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Reporting Summary

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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	Task was coded using the publicly available programming library PandaEPL. Data was recorded using commercial software from BlackRock Microsystems (v 7.0.5.0) and Neuralynx (v 5.6.0).
Data analysis	Analysis was performed in Matlab (v 2015b) and spike sorting in Python using the publicly available code Combinato (no version #).

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

The data that support the findings of this study are available on reasonable request from the corresponding author. The data are not publicly available because they could compromise research participant privacy/consent.

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 pre-determine sample sizes but our sample sizes are similar to those reported in previous publications.
Data exclusions	Individual cells were excluded based on standard criteria for recording quality, described in the Methods. Spike sorting was done using Combinato, which uses a technique called super-paramagnetic clustering to identify potential waveform clusters based on recorded threshold-crossings. Then, the algorithm over-clusters and performs iterative template-matching to yield putative single-units. After identifying putative single-unit activity, we excluded neurons that had a mean firing rate below 0.2 Hz or above 15 Hz (potential interneurons).
Replication	Findings replicated across multiple subjects, and findings also replicated from multiple sessions within some subjects.
Randomization	Subjects were all allocated into one group for analysis.
Blinding	Data collection and analysis were not performed blind to the conditions of the experiments. Blinding was not relevant to our study. The data collected requires many processing steps to become interpretable, so there is no way for the experimenter to be biased during data collection by results coming in.

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

Human research participants

Policy information about studies involving human research participants

Population characteristics	All subject demographic information is in Supplementary Table 1 of the manuscript. Briefly, all subjects were patients undergoing surgical treatment for epilepsy. We included data from 19 such patients (13 male, 6 female). Mean age was 34.1 years, with a standard deviation of 11.9 years.
Recruitment	Subjects were recruited from the pool of epilepsy patients between the ages of 18 and 65 years, with close to normal neuropsych evaluation, who were undergoing chronic implantation of subdural and/or intracortical electrodes with long term EEG recording for clinical purposes. It is possible that self-selection bias may be present, i.e. patients with depression or low-motivation levels may have opted out of research, but we do not believe this affected our electrophysiological findings.
Ethics oversight	Study protocol was approved by IRB at Emory University Hospital (Atlanta, GA), UT Southwestern Medical Center (Dallas, TX), Thomas Jefferson University Hospital (Philadelphia, PA), and Columbia University Medical Center (New York, NY).

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

Magnetic resonance imaging

Experimental design

Design type	MRI were acquired purely for clinical purposes to indicate electrode placement, and were not a part of the experiment.
Design specifications	MRI were acquired purely for clinical purposes to indicate electrode placement, and were not a part of the experiment.
Behavioral performance measures	MRI were acquired purely for clinical purposes to indicate electrode placement, and were not a part of the experiment.

Acquisition

Imaging type(s)	Structural MRI and CT
Field strength	3T MRI - before electrode implantation, 1.5 T MRI - after implantation
Sequence & imaging parameters	Sequence & imaging parameters: Imaging parameters varied somewhat among institutions in this multisite study. In general, sequences required for macroelectrode and microwire localization included 3D T1-weighted with 1 mm or less isotropic resolution, coronal fast spin echo T2-weighted with 0.4 x 0.4 mm in-plane resolution and 2 mm slice thickness, and CT with less than 1 mm slice thickness. Representative examples are as follows: Pre-implant 3D T1-weighted MPRAGE (TR 1900 ms, TE 2.52 ms, flip angle 9, 1 mm isotropic resolution, 216 x 256 x 174 matrix), pre-implant coronal FSE T2-weighted (TR 7200 ms, 76 ms, ETL 15, flip angle 139, 0.4 x 0.4 x 2 mm, 448 x 448 x 30), post-implant CT (0.5 x 0.5 x 0.625 mm, 512 x 512 x 384).
Area of acquisition	T1 - whole brain, T2 - temporal lobes spanning and oriented perpendicular to the hippocampal long axis

Diffusion MRI ☐ Used ☒ Not used

Preprocessing

Preprocessing software	Segmentations of hippocampal subfields and parahippocampal cortical regions including the entorhinal cortex were generated from 3D T1-weighted and coronal T2-weighted images using Automatic Segmentation of Hippocampal Subfields (ASHS) software.
Normalization	Pre-implant MRI, post-implant CT, and when available post-implant MRI scans were all aligned to each other using rigid registration based on mutual information with Advanced Normalization Tools (ANTS) softwar
Normalization template	No normalization template was used.
Noise and artifact removal	No noise or artifact removal was used.
Volume censoring	No volume censoring was used.

Statistical modeling & inference

Model type and settings	No statistical modeling was used as MRI were acquired for clinical purposes to indicate electrode placement.
Effect(s) tested	No effects tested as MRI were acquired for clinical purposes to indicate electrode placement.

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

Anatomical location(s)	Pre and post-implant MRI and post-implant CT scans were co-registered based on maximal mutual information using ANTS software. Segmentations of hippocampal subfields and parahippocampal cortical regions including the entorhinal cortex were generated from 3D T1-weighted and coronal T2-weighted images using Automatic Segmentation of Hippocampal Subfields (ASHS) software.
Statistic type for inference (See Eklund et al. 2016)	No inference was done as MRI were acquired for clinical purposes to indicate electrode placement.
Correction	No correction was used as MRI were acquired for clinical purposes to indicate electrode placement.

Models & analysis

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