

***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), life science research (see the BioSharing Information Resource), or the ARRIVE guidelines for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this form.

If you have any questions, please consult our Journal Policies and/or contact us:

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

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| In all cases our numbers were made as large as possible within the limitations of the numbers of fish we would obtain from a cross and the number we could test in a single experimental run. Our sample size was determined by the number of fish that could be studied from each cross within a single experimental 1-2 day period. Where many fish in a single dish or well could be imaged simultaneously, we were limited by the number of fish that could be placed in one dish or the number of wells that could be imaged at once, the duration of the adaptation period before behavioral analysis could begin, the duration of behavioral monitoring and the experiment window in which we tested fish during the same portion of the day. Where individual fish were semi-immobilized and behavior and/or neural activity was monitored in response to virtual or live prey, the number of animals was, of necessity, smaller because we were limited by the time it takes to mount the fish, adapt it, the monitoring time and the time to remove the fish for later analysis. Where individual fish were monitored in single wells, we could image 9 wells simultaneously and the adaptation time of 10 minutes and imaging period of 30 minutes limited the total number we could do in a single day. Where possible, we used offspring of a single parental pair to minimize behavioral variation that comes from genetic diversity (Pantoja et al., 2018). |

# 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:

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|  All information about replications and exclusions is included in the figure legends or Methods. |

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# 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:

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| Statistical analysis methods, sample sizes and p values are reported in the figure legends, Experimental Procedures or Supplemental Experimental Procedures. |

(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:

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| The group allocation methods are indicated in Experimental Procedures or figure legends. |

# 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:

|  |
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| A source data table is presented for each figure and supplemental figure. |

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