

Corresponding author(s): Michael SuretteLast updated by author(s): Mar 14, 2025

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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☐ | ☒ | 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
<i>Give P values as exact values whenever suitable.</i> |
| ☒ | ☐ | 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

No software was used for data collection.

Data analysis

We exclusively used open-source software and publicly available in-house custom code. All code used for figure generation and statistical analyses in this paper is available in the GitHub repository: <https://github.com/SShekariz/UCFMT1>. A full description of the software and their versions is provided in the Methods section

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](#)

All data collected for this study consist of DNA sequencing data from our lab, which have now been deposited in the SRA and will be made available upon publication. Shotgun metagenomic sequences used in this study are available via the SRA under BioProject number PRJNA1220173. These samples include fecal samples from donor B and patients with ulcerative colitis, as well as plate pool metagenomes from donor B. In addition, we utilized metagenomic reads from a

publicly available dataset (PRJNA4000722935) to confirm some of the findings from this study.

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

This study uses DNA extracted from stool samples from a completed randomized control trial ClinicalTrials.gov Number: NCT01545908. This study was approved by the Hamilton Health Sciences Research Ethics Board (REB # 11-600) The results of the trial are published as are published (PMID: 25857665). Sex was reported in the original trial, but given the small samples size in this study which was a subset of the original trial, it was not evaluated here.

Reporting on race, ethnicity, or other socially relevant groupings

Race and ethnicity were reported in the original trial, but given the small samples size in this study which was a subset of the original trial, it was not evaluated here.

Population characteristics

Population characteristics were reported in the original trial, but given the small samples size in this study which was a subset of the original trial, it was not evaluated here.

Recruitment

Recruitment was not part of this analysis.

Ethics oversight

Hamilton Health Sciences Research Ethics Board, Hamilton ON Canada (REB # 11-600). Written informed consent for microbiome analysis was obtained by all participants.

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](https://www.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 were limited by the number of samples available from a randomized controlled trial. No sample size calculation was performed for inclusion in this study.

Data exclusions

No data were excluded for our analysis.

Replication

The data used in this paper consisted of previously published 16S amplicon data (re-analyzed with newer approaches) and shotgun metagenomic data. There was no replication of this data in this study. We have rigorous internal controls in our process including standard positive controls and negative controls. For the 16S sequencing included negative control samples which were found to be free of contamination. We did not include negative control samples in the shotgun metagenomic sequencing however we do include negative control in the library preparation. We do not use a library where the negative control has a signal at the end of the library construction (did not occur for any samples in this study). The samples were not all obtained and processed at the same time. We utilized metagenomic reads from a publicly available dataset (PRJNA4000722935) to confirm some of the findings from this study.

Randomization

The treatment allocation for the original RCT was random and approved by the research ethics board. The number of placebo-controlled samples included in this study was also selected randomly and matched to the number of patients who received FMT to ensure a balanced analysis.

Blinding

Investigators and participants in the RCT were blinded. The analysis of DNA sequencing data was conducted after unblinding.

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

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, mosaicism, off-target gene editing) were examined.