



Supplemental Fig S4. MeD-seq and other technologies to detect DNA methylation genome wide.

- MeD-seq, WGBS, and MeDIP DNA methylation profiles and Infinium 450K scores for the *HOXA* locus obtained with human ES cell DNA. MeD-seq and MeDIP read count or relative DNA methylation level (0-1) is shown for all CpG sites. Infinium 450 scores are: dark blue = high CpG methylation, light blue = intermediate DNA methylation, green = low DNA methylation.
- MeD-seq coverage showing amount of reads from the respective genomic region for both huES and 100% methylated DNA samples.
- Correlation plots for MeDIP-WGBS comparison of CpG islands.
- Correlation plots for MeDIP-WGBS comparison of TSS.
- WGBS scores in a 100 base pair window plotted against Infinium 450K scores binned in 10 different groups with increasing methylation scores for human ES cells.
- MeDIP reads in a 100 base pair window plotted against Infinium 450K scores binned in 10 different groups with increasing methylation scores for human ES cells.