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

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* You should state whether an appropriate sample size was computed when the study was being designed
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All measurements in this work are replicated and error analysis is performed throughout the paper. Conclusions are based on analysis of the replicates performed.

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* You should report how often each experiment was performed
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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 replicate numbers are included in the figure legends or in supplemental file 9. Definitions of biological versus technical replicates and information on exclusion/inclusion of data are included in the methods. Barcode counts from HTS are included in supplementary file 12.

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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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* 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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Not applicable.

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* 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
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Source code and raw data for computing gene scores and GO category enrichment scores are provided in supplementary file 12. Scores for all genes and GO categories are included in supplemental files 1, 4, 5.