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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 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	GraphPad Prism V.8 Microsoft Excel V16.16.27 (201012) BD FACSDiva 6.1.2
Data analysis	GraphPad Prism V.8 Microsoft Excel V16.16.27 (201012) BD FlowJo V.10

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

Source data for Figure 3 (i.e. uncropped gel pictures, OD values, yields, and concentrations) are provided as Source Data files with this paper.

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 relevant for our study.
Data exclusions	No data was excluded from the study.
Replication	Reproducibility of the experimental findings was verified in mutliple, independent experiments. Results have already been published in primary research papers . Please refer to "Related links" section.
Randomization	Randomization was not relevant for our study.
Blinding	Blinding was not relevant for our 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 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	• Alexa Fluor 700 mouse anti-human CD20 (BD biosciences, cat. no. 560631) • APC mouse anti-human IgG (BD biosciences, cat. no. 550931) • HRP-conjugated polyclonal goat anti-human IgG (Fcγ Fragment Specific) (Jackson ImmunoResearch, cat. no. 109-035-098) • IgG1 kappa from human myeloma plasma (Sigma Aldrich, cat. no. I5154) • Polyclonal goat anti-human IgG (Fcγ Fragment Specific) (Jackson ImmunoResearch, cat. no. 109-005-098)
Validation	Antibodies were used for ELISA or flow cytometry assays and were validated using relevant positive and negative controls. Used concentrations were determined by titration experiments. Validation available upon request.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	human embryonic kidney cell line HEK293-6E (National Research Council of Canada, NRC file 11565)
Authentication	Cell line were authenticated with STR analysis.
Mycoplasma contamination	Cell line was tested negative for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used in the study.

Human research participants

Policy information about studies involving human research participants

Population characteristics	Population characteristics are not relevant for this study.
Recruitment	Study participants with age ≥18 years, sound physical condition (Karnofsky Performance Scale ≥80), who suffer or have suffered from a severe or acute chronic infection within the last ten years, for example Acinetobacter baumanii, Cytomegalovirus, Human Immunodeficiency Virus, Hepatitis, or Ebola Virus Disease, were recruited.
Ethics oversight	Samples were obtained under a study protocol approved by the Institutional Review Board of the University of Cologne and respective local IRBs (study protocol 16-054).

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	PBMCs are purified by density gradient centrifugation and CD19+ cells are enriched with CD19 microbeads.
Instrument	BD FACS Aria Fusion
Software	BD FACSDiva was used to collect data. BD FlowJo V.10 was used to analyse data.
Cell population abundance	Relevant were viable B cell frequencies and sorted target population.
Gating strategy	Lymphocyte population in FCS-A/SSC-A and single cells were identified in FCS-H/FCS-A. Cells were displayed in FCS-A/DAPI and it was gated into DAPI negative cells. B cells were identified, cells plotted in FCS-A/CD20 and it was gated into CD20 positive cells. It was continued with a plot for CD20/IgG cells and gated into CD20 and IgG positive cells. The final sorting gate, displayed the bait protein against IgG and it was gated to the bait and IgG positive fraction. In case of double staining with two differently labelled baits, it was gated on IgG positive cells in the FCS-A/IgG plot first, the two colours of the differently labelled bait proteins were displayed and a sorting gate placed on double positive cells.

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