

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 <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. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted <i>Give P 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 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	Neural data were collected using the Cerebus Central Suite (BlackRock).
Data analysis	Data preprocessing: MATLAB (2020b, MathWorks) and Python (v3.9); Data analysis: Python (v3.9 and V3.11).

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](#)

Deidentified recording data is on the Data Archive BRAIN Initiative (DABI, <https://dabi.loni.usc.edu/home>) in the iEEG BIDS format. The raw neural recording data and processed data have been deposited to the DABI database under accession code M6RES1N4MVA3 (<https://doi.org/10.18120/5jg5-j555>). Source data are provided with this paper.

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 included 8 male and 6 female participants. Sex is included in the information provided in Table S1. The study participants were patients with epilepsy undergoing intracranial investigation to determine the nature and focality of their seizures. They participated in this study under a consent procedure approved by our IRB. Their enrollment was not influenced by their sex but purely based on the vagaries of who was scheduled for clinical investigation. The disaggregated results for sex, presented in Figure S6, indicate that sex did not have a significant impact on the study outcomes. Sex was determined by biological factors while gender was self-reported. In all cases the sex and gender were the same.
Reporting on race, ethnicity, or other socially relevant groupings	The participants were recruited for this study independently of race, ethnicity or other socially relevant groupings. The study does not involve analyzing data on these variables.
Population characteristics	The participants were recruited for this study independently of age or sex. Information on participants' sex is presented in Table S1; however, individual ages are not disclosed to ensure the privacy of participants.
Recruitment	Patients were asked whether they were interested in participating in the research. Participants were informed that participation in the experiment would not alter their clinical treatment in any way, and that they could withdraw at any time without affecting their clinical care.
Ethics oversight	All patients voluntarily participated after informed consent according to guidelines as monitored by the Partners Institutional Review Board (IRB) Massachusetts General Hospital (MGH).

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	A total of 14 participants were recruited for sEEG recordings. The neural analysis was based on 1910 bipolar-referenced channels, as explained in Methods.
Data exclusions	No subjects were excluded from analysis. Electrode exclusions were based on the quality of the neural recording signal and the frequency of interictal epileptiform discharges.
Replication	Similar results were observed across participants, and removing an individual participants did not result in significant changes of the results, as explained in Figure S5.
Randomization	Randomization was not applicable to this study because all participants were involved in the task.
Blinding	Human data were de-identified and assigned a unique numerical code. Subsequent preprocessing and analysis were performed blinded to the conditions of the data acquisition.

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