



Figure S14. Comparison with the methylation array data.

(A) Venn diagram showing the concordance rate of the t^{dm} CGIs and the the Infinium HumanMethylation450 BeadChip data from Song, et al and the TCGA database (21 tumor and 11 non-tumor samples). A total of 3,890 auto chromosome CGIs that exhibited a minimum of 16 MePM in at least one tissue sample of this study and a minimum of 0.1 Beta value in at least one tissue sample of TCGA data, were selected. Of these CGIs, 837, 880 and 146 were identified as differentially methylated CGIs in these three studies, respectively. For the TCGA data, the CGIs were identified as $FDR < 0.1$, average methylation difference > 0.1 , two-tailed MWW test. **(B)** Boxplots of the TCGA data showing the methylation levels in HCC (red) and non-tumor liver tissues (green) for representative type I and type II markers. **: $P < 0.01$; *: $P < 0.05$; nd: no statistical difference. Two-tailed MWW test.