



Supplemental Fig S3. LpnPI mediated digestion of genomic DNA.

a) Pearson correlation analysis of MeD-seq read counts of TSSs for technical (left) and biological (right) replicates.

b) MeD-seq tracks showing methylation profiles in the INS-IGF2 locus for fibroblast DNA and 100% methylated control DNA. Two biological replicates are shown for fibroblasts, two technical replicates for 100% methylated DNA.

c) Profiles of all LpnPI sites (light blue), undetected LpnPI sites (blue), and the ratio of undetected versus all LpnPI sites (red). Shown are sites and ratio in 100 bins before the TSS, inside the gene body, and behind the TES.

d) Methylation profiles in the HOXA locus using 6, 8, 10 and 12 PCR amplification cycles after library preparation of 100% methylated DNA.

e) List of detection frequencies of hexanucleotides containing LpnPI recognition sequences. Only read counts, site counts and read frequencies of LpnPI sites that contain a CpG are shown.