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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	NMR: Chenomx NMR suite 8.2 QPCR: CFX Maestro 2017 Seahorse: Wave 2.4
Data analysis	Peptide mass spectra were processed with an house SEQUEST-based software pipeline (Huttlin, E.L., et all. Cell. 143, 1174–1189 (2010). Details available upon reasonable request GraphPad Prism, 7 Microsoft office Excel 2016 limma (v3.32.10) package in R

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

The data that support the findings of this study are available from the corresponding author upon request.

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	Sample sizes were predetermined based on effect size, standard deviation, and significance level required to attain statistical significance of p<0.05 with a 90% probability on the basis of previous experiments using similar methodologies and were deemed sufficient to account for any biological/technical variability.
Data exclusions	No data were excluded
Replication	All attempts of in vivo replication were successful. Proteomics was performed with five independent samples at two environmental temperatures. Only replicated proteomic data are discussed, effectively increasing independent sample number to 10 per genotype. Proteomic data were further followed up by alternative approaches, such as RT-qPCR.
Randomization	For in vivo studies, mice in each genotype were randomly assigned to treatment groups. For MS analyses, samples were processed in random order and experimenters were blinded to experimental conditions.
Blinding	For MS analyses, samples were processed in random order and experimenters were blinded to experimental conditions.

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)	Primary brown adipocytes from CrT(lox/y) mice (strain: C57BL6/J, Stock#: 000664). Mice were bred and cells were isolated in-house.
Authentication	N/A
Mycoplasma contamination	N/A
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used

Animals and other organisms

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

Laboratory animals	Mice were housed at 22°C under a 12 hr light/dark cycle with free access to food and water until 8 weeks of age. CrT(lox/y) animals were obtained from the Jackson Laboratory [B6(SJL)-Slc6a8tm1.1Clar/J), Stock No: 020642]. Adiponectin-Cre mice (B6;FVB-Tg(Adipoq-cre)1Evdr/J, Stock No: 010803), maintained on a C57BL/6J background, were bred to CrT(lox/y) animals to generate experimental groups. All experiments used age-matched male littermates and were conducted at either 30°C or 22°C. Animal experiments were performed according to procedures approved by the Animal Resource Centre at McGill University and

	comply with guidelines set by the Canadian Council of Animal Care, and experiments were performed according to procedures approved by the Institutional Animal Care and Use Committee (IACUC) of the Beth Israel Deaconess Medical Center or the Harvard Center for Comparative Medicine. Unless otherwise stated, mice used were age-matched littermates (8–12 weeks of age), and housed in at (22 °C or 30 °C) on a 12 h light/dark cycle. AdCrTKO (CrT[lox/y]; AdipoQ-Cre) and age-matched littermates (CrT[lox/y]) were used. Brown adipocytes were cultured from male and female pups after genotyping (14 days old).
Wild animals	N/A
Field-collected samples	N/A
Ethics oversight	Animal experiments were performed according to procedures approved by the Animal Resource Centre at McGill University and comply with guidelines set by the Canadian Council of Animal Care. Experiments were performed according to procedures approved by the Institutional Animal Care and Use Committee (IACUC) of the Beth Israel Deaconess Medical Center.

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

Human research participants

Policy information about studies involving human research participants

Population characteristics	Inclusion criteria included healthy male and female subjects, ages 18-64 receiving abdominal surgery. Exclusion criteria were diagnosis of diabetes, any subjects taking insulin-sensitizing medications like thiazolidinediones or metformin, chromatin modifying enzymes such as valproic acid, and drugs known to induce insulin resistance such as mTOR inhibitors (e.g. sirolimus, tacrolimus) or systemic steroid medications.
Recruitment	Subjects recruited from plastic surgeon operating room schedule at Beth Israel Deaconess Medical Center in consecutive fashion as scheduling permitted to process the sample.
Ethics oversight	Subcutaneous adipose tissue was collected under IRB 2011P000079, and approved by the Beth Israel Deaconess Medical Center Committee on Clinical Investigations

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