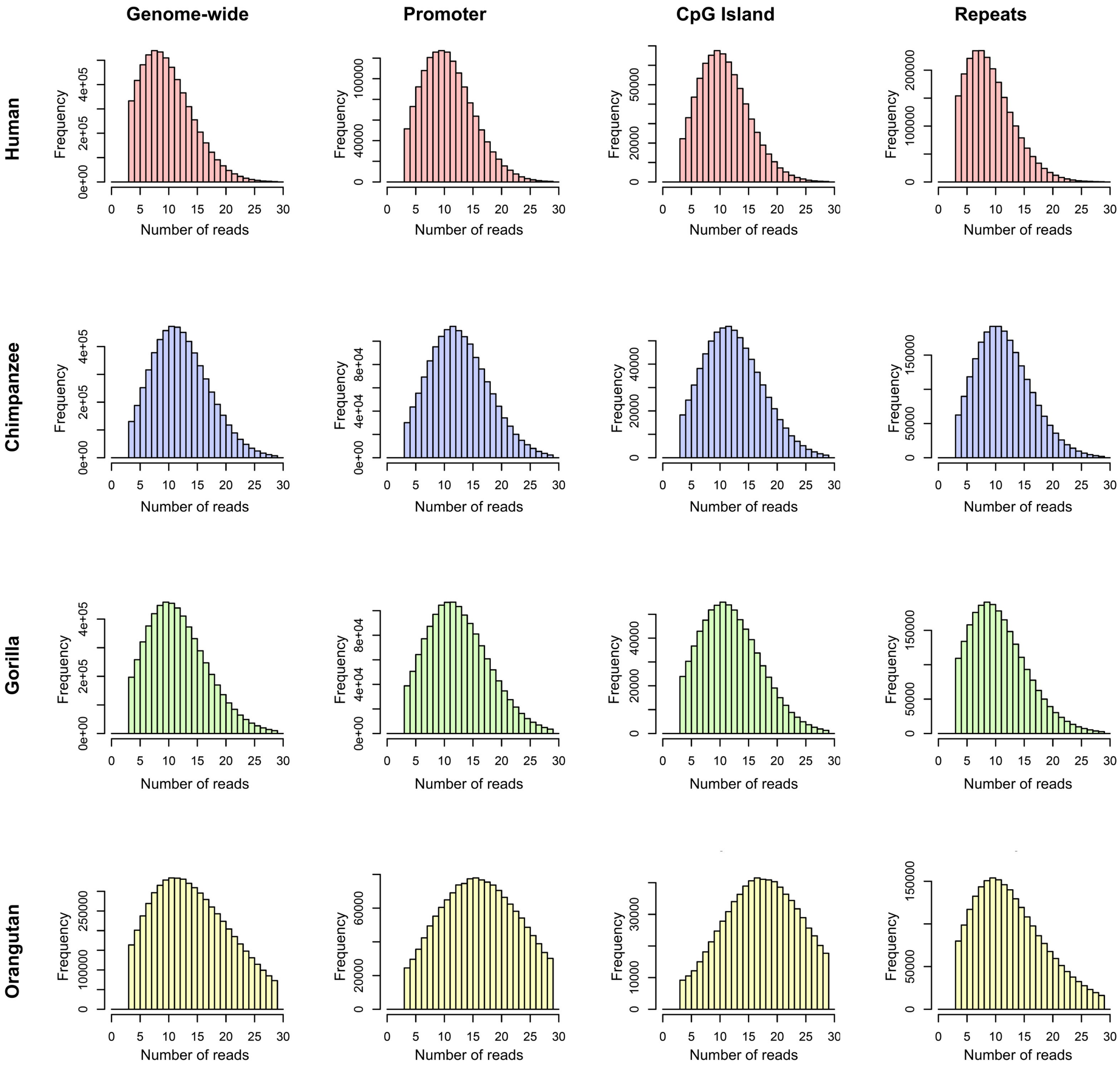

Figure S3: Read coverage across genomic regions and samples.

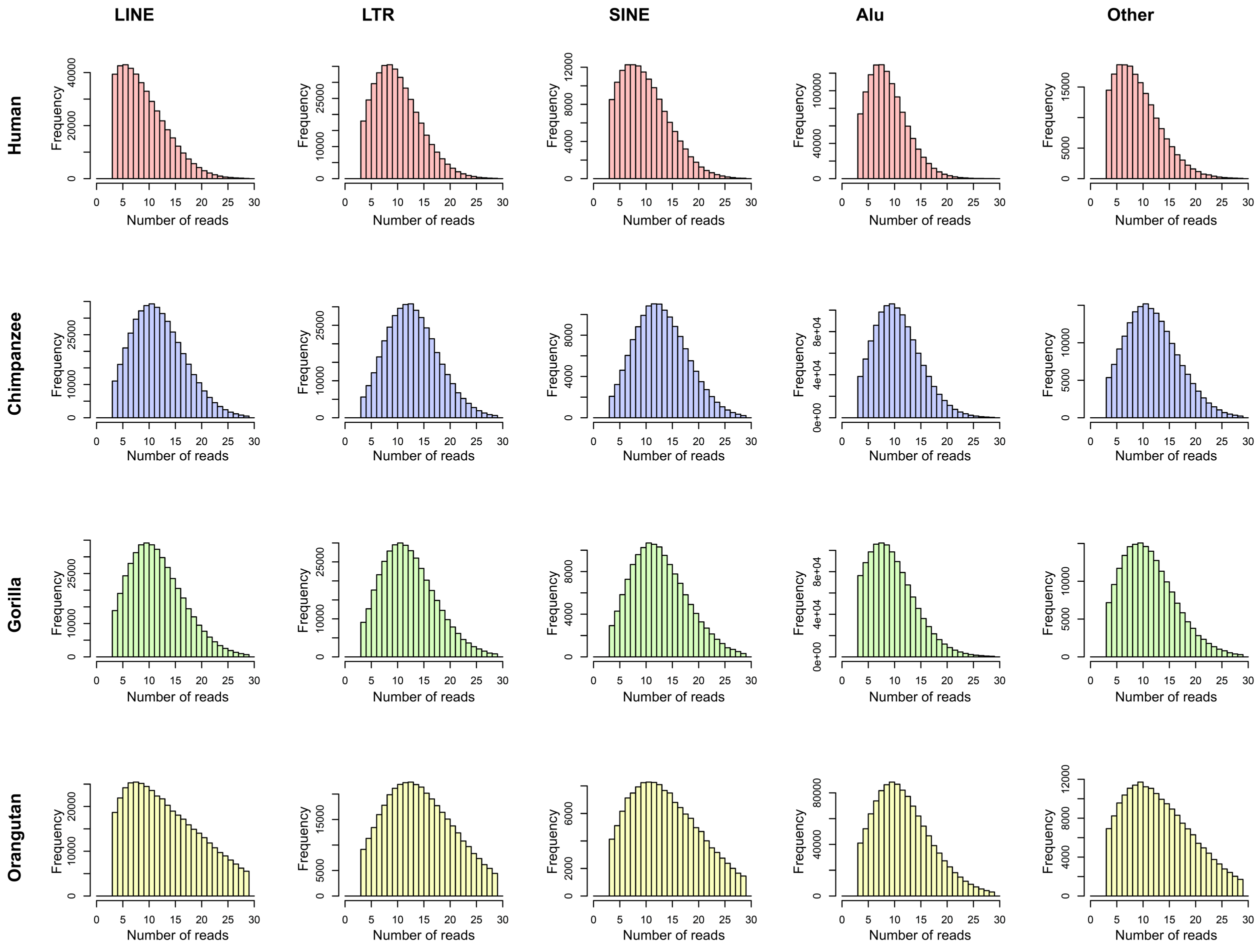

Figure S4: Read coverage across major repeat families and samples.

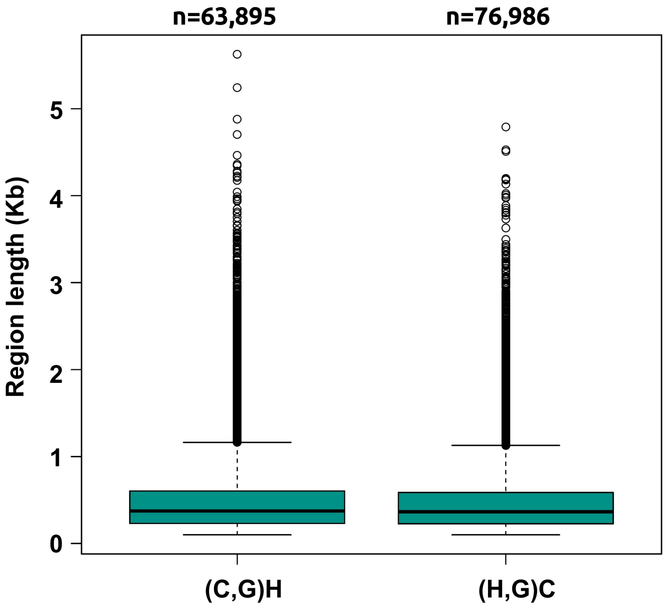

Figure S5: Size of incomplete lineage sorting regions.

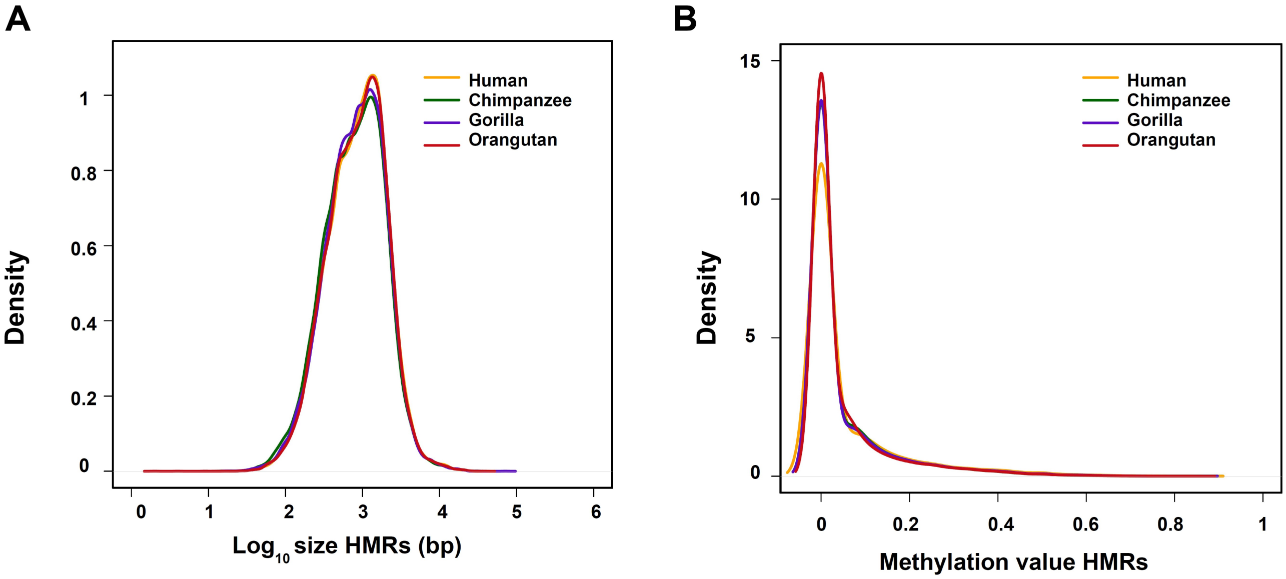

Figure S6: Distribution of (A) size and (B) methylation value of hypomethyated regions (HMRs) across samples.

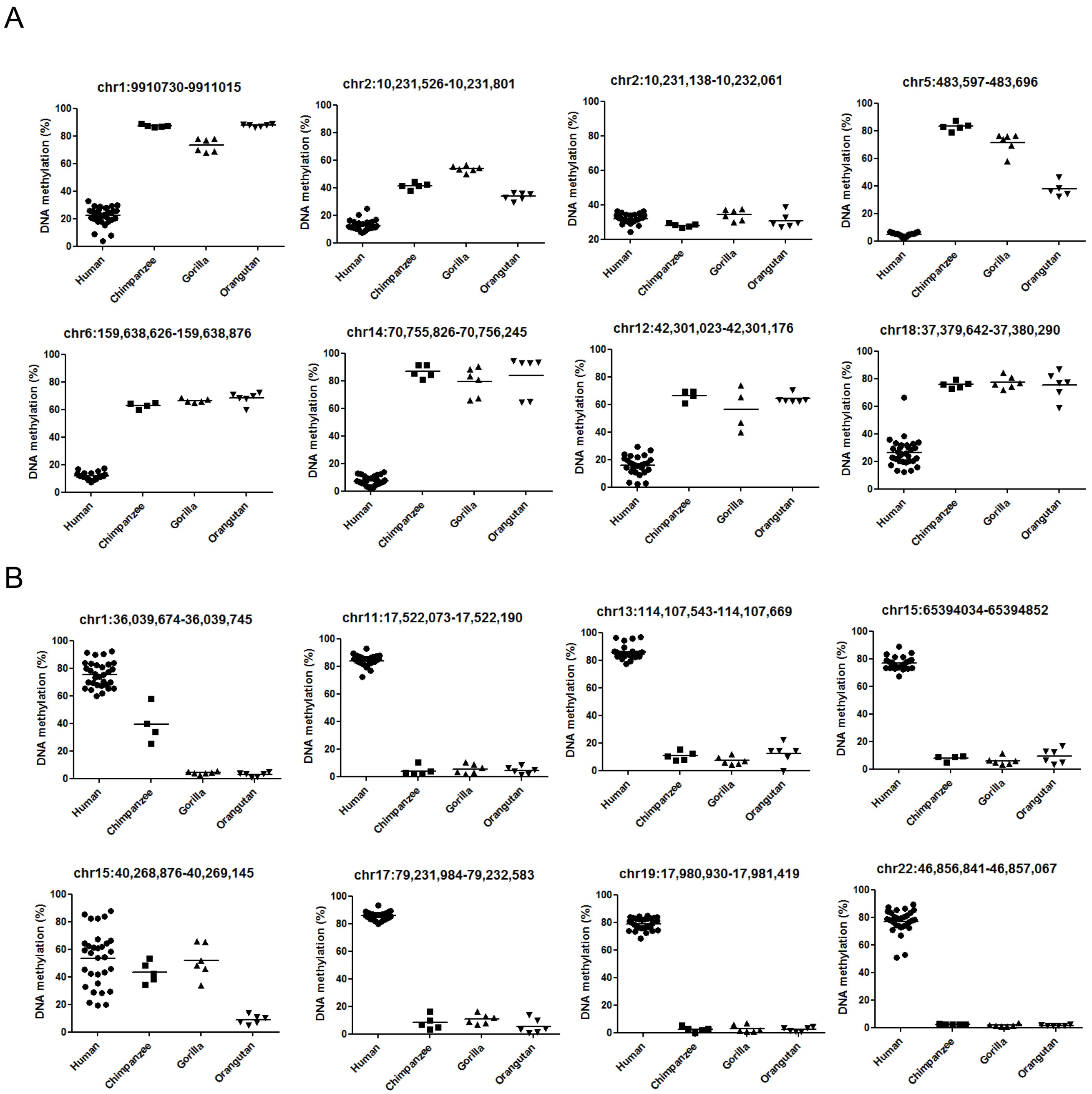

Figure S7: DNA methylation analysis of randomly selected human specific DMRs, 8 Hypo- (A) (DMRs and 8 Hyper-DMRs (B), using bisulfite pyrosequencing. A total of 31 humans, 5 chimpanzees, 6 gorillas and 6 orangutans samples were screened for differential DNA methylation. The averaged CpG methylation level for each region and individual are displayed with mean methylation values being indicated (bar) per species.

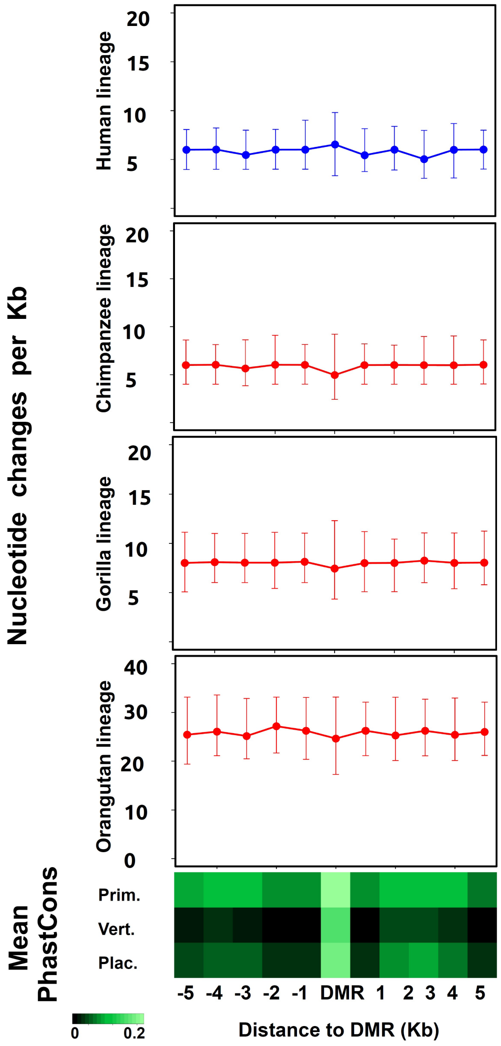

Figure S8: Nucleotide divergence at human hypomethylated DMRs. Top, nucleotide changes of human hypomethylated DMRs estimated in each species lineage. The color plot represents the methylation state of the lineage species, red hypermethylated and blue hypomethylated. Data are represented as mean ± 2 standard deviations above and below the mean. Bottom, PhastCons score (Cons 46-Way) from all species (vertebrate) and two subsets (primate and placental mammal).

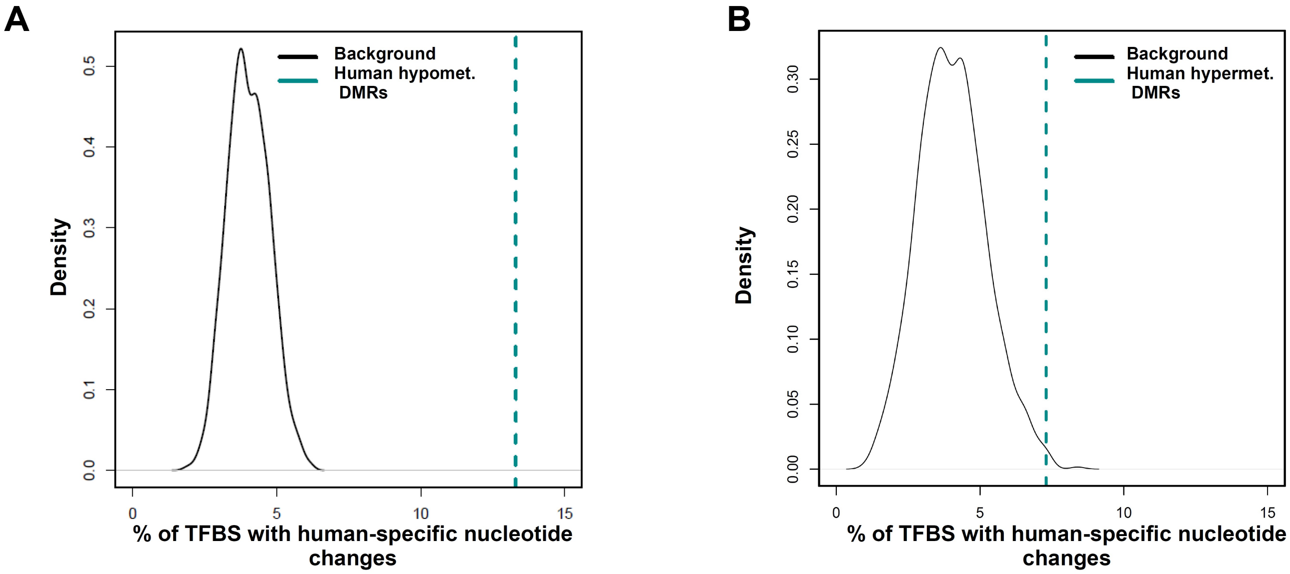

Figure S9: Proportion of binding sites with human-specific nucleotide changes at DMRs (green) and background (black). (A) Human hypomethylated DMRs. (B) Human hypermethylated DMRs.

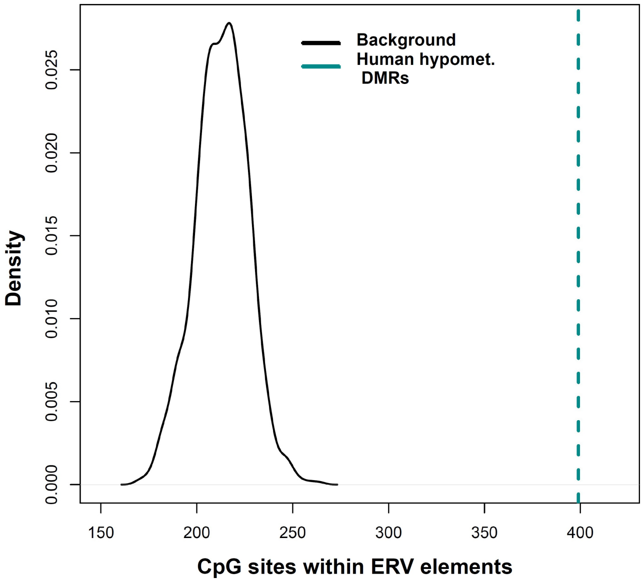

Figure S10: CpG sites within a ERV repeat elements at human hypomethylated DMRs and background.

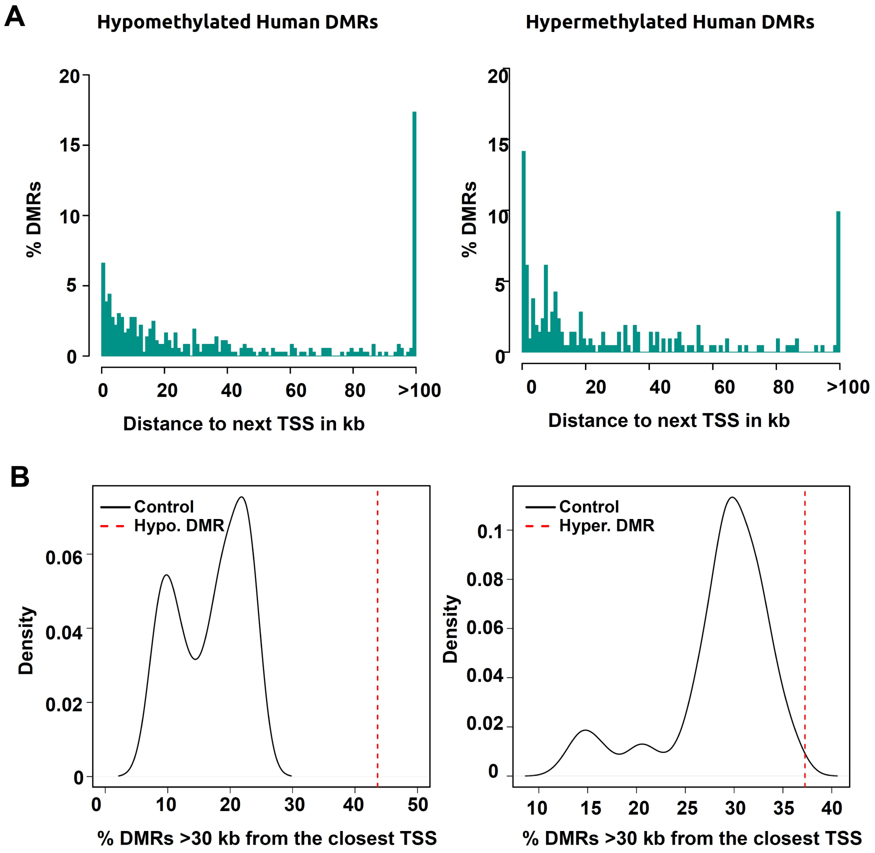

Figure S11: (A) Distance distribution of human hypo- and hypermethylated DMRs to the closest RefSeq TSS truncated at 100kb. (B) Proportion of human DMRs (red) and control datasets (black) located > 30kb away from the closest TSS.