BAMscale: quantification of next-generation sequencing peaks and generation of scaled coverage tracks

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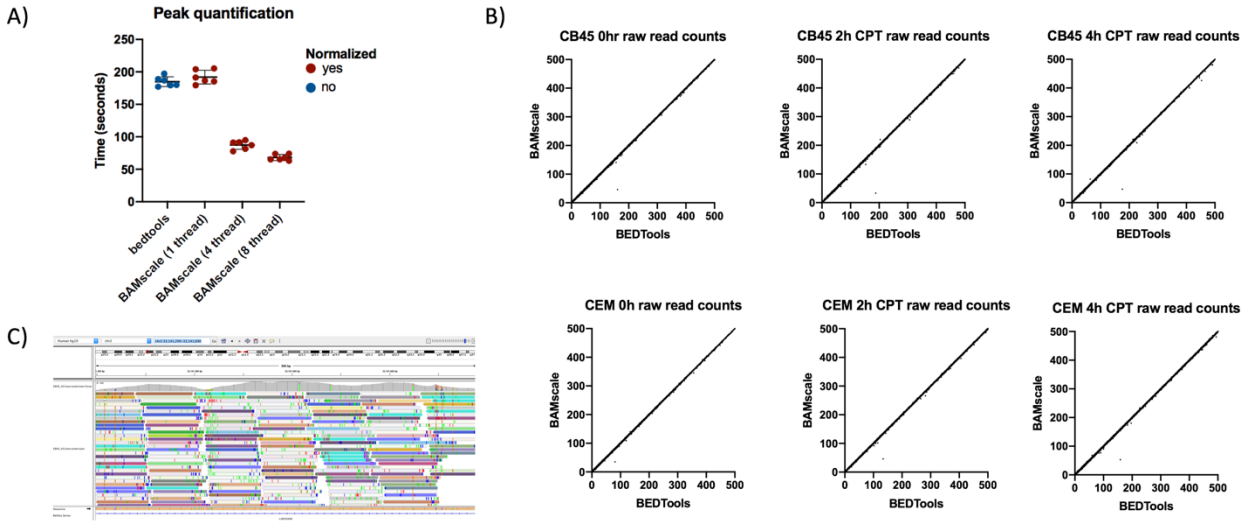
SUPPLEMENTARY TABLES LEGENDS

Supplementary table 1. Detailed list of processed samples.

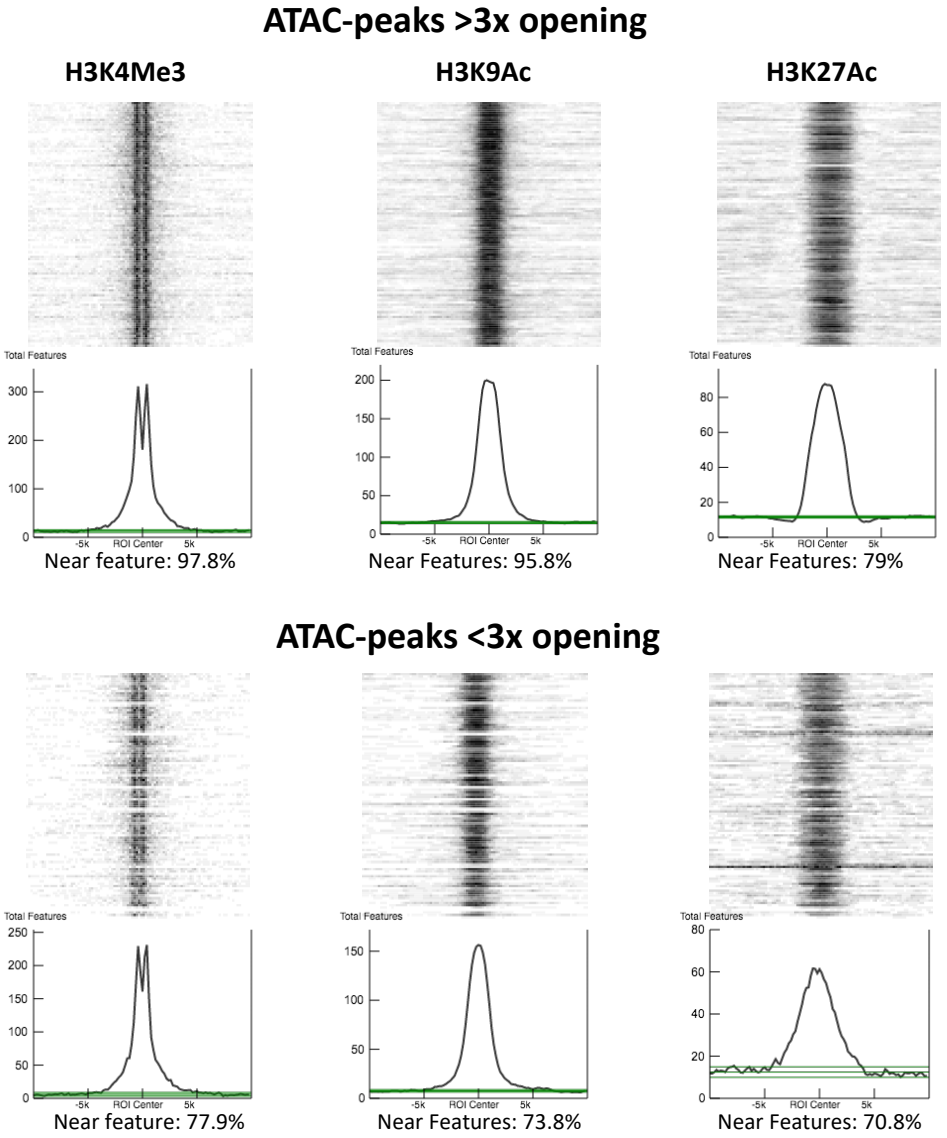
Supplementary table 2. Colocalization statistics of ATAC-seq peaks with >3x opening and <3x opening induced by camptothecin (CPT) treatment in human leukemia CCRF-CEM SLFN11 wild type and KO.

Supplementary table 3. Differential expression analysis results between *Top1mt* wild type and knockout murine liver tumor samples.

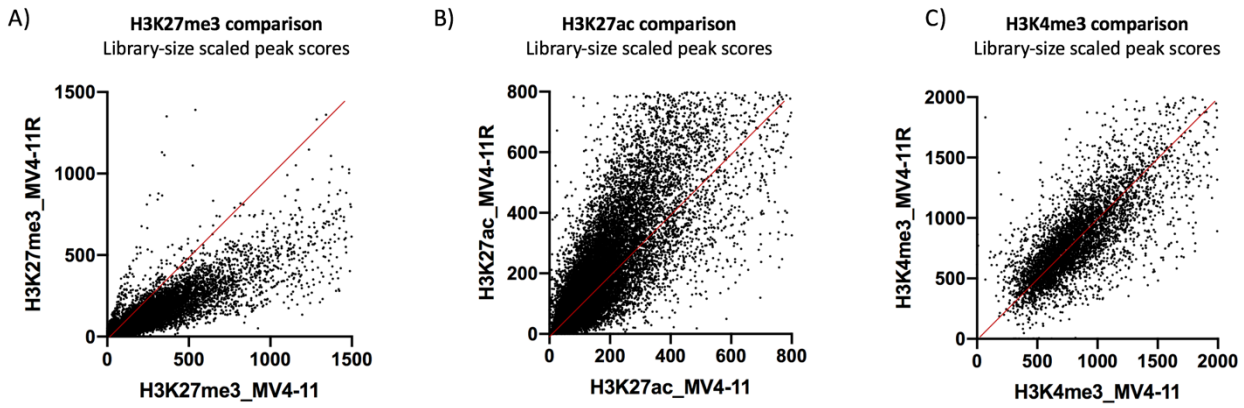
SUPPLEMENTARY FIGURES



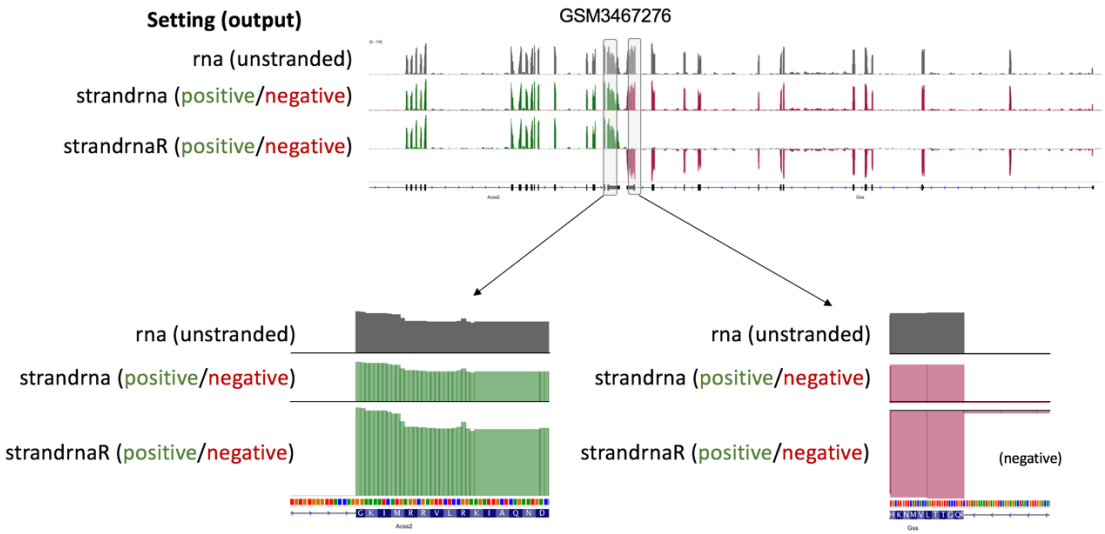
Supplementary figure 1. Benchmarking and comparison of different tools using ATAC-seq data. A) Peak quantification performance using *bedtools* and *BAMscale* (1, 4 and 8 execution threads). B) Comparison of raw read counts between *bedtools* and *BAMscale* in six ATAC-seq samples. C) IGV screenshot of a peak overestimated by *bedtools* in all samples, where read pairs align to different chromosomes.



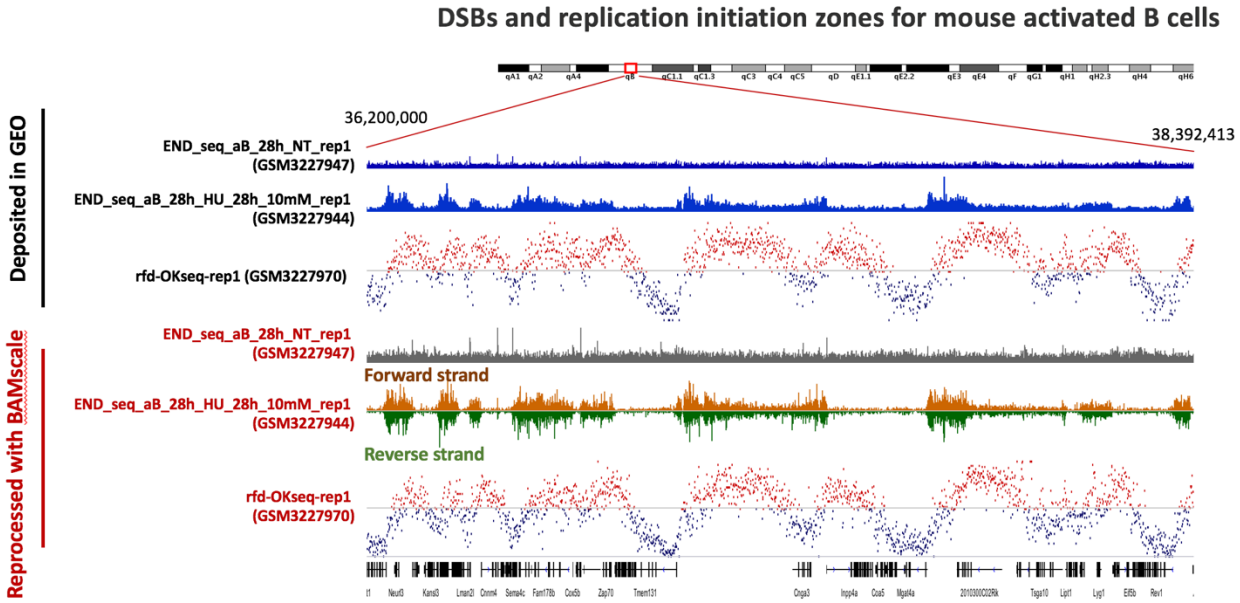
Supplementary figure 2. Colocalization of ATAC-seq peaks. Peaks with >3-fold opening had increased colocalization with H3K4me3 and H3K9ac compared to peaks with weaker or no increase.



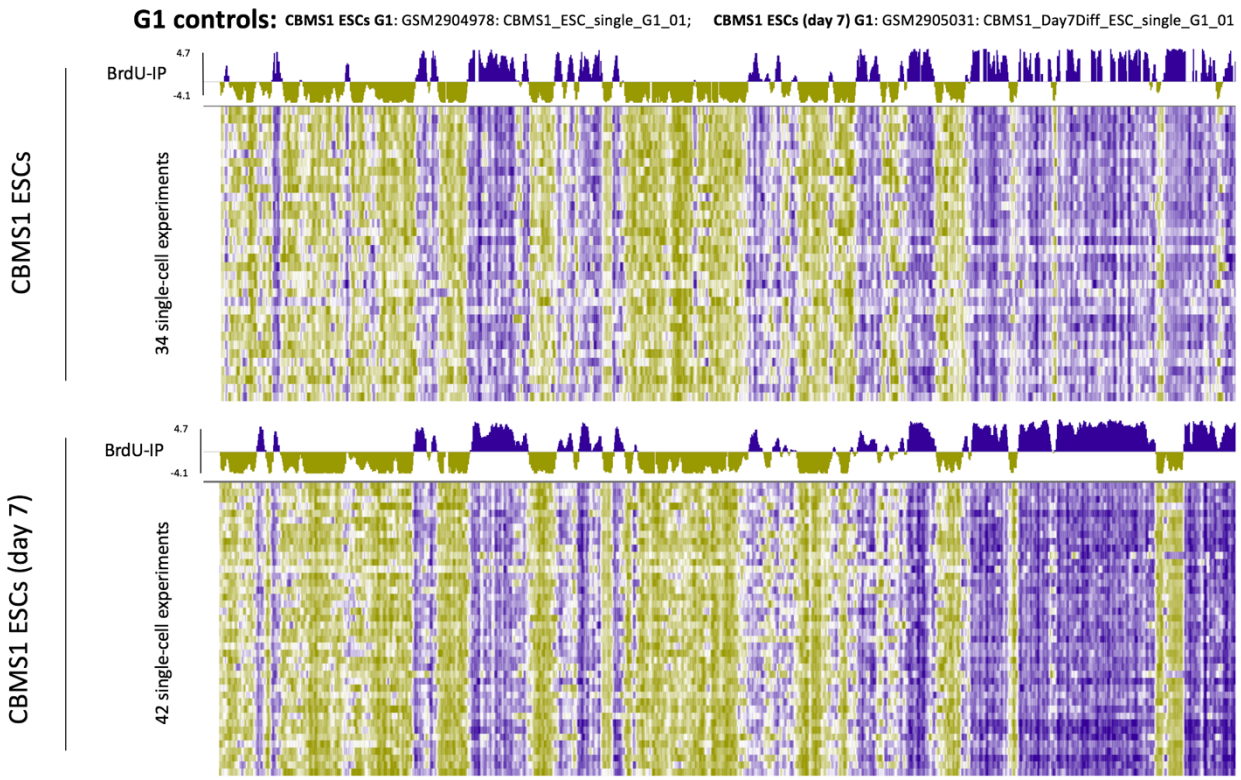
Supplementary figure 3. Changes in histone ChIP-seq signal between MV4-11 and MV4-11R cells. A) H3K27me3 signal decreased, B) H3K27ac signal increased, and C) H3K4me3 signal did not change in the MV4-11R cells compared to the MV4-11 cells.



Supplementary figure 4. Stranded and unstranded RNA-seq coverage tracks created with BAMscale.



Supplementary figure 5. Comparison of deposited END-seq and OK-seq data reprocessed with BAMscale.



Supplementary figure 6. Reproducing replication timing from single-cell Repli-seq data.