nature research

Corresponding author(s): Olivier Schwartz

Last updated by author(s): Mar 5, 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	Harmony Software v4.9 (Perkin-Elmer), Attune Nxt Software v3.2.1 (ThermoFischer), Flowjo Software v10.7.1
Data analysis	Excel 365 v16.46 (Microsoft), Prism v9.0.2 (GraphPad Software)

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

All data supporting the findings of this study are available within the paper and are available from the corresponding author upon request.

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	83 sera from 58 convalescent individuals, 46 sera and 41 nasal swabs from 19 vaccinees were analyzed in the study. Given the exploratory nature of the study, we did not use statistical methods to predetermine sample size. We included between 15 and 30 patients per group.
Data exclusions	None.
Replication	All experiments were performed and verified in multiple replicates as indicated in their methods/figure legends.
Randomization	The experiments were not randomized as we tested all available samples.
Blinding	The investigators were not blinded to allocation during experiments and outcome assessment. However, the clinical sampling and biological measurement were performed by different teams. Only the final assembly of the data revealed the global view of the results.

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	mAb10, 48 and 102 are human anti-S monoclonal antibodies isolated and produced by Hugo Mouquet (Institut Pasteur). The Goat anti-Human IgG (H+L) Cross-Adsorbed Secondary Antibody, Alexa Fluor 647 (A21445) was obtained from thermoFisher Scientific.
Validation	mab10,48 and 102 were validated using ELISA binding assays (against the trimeric S, RBD, and S2 proteins) by the team of Hugo Mouquet. Validation of the goat anti-human IgG is available from the ThermoFisher website.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	Vero E6 (ATCC® CRL-1586™), 293T cells (ATCC CRL- 3216) and U2OS cells (ATCC® HTB-96™), were obtained from ATCC. Freestyle 293-F were fromThermoFisher
Authentication	Cell lines were not authenticated
Mycoplasma contamination	All cells are negative for mycoplasma contamination. Tests were performed on a monthly basis
Commonly misidentified lines (See ICLAC register)	None

Human research participants

Policy information about studies involving human research participants

Population characteristics	Orleans' Cohort of convalescent and/or vaccinated individuals: since April 2020, a prospective, monocentric, longitudinal, cohort clinical study enrolling 170 SARS-CoV-2-infected individuals and 30 non-infected healthy controls is on-going, aiming to describe the persistence of specific and neutralizing antibodies over a 24-months period. Strasbourg Cohort of convalescent individuals: Since April 2020, a prospective, interventional, monocentric, longitudinal, cohort clinical study enrolling 308 RT-PCR-diagnosed SARS-CoV-2 infected hospital staff from the Strasbourg University Hospitals is on-going. Given the exploratory design of the two studies, the characteristics of participants were not pre-established when entering the cohorts. Relevant co-variates are provided in the corresponding supplementary tables.
Recruitment	Orléans cohort : Individuals admitted to the hospital for COVID-19 or with known COVID-19 consulting for a chronic disease were invited to participate. Strasbourg Cohort : Hospital staff with PCR-confirmed COVID-19 were invited to participate. Individuals were included without any selection other than those imposed by the entry criteria (known COVID-19 or vaccination). Under these conditions, no particular bias is envisaged.
Ethics oversight	Orléans cohort was approved by national external committee (CPP Ile de France IV, IRB No. 00003835). Strasbourg cohort was approved by the institutional review board of Strasbourg University Hospitals. At enrolment a written informed consent was collected for all participants.

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

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

Clinical trial registration	NCT04750720 and NCT04441684
Study protocol	All protocols can be accessed on clinicaltrial.gov
Data collection	Cohorts started at Hopitaux Universitaires de Strasbourg on April 2020 and Centre hospitalier Régional Orléans on August 2020 and are ongoing.
Outcomes	The primary outcome was the presence of SARS-CoV-2 antibodies binding to the Spike protein (S-Flow assay). The secondary outcome was the presence of neutralizing antibodies (S-Fuse assay)

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	Freshly prepared (<24h) 293T cells were stained as indicated in the method section. All samples were acquired within 24h.
Instrument	Attune NxT Acoustic Focusing Cytometer, blue/red/violet/yellow (catalog number : 15360667)
Software	AttuneNxT Software v3.2.1
Cell population abundance	At least 10,000 cells were acquired for each condition.
Gating strategy	All gates were set on 293T cells transfected with an empty plasmid.

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