nature portfolio

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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	Fluorescent image data corrected by a Zeiss LSM 780 confocal microscope system with ZEN 2009 software. Nissle staining data were corrected by all in one fluorescent microscopy BZ700 (Keyence). Electron microscopy data corrected by TEM, JEM-3200FS. WB data collected by ImageQuant LAS-4000 mini (Fujifilm). Differentially expressed genes in RNA-seq were identified using DESeq2 (version 1.8). Current responses in electrophysiological analyses were recorded using an Axopatch 200 B amplifier, and the pCLAMP system (v9.2) was used for data acquisition and analysis.
Data analysis	All statistical analyses were preformed by ImageJ (Open source), Microsoft Excel (Microsoft), and Prism V8 (GraphPad).

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.

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 calculations were performed. Sample size was determined to be adequate based on similar sample sizes that have previously reported using similar experiments reported in references of this manuscript.
Data exclusions	No other data were excluded from the analyses.
Replication	For each experimental condition, at least 3 sections were analyzed per animal and at least 3 animals were used per conditions. All attempts at replication were successful expect for the failures due to sickness or death of animals during the experimental period.
Randomization	Mice and samples were randomized from each group.
Blinding	Data collection and analysis were blinded only for those that could not be automated or arbitrarily extracted.

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
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	Supplier name, catalog number and dilution about all antibodies used in this manuscript are noted in methods.
Validation	We used antibodies which already validated about each specificity and profiles in relevant citations.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	COS7 cells
Authentication	We verified that cells exhibited the expected morphology and transfection efficiency as previously reported.
Mycoplasma contamination	The cell line was tested negative for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell line has been used in the study.

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	Species: ICR and C57BL/6; Pcp2Cre-cKO, Ptf1aCre-cKO, Atoh1-Cre-cKO; Sex: n/a; Age: between 2dpf and 14 dpf Transgenic lines in mixed (BALB/cCrSlc and C57BL/6) backgrounds: Dscamdel17/ del17, En1Cre-cKO; Sex: n/a; Age: between postnatal day 0 and 90
Wild animals	The study did not involve wild animals.
Field-collected samples	The study did not involve samples collected from the field.
Ethics oversight	All animal experiments in this study were approved by the Animal Care and Use Committee of the National Institute of Neuroscience, Japan (#2019027).

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