

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

Image data collection: Zen-2012, Germany; RNA-seq data collection: published database in modEncode (ID-4658) or NCBI (GEO: GSE106930; GSM838792; GSM838789; GSM838784; GSM838752; GSM838787; GSM2052238; GSM2052220; GSM2052244; GSM2052262; GEO: GSE52564).

Data analysis

Image data analysis: Imaris (x64 9.3.0), GraphPad Prism (9.0.0.); RNA-seq data analysis: IGV (2.7.2) and NCBI genome data viewer; Fleximaging: V3.0; Microsoft Excel: 16.45

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

All data supporting the findings in this study are available from the corresponding author upon reasonable request. The source data underlying Figures 1d, 2c, e, 3b-d, 4b, 5d, 6c, f, 7a, and Supplementary Figures 4, 5 and 10 are provided as a Source Data file. The RNA-seq data are available in modEncode (ID-4658) or NCBI (GEO: GSE106930; GSM838792; GSM838789; GSM838784; GSM838752; GSM838787; GSM2052238; GSM2052220; GSM2052244; GSM2052262; GEO: GSE52564).

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	For dendrite volume imaging and Nile red staining experiments, we collected 10 to 20 samples for each genotype and condition. For FISH experiments, we collect ≥ 20 samples for each genotype and condition. These sample numbers are limited by the number of animals with desired genotypes from genetic crosses, and are similar to those reported in previous studies (Sheng C. et al., 2018, Yin J., et al., 2018).
Data exclusions	No data were excluded.
Replication	We performed genetic analyses using different genetic reagents to ensure the reproducibility of the experimental findings. Experiments were performed and repeated by three different lab members. All findings can be reproduced.
Randomization	The sample collection was randomized within each genotype and condition.
Blinding	The group allocation in data collection can not be blinded due to the needs of the experiments. Specific genotypes and conditions are collected for data analyses. The data quantifications were performed blindly by co-authors without knowing the genotype and condition of the groups.

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	Involved in the study
☐	☒ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☐	☒ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	mouse anti-PDF (DSHB PDF C7, 1:10), mouse anti-Chp (DSHB 24B10, 1:10), rat anti-HA (Sigma, 11867423001, 1:200 for immunohistochemistry, 1:2000 for western-blots), rabbit anti-GFP antibody (Abcam, Ab6556, 1: 2000), goat anti-mouse Alex 488 (Invitrogen, A-32723, 1:500), goat anti-mouse Alex647 (Invitrogen, A-32728, 1:500), donkey anti-mouse CY3 (Jackson Immuno Research Labs, 715165150, 1:500), goat anti-rat Alex 647 (Invitrogen, A-21247, 1:500), Donkey anti-Rabbit IgG (H+L) HRP (Thermo Fisher, SA1-200, 1:10,000), Donkey anti-Rat IgG HRP (Thermo Fisher, A18745, 1:10,000)
Validation	Validation statements for the commercial antibodies are available on the manufactures websites.

Animals and other organisms

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

Laboratory animals	Drosophila melanogaster is used in the study. for FISH, dendrite phenotype and lipid droplets study, both male and female are collected at the wandering third instar larval stage. For MALDI study, both male and female flies are collected at adult stage, 5
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days after hatching. The genotypes are described in the main text and Methods. No animal protocol is required for studies using *Drosophila*.

Wild animals

none

Field-collected samples

none

Ethics oversight

The study does not require an ethical approval.

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