

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 our [Editorial Policies](#) 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 analysis

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 and 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

High-throughput m6A-seq data were deposited into the GEO database with accession number:GSE155662. It includes all raw files, peak text files, FPKM value text files, and bigWig files for visualization.

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

Life sciences study design

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

- Sample size
- Data exclusions
- Replication
- Randomization
- Blinding

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 |
|-------------------------------------|---|
| <input type="checkbox"/> | <input checked="" type="checkbox"/> Antibodies |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> Eukaryotic cell lines |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Palaeontology and archaeology |
| <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 |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Dual use research of concern |

Methods

- | n/a | Involved 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 |

Antibodies

- Antibodies used
- Validation

Studies Hybridoma Bank and their information are described in <https://dshb.biology.uiowa.edu>. rabbit anti-GFP (A6455, Molecular Probes), rat anti-HA (3F10, Roche), and rabbit anti-m6A (202003, Synaptic Systems) are widely-used commercial antibodies and their information are described in the companies' websites.

Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s)	Drosophila S2 cells were kindly provided by Prof Yongzhen Xu at Wuhan University as described in: Li, L et al. Nat. Commun. 11:5608 (2020). HeLa cells were purchased from the Cell Bank of the Chinese Academy of Sciences (Shanghai, China).
Authentication	None
Mycoplasma contamination	Not tested for mycoplasma contamination
Commonly misidentified lines (See ICLAC register)	None

Animals and other organisms

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

Laboratory animals	Drosophila Melanogaster of the following genotypes were used: w1118 yw Mettl3SK2 Mettl14SK1 Df(3R)Exel6197 ap-Gal4 Hakai shRNA (VDRC 330548) vir shRNA (HMC03908, Bloomington 55694) fl(2)d shRNA (HMC03833, Bloomington 55674) flacc shRNA (VDRC 35212GD) actin-Cas9 (Bloomington 54590) nanos-Cas9 (Bloomington 78782) U6-Hakai-sgRNA HakaiSH2 HakaiSH4 Hakai shRNA (TH14422.S) Hakai shRNA (TH14423.S) Immunostaining was performed on 3rd instar larval wing discs. Adult flies used in the paper were about 1-2 days old; the sex of these flies were indicated in Fig. 3b, Fig. 6d-g, Fig. S4, Fig. 2 legend, Fig. 3 legend, Fig. 6 legend, and Fig. 7 legend.
Wild animals	The study did not involve wild animals.
Field-collected samples	The study did not involve field-collected samples.
Ethics oversight	Not applicable.

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