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* You should state whether an appropriate sample size was computed when the study was being designed
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* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

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For the analysis of phenotypes, three to five﻿ animals per treatment were routinely used, with pilot and independent replicates confirming observed responses. With effects sizes similar to those previously observed for RNAI mediated loss of developmental competence (0.637 to 1.804; e.g.[9]) a sample size of three to five animals per group (+ or − DOX)﻿, or a total of six to ten, allows 80% power for test genes. Data were examined before analysis to ensure normality and that no transformations were required. *P* values of less than 0.05 were considered statistically significant. This is reported in the Materials and Methods “Statistical analyses”.

Other statistical analyses are reported in the materials and methods

**Replicates**

* You should report how often each experiment was performed
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Experimental replicates, and n values are reported in each figure legend where relevant.

Other statistical analyses are reported in the materials and methods

**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.

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(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.)

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* 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
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* Include model definition files including the full list of parameters used
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Provided in Supplementary files 2-4.