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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	No commercial, open source software, custom code was used in data collection.
Data analysis	Statistical analyses were performed using R software, version 3.6.0.

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

Raw data in this study are provided in the Supplementary Dataset. Additional supporting data are available from the corresponding authors on request. All request for raw and analyzed data and materials will be reviewed 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

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	There were 178 laboratory-confirmed COVID-19 patients in Wanzhou District (by March 2, 2020), after the symptoms screening, 135 COVID-19 patients were excluded, 6 of the 43 asymptomatic cases developed typical symptoms and were also excluded. The sex- and age-frequency matched controls including 37 symptomatic patients and 37 health subjects were also included in this study.
Data exclusions	All patients were included.
Replication	Technical replicates of our assay have been well evaluated. First, the precision and reproducibility of this assay have been evaluated by an independent third-party testing institution (National Institutes for Food and Drug Control), which is required by CFDA Based on the reports given by National Institutes for Food and Drug Control, both the within-run coefficient of variation (CV) and between-run CV were less than 8%, revealing a very good precision and reproducibility of our assay. Second, we also conducted experiments to evaluate the precision and reproducibility of our assay. Thirty serum sample from COVID-19 patients showing different titers of IgG (Range from 0.43 to 187.82) and IgM (Range from 0.26 to 24.02) were tested. Each individual sample was tested in three independent experiments, each involving technical triplicates. Third, we also tested 46 serum sample from COVID-19 patients by using different batches of diagnostic kit for novel coronavirus IgG or IgM antibody. Very good correlation was found for IgG (r = 0.996) and IgM (r = 0.997). The detailed data has been provided in our previous published paper (QX Long, et al. Antibody responses to SARS-CoV-2 in patients with COVID-19. Nature medicine. 2020 Apr 29. doi: DOI: 10.1038/s41591-020-0897-1; Table 1 and Extend Data Figure 1). After proving the good precision and reproducibility of our assay, the serum sample of each patients was measured once in hospital.
Randomization	Our study is an observation study, so no randomization is needed here.
Blinding	Serum extraction and antibody detection were performed independently by researchers blind to samples information; data analysis were performed by two trained researchers, and investigators were blinded during data analysis.

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

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	293T cell was obtained from ATCC.
Authentication	Authentication was performed regularly based on morphology and gene/protein expression (in case of genetic alterations)
Mycoplasma contamination	Cell line was tested for Mycoplasma contamination, no Mycoplasma contamination found.
Commonly misidentified lines (See ICLAC register)	None of the cell line was misidentified in this study.

Human research participants

Policy information about studies involving human research participants

Population characteristics	For the asymptomatic group, the median age was 41 years, ranged from 8 months to 75 years, and 15 of 37 were male. For the symptomatic group, the median age was 41 ranged from 9 to 75 years, and 19 of 37 were male. For the healthy control group, the median age was 35 ranged from 17 to 72 years, and 16 of 37 were male.
Recruitment	37 individuals with asymptomatic infections without any symptoms in preceding 14 days after exposure and during hospitalization in Wanzhou District were recruited. In order to reduce the confounding bias, 37 sex-, age-frequency and comorbidity-matched symptomatic patients were selected for comparison with the asymptomatic individuals. To minimize self-selection bias, no participants (including asymptomatic and symptomatic patients) had dropped out of this study. In addition, the sex- and age- frequency matched 37 control subjects with negative RT-PCR result for SARS-CoV-2 were also included in this study. Control subjects with lung, liver, kidney, cardiovascular, metabolic or immunodeficiency diseases were excluded. However, the asymptomatic infections were identified from those who were at high risk for infection (including close contacts and individuals with a history of travel to Wuhan) in a single district, not a random sample of people representative of the general population. Therefore, sample selection bias might impact results.
Ethics oversight	The study was approved by the Ethics Commission of Chongqing Medical University (reference number: 2020004). Written informed consent for participation in this study was obtained from all adult participants or guardians on behalf of the children enrolled in this study.

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