***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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Not applicable, because no new data were generated for this study.

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Not applicable, because no new data have been generated. No outliers were removed.

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* Statistical analysis methods should be described and justified
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* 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)
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Data sets published previously and used in this study are summarized in the Methods and Results sections in which they are presented. Statistical tests are described in the Methods and Results sections. Outcomes are reported even when not sufficiently significant to reject the null hypothesis.

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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
* Indicate if masking was used during group allocation, data collection and/or data analysis

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Not applicable, as no experimental data were generated de novo for this study. In the bootstrap resampling analysis (Supplemental Materials), restricted randomization was not applied and resampling with replacement was utilized.

**Additional data files (“source data”)**

* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
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* Include model definition files including the full list of parameters used
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We have stated software version numbers and cited the publications associated with each of the R methods utilized, and listed a web address for experimentalists to use these methods with their data (http://hiv.lanl.gov/content/sequence/NI/ni.html).