

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 (<i>n</i>) 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give <i>P</i> 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 <i>d</i> , Pearson's <i>r</i>), 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	). The electrophysiology data acquisition software (MIES v2.0-2.6) used for this study is available at https://github.com/alleninstitute/mies. The morphological reconstruction software (Vaa3D-TeraFLY-Mozak) is freely available at http://home.penglab.com/proj/vaa3d/home/index.html and the code is available at https://github.com/Vaa3D.
Data analysis	The code for electrophysiological and morphological feature analysis and clustering is available as part of the open-source Allen SDK repository (https://github.com/AllenInstitute/AllenSDK), skeleton-keys repository (https://skeleton-keys.readthedocs.io/en/latest/), pyropractor repository (https://github.com/AllenInstitute/pyropractor/), IPFX repository (https://github.com/alleninstitute/ipfx), and DRCME repository (https://github.com/alleninstitute/drcme). The code for processing and quantifying WNM reconstructions is part of the morph-utils repository (https://github.com/matthewMallory/morph_utils). The code for transcriptomic analysis and clustering is available as part of the scratth.hicat package (https://github.com/AllenInstitute/sratth.hicat/). Gene counts were computed using the R Genomic Alignments package. (https://doi.org/doi:10.18129/B9.bioc.GenomicAlignments). The original sparse reduced-rank regression (sparse RRR) Python code is publicly available (https://github.com/berenslab/patch-seq-rrr) in the R language using the glmnet package. Whole brain fMOST images were registered to the average mouse brain template of CCFv3 by one of two methods: BrainAligner (https://github.com/Vaa3D/vaa3d_tools/blob/master/hackathon/mBrainAligner) or DeepMAPI (http://atlas.brainsmatics.org/a/ni2020). Analysis and figure generation code for this study is available for reference (https://github.com/AllenInstitute/exc_vis_manuscript).

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](#)

Transcriptomic data supporting the findings of this study are available at the NeMO archive (https://data.nemoarchive.org/other/grant/aibs_internal/zeng/transcriptome/scell/PATCHseq/mouse/raw/). Electrophysiological data for this study are available in the DANDI archive (<https://dandiarchive.org/dandiset/001455>). Morphological reconstructions from this study, as well as the fMOST whole brain images used for WNM reconstructions, are available in the BIL archive (<https://doi.org/10.35077/g.1177>).

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

1,528 neurons of which all had transcriptomics and electrophysiology data and 389 had a manual reconstruction (Patch-seq); 341 neurons had manual Whole Neuron Morphology reconstructions. No statistical methods were used to predetermine sample sizes, but the sample sizes here are similar to those reported in previous publications.

Data exclusions

Describe any data exclusions. If no data were excluded from the analyses, state so OR if data were excluded, describe the exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.

Replication

Describe the measures taken to verify the reproducibility of the experimental findings. If all attempts at replication were successful, confirm this OR if there are any findings that were not replicated or cannot be reproduced, note this and describe why.

Randomization

No randomization was used during data collection as there was a single experimental condition for all acquired data. The different stimulus

Randomization ☐ protocols were not presented in a randomized order.Blinding ☐ Data collection and analyses were not performed blind to the conditions of the experiments as there was a single experimental condition for all acquired data.

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

Methods

- 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

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

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

All animals used in this study were house mice (*Mus musculus*) maintained on the C57BL/6J background. Mice used for Patch-seq studies were between the ages of P45 and P70. Mice used for fMOST/WNM studies were from at least postnatal day 56 (P56). Due to space constraints of this field, each animal's unique ID, sex, age, and genotype are included in Supplementary Table 1. Mice were housed ≤ 5 mice per cage and were maintained on a 12-hour light/dark cycle, in a humidity- and temperature-controlled room with water and food available ad libitum.

Wild animals

no wild animals were used in this study.

Reporting on sex

Male and Female mice were used.

Field-collected samples

no field samples were collected

Ethics oversight

Experimental procedures that involved the use of mice were all conducted with approved protocols in accordance with NIH guidelines. They were also approved by the Allen Institute for Brain Science Institutional Animal Care and Use Committee (IACUC).

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

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, mosaicism, off-target gene editing) were examined.