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eLife's transparent reporting form

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. Authors can upload supporting documentation to indicate the use of appropriate reporting guidelines for health-related research (see EQUATOR Network), life science research (see the BioSharing Information Resource), or the ARRIVE guidelines for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this form.

If you have any questions, please consult our Journal Policies and/or contact us: editorial@elifesciences.org.

Sample-size estimation

- You should state whether an appropriate sample size was computed when the study was being designed
- You should state the statistical method of sample size computation and any required assumptions
- If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

Biological triplicates are always a starting baseline for biological experiments; all plots in the manuscript represent at least biological triplicates, unless otherwise indicated in the Methods. Experiments and controls are always paired to allow for paired statistical analysis.

Replicates

- You should report how often each experiment was performed
- You should include a definition of biological versus technical replication
- The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
- If you encountered any outliers, you should describe how these were handled
- Criteria for exclusion/inclusion of data should be clearly stated
- High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

Replicates are listed in the Methods section. All plots in the manuscript represent at least biological triplicated experiments, done on different days with paired controls. The only experiments with two biological replicates are RNA-seq samples for W303_Chr8,15 and W3030_Chr8,10,16 in Fig 2A – these experiments were not analyzed in the manuscript, but the set of RNA-seq samples together with W3030_Chr8 confirm that the same trends occur in different W303 aneuploids, as also shown in Fig 2A Torres data. We do not remove outliers unless there is sign that the culture was not growing properly at the outset of the experiment. We pay close attention to proper statistical handling of all our data.

Statistical reporting

- Statistical analysis methods should be described and justified
- Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
- For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
- Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

Statistical tests are listed after p-values for the first call out in a section. We pay careful attention to statistical tests, using parametric or nonparametric where appropriate. Multiple-test correction methods are listed in the Methods section. We use standard devation or SEM appropriately, as specified in the figure legends. We report exact p-values, except when using an asterisk in figures to indicate significance below a particular threshold; we do cite a general FDR cutoff (e.g. "FDR < 0.05") when used for selection of a data subset. All statistical details are outlined in detail in the extensive Methods section.

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

Group allocation

- Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
- Indicate if masking was used during group allocation, data collection and/or data analysis

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

Groups are defined by genotype; all replicates are paired with controls (i.e. data were collected together at the outset of the experiment and built into the experimental design).

Additional data files ("source data")

- We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
- Where provided, these should be in the most useful format, and they can be uploaded as "Source data" files linked to a main figure or table
- Include model definition files including the full list of parameters used
- Include code used for data analysis (e.g., R, MatLab)
- Avoid stating that data files are "available upon request"

Please indicate the figures or tables for which source data files have been provided:

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All sequencing and proteomic data are available in public repositories, with accession numbers listed. All mapping output files are provide, normalized data and defined groups are provided, normalized but otherwise unprocessed proteomic data is also available.