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

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. Authors can upload supporting documentation to indicate the use of appropriate reporting guidelines for health-related research (see [EQUATOR Network](about:blank)), life science research (see the BioSharing Information Resource), or the [ARRIVE guidelines](about:blank) for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this 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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* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

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Sample sizes are detailed throughout the text and explicitly in figure legends. In all cases each observation is a single molecule sequenced on a PacBio sequencer.

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Replicate information is included in Figures and Figure Legends. All experiments were performed at least in biological duplicate, with technical replicates representing multiple sequencing runs of the same library.

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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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All statistical analyses are explored in detail in the Methods section of this paper. All code used for statistical analyses are, moreover, freely available on the publicly released Ramani Lab github (URL in paper).

(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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This is not applicable as no statistical analyses performed in our paper involve group allocation.

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* Include model definition files including the full list of parameters used
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Please indicate the figures or tables for which source data files have been provided:

All source data is freely available and downloadable @ Zenodo (dx.doi.org/10.5281/zenodo.3834706)