



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:

This information can be found in the figure legends for functional imaging experiments and in the section 'materials and methods' for behavioral experiments. The sample size used corresponds to the common sample sizes in the field of *Drosophila* olfaction functional/behavioral analysis. Statistical analyses are mentioned in the figure legends. In general, the 'Past' software was used to identify the appropriate statistical method according to the type of data, data distribution etc. No power analysis was used and replicates were determined according to the standard procedures in the field.

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:

N-values are specified in each figure legend. Briefly, all experiments were independently carried out several times and several experiments were independently repeated in a similar way. No data were excluded.



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:

The information on statistical methods is given in the appropriate figure legends. The figures show mainly raw data distributions within box plots or bar plots. Exact p-values are mentioned in the corresponding figures; in addition p-values are reported using number of stars defined in the figure legends. Analyzing methods were chosen according to sample distribution, variation, size, groups and appropriate tests were determined using the 'Past' software.

(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:

For functional imaging experiments, groups were defined by the genotype of the flies. For the data analyses, groups were chosen based on hedonic valence of the odors, which are defined in the figures, figure legends and in the appropriate text. For behavioral experiments with wild type flies, groups were chosen randomly and aged to the appropriate ages (as described in the Methods).

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 all source data of this study. The fluorescent changes of GCaMP6f obtained by 2-photon functional imaging deriving from the experiments that are represented as graphs in the main and supplementary figure are provided as excel files (Figs. 2, 3, 5, 6). All raw data files of the functional imaging experiments (Figs. 2, 3, 5, 6), the behavioral experiments (Fig. 3), the photoactivation and immunohistochemistry experiments (Figs. 1, 4) have been deposited on the Edmond server, the Open Research Data Repository of the Max Planck Society, which can be accessed via the following link once the article is published:
<https://dx.doi.org/10.17617/3.88>