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* You should state whether an appropriate sample size was computed when the study was being designed
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Our study does not contain experiments and this information does not apply to our submission.

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* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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Our study does not contain experiments and this information does not apply to our submission. As for the data processing where certain reconstructions are dropped or corrected, we outlined the steps we took in the Data preparation section in the Materials and methods.

**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.

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The statistical analysis methods are described in detail in the Materials and methods section. The exact p-values are available in Tables S1 and S2. Raw values of mutual information study are available in the Supplementary Materials. Other necessary statistical information, such as data size, cluster size, and dispersion measures, can be found in the main text and figures. The matrices of inter-neuronal distances for three neuropils are provided in the binary format (morph\_dist\_AL\_r\_new.npy, morph\_dist\_calyx\_r\_new.npy, morph\_dist\_LH\_r\_new.npy), which can be analysed with a python script (drosophila\_analysis.py) to generate Figures 3, S1, S2, and S3. The binary files and drosophila\_analysis.py are also available from our Github repository (https://github.com/kirichoi/DrosophilaOlfaction).

(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

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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
* 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:

The original source data published by Zheng et al. (2018) is publicly available, including the neuron reconstructions in .swc format and glomerulus labels information. A copy of the source data as well as the script for the data analysis and figure reproduction is available at our Github repository (https://github.com/kirichoi/DrosophilaOlfaction).