***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](http://www.equator-network.org/%20)), life science research (see the [BioSharing Information Resource](https://biosharing.org/" \t "_blank)), or the [ARRIVE guidelines](http://www.plosbiology.org/article/info:doi/10.1371/journal.pbio.1000412) for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this 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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The sample size used is described in the figure legends, Methods and/or in the Results section as appropriate.

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* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
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* Criteria for exclusion/inclusion of data should be clearly stated
* 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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The number of replicates and replicate information is described in the figure legends, Results and/or Methods section as appropriate. The 16S rRNA sequencing abundance data and community OD are available at Dryad: <https://datadryad.org/stash/share/GY93Mt6d49j43K57N-VnvGDrPInJjLk-Dfm1EYCsjHQ>

**Statistical reporting**

* 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)
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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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There are no experimental groups in our work.

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

The source data files and codes used to generate the figures will be available at https://github.com/sylestrela. The codes for the CRM and FBA simulations will be available at https://github.com/vilacelestin.