

## 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 software was used for data collection.

Data analysis

GraphPad Prism 7.05

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

The data shown in the manuscript is available upon request from the corresponding author.

### 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://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	Sample size was determined/limited by available number of samples. The maximum number of samples available was analyzed. Positive and negative control samples for assay development showed a clear difference in reactivity that could already be detected with an n of 4 positive samples.
Data exclusions	All data was included in the analysis
Replication	Assays were repeated with 4 different substrates. ELISAs for each substrate were run once each. All attempts at replication were successful.
Randomization	Randomization was not performed since the purpose of this work was assay development.
Blinding	Blinding was not performed since the purpose of this work was assays development. Performance tests of this assay setup in our clinical laboratory have been conducted using blinded operators.

## 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

### Methods

n/a	Involved 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
<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

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

## Antibodies

Antibodies used	mAb CR3022 is a published antibody with known reactivity to the RBD of SARS-CoV-1 and 2. 1C7 is an unpublished in-house mAb with reactivity to the N protein of SARS-CoV-1 and 2.
Validation	Both mAbs were validated by binding studies to cells infected with SARS-CoV-2.

## Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s)	Sf9, High Five and and Vero.E6 cells were sourced from ATCC. Expi293F cells were sourced from ThermoFisher.
Authentication	No authentication was performed. All expression constructs were Sanger sequenced.
Mycoplasma contamination	The cell lines were not tested for mycoplasma.
Commonly misidentified lines (See <a href="#">ICLAC</a> register)	No commonly misidentified cell lines were used.

## Human research participants

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

Population characteristics	Only de-identified samples were used. This is considered non-human subject research. 16 samples were from COVID19 survivors, 109 negative control samples were from a non-COVID19 infected cohort age 20 to 65+.
Recruitment	No participants were enrolled. All samples were preexisting.
Ethics oversight	Alfred Hospital (ID #280/14) and University of Melbourne (ID #1442952.1, 1955465.2) Human Research Ethics Committees, under research permit for project TYH2018322 of Helsinki University Hospital Laboratory and by the IRB of the Icahn School of Medicine at Mount Sinai, NY

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