nature research

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Last updated by author(s): Mar 28, 2020

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 Authors & Referees 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	Data were collected based on existing resources and no software was used.
Data analysis	Retrieved data clustering information was retained or reprocessed using scanpy (version 1.4.3) and harmony. Illustration of the results was generated using scanpy (version 1.4.3) and Seurat (version 3.1). The Spearman's correlation with statistical tests were done using the R Hmisc package (version 4.3-1) and the p values were adjusted with Benjamini-Hochberg method with the R stats package (version 3.6.1). Analysis notebooks are available at github.com/Teichlab/covid19_MS1.

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/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

The published datasets can be found as followed: pulmonary airways (European Genome-phenome Archive: EGAS00001001755, EGAS00001002649; lungcellatlas.org and www.genomique.eu/cellbrowser/HCA), ileum (NCBI: GSE134809), colon (Single Cell Portal: SCP259; portals.broadinstitute.org/single_cell), pancreas (NCBI: GSE84133), liver (NCBI: GSE115469), kidney (www.kidneycellatlas.org), placenta/decidua (EBI Array Express: E-MTAB-6701; maternal-fetal-interface.cellgeni.sanger.ac.uk), testis (NCBI: GSE120508), brain (www.gtexportal.org/home/data-sets), retina (NCBI: GSE135922), skin (European Genome-phenome Archive: EGAS00001002927), spleen and esophagus (tissuestabilitycellatlas.org) and fetal tissues (Array Express: E-MTAB-7407 and E-MTAB-8581; developmentalcellatlas.ncl.ac.uk).

All of the published datasets and relevant data from unpublished sources in this study can be visualized and assessed through a website portal (covid19cellatlas.org).

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

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. Selection of sample size was not relevant to this study.
Data exclusions	No data were excluded in the study.
Replication	Each dataset has biological replicates based on particular studies. The findings on airways were confirmed based on 2 independent ex vivo datasets and another in vitro culture dataset.
Randomization	This is not relevant to the study as we collected datasets from existing resources based on availability.
Blinding	This is not relevant to the study as we collected datasets from existing resources based on availability.

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
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

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