



## 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](mailto: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:

No explicit statistical methods were used to determine sample sizes. Sample sizes were pre-determined during experimental design based on our previous experience, and are similar to those reported in previous publications.

### 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:



eLIFE

1st Floor  
24 Hills Road  
Cambridge CB2 1JP, UK

P 01223 855340  
W [elifesciences.org](http://elifesciences.org)  
T @elife

In all cases, biological replicates were used, i.e. independent tissue or culture samples from separate cultures (*in vitro* studies) or mouse cohorts. Detailed information on the number of biological replicates can be found in each figure legend, and individual data points are included in each graph.

We did not exclude statistical outliers; any data excluded was for obvious confounds that corrupted the data (defective blot transfer or corner effects; failed positive or negative controls)

Key *in vitro* findings were replicated by two independent researchers (Conde-Dusman, and Dey). All attempts at replication were successful.

RNA sequencing data are available in GEO, as indicated.



### 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 analysis methods, exact N values, and statistical significance can be found in the Methods section (Statistical Analysis), and figure legends. Individual data points are show on figures.

(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:

Randomization: Mice were allocated to different groups based on genotype or sex. Biological samples (i.e. culture wells)/mice were randomly distributed into experimental groups. Experimenter was blind to treatment/genotype whenever possible, and always during data analysis.

### 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:



eLIFE

1st Floor  
24 Hills Road  
Cambridge CB2 1JP, UK

P 01223 855340  
W [elifesciences.org](http://elifesciences.org)  
T @elife

All source data generated in this study will be included with the publication. In biochemical experiments, source data files are linked to the submission