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

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**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

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A statistical method for sample size computation was not used, however, sample sizes used are in line with other studies with similar experiments. These include:

Esterberg, Robert, et al. "Mitochondrial calcium uptake underlies ROS generation during aminoglycoside-induced hair cell death." *The Journal of clinical investigation* 126.9 (2016): 3556-3566.

Hailey, Dale W., et al. "Fluorescent aminoglycosides reveal intracellular trafficking routes in mechanosensory hair cells." *The Journal of clinical investigation* 127.2 (2017): 472-486.

Sebe, Joy Y., et al. "Ca2+-Permeable AMPARs Mediate Glutamatergic Transmission and Excitotoxic Damage at the Hair Cell Ribbon Synapse." *Journal of Neuroscience* 37.25 (2017): 6162-6175.

**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
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* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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This information is provided in the Results section and the “Quantification and Statistical Analysis” section of the Methods.

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* 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.

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The statistical analyses used are listed in the “Quantification and Statistical Analysis” section of the Methods, as well as in the Results and figure legends. All other values listed above can be found in the text of the Results section and in the figure legends for corresponding experiments.

(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.)

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* 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:

Zebrafish larvae were randomly selected and sorted into experimental groups. Masking was not used during group allocation, data collection, or analysis. This is stated in the Methods section.

**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
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* Include model definition files including the full list of parameters used
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