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

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* You should state whether an appropriate sample size was computed when the study was being designed
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* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

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Sample sizes were determined based on our previous studies using similar techniques (no power calculations were performed). This information is provided under “Animals” in Materials and Methods.

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* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
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Materials and methods: “Statistical analysis”. Number of trials and observations are given in the section “Modelling”

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* Statistical analysis methods should be described and justified
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* 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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(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
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* 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
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Numerical data for Figures 2 and 3 are provided as Source Data 1. A complete dataset of raw and processed data including Ca2+ signal traces, behavioral monitoring traces (all sampled and time aligned to 30Hz) and pupil tracking data are provided at: <https://doi.org/10.11582/2021.00100>. Data analyses were performed with the Begonia toolkit [(Bjørnstad et al. 2021)](https://paperpile.com/c/q14pSW/gNl0), which is available at <https://github.com/GliaLab/Begonia>.