



Supplementary Figure S11. MBS and gene expression analysis in the comparison of hepatoma cells to Liver cells.

(A, B) Methylation boundary shift in the LM3 cells and primary liver cancer comparing with Liver cells. 11290 genes with MBS to either upstream or downstream from TSS in LM3 cell comparing with Liver cells in A and 6341 genes in primary liver cancer sample in B. (C) In the comparison of Liver to 97L, gene expression alteration and MBS extension to the downstream of TSS were positively correlated (left panel, $\rho = 0.96$, P-value $< 2.2 \times 10^{-16}$, Spearman's rank correlation), while gene expression and MBS extension to the upstream of TSS show less correlation (median panel, $\rho = 0.19$, P-value = 0.6076, Spearman's rank correlation). Gene expression also shows less correlation with promoter methylation (right panel, $\rho = 0.20$, P-value = 0.5835, Spearman's rank correlation). The x-axis shows the difference of MBS length or promoter methylation level while the y-axis represents the log ratio of expression. (D,E) Similar results were found in the comparison of Liver to LM3 and Liver to primary liver cancer cells, respectively. (F) Correlation between H3K4me3 peak length and gene expression. Gene expression was up-regulated while the H3K4me3 peak length increased.