***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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* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
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* We have three or more biological replicates for each experiment, except for Supplemental Figure 5–figure supplement 1 G and H, and reproduced the main findings with these replicates. This information can be found in the figure legends or materials and methods.
* No data were excluded for this study.
* Fastq files of RNA-seq data have been submitted to NCBI SRA, and these data can be accessed through the BioProject ID: PRJNA342736. This information is described in Materials and methods.

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* Statistical analysis methods should be described and justified
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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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Samples were allocated to groups of a given genotype, detected by standard genetic/ genomic approaches. Otherwise samples were randomly selected within these groups. Phenotypic analyses was performed without taking into account the genotype of sample groups, when possible.

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