***eLife’s* transparent reporting form**

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. If you have any questions, please 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., page numbers or figure legends), or explain why this information doesn’t apply to your submission:

The experiments mostly involve cutting individual axons and observing results axon by axon, which is slow. Similar experiments have been done in previous published work *in vitro* and in c.elegans. Our experiments and numbers were based on this body of published work, which often involves rather few axotomies. We had no previous information about variance and effect size so a power calculation would have been based on fantasy numbers. Based on previous work we expected that 15-30 axotomies would give meaningful results. In fact we did many more, 35,69 and 102 for the three time points so that we could perform more in depth analysis and reach valid conclusions.

**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., page numbers or figure legends), or explain why this information doesn’t apply to your submission:

We state in the paper that each result is based on more than 3 replicates. By this we mean a variable number of axotomies from different cultures made at different times. In fact we had only one measure for which there were only 3 replicates, and for most of the results we had many more replicates than this.

No data was excluded.

Our array data is uploaded and the link is given in the paper.

**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.

The statistical methods are given in the methods section on page 18. The raw data is present in graphical form in most of the figures, where we have plotted each axotomy result as an individual point without any exclusions. The tests used are stated in the results section and/or in the figure legends for each experiment. At present our p values are given as ranges, but if the paper is accepted we are happy to change these to exact numbers.

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

(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 page numbers in the manuscript.)

**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:

Most of our data is very visible as the individual points in the figures. However if the paper is accepted we are happy to upload data files in addition, although this will not provide much more information.