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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 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	SoftMax Pro 7.0.2 (Molecular Devices, LL) was used to measure luminescence in the pseudovirus neutralization assays
Data analysis	This study used commercially available GraphPad Prism software v8.4 for data representation and statistical analysis (GraphPad Prism; RRID: SCR_002798).

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

Materials used in this study will be made available but may require execution of a materials transfer agreement. Source data are provided herein.

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	We obtained convalescent plasma from 20 patients, vaccinee sera from 12 Moderna SARS-Co-2 mRNA-1273 Vaccine participants and 10 Pfizer BNT162b2 Covid-19 Vaccine participants. The sample size is appropriate within technical capability to compare the difference between groups
Data exclusions	No data were excluded from the analysis
Replication	Studies that were repeated are noted in figure captions and include all studies that demonstrated the key results reported in the manuscript.
Randomization	Randomization is not relevant as this is an observational study.
Blinding	The investigators were not blinded as this is an observational study.

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	Monoclonal antibodies tested in this study were constructed and produced at Columbia University as previously described20, except REGN10933, REGN10987, REGN10985, COV2-2196, and COV2-2130 were provided by Regeneron Pharmaceuticals, Inc., Brii-196 and Brii-198 were provided by Brii Biosciences, and CB6 was provided by B.Z. and P.D.K. Most mAbs were serially diluted (5-fold dilutions) starting at 10 µg/mL. Some clinical antibodies were tested from starting concentrations of 1 µg/mL.
Validation	All of the SARS-CoV2 spike antigen-specific monoclonal antibodies have been validated by binding to SARS-CoV-2 spike and neutralizing SARS-CoV-2 pseudovirus in previous publications cited in this paper.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	In this study we used the following cell lines: Vero E6 (ATCC, Cat# CRL-1586) and HEK293T (ATCC Cat# CRL-3216).
Authentication	All cell lines were obtained from authenticated vendors. Cells were recovered as healthy logarithmically growing cells within 4 to 7 days after thawing. Viability was measured and found to be >90%.
Mycoplasma contamination	Mycoplasma is negative (Detected mycoplasma contamination using Mycoplasma PCR ELISA ,Sigma,catalog number is 11663925910)
Commonly misidentified lines (See ICLAC register)	None

Human research participants

Policy information about studies involving human research participants

Population characteristics	Plasma samples were obtained from patients (age 34-79; mean 54) convalescing from documented SARS-CoV-2 infection approximately one month after recovery or later.
Recruitment	Convalescing patients volunteered for the cohort study. These cases were enrolled into an observational cohort study of convalescent patients followed at the Columbia University Irving Medical Center starting in the Spring of 2020. From their documented clinical profiles, plasma samples from ten with severe Covid-19 were selected, along with plasma from 10 with non-severe infection, for this study.
Ethics oversight	The study protocol was approved by the CUIMC Institutional Review Board (IRB), and all participants provided written informed consent. Sera were obtained from 12 participants in a Phase 1 clinical trial of Moderna SARS-CoV-2 mRNA-1273 Vaccine conducted at the NIH, under a NIH IRB-approved protocol. Sera were also obtained from 10 individuals followed in a CUIMC IRB-approved protocol to assess immunological responses to SARS-CoV-2 who received the Pfizer BNT162b2 Covid-19 Vaccine as a part of the emergency use authorization.

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