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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 Authors & Referees 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	The OD600nm values, luminescence and fluorescence intensity were collected by Tecan Infinite M200 Microplate reader;Fluorescent images of stained bacteria were obtained by Leica TCS SP8 confocal laser scanning microscope;The Ct values of RT-PCR were collected using ABI quantstudio™ 7 detection system.
Data analysis	GraphPad Prism 7 was used to plot graphs; Statistical analysis was performed by GraphPad Prism 5 and SPSS. pharmacokinetic parameters were obtained using a non-compartmental analysis model by WinNonlin 6.4; R v3.5.1 and Heatmap package were used to analyze the transcriptome data.

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. 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 supporting the findings of this study are included in the article. RNA-seq data have been deposited in NCBI SRA with accession number PRJNA610702.

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	All experiments were performed with at least two independent biological replicates. Each value shown in figures was presented as the mean value of the biological replicates, with standard deviation shown as error bars.
Data exclusions	For differential expression analysis,the RNA expression levels for each gene with fragments per kilobase per million reads mapped (FPKM) lower than1 were removed from consideration before downstream analysis.
Replication	All of the reported results were reproducible.
Randomization	For animal studies, six to eight-week-old female BALB/c mice and larvae of Galleria mellonellas were randomly assigned to the experimental and the control groups by the experimenter.
Blinding	No blinding was required because all measurements are not subject to investigator's bias or ambiguity.

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
☐	☒ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

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

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	All eukaryotic cell lines used in this paper were obtained from ATCC.
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.

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	Six to eight-week-old female BALB/c mice
Wild animals	None
Field-collected samples	None

Ethics oversight	The laboratory animal usage license number is SYXK-2016-0008, certified by Beijing Association for Science and Technology and the animal study protocols were performed in accordance with the relevant guidelines and regulations (ID: SKLAB-B-2010-003).

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