Regeneration in starved planarians depends on TRiC/CCT subunits modulating the unfolded protein response

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(Note: With the exception of the correction of typographical or spelling errors that could be a source of ambiguity, letters and reports are not edited. Depending on transfer agreements, referee reports obtained elsewhere may or may not be included in this compilation. Referee reports are anonymous unless the Referee chooses to sign their reports.)
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Reporting checklist for Life Sciences Articles (Rev. June 2017)

This checklist is used to ensure good reporting standards and to improve the reproducibility of published results. These guidelines are consistent with the Principles and Guidelines for Reporting Preclinical Research issued by the NIH in 2014. Please follow the journal’s authorship guidelines in preparing your manuscript.

A- Figures

1. Data

The data shown in figures should satisfy the following conditions:

- the data were obtained and processed according to the field’s best practice and are presented to reflect the results of the experiments in an accurate and unbiased manner.
- figure panels include only data points, measurements or observations that can be compared to each other in a scientifically meaningful way.
- graphs include clearly labeled error bars for independent experiments and sample sizes. Unless justified, error bars should not be shown for technical replicates.
- if n ≤ 5, the individual data points from each experiment should be plotted and any statistical test employed should be justified.

Source data should be included to report the data underlying graphs. Please follow the guidelines set out in the authorship guidelines on Data Presentation.

2. Captions

Each figure caption should contain the following information, for each panel where they are relevant:

- a specification of the experimental system investigated (e.g. cell line, species name).
- the assay(s) and method(s) used to carry out the reported observations and measurements.
- an explicit mention of the biological and chemical entity(ies) that are altered/varied/perturbed in a controlled manner.
- an explicit mention of the biological and chemical entity(ies) that are being measured.
- the assay(s) and method(s) used to carry out the reported observations and measurements.
- a statement of how many times the experiment shown was independently replicated in the laboratory.
- definitions of statistical methods and measures:
  - common terms, such as n=1 test (please specify whether paired or unpaired), simple Z tests, Fischer’s exact test, Mann-Whitney U tests, can be unambiguously identified by name only, but more complex techniques should be described in the methods section.
  - are tests one-sided or two-sided?
  - are there adjustments for multiple comparisons?
  - exact statistical test results, e.g., F values ≤ x but not P values < y;
  - definition of “center values” as median or average;
  - definition of error bars as s.d. or s.e.m.

Any descriptions too long for the figure legend should be included in the methods section and/or with the source data.

In the pink boxes below, please ensure that the answers to the following questions are reported in the manuscript itself.

Every question should be answered. If the question is not relevant to your research, please write NA (non-applicable).

We encourage you to include a specific subsection in the methods section for statistics, reagents, animal models and human subjects.

B- Statistics and general methods

| Question                                                                 | Answer |
|-------------------------------------------------------------------------|--------|
| 1a. How was the sample size chosen to ensure adequate power to detect a pre-specified effect size? | The sample size calculations were performed. Sample sizes were chosen to be similar to previously published data for highly penetrant phenotypes. |
| 1b. For animal studies, include a statement about sample size estimate even if no statistical methods were used. | At least 5 planarians per independent experiment. In case of qPCR we always did 3 biological replicates with 5 planarians per replicate. At least 3 mice were used per experiment. |
| 2. Describe inclusion/exclusion criteria if samples or animals were excluded from the analysis. Were the criteria pre-established? | No data was excluded. The only exception was if a planarian was completely broken because of handling during FISH or SH. |
| 3. Were any steps taken to minimize the effects of subjective bias when allocating animals/samples to treatment (e.g., randomization procedure)? If yes, please describe. | Animals were randomly assigned to RNAi condition and stainings. |
| For animal studies, include a statement about randomization even if no randomization was used. | Animals were randomly assigned to RNAi condition and stainings. |
| 4a. Were any steps taken to minimize the effects of subjective bias during group allocation or when assessing results (e.g., blinding of the investigator)? If yes please describe. | Investigators were blinded to RNAi condition and stainings. |
| 5. For every figure, are statistical tests justified as appropriate? | Yes. |
| Do the data meet the assumptions of the tests (e.g., normal distribution)? Describe any methods used to assess it. | Yes. When appropriate we performed D’Agostino and Pearson normality test. |
| In there an estimate of variation within each group of data? | The tests we performed assumed equal sample variance. |

Please fill out these boxes (Do not worry if you cannot see all your text once you press return)
| 22. Could your study fall under dual use research restrictions? Please check biosecurity documents in a public repository or included in supplementary information. | Yes |
|---|---|
| 21. Computational models that are central and integral to a study should be shared without restrictions and provided in a controlled repositories such as dbGAP. | Does not apply |
| 20. We recommend consulting the ARRIVE guidelines (see link list at top right) (Qureshi et al., 2010) to ensure all other relevant aspects of animal studies are adequately reported. See also: NIH (see link list at top right) and MRC (see link list at top right) recommendations. Please confirm you have followed these guidelines. | Does not apply |
| 19. Deposited is strongly recommended for any datasets that are central and integral to the study; please consider the journal’s data policy. If no structured public repository exists for a given data type, we encourage the provision of datasets in the manuscript as a Supplementary Document (see author guidelines, under ‘Reporting Guidelines’. Please confirm you have followed these guidelines. | Does not apply |
| 18. For tumor marker prognostic studies, we recommend that you follow the REMARK reporting guidelines (see link list at top right) and submit the CONSORT checklist (see link list at top right) with your submission. See author guidelines, under ‘Reporting Guidelines’. Please confirm you have followed these guidelines. | Does not apply |
| 17. Identify the source of cell lines and report if they were recently authenticated (e.g., by STR profiling) and tested for mycoplasma contamination. | Does not apply |
| 16. Sequence of cct8A has been previously deposited in GenBank: MF669570 (Counts et al., 2017). Sequences of ccl4A, cct1A, cct2B, cct3A, cct4A, cct5, cct6, bip-1, bip-2 and bip-3 have been deposited in GenBank with the accession numbers MN171093-MN171100, MN380639 and MN173562-MN173566. RNA-Seq data has been deposited in GEO with the accession numbers GSE39462 and GSE134013. | Does not apply |
| 15. Report the clinical trial registration number (at ClinicalTrials.gov or equivalent), where applicable. | Does not apply |
| 14. Report any restrictions on the availability (and/or on the use) of human data or samples. | Does not apply |
| 13. For publication of patient photos, include a statement confirming that consent to publish was obtained. | Does not apply |
| 12. Identify the committee(s) approving the study protocol. | Does not apply |
| 11. Identify the committee(s) approving the experiments. | Does not apply |
| 10. For experiments involving live vertebrates, include a statement of compliance with ethical regulations and identify the committee(s) approving the experiments. | Does not apply |
| 9. For experiments involving live vertebrates, include a statement confirming that informed consent was obtained from all subjects and that the experiments conformed to the principles set out in the WHA Declaration of Helsinki and the Department of Health and Human Services Belmont Report. | Does not apply |
| 8. Report species, strain, gender, age of animals and genetic modification status where applicable. Please detail housing and husbandry conditions and the source of animals. | Does not apply |
| 7. Identify the source of cell lines and report if they were recently authenticated (e.g., by STR profiling) and tested for mycoplasma contamination. | Does not apply |
| 6. To show that antibodies were profiled for use in the system under study (assay and species), provide a citation, catalog number and/or clone number, supplementary information or reference to an antibody validation profile. e.g., Antibodypedia (see link list at top right), 1D4gnw02a (see link list at top right). | Does not apply |
| 5. For data accessibility, provide a “Data Availability” section at the end of the Materials & Methods, listing the accession codes for data generated in this study and deposited in a public database (e.g. RNA-Seq data: Gene Expression Omnibus GSE31962; Proteomics data: PRIDE P0000208 etc). Please refer to our author guidelines for ‘Data Deposition’. | Does not apply |
| 4. To show that antibodies were profiled for use in the system under study (assay and species), provide a citation, catalog number and/or clone number, supplementary information or reference to an antibody validation profile. e.g., Antibodypedia (see link list at top right), 1D4gnw02a (see link list at top right). | Does not apply |
| 3. Provide a “Data Availability” section at the end of the Materials & Methods, listing the accession codes for data generated in this study and deposited in a public database (e.g. RNA-Seq data: Gene Expression Omnibus GSE31962, Proteomics data: PRIDE P0000208 etc). Please refer to our author guidelines for ‘Data Deposition’. | Does not apply |
| 2. Provide a “Data Availability” section at the end of the Materials & Methods, listing the accession codes for data generated in this study and deposited in a public database (e.g. RNA-Seq data: Gene Expression Omnibus GSE31962, Proteomics data: PRIDE P0000208 etc). Please refer to our author guidelines for ‘Data Deposition’. | Does not apply |
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