

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 Zen Black Imaging Software (ZEISS), ImageJ, GraphPadPrism. All sequencing was done on the NovaSeq 6000.

Data analysis Western Blots and immunofluorescence images were analyzed by ImageJ. Plotting and statistics were done in GraphPadPrism. Sequencing reads were mapped to the mm10 reference genome using CellRanger-ARC (version 2.0.2). Analysis was performed with Seurat (

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](#)

GSE272154 BioProject Number is PRJNA112533

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

The sample size was determined by based on previous studies. All experiments were repeated a minimum three times.

Data exclusions

No data was excluded.

Replication

All experiments were repeated at least three independent times and were reproducible

Randomization

Male and female mice were used evenly throughout all the manuscripts experiments.

Blinding

Investigators were not blinded during data collection as experiments had quantitative output.

Behavioural & social sciences study design

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

Study description

N/A

Research sample

N/A

Sampling strategy

N/A

Data collection

N/A

Timing

N/A

Data exclusions

N/A

Non-participation

N/A

Randomization

N/A

Ecological, evolutionary & environmental sciences study design

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

Study description

N/A

Research sample

N/A

Sampling strategy

N/A

Data collection

N/A

Timing and spatial scale

N/A

Data exclusions

N/A

Reproducibility

N/A

Randomization

N/A

Blinding

N/A

Did the study involve field work? ☐ Yes ☒ No

Field work, collection and transport

Field conditions

N/A

Location

N/A

Access & import/export

N/A

Disturbance

N/A

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	Tbx5 (Thermo Fisher; 42-6500), Gata4 (SantaCruz; SC-25310), Mef2c (Cell Signaling; #5030), Nkx2.5 (Abcam; ab97355), MF20 (Developmental Studies Hybridoma Bank; MF20), cTnT (Developmental Studies Hybridoma Bank; CT3); cTnT (ProteinTech; 15513-1-AP), Nppa (ProteinTech; 27426-1-AP), Sox5 (Developmental Studies Hybridoma Bank; PCRP-Sox5-1E3) Irx1 (Sigma; HPA 043160), Pitx2 (Capra; 1021-100), Gapdh (SantaCruz; SC32233)
Validation	All antibodies used were previously validated by the manufactures.

Eukaryotic cell lines

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

Cell line source(s)	HEK293T and C166 cells were obtained from ATCC. MEC1 (Cat. SCC187) and HCFs (Cat. 306-05F) were obtained from Millipore Sigma. AC16 cells were gifted from Dr. James F. Martin (Baylor School of Medicine).
Authentication	Cell lines were authenticated by the previously by manufacturer . AC16 cells were authenticated by qPCR .
Mycoplasma contamination	Cells were cultured in a mycoplasma free enviornment.
Commonly misidentified lines (See ICLAC register)	No misidentified cells were used in this study.

Palaeontology and Archaeology

Specimen provenance	N/A
Specimen deposition	N/A
Dating methods	N/A
☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.	
Ethics oversight	N/A

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	PMIS transgenic mice were generated in the C57/B6 background. All mice used in the study were of this background.
Wild animals	N/A
Reporting on sex	Male and female mice used were used equally throughout all of the experiments and were randomly assigned .
Field-collected samples	N/A

Ethics oversight

IACUC approvals is under ACRUF #4021420

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 N/A

Study protocol N/A

Data collection N/A

Outcomes N/A

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 N/A

Novel plant genotypes N/A

Authentication N/A

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

May remain private before publication.

N/A

Files in database submission

N/A

Genome browser session
(e.g. [UCSC](#))

N/A

Methodology

Replicates

N/A

Sequencing depth

N/A

Antibodies

N/A

Peak calling parameters

N/A

Data quality

N/A

Software

N/A

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

N/A

Instrument

N/A

Software

N/A

Cell population abundance

N/A

Gating strategy

N/A

- ☐ 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

N/A

Design specifications

N/A

Behavioral performance measures

N/A

Acquisition

Imaging type(s)

N/A

Field strength

N/A

Sequence & imaging parameters

N/A

Area of acquisition

N/A

Diffusion MRI

☐

Used

☐

Not used

Preprocessing

Preprocessing software

N/A

Normalization

N/A

Normalization template

N/A

Noise and artifact removal

N/A

Volume censoring

N/A

Statistical modeling & inference

Model type and settings

N/A

Effect(s) tested

N/A

Specify type of analysis: ☐ Whole brain ☐ ROI-based ☐ Both

Statistic type for inference

N/A

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

Correction

N/A

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

N/A

Graph analysis

N/A

Multivariate modeling and predictive analysis

N/A