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	Bruker Avance III HD console spectrometer, Agilent 6530 LC Q-TOF mass spectrometer, Tosoh EcoSEC size exclusion chromatography system, Shimadzu UV-3600 Plus UV-VIS-NIR spectrophotometer, Shimadzu IRTracer-100 Fourier transform infrared spectrometer, Bruker Multimode 8 AFM, Kratos AXIS Nova with a monochromatic Al Kα X-ray source and a delay line detector (DLD) system, CLARIUS V1.9, Keithley 2450, Digidata 1550 digitizer with Clampex software (Molecular Devices)
Data analysis	OriginPro 2021, Microsoft Office 365, GraphPad Prism 9, FlowJo 9 (TreeStar)

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

All relevant data that support the findings of this study are available in the article and its supplementary files and are available from the corresponding authors upon request. Source data of plots are provided with this paper.

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	N/A
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	N/A

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	Sample sizes were predetermined from pilot experiments and/or experiments that have been done in the past, to obtain statistically significant data. We conducted a pilot experiment to determine the effect size and sample size of the experiment. Then, we determined the sample size at which statistical significance was observed ($P < 0.05$) in the result value of each group through a one-way ANOVA test.
Data exclusions	No data were excluded from the analyses.
Replication	Experimental results were successfully reproduced. To ensure the independence of the replication, we performed repeated experiments at four-month intervals. We used the same condition mice (Male, C57BL/6 6-8 weeks from Charles River Laboratory). Also, we provided the same animal room, same condition, same mice number in a cage, and same diet to the experimental animal.
Randomization	Samples were randomly allocated into experimental groups.
Blinding	The sample preparation, the surgical experiments, and the data analysis were divided, and information on the substance was not provided to the animal experimenter. During the experiment, data collection, and data analysis, grouping allocation was not provided to the researchers.

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
☒	☐ Plants

Methods

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

Antibodies

Antibodies used

Anti-alpha smooth muscle Actin antibody (EPR5368, abcam, Cat#: ab124964), CD68 Monoclonal Antibody (FA-11, Invitrogen, Cat#: 14-0681-82), Donkey anti-Rat IgG (H+L) Alexa FluroTM 594 Secondary Antibody (Polyclonal, Invitrogen, Cat#: A-21209), and Goat anti-Rabbit IgG Alexa FluorTM 647 Secondary Antibody (Polyclonal, Invitrogen, Cat#: A-21244).
Anti-pERK BV421 (clone: 6B8B69, Biolegend, Cat#: 369509), anti-p-p38 PE (clone: A16016A, Biolegend,Cat#: 690203), anti-iNOS Alexa FluroTM 488 (clone: CXNFT, Invitrogen, Cat#: 53-5920-82), anti-pJNK Alexa FluroTM 647 (clone: N9-66, BD, Cat#: 562481), Fc blocking (clone: 93, Biolegend, Cat#: 101302), anti-CD45 APC-Cy7 (clone: 30-F11, Biolegend, 103115), anti-MHC2 Percp-Cy5.5 (clone: M5/114.15.2, Biolegend, Cat#: 107625), anti-CD86 PE-Dazzle 594 (clone GL-1, Biolegend, Cat#: 105041), and anti-Gr-1 BV605 (clone: RB6-8c5, Biolegend, Cat#: 108439)

Validation

Anti-alpha smooth muscle Actin antibody (EPR5368, abcam, Cat#: ab124964) was validated using human stomach tissue. Antigen retrieval by heating was performed.
CD68 Monoclonal Antibody (FA-11, Invitrogen, Cat#: 14-0681-82) was validated using a mouse spleen.
Anti-pERK BV421 (clone: 6B8B69, Biolegend, Cat#: 369509) was validated using activated human peripheral blood lymphocytes. The isolated peripheral blood lymphocytes were stimulated with a cell activation cocktail without Bredfeldin A for 15 min, followed by intracellular staining process.
anti-p-p38 PE (clone: A16016A, Biolegend,Cat#: 690203) was validated using activated human peripheral blood lymphocytes. The isolated peripheral blood lymphocytes were stimulated with a cell activation cocktail without Bredfeldin A for 15 min, followed by intracellular staining process.
anti-iNOS Alexa FluroTM 488 (clone: CXNFT, Invitrogen, Cat#: 53-5920-82) was validated using LPS-stimulated mouse thioglycolate-elicited peritoneal exudate cells.
anti-pJNK Alexa FluroTM 647 (clone: N9-66, BD, Cat#: 562481) was validated using LPS-stimulated C57BL/6 mice's splenocytes.
Fc blocking (clone: 93, Biolegend, Cat#: 101302) was validated using C57BL/6 mice's splenocytes. The isolated splenocytes were stained with Fc blocking (clone: 93, Biolegend, Cat#: 101302), followed by anti-rat IgGs FITC.
anti-CD45 APC-Cy7 (clone: 30-F11, Biolegend, 103115) was validated using C57BL/6 mice's splenocytes.
anti-MHC2 Percp-Cy5.5 (clone: M5/114.15.2, Biolegend, Cat#: 107625) was validated using C57BL/6 mice's splenocytes.
anti-CD86 PE-Dazzle 594 (clone GL-1, Biolegend, Cat#: 105041) was validated using LPS-stimulated C57BL/6 mice's splenocytes.
anti-Gr-1 BV605 (clone: RB6-8c5, Biolegend, Cat#: 108439) was validated using C57BL/6 mice's bone marrow cells.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	RAW 264.7 cell line from ATCC
Authentication	The cell lines were not authenticated
Mycoplasma contamination	The cells were routinely checked for mycoplasma contamination, with negative results
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used

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	Male C57BL/6 mice (6-8 weeks) were purchased from Charles River Laboratory. The animal room is maintained on a 12 hrs light/12 hrs dark cycle using artificial lighting (6 am to 6 pm light and 6 pm to 6 am dark). The temperature of the room is maintained at 18-23 ℃ and the humidity is maintained at 40–60 %.
Wild animals	This study did not involve wild animals.
Reporting on sex	Male mice were used in this study.
Field-collected samples	This study did not involve samples collected from the field.

Ethics oversight	All protocols used in this study were approved by the Institutional Animal Care and Use Committee of the University of Chicago. (Protocol numbers 72450, 72702 and 72470)

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

Plants

Seed stocks	*Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*
Novel plant genotypes	*Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*
Authentication	*Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*

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	After the LPS activation process, RAW 264.7 cells placed in 48-well plate were harvested by gently pipetting
Instrument	BD LSR flow cytometer
Software	FlowJo (TreeStar)
Cell population abundance	No sorting was performed
Gating strategy	A representative gating strategy is shown in Supplementary Fig. 21 and 27

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