

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 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

Data 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 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

All data in the main text and the supplementary materials have been uploaded into a password-protected cloud drive (<https://cdo.e-pro-vision.com:81/html/index.html>). Readers have read access to the data but are not allowed to export the data. The full access to the data will be available to researchers for purposes of research or regulatory decision making with a signed data access agreement after approval of a proposal. All data requests will be reviewed by the research committee at Chongqing Medical University and by the corresponding authors to verify whether the request is subject to any intellectual property or confidentiality obligations.

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	We did not perform statistical analyses to predetermine sample sizes. Individual-level data from 183 laboratory-confirmed COVID-19 cases and 1983 close contacts tested negative for RT-PCR were extracted from the epidemiological investigation reports and contract tracing records conducted by Wanzhou Center for Disease Prevention and Control, Chongqing, China from January 21 through April 10, 2020. We included all confirmed COVID-19 cases and identified close contacts in Wanzhou throughout this period. For the multilevel logistic regression which included 1398 individuals (55 cases and 1343 negative close contacts) with information on contact patterns, we performed a power calculation and found that we had a power of 0.999 to detect the associations that we observed.
Data exclusions	All confirmed cases and close contacts were included. Six imported cases who were not registered in Wanzhou, only traveled to and stayed in Wanzhou for a very short period of time, and were not administrated by Wanzhou CDC were not included as no data on them were available.
Replication	Our study is an observation study based on official records, therefore no replication is needed.
Randomization	Our study is an observation study based on official records, therefore no randomization is needed.
Blinding	Data were de-identified and analyzed by two trained researchers.

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

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

Human research participants

Policy information about [studies involving human research participants](#)

Population characteristics	The sample included 2166 COVID-19 cases and their close contacts with a mean age of 42.7 years and a standard deviation of 19.5 years. Of them, 1170 were men and 988 were women.
Recruitment	All laboratory-confirmed COVID-19 cases and their close contacts were extracted from the epidemiological investigation reports and contract tracing records conducted by Wanzhou Center for Disease Prevention and Control, Chongqing, China from January 21 through April 10, 2020.
Ethics oversight	The study was approved by the Chongqing Medical University Institutional Review Board. Written informed consent was waived, as the study retrospectively analyzed data extracted from reports of the Wanzhou District Center for Disease Control and Prevention

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