



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:

Two cohorts of 20-25 mice from each group (Control vs knockout) were used. In electrophysiological study, 3 – 4 cells were sampled per mice, from at least 3 mice. Most data are displayed as scatter plots (each dot represent a value). All statistical methods are listed in figure legends.

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:



Two cohorts were used in the behavioral assays. The first cohort (control and KO) was tested with open field, elevated plus maze, fear conditioning and hot plate. The second cohort was tested with light/dark box and pre-pulse inhibition. There was at least one week of rest between consecutive assays, starting from assays with weak stimulation and followed with tests with progressively stronger stimulation.

Every recording was a biological replication. One cell was recorded from one brain slice, 3 – 4 cells per mouse for each assay. Most data are displayed as scatter plots (each dot represents a value).

During recording, access resistance was compensated by up to 80%. Neurons with series resistance above 20 MΩ and > 20% of changes throughout the recording were discarded, otherwise all data were used for analysis.

**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 statistical methods are listed in figure legends, including statistical tests, exact values of N, definitions of center. Data are presented as mean \pm SEM, as mentioned in the legends.

Most raw data are presented in figures, whenever N is less 10 or not.

Exact p-values is reported for all key questions.

(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:

One cell was recorded from one brain slice, 3 – 4 cells per mouse for each assay. For critical experiments, recordings were performed on different days. Control and KO mice were from littermates of matched age.

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:



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We uploaded the model panel (Figure 8) for further illustration. We used scatter plots for most of the experiments, which represent raw data.
All the data analyses were performed with Graphpad, which are mentioned in Methods.