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Reporting Summary

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Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
☐	☒ An indication of 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 statistics 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
☐	☒ Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	SteoOne Software v2.3, BD FACSDiva V8.0
Data analysis	GraphPad Prism v.6 and v.7, SPSS v.22, Photoshop CS6, R v3.3.2, Gephi v.0.8.2 beta, FlowJo v.8 Mac and v.10 PC.

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/reviewers upon request. 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

Data Availability
RNA sequencing data presented in this study have been deposited in NCBI GEO repository under the accession #GSE119273.

Code Availability
All code used in this manuscript can be accessed from the Github repository perryjs/Perry-R.

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

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

Sample size	No statistical tests were used to predetermine sample size. For in vivo experiments, sample sizes were determined based on the numbers required to achieve statistical significance using non-parametric statistics.
Data exclusions	Statistical tests for outliers are routinely performed,Grubbs' test for outliers was used for excluding outliers.
Replication	Consistent results obtained from at least two or three biological replicates with more than two technical replicates per experiment were used in the manuscript. A significant number of the experiments used 3-4 biological replicates and 3-4 technical replicates.
Randomization	Allocation of mice was random in all in vivo experiments, taken from littermates.
Blinding	The investigators were not blinded to allocation during the experiments and outcome assessment. All experiments required known injections of substances, including apoptotic cells, inhibitors, etc. Therefore, it was not possible to blind the investigator for such experiments.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☒	☐ Unique biological materials
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants

Methods

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

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	Reported under Methods, in "In vivo engulfment assay and quantitative RT-PCR","In vivo engulfment assay and quantitative RT-PCR", "In vivo thymus efferocytosis assay" and "Macrophages isolation and analysis". Peritoneal exudates were obtained via cold PBS flush. Thymocytes were obtained by gentle mechanical disruption. Bone marrow cells for BMDMs was obtained by flushing tibia and fibia using serum-complete media. All samples were filtered prior to staining. Samples were kept on ice during staining and collection. All fluorescent antibodies were aliquotted in a sterile hood with minimal light exposure. Staining of samples were protected from light throughout.

Instrument	Data were collected on a FACS Canto I (Becton Dickinson).
Software	Data were collected analyzed with FlowJo v8 and v10 (Treestar, Inc).
Cell population abundance	Purity of isolated samples was obtained by antibody stain and FACS. Sample purity was greater than 95% in all experiments.
Gating strategy	Standard lymphocyte gates were applied, following by doublet exclusion using FSCHxW and SSC-HxW. In our studies, macrophages were gated using a combination of CD11b and F4/80. For in vitro experiments, all phagocytes were labeled with GFP or CFSE, whereas all apoptotic cells were labeled with a reporter dye such as CypHer5E or TAMRA. Singlets were similarly gated for in vitro experiments prior to analysis of GFP+/CFSE+, CypHer5E+/TAMRA+ cells.

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