



Figure 3-figure supplement 1:

(A-B) Estimation of the abundance of transcription factor binding motifs in mouse (grey line) and E.coli (purple lines) sequences used in the comparisons. Depicted are the mean abundance per CG density bin of the total counts of motifs for the fragment of each origin. The motifs counts were calculated separately for all motifs (A) and for GC rich motifs only (B). (C) Comparison of the distance between predicted and observed values and the presence of DNase Hypersensitivity within fragments. The difference between the observed methylation levels and the CG density based prediction were calculated and used to bin fragments. The median of DHS signal for each bin was computed and plotted as a dotted line showing that fragments that negatively deviate from the prediction have DHS signal that could explain their unmethylated state.