

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 (<i>n</i>) 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> 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 <i>d</i> , Pearson's <i>r</i>), 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	Illumina NovaSeq6000 sequencer was used for 4C-seq. Publicly available ChIP-seq, ATAC-seq, and DHS-seq data used in this study were downloaded from the EBI ENA database (https://www.ebi.ac.uk/ena/browser/home). Quantitative real-time PCR was performed on the CFX Connect Real-Time System (Bio-Rad, USA) eBlot Touch Imager was used to obtain images of Western Blots (eBlot Photoelectric Technology, China). Whole-body energy metabolism was measured using an Animal Metabolism Monitoring System (EM-8M-WA, Tow-Int Tech, China).
Data analysis	Demultiplexing, trimming, and alignment were performed using the pipe4C pipeline. 4C-seq data analysis was performed using the r3Cseq package. ChIP-seq, ATAC-seq, and DHS-seq reads were aligned to mouse (mm10) or human (hg38) genome using Bowtie2 (v2.4.2) with the default parameters. Peak calling was performed using MACS2 (v2.2.7.1) with the q-value cut-off of 0.05. BedGraph files were converted to BigWig files using bedGraphToBigWig (v4), and then BigWig was visualized by Integrative Genomics Viewer (IGV). Western blot and fluorescence image quantifications: ImageJ v1.5.4. Statistics and Data Figure Panel: Graphpad Prism 8.

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 (Genomics, Proteomics & Bioinformatics 2021) in National Genomics Data Center (Nucleic Acids Res 2022), China National Center for Bioinformation / Beijing Institute of Genomics, Chinese Academy of Sciences (GSA: CRA017780) that are publicly accessible at <https://ngdc.cncb.ac.cn/gsa>.

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

Reporting on race, ethnicity, or other socially relevant groupings

Population characteristics

Recruitment

Ethics oversight

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

Data exclusions

Replication

Randomization

Blinding

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	UCP1 (ABclonal, A5857, 1:100) for Immunocytochemistry UCP1 (Cell Signaling Technology, 72298, 1:1000) for Western blot UCP1 (Servicebio, GB112174, 1:200) for Immunofluorescence Total OXPHOS cocktail (Abcam, ab110413, 1:1000) for Western blot Vinculin (Cell Signaling Technology, 13901, 1:1000) for Western blot EBF2 (R&D Systems, AF7006, 2 µg) for ChIP assay CBP (Cell Signaling Technology, 7389, 2 µg) for ChIP assay H3K27ac (Abcam, ab4729, 2 µg) for ChIP assay
Validation	All antibodies used were validated by the suppliers for their particular application. Validation statements and relevant references for the used antibodies can be found on the manufacture's website.

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)	H293T cell line was purchased from ATCC.
Authentication	The H293T cell line was authenticated using Short Tandem Repeat (STR) profiling.
Mycoplasma contamination	H293T cell line tested negative for Mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were 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	5-9 weeks male C57BL/6J mice were used in this study.
Wild animals	This study did not involve wild animals
Reporting on sex	Male mice were used in this study which allows for housing of 5 mice per cage. Sex consideration was based on practical feasibility issues. Body Weight and Fat Distribution: Male mice typically have more body weight and different fat distribution compared to female mice, which can be advantageous for studying specific aspects of BAT and its metabolic effects. Consistency with Previous Studies: Many previous studies on BAT have used male mice, allowing for better comparison and replication of results. This continuity helps in building on existing knowledge without introducing new variables.
Field-collected samples	This study did not involve field collected samples
Ethics oversight	All animal experiments were conducted according to the Regulations for the Administration of Affairs Concerning Experimental Animals (Ministry of Science and Technology, China, revised in March 2017) and approved by the Animal Ethical and Welfare Committee (AEWC) of Sichuan Agricultural University under permit No. DKY-B3022102011.

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Plants

Seed stocks

N/A

Novel plant genotypes

N/A

Authentication

N/A