# 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<br>*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<br>*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 software was used. |
|---|---|
| Data analysis | Data were analyzed using Graphpad Prism 8.2.1 |

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

Data have been deposited in Figshare: https://doi.org/10.35092/yhjc.12026910

# 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 | Since this is a model with no prior data, it was not possible to perform a power analysis. The sample size was based on experience with other nonhuman primate models of respiratory disease. |
|---|---|
| Data exclusions | No data were excluded. |
| Replication | Lung histology: for each animal (n=4), 3 sections were evaluated from all 6 lung lobes.<br>Gastrointestinal tract, trachea, tonsil histology: Tissue sections were collected from the same anatomical location for each animal (n=4) and organ; three tissue sections were evaluated from each animal and organ.<br>Nasal turbinate histology: Tissue sections were collected from the same anatomical location for each animal (n=4) and organ; one tissue section was evaluated from each animal and organ.<br>Radiographs: Three chest radiographs were taken from each animal at each clinical exam: right-lateral, left-lateral and ventro-dorsal; only the ventro-dorsal radiograph is shown.<br>Cytokine analysis: serum samples were analyzed in duplicate from each animal for each timepoint; n= 8 animals on 0, 1, and 3 dpi and n=4 animals thereafter.<br>Ultrastructural analysis: Three tissue samples were collected from each animal (n=4) and cut into 6 samples for analysis; a minimum of 2 samples were analyzed per animal (n=4).<br>Serological analysis: Serum samples were analyzed in duplicate from each animal (n=4)for each timepoint. |
| Randomization | Animals were randomly assigned to the group euthanized at 3 dpi or 21 dpi. |
| Blinding | Blinding was not used since there was only a single treatment (inoculation with SARS-CoV-2). |

# 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 |

## Antibodies

| Antibodies used | anti-SARS nuclocapsid protein antibody; Novus Biologicals, cat.no. NB100-56576, lotno.111003003<br>anti-monkey IgG (gamma) antibody, peroxidase-labeled; KPL, cat.no. 5220-0333, lot no. 10329492 |
|---|---|
| Validation | Validation of cross-reactivity of SARS-CoV to SARS-CoV-2 in IHC was done in-house by embedding SARS-CoV-2 infected Vero cells in histogel and producing and staining histology slides. |

## Eukaryotic cell lines

Policy information about cell lines

| Cell line source(s) | VeroE6: Ralph Baric, University of North Carolina, Chapel Hill, USA |
|---|---|
| Authentication | Not authenticated in-house. |
| Mycoplasma contamination | Mycoplasma testing confirmed negative at regular intervals. |
| Commonly misidentified lines<br>(See ICLAC register) | No commonly misidentified cell lines were used. |

## Animals and other organisms

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

| | |
|---|---|
| Laboratory animals | Rhesus macaques, Chinese origin, adult (4-6 years), 4 males, 4 females |
| Wild animals | No wild animals were used. |
| Field-collected samples | No samples were collected in the field. |
| Ethics oversight | All animal experiments were approved by the Institutional Animal Care and Use Committee of Rocky Mountain Laboratories, NIH and carried out by certified staff in an Association for Assessment and Accreditation of Laboratory Animal Care (AAALAC) International accredited facility, according to the institution's guidelines for animal use, following the guidelines and basic principles in the NIH Guide for the Care and Use of Laboratory Animals, the Animal Welfare Act, United States Department of Agriculture and the United States Public Health Service Policy on Humane Care and Use of Laboratory Animals. |

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