

Reporting Summary

Nature Portfolio 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 Portfolio 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 (<i>n</i>) 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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☒ | ☐ 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted
<i>Give P values as exact values whenever suitable.</i> |
| ☒ | ☐ 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 <i>d</i> , Pearson's <i>r</i>), 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 software was used.
Data analysis	Single-cell gene expression data were aligned to the Macaca fascicularis reference genome (macFas6) and processed for barcode assignment and unique molecular identifier (UMI) counting using the Cell Ranger v3.1.0 pipeline (10x Genomics). Filtered count matrices from the Cell Ranger pipeline were converted to sparse matrices using Seurat package (v4.0.0) in R, and cells expressing more than 4000 genes or less than 200 genes and more than 20% of mitochondrial genes expressing in UMI counts were filtered out before downstream analysis. Filtered data were then log normalized and scaled, with cell-cell variation due to UMI counts and percent mitochondrial reads regressed out. Then, we log normalised and scaled the filtered data to avoid cell-to-cell variation caused by UMI counts and percent mitochondrial reads removal. As the samples involved the integration of large multi-organ samples such as trachea and spleen, Seurat's Robust Principal Component Analysis (RPCA) method was adopted for data integration. Cell clustering was performed at 0.8 resolution using the "FindClusters" function, and cell identity were defined using the top 20 principal components (PCs), and 17 clusters were identified. Dimensionality was reduced by the "RunUMAP" function and by visual Uniform Manifold Approximation and Projection (UMAP). Different types of cells were extracted for subgroup cell clustering, and their first 20 PCs were used for clustering. In the end, we identified 40 different subgroups. To ensure the accuracy of subsequent analysis, all 40 different subgroups were processed to remove double cells. Wilcoxon rank-sum test (FindAllMarkers function with default parameters) was used to identify markers for each cluster. The scATAC-seq sequencing data are pre-processed by cellranger-atac (v1.2.0) with the count command line. The running parameters are used by default except for "--force-cells=". The "--force-cell" is 10000 for liver, lung and colon, 8000 for spleen, and the rest of the organs have no restriction on this parameter. For the subsequent scATAC-seq data processing and analysis, we used the ArchR (v1.0.1) package. Macaca fascicularis genome were constructed and annotated by createGenomeAnnotation and createGeneAnnotation function respectively. Then arrow file were created by createArrowFiles function with the default parameters. We used the addDoubletScores function to infer the doublet, filterDoublets function was used to remove the potential doublets with the "filterRatio = 1.0" parameter. ArchR project was created

by ArchRProject function with the default parameters. For dimensionality reduction, we use the addIterativeLSI function in ArchR with the following parameters: “iterations = 4, clusterParams = list (resolution = c(0.2, 0.4, 0.6), sampleCells = 10000, n.start = 10, maxClusters = 6), varFeatures = 20000, dimsToUse = 1:50, scaleDims=FALSE”. Next, the Harmony package were utilized to remove the batch effect by addHarmony function⁵⁸. AddClusters function was used to cluster cells by its default parameters. For single cell embedding, we selected the reducedDims object with harmony and used addTSNE function with the parameter “perplexity = 30” for visualization.

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 Portfolio [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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

The raw files are available from China National GeneBank (CNGB) (<https://db.cngb.org/>): RNA: CNP0002427; ATAC: CNP0002441. Gene counts and metadata are available at Zenodo (<https://zenodo.org/>): DOI: 10.5281/zenodo.5881495.

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	Tissues were collected from 16 organs including trachea, spleen, stomach, kidney, uterus, tongue, testis, muscle, lung, liver, heart, colon, breast, bladder, adipose and aorta from two cynomolgus monkeys.
Data exclusions	Not applicable
Replication	Not applicable
Randomization	Not applicable
Blinding	Not applicable

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

Animals and other organisms

Policy information about [studies involving animals](#); ARRIVE [guidelines](#) recommended for reporting animal research

Laboratory animals

Wild animals	This study did not involve wild animals
Field-collected samples	This study did not involve samples collected from the field.
Ethics oversight	The cynomolgus monkey sample collection and research conducted in this study were approved by the Research Ethics Committee of the Changchun Biotechnology Development Co., Ltd. (Approval Number: 21001).

Note that full information on the approval of the study protocol must also be provided in the manuscript.