nature portfolio

Corresponding author(s): Anna Kuchina, Neelendu Dey

Last updated by author(s): 2/09/2026

Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☒	☐	A description of all covariates tested
☐	☒	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☒	☐	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☐	☒	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	Software not used to collect data.
Data analysis	BBDuk (BBMap version 38.92), MEGAHIT v1.2.9, Prokka v1.14.5, Pharokka v1.7.3, NCBI BLASTp v2.9.0, phold v0.2.0, PhageScope, AlphaFold 3, Dali, VIRIDIC Web, STAR, STARsolo (STAR-2.7.10b), AnnData v0.10.9, Scanpy v1.10.3, DefenseFinder v2.0.1, SnapGene v8.2, snippy v 5.2, SPAdes v3.15.5, Minced v0.4.2, Dorado v1.1.1, samtools v1.18, modkit v0.5.0, bwa v0.7.17, iLund4u v0.1.0, MEGAHIT v1.2.9, custom Python 3.11 code (https://github.com/anika-gupta-8/B_fragilis_phage_microSPLiT), R 4.3.1

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

MicroSPLiT sequencing data generated in this study have been deposited in the Gene Expression Omnibus series under accession code GSE309504[https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=309504]. The bulk RNA sequencing data are available under GSE318809[https://www.ncbi.nlm.nih.gov/geo/query/

acc.cgi?acc=GSE318809]. WGS data for Bacteroides fragilis strains and Bf12P1 phage are available in the Sequence Read Archive under BioProject PRJNA1335357 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1335357]. Sequencing datasets generated in this study are summarized in Supplementary Data 9. The Bf12P1 genome is deposited in GenBank under accession number PX436277. Source data are provided with this paper.

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	N/A
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	N/A

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	We collected sequencing and growth data and used all processed data for analyses.
Data exclusions	None
Replication	We performed two biological replicates of phage infection assay in liquid culture, with separate microSPLiT experiments performed for each of these samples. For the growth curves of phase-locked strains in Fig. 4a, we measured four (4) biological replicates. For the plaque assays in Fig. 4b, we performed three (3) biological replicates. Three (3) biological replicates were collected for bulk RNA-sequencing of control and Bf12P1 phage-infected B. fragilis cultures.
Randomization	None
Blinding	None

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☐	☒ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals	None
Wild animals	None
Reporting on sex	None
Field-collected samples	Bf12P1 bacteriophage isolated from municipal wastewater.
Ethics oversight	No approval was required as we used laboratory bacterial cultures.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Plants

Seed stocks	*Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*
Novel plant genotypes	*Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*
Authentication	*Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*