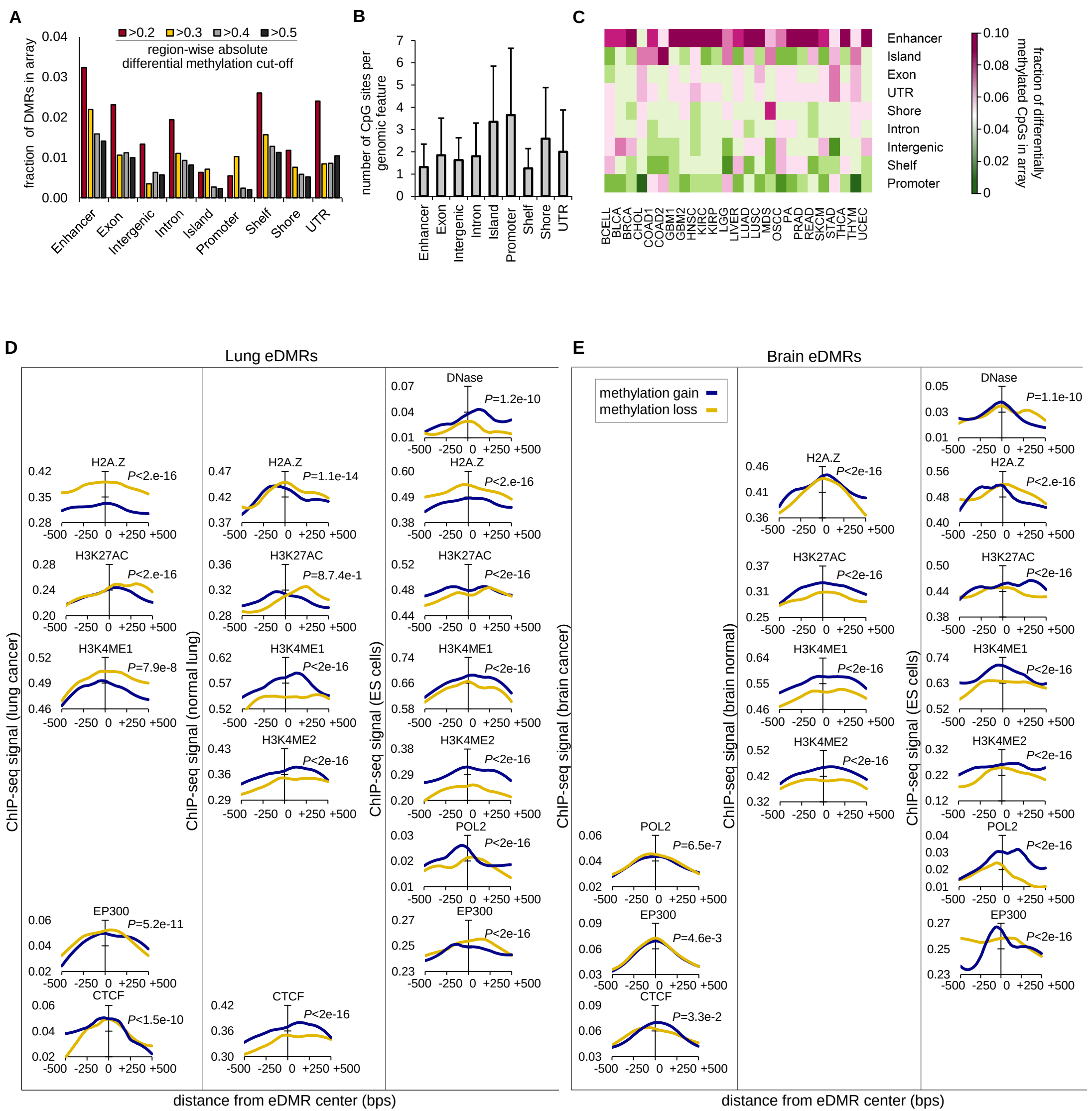

Supplemental Figure S1: Enhancers exhibit highly dynamic methylation patterns upon malignant transformation

Bell et al., 2015

Supplemental Figure S1: Enhancers exhibit highly dynamic methylation patterns upon malignant transformation

(A) The bar plot compares the fraction of differentially methylated regions (DMRs) using various cut-offs (absolute methylation values 0.2-0.5). Consistently, eDMRs are the most variable regions. (B) The average number of CpG sites within the intervals of each genomic feature (islands, promoters, enhancers, shores, shelves, UTRs, introns, exons, and intergenic). Error bars represent the standard deviation; the data relates to the results presented in Fig. 1A. (C) Heatmap shows that across 25 cancer datasets (x-axis) most of the differentially methylated CpG sites occur at enhancers. Colors indicate high (pink) to low (green) fraction of differentially methylated CpGs in each genomic feature (N=9; y-axis). (D-E) EDMRs at different cell state (embryonic, normal and transformed) from lung and brain tumors. *Left panels:* eDMRs exhibit markers of active chromatin in lung and brain cancer cell lines. *Middle panels:* eDMRs exhibit mostly markers of inactive chromatin in normal cell lines, and in *Right panels:* embryonic stem (ES) cell lines. Examples of eDMRs from (D) lung cancers (LUAD, LUSC) and (E) brain cancers (GBM1, GBM2, LGG, PA) are shown. Curves show enhancers with methylation gain (blue) or loss (yellow) upon tumorigenesis (from normal to primary tumors). *P*-values were calculated with two-sample Student's t-tests and were FDR adjusted. Chromatin marks were derived from the ENCODE Project (Supplemental Table S2).