***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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Replicates numbers were decided from experience of the techniques performed and practical considerations. N numbers and statistical tests are given in Supplementary File 8. All statistical comparisons were conducted on data originating from three or more biologically independent experimental replicates.

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* Criteria for exclusion/inclusion of data should be clearly stated
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We describe the number of replicates, and the criteria used to exclude samples, if applicable, in the “Methods” section and in Supplementary File 8.

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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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Statistical analysis methods are described in "Methods" section and Supplementary File 8. All data are shown as means ± SEM. P-values are included in Figure legends and Supplementary tables.

(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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Please indicate the figures or tables for which source data files have been provided:

All available data is reported in the manuscript. The source code for the computational method SPACED and M-CRITIC are available at Github. For details, please see "Results" and "Methods" sections.