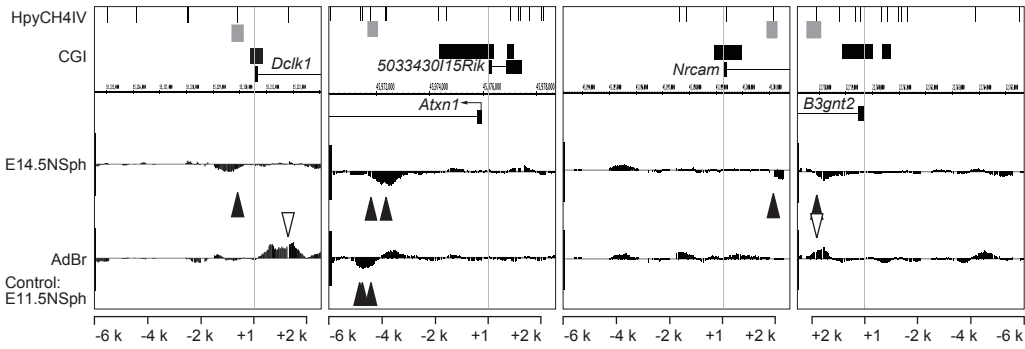
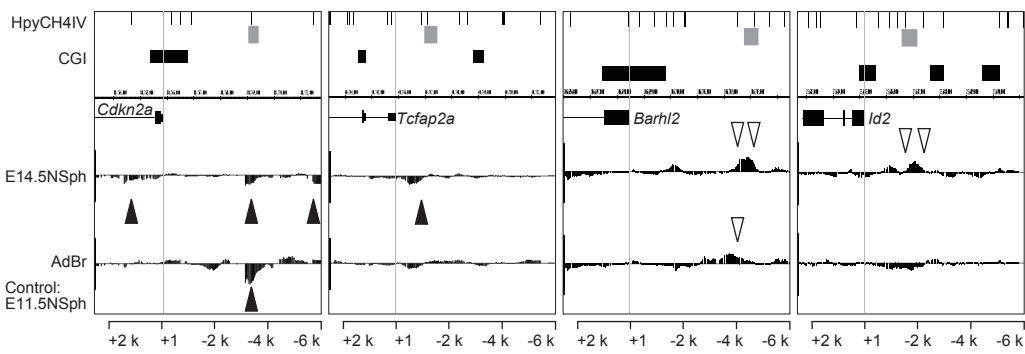


A



B

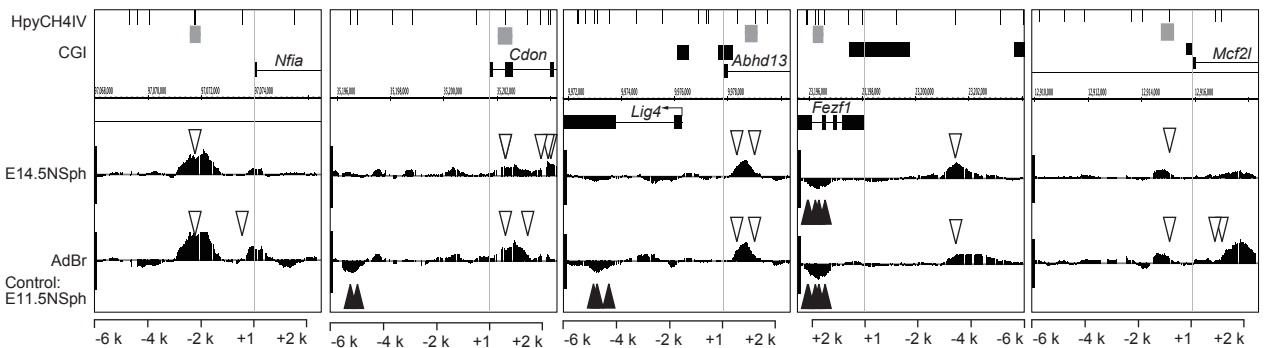
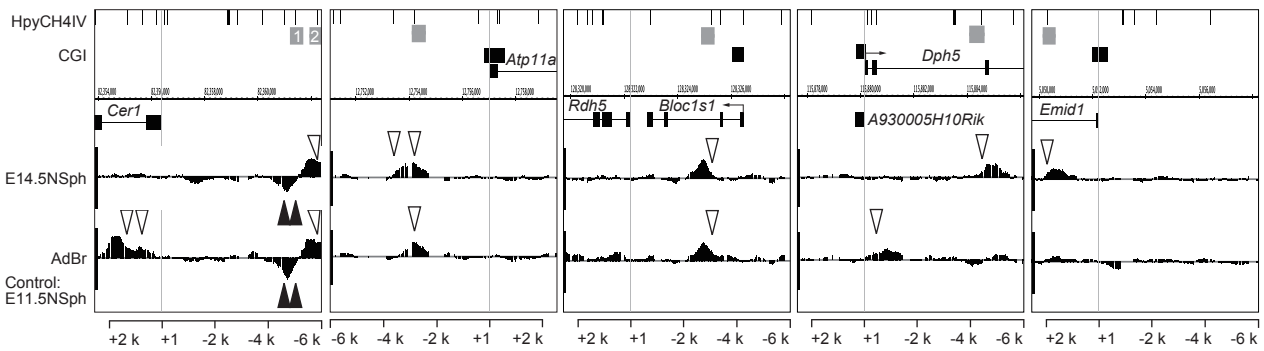
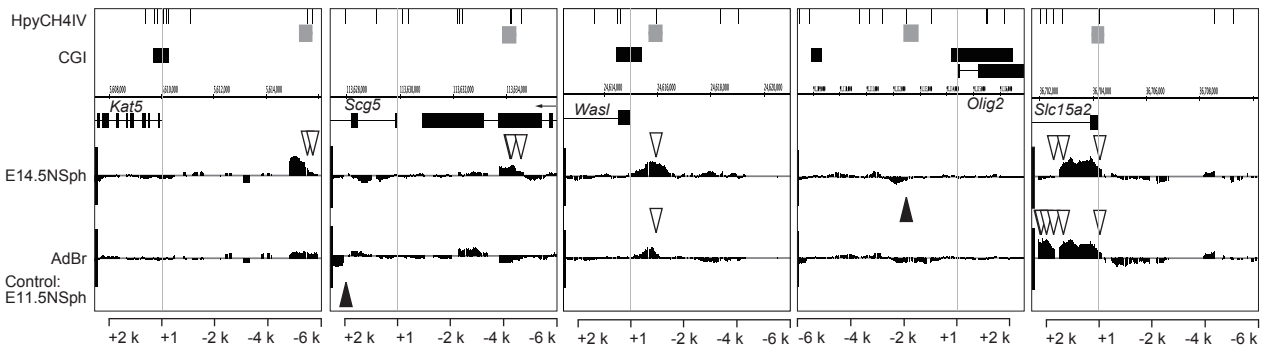


Figure S2. Positions of T-DMRs identified by D-REAM analysis

Panels indicate Integrated Genome Browser (IGB) images for the genes (Ensembl Transcripts) with E11Hypo- (A) and E14Hypo-T-DMRs (B). Comparative MATscores of E14.5NSph and the adult brain (AdBr) to E11.5NSph as the control were plotted and displayed from 6 kb upstream to 2.5 kb downstream of the transcription start site (TSS) at the middle parts of each panel. Filled and open arrowheads indicate T-DMRs hypermethylated and hypomethylated in comparison to E11.5NSph, respectively. Regions analyzed by bisulfite sequencing or COBRA are indicated by gray rectangles.