

Corresponding author(s): Zheng Yu

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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
<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 MD3000-C force transducers system

Data analysis MEGA (v6.0), FastANI (v1.33), Fastp (v0.23.4), FastUniq (v1.1.0), Bowtie (v2.3.5), unicycler (v0.4.8), Megahit (v1.2.9), checkm2 (v1.0.1), gtdbtk (v1.7.0), Bakta (v1.9.2), CoverM (v0.6.1), Diamond (v2.0.2), mmseq2 (version 13.45111)

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 raw sequence data reported in this paper have been deposited in the Genome Sequence Archive in National Genomics Data Center, China National Center for Bioinformation/Beijing Institute of Genomics, Chinese Academy of Sciences, under accession number CRA025930 (RNA sequencing data), CRA025960 (Subculture sample metagenomic sequencing data), CRA025961 (Mice fecal sample metagenomic sequencing data) that are publicly accessible at <https://bigd.big.ac.cn/gsa>. The methane oxidation gene database generated in this study have been deposited in the zenodo (<https://doi.org/10.5281/zenodo.15124190>). The public metagenomic

sequencing dataset in this study are stored in Source data file. 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

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](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

Data sets were analyzed without a normality assumption, therefore normality was tested to determine the use of parametric or non parametric statistical tests. The number of samples to analyze was based on the outcome of previous experiments with similar aims and/or with the expected effects in each assay.

Data exclusions

No data were excluded from the analyses

Replication

Groups of mice were randomly treated such that each group would have similar numbers of mice. We used different strains of animals to carry out experiments to ensure that the results were repeated. In addition, the data collected from public data sets supported our results. Groups of mice were randomly treated such that each group would have similar numbers of mice. We used different strains of animals to carry out experiments to ensure that the results were repeated. In addition, the data collected from public data sets supported our results.

Randomization

All the mice were randomly allocated into different groups. For molecular experiments and microscopic observation experiments did not involve in allocation.

Blinding

All mice were blinded to group allocation during data collection and analysis.

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 |

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	Kunming mice 5-week-old bred in house Strain C57BL/6 5-week-old bred in house Strain Sprague-Dawley rats 8-month-old bred in house Strain
Wild animals	Not used
Reporting on sex	Only the male mice are considered in the study because of the practical feasibility issues of epididymal fat.
Field-collected samples	Fecal samples were collected via the stress defecation method one day prior to mice sacrifice. Sterile cotton swabs were used to gently stimulate defecation by wiping the anal area, and the feces were collected in sterile tubes for storage at -80°C. Blood samples were obtained during sacrifice after isoflurane anesthesia, via orbital vein puncture, followed by immediate euthanasia through cervical dislocation. The collected blood was immediately collected. Animals were perfused with formaldehyde, and various adipose tissue depots (epididymal, inguinal, mesenteric and interscapular BAT) weighted, and stored in PBS.
Ethics oversight	All animal experiments were carried out in compliance with the National Institutes of Health Guide for the Care and Use of Laboratory Animals and approved by the Institutional Ethics Committee of Central South University (CSU-2024-0315).

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

Clinical data

Policy information about [clinical studies](#)

All manuscripts should comply with the ICMJE [guidelines for publication of clinical research](#) and a completed [CONSORT checklist](#) must be included with all submissions.

Clinical trial registration	N/A
Study protocol	All research conducted for this manuscript complies with ethical regulations including approval by the Institutional Review Board (IRB) of School of Xiangya Basic Medical Sciences and Institutional Ethics Committee (2021-KT75)
Data collection	The feces of 10 adult healthy volunteers in Changsha, China were collected in 2021-2023 years
Outcomes	Gut microbial culture, and metagenomic sequencing data analysis

Plants

Seed stocks	N/A
Novel plant genotypes	N/A
Authentication	N/A