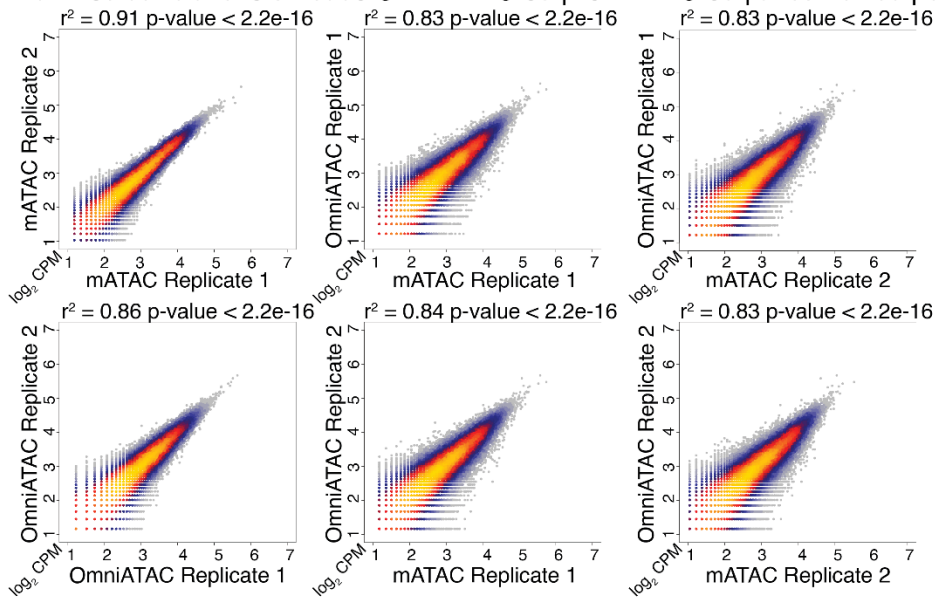
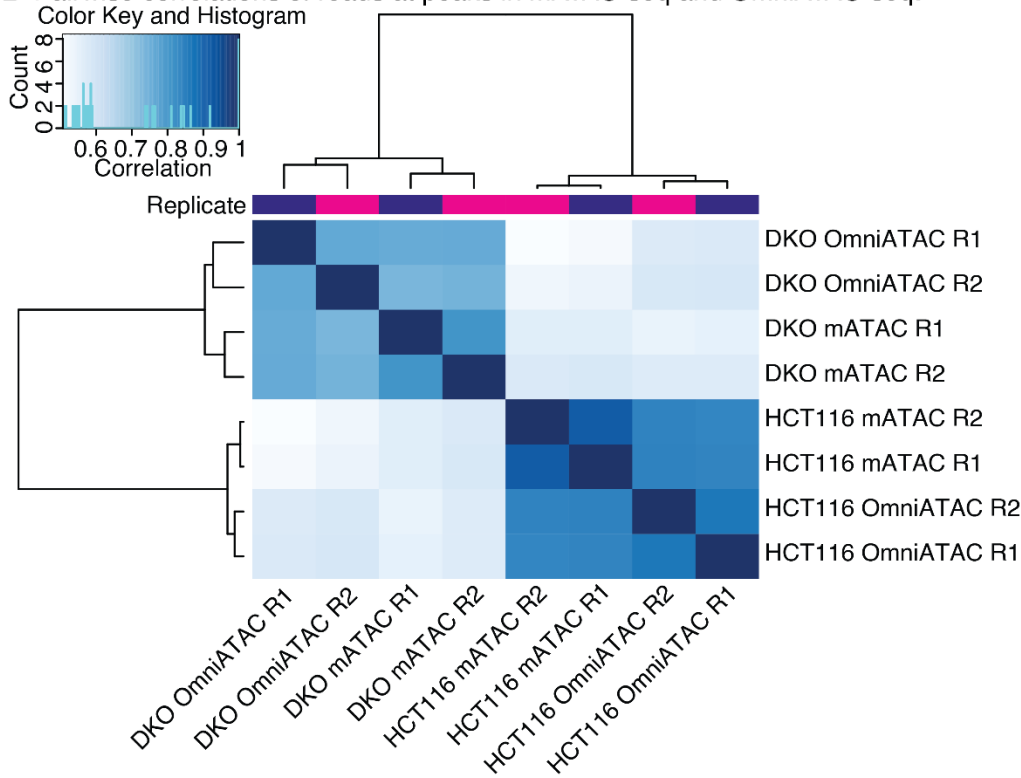


A Pairwise correlations of reads Omni-ATAC-seq vs mATAC-seq at combined peaks.



B Pairwise correlations of reads at peaks in mATAC-seq and OmniATAC-seq.



C HOMER peak annotations (% total) in mATAC-seq / Omni-ATAC-seq from Fig.2a

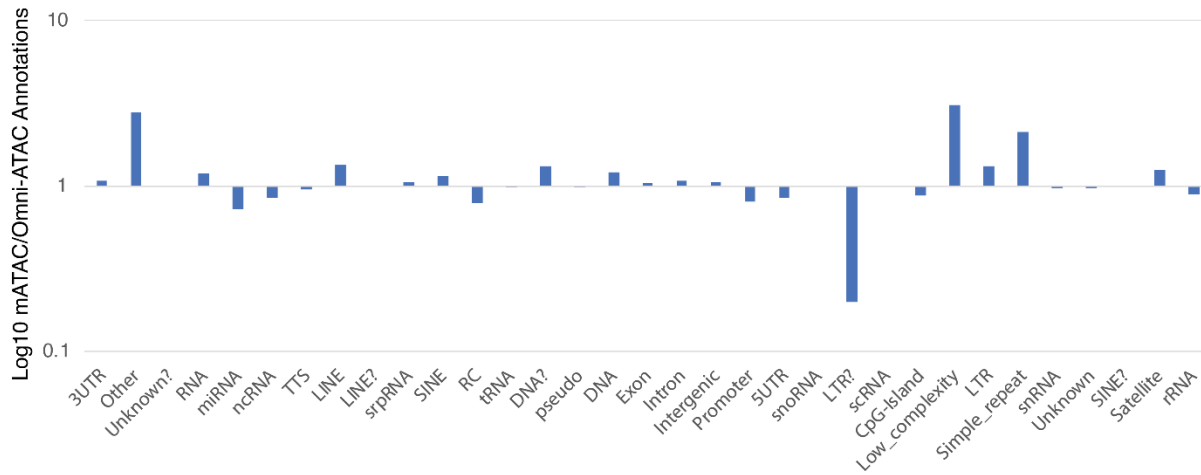
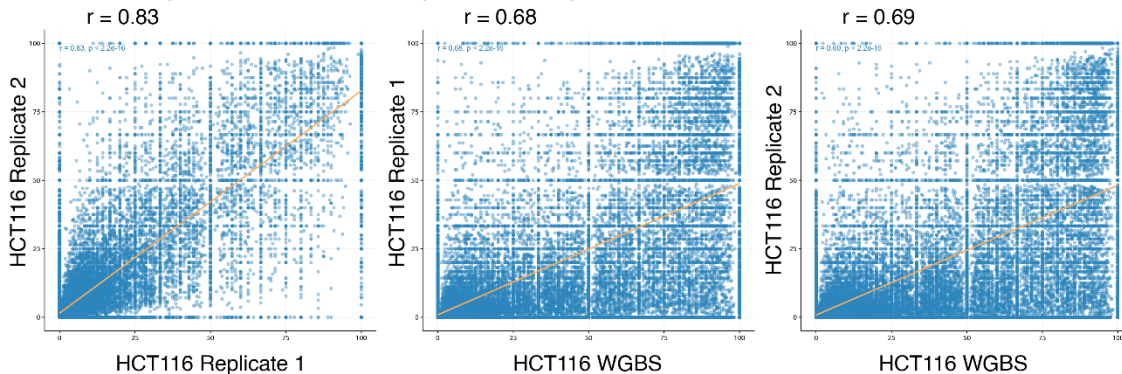
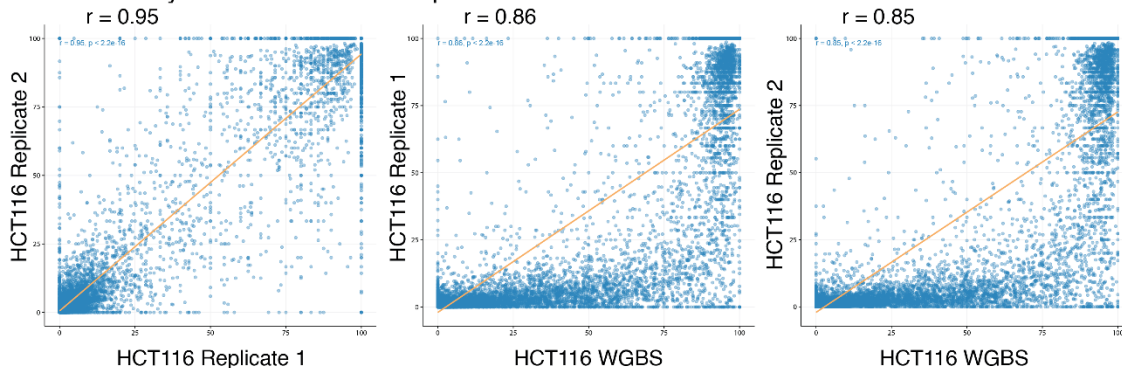


Figure S1: (A) Scatterplots of HCT116 mATAC-seq reads at peaks in libraries downsampled to 5M reads. (B) Pairwise Pearson correlations between mATAC-seq and Omni-ATAC-seq of HCT116 and *DNMT1/DNMT3b* Double Knockout (DKO) cells in downsampled libraries. (C) Annotations from peaks (% total) in Omni-ATAC-seq/mATAC-seq in Fig 2A.

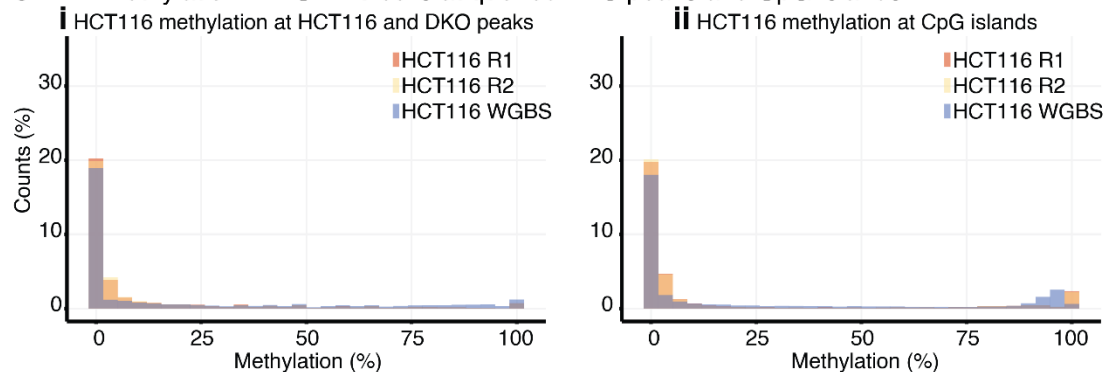
A DNA methylation correlation at queried THS peaks



B DNA methylation correlation at CpG Islands



C DNA methylation in HCT116 cells at queried THS peaks and CpG islands



D DNA methylation in DKO cells at queried peaks and CpG islands

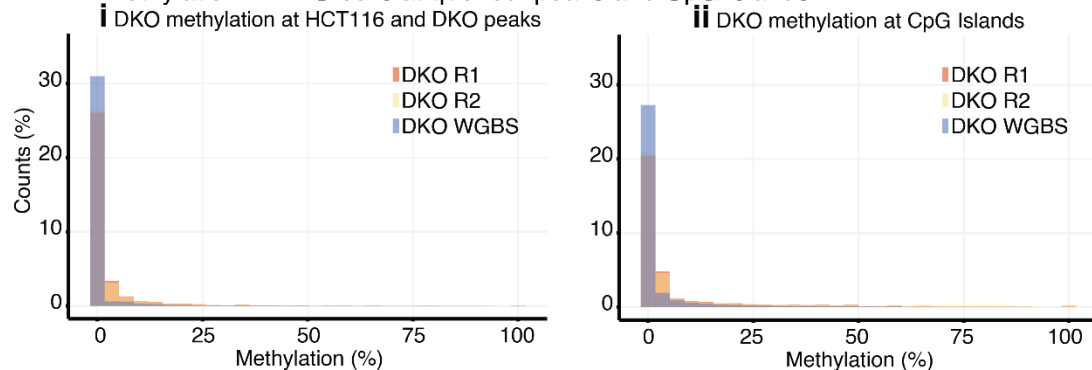
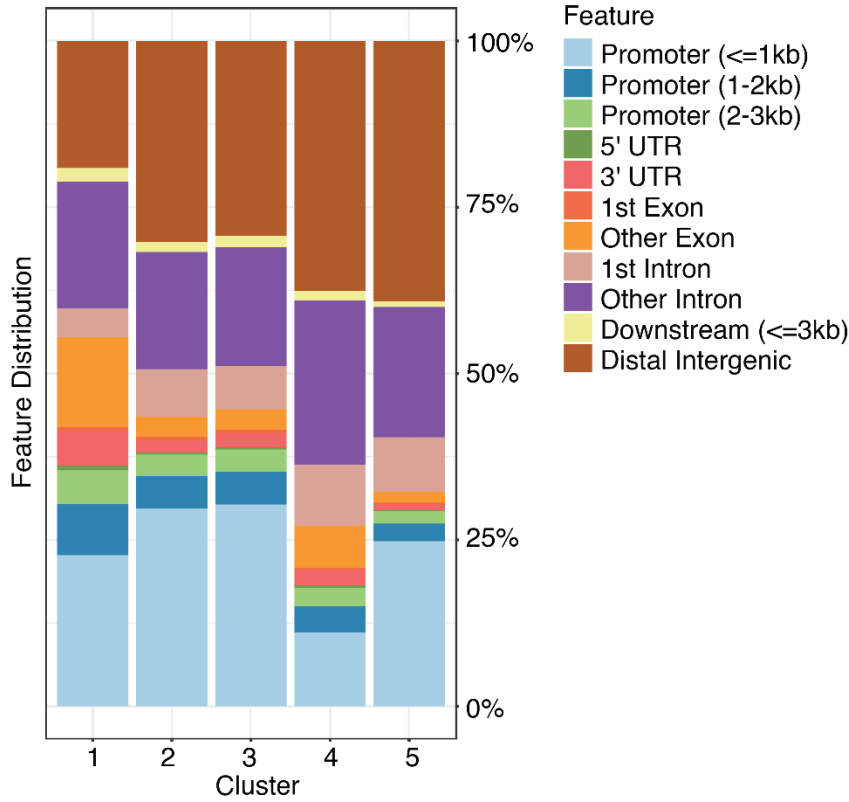


Figure S2: Scatterplots of HCT116 mATAC-seq libraries vs WGBS at (A) THS sites and (B) CpG Islands. DNA methylation in mATAC-seq and WGBS in (C) HCT116 at i. merged HCT116 and DKO peaks and ii. CpG islands and (D) DKO at i. merged HCT116 and DKO peaks and ii. CpG islands. Grey bars denote an overlap of all labeled samples, orange bars denote an overlap of mATAC-seq Replicate1 and Replicate2 samples.

A Genomic features at THS peaks in clusters



B HOMER annotations at Clusters

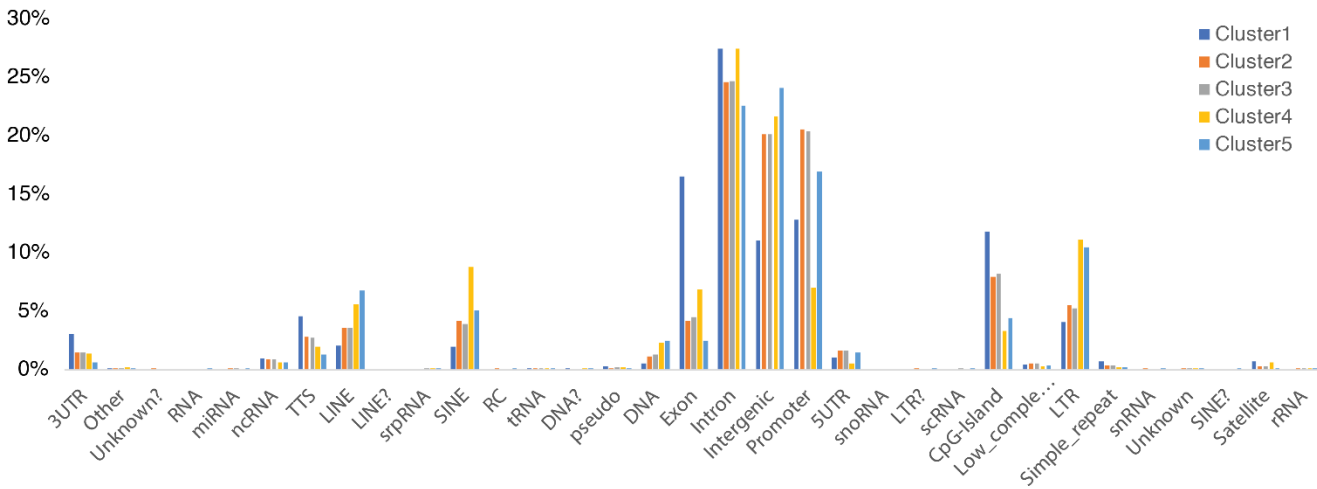


Figure S3: (A) Genomic features, and (B) HOMER annotations for clusters shown in Fig. 4.

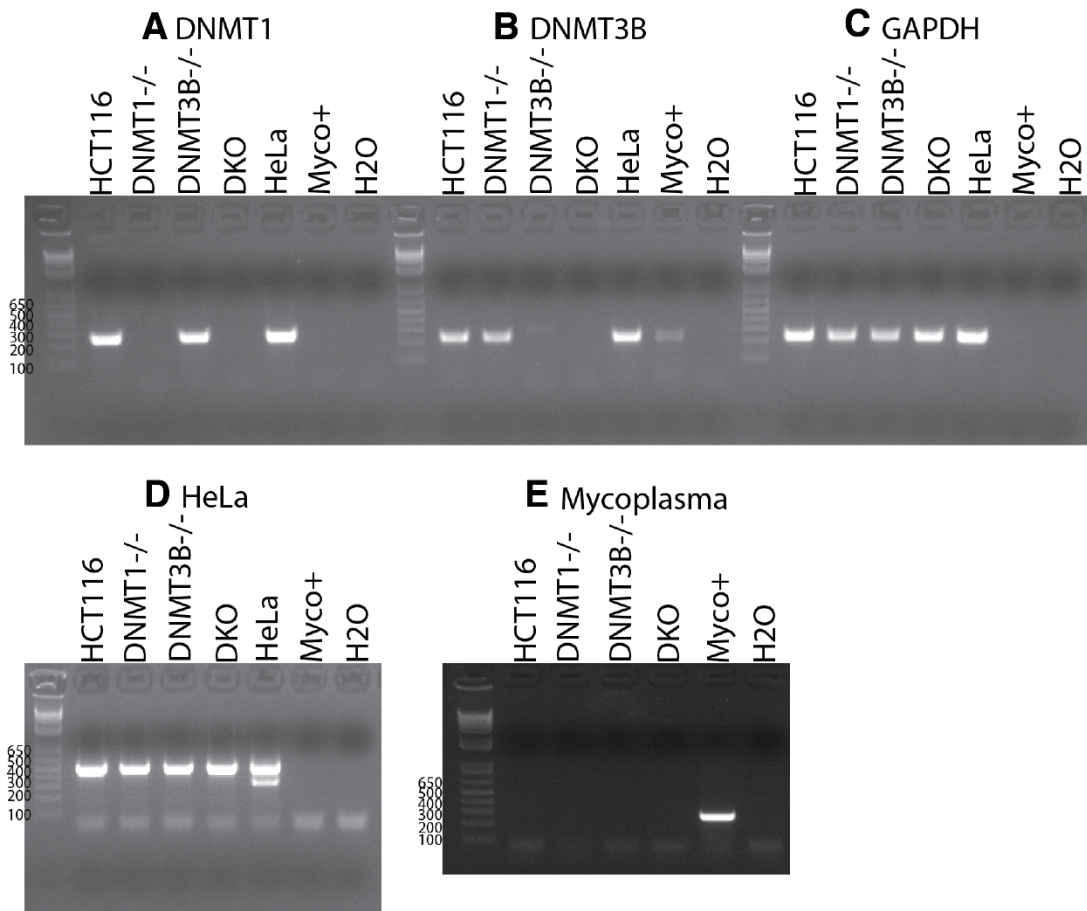


Figure S4: Genotyping by PCR to test for presence of *DNMT1* (A), *DNMT3B* (B), *GAPDH* (C), HeLa cell contamination (D), and Mycoplasma (E) in cells used for this study.

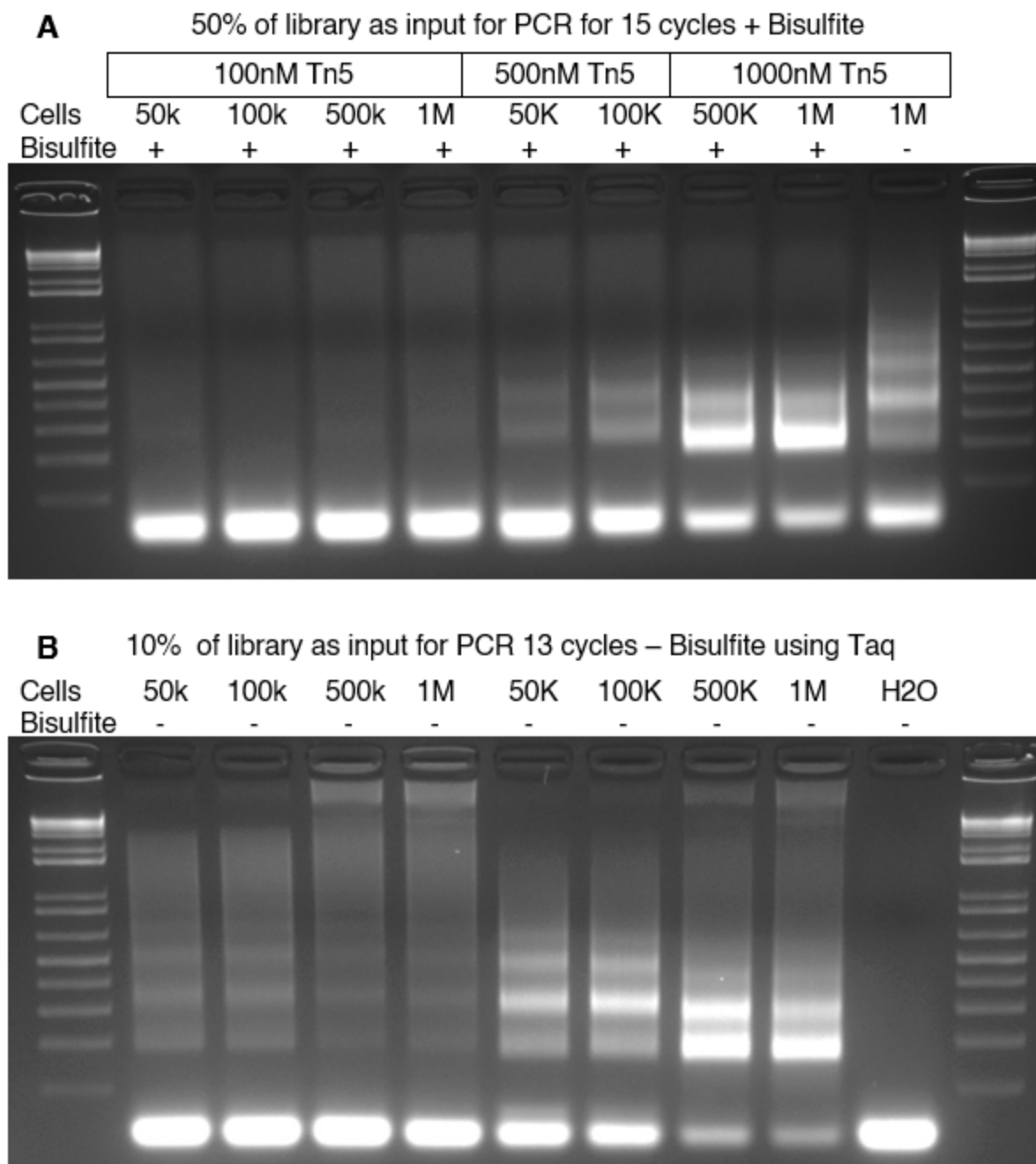


Figure S5: Titration of Tn5 transposase compared to input nuclei. An input range of nuclei and Tn5 were tested using libraries either (A) Bisulfite converted library amplified with PfuTurbo Cx (B) not converted library amplified with Taq to assay viable product for sequencing. Samples were run using a 3.5% Agarose gel in TAE; samples were resuspended in loading buffer containing 1X SYBR Gold.

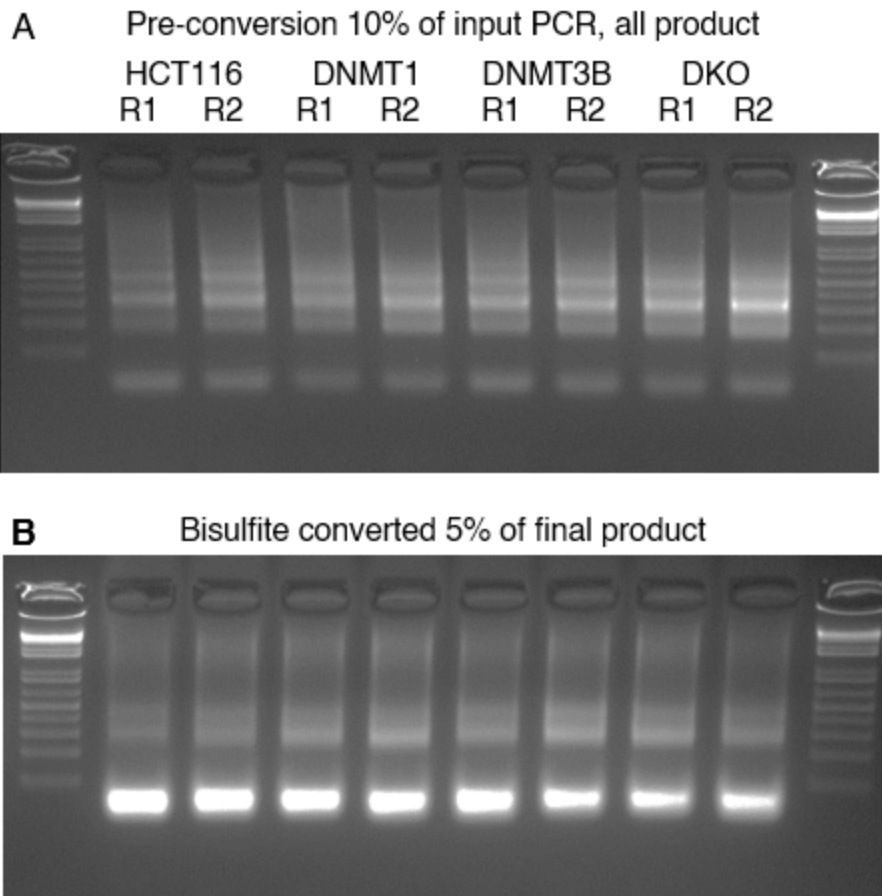


Figure S6: QC of final methyl-ATAC-seq libraries. PCR was performed on (A) 10% of pre-converted libraries using Taq (B) bisulfite converted libraries using PfuTurbo Cx. Samples were run using a 3.5% Agarose gel in TAE; samples were resuspended in loading buffer containing 1X SYBR Gold.