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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	Living Image 4.1,
Data analysis	ChemDraw 16.0.1.4 (77), Living Image 4.1, Geneious prime 2019.0.4, Microsoft Word 2016, Microsoft Excel 2016, Microsoft Powerpoint 2016, GraphPad Prism 8.0.2, Adobe Illustrator CC 22.1, Osirix 3.8, EVOS FL Auto, Tecan i-Control 1.11, Nanodrop 8000 2.3.2, cSeries software 1.9.8.0403.

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	No sample-size calculations were performed. Sample size was determined to be adequate based on the magnitude and consistency of measurable differences between groups.
Data exclusions	Non of the data were excluded.
Replication	All experiments were repeated at least twice.
Randomization	Mice were randomly divided into experimental groups.
Blinding	Blinding was not relevant to the study, because it would not affect the results.

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

Antibodies

Antibodies used	Glut1 (abcam, ab15309, polyclonal, dilution 1:400), Beta-Acitn (abcam, ab8229, polyclonal, dilution 1:1000), donkey anti-goat IgG HRP (abcam, ab97110,polyclonal, dilution 1:10000),Goat anti-Rabbit IgG H&L HRP (abcam, ab97051, polyclonal, dilution 1:10000), Glut4 (abcam, ab654, polyclonal, dilution 1:2000), Myosin (abcam, ab124205,polyclonal, dilution 1:900), Glycogen Synthase (abcam, ab40810, monoclonal [EP817Y], dilution 1:10000), a-Tubulin (Sigma, #T6074Akt, dilution 1:4000), Akt (Cell Signaling , #9271, dilution 1:1000) and P-Akt (Cell Signaling, #9272, dilution 1:1000).
Validation	All the antibodies were validated by the manufacturer.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	C2C12-luc (it was a kind gift form Prof. Patrick Aebischer - LEN, EPFL, Lausanne, Switzerland), HT1080-luc2, 4T1-Redluc, HepG2-luc2 (PerkinElmer), 3T3-L1 (it was a kind gift form Prof. Andreas Stahl, Stanford University) and HEK293 TN (it was a kind gift form Prof. Dean Felsher, Stanford University).
Authentication	None of the cell lines were authenticated.
Mycoplasma contamination	Cell lines were tested with the MycoProbe kit(R&D Systems) and results were negative for mycoplasma contamination.
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	Mus musculus (FVB-Tg[CAG-luc,-GFP]L2G85Chco/ J, females, 12 - 25 weeks, Jackson Lab) Mus musculus (Swiss nu/nu, females, 12 - 25 weeks, Charles river labs)
Wild animals	The study did not involve wild animals.
Field-collected samples	The study did not involve samples collected from the field.
Ethics oversight	Swiss Cantonal Veterinary Office Committee for Animal Experimentation, University of California Los Angeles (UCLA, USA) Animal Research Committee.

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

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	300 000 cells were diluted in 500 ul PBS and sorted for GFP positive.
Instrument	FACSAria Fusion
Software	FACSDiva Version 6.1.2
Cell population abundance	We had population of 785 GFP positive cells that were sorted as 1 cell per well in 96-well plate.
Gating strategy	Describing the gating strategy used for all relevant experiments, specifying the preliminary FSC/SSC of the starting cell population, indicating where boundaries between "positive" and "negative" staining cell populations are defined.

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