nature research

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Last updated by author(s): Jul 1, 2020

Reporting Summary

Nature Research 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 Research policies, see Authors & Referees 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	Electrophysiology data were acquired using Clampex (version 10, Molecular Devices). Histological data were acquired using Zeiss Zen software (2.3 SP1). Behavioral experiments were conducted using Doric Neuroscience Studio (4.1.5.2) and custom codes written in Bonsai (2.3.1) and Arduino (1.8.7) software, which are available at GitHub (https://github.com/SebastianChoi/Choi-et-al-Nature2020) or upon request.
Data analysis	GraphPad Prism (Version 8, GraphPad Software), Image J (2.0.0-rc-69/1.52p), Zeiss Zen software (2.3 SP1), Clampfit (10.4), and custom codes written in Bonsai (2.3.1) and CellProfiler (3.1.9) software. Custom codes are available at GitHub (https://github.com/SebastianChoi/Choi-et-al-Nature2020) or upon request.

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/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research 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 list of figures that have associated raw data
- A description of any restrictions on data availability

All data 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	Statistical methods to predetermine sample size were not used. Sample sizes were based on previous studies from our lab and others (Li et al., Cell, 2011), (Abraira et al., Cell, 2017), (Hachiska et al., eLife, 2016), (Rodriguez et al., Nature Neuroscience, 2017).
Data exclusions	For real-time place preference and texture aversion assays, animals that spent less than 20% or more than 80% in one side of chambers during baseline/prestimulation period were excluded from further experiments. For lever-pressing assay, animals that exhibit less than 10 lever-presses during baseline session were excluded from further experiments. Those animals were excluded from further experiments because they exhibited anxiety and did not engage in experimental tasks (e.g. sitting in one corner of the chambers, not exploring chambers).
Replication	We performed experiments with multiple animals to confirm reproducibility. All attempts at replication were successful. The number of replications is noted in the figure legends.
Randomization	The mice were randomly allocated into different experimental groups whenever possible. For place preference assays and lever pressing assays, the sides of chambers and the levers associated with photostimulation were randomized and counterbalanced.
Blinding	For histological experiments, images were collected and analyzed by investigators who were blinded to genotype whenever possible. Blinding was not used for electrophysiological recordings as we used all mice with the correct genotype, not comparing to littermate controls by our study design. Electrophysiological data were analyzed automatically with the same software (Clampfit (10.4)) run for each experimental group. Tactile and thermal behavioral experiments were performed and analyzed by investigators who were blinded to genotype. For optogenetic behavioral experiments, approximately the initial half of the experiments were performed by investigators who were not blinded to genotype to make sure that new experimental setups and optogenetic activations were working, and the remainder of the experiments were repeated by investigators who were blinded to genotype, and the results were successfully reproduced. The data were analyzed either by investigators who were blinded to genotype or automatically using Bonsai software (2.3.1) with the same scripts run for each experimental group.

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
☐	☒ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

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

Antibodies

Antibodies used	IB4 (Alexa 647 conjugated, I32450, ThermoFisher) was diluted at 1:300 and incubated together with secondary antibodies. Primary antibodies used in this study include rabbit anti-DsRed (1:1000, 632496, Clontech), goat anti-mCherry (1:1000, AB0040-200, Acris), chicken anti-GFP (1:1000, GFP-1020, Aves Labs), rabbit anti-GFP (1:1000, A-11122, Life Technologies), mouse anti-NeuN (1:1000, MAB377, Millipore), rabbit anti-tagRFP (for BFP detection, 1:1000, EVN-AB233-C100, Axxora), rabbit anti-TACR1 (1:2000, S8305, Sigma), rabbit anti-PKCγ (1:1000, SC-211, Santa Cruz Biotechnology), mouse anti-c-Fos (1:1000, M-1752-100, Biosensis), rabbit anti-phospho-c-Fos (1:500, #5348, Cell Signaling), and rabbit anti-CGRP (1:1000, 24112, Immunostar). Secondary antibodies included Alexa 488 or 546 conjugated goat anti-rabbit antibodies, Alexa 488 or 546 conjugated goat anti-chicken antibodies, Alexa 488 or 647 conjugated goat anti-mouse antibodies (IgG1, IgG2b), Alexa 647 conjugated goat anti-gunea pig antibodies, Alexa 488 conjugated donkey anti-chicken antibodies, Alexa 546 conjugated donkey anti-goat antibodies, and Alexa 488 or 647 conjugated donkey anti-rabbit antibodies. All secondary antibodies were purchased from Life Technologies except for Alexa 488 conjugated donkey anti-chicken antibodies, which was purchased from Jackson ImmunoResearch, and used at 1:500 dilution.

Validation	rabbit anti-DsRed (1:1000, 632496, Clontech): Abraira et al. Cell, 2017 goat anti-mCherry (1:1000, AB0040-200, Acris): Abraira et al. Cell, 2017 chicken anti-GFP (1:1000, GFP-1020, Aves Labs): Abraira et al. Cell, 2017 rabbit anti-GFP (1:1000, A-11122, Life Technologies): Abraira et al. Cell, 2017 mouse anti-NeuN (1:1000, MAB377, Millipore): Abraira et al. Cell, 2017 rabbit anti-tagRFP (for BFP detection, 1:1000, AB233, Evrogen): Tang et al., Nature Neuroscience, 2015 rabbit anti-TACR1 (1:2000, S8305, Sigma): Polgar et al., PLOS one, 2013 rabbit anti-PKCγ (1:1000, SC-211, Santa Cruz Biotechnology): Abraira et al. Cell, 2017 mouse anti-c-Fos (1:1000, M-1752-100, Biosensis): Bai et al., Cell, 2019 rabbit anti-phospho-c-Fos (1:500, #5348, Cell Signaling): Wilson et al., Cell Reports, 2019 rabbit anti-CGRP (1:1000, 24112, Immunostar): Bai et al., Cell, 2015

Animals and other organisms

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

Laboratory animals	Mice were handled and housed in accordance with Harvard Medical School and IACUC guidelines. Mice were kept in a temperature- and humidity-controlled room with a 12-hour light/dark cycle. Mice (2-24 weeks of age) from both genders were used in experiments. Robo3CreERT2, Tacr1CreERT2, Gpr83CreERT2, AdvillinFlpO, TauFSFiAP knockin mouse lines were generated and characterized in this study. Other published knockin mouse lines used in this study include Lbx1FlpO, Rosa26FSF-LSL-tdTomato (Ai65) (JAX#021875), Rosa26LSL-tdTomato (Ai14) (JAX#007908), Rosa26LSL-EYFP (Ai3) (JAX#007903), Rosa26LSL-synaptophysin-tdTomato (Ai34) (JAX#012570), Rosa26FSF-tdTomato (generated from the cross between Ai65 and EIIa-Cre mouse lines; germline excision of LSL), Rosa26LSL-FSF-ReaChR (JAX#024846), Rosa26LSL-FSF-TeTx, Rosa26FSF-LSL-Synaptophysin-GFP, AdvillinCre, Ntrk2CreER, Mrgprb4Cre, MrgprdCre, Tac1IRES2-Cre (JAX#021877), Gad2NLS-mCherry (JAX#023140). The Calca-FlpE BAC transgenic mouse line was generated and characterized in this study. The Gpr83-EGFP BAC transgenic mouse line was imported from the MMRRC (Stock number: 010442-UCD). Other published transgenic mouse lines used in this study include Cdx2-Cre (JAX#009352), Cdx2-NSE-FlpO, and Calca-GFP (MMRRC, Stock number: 011187-UCD).
Wild animals	No wild animals were used.
Field-collected samples	No field-collected samples were used.
Ethics oversight	Experimental protocols were approved by Harvard Medical School IACUC following the NIH Guide for the Care and Use of Laboratory Animals.

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