***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/%22%20%5Ct%20%22_blank)), or the [ARRIVE guidelines](http://www.plosbiology.org/article/info%3Adoi/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 statistical methods were used to predetermine sample size”. This sentence is reported in the Section: Materials and methods-Statistics. Sample sizes in this manuscript are similar to those used in previous studies (Attardo et al., 2015; Meng et al., 2019).

**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:

“The number of samples (n) and p values are reported in the Figure legends or in the text. All recordings with no technical issues were included in the analysis”. These sentences are reported in the Section: Materials and methods-Statistics.

The experiments reported in this work were repeated independently in at least three-four animals of both sexes and from different litters. Animals with misplaced microendoscope implant or without significant calcium indicator expression were not included in the 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:

“Values are expressed as mean ± sem, unless otherwise stated; the number of samples (n) and p values are reported in the Figure legends or in the text.” This information is reported in the Section: Materials and methods-Statistics. In the same paragraph, we describe all the statistical tests used. Information about sample size, p value, and statistical test used is also reported in the Figure legends or in the text.

Raw data are presented in figures.

(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:

Randomization: transgenic animals were chosen based on correct genotyping. Each experiment contained both male and female animals from different litters.

Blinding: “blinding was not used in this study”. This sentence is reported in the Section: Materials and methods-Statistics. Blinding was not possible because all mice were implanted with microendoscopes and all were expressing GCaMP. The same researcher trained animals, collected, and analyzed data.

**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 provide numerical data for graphs represented in figures 3-7, figure 2-figure supplement 2-4, figure 3-figure supplement 4, figure 4-figure supplement 1-2. The code used to simulate and analyze synthetic calcium data is shared through the following link: <https://github.com/moni90/eFOV_microendoscopes_sim>

The datasets shown in Figures 4, 6, 7 and corresponding figure supplements are available at:

<https://data.mendeley.com/datasets/wm6c5wzs4c/draft?a=56f1660e-a036-40ee-83ef-458dc2457b6a>