nature portfolio

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Last updated by author(s): May 26, 2023

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	Microsoft Excel, Waters Empower 3, R Studio, FacsDiva, and FlowJo software were used to collect data
Data analysis	Microsoft Excel, GraphPad Prism 8, Waters Empower 3, R Studio, and FlowJo software were used to analyze data

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

All data supporting the findings of this study are available within the paper and its Supplementary Information.

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	This study collected information on participant sex as noted within the electronic medical record. We note two typos in the statistical analysis section of the methods where the word 'gender' is erroneously used instead of the word 'sex'. If we are granted the opportunity to respond to reviewer comments, we will replace the word 'gender' with the correct nomenclature of 'sex.'
Reporting on race, ethnicity, or other socially relevant groupings	This study collected information on participant race and ethnicity as noted within the electronic medical record. The details of the IMPACC study have been published in the manuscript and is cited throughout the methods section. For more information, please see the manuscript published in Science Immunology in 2021 "Immunophenotyping assessment in a COVID-19 cohort (IMPACC): A prospective longitudinal study" detailing the data collection approach: https://www.science.org/doi/10.1126/sciimmunol.abf3733
Population characteristics	This study collected information on participant comorbitiy, body mass index, time from symptom onset to hospitalization for COVID-19 infection, levels of respiratory support, SOFA score, prescription of Remdesivir, and clinical laboratory assessment of D-dimer, BUN, creatinine, and potassium as noted within the electronic medical record. For more information, please see the manuscript published in Science Immunology in 2021 "Immunophenotyping assessment in a COVID-19 cohort (IMPACC): A prospective longitudinal study" detailing the data collection approach: https://www.science.org/doi/10.1126/sciimmunol.abf3733
Recruitment	This study recruited participants admitted to the hospital and diagnosed with an acute case of COVID-19 within the first 48 hours. For more information, please see the manuscript published in Science Immunology in 2021 "Immunophenotyping assessment in a COVID-19 cohort (IMPACC): A prospective longitudinal study" detailing the data collection approach: https://www.science.org/doi/10.1126/sciimmunol.abf3733
Ethics oversight	This study was approved by Drexel's IRB Protocols 2004007753 and 2102008337

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

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	The sample size (n=22) was limited by the number of consenting participants recruited during the spring of 2020 and the remaining plasma samples available for analysis in 2022.
Data exclusions	The only cause for a clinical parameter or assayed biomarker to be excluded was due to dataset incompleteness. Any datasets missing greater than 3 of 22 values were excluded from analysis to reduce potential bias due to incomplete datasets as advised in Dong et al. 2013.
Replication	Analysis of immunoglobulin N-glycan profiles and complement deposition were experimentally repeated a minimum of two times. Clinical data, transcription data, and other parameters were collected in accordance with industry standards and these data have previously been approved for publication through other IMPACC-sponsored manuscripts.
Randomization	Patient samples were analyzed for N-glycan profiles in a randomized fashion to avoid bias in the UPLC-FLR-ESI-MS analysis pipeline due to order of samples run. During analysis of the collected datasets, samples were sorted by their IMPACC trajectory.
Blinding	Blinding of the samples during analysis was not applicable to this study as the randomized experimental methods used to analyze complement deposition and N-glycan profiles did not provide opportunity for experimental-bias or participant bias.

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
☐	☒ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

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

Antibodies

Antibodies used	FITC labeled Goat anti-Guinea pig Complement C3 antibody (MP Biomedicals, 085538)
Validation	This antibody was validated internally during the complement deposition assays by performing Flow-minus-one (FMO) to confirm the antibody does not bind non-specifically to elements other than deposited Guinea pig C3. Furthermore, this antibody has been employed in complement deposition assays developed in the Galit Alter lab in 2019. DOI: 10.1016/j.jim.2019.07.002

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJEguidelines for publication of clinical research and a completedCONSORT checklist must be included with all submissions.

Clinical trial registration	This study was not a clinical trial.
Study protocol	This study was not a clinical trial.
Data collection	We followed the protocol developed by the Drexel University IRB 2004007753 and 2102008337 during patient data collection and analysis.
Outcomes	This study was not a clinical trial.

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	We analyzed the deposition of complement onto a FluoSpheres™ NeutrAvidin™-Labeled Microspheres presenting the RBD or Spike S1 antigen to patient antibodies, adapted from the complement deposition assay protocol developed by the Galit Alter lab in 2019. DOI: 10.1016/j.jim.2019.07.002
Instrument	Fortessa Flow Cytometer (BD)
Software	We used FacsDiva and FlowJo for flow cytometry analysis
Cell population abundance	We did not analyze cells, rather we analyzed the abdunance of complement deposition on FluoSpheres™ NeutrAvidin™-Labeled Microspheres as adapted from the complement deposition assay protocol developed by the Galit Alter lab in 2019. DOI: 10.1016/j.jim.2019.07.002.
Gating strategy	Please see figure 5B for an example of the gating strategy. We followed the gating strategy adapted from the complement deposition assay protocol developed by the Galit Alter lab in 2019. DOI: 10.1016/j.jim.2019.07.002.

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