***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](http://www.equator-network.org/%20" \t "_blank)), life science research (see the [BioSharing Information Resource](https://biosharing.org/" \t "_blank)), or the [ARRIVE guidelines](http://www.plosbiology.org/article/info:doi/10.1371/journal.pbio.1000412" \t "_blank) 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:

Sample sizes (i.e. number of broods counted, number of clones sequenced, number of transgenic lines assayed) are normally listed explicitly in the figures or provided in the figure legends. Occasionally, sample sizes are given the Methods section, if a longer description is needed than appropriate for a legend. The sample sizes are based on years of experience with nematode genetics to ensure that variation would be detected from sample to sample, if it existed. Typically, brood characteristics from different mothers of a particular genotype are very similar and reproducible. Given the low variability from experiment to experiment, we have high confidence in the results. Indeed, the number of replicates was sufficiently high in all experiments such that comparisons between different genotypes using an unpaired t-test revealed clearly whether the samples were statistically different or not.

**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:

The number of times an experiment was performed is given in the figures, figure legends or in the methods section. All replicates are biological replicates. These replicates are independent experiments performed on separately derived biological extracts, or in the case of viability counts, on different progeny cohorts produced from different mothers of the same genotype. No data were excluded from analysis, and rare outlier data, if it existed, were not omitted.

**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:

For our statistical comparisons, we examined the differences between two independent samples, a control group and a single test group or between two different test groups. To do so, we used the well-established unpaired t-test. Statistical analysis, including Standard Error of the Mean (SEM) and p values calculated from unpaired t-tests, were provided in Figures, Figure legends, or directly in the Results and Discussion sections.

(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:

Our data analyses compare animals with different genotypes or compare FOX protein binding to different RNA sequences. Group allocation was based on the clear biological differences or genotypes that were compared.

**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:

All data for this manuscript are included in the main and supplemental figures and tables. No data from any other data files were used for this study. That is, we have no "source data" to upload.