

Descriptions of Additional Supplementary Files

Supplementary Data 1

Description: Tumor suppressor gene DMR overlap analysis.

Supplementary Data 2

Description: Tumor suppressor genes with core promoter hyperDMRs in both EAC and GBM.

Supplementary Data 3

Description: Tumor suppressor gene promoter and/or enhancer overlaps with EAC and GBM hyperDMRs. The full list of 1217 tumor suppressor genes (TSGs) analyzed in this study^{6,7} are displayed, along with any relevant aliases. A value of 1 is given in the 3rd and 4th column if the gene's promoter or enhancer, respectively, overlaps with the hyperDMR set (1st tab: EAC hyperDMR overlaps, 2nd tab: GBM hyperDMR overlaps). The union of all TSGs with either promoter and/or enhancer overlaps to the hyperDMR set is given to the right. In the case of EAC hyperDMRs, two TSGs with regulatory regions overlapping DMRs (*BRINP1* and *CCAR2*) had the same alias: *DBC1*. Since the expression data was associated with the alias, *BRINP1* and *CCAR2* were replaced by *DBC1* on the right. TSGs without expression data are highlighted in orange.

Supplementary Data 4

Description: GREAT⁸ GO Biological Processes significantly enriched terms for DMRs overlapping active enhancers outside of promoters (ceDMRs). Terms reported are significant in both the binomial and hypergenometric tests (BinomFDRQ \leq 0.05 and HyperFDRQ \leq 0.05, are within the top 500 ranked binomial test terms, and have a region fold change of 2 or greater). Tab1: EAC ce-hyperDMRs, Tab2: EAC ce-hypoDMRs, Tab3: GBM ce-hyperDMRs, Tab4: ce-GBM hypoDMRs.

Supplementary Data 5

Description: VISTA Enhancer IDs¹² and Roadmap chromHMM 18-state map IDs¹.