nature portfolio

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Last updated by author(s): Apr 18, 2025

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 *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	None to report.
Data analysis	All statistical processing used in this paper was performed in GraphPad prism 9.5.1. Experimenters who collected or quantified data were blinded to genotype, drug treatment, and surgery groups. The reproducibility of our findings was confirmed by at least three independent experiments. Data are shown as mean ± standard error of the mean (SEM). For multiple comparisons, analyses of variance with Dunnett's post hoc tests or Tukey–Kramer tests were performed as appropriate. A t-test was used for comparison between two groups.

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 data that support the findings of this study are available from the corresponding author upon reasonable 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	Not applicable.
Reporting on race, ethnicity, or other socially relevant groupings	Not applicable.
Population characteristics	Not applicable.
Recruitment	Not applicable.
Ethics oversight	Not applicable.

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

Life sciences study design

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

Sample size	For each experiment, at least 3 samples were set up in the control group and the experimental group, and at least 3 times were repeated.
Data exclusions	Data points were excluded If the animal's growing conditions are very different.
Replication	All experiments were performed with at least three biological replicates, and each sample was measured in triplicate as technical replicates.
Randomization	Mice of each genotype were tested in a random and blinded fashion.
Blinding	Mice of each genotype were tested in a random and blinded fashion.

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	The following antibodies were used for immunostaining and immunoblot analysis: anti-LTCC (Alomone, 1:1000 dilution), anti-SERCA2a (Thermo, 1:1000 dilution), anti-GAPDH (Abcam, 1:1000 dilution), anti-caveolin3 (BD biosciences, 1:1000 dilution), anti-junctophilin2 (Santa Cruz, 1:1000 dilution), anti-IGF-1 receptor (Cell Signaling, 1:1000 dilution), anti-phospho-IGF-1 receptor (Cell Signaling, 1:1000 dilution), anti-Akt (Cell Signaling, 1:1000 dilution), anti-phospho-Akt (Cell Signaling, 1:1000 dilution), anti-mTOR

(Cell Signaling, 1:1000 dilution), anti-PI3K (Cell Signaling, 1:1000 dilution), anti-p70S6K (Cell Signaling, 1:1000 dilution), anti-phospho-p70S6K (Cell Signaling, 1:1000 dilution), anti-MEF2C (Cell Signaling, 1:1000 dilution), anti-p-HDAC (Sigma, 1:1000 dilution), anti-IGF-1 (Santa Cruz, 1:1000 dilution), and anti-SRF (Santa Cruz, 1:1000 dilution). Anti-NCX1 antibody (1:1000 dilution) was generated in our laboratory as previously described (Katanosaka et al., 2005, J Bio Chem.).

Validation

Of the antibodies used, anti-SRCA2a, anti-caveolin3, anti-IGF-1, and anti-SRF were produced in mice. Anti-junctophilin2 was produced in goats. Other antibodies were produced in rabbits. All antibodies used for antibody staining were confirmed by immunoblotting to have one main band corresponding to their molecular weight against mouse cardiac tissue. We also checked the description of validation on the manufacturer's website and relevant citations to determine that they were reliable.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	Cardiomyocytes isolated from neonatal mice were cultured and used in the experiments. Cell line is not used.
Authentication	N/A
Mycoplasma contamination	Cardiac function differed between males and females. For this reason, only male mice were used in this experiment. Mice used ranged from 2 to 12 weeks of age. When heart failure was induced, a maximum of 38 weeks old was used.
Commonly misidentified lines (See ICLAC register)	N/A

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	Knockout mice generated from C57BL/6 mice were used. The generation of TRPV2flox/flox;MerCreMer+/– (MCM-TRPV2-cKO) and TRPV2flox/flox;MerCreMer–/– (Floxed-TRPV2) mice was previously described in detail (Katanosaka et al., 2014, Nat. Comms.).
Wild animals	N/A
Reporting on sex	Cardiac function differed between males and females. For this reason, only male mice were used in this experiment. Mice used ranged from 2 to 12 weeks of age. When heart failure was induced, a maximum of 38 weeks old was used.
Field-collected samples	N/A
Ethics oversight	The Institutional Animal Care and Use Committee at Okayama University approved the animal experiments conducted in this study (approval number OKU-2022397, 2021119). All methods were carried out in accordance with the Guide for the Care and Use of Laboratory Animals published by the U.S. National Institutes of Health.

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

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, mosiacism, off-target gene editing) were examined.*