***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](http://www.equator-network.org/%20)), life science research (see the [BioSharing Information Resource](https://biosharing.org/" \t "_blank)), or the [ARRIVE guidelines](http://www.plosbiology.org/article/info:doi/10.1371/journal.pbio.1000412) for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this 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

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:

No explicit power analysis was used, sample size can be found in the figure legend. For WT samples, 10 brains were stained for each developmental stage for three replicates or more.

**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:

For intensity of immunotaining, sample size can be found in every figure legend. The measurement of the intensity can be found in the methods. When we encountered outliers, we analyzed more samples and removed not representative one (outliers, n<3).

For Mamo-positive neurons in the brains of wild type and *OK107>chinmo-RNAi*, Mean and Standard error of the mean (SEM) were calculated for all the brains. Two time points were collected. Sample size can be found in figure legend. All the results were included in the Figure 2-Source Data 1.

**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:

Detailed information of the statistical analysis can be found in the legend of Figure 1-figure Supplemental 1 and Figure 2G and Figure 2-Source Data 1 and Figure 3-figure Supplemental 1&2 and Figure 4-figure Supplemental 1 and Figure 5-figure Supplemental 2 and Figure 5-figure Supplemental 3 and Figure 6.

Sample size can be found in figure legend.

(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:

This information doesn’t apply to our submission since samples were not allocated into groups.

**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:

Figure 1-Source Data 1 includes raw data and statistical analysis for the Figure 1 and the Figure 1-figure Supplemental 1A.

Figure 2-Source Data 1 includes raw data and statistical analysis for the Figure 2G.

Figure 2-Source Data 2 includes raw data and statistical analysis for the Figure 2 and the Figure 2- figure Supplemental 1.

Figure 3-Source Data 1 includes raw data and statistical analysis for the Figure 3 and the Figure 3- figure Supplemental 2.

Figure 3-Source Data 2 includes raw data and statistical analysis for the Figure 3- figure Supplemental 1.

Figure 4-Source Data 1 includes raw data and statistical analysis for the Figure 4 and the Figure 4- figure Supplemental 1.

Figure 4-Source Data 2 includes FISH probe sequences for *mamo* nascent and mature transcripts.

Figure 5-Source Data 1 includes raw data and statistical analysis for the Figure 5 and the Figure 5- figure Supplemental 3.

Figure 5-Source Data 2 includes raw data and statistical analysis for the Figure 5- figure Supplemental 2.

Figure 6-Source Data 1 includes raw data and statistical analysis for the Figure 6E.

Source code file 1 includes customized MATLAB and Python scripts for Figure 5-figure Supplemental 1A&B.