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	Commercially available software from NeuroNexus (Radiens Suite) was used for mouse data collection. Intracranial EEG data were recorded using ATLAS recording setup running Cheetah software (Neuralynx Inc.).
Data analysis	Matlab R2023a was used for data analysis. All custom code for preprocessing the data is freely available on the Buzsaki Lab and HippoCookBook repositories: https://github.com/buzsakilab; https://github.com/valegarman/HippoCookBook. Code specifically developed for this analyzis is available in the Ripmap repository: https://github.com/acnavasolive/ripmap

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

Data availability

The rodent data generated in this study as well as the human datasets used in this study have been deposited on the Buzsáki Lab web share under https://buzsakilab.nyumc.org/datasets/MaslarovaA/MaslarovaShin2025. The source data are available as a source data file in the same repository. Due to privacy and ethical considerations, the raw electrophysiological recordings from human participants are protected and cannot be shared publicly. Access to raw data may be considered upon reasonable request and subject to institutional data-sharing agreements and IRB approval. Access can be obtained by emailing Anna Maslarova at amaslarova@gmail.com. Please allow up to two weeks for sharing the data, due to NYU archiving policies.
Code availability
Ripmap is available on https://github.com/acnavasolive/ripmap99, which also includes an example script for optimal ripple-channel detection in https://github.com/acnavasolive/ripmap/tree/main/select_channel. Further custom written scripts that are not part of ripmap or other published toolboxes have been added to the data repository: https://buzsakilab.nyumc.org/datasets/MaslarovaA/MaslarovaShin2025.

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	We report self-reported gender of 13 Patients, female - 4, male -9 in Table 1. We did not perform any gender-based analysis.
Reporting on race, ethnicity, or other socially relevant groupings	We did not collect any race or ethnicity based information.
Population characteristics	13 patients with drug-resistant epilepsy, age: average 28, range 20-38 (see Table 1)
Recruitment	Patients in the preoperative epilepsy program of the Level 4 Epilepsy Center of Erlangen University Hospital, Germany, were recruited and consented from 2019 – 2022 years. Inclusion criteria were: at least one hippocampal microwire.
Ethics oversight	Ethical approval was granted by the "Ethik Kommission" of Friedrich-Alexander Universität Erlangen-Nürnberg (142_12B), and all patients consented to implantation of hippocampal macro/microwire bundles (Behnke-Fried Electrodes).

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	The sample size was determined by availability of eligible epilepsy patients during the recruitment period. The sample size is similar or larger than those reported in previous publications.
Data exclusions	Patients were excluded from analysis if none of the macro/microwires were in the hippocampus. One patient was excluded due to insufficient anatomical information. In mice, all 5 mice were included in the study. Recording sessions with poor signal were excluded after initial quality check and were not reported in the study (n = 7 sessions from 4 mice). All other 9 sessions were included.
Replication	Data was collected from 5 mice. The results were consistent across animals.
Randomization	randomization was not relevant for this study as there were no comparisons between groups or treatments
Blinding	blinding was not relevant to the study as there were no interventions or groups to be compared

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

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	APP/PS1 hemizygous male mice (n = 5, age 3-9 months, JAX Stock No. 004462). Mice were housed at a vivarium on a 12 hour dark/light cycle. Ambient temperature was maintained at ~22 ± 2 °C, with relative humidity of 40–60%. Animals had ad libitum access to food and water and were housed in standard ventilated cages with appropriate environmental enrichment.
Wild animals	n/a
Reporting on sex	male
Field-collected samples	n/a
Ethics oversight	Institutional Animal Care and Use Committee at New York University Medical Center

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 not a clinical trial
Study protocol	Ethical approval was granted by the "Ethik Kommission" of Friedrich-Alexander Universität Erlangen-Nürnberg (142_12B)
Data collection	Data was collected at Erlangen University Hospital, Germany between 2019 – 2022
Outcomes	n/a not a clinical trial

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, mosiacism, off-target gene editing) were examined.*

Magnetic resonance imaging

Experimental design

Design type	This study retrospectively analyzed structural MRI data (T1-weighted and T2-weighted images) obtained during standard clinical evaluations. The MRI scans were not acquired specifically for this research project, and no functional MRI (fMRI) or task-based paradigms were involved.

Design specifications: n/a

Behavioral performance measures: n/a

Acquisition

Imaging type(s): structural

Field strength: 3

Sequence & imaging parameters: T1, T2

Area of acquisition: whole brain

Diffusion MRI ☐ Used ☒ Not used

Preprocessing

Preprocessing software: Freesurfer

Normalization: *If data were normalized/standardized, describe the approach(es): specify linear or non-linear and define image types used for transformation OR indicate that data were not normalized and explain rationale for lack of normalization.*

Normalization template: Subject space and MNI152

Noise and artifact removal: *Describe your procedure(s) for artifact and structured noise removal, specifying motion parameters, tissue signals and physiological signals (heart rate, respiration).*

Volume censoring: *Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.*

Statistical modeling & inference

Model type and settings: *Specify type (mass univariate, multivariate, RSA, predictive, etc.) and describe essential details of the model at the first and second levels (e.g. fixed, random or mixed effects; drift or auto-correlation).*

Effect(s) tested: *Define precise effect in terms of the task or stimulus conditions instead of psychological concepts and indicate whether ANOVA or factorial designs were used.*

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

Statistic type for inference (See Eklund et al. 2016): *Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.*

Correction: *Describe the type of correction and how it is obtained for multiple comparisons (e.g. FWE, FDR, permutation or Monte Carlo).*

Models & analysis

n/a	Involved in the study
☒	☐ Functional and/or effective connectivity
☒	☐ Graph analysis
☒	☐ Multivariate modeling or predictive analysis