nature portfolio

https://doi.org/10.1038/s41587-021-00902-x

Supplementary information

Profiling the genetic determinants of chromatin accessibility with scalable single-cell CRISPR screens

In the format provided by the authors and unedited

Supplementary materials

Scalable pooled CRISPR screens with single-cell chromatin accessibility profiling

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Supplementary tables

Supplementary Table 1.	Number of cells in each step of the CRISPR-sciATAC protocol.
Supplementary Table 2.	Sequences of oligonucleotides for CRISPR-sciATAC, CRISPR libraries and qRT-PCR.
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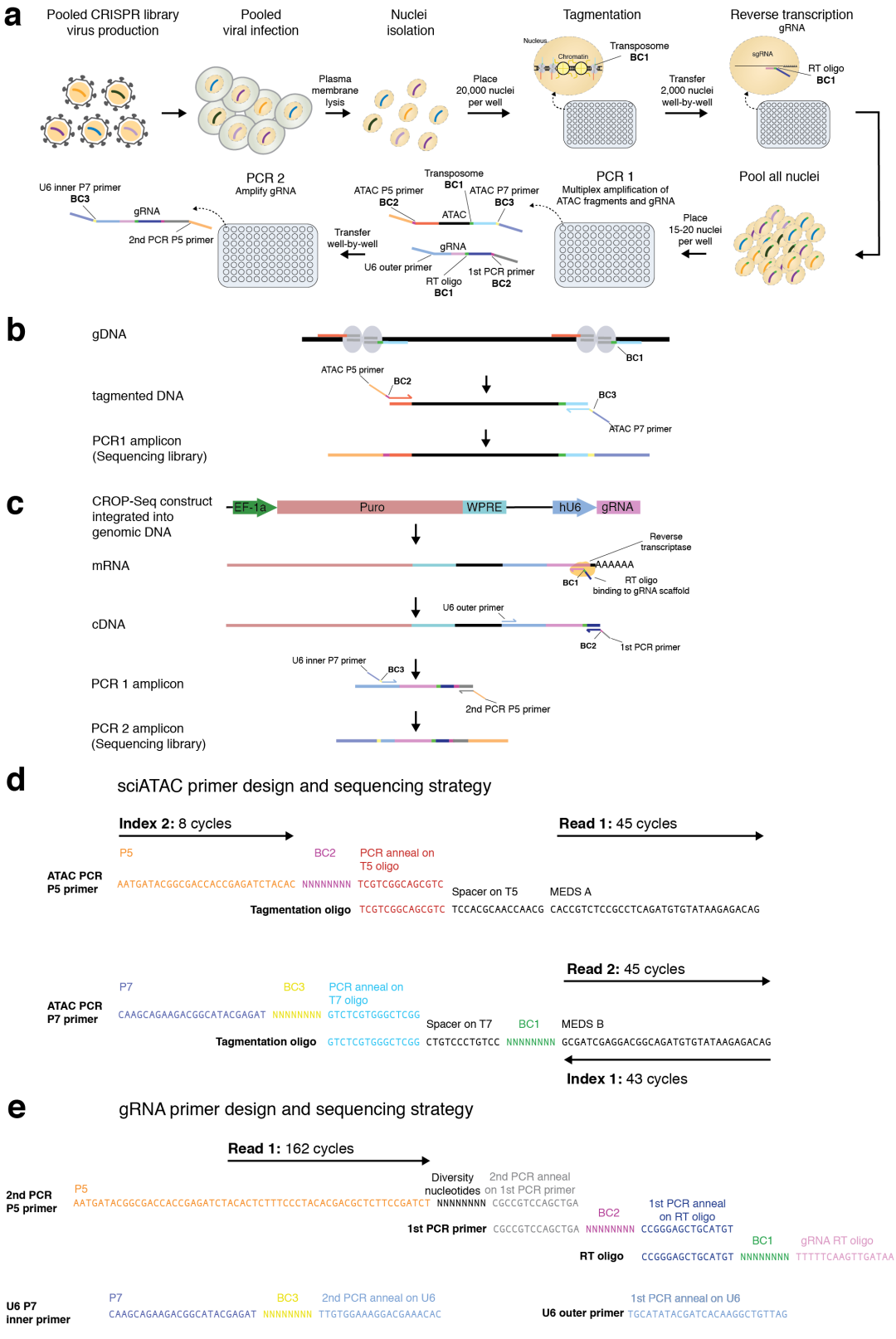
Supplementary Table 6.	GO enrichment results of differential accessibility in *EZH2*-targeted cells.
Supplementary Table 7.	Transcription factor binding site differential accessibility.
Supplementary Table 8.	Cost comparison between CRISPR-sciATAC and Perturb-ATAC protocols.
Supplementary Table 9.	Time comparison between CRISPR-sciATAC and Perturb-ATAC protocols.



Supplementary Figure 1. CRISPR-sciATAC library preparation and sequencing. (**a**) Workflow for CRISPR-sciATAC. BC, barcode. Cell barcodes consist of a unique combination of

BC1, BC2, and BC3. (**b**) CRISPR-sciATAC schematic for ATAC-seq library preparation. (**c**) CRISPR-sciATAC schematic for guide RNA (gRNA) library preparation. (**d**) CRISPR-sciATAC primer design and sequencing strategy for ATAC fragments. (**e**) CRISPR-sciATAC primer design and library sequencing strategy for gRNA amplicons. Staggered P5 oligos were introduced in the library preparation to introduce sequence diversity. BC 1, 2, and 3 are matched for ATAC-seq and gRNA libraries, e.g. the ATAC-seq BC 1 in well A1 in the 96-well plate where tagmentation is performed is the same as the gRNA BC 1 in well A1 in the 96-well plate where reverse transcription is performed.