eLife's transparent reporting form

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. Authors can upload supporting documentation to indicate the use of appropriate reporting guidelines for health-related research (see EQUATOR Network), life science research (see the BioSharing Information Resource), or the ARRIVE guidelines for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this form.

If you have any questions, please consult our Journal Policies and/or contact us: editorial@elifesciences.org.

Sample-size estimation
- You should state whether an appropriate sample size was computed when the study was being designed
- You should state the statistical method of sample size computation and any required assumptions
- If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

The information on sample size is provided in methods section in subsection Human subjects and brain tissue and in Figure legend for Figures 2,3 and 5. Our experiments were performed in the resected cortical tissue from subjects undergoing brain surgery for epilepsy or tumor. Based on the size of the effects and variation in the data, power calculations showed that approximately sample size of 30 should be needed for >0.90 power at significance level of 0.05. Our total dataset included multiple cells from totally 46 subjects in accordance with these calculations.

Replicates
- You should report how often each experiment was performed
- You should include a definition of biological versus technical replication
- The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
- If you encountered any outliers, you should describe how these were handled
- Criteria for exclusion/inclusion of data should be clearly stated
- High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

eLIFE

1st Floor
24 Hills Road
Cambridge CB2 1JP, UK

P 01223 855340
W elifesciences.org
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> Biological replication was handled by recordings/morphology from multiple cells from the same subject (up to 14 cells per subject) and from multiple subjects (total n=46) Data inclusion is described in methods section, no outliers were excluded.
> - MRI data– all data included
> - Cellular morphology: all complete dendritic structures in layer 2, 3 and 4 pyramidal cells were included; cells with cut dendrites due to slicing procedure were excluded
> - Cellular electrophysiology: all complete AP recordings corresponding to pyramidal cell types were included (bridge balance of < 20 MOhm)

Statistical reporting
- Statistical analysis methods should be described and justified
- Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
- For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
- Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

> Raw data and examples are represented in figures and graph insets. The information on statistics is provided in Methods section, subsection Statistical Analysis and in Figure legends, Pearson's r and p values for correlations are shown in graph insets. All graphs for correlations include representation of 95% confidence interval.

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

Group allocation
- Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
- Indicate if masking was used during group allocation, data collection and/or data analysis

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

> All data were split based on IQ scores after all data analyses were performed. The data for individual cells were recorded, processed and analyzed double blind.

Additional data files ("source data")
- We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table

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- Where provided, these should be in the most useful format, and they can be uploaded as "Source data" files linked to a main figure or table
- Include model definition files including the full list of parameters used
- Include code used for data analysis (e.g., R, MatLab)
- Avoid stating that data files are "available upon request"

Please indicate the figures or tables for which source data files have been provided:

We provide all numerical data for Figures 2, 3, 4, 5 and patient information. These data are arranged in an overview table.
Matlab converted e-phys files will be made available on Dryad after publication.