

Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see [Authors & Referees](#) and the [Editorial Policy Checklist](#).

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- The statistical test(s) used AND whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- A description of all covariates tested
- A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection

Data was collected using custom-written code run on Matlab 2017a or custom-written code for data acquisition written using Python 3.6.

Data analysis

A full description of the software used for analysis is described in the Methods and is available at <https://github.com/murthylab/GLM-HMM> and <https://github.com/murthylab/DeepFlyTrack> (any additional code available upon request). Analyses were run on Matlab 2017a or custom-written code using Python 3.6.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

Data available at <http://arks.princeton.edu/ark:/88435/dsp01rv042w888>.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

Life sciences Behavioural & social sciences Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	Sample sizes for behavioral experiments were determined by comparison with experiments in previous literature.
Data exclusions	No data was excluded.
Replication	Each experiment presented in the paper was repeated in multiple animals. The effects identified were consistent across animals. Analysis was performed with code that is freely available to promote replication.
Randomization	Animals of the same genotype were randomly placed into experimental groups (+/- ATR).
Blinding	Blinding was not performed. All experiments were analyzed and data analysis performed by automatic tracking methods.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology
<input type="checkbox"/>	<input checked="" type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data

Methods

n/a	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals	D. melanogaster strains CM07, CarM03, N30, NM91, TZ58, ZH23, ZW109 (provided by Peter Andolfatto or the Drosophila species stock center), and Canton S (lab stock). UAS-CsChrimson was obtained from the Bloomington stock center (UAS-CsChrimson was contributed to the stock center by Vivek Jayaraman). P1a: UASCsChrimson/+; GMR15A01-AD (attp40)/+; GMR71G01-DBD (attp2)/+ (GMR15A01-AD (attp40); GMR71G01-DBD (attp2) kindly provided by David Anderson. ppIP10: w/+; UAS>stop>CsChrimson/+; VT40556, Fru-FLP/+ (VT40556 and FruFLP were kindly provided by Barry Dickson and UAS>stop>CsChrimson was kindly provided by Vivek Jayaraman. vPR6: w/+; UAS>stop>CsChrimson/+; VT57239, FruFLP/+ (VT57239) All experiments used 4 - 7 day old virgin males courting 4 - 7 day old virgin PIBL (GMR-hid/GMR-hid; orco-/orco-).
Wild animals	n/a
Field-collected samples	n/a
Ethics oversight	n/a

Note that full information on the approval of the study protocol must also be provided in the manuscript.