

Supplemental Figure 1. Confirming efficient detection of methylation by MeDIP-seq

(a) Real time quantitative PCR analysis for known methylated (AX1) and unmethylated (GAPDH) promoters. Positive control DNA fragments processed by in vitro methylation reactions and unprocessed negative control DNA fragments were mixed in input samples and enriched by MeDIP. Unmethylated DNA fragments were efficiently removed in MeDIP samples, and detected in input samples. (b) Pie chart representing the fraction of CpGs covered with each depth. (c) Scatter plot showing the correlation between two replicated MeDIP-seq experiments. HMEC methylations for each 100kb segments (left panel) and CGIs (right panel) are shown. (d) Box-and-whisker plot showing correlation between MeDIP-seq data and MeDIP-chip data (GSM263125). Boxes, bars and whiskers represent interquartile range, median and 1.5 times extended interquartile range of MeDIP-chip signal distributions, respectively. Overall, regions detected by MeDIP-seq were found to have higher methylation levels in MeDIP-chip results. (e) Representative methylation patterns of HSATII.

Supplementary Figure 1

