



Figure 5-figure supplement 2:

(A-B) Motif MA plots representing the counts for known TF motifs in the surroundings (300bp) of hypomethylated (A) or hypermethylated (B) CGs versus counts in CGs not changing methylation. For each set, control sequences with similar CG density distribution were used. The name of enriched TF matrices were depicted and matrices for which expression data could be mapped were depicted in red and represented in Figure 5A