nature portfolio

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Reporting Summary

Nature Portfolio 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 Portfolio 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	No Software was used for data collection
Data analysis	MIP (Max-Intensity-Projection) processing of images was performed using Imaris 9.5.0 (Bitplane, http://www.bitplane.com/, RRID:SCR_007370). Costume codes are deposited in GitHub- https://github.com/WIS-MICC-CellObservatory/compensatory-proliferation-in-the-Drosophila-wing-

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 Portfolio 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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

The authors declare that the data supporting the findings of this study are available within the paper and its supplementary information files, and that all additional data (proteomics data, custom codes) are publicly available. All unique materials generated are readily available from the authors.

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	*Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used.* *Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected.* *Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.*
Reporting on race, ethnicity, or other socially relevant groupings	*Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status).* *Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.)* *Please provide details about how you controlled for confounding variables in your analyses.*
Population characteristics	*Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."*
Recruitment	*Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.*
Ethics oversight	*Identify the organization(s) that approved the study protocol.*

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

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	Sample size was chosen according to standard practices in the field. The vast majority of our samples are above 20
Data exclusions	All the obtained data were included in our analysis.
Replication	All experiments were conducted with at least two biological replicates
Randomization	The order of imaginal disc dissections by genotype was randomized for each experiment
Blinding	Blinding is not necessary or applicable to our approach, as all of our data consist of well-controlled wild-type versus RNAi knockdown comparisons. Moreover, the distinct nature of the knockdown phenotypes eliminates the need for blinding, as each of the co-authors who examined the wing imaginal discs could easily distinguish between RNAi and wild-type phenotypes.

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
[ ]	[x] Antibodies
[x]	[ ] Eukaryotic cell lines
[x]	[ ] Palaeontology and archaeology
[ ]	[x] Animals and other organisms
[x]	[ ] Clinical data
[x]	[ ] Dual use research of concern
[x]	[ ] Plants

Methods

n/a	Involved in the study
[x]	[ ] ChIP-seq
[x]	[ ] Flow cytometry
[x]	[ ] MRI-based neuroimaging

Antibodies

Antibodies used

Rabbit polyclonal anti-cleaved human PARP Abcam Ab2317
Rabbit polyclonal anti-pHH3 Millipore 06-570
Rabbit anti-cleaved Dcp-1 Cell Signaling 9578
Biotin Anti-GFP antibody Abcam Ab6658
Mouse anti-Fasciclim III DSHB 7G10
Alexa Fluor® 488-Streptavidin Jackson Immuno-Research 016-540-084
Goat anti-mouse Atto647 Sigma-Aldrich 50185
Mouse anti V5 Tag Antibody (SV5-Pk1) Thermo Fisher Scientific R960-25
Goat anti-Rabbit Rhodamin-Red Jackson ImmunoResearch 111-295-144
Goat anti-Rabbit Cy5 Jackson ImmunoResearch 111-175-144
Anti-Digoxigenin-Rhodamine, Fab fragments Roche 11207750910
Rhodamine (TRITC) AffiniPure® Goat Anti-Mouse IgG (H+L) Jackson Immuno-Research 115-025-166

Validation

Rabbit polyclonal anti-cleaved human PARP Abcam Ab2317: This antibody was referenced in at least 19 studies. For the specific studies please refer to the following link: https://www.citeab.com/antibodies/723575-ab2317-anti-cleaved-parp1-antibody
Rabbit polyclonal anti-pHH3 Millipore 06-570: This antibody was referenced in at least 2506 studies. For the specific studies please refer to the following link: https://www.citeab.com/antibodies/220443-06-570-anti-phospho-histone-h3-ser10-antibody-mito
Rabbit anti-cleaved Dcp-1 Cell Signaling 9578: This antibody was referenced in at least 286 studies. For the specific studies please refer to the following link: https://www.citeab.com/antibodies/654396-9578-cleaved-drosophila-dcp-1-asp215-antibody
Biotin Anti-GFP antibody Abcam Ab6658: This antibody was referenced in at least 163 studies. For the specific studies please refer to the following link: https://www.citeab.com/antibodies/732949-ab6658-biotin-anti-gfp-antibody?des=8df8d3c27ba48fd0
Mouse anti-Fasciclim III DSHB 7G10: This antibody was referenced in at least 44 studies. For the specific studies please refer to the following link: https://www.citeab.com/antibodies/150883-7g10-anti-fasciclin-iii-7g10-anti-fasciclin-iii?des=b8e82eba2c52ab3b
Alexa Fluor® 488-Streptavidin Jackson Immuno-Research 016-540-084: This antibody was referenced in at least 164 studies. For the specific studies please refer to the following link: https://www.jacksonimmuno.com/catalog/products/016-540-084
Goat anti-mouse Atto647 Sigma-Aldrich 50185: This antibody was referenced in at least 78 studies. For the specific studies please refer to the following link: https://www.citeab.com/antibodies/1476285-50185-anti-mouse-igg-atto-647n-antibody-produced-i?des=29cf2cffafcebe1e
Mouse anti V5 Tag Antibody (SV5-Pk1) Thermo Fisher Scientific R960-25: This antibody was referenced in at least 2025 studies. For the specific studies please refer to the following link: https://www.citeab.com/antibodies/2950355-r960-25-v5-tag-monoclonal-antibody-sv5-pk1?des=6eba639be453f13b
Goat anti-Rabbit Rhodamin-Red Jackson ImmunoResearch 111-295-144: This antibody was referenced in at least 100 studies. For the specific studies please refer to the following link: https://www.citeab.com/antibodies/2036905-111-295-144-rhodamine-red-x-rrx-affinipure-goat
Goat anti-Rabbit Cy5 Jackson ImmunoResearch 111-175-144: This antibody was referenced in at least 224 studies. For the specific studies please refer to the following link: https://www.citeab.com/antibodies/2036181-111-175-144-cy-5-affinipure-goat-anti-rabbit-igg-h
Anti-Digoxigenin-Rhodamine, Fab fragments Roche 11207750910: This antibody was referenced in at least 68 studies. For the specific studies please refer to the following link: https://www.citeab.com/antibodies/7015944-11207750910-anti-digoxigenin-rhodamine-fab-fragment
Rhodamine (TRITC) AffiniPure® Goat Anti-Mouse IgG (H+L) Jackson Immuno-Research 115-025-166: This antibody was referenced in at least 14 studies. For the specific studies please refer to the following link: https://www.citeab.com/antibodies/2037140-115-025-166-rhodamine-tritc-affinipure-goat-anti?des=db396b8150712019

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals

Drosophila melanogaster strain: Does not require Institutional Animal Care and Use Committee (IACUC) oversight. The mutant and transgenic strains used in the study are listed under "Fly strains" in the Methods section.

Wild animals	This study did not involve wild animals.
Reporting on sex	Apart for Fig.8F, mixed sex animals were used and data were not analyzed deferentially with respect to sex.
Field-collected samples	This study did not involve samples collected from field.
Ethics oversight	*Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance was required and explain why not.*

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

Plants

Seed stocks	*Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*
Novel plant genotypes	*Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*
Authentication	*Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*