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:

No explicit power analyses were performed before data collection. We decided on the sample sizes based on comparable studies (Jun et al. 2017 and Juavinett et al. 2019).

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:

The number of replicates (biological and technical) are clearly stated as appropriate throughout the manuscript. In particular, the Methods and Figure 4--table supplement 1 ("All implantations") clearly state the number of animals, recording sessions and cells used, as well as what criteria were used for inclusion of data.

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:

> All non-standard statistical analysis methods are described in detail in the Methods. Standard statistical tests (ANOVA, bootstrap test, etc.) are described as they are presented in the text, in the Figure legends, and and/or in the Methods. Sample sizes are described as appropriate in the text, Figure legends, and Methods. We have used exact p-values exclusively, and individual raw data are not shown except when presented as examples.

(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:

> Several comparisons were made between groups of data. The first involved an analysis of neuronal yields across brain areas. These comparisons were made in a non-blinded way after data collection to highlight unpredicted differences observed in the data. As these differences depended on differences in implantation location across animals, there was no way to blind the experimenters. Furthermore, performance comparisons were done between explanted and new (unimplanted) neural probes. Because these measurements, as well as the implantations and explantations themselves, were performed by the experimenters, there was no way to perform these comparisons in a blinded way.

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
- 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"

2

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

Source data and code to reproduce all figures in the manuscript have been posted in public repositories.
Code is available on Github: https://github.com/Brody-Lab/chronic_neuropixels
Data is available on Dryad: https://doi.org/10.5061/dryad.m63xsj3zw