

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 Behavioural data were collected by Ethovision XT14. Calcium imaging data were collected by Inscopix DAQ (nVoke2). Images were acquired by LAS X software. Electrophysiological data were acquired using pCLAMP10 (Molecular Devices).

Data analysis Data were analyzed by following tools: Ethovision XT14, Inscopix IDPS (v1.8), Python (v3.8.0), GraphPad Prism (v10.2.0), image j, CEBRA (v0.2.0) and Clampex 10.3 software (Molecular Devices, Sunnyvale, CA).

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](#)

Source Data are provided with this paper. Additional raw data from this study are available from the corresponding author upon request. They are not deposited to a public database due to their large size and size limitations of online depositories.

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](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

No statistical method was used to predetermine sample size. Sample sizes were chosen based on published studies and reported power analyses in the field, and are comparable to those in our previous publications.

Data exclusions

Mice showing incorrect lens placement, injection sites or optic fiber placement were excluded from analysis. These criterion were pre-established.

Replication

All attempts at replication were successful. Cell counting of histological sections: all experiments were performed using a minimum of three sections per mouse from three mice.

Randomization

Mice were randomly allocated into different experimental groups and sequences of behaviour tests are assigned randomly. No specific randomization method was used. Age-matched littermates were used as controls in all experiments.

Blinding

Experiments were conducted by an investigator with knowledge of the animal genotype and treatment. For behavior experiments, the need for post-hoc verification of virus expression and optic fiber placement ensured data collection was unbiased.

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	Primary antibodies: goat anti-mCherry (1:1000) (Origene AB0040-200) chicken anti-GFP (1:500) (Aves, GFP-1020) rabbit anti-Wfs1 (1:200) (made by the lab of Prof. Dr. Jens F. Rehfeld, University of Copenhagen, Denmark) mouse anti-PKC δ (1:100; 610398, BD Biosciences)
Validation	The goat anti mcherry was validated by manufacturer: https://www.origene.com/catalog/antibodies/tag-antibodies/ab0040-200/mcherry-goat-polyclonal-antibody The chicken anti-GFP was validated by manufacturer: https://www.aveslabs.com/products/anti-green-fluorescent-protein-antibody-gfp The rabbit anti-Wfs1 was made by the lab of Prof. Dr. Jens F. Rehfeld, University of Copenhagen, Denmark. Validation in https://doi.org/10.1002/cne.21777 The mouse anti-PKC δ was validated by manufacturer: https://www.bdbiosciences.com/en-eu/products/reagents/microscopy-imaging-reagents/immunofluorescence-reagents/purified-mouse-anti-pkc.610398

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	Mice are group-housed under standard laboratory conditions and maintained under a 12-hour light/12-hour dark cycle with food and water ad libitum. The following mouse lines are used: the Htr2a-Cre BAC transgenic line (stock Tg(Htr2a-Cre)KM208Gsat/Mmucd) was imported from the Mutant Mouse Regional Resource Center 482 (https://www.mmrrc.org/). SOM-IRES-cre (SSTtm2.1(cre)Zjh/J) mice were acquired from the Jackson Laboratory. Ai9Isl-TdTomato (B6.Cg- Gt(ROSA)26Sortm9(CAG-tdTomato)Hze/J), FPD1 (B6;129S6Gt(ROSA)26Sortm9 (CAG-mCherry, -CHRM4*)Dym) mouse lines were as described previously (https://doi.org/10.1038/nn.2467 . https://doi.org/10.1126/science.1205295). All mice were backcrossed into a C57BL/6NRj background (Janvier Labs - http://www.janvier-labs.com).
Wild animals	This study did not involve wild animals.
Reporting on sex	Experiments are conducted with adult male mice or mixed gender groups of mice (adult mice > 12 weeks). Samples sizes are not large enough for determination of sex differences.
Field-collected samples	This study did not involve samples collected from the field.
Ethics oversight	All the experiments were performed following regulations from the government of Upper Bavaria, Germany.

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

Plants

Seed stocks	<i>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.</i>
Novel plant genotypes	<i>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.</i>
Authentication	<i>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, mosaicism, off-target gene editing) were examined.</i>