

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
<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

Data analysis

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](#)

Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research.](#)

Reporting on sex and gender

NA

Population characteristics

NA

Recruitment

NA

Ethics oversight

NA

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](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

Each group contained 8 animals (4 male and 4 female). Using PASS 13 software we determined that in a repeated measures design with 8 animals measured at 4 post-treatment time points there is 80% power to detect a difference of 1.16 standard deviations (SD) between groups for an outcome of interest using a compound symmetry covariance structure and a correlation between repeated measures of 0.58 (based on our previous work) with alpha=0.05 (2-sided). Based on our previous data, the estimated SD for IgG was at most 1.5 and the correlation between repeated observations was 0.58. Using these inputs we can detect a difference in IgG value of 1.74 titer units with 80% power and alpha=0.05 (2-sided test). For analyses that may focus on one timepoint, we would have 80% power to detect a difference between groups of 2.26 titer units based on our estimate of the variability in IgG measures.

Data exclusions

Data are not excluded.

Replication

Findings are replicated with individuals animals.

Randomization

Newborns were randomized to the experimental groups.

Blinding

Blinding was not possible as the animals were numbered by sample and analyzed by researchers involved in the 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
☒	☐ 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-monkey IgM-HRP Fitzgerald #43R-IG074hrp 1:10,000
Anti-monkey IgG-HRP Fitzgerald #43C-CB1603 1:5,000
Anti-monkey IgA-Biotin Fitzgerald 43R-IG002bt 1:5,000

Anti-CD107a-PE Biolegend, #328608 1:50
Anti-guinea pig C3-FITC MP Biomedicals, # 855385 1:100

Validation

Antibodies were validated by the vendor.

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)

THP-1 cells were obtained from the WFUSM CCC Core via ATCC (lot number #70035863), KHYG-1 cells transduced with rhesus macaque CD16 (kind gift of Dr. David Evans)

Authentication

THP-1 cells were authenticated by the vendor. CD16 expression of KHYG-1 cells was tested for flow cytometry.

Mycoplasma contamination

The cell lines were not tested for mycoplasma just prior to the analysis.

Commonly misidentified lines
(See [ICLAC](#) register)

NA

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

African green monkeys were from the breeding colony at Wake Forest University School of Medicine.

Wild animals

NA

Reporting on sex

Equal numbers of male and female animals were used. Sex was considered in the results. No sex dependent differences were observed.

Field-collected samples

NA

Ethics oversight

The animal care and use protocol was adherent to the US Animal Welfare Act and Regulations and approved by the Wake Forest University Institutional Animal Care and Use Committee. AGM were housed and cared for in accordance with state, federal, and institute policies in facilities accredited by the American Association for Accreditation of Laboratory Animal Care (AAALAC) under standards established in the Animal Welfare Act and the Guide for the Care and Use of Laboratory Animals.

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