

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 (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

FinePointe software version 2.8.0.12146(SATRR)
iSeq 100 System (Illumina)
CLC Genomics Workbench (version 22, Qiagen)
LightCycler® 96 System (Roche)
QuantStudio 6 Flex (Applied Biosystems)

Data analysis

Prism 8.0 was used for the statistical analysis.

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](#)

All data supporting the findings of this study are available in the paper. There are no restrictions in obtaining access to primary data. Source data are provided with this paper. The sequences of BA.2.75 (NCD1757) and BA.2.75 (NCD1759) determined in this study have been deposited in the Genbank with accession IDs: OQ326841 (<https://www.ncbi.nlm.nih.gov/nuccore/OQ326841>), and OQ326844 (<https://www.ncbi.nlm.nih.gov/nuccore/OQ326844>), respectively.

Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research](#).

Reporting on sex and gender

NA

Population characteristics

NA

Recruitment

NA

Ethics oversight

NA

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

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 calculations were performed. No statistical method was used to determine sample size. Wild-type and hACE2-expressing hamster experiments were performed with at least n = 4 respectively, per group. All sample sizes were chosen based on prior experience (PMID:34140350, and 32571934).

Data exclusions

No data exclusions.

Replication

All experiments with multiple biological replicates are indicated in the figure legends.

Randomization

No method of randomization was used to determine how the animals were allocated to the experimental groups and processed in this study. However, covariates including sex and age were identical in groups. Regarding the the analysis of transitions in Omicron variant, randomization is not applicable.

Blinding

No blinding was carried out due to the limited number of staff available to conduct these studies.

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	Included 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 and archaeology
<input type="checkbox"/>	<input checked="" type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern

Methods

n/a	Included 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	A rabbit polyclonal antibody for SARS-CoV nucleocapsid protein (ProSpec) was used for immunohistochemical staining.
Validation	The rabbit polyclonal antibody for SARS-CoV nucleocapsid protein (ProSpec, Catalog#:ANT-180) was validated in previous publications: Imai, M. et al. Syrian hamsters as a small animal model for SARS-CoV-2 infection and countermeasure development. Proc Natl Acad Sci U S A 117, 16587-16595, doi:10.1073/pnas.2009799117 (2020); Imai, M. et al. Characterization of a new SARS-CoV-2 variant that emerged in Brazil. Proc Natl Acad Sci U S A 118, doi:10.1073/pnas.2106535118 (2021); Halfmann, P. J. et al. SARS-CoV-2 Omicron virus causes attenuated disease in mice and hamsters. Nature, doi:10.1038/s41586-022-04441-6 (2022).

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)	VeroE6/TMPRSS2 cells (available at Japanese Collection of Research Bioresources Cell Bank, JCRB 1819), Vero E6-TMPRSS2-T2A-ACE2 cells, VRC/NIH (available at BEi Resources, NR-54970).
Authentication	Vero/TMPRSS2 and Vero E6-TMPRSS2-T2A-ACE2 cells were assumed to be authentic by the cell bank or manufactures by karyotype analysis or IFA, respectively. No further authentication was performed by the authors.
Mycoplasma contamination	All cell lines are routinely tested each month and were negative for mycoplasma.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified lines were used in this study.

Animals and other research organisms

Policy information about [studies involving animals; ARRIVE guidelines](#) recommended for reporting animal research, and [Sex and Gender in Research](#)

Laboratory animals	Male or female Syrian hamsters (6-week-old) were obtained from Japan SLC Inc., Shizuoka, Japan or Envigo, Indianapolis, USA. The K18-hACE2 transgenic hamsters (lineM41; female, 6- to 8-week-old) are described in detail elsewhere (lines M41; Gilliland T. et al. bioRxiv, doi:10.1101/2021.07.26.453840).
Wild animals	No wild animals were used in this study.
Reporting on sex	Male or female Syrian hamsters were used in the study. Female K18-hACE2 transgenic hamsters were used, due to the limited availability.
Field-collected samples	This study did not involve samples collected from the field.
Ethics oversight	Animal studies were carried out in accordance with the recommendations in the Guide for the Care and Use of Laboratory Animals of the National Institutes of Health. The protocols were approved by the Institutional Animal Care and Use Committee at University of Wisconsin, Madison (V006426) and the Animal Experiment Committee of the Institute of Medical Science, the University of Tokyo (approval number PA19-75).

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