

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
<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. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P 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 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 N/A

Data analysis N/A

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](#)

GSE270889

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	N/A
Reporting on race, ethnicity, or other socially relevant groupings	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](https://www.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	In-vitro sample size 3-6 and 3-10 animals
Data exclusions	NO
Replication	Western blot were done by 4-6 independent biological replicates; 3-4 independent Seahorse experiments were performed with 3-4 technical replicates; Metabolic profiling was done with 6 biological replicates; 6 biological samples (mice) were used for RNA sequencing study.
Randomization	N/A
Blinding	Blinding were done for saffroninO/fast-green stained histological grading

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	All antibody details including clone and manufacturer information are included in methods and also listed below: Antibody Manufacturer Catalog number and Concentration mouse monoclonal anti-OPA1 (BD Bioscience, 612607, 18/OPA1, WB 1:2000, IF 1:200) rabbit polyclonal anti-PMP70 (Thermo Fisher, PA1-650, 5ug/ml)
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rabbit monoclonal anti-GM130 (Thermo Fisher, MA5-35107, 1:100)
 rabbit polyclonal anti-EEA1 (Cell Signaling Technology, 2411, 1:100)
 rabbit polyclonal anti-BNIP3 (Cell Signaling Technology, 3769, WB-1:1000, IF-1:100)
 rabbit monoclonal anti-LC3A/B (Cell Signaling Technology, D3U4C, 12741, WB-1:1000, IF- 1:100)
 rabbit polyclonal anti-TGN46 (Abcam, 16059, 1 ug/ml)
 rabbit monoclonal anti-LAMP1 (Cell Signaling Technology, D2D11, 9091, WB- 1:1000, IF-1:100)
 rabbit monoclonal anti-BNIP3L (Cell Signaling Technology, D4R4B, 12396, WB 1:1000, IF-1:100)
 mouse monoclonal anti-Rab7 (EMD Millipore, 117, R8779, IF-10ug/ml)
 rabbit polyclonal anti-SQSTM1/p62 (Cell Signaling Technology, 5114, 1:1000)
 mouse monoclonal anti-CHOP (Cell Signaling Technology, L63F7, 78063, 1:1000)
 rabbit polyclonal anti-Beclin-1 (Cell Signaling Technology, 3738, 1:1000)
 rabbit monoclonal anti-MFF (Cell Signaling Technology, E5W4M, 84580, 1:1000)
 rabbit monoclonal anti-MFN2 (Cell Signaling Technology, D2D10, 9482, 1:1000)
 rabbit monoclonal anti-FIS1 (Cell Signaling Technology, E3K90, 32525, 1:1000)
 rabbit polyclonal anti-Ubiquitin (Cell Signaling Technology, 3933, 1:1000)
 rabbit monoclonal anti-phospho-Ubiquitin (Cell Signaling Technology, E2J6T, 62802, 1:1000)
 rabbit monoclonal anti-GAPDH (Cell Signaling Technology, D16H11, 5174, 1:1000)
 mouse monoclonal anti-DLP1 (BD Bioscience, 8/DLP1, 611113, 0.5ug/ml)
 mouse monoclonal anti-Parkin (Santa Cruz, sc32282, 1:1000)
 mouse monoclonal anti-MFN1 (Abcam, 11E91H12, ab126575, 1:1000)
 rabbit monoclonal anti-OPA1 (Abcam, EPR11075, ab157457, 1:250)
 rabbit polyclonal anti-LC3B (Novus Biologicals, NB100-2220, 1:200)
 rabbit monoclonal anti-GLUT1 (Abcam, SPM498, Ab40084, 1:200)
 rabbit polyclonal anti-CA3 (Abcam, ab196835, 1:200)
 rabbit polyclonal anti-Collagen X (Abcam, ab58632, 1:500)
 rabbit polyclonal anti-Collagen I (Thermo Fisher, PA1-26204)
 rabbit polyclonal anti-COMP (Abcam, ab231977, 1:200)
 rabbit polyclonal anti-MMP13 (Abcam, ab39012, 1:200)
 mouse monoclonal anti_ARGxx (Abcam, BC-3, ab3773, 1:200)
 mouse polyclonal anti-Aggregan (Millipore Sigma, AB1031, 1:50)
 mouse monoclonal anti-Krt19 (DSHB, TROMA-II, AB_2133570, 1:3)
 anti-rabbit Alexa Fluor 488 (Jackson Laboratories, 111-545-003, 1:400)
 anti-mouse Alexa Fluor 488 (Jackson Laboratories, 115-545-006, 1:400)
 anti-mouse Alexa Fluor 594 (Jackson Laboratories, 115-585-003, 1:400)
 anti-rabbit Alexa Fluor 594 (Jackson Laboratories, 111-585-003, 1:400)
 anti-rabbit Alexa Fluor 647 (Jackson Laboratories, 111-605-003, 1:400)
 anti-mouse Alexa Fluor 647 (Jackson Laboratories, 115-605-003, 1:400)

Validation

All antibodies used in this study have been commercially available and previously used by our group (Madhu et al., JBMR 2020: Autophagy 2023; Johnston et al JBMR 2022; JCI Insight 2023; Boneski et al Front. Cell Dev Biol 2022). The complete information and validation information for each antibody as well as previous publications that have used each antibody can be found on the manufacturer's website.

Eukaryotic cell lines

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

Cell line source(s)	Primary rat nucleus pulposus cells were isolated and culture. HEK293T (Human embryonic kidney) (ATCC; CRL-3216)
Authentication	Gelatinous tissue in rat NP compartment.
Mycoplasma contamination	Mycoplasma contamination test results were negative
Commonly misidentified lines (See ICLAC register)	There is no commonly misidentified lines.

Palaeontology and Archaeology

Specimen provenance	<i>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). Permits should encompass collection and, where applicable, export.</i>
Specimen deposition	<i>Indicate where the specimens have been deposited to permit free access by other researchers.</i>

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.

Ethics oversight

Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance was required and explain why not.

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

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

10-week-old male Sprague Dawley rats (Charles River). Opa1 fl/fl on mixed C57BL/6-129/SvEv background and Aggrecan-CreERT2 (C57BL/6J) from Jackson laboratories (Stock #019148). For mutant experiments, Opa1 fl/fl mice were bred to Acan (aggrecan)-CreERT2 to generate inducible mouse model. Cre negative mice were used as litter mate control. Mice were analyzed at 7, 12, and 20 month. All animal experiments were conducted in accordance with Thomas Jefferson University institutional guidelines, Philadelphia, Pennsylvania, USA.

Wild animals

No wild animals were used in this study.

Reporting on sex

Male and female were presented together, but mentioned in the legend and methods how many were male and female.

Field-collected samples

No field collected samples were used in this study.

Ethics oversight

All the animal studies were carried out in conformity with the Institutional Animal Care and Use Committee (IACUC) of Thomas Jefferson University's applicable rules and regulations. Mice were housed in pathogen-free conditions in individually ventilated cages with a consistent light/dark cycle, food, water and controlled temperature.

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

Clinical data

Policy information about [clinical studies](#)

All manuscripts should comply with the ICMJE [guidelines for publication of clinical research](#) and a completed [CONSORT checklist](#) must be included with all submissions.

Clinical trial registration

Provide the trial registration number from ClinicalTrials.gov or an equivalent agency.

Study protocol

Note where the full trial protocol can be accessed OR if not available, explain why.

Data collection

Describe the settings and locales of data collection, noting the time periods of recruitment and data collection.

Outcomes

Describe how you pre-defined primary and secondary outcome measures and how you assessed these measures.

Dual use research of concern

Policy information about [dual use research of concern](#)

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

- | No | Yes | |
|--------------------------|--------------------------|----------------------------|
| ☐ | ☐ | Public health |
| ☐ | ☐ | National security |
| ☐ | ☐ | Crops and/or livestock |
| ☐ | ☐ | Ecosystems |
| ☐ | ☐ | Any other significant area |

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes
☐	☐ Demonstrate how to render a vaccine ineffective
☐	☐ Confer resistance to therapeutically useful antibiotics or antiviral agents
☐	☐ Enhance the virulence of a pathogen or render a nonpathogen virulent
☐	☐ Increase transmissibility of a pathogen
☐	☐ Alter the host range of a pathogen
☐	☐ Enable evasion of diagnostic/detection modalities
☐	☐ Enable the weaponization of a biological agent or toxin
☐	☐ Any other potentially harmful combination of experiments and agents

Plants

Seed stocks	Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.
Novel plant genotypes	Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.
Authentication	Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.

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 <i>May remain private before publication.</i>	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

Describe the sample preparation, detailing the biological source of the cells and any tissue processing steps used.

Instrument

Identify the instrument used for data collection, specifying make and model number.

Software

Describe the software used to collect and analyze the flow cytometry data. For custom code that has been deposited into a community repository, provide accession details.

Cell population abundance

Describe the abundance of the relevant cell populations within post-sort fractions, providing details on the purity of the samples and how it was determined.

Gating strategy

Describe the gating strategy used for all relevant experiments, specifying the preliminary FSC/SSC gates 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.

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

Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.

(See [Eklund et al. 2016](#))

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.