

Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see our [Editorial Policies](#) and the [Editorial Policy Checklist](#).

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- ☒ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- ☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- ☒ The statistical test(s) used AND whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- ☒ A description of all covariates tested
- ☒ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- ☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- ☒ For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- ☒ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- ☒ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- ☒ Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection No data was collected for this study. All public data sources are listed in the methods section. No software for data collection was used.

Data analysis The code generated for this study is available on GitHub: <https://github.com/sandberg-lab/dataprivacy>
Further software used in the data analysis of this study is: zUMIs (Parekh et al., 2018; v2.9.4f), STAR (Dobin et al., 2014; v2.5.4b), Seurat (Hao et al, 2020; v3.1.5), CellRangerATAC (v1.2.0), cellsnp-lite (Huang & Huang 2021; v1.2.0), picard-tools (v2.25.0) vireo (Huang et al, 2020; v0.4.2)

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

No new data was generated in this study. Raw data in fastq format for the 10x Genomics v2 single-cell RNA sequencing experiment of five human cell lines (H2228, H1975, A549, H838 and HCC827) was obtained from the European Nucleotide Archive (accession: SRR8606521). Raw fastq data from scRNA-seq data generated using the Smart-seq3 protocol from PBMC and HEK cells were obtained from ArrayExpress (accession: E-MTAB-8735). Single-cell ATAC-seq data for human PBMCs and GM12878 cells was downloaded as preprocessed (CellRangerATAC v 1.2.0) .bam files from the 10x Genomics website (https://support.10xgenomics.com/single-cell-atac/datasets/1.2.0/atac_hgmm_1k_nextgem; https://support.10xgenomics.com/single-cell-atac/datasets/1.2.0/atac_pbmc_1k_nextgem).

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	No sample size calculation was performed as the analysis was based on publicly available datasets. The datasets were selected for being representative data with several human donors from popular sample preparation techniques to represent well the spectrum of functional genomics assays.
Data exclusions	No data exclusions were performed.
Replication	Effectiveness of our code was demonstrated in three independent datasets.
Randomization	No randomization was performed. Randomization was not applicable in our study because the study outcomes were results of software processing and not subject to human interaction.
Blinding	Research was not performed blinded. Blinding was not applicable in our study because the study outcomes were results of software processing and not subject to human interaction.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging