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* You should state whether an appropriate sample size was computed when the study was being designed
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Information regarding the statistical methods and sample size are available in the Materials and Methods and Figure Legends.

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* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
* The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
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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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* 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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* 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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It does not apply because our study does not involve samples allocated into experimental groups or masking.

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* Include model definition files including the full list of parameters used
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Source data for Figure 1, 2, 4B, S1-3 and S5 is provided as Supplemental Tables 3 and 5, which contain the source files for DNA sequencing. Source data for Figure 4C is provided as a separate file.