***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
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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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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.

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* You should report how often each experiment was performed
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* The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
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* 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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(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
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