



Figure 2-figure supplement 1:

(A) Estimation of the measurement error in methylation levels determination for the Mouse and the E.coli samples. Technical replicates represent the same library insertion profiled twice using the same starting gDNA as a template for PCR. (B) Estimation of the biological variation in methylation acquisition for the mouse and E.coli based libraries. Biological replicates represent separate library insertion events. Pearson correlation coefficients R are depicted. (C) Validation of single fragments methylation levels by standard bisulphite sequencing. Black dots represent the single CG endogenous methylation levels as measured by shotgun bisulphite sequencing (Stadler et al, 2012). Blue boxes represent the endogenous location of the inserted fragment. Red dots represent the ectopic methylation levels of the inserted fragments as measured by next generation sequencing (upper track) or Sanger sequencing (lower track).