Supplementary Figure 2. mCH is enriched at long and repressed genes. A) Gene ontology enrichment of genes with high levels of mCAC/CAC. B) Spearman correlation coefficients between diverse genomic and epigenomic features and gene body mCH/CH levels at all genes and the top and bottom 10% of CH methylated genes (left). Log2(relative levels) of diverse genomic and epigenomic features at all genes and the top and bottom 10% of CH methylated genes (right).