nature portfolio

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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	SPR binding assays collected and analyzed using Biacore Evaluation and Biacore Insight software SerialEM automated image acquisition software version 3.8.7 Fortebio Octet RED96 instrument software (available and referenced in the Methods section)
Data analysis	Flow cytometry data were analyzed using FlowJo v10. ELISA data was analyzed using Prism v8. Binding, Neutralization assays analyzed using PRISM (V8.0) as described in Methods. CryoEM data processing (all available and referenced in methods): RELION v4.0; MotionCor2 algorithm; Warp 1.0.7. Modelling/structure refinement/visualization (all available and referenced in methods): Coot; Namdinator; PHENIX 1.20.1; UCSF Chimera 1.14; PISA; Glyprot. Single cell sequencing data analysis: Cell Ranger v6.1.2; R statistical software v4.1.2; Seurat v4.0.5; SingleR v1.8.0; IgBlast v1.18.0; Biostrings v2.60.2. Kinetic constants calculating: Fortebio Octet Data Analysis Software. Polyreactivity data analysis: Graphpad Prism 8. Sequence alignment: IMGT/V-QUEST (http://imgt.org).

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

The raw sequencing data has been deposited in the Genome Sequence Archive of the BIG Data Center, Beijing Institute of Genomics (BIG), Chinese Academy of Science, under accession number .
All datasets and custom codes generated in the study are available from the corresponding author on reasonable request.
Databases used in this study include COV-AbDab database: http://opig.stats.ox.ac.uk/webapps/covabdab/.
EM density maps and atomic models will be deposited in the EMDB and wwPDB before publication.

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	Not applicable to this study, because no sample size calculation was performed to design the study.
Data exclusions	No data were excluded.
Replication	Experimental assays were performed in biological duplicate or triplicate (or more) according to or exceeding standards in the field. We conducted all neutralization and antibody functional assays in biological duplicate, triplicate, or more, as indicated in relevant figure legends. In all cases, representative figure displays were appropriately replicated.
Randomization	Not applicable to this study, as we do not report experiments that use randomized data.
Blinding	The investigators were not blinded to allocation during experiments and outcome assessment. Data collection and analysis were performed by different team, the sample classification were replaced by marks 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 and archaeology
☒	☐ Animals and other organisms
☐	☒ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☐	☒ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	HRP-labeled Goat Anti-Human IgG(H+L) (Beyotime, cat. A0201, dilution 1:5000); HRP-Mouse Anti-M13 antibody (NBbiolab, cat. S004H, dilution 1:5000).
Validation	HRP-labeled Goat Anti-Human IgG(H+L) is an established commercial antibody;

HRP-Mouse Anti-M13 antibody is an established commercial antibody.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	293T cells: ATCC, CRL-3216; 293T-ACE2 cells (derived from 293T): described by previously study (Feng et al., 2020); Vero E6 cells: ATCC, CRL-1586; Expi293F: ThermoFisher, cat. A14527.
Authentication	Not authenticated after purchase.
Mycoplasma contamination	The cell lines were not contaminated by mycoplasma as determined by using the Lonza Mycoplasma Detection Kit.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used.

Human research participants

Policy information about studies involving human research participants

Population characteristics	Samples were obtained from convalescent COVID-19 patients in Guangzhou Eighth People's Hospital, China.
Recruitment	The patients agreed to provide the biospecimen for detection, further diagnostic and scientific research when hospitalization.
Ethics oversight	Ethics Committee of Guangzhou Eighth People's Hospital (No. 202001134 and 202115202).

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

Flow Cytometry

Plots

Confirm that:

☒ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☒ All plots are contour plots with outliers or pseudocolor plots.

☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	Primary human B lymphocytes were obtained by purification of human blood CD19+B cells with immunomagnetic bead isolation (Miltenyi). CD27 and biotinylated spike/RBD protein incubated with enriched B cells at room temperature for 30 mins. After incubation, CD27+ and antigen-binding memory B cells were isolated by FACs (AriaFusion, BD).
Instrument	AriaFusion, BD
Software	FlowJo v10 GraphPad Prism version 8.0.
Cell population abundance	The SARS-COV-2 antigen-specific B cells constitute about 0.5%-3.0% among the CD27+B cells population.
Gating strategy	The SARS-COV-2 antigen-specific B cells were gated as CD19+CD27+RBD+S1+ cells. More information available on Extended Data Figure s1 and Methods sections.

☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.