

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 (<i>n</i>) 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> 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 <i>d</i> , Pearson's <i>r</i>), 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	Data collection was performed using CytoExpert software (Beckman Coulter) for flow cytometry, NIS-Elements software (Nikon) for confocal microscopy, MoorLDI software (Moor Instruments) for Laser Doppler perfusion imaging, VevoLab software (VisualSonics) for cardiac ultrasound, and Living Image software (PerkinElmer) for small animal in vivo imaging. No custom code or unpublished software was used for data collection.
Data analysis	Flow cytometry data were analyzed using FlowJo (BD Biosciences). Confocal microscopy images were analyzed using ImageJ (Fiji). Statistical analyses were performed using GraphPad Prism. No custom code or unpublished software was used for data analysis.

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](#)

The single-cell RNA sequencing data generated in this study have been deposited in the NCBI BioProject database under accession code PRJNA1344814 [<https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1344814>] and are publicly available. The mass spectrometry proteomics data generated in this study have been deposited in the ProteomeXchange Consortium via the iProX partner repository under accession code PXD069416 [<https://www.iprox.cn//page/subproject.html?id=IPX0013796001>] and are publicly available. Source data are provided with this paper. All other data supporting the findings of this study are available within the article and supplementary information. This paper does not report original code. Any additional information required to reanalyze the data reported in this paper is available from the lead contact upon request.

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	No human participants were recruited in this study. The human cell lines used (hiPSCs and THP 1) are derived from male donors.
Reporting on race, ethnicity, or other socially relevant groupings	Not applicable
Population characteristics	No human participants were involved in this study.
Recruitment	No human participants were recruited.
Ethics oversight	All experiments involving human-derived cell lines were performed in accordance with institutional guidelines and commercial provider recommendations. No human participants were involved. Animal experiments were approved by the Institutional Animal Care and Use Committee of Peking University Health Science Center. (Animal Protocol Approval Number: BCJ0257).

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	Sample sizes were chosen based on previous experience with similar ischemic mouse models and arterial organoid transplantation experiments, which have been shown to detect biologically relevant effects. No formal sample size calculation was performed.
Data exclusions	No data were excluded from the analyses.
Replication	All experiments were independently repeated at least three times with consistent results. Findings reported in the study were reproducible across biological replicates.
Randomization	Animals were purchased at the same age and with similar body weight. Mice were randomly assigned to experimental groups to ensure comparable baseline characteristics, and outcome measurements were analyzed in a standardized manner to minimize potential bias.
Blinding	Investigators were not blinded to group allocation during experiments due to the nature of the interventions; however, outcome analyses (e.g., flow cytometry, imaging quantification) were performed in a standardized manner to minimize bias.

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 antibodies used in this study are listed in Supplementary Table 1 and Table 2, including supplier, catalog number and dilution.
Validation	Primary antibodies were validated for the indicated species and applications by the manufacturers, as described on the supplier websites.

Eukaryotic cell lines

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

Cell line source(s)	Arterial organoids (AOs) were generated from human iPSCs (Takara Bio, Cat. No. Y00305, male donor). THP 1 cells (Ubigen, Cat. No. YC D011 EGFP P) were used as a human monocytic line (male origin).
Authentication	Cell lines were not independently authenticated; the original source maintains authentication.
Mycoplasma contamination	All cell lines tested negative for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used in this 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	Laboratory mice (Mus musculus, NCr nu/nu, male and female, 8 weeks old) were used for all experiments. Mice were purchased from the department of laboraroty animal science of Peking university health science center and maintained under standard laboratory conditions (22±22°C, 12-h light/dark cycle, ad libitum access to food and water).
Wild animals	No wild animals were used in this study.
Reporting on sex	Eight-week-old male mice were used for all experiments and randomly allocated to different experimental groups. Experimental analyses were performed in a double-blind fashion.
Field-collected samples	No field-collected samples were used in this study.
Ethics oversight	All animal experiments were approved by the Institutional Animal Care and Use Committee of Peking University Health Science Center (Animal Protocol Approval Number: BCJ10257) and conducted in accordance with institutional guidelines.

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

Plants

Seed stocks	Not applicable
Novel plant genotypes	Not applicable
Authentication	Not applicable

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	Single-cell suspensions were prepared from mouse ischemic muscle tissues or arterial organoids (AOs) by enzymatic digestion, followed by filtration through a 70-µm cell strainer. Cells were washed and resuspended in staining buffer prior to antibody incubation.
Instrument	Flow cytometry data were acquired on a Beckman Coulter CytoFLEX flow cytometer.
Software	Data were collected using CytoExpert software and analyzed with FlowJo.
Cell population abundance	Cell population abundance was quantified as the percentage of parent populations. Post-sort purity was assessed by re-analysis and was typically >90%.
Gating strategy	Cells were first gated based on FSC/SSC to exclude debris, followed by doublet exclusion. Positive and negative populations were defined based on fluorescence minus one (FMO) controls or unstained controls.

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