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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 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	BD FACS DIVA v8.0.1
Data analysis	FlowJo v10.5.3, Prism v8.3.1,

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

FACS plots, immunofluorescence and X-rays show raw data. Source data are supplied in "Source Data.xlsx" file

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 was determined by the availability of samples: this is a COVID-2019 patient case report.
Data exclusions	No data were excluded.
Replication	Experiments in figure 1 c were repeated twice in duplicates, with similar results. We have performed repeated flow cytometry stains and analyses, when feasible given the limited clinical material: Staining for COVID patient ASC (Fig 1d) was repeated twice for d7 and d20, and three times for d8, d9 time-points, with similar results. Staining for CD38+HLA-DR+ CD8+ T cells (fig 1e) was repeated twice for d8 and d20, with similar results. Due to a limitation in clinical specimens, the remaining stains for Tfhs, NK cells, CD38+HLA-DR+ CD4+ T cells and monocytes was performed once.
Randomization	It is a case study this randomization was not applicable
Blinding	Experiments were not blinded as this was a Case 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
☒	☐ Animals and other organisms
☐	☒ Human research participants
☒	☐ Clinical data

Methods

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

Antibodies

Antibodies used

We used commercially-available antibodies:
Antibody/Clone/Fluorochrome/Dilution/Vendor/Cat number:
CD45RA HI100 FITC 1:50 BD Pharmingen 555488
CD8a SK1 PerCP-Cy5.5 1:50 BD Pharmingen 565310
CD56 MEM-188 APC 1:50 Biolegend 304610
CD16 3G8 AF700 1:50 Biolegend 302026
CD14 MΦP9 APC-Cy7 1:50 BD Pharmingen 560180
CD19 HIB19 BV570 1:200 Biolegend 302236
HLA-DR L243 BV605 1:50 Biolegend 307640
CD4 SK3 BV650 1:200 BD Biosciences 563875
CD27 L128 BV711 1:100 BD Horizon 563167
CD38 HIT2 BV786 1:400 BD Horizon 563964
CD3 UCHT1 PECF594 1:600 BD Biosciences 562280
Granzymes/perforin panel:
Surface
CD45RA HI100 FITC 1:50 BD Pharmingen 555488
CD8a RPA-T8 BV421 1:200 BD Pharmingen 301036
CD14 MΦP9 APC-H7 1:100 BD Pharmingen 560180
CD19 SJ25C1 APC-H7 1:100 Biolegend 560177
HLA-DR L243 BV605 1:50 Biolegend 307640
CD4 SK3 BV650 1:200 BD Biosciences 563875
CD27 L128 BV711 1:400 BD Horizon 563167
CD38 HIT2 BV786 1:400 BD Horizon 563964
CD3 UCHT1 PECF594 1:600 BD Biosciences 562280
Intracellular
Granzyme A CB9 PE 1:50 eBioscience 12-9177-42

Granzyme B GB11 AF700 1:50 BD Pharmingen 560213
Granzyme K G3H69 PerCP-eFluor710 1:50 eBioscience 46-8897-42
Granzyme M 4B2G4 eFluor660 1:50 eBioscience 50-9774-42
Perforin B-D48 Pe-Cy7 1:10 Biolegend 353316

Validation

Each antibody used had a validated technical data sheet as per manufacturer's website showing positive staining, and titrated in our laboratory prior to their use.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)

Vero cells are African Green monkey kidney cells; were used for SARS-CoV-2 infections. Source ATCC – CRL01586 (Vero C1008 Kidney, Monkey). Lot 3338237

Authentication

Cells line was not authenticated

Mycoplasma contamination

Mycoplasma free (tested recently)

Commonly misidentified lines
(See ICLAC register)

The cell line used is not listed in the ICLAC database

Human research participants

Policy information about studies involving human research participants

Population characteristics

This is a case report:
A 47-year old woman from Wuhan, Hubei province, China presented to an emergency department in Melbourne, Australia. Her symptoms commenced 4-days earlier with lethargy, sore throat, dry cough, pleuritic chest pain, mild dyspnoea and subjective fevers (Fig.1a). She travelled 11 days prior to presentation from Wuhan to Australia. She had no contact with the Huanan seafood market or known COVID-19 cases. She was otherwise healthy, non-smoker, taking no medications. Clinical examination revealed a temperature of 38.5□C, pulse rate 120 beats/minute, blood pressure 140/80 mmHg, respiratory rate 22 breaths/minute, and oxygen saturation 98%, while breathing ambient air. Lung auscultation revealed bibasal rhonchi. At presentation day (d) 4, SARS-CoV-2 was detected by real-time reverse-transcriptase polymerase-chain-reaction (rRT-PCR) from a nasopharyngeal swab specimen. SARS-CoV-2 was again detected at d5-6 from nasopharyngeal, sputum and faecal samples, but undetectable from d7 (Fg.1a). Blood C-reactive protein was elevated at 83.2, with normal lymphocyte (4.3x109/L [range 4.0-12.0x109/L]) and neutrophil counts (6.3x109/L [range 2.0-8.0x109/L]). No other respiratory pathogens were detected. Her management was intravenous fluid rehydration without supplemental oxygenation. No antibiotics, steroids or antiviral agents were administered. Chest radiography demonstrated bibasal infiltrates at d5, which cleared on d10 (Fig.1b). She was discharged to home isolation on d11. Symptoms resolved completely by d13 and she remained well at d20.

Healthy donors (n=10), 4 females, 6 males, mean age of 34.
Influenza-patients (n=5), 1 female, 4 males, mean age of 55.
Human HCoV-229e Cov patient (n=1), 1 male, age 27.

Recruitment

Healthy volunteer donors >18 years old were recruited through University of Melbourne (UoM) and virus-infected patients were recruited at Royal Melbourne Hospital (RMH). Signed informed consents were obtained from all blood donors prior to study.

Ethics oversight

Human experimental work was conducted according to the Declaration of Helsinki Principles and according to the Australian National Health and Medical Research Council Code of Practice. Participants provided written informed consent prior to the study. The study was approved by the Royal Melbourne Hospital (HREC Reference number: HREC/17/MH/53 and HREC/15/MonH/64/2016.196) and University of Melbourne (ID #1442952.1 and #1443389.4) Human Research Ethics Committees.

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

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	Whole blood staining was performed as outlined in fig legends to Extended Data
Instrument	BD LSR Fortessa was used for acquisition of data
Software	BD FACS Diva v8.0.1, FlowJo v10.5.3
Cell population abundance	We have not sorted the PBMCs
Gating strategy	Gating strategy has been described in methods, figure legends and as Extended Data figure 3

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