***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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The data analyzed in this work consist solely of bacterial genome sequences. The entire paper concerns development of methodology for analysis of such data, and as such the justification of the methods we present is actually the topic of the paper.

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* You should report how often each experiment was performed
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All datasets used are publicly available and we provide explicit links to all of them (i.e. database URLs and accession IDs).

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

The source data (i.e. genome sequences) from which all results derive are publicly available as mentioned above. In addition, we have prepared a comprehensive collection of processed data files to help reproduce the results shown in the paper, which are available from <https://zenodo.org/record/4420880> (as also stated in the paper).