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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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* 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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Methods section

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* Statistical analysis methods should be described and justified
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Table 1

All Figures contain descriptions of statistical analyses performed

(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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This does not apply to this submission as samples were not allocated into experimental groups and randomization was not used

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* Include model definition files including the full list of parameters used
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Shotgun metagenomic sequence data reported in this study were submitted to the National Center for Biotechnology Information (NCBI) Sequence Read Archive (SRA) archive and are publicly available via the accession numbers SRA: SRP167939 and BioProject: PRJNA503909. This is described in the “Bioinformatic processing” section of the Methods.

Certain restrictions apply to providing access to participant metadata for this study.

The code used in data formatting and analysis, its corresponding Markdown document, and relevant output files are archived at https://github.com/fmobegi/TSI-Data-Analysis.