

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

Experimental data were recorded in Microsoft Excel for Mac, version 16.35. Images were captured using a Leica DFC 5400 digital camera and were processed using Leica Application Suite v4.13

Data analysis

Data were analyzed in Microsoft Excel for Mac, version 16.35 and GraphPad Prism version 8.4.1.

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

The accession number for the SARS-CoV-2 virus used for the study was provided.
There are two figures that have associated raw data. All data will be provided upon request.

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	This is an observational study investigates the suitability of using golden Syrian hamsters as an animal model for SARS-CoV-2. There is no comparison to be made with another virus, and a sample size of 3 was selected to evaluate the level of variation between individuals. Transmission studies are generally performed in 3-4 pairs of donor: contact at 1:1 ratio (Nishura et al., PLOS ONE 2013 and Belser et al., Future Microbiol 2013).
Data exclusions	No data was excluded in the analyses.
Replication	The challenge experiment was repeatedly performed three times. Direct contact transmission experiments were independently performed twice and naive animals were co-housed with inoculated donors on day 1 and day 6, respectively. Each experiment was performed with three pairs of donor: contact at 1:1 ratio. Aerosol transmission and fomite transmission experiments were each performed once with three pairs of donor: contact at 1:1 ratio.
Randomization	Randomization was performed while assigning the animals from different litters into experimental groups.
Blinding	Blinding was not possible for the experimental design due to the need to identify each animal (inoculated or contact) accurately.

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
<input type="checkbox"/>	<input checked="" type="checkbox"/> Antibodies
<input type="checkbox"/>	<input checked="" type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology
<input type="checkbox"/>	<input checked="" type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data

Methods

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

Antibodies

Antibodies used	SARS-CoV-2 N protein was detected using monoclonal antibody (4D11). CD3 was detected using polyclonal rabbit anti-human CD3 antibody purchased from DAKO. Neuron-specific beta-III tubulin was detected using monoclonal clone TuJ1 (R&D Systems).
Validation	4D11 monoclonal antibody was reported in Nicholls et al. PLoS Med. 2006 Feb;3(2):e27. PubMed PMID: 16379499 Other antibodies are available commercially.

Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s)	Vero E6 (ATCC CRL-1586)
Authentication	The cell line was purchased from ATCC (ATCC CRL-1586). The cell line has not been authenticated since it was purchased from ATCC.
Mycoplasma contamination	The cell line was tested negative for mycoplasma.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified lines were used.

Animals and other organisms

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

Laboratory animals

Male golden Syrian hamsters, at 4-5 weeks old

Wild animals

This study does not involve wild animals.

Field-collected samples

This study does not involve field-collected samples.

Ethics oversight

Animal ethics was approved by the the Committee on the Use of Live Animals in Teaching and Research, The University of Hong Kong (CULATR # 5323-20).

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