nature portfolio

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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 *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	Agilent Wave, Agilent MassHunter Acquisition, Visualsonics Vevo Lab, Zeiss Zen Blue, and Applied Biosystems StepOne Software were used for Seahorse, GCMS, Doppler, Histology, and qPCR data acquisition respectively.
Data analysis	Agilent MassHunter Quantitative Analysis was used for GCMS data analysis. EI-MAVEN and Compound Discoverer was used for LCMS data analysis. GraphPad Prism was used for graphs and statistical analysis. Code is available: https://github.com/johnnl15/Bootstrapping_AUC_NitrogenFL_BATLiverSerum

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

All data in the main and extended figures is available.

Human research participants

Policy information about studies involving human research participants and Sex and Gender in Research.

Reporting on sex and gender	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

Life sciences study design

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

Sample size	Arteriovenous sampling experiments used a sample size of 14-20 due to the high amount of variation. For all other animal experiments a sample size of 4-7 was used. For cell experiments a sample size of 3-6 was used due to smaller biological variation, except in the case of the seahorse where a samples size of 15 was used due to the assay's sensitivity.
Data exclusions	In the doppler studies, mice were excluded if heart rate dropped below 400 beat per minute.
Replication	All experimental findings were replicated at least 3 times.
Randomization	Samples and mice were randomly assigned experimental conditions.
Blinding	Mouse dissections were not blinded as the phenotypes are different enough that the different temperature conditions can be identified. However, all sample processing was blinded.

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

Methods

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

Antibodies

Antibodies used	GS (BD#610517), UCP1 (CST#14670 for tissue and Abcam#ab10983 for cells), VINC (SantaCruz#sc-73614), GLS (ProteinTech#12855), GLUD1 (ProtienTech#14299), FASN (CST#3180), PPARγ (CST#2443).
Validation	All antibodies have been validated by manufacturer or by knockdown/knockout studies.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	Brown preadipocytes were isolated from C57BL/6J neonates at postnatal day 1 and immortalized with pBabe-SV40 Large T. The sex of each neonate was not determined.
Authentication	Cell lines were authenticated to be BAT cell lines by differentiating them and confirming the presence of BAT markers by qPCR.
Mycoplasma contamination	Cell line tested negative for mycoplasma.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used in the 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	C57BL/6J, Male, 10-12 weeks of age,
Wild animals	No wild animals were used in this study.
Reporting on sex	All experiments were done in male mice. We plan to followup with female mice in the future.
Field-collected samples	No field-collected samples were used in this study.
Ethics oversight	UMass Chan Medical School IACUC approved all animal experiments (Protocol #'s: 202100035, 202200006)

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