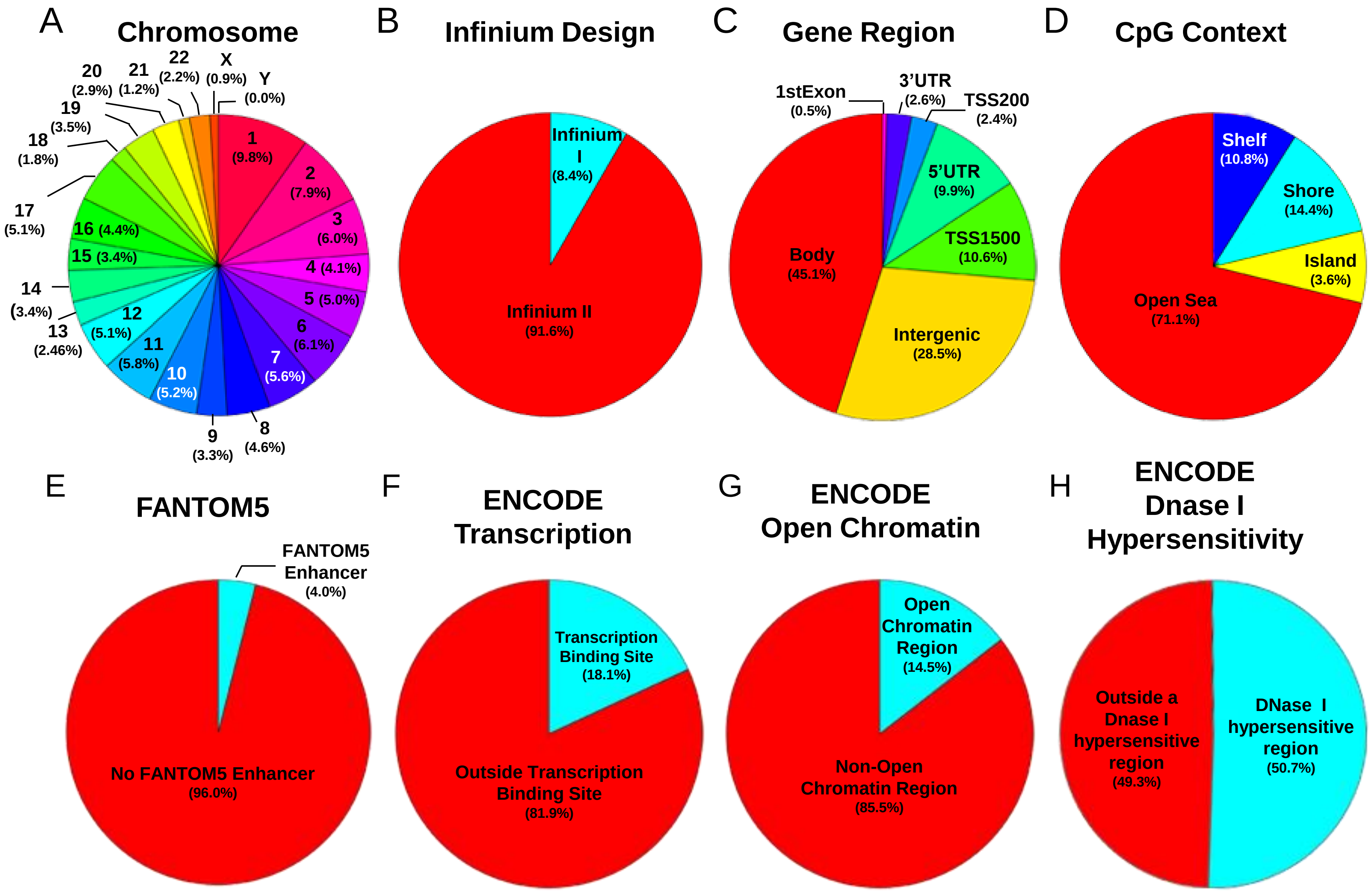

Supplementary Figure 1. Genomic and functional context of the 361,351 hydroxymethylated (oxBS-BS ≥ 0.2) CpG sites detected using the MethylationEPIC BeadChip microarray (850K) on sorted normal neurons (N229), based on chromosome location (**A**); Infinium design chemistry (Infinium I, II) (**B**); UCSC gene region feature category (TSS200, TSS1500, 5'UTR, 1stExon, Body, 3'UTR) (**C**); location of the CpG relative to the CpG island (Open Sea, Island, Shore, Shelf) (**D**); FANTOM5 associated enhancer regions (**E**); and ENCODE project annotation for transcription binding site (**F**), open chromatin (**G**) and Dnase I hypersentitive (**H**) regions.