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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.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
☐	☒	An indication of 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 statistics 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
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	*Provide a description of all commercial, open source and custom code used to collect the data in this study, specifying the version used OR state that no software was used.*
Data analysis	Graphpad Prism version 5.0b was used for statistical analysis. BD FACS DIVA (v6.1.3) or FlowJo, LLC v9.9.6 or v10.4.2 were used for flow cytometry analysis. For microarray analyses, RNA quality was measured using the TapeStation Analysis (Software A.02.01, Agilent Technologies). Heatmaps were generated using Partek Genomics Suite version 6.6 (Partek, St. Louis, MO). Pathway enrichment analyses were performed using the bioinformatic tools DAVID and WebGestalt (ref 26, 27). Image J was used to calculate the densitometry of immunoblots.

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 upon request. 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

Reagents for ELISA and immunoblot for S100A8/A9 were uniquely provided by Prof. Thomas Vogl (Munster University, Germany). [D-Ala2]-GIP was synthesized by Bio-Synthesis (Lewisville, Tx). All other reagents are commercially avalilable as indicated in the method section.

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

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

Sample size	Sample size and experiment repeats are clearly indicated in figure legends. The amount of mice used in each of the in vivo experiments was determined in order to meet the requirements of applied measurements and to allow a wide enough representative sample. Sample size was estimated based on our previous experience (see ref 10 for example) as optimal for in-vivo evaluation. For metabolic measurements of body weight, food intake, ITT, serum parameters, and qRT-PCR analyses of metabolic genes all groups contained at least 9 mice and experiments repeated 3 times. Computed tomography calculation of lean and fat mass was as well as metabolic cages analyses in individual caging systems were performed in groups of 5 mice to allow simultaneous observations in these instruments and experiments repeated once. Experiments in cold-exposure challenge included 5 mice per group and repeated twice. Immunological analyses including flow cytometry and qRT-PCR analyses included at least 6 mice per group and repeated twice. For sorting experiments of ATMs, each group contained three repeats, each repeat was extracted from pools of 5 mice. Finally, epiWAT and ingWAT microarray analyses were performed on groups of 3-4 repeats.
Data exclusions	One way or two way ANOVA and unpaired two tailed Student t test were performed using GraphPad Prism (San Diego, CA) and statistical outliers defined by the tests were then excluded from data analysis. Indicated mouse numbers do not include outliers.
Replication	All experiments contain biological replicates as indicated in the legends. Experiments that were repeated on different days showed reproducibility independent of minor day to day variation.
Randomization	Control and experimental groups were initiated at the same age and average body weight.
Blinding	The experiments were not performed with blinding.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
[ ]	[x] Unique biological materials
[ ]	[x] Antibodies
[ ]	[ ] Eukaryotic cell lines
[ ]	[ ] Palaeontology
[ ]	[x] Animals and other organisms
[ ]	[ ] Human research participants

Methods

n/a	Involved in the study
[ ]	[ ] ChIP-seq
[ ]	[x] Flow cytometry
[ ]	[ ] MRI-based neuroimaging

Unique biological materials

Policy information about availability of materials

Obtaining unique materials

Describe any restrictions on the availability of unique materials OR confirm that all unique materials used are readily available from the authors or from standard commercial sources (and specify these sources).

Antibodies

Antibodies used

Flow cytometry antibodies:

Anti-mouse CD45 FITC Biolegend Cat# 103107 (1:100)

Anti-mouse CD45 APC-Cy7 Antibody Biolegend Cat# 1103116 (1:100)

Anti-mouse F4/80 PE Bio-Rad Cat# MCA497RT (1:50)

Anti-mouse/human CD11b PE-Cy7 Antibody Biolegend Cat# 101216 (1:300)

Anti-mouse Ly6C PerCP/Cy5.5 Antibody Biolegend Cat# 128012 (1:300)

Anti-mouse CD64 APC (FcγRI) Antibody Biolegend Cat# 139306(1: 50)

Anti-mouse Ly6G Brilliant Violet421 Antibody Biolegend Cat# 127628 (1:100)

Anti-Mouse Ly6G FITC Antibody Biolegend Cat# 127606 (1:100)

Anti-mouse CX3CR1 Alexa Fluor® 488 Antibody Biolegend Cat# 149022 (1:100)

Anti-mouse I-A/I-E Pacific Blue Antibody Biolegend Cat# 107620 (1:100)

Rabbit polyclonal anti S100A8 (prof Vogel, house production)(used at concentration of 1ug/ml)

Donkey anti-rabbit Alexa 647 Jackson ImmunoResearch laboratories cat #711-605-152 (1:500)

Immunoblot antibodies:

Rabbit monoclonal anti p-Akt (Ser473) Cell Signaling Cat# 4060(1:1000)

Rabbit polyclonal anti Akt Cell Signaling Cat# 9272 (1:1000)

Rabbit polyclonal anti- S100A8 (MRP8, V/4) (prof. T. Vogl lab. house production)(used at concentration of 1ug/ml)

Rabbit polyclonal anti-PGC1α Abcam cat# ab54481 (1:500)

Rabbit polyclonal anti-UCP1 Abcam cat# ab23841 (1:500)

p97 (rabbit polyclonal prepared in the lab of prof. Boaz Tirosh, Hebrew University, Jerusalem)(1:2000)

Peroxidase conjugated Goat anti-rabbit IgG (Jackson ImmunoResearch laboratories cat #111-035-144 (1:10000)

Validation

Flow cytometry antibodies:

Anti-mouse CD45 FITC Biolegend Cat# 103107 (1:100)

https://www.biolegend.com/en-us/products/fitc-anti-mouse-cd45-antibody-99

Anti-mouse CD45 APC-Cy7 Antibody Biolegend Cat# 1103116 (1:100)
https://www.biolegend.com/en-us/products/apc-cy7-anti-mouse-cd45-antibody-2530

Anti-mouse F4/80 PE Bio-Rad Cat# MCA497RT (1:50)
https://www.bio-rad-antibodies.com/static/datasheets/mca49/mouse-f4-80-antibody-cl-a3-1-mca497rt.pdf

Anti-mouse/human CD11b PE-Cy7 Antibody Biolegend Cat# 101216 (1:300)
https://www.biolegend.com/en-us/products/pe-cy7-anti-mouse-human-cd11b-antibody-1921PE/Cy7 anti-mouse I-Ab Antibody Biolegend Cat# 116420

Anti-mouse Ly6C PerCP/Cy5.5 Antibody Biolegend Cat# 128012 (1:300)
https://www.biolegend.com/en-us/products/percp-cy5-5-anti-mouse-ly-6c-antibody-5967

Anti-mouse CD64 APC (FcγRI) Antibody Biolegend Cat# 139306(1: 50) https://www.biolegend.com/en-us/products/apc-anti-mouse-cd64-fcgammari-antibody-7874

Anti-mouse Ly6G Brilliant Violet421 Antibody Biolegend Cat# 127628 (1:100)
https://www.biolegend.com/en-us/products/brilliant-violet-421-anti-mouse-ly-6g-antibody-7161

Anti-Mouse Ly6G FITC Antibody Biolegend Cat# 127606 (1:100)
https://www.biolegend.com/en-us/products/fitc-anti-mouse-ly-6g-antibody-4775

Anti-mouse CX3CR1 Alexa Fluor® 488 Antibody Biolegend Cat# 149022 (1:100)
https://www.biolegend.com/en-us/products/alexa-fluor-488-anti-mouse-cx3cr1-antibody-11879

Anti-mouse I-A/I-E Pacific Blue Antibody Biolegend Cat# 107620 (1:100)
https://www.biolegend.com/en-us/products/pacific-blue-anti-mouse-i-a-i-e-antibody-3136

Rabbit polyclonal anti S100A8 (prof Vogel, house production)(used at concentration of 1ug/ml)

Donkey anti-rabbit Alexa 647 Jackson ImmunoResearch laboratories cat #711-605-152 (1:500)
https://www.jacksonimmuno.com/catalog/products/711-605-152

Immunoblot antibodies:

Rabbit monoclonal anti p-Akt (Ser473) Cell Signaling Cat# 4060(1:1000)
https://www.cellsignal.com/products/primary-antibodies/phospho-akt-ser473-d9e-xp-rabbit-mab/4060

Rabbit polyclonal anti Akt Cell Signaling Cat# 9272 (1:1000)
https://www.cellsignal.com/products/primary-antibodies/akt-antibody/9272?site-search-type=Products&N=4294956287&Ntt=9272s&fromPage=plp&_requestid=449128
Rabbit polyclonal anti- S100A8 (MRP8, V/4) (prof. T. Vogl lab. house production)(used at concentration of 1ug/ml)

Rabbit polyclonal anti-PGC1α Abcam cat# ab54481 (1:500)
https://www.abcam.com/pgc1-alpha-antibody-ab54481.html

Rabbit polyclonal anti-UCP1 Abcam cat# ab23841 (1:500)
https://www.abcam.com/ucp1-antibody-ab23841.html

p97 (rabbit polyclonal prepared in the lab of prof. Boaz Tirosh, Hebrew University, Jerusalem)(1:2000)

Peroxidase conjugated Goat anti-rabbit IgG (Jackson ImmunoResearch laboratories cat #111-035-144 (1:10000)
www.jacksonimmuno.com/catalog/products/111-035-144

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	No eukaryotic cell lines were used
Authentication	No eukaryotic cell lines were used
Mycoplasma contamination	No eukaryotic cell lines were used
Commonly misidentified lines (See ICLAC register)	No eukaryotic cell lines were used

Palaeontology

Specimen provenance

Provide provenance information for specimens and describe permits that were obtained for the work (including the name of the issuing authority, the date of issue, and any identifying information).

Specimen deposition

Indicate where the specimens have been deposited to permit free access by other researchers.

Dating methods

If new dates are provided, describe how they were obtained (e.g. collection, storage, sample pretreatment and measurement), where they were obtained (i.e. lab name), the calibration program and the protocol for quality assurance OR state that no new dates are provided.

☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.

Animals and other organisms

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

Laboratory animals

C57BL/6JOlaHsd male mice (Envigo, Jerusalem), Gipr-/- mice (provided by Dr Y. Yamada, Akita University, Japan), S100a9-/- mice (on C57Bl/6 background, provided by Prof. T. Vogl, Munster University, Germany) were used fto generate bone marrow chimeras.
Gipr fl/fl (on C57Bl/6 background, provided by Prof.D Drucker,Toronto) and LysM cre (B6.129P2-Lyz2tm1(cre)Ifo/J from Jackson laboratories) were used for generate Lysm -cre. Gipr fl/fl mice. All mice were maintained in specific pathogen-free animal facility and experiments were performed according to protocols approved by the Animal Care Use Committee of the Sourasky Medical Center. Mice were housed with 12 hr light cycles and a constant temperature of 22°C.

Wild animals

Provide details on animals observed in or captured in the field; report species, sex and age where possible. Describe how animals were caught and transported and what happened to captive animals after the study (if killed, explain why and describe method; if released, say where and when) OR state that the study did not involve wild animals.

Field-collected samples

For laboratory work with field-collected samples, describe all relevant parameters such as housing, maintenance, temperature, photoperiod and end-of-experiment protocol OR state that the study did not involve samples collected from the field.

Human research participants

Policy information about studies involving human research participants

Population characteristics

Describe the covariate-relevant population characteristics of the human research participants (e.g. age, gender, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."

Recruitment

Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.

ChIP-seq

Data deposition

☐ Confirm that both raw and final processed data have been deposited in a public database such as GEO.

☐ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links
May remain private before publication.

For "Initial submission" or "Revised version" documents, provide reviewer access links. For your "Final submission" document, provide a link to the deposited data.

Files in database submission

Provide a list of all files available in the database submission.

Genome browser session
(e.g. UCSC)

Provide a link to an anonymized genome browser session for "Initial submission" and "Revised version" documents only, to enable peer review. Write "no longer applicable" for "Final submission" documents.

Methodology

Replicates

Describe the experimental replicates, specifying number, type and replicate agreement.

Sequencing depth

Describe the sequencing depth for each experiment, providing the total number of reads, uniquely mapped reads, length of reads and whether they were paired- or single-end.

Antibodies

Describe the antibodies used for the ChIP-seq experiments; as applicable, provide supplier name, catalog number, clone name, and lot number.

Peak calling parameters	*Specify the command line program and parameters used for read mapping and peak calling, including the ChIP, control and index files used.*
Data quality	*Describe the methods used to ensure data quality in full detail, including how many peaks are at FDR 5% and above 5-fold enrichment.*
Software	*Describe the software used to collect and analyze the ChIP-seq data. For custom code that has been deposited into a community repository, provide accession details.*

Flow Cytometry

Plots

Confirm that:

☒ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☒ All plots are contour plots with outliers or pseudocolor plots.

☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	Epididymal fat pads or inguinal subcutaneous fat stromal vascular fractions (SVF) - fat pads were surgically removed from mice, weighted, cut into small pieces and subsequently incubated in digestion buffer [DMEM, 12.5 mM HEPES pH 7.4, 2% BSA and 10mg collagenase type II] for 30 min at 37 degrees C in a shaking bath at 150 rpm. The digested tissue was filtered through a 100µM mesh and centrifuged at room temperature at 500Xg for 5 min. The pellet was washed and erythrocytes were lysed with red blood cells lysis solution. Blood peripheral blood mononuclear and polymorphonuclear cells were isolated using the BD FACS(TM) Lysing Solution, according to manufacturer's instructions. Cells from SVF and blood were stained according to the manufacturer orders using the listed antibodies and dilutions. With respect to S100A8 staining, after surface antigen staining, cells were fixed and permeabilized with BD Cytofix Cytoperm kit and stained intracellularly with an isotype control or S100A8 (provided by Prof. T. Vogl, Munster University, Germany) antibodies, followed by staining with Alex 647 anti-rabbit antibodies.
Instrument	FACSCanto™ II machine(BD Biosciences, USA)
Software	Data were analyzed using BD FACS DIVA (v6.1.3) or FlowJo (LLC, v9.9.6 or v10.4.2) softwares
Cell population abundance	EpiWAT ATMs, Ly6Chi monocytes or CD11b(neg) lymphocytes were sorted to high purity using the cell sorter BD FACSAria™ III machine (BD Biosciences, USA). For all populations, purity was above 90% as calculated out of total living cells.
Gating strategy	Blood monocytes: CD45+CD11b+CD115+Ly6G- monocytes were dissected into Ly6Chi and Ly6Clo subsets Blood neutrophils: CD45+CD11b+CD115-Ly6Ghi EpiWAT or IngWAT ATMs: CD45+CD11b+MHCII+CD64+F4/80+ EpiWAT or IngWAT neutrophils: CD45+CD11b+MHCII-CD64-/loF4/80-/loLy6Ghi EpiWAT or IngWAT Ly6Chi monocytes: CD45+CD11b+MHCII-CD64loF4/80lo Ly6G-Ly6Chi All gating strategies are exemplified at Figure 2 and Supplementary Figure 8.

☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.

Magnetic resonance imaging

Experimental design

Design type	*Indicate task or resting state; event-related or block design.*
Design specifications	*Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial or block (if trials are blocked) and interval between trials.*
Behavioral performance measures	*State number and/or type of variables recorded (e.g. correct button press, response time) and what statistics were used to establish that the subjects were performing the task as expected (e.g. mean, range, and/or standard deviation across subjects).*

Acquisition

Imaging type(s) — *Specify: functional, structural, diffusion, perfusion.*

Field strength — *Specify in Tesla*

Sequence & imaging parameters — *Specify the pulse sequence type (gradient echo, spin echo, etc.), imaging type (EPI, spiral, etc.), field of view, matrix size, slice thickness, orientation and TE/TR/flip angle.*

Area of acquisition — *State whether a whole brain scan was used OR define the area of acquisition, describing how the region was determined.*

Diffusion MRI ☐ Used ☐ Not used

Preprocessing

Preprocessing software — *Provide detail on software version and revision number and on specific parameters (model/functions, brain extraction, segmentation, smoothing kernel size, etc.).*

Normalization — *If data were normalized/standardized, describe the approach(es): specify linear or non-linear and define image types used for transformation OR indicate that data were not normalized and explain rationale for lack of normalization.*

Normalization template — *Describe the template used for normalization/transformation, specifying subject space or group standardized space (e.g. original Talairach, MNI305, ICBM152) OR indicate that the data were not normalized.*

Noise and artifact removal — *Describe your procedure(s) for artifact and structured noise removal, specifying motion parameters, tissue signals and physiological signals (heart rate, respiration).*

Volume censoring — *Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.*

Statistical modeling & inference

Model type and settings — *Specify type (mass univariate, multivariate, RSA, predictive, etc.) and describe essential details of the model at the first and second levels (e.g. fixed, random or mixed effects; drift or auto-correlation).*

Effect(s) tested — *Define precise effect in terms of the task or stimulus conditions instead of psychological concepts and indicate whether ANOVA or factorial designs were used.*

Specify type of analysis: ☐ Whole brain ☐ ROI-based ☐ Both

Statistic type for inference (See Eklund et al. 2016) — *Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.*

Correction — *Describe the type of correction and how it is obtained for multiple comparisons (e.g. FWE, FDR, permutation or Monte Carlo).*

Models & analysis

n/a	Involved in the study
☐	☐ Functional and/or effective connectivity
☐	☐ Graph analysis
☐	☐ Multivariate modeling or predictive analysis

Functional and/or effective connectivity — *Report the measures of dependence used and the model details (e.g. Pearson correlation, partial correlation, mutual information).*

Graph analysis — *Report the dependent variable and connectivity measure, specifying weighted graph or binarized graph, subject- or group-level, and the global and/or node summaries used (e.g. clustering coefficient, efficiency, etc.).*

Multivariate modeling and predictive analysis — *Specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.*