

## eLife's transparent reporting form

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. If you have any questions, please 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., page numbers or figure legends), or explain why this information doesn't apply to your submission:

Sample sizes for all experiments exceed accepted standards in the field. Each explant contains on the order of 1000 cells whose response to perturbation is being assayed. Every experiment includes a minimum of 10 explants per perturbation and gene examined which are each unique biological replicates within the same experiment. Each experiment is repeated a minimum of three times. This ensures that sample size is large enough to detect even small variations in response to perturbation. Sample sizes and percent of samples displaying a given response are noted throughout the Results section (pages 5, 6, 8-13). That each experiment is repeated a minimum of three times is noted in the Methods on page 17, line 386.

### 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., page numbers or figure legends), or explain why this information doesn't apply to your submission:

Each experiment was performed a minimum of three independent times. This is noted in the Methods on page 17, line 386. For types of experiments reported in this paper all replicates are biological not technical replicates. Outliers are handled by reporting the percent of n that shows the reported phenotype. All samples are reported, no data are excluded.

### 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., page numbers or figure legends), or explain why this information doesn't apply to your submission:

N/A

(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 page numbers in the manuscript.)

### 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"



eLIFE

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

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

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

N/A