Supplemental Figure 4. Aberrant methylation at the region distal from TSS.

(a) Distribution of the distance from transcription start sites to differentially methylated sites in CpG islands. CpG density is shown as a black line. Dotted lines show the ratio of hyper- or hypomethylated CpGs to CpG density. (b) Correlation analysis between gene expression and methylation patterns of regions around TSS. The fraction of genes positively or negatively correlated (ppc: pearson’s correlation constants > 0.6 or < -0.6, respectively) was plotted.
Supplemental Figure 4

(a) Density and Ratio graphs showing the distribution of CpG sites across different distances from the TSS (Transcription Start Site).

(b) Fraction of correlated genes across different distances from the TSS, with red and blue lines representing positive (ppc > 0.6) and negative (ppc < -0.6) correlations, respectively.