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	Open-source software SpikeGLX 3.0 and OpenEphys version 0.6x were used for data acquisition. The probe was positioned using the ROSA ONE Brain (Zimmer Biomet) robotic arm and lowered using an AlphaOmega (Alpha Omega Engineering) microdrive. MATLAB (R2024b) was used to generate the TTL pulses that synchronized the neural and audio signal capture. Stealth navigation was used to localize the probe entry site (StealthStation, Medtronic)
Data analysis	Custom code written in MATLAB (R2024b) and Python (3.12.9) was used for analysis. Software packages included DREDge (https://github.com/evarol/DREDge), Kilosort (https://github.com/MouseLand/Kilosort), Phy (https://github.com/cortex-lab/phy), and FOOOF (https://fooof-tools.github.io/fooof/), and RAVE (https://github.com/rave-ieeg) The computational modeling software has been made publicly available (https://github.com/NuttidaLab/rnn_oddball)

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

Core data used for analysis have been uploaded to DABI and is available to anyone with a university affiliation: https://dabi.loni.usc.edu/dsi/U01NS108923

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	Summary statistics are reported in the methods. Sex and gender were not considered in the analysis.
Reporting on race, ethnicity, or other socially relevant groupings	Race, ethnicity, and other socially relevant groupings were not considered in the analysis.
Population characteristics	Summary statistics are reported in the methods. This feature was not considered in the analysis.
Recruitment	Anesthetized Neuropixels: All patients diagnosed with drug resistant temporal lobe epilepsy and scheduled to undergo an anteromesial temporal lobectomy for seizure control from 3/1/2023 to 6/1/2025 were offered participation in our study. Awake EMU:All patients diagnosed with drug resistant temporal lobe epilepsy and scheduled to undergo stereotactic encephalography from 3/1/2024 to 6/1/2025 were offered participation in our study. All patients provided written informed consent to participate in the study and were aware that participation was voluntary and would not affect their clinical course. There were no potential biases in the recruitment.
Ethics oversight	Experiments were conducted according to protocol guidelines approved by the Institutional Review Board for Baylor College of Medicine and Affiliated Hospitals, Houston TX (H-50885 for the Neuropixel recordings and H-18112 for the EMU recordings).

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	No statistical methods were used to predetermine sample size. Patient recruitment was constrained by the availability of eligible neurosurgical cases and limited intraoperative experimental time, and data were collected from all available participants during the study period. Data analysis was performed after completion of data collection. Within patients, units were included based on data quality, and only well-isolated neurons were analyzed. Sample sizes are consistent with, or larger than, most typically reported in human intracranial single-unit electrophysiology studies. Data were analyzed on an individual patient basis with replication across patients.
Data exclusions	One patient was excluded from analysis after analysis post collection demonstrated high amplitude noise was unable to be accounted for and precluded single clustering based on independent analyses from two separate institutions. Within included patients all data were used for analysis.
Replication	10-fold cross validation was used to ensure the reproducibility of all classification and regression analyses.
Randomization	Patients were assigned to maximize the dataset across stimuli. No covariates would be expected between the tasks performed and patient specific features. Additionally, the majority of analyses were performed within patients, with replication across patients demonstrating generalization.
Blinding	Blinding was not possible due to the features of data collection and analysis. However, all methods were equally applied across patients and across neurons, so blinding is not relevant to this study.

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

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.