nature portfolio

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Last updated by author(s): May 30, 2026

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	Bacterial colonies on the plates were quantified using a colony counting and measuring instrument (SupcreG10, Shineso, China); The OD600nm values, luminescence and fluorescence intensity were collected by Tecan Infinite Spark microplate reader; Fluorescent images of the stained bacteria were captured using a confocal laser scanning microscope (AIR HD25, Applied Biosystems, Carlsbad, USA) and an inverted fluorescence microscope (TS2R-FL, Caikang Optical Instrument, Shanghai, China); The mRNA expression levels were quantified using a CFX96-C1000 Touch Real-Time PCR Detection System (Bio-Rad, USA); RNA sequencing was performed on the Illumina HiSeq™ platform (Illumina, San Diego, CA, USA) to obtain transcriptomic data; The protein bands on the membranes were visualized using the BIO-RAD ChemiDoc™ XRS+ imaging system (Bio-Rad, USA); NMR data were acquired using a BRUKER AVANCE NEO 400 MHz nuclear magnetic resonance spectrometer (Bruker, Germany); HPLC analysis was performed using a Shimadzu Prominence UFLC system.
Data analysis	GraphPad Prism version 9.4.1; Image J 1.54d; Origin 7.0; NIS Elements v. 5.21.00.

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 gene knockout strain sequences generated in this study have been deposited in the NGDC BioProject database under accession number PRJCA065442, and the transcriptome-related data have been deposited in Figshare under DOI 10.6084/m9.figshare.32507898. Both datasets are under embargo and will be made publicly available upon publication of this article. All other data are available in thearticle and its Supplementary files. Source data 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	None
Reporting on race, ethnicity, or other socially relevant groupings	None
Population characteristics	None
Recruitment	None
Ethics oversight	None

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 formal sample size calculation was performed for in vitro experiments; sample sizes of at least three independent biological replicates were chosen based on standard practice for comparable biological assays and were considered sufficient because consistent effects were observed across independent experiments. Each value shown in figures was presented as the mean value of the biological replicates, with standard deviation shown as error bars. Sample size for mouse experiments (n=8), was chosen based on previous mouse infection model experiments (Elisabeth et al 2005).
Data exclusions	No data was excluded.
Replication	All results presented are reproducible. The experiment was repeated at least three times over several days and each repetition was successful.
Randomization	In animal experiments, all animals were randomly assigned to different groups and given completely equal living conditions. For other experiments, we randomized sample measurements as much as possible by naming the samples as numbers that did not contain sample attributes. In addition, we did not randomize if the act of randomization was not feasible or did not have an effect on the results of the experiment, such as in many experiments where measurements were made by detecting absorbance and subjective factors did not affect the results.
Blinding	The results of most experiments are not affected by the bias of the experimenter. For some of the results that are affected by the subjectivity of the experimenter, we use auxiliary means to accurately quantify the results as much as possible in a blinded manner, such as imageJ to accurately quantify the area of the wound in the mice.

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	CSE(Proteintech, Cat#60234-1-Ig, clone 2C7F9, 1:20000), 3-MST(Proteintech, Cat#19499-1-AP, polyclonal, 1:2000), GAPDH(Cell Signaling Technology, Cat#97166T, clone D4C6R, 1:3000), β-actin(Cell Signaling Technology, Cat#4970T, clone 13E5, 1:2000), Akt (Cell Signaling Technology, Cat#4691T, clone C67E7, 1:1500), Phospho-Akt(Cell Signaling Technology, Cat#4060T, clone D9E, 1:2000), HRP-conjugated Secondary antibodies of Goat anti-mouse IgG(Proteintech, Cat#SA00001-1, polyclonal, 1:10000), HRP-conjugated Secondary antibodies of Goat anti-rabbit IgG(Proteintech, Cat#SA00001-2, polyclonal, 1:10000)
Validation	All primary antibodies used in this study have been validated for Western blot (WB) applications according to the manufacturer's datasheets available on their official websites.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	Mouse mononuclear macrophages, RAW264.7 (Catalog number: TCM13), were purchased from National Collection of Authenticated Cell Cultures (https://www.cellbank.org.cn/).
Authentication	None of the cell lines were authenticated.
Mycoplasma contamination	The cell lines were not tested for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified species used in this study.

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	6-8 weeks old female BALB/c mice.
Wild animals	None.
Reporting on sex	All experimental animals were female. Only female BALB/c mice were used in the peritonitis model to avoid the potential confounding effects of testosterone and aggressive behavior commonly observed in male mice, which can significantly modulate the immune response and increase variability in survival studies. This approach ensures a more consistent baseline for evaluating the anti-inflammatory effects of the treatment.
Field-collected samples	No field-collected samples were used.
Ethics oversight	Mice were housed under specific pathogen-free conditions with unrestricted access to food and water, a 12 h light/dark cycle, an ambient temperature of 22 ± 2°C, and relative humidity of 50 ± 10%. AAll animal experiments were approved by the Animal Research and Ethics Committee of Chengdu Institute of Biology, Chinese Academy of Sciences (under NO. CIBDWLL2023). All animal testing protocols were conducted in compliance with Animal Welfare Act regulations and the 1996 National Research Council's Guide for Laboratory Animal Care and Use.

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

Plants

Seed stocks	None
Novel plant genotypes	None
Authentication	None