

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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☒ | ☐ 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
<i>Give P values as exact values whenever suitable.</i> |
| ☒ | ☐ 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; Flowjo Version 10.6.2; ImmunoSpot 7.0.26.0
Viral sequences were aligned using the MUSCLE algorithm (3.8.425) with default parameters and percentage identity was calculated in Geneious Prime 2020.1.2 (<https://www.geneious.com>). Alignment figures were made in Snapgene 5.1 (GSL Biotech).

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

Coronavirus reference protein sequences for ORF1ab and Nucleocapsid Protein were downloaded from the NCBI database. All other data are included in this 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](https://www.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	Aim of the study was to characterize SARS-CoV-2-specific T cells in patients who recovered from SARS 17 years ago. 23 of those individuals gave informed consent and were available to donate blood samples. Therefore similar numbers of COVID-19 convalescents and non-infected controls were selected.
Data exclusions	No data points were excluded.
Replication	We evaluated the SARS-CoV-2 specific T cell responses in 36 COVID-19 convalescents, in 23 SARS-recovered, and in 37 uninfected donors.
Randomization	No randomization was used in this study, since we are comparing 3 different well defined cohorts: COVID-19 convalescents, SARS recovered patients and SARS-CoV-1/2 non-exposed individuals.
Blinding	Blinding was not done for this study. The groups were defined by their infection history and studied by the investigators using standard protocols.

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	ELISpot: IFN- γ coating antibody (clone: 1-D1K, MabTech, Cat. Nr. 3420-3-1000); biotinylated IFN- γ detection antibody (clone: 7-B6-1, MabTech, Cat. Nr. 3420-6-1000) Flow cytometry: anti-human CD3-PerCP-cy5.5 (BD Pharmingen, clone: SK7, Cat. Nr. 340949); anti-human CD4-PECy7 (BD Pharmingen, clone: SK3, Cat. Nr. 557852); anti-human CD8-APC-Cy7 (BD Pharmingen, clone: SK1, Cat. Nr. 557834); anti-human TNF α -APC (BD Pharmingen, clone: MAb11, Cat. Nr. 554514); anti-human IFN γ -PE (R&D Systems, clone: 25273, Cat. Nr. IC285P); anti-human CCR7-BV421 (BD Pharmingen, clone: 150503, Cat. Nr. 562555); anti-human CD45RA-FITC (BD Pharmingen, clone: HI100, Cat. Nr. 555488)
Validation	All antibodies were obtained from commercial vendors and we based specificity on descriptions and information provided in corresponding Data Sheets available and provided by the Manufacturers.

Human research participants

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

Population characteristics	The characteristics of the human research participants are described in Extended Data Table 1 of the manuscript.
Recruitment	All donors were recruited based on the infection history. COVID-19 convalescents were previously PCR positive for SARS-CoV-2; SARS-recovered donors were tested PCR positive 17 years ago for SARS-CoV. Written informed consent was obtained from all subjects. All donors were recruited and resident in Singapore, were of mixed ethnicity and age.
Ethics oversight	Written informed consent was obtained from all subjects. The study was conducted in accordance with the Declaration of Helsinki and approved by the NUS institutional review board (H-20-006); SingHealth Centralised Institutional Review Board (reference CIRB/F/2018/2387)

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	PBMC and T cell lines were prepared and stained according to standard protocols
Instrument	BD-LSR II FACS Scan
Software	Flowjo Version 10.6.2
Cell population abundance	N/A. No sorting was performed.
Gating strategy	Gating strategy: live cells (yellow LIVE/DEAD positive cells were excluded); singlets (SSC-H/SSC-A); Lymphocytes (FSC-A/SSCA); CD3+ (CD-3-PerPC-Cy5.5/CD8-APC-Cy7); CD4+ and CD8+ (CD4-PECy7/CD8-APC-Cy7); IFNg+ and TNFa+ gates were based on the unstimulated control sample.

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