

Supplementary Materials

Table S1. Methylation-specific primers used

Table S2. Gene primers used

Table S3. Medip-seq data for read alignments in SP and NSP cells in the MS1 cell line

Table S4. Information for peak regions between SP and NSP samples

Table S5. Numbers of differentially methylated genes between SP and NSP cells in different gene regions

Table S6. RNA-seq reads between SP and NSP samples

Table S7. Differentially regulated genes showing concomitant changes in mRNA expression and DNA methylation

Table S8. GO terms with a p-value less than 0.05

Figure S1. Distribution and coverage of peaks in SP and NSP cells in the MS1 cell line.

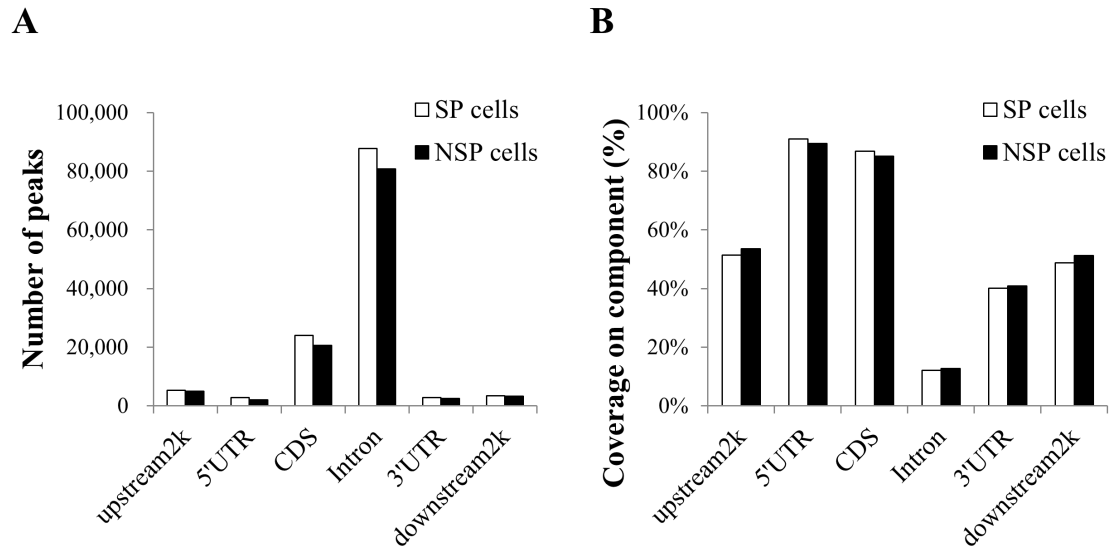


Figure S2. Differentially methylated genes containing altered methylated sequences in CpG islands. A total of 10 genes positively correlated with gene expression showed the methylation of CpG islands inside various genomic regions as follows: (A) CDS; (B) downstream 2k; (C) intron; (D) upstream 2k.

