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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:

Numbers of recorded units and numbers of experimental animals were estimated to allow population slope confidence intervals as low as ~0.1 (e.g. Fig. 6h; via nonparametric bootstrap; see Methods). An explicit a priori power analysis was not performed.

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:

Waveforms were sorted independently by two different authors (B.A. and M.H.). All results were qualitatively identical with both classifications. Similar results are seen within each animal, so we pooled data across animals for each experimental manipulation. Our inclusion/exclusion data criteria are described in Methods. Notably, SU/MU were differentiated both manually and confirmed by SNR (Kelly et al., 2007), and we repeated analyses with different SNR thresholds (Methods; Supp. Figures). We also report SNR as a metric of data quality (Methods).

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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 is shown throughout where feasible (i.e. Fig. 2b,e,c; Fig. 6h.). We have taken extra steps to show population slope data in most figures. Because most unit measurements contain many more data points than 10, we show distributions across the entire population (e.g. Fig. 2jk). In that figure we show both PDFs and corresponding CDFs for maximum clarity, despite slight redundancy for those readers who prefer CDFs. For every following experiment we show CDFs. We show 95% Cis wherever possible (often via bootstrap), and report thresholded p-values when small and exact p-values when near 0.05 or larger.

(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:

Animals were not preselected except that animals with poor optical windows were not used. Data exclusion was limited and is described in Methods.

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"

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

Data and code to generate plots are available at:
https://github.com/histedlab/code-Sanzeni-inhibition-stabilization-cortex

Source data files have been provided for Figs. 2-8. (Fig. 1 has no data).