nature research

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Last updated by author(s): Mar 6, 2021

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	"R" is a free software program for statistical computing and graphics. Version 4 was used in this manuscript for analysis of PRNT data. SoftMax Pro Softwares is a statistical analysis program capable of analysing microplate readouts to GxP standards. Version 7.0.3 was used in this manuscript for analysis of MNA and PNA data.
Data analysis	The R script code for analysis of PRNT data has been supplied in the supplementary files. SoftMax Pro code has not been supplied but could be supplied on reasonable request to the authors.

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

The data that support the findings of this study are available from the corresponding author upon reasonable request. Some data are not publicly available due to them containing information that could compromise trial participant privacy/consent.

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	This is discussed and reported in the associated clinical trial publications.
Data exclusions	None
Replication	During qualification of the MNA; 3 operators, over 3 separate testing days, tested 6 mock-samples to generate the qualification data presented in Extended Data Figure 1.
Randomization	In the assay qualification protocol, mock-samples were allocated to plate locations randomly to minimise the impact of edge-effects on results.
Blinding	Operators were not blinded to the relative concentrations of the qualification mock-samples - blinding was not possible as the operators produced their own mock-sample panels

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	Anti-Spike Rabbit Polyclonal antibody (Sino Biologicals; 40592-T62)
Validation	Manufacturer states some cross-reactivity with SARS-CoV Spike S1 and RBD. The authors have demonstrated satisfactory virus foci staining with variants including Victoria/1/2020, B.1.1.7, B.1.351 and SARS-CoV-2 cluster 5.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	Vero E6 (ECACC), Vero hSLAM (ECACC)
Authentication	Speciated by DNA barcoded sequencing of the mitochondria cytochrome c oxidase subunit 1 gene by ECACC
Mycoplasma contamination	Tested by PCR and Hoechst 33258 by ECACC; mycoplasma not detected
Commonly misidentified lines (See ICLAC register)	None listed in ICLAC register for Vero