nature portfolio

Corresponding author(s): Duanqing Pei

Last updated by author(s): Aug 18, 2024

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	ZEN software 3.4 for immunofluorescence, Clampfit 10.7 for electrophysiology, bulk seq data are collected at home by using the specific commercial kit (Vazyme, #701). scRNA data was constructed using 10× Genomics single-cell transcriptome libraries and PE150 paired-end sequencing was performed using the illumina NovaSeq platform.
Data analysis	RNA-seq data were mapped to the hg38 reference genome with STAR(v2.7.10a), RSEM(v1.3.1) tool was used to do quantification. Differential expression analysis was performed using the DESeq2(v1.42.1) software package and the results were output. The scRNA data were demultiplexed, baecoded, counted, and aggregated using Cell Ranger software(v7.0.0). Downstream analysis was performed using the Seurat(v4.4.0) software package.

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

RNA sequencing data have been deposited in the NCBI Gene Expression Omnibus and are accessible through GEO accession numbers GSE269571 ((for reviewers, the access token is ctepiwkgtvutrqx) and GSE269572 ((for reviewers, the access token is upkbaagwfpwtnoj)
https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE269571
https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE269572

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	*Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used.* *Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected.* *Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.*
Reporting on race, ethnicity, or other socially relevant groupings	*Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status).* *Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.)* *Please provide details about how you controlled for confounding variables in your analyses.*
Population characteristics	*Describe the covariate-relevant population characteristics of the human research participants (e.g. age, 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.*
Ethics oversight	*Identify the organization(s) that approved the study protocol.*

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	No sample size calculation was performed. Sample size was chosen based on our experience and experiments. No statistical method was used to predetermine sample size.
Data exclusions	No data were excluded from analysis
Replication	All experiments were replicated at least three times, data are shown as means with SEM or SD
Randomization	The authors thought there were no relevant for randomization to our study
Blinding	None

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

HAND1 (R&D Systems, AF3168; Genetex, GTX56230), NKX2.5 (Cell Signaling Technology, 8792), WT1 (Abcam, ab89901), VIM (Cell Signaling Technology, 5741S), VE-cadherin/CDH5 (R&D Systems, AF938-SP), TNNT2 (Abcam, ab8295), NR2F2 (R&D Systems, PP-H7147-00; Abcam, ab211777), MYL3 (Abcam, ab108923), COL1A1 (Invitrogen, PA5-29569), HRP-linked Goat anti Mouse IgG(H+L) (Beyotime, A0216), HRP-linked Goat anti Rabbit IgG(H+L) (Beyotime, A0208), HRP-linked Donkey anti Goat IgG(H+L) (Beyotime , A0516), Anti-mouse IgG (H+L), F(ab')2 Fragment (Alexa Fluor® 488 Conjugate) (Cell Signaling Technology, 4408S), A mouse IgG (H+L), F(ab')2 Fragment (Alexa Fluor® 594 Conjugate) (Cell Signaling Technology, 8890S), Anti-mouse IgG (H+L), F(ab')2 Fragment (Alexa Fluor® 647 Conjugate) (Cell Signaling Technology, 4410S), Anti-rabbit IgG (H+L), F(ab')2 Fragment (Alexa Fluor® 488 Conjugate) (Cell Signaling Technology, 4412S), Anti-rabbit IgG (H+L), F(ab')2 Fragment (Alexa Fluor® 594 Conjugate) (Cell Signaling Technology, 8889S), Anti-rabbit IgG (H+L), F(ab')2 Fragment (Alexa Fluor® 647 Conjugate) (Cell Signaling Technology, 4414S)

Validation

HAND1: https://www.rndsystems.com/cn/products/human-hand1-antibody_af3168
HAND1: https://www.genetex.com/Product/Detail/HAND1-antibody/GTX56230
NKX2.5: https://www.cellsignal.com/products/primary-antibodies/nkx2-5-e1y8h-rabbit-mab/8792
WT1: https://www.abcam.com/en-us/products/primary-antibodies/wilms-tumor-protein-antibody-can-r9ihc-56-2-ab89901
VIM: https://www.cellsignal.com/products/primary-antibodies/vimentin-d21h3-xp-rabbit-mab/5741
VE-cadherin/CDH5: https://www.rndsystems.com/cn/products/human-ve-cadherin-antibody_af938
TNNT2: https://www.abcam.cn/products/primary-antibodies/cardiac-troponin-t-antibody-1c11-ab8295.html
NR2F2: https://www.rndsystems.com/cn/products/human-coup-tf-ii-nr2f2-antibody-h7147_pp-h7147-00
NR2F2: https://www.abcam.cn/products/primary-antibodies/nr2f2-antibody-epr18443-ab211777.html
MYL3: https://www.abcam.cn/products/primary-antibodies/myosin-light-chain-3-antibody-epr4160-ab108923.html
COL1A1: https://www.thermofisher.cn/cn/zh/antibody/product/COL1A1-Antibody-Polyclonal/PA5-29569
HRP-linked Goat anti Mouse IgG(H+L): https://www.beyotime.com/product/A0216.htm
HRP-linked Goat anti Rabbit IgG(H+L): https://www.beyotime.com/product/A0208.htm
HRP-linked Donkey anti Goat IgG(H+L): https://www.beyotime.com/product/A0516.htm
Anti-mouse IgG (H+L), F(ab')2 Fragment (Alexa Fluor® 488 Conjugate): https://www.cellsignal.com/products/secondary-antibodies/anti-mouse-igg-h-l-f-ab-2-fragment-alexa-fluor-488-conjugate/4408
Anti-mouse IgG (H+L), F(ab')2 Fragment (Alexa Fluor® 594 Conjugate): https://www.cellsignal.com/products/secondary-antibodies/anti-mouse-igg-h-l-f-ab-2-fragment-alexa-fluor-594-conjugate/8890
Anti-mouse IgG (H+L), F(ab')2 Fragment (Alexa Fluor® 647 Conjugate): https://www.cellsignal.com/products/secondary-antibodies/anti-mouse-igg-h-l-f-ab-2-fragment-alexa-fluor-647-conjugate/4410
Anti-rabbit IgG (H+L), F(ab')2 Fragment (Alexa Fluor® 488 Conjugate) : https://www.cellsignal.com/products/secondary-antibodies/anti-rabbit-igg-h-l-f-ab-2-fragment-alexa-fluor-488-conjugate/4412
Anti-rabbit IgG (H+L), F(ab')2 Fragment (Alexa Fluor® 594 Conjugate) : https://www.cellsignal.com/products/secondary-antibodies/anti-rabbit-igg-h-l-f-ab-2-fragment-alexa-fluor-594-conjugate/8889
Anti-rabbit IgG (H+L), F(ab')2 Fragment (Alexa Fluor® 647 Conjugate): https://www.cellsignal.com/products/secondary-antibodies/anti-rabbit-igg-h-l-f-ab-2-fragment-alexa-fluor-647-conjugate/4414

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)

Human H9 (WA09) and H1 (WA01) ESCs were purchased from WiCell Research Institute. Human UiPSC were homemade.

Authentication	All the cell line used were authenticated
Mycoplasma contamination	All cell lines were tested negative for mycoplasma with the Kit from Lonza (LT07-318).
Commonly misidentified lines (See ICLAC register)	None

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.*