

## 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](mailto: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 sample sizes in this study, which is essentially exploratory as to its nature, were chosen as a trade-off between the maximum number of animals per group allowed by the technical constraints and the minimum needed to effectively explore the design space.

### 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:

We first run the pharmacogenetic inhibition of the ACA followed by the functional tracing of the ACA inputs during the acquisition and expression of contextual fear. Next, we examined how silencing the AM > ACA pathway influences contextual fear acquisition to the predatory threat. In the following experiments, we silenced the ACA projections to different targets and examined how it influences the acquisition and/or expression of contextual fear. The experiments were not replicated and followed the sequence of the findings. There was no outlier exclusion, and the criteria for including the experiments were based on the correct position of viral transfection and optic fiber placement, as stated in the manuscript (see Methods page 30 lines 7 and 32)

## 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:

Statistical analysis methods were fully described in the Methods Section (see page 34 line 8 and 29). The raw data for the behavior experiments are plotted in the figure graphs, indicating the mean ( $\pm$  SEM) values. Complete statistical analyses for behavioral experiments are described in the Figure Legends, and the statistical analyses for the cell counting can be found in the Results Section. In both instances, exact values of N, means, SEM, and effect sizes are fully reported, and exact p-values whenever possible for significant and non-significant results.

(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:

The animals were randomly allocated to each experimental group without utilizing a restricted randomization criterium. As indicated in the manuscript, behavioral sessions were blindly scored by a trained observer (see Methods page 29 line 14), and the statistical analyses were conducted by an experimenter (MVCB) without previous knowledge of the experimental results (see Methods page 35 line 8).

## 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:

We provided as “source data” for Figures 1 to 8 additional data files containing the complete raw data of cell counting and behavioral results.