***eLife’s* transparent reporting form**

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**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

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No statistical method was used to estimate the sample size. For RT-qPCR and WISH experiments a minimal of 3 embryos per genotype were analyzed, which is standardly accepted for these kinds of experiments. For RNA-seq and ATAC-seq experiments we used at least 2 replicates to reduce the chance of any technical inferences on the results. For 4C-seq experiments regarding the mutant alleles we used 2 replicates per condition. The 4C-seq experiments regarding the “development time series” was done as singletons. The results of the ChIP-seq experiments were in line with previous work, as such and because of the large number of animal necessary to perform these experiments only one replicate was analyzed. The CUT&RUN experiments were done as singletons.

**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)

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Information on replicates can be found in the figure legends and in the materials and methods section of the manuscript. High-throughput sequence data can be found under the GEO accession number GSE138514

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* 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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Information on statistical reporting can be found in the figure legends, results, and materials and methods sections of the manuscript.

(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

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* Include model definition files including the full list of parameters used
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