nature portfolio

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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: for data collection no software was used

Data analysis:

FlowJO 10.8
GraphPad Prism 7
GraphPad Prism 8
Excel2013

R language version 4.2.2, with packages:
tidyverse version 1.3.2
Seurat verseion 4.3.0
vroom version 1.6.0
cluster version 2.1.4
enrichR version 3.1
KEGGREST version 1.36.3
censReg version 0.5.36
ggplot2 version 3.4.0
readxl version 1.4.1

Python version 3.9.7, with packages:
numpy version 1.22.4
pandas version 1.5.0

Julia version 1.7.0, with packages
HCubature
XLSX version 0.8.4
DataFrames version 1.3.6
Distributions version 0.25.6
QuadGK version 2.8.1
FastGaussQuadrature version 0.5.0
LinearAlgebra -> no version number
ForwardDiff version 0.10.35
Optim version 1.7.4
LineSearches version 7.2.0
Random version -> no version number availbe

multiple graphic libraries
The code will be made public on GitHub as soon as the manuscript is accepted.
Respective link to the repository is included in the manuscript

https://github.com/TropI-LMU/Eser2022
https://github.com/manuhuth/early_t_cell_control.git

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

The RNA sequencing data of CoKo19 patients are available under restricted access upon request from the corresponding author Christof Geldmacher [Christof.Geldmacher@lrz.uni-muechen.de] This restriction is necessary due to applicable data privacy laws in Germany.
Single cell datasets used in this publication have been previously published by Ziegler et. al. [https://singlecell.broadinstitute.org/single_cell/study/SCP1289/impaired-local-intrinsic-immunity-to-sars-cov-2-infection-in-severe-covid-19] and Yoshida et. al. [https://www.covid19cellatlas.org/index.patient.html ; COVID-19 airway and matched PBMCs from UCL-Sanger, only airway set was used].
Pathway information and gene lists are available at the website of Kyoto Encyclopedia of Genes and Genomes. [https://www.genome.jp/kegg-bin/get_htext?ko00001.keg]. Gene Onthology Terms are available at http://geneontology.org/docs/download-go-annotations/ . Both KEGG and GO terms were accessed via the enrichR package from R language.
Code used to generate RNA and single cell analysis is available at https://github.com/TropI-LMU/Eser2022 .

Human research participants

Policy information about studies involving human research participants and Sex and Gender in Research.

Reporting on sex and gender	We report on the biological sex of participants in table 1 and in the text. The Data is not analyzed in relation to sex.
Population characteristics	Patient characteristics are provided in table 1.
Recruitment	Recruitment of study patients is detailed in the materials and methods "Study participants". The Division of infectious diseases and tropical medicine hosted a SARS-CoV-2 Corona test center primarily for employees of the LMU University clinics. All individuals with a positive SARS-CoV-2 PCR result were informed and asked to participate in the study. Those who consented were then recruited without further delay. There was no further selection applied and we do not see bias that possibly could have negatively impacted on the results.
Ethics oversight	Ethics Committee of the Faculty of Medicine at LMU Munich (20–371)

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	No sample size calculations were performed in advance, because this was a purely observational study to investigate events and host responses during and after acute SARS-CoV-2 infection.
Data exclusions	No data were excluded from the analyses of the primary KoCo19-Immun data (Figure 1-4). For the scRNA sequencing analyses (Figure 5), patient 19 from the SARS-CoV-2 positive group from the Ziegler et.al. dataset wa s excluded due to abnormal number of monocytes (order of magnitude above the rest of COVID-19 positive subjects). This step was performed before any attempts of differential gene expression or gene set enrichment analyses. The exclusion of COVID-positive patient 19 was not planned before the analysis, but was done based on the quality control (QC). After QC of the data we noticed that patient 19 had an abnormally high amount of macrophages (orders of magnitude above the rest of the cohort). Hence before proceeding with the analysis we have excluded all cells assigned to this patient. So, in summary, the exclusion was not predetermined, but was made after the QC and before the differential expression analysis.
Replication	We report results regarding differentially expressed genes that were differentially expressed two analysed scRNA sequencing data sets and differentiate from those that were identified only in one data set.
Randomization	not applicable, it was a purley observation study without diffrent study groups,
Blinding	Immunological results were generated "blinded" to other relevant immunological parameters and upper airway viral loads.

Behavioural & social sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	*Briefly describe the study type including whether data are quantitative, qualitative, or mixed-methods (e.g. qualitative cross-sectional, quantitative experimental, mixed-methods case study).*
Research sample	*State the research sample (e.g. Harvard university undergraduates, villagers in rural India) and provide relevant demographic information (e.g. age, sex) and indicate whether the sample is representative. Provide a rationale for the study sample chosen. For studies involving existing datasets, please describe the dataset and source.*
Sampling strategy	*Describe the sampling procedure (e.g. random, snowball, stratified, convenience). Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient. For qualitative data, please indicate whether data saturation was considered, and what criteria were used to decide that no further sampling was needed.*
Data collection	*Provide details about the data collection procedure, including the instruments or devices used to record the data (e.g. pen and paper, computer, eye tracker, video or audio equipment) whether anyone was present besides the participant(s) and the researcher, and whether the researcher was blind to experimental condition and/or the study hypothesis during data collection.*
Timing	*Indicate the start and stop dates of data collection. If there is a gap between collection periods, state the dates for each sample cohort.*
Data exclusions	*If no data were excluded from the analyses, state so OR if data were excluded, provide the exact number of exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.*
Non-participation	*State how many participants dropped out/declined participation and the reason(s) given OR provide response rate OR state that no participants dropped out/declined participation.*
Randomization	*If participants were not allocated into experimental groups, state so OR describe how participants were allocated to groups, and if allocation was not random, describe how covariates were controlled.*

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	*Briefly describe the study. For quantitative data include treatment factors and interactions, design structure (e.g. factorial, nested, hierarchical), nature and number of experimental units and replicates.*
Research sample	*Describe the research sample (e.g. a group of tagged Passer domesticus, all Stenocereus thurberi within Organ Pipe Cactus National*

Research sample	*Monument), and provide a rationale for the sample choice. When relevant, describe the organism taxa, source, sex, age range and any manipulations. State what population the sample is meant to represent when applicable. For studies involving existing datasets, describe the data and its source.*
Sampling strategy	*Note the sampling procedure. Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient.*
Data collection	*Describe the data collection procedure, including who recorded the data and how.*
Timing and spatial scale	*Indicate the start and stop dates of data collection, noting the frequency and periodicity of sampling and providing a rationale for these choices. If there is a gap between collection periods, state the dates for each sample cohort. Specify the spatial scale from which the data are taken*
Data exclusions	*If no data were excluded from the analyses, state so OR if data were excluded, describe the exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.*
Reproducibility	*Describe the measures taken to verify the reproducibility of experimental findings. For each experiment, note whether any attempts to repeat the experiment failed OR state that all attempts to repeat the experiment were successful.*
Randomization	*Describe how samples/organisms/participants were allocated into groups. If allocation was not random, describe how covariates were controlled. If this is not relevant to your study, explain why.*
Blinding	*Describe the extent of blinding used during data acquisition and analysis. If blinding was not possible, describe why OR explain why blinding was not relevant to your study.*

Did the study involve field work? ☐ Yes ☒ No

Field work, collection and transport

Field conditions	*Describe the study conditions for field work, providing relevant parameters (e.g. temperature, rainfall).*
Location	*State the location of the sampling or experiment, providing relevant parameters (e.g. latitude and longitude, elevation, water depth).*
Access & import/export	*Describe the efforts you have made to access habitats and to collect and import/export your samples in a responsible manner and in compliance with local, national and international laws, noting any permits that were obtained (give the name of the issuing authority, the date of issue, and any identifying information).*
Disturbance	*Describe any disturbance caused by the study and how it was minimized.*

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

Methods

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

Antibodies

Antibodies used	anti-CD28 (L293) (pure BD) anti-CD49 (L49) (pure BD) anti-CD4–ECD (clone SFCI12T4D11, Beckman Coulter) anti-CD8–APC-AF750 (clone B9.11, Beckman Coulter) CD3–APC-AF700 (clone UCHT1, Beckman Coulter) anti-IFN-γ–FITC (clone 4S.B3, BioLegend)

	in addition to these other antibodies were used in the staining panel as detailed below and in the manuscript, but results were not provided or relevant for this analyses.
Validation	FMO control and titration experiments were performed to define the optimal amount of each antibody for our experiments. All antibodies are suited for staining human samples. Any further information on antibody validation can be found on the respective webpages of the producing company.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	HEK-293T-ACE2 cells available from ATCC 293T-ACE2 cells available from BEI resources Catalog # 52511
Authentication	Cell lines were not authenticated
Mycoplasma contamination	Cells lines were not checked for Mycoplasma contamination
Commonly misidentified lines (See ICLAC register)	*Name any commonly misidentified cell lines used in the study and provide a rationale for their use.*

Palaeontology and Archaeology

Specimen provenance	*Provide provenance information for specimens and describe permits that were obtained for the work (including the name of the issuing authority, the date of issue, and any identifying information). Permits should encompass collection and, where applicable, export.*
Specimen deposition	*Indicate where the specimens have been deposited to permit free access by other researchers.*
Dating methods	*If new dates are provided, describe how they were obtained (e.g. collection, storage, sample pretreatment and measurement), where they were obtained (i.e. lab name), the calibration program and the protocol for quality assurance OR state that no new dates are provided.*

☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.

Ethics oversight	*Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance was required and explain why not.*

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

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals	*For laboratory animals, report species, strain and age OR state that the study did not involve laboratory animals.*
Wild animals	*Provide details on animals observed in or captured in the field; report species and age where possible. Describe how animals were caught and transported and what happened to captive animals after the study (if killed, explain why and describe method; if released, say where and when) OR state that the study did not involve wild animals.*
Reporting on sex	*Indicate if findings apply to only one sex; describe whether sex was considered in study design, methods used for assigning sex. Provide data disaggregated for sex where this information has been collected in the source data as appropriate; provide overall numbers in this Reporting Summary. Please state if this information has not been collected. Report sex-based analyses where performed, justify reasons for lack of sex-based analysis.*
Field-collected samples	*For laboratory work with field-collected samples, describe all relevant parameters such as housing, maintenance, temperature, photoperiod and end-of-experiment protocol OR state that the study did not involve samples collected from the field.*
Ethics oversight	*Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance was required and explain why not.*

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	not applicable

Study protocol	The study protocol "PROSPEKTIVE COVID-19 KOHORTE MÜNCHEN – IMMUNOLOGIE" is not publicly available but can be made available upon reasonable request.
Data collection	Patients with acute COVID-19 and controls were recruited into this study between May and December 2020 in Munich under the umbrella of the longitudinal KoCo19 study.
Outcomes	This was an observational study without predefined outcomes.

Dual use research of concern

Policy information about dual use research of concern

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No	Yes	
☐	☐	Public health
☐	☐	National security
☐	☐	Crops and/or livestock
☐	☐	Ecosystems
☐	☐	Any other significant area

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes	
☐	☐	Demonstrate how to render a vaccine ineffective
☐	☐	Confer resistance to therapeutically useful antibiotics or antiviral agents
☐	☐	Enhance the virulence of a pathogen or render a nonpathogen virulent
☐	☐	Increase transmissibility of a pathogen
☐	☐	Alter the host range of a pathogen
☐	☐	Enable evasion of diagnostic/detection modalities
☐	☐	Enable the weaponization of a biological agent or toxin
☐	☐	Any other potentially harmful combination of experiments and agents

ChIP-seq

Data deposition

☐ Confirm that both raw and final processed data have been deposited in a public database such as GEO.

☐ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links *May remain private before publication.*	*For "Initial submission" or "Revised version" documents, provide reviewer access links. For your "Final submission" document, provide a link to the deposited data.*
Files in database submission	*Provide a list of all files available in the database submission.*
Genome browser session (e.g. UCSC)	*Provide a link to an anonymized genome browser session for "Initial submission" and "Revised version" documents only, to enable peer review. Write "no longer applicable" for "Final submission" documents.*

Methodology

Replicates	*Describe the experimental replicates, specifying number, type and replicate agreement.*
Sequencing depth	*Describe the sequencing depth for each experiment, providing the total number of reads, uniquely mapped reads, length of reads and whether they were paired- or single-end.*
Antibodies	*Describe the antibodies used for the ChIP-seq experiments; as applicable, provide supplier name, catalog number, clone name, and lot number.*
Peak calling parameters	*Specify the command line program and parameters used for read mapping and peak calling, including the ChIP, control and index files used.*

Data quality	*Describe the methods used to ensure data quality in full detail, including how many peaks are at FDR 5% and above 5-fold enrichment.*
Software	*Describe the software used to collect and analyze the ChIP-seq data. For custom code that has been deposited into a community repository, provide accession details.*

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	PBMCs were isolated within 6 h of blood collection via density gradient centrifugation (Cytiva Sweden AB). In the final step Complete Medium (RPMI medium (R)= 442.5ml RPMI 1640 W/Glutamax + 5ml Penicillin-Streptomycin+ 50 ml FCS) was added and the fresh PBMCs were directly stimulated with 15mer peptide pools overlapping by 11 amino acids representing the NC or S proteins of SARS-CoV-2 (1 µg/ml/peptide, Miltenyi Biotec Peptivator SARS-CoV-2 Prot_S and Prot_N) for 16 h at 37°C in the presence of anti-CD28 (clone L293, 1 µg/ml, BD Biosciences), anti-CD49d (clone L25, 1 µg/ml, BD Biosciences), and brefeldin A (5 µg/ml, Sigma-Aldrich). Negative control wells lacked stimulants (complete medium alone) and positive control wells contained staphylococcal enterotoxin B (SEB, 0.6 µg/ml, Sigma-Aldrich). Cells were then stained with anti-CD4–ECD (clone SFCI12T4D11, Beckman Coulter), anti-CD8–APC-AF750 (clone B9.11, Beckman Coulter), anti-CD57–APC (clone HNK-1, BioLegend), anti-PD1–PE-Cy5.5 (clone NAT105, BioLegend), and anti-CXCR5–PE-Cy7 (clone J252D4, BioLegend). Labeled cells were fixed/permeabilized using a FoxP3 / Transcription Factor Staining Buffer Set (eBioscience) and further stained intracellularly with anti-CD3–APC-AF700 (clone UCHT1, Beckman Coulter), anti-IFN-γ–FITC (clone 4S.B3, BioLegend), anti-IL2–PE (clone MQ1-17H12, BioLegend), anti-TNF-α–BV510 (clone mAb11, BioLegend), anti-CTLA-4–BV421 (clone BNI3, BioLegend), anti-Ki-67–BV605 (clone Ki-67, BioLegend), and anti-CD40L–BV785 (clone 24-31, BioLegend).
Instrument	CytoFLEX Flow Cytometer (Beckman Coulter)
Software	Data analysis was performed using FlowJo software version 10.8 (FlowJo LLC)
Cell population abundance	SARS-CoV-2-specific T cell responses were defined on the basis of IFN-γ production and were considered positive at a frequency of ≥0.01% after background subtraction if greater than the corresponding unstimulated values by a factor of ≥2.
Gating strategy	The gating strategy is shown in supplementary figure 2. The red lines/ boxes indicatet the cutoffs.

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

Magnetic resonance imaging

Experimental design

Design type	*Indicate task or resting state; event-related or block design.*
Design specifications	*Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial or block (if trials are blocked) and interval between trials.*
Behavioral performance measures	*State number and/or type of variables recorded (e.g. correct button press, response time) and what statistics were used to establish that the subjects were performing the task as expected (e.g. mean, range, and/or standard deviation across subjects).*

Acquisition

Imaging type(s)	*Specify: functional, structural, diffusion, perfusion.*
Field strength	*Specify in Tesla*
Sequence & imaging parameters	*Specify the pulse sequence type (gradient echo, spin echo, etc.), imaging type (EPI, spiral, etc.), field of view, matrix size, slice thickness, orientation and TE/TR/flip angle.*
Area of acquisition	*State whether a whole brain scan was used OR define the area of acquisition, describing how the region was determined.*

Diffusion MRI ☐ Used ☐ Not used

Preprocessing

Preprocessing software — *Provide detail on software version and revision number and on specific parameters (model/functions, brain extraction, segmentation, smoothing kernel size, etc.).*

Normalization — *If data were normalized/standardized, describe the approach(es): specify linear or non-linear and define image types used for transformation OR indicate that data were not normalized and explain rationale for lack of normalization.*

Normalization template — *Describe the template used for normalization/transformation, specifying subject space or group standardized space (e.g. original Talairach, MNI305, ICBM152) OR indicate that the data were not normalized.*

Noise and artifact removal — *Describe your procedure(s) for artifact and structured noise removal, specifying motion parameters, tissue signals and physiological signals (heart rate, respiration).*

Volume censoring — *Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.*

Statistical modeling & inference

Model type and settings — *Specify type (mass univariate, multivariate, RSA, predictive, etc.) and describe essential details of the model at the first and second levels (e.g. fixed, random or mixed effects; drift or auto-correlation).*

Effect(s) tested — *Define precise effect in terms of the task or stimulus conditions instead of psychological concepts and indicate whether ANOVA or factorial designs were used.*

Specify type of analysis: ☐ Whole brain ☐ ROI-based ☐ Both

Statistic type for inference (See Eklund et al. 2016) — *Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.*

Correction — *Describe the type of correction and how it is obtained for multiple comparisons (e.g. FWE, FDR, permutation or Monte Carlo).*

Models & analysis

n/a	Involved in the study
☐	☐ Functional and/or effective connectivity
☐	☐ Graph analysis
☐	☐ Multivariate modeling or predictive analysis

Functional and/or effective connectivity — *Report the measures of dependence used and the model details (e.g. Pearson correlation, partial correlation, mutual information).*

Graph analysis — *Report the dependent variable and connectivity measure, specifying weighted graph or binarized graph, subject- or group-level, and the global and/or node summaries used (e.g. clustering coefficient, efficiency, etc.).*

Multivariate modeling and predictive analysis — *Specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.*