



**Supplemental Figure 11.** Four lines of evidence supporting the usage of distal CGI as alternative promoter by MethExp genes in contrast to MethNotExp genes in the human spleen (E113). The boxplots show the distribution of (i) fractional methylation at upstream CGIs (top-left), (ii) genomic distance between distal CGI and gene (top-right), (iii) RNA-seq RPKM signal (bottom-left), and (iv) RNA-seq coverage (bottom-right) at the segment region corresponding to MethExp (yellow) vs. MethNotExp genes (red) computed using the GRCh38/hg38 genome annotation and "lifted-over" RNAseq and methylation data.