**SUPPLEMENTARY MATERIALS**

**Methods for 16S rRNA gene sequencing**

***DNA isolation from stool samples***

DNA was isolated from each stool sample using a modified version of a method previously described [1]. Because both the FMT material and the patient’s stool samples were liquid, 200 µL of each sample were used for DNA isolation. Each sample was combined with 300 mg of 0.1 mm glass beads and 750 µL of lysis buffer comprising 200 mM NaCl, 100 mM Tris (pH 8.0), 20 mM EDTA, and 20 mg/mL lysozyme from chicken egg white (Sigma L4919, Saint Louis, Missouri) that had been dissolved by incubating in a 37°C water bath for 30 minutes. The solution of lysis buffer and stool was vortexed briefly and incubated at 37°C for 30 minutes.

Following incubation, 85 µL of 10% SDS and 20 µL of Proteinase K from the Qiagen QIAamp DNA Stool Mini Kit (catalog number 51504, Qiagen, Valencia, California) were added, and the mixture was incubated at 60°C for 30 minutes. 500 µL of 25:24:1 solution of phenol:chloroform:isoamyl alcohol was then added before the samples were placed in a TeSeE Precess 48 Homogenizer (Bio-Rad, Hercules, California) and beaten for 90 seconds at 5300 rpm. Once homogenized, the samples were centrifuged at 15,871 rcf (13,000 rpm) for 5 minutes at 20°C in an Eppendorf 5424 R Microcentrifuge (Eppendorf, Hamburg, Germany).

Following centrifugation, supernatants were successively vortexed with the three different solutions listed below, with each addition separated by a 5 minute/20°C/15,871 rcf centrifugation. First, supernatants were transferred to a second 500 µL volume of 25:24:1 phenol:chloroform:isoamyl alcohol and vortexed. These solutions were then centrifuged and the resulting supernatants were transferred to 500 µL of 100% chloroform and vortexed. Last, the solutions were centrifuged and the supernatants were transferred to a solution of 1 mL100% ethanol with 50 µL of 3 M sodium acetate, and gently mixed. This solution was precipitated at -80°C for 75 minutes.

To pellet the precipitated DNA, samples were centrifuged again for 5 minutes at 15,871 rcf and 20°C. The ethanol/sodium acetate supernatant was carefully removed and discarded, and the pelleted DNA was allowed to air dry for 5 minutes before being re-suspended in 200 µL of molecular-grade, nuclease-free water. This DNA was then purified using additional 100% ethanol and buffers from the Qiagen QIAamp DNA Stool Mini Kit (AL, AW1, AW2) per the manufacturer’s accompanying instructions for “Isolation of DNA from Stool for Pathogen Detection,” beginning at step 11 and skipping steps 12 (10 minute, 70°C incubation) and 18 (this isolation method does not employ buffer AE).

***16S rRNA gene library preparation***

The V4 region of the 16S rRNA gene was amplified using a two-PCR method as previously described [2]. Sequences of the primers used are given in Supplementary Table 1. The first PCR amplifies the V4 region of the 16S rRNA gene using a mixture of six staggered forward and six staggered reverse primers to increase sequence complexity. The second PCR amplifies this region of the gene further, while also appending Illumina MiSeq adapter primers and a single 12-nucleotide Golay error-correcting index to each sample’s amplicons to enable multiplexing [3]. After each PCR, amplicons were cleaned using the HighPrep PCR reagent (MagBio, Lausanne, Switzerland) on a DynaMag-96 side magnet (Life Technologies, Carlsbad, California) following the manufacturer’s instructions.

For the first PCR, 120 ng of template DNA and the twelve primers at a concentration of 0.03 µM each (for a total primer concentration of 0.8 µM) were combined with reagents (Buffer A, Enhancer, dNTPs, Robust DNA polymerase) from the KAPA2G Robust PCR Kit (#KK5005, Kapa Biosystems, Roche, Wilmington, Massachusetts). These were amplified with the following parameters: 95°C/3min; [95°C/30s; 50°C/30s; 72°C/30s] x 10 cycles; 72°C/5 min; 4°C/hold. In the second PCR, 5 µL of cleaned product from the first PCR was added to the KAPA HiFi HotStart ReadyMix reagent (#KK2602, Kapa Biosystems, Roche, Wilmington, Massachusetts) with a 1.25 µM final combined concentration of both the forward MiSeq adapter primer and reverse Golay index primer. These were amplified with the following parameters: 95°C/3min; [95°C/30s; 50°C/30s; 72°C/30s] x 22 cycles; 72°C/5 min; 4°C/hold. Equimolar amounts of the final products of the two PCRs were then pooled for sequencing.

***Sequencing and sequence data processing***

The pool of amplicons was sequenced at the High Throughput Sequencing Facility of the University of North Carolina at Chapel Hill School of Medicine on an Illumina MiSeq benchtop sequencer (Illumina, San Diego, California) generating 2x250 bp reads. The pool was combined with a 15% phiX spike, and data were processed using bcl2fastq version 1.19. Sequence data are available on the NCBI’s Sequence Read Archive under the accession number SRP129013 (<https://www.ncbi.nlm.nih.gov/sra/SRP129013>). During the process of being uploaded to the SRA, human contaminant sequences were filtered from the dataset, removing at most 17 sequences per sample. Analysis of the 16S rRNA reads was performed using DADA2 (v. 1.6.0), phyloseq (v. 1.22.3), and the Silva reference database (v. 128) in R (v. 3.4.3) [4-6]. The code and data used to analyze the 16S rRNA sequences and generate figures are in additional supplemental files.

**Supplementary Table 1:** Primers used in amplifying the V4 region of the 16S rRNA gene, modified from Caporaso et al. (2012) [3].

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| **Primer Name** | **Primer Sequence (5'–3')** | **PCR #** |
| Var4v5\_F1 | GCCTCCCTCGCGCCATCAGAGATGTGTATAAGAGACAGNNNNNNNNGAGTGCCAGCMGCCGCGGTAA | PCR 1 |
| Var4v5\_F2 | GCCTCCCTCGCGCCATCAGAGATGTGTATAAGAGACAGNNNNTNNNNGAGTGCCAGCMGCCGCGGTAA | PCR 1 |
| Var4v5\_F3 | GCCTCCCTCGCGCCATCAGAGATGTGTATAAGAGACAGNNNNCTNNNNGAGTGCCAGCMGCCGCGGTAA | PCR 1 |
| Var4v5\_F4 | GCCTCCCTCGCGCCATCAGAGATGTGTATAAGAGACAGNNNNACTNNNNGAGTGCCAGCMGCCGCGGTAA | PCR 1 |
| Var4v5\_F5 | GCCTCCCTCGCGCCATCAGAGATGTGTATAAGAGACAGNNNNGACTNNNNGAGTGCCAGCMGCCGCGGTAA | PCR 1 |
| Var4v5\_F6 | GCCTCCCTCGCGCCATCAGAGATGTGTATAAGAGACAGNNNNTGACTNNNNGAGTGCCAGCMGCCGCGGTAA | PCR 1 |
| Var4v5\_R1 | GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTNNNNNACGGACTACHVGGGTWTCTAAT | PCR 1 |
| Var4v5\_R2 | GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTNNTNNNACGGACTACHVGGGTWTCTAAT | PCR 1 |
| Var4v5\_R3 | GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTNNCTNNNACGGACTACHVGGGTWTCTAAT | PCR 1 |
| Var4v5\_R4 | GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTNNACTNNNACGGACTACHVGGGTWTCTAAT | PCR 1 |
| Var4v5\_R5 | GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTNNGACTNNNACGGACTACHVGGGTWTCTAAT | PCR 1 |
| Var4v5\_R6 | GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTNNTGACTNNNACGGACTACHVGGGTWTCTAAT | PCR 1 |
| Adapter | AATGATACGGCGACCACCGAGATCTACACGCCTCCCTCGCGCCATCAGAGATGTG | PCR 2 |
| Index | CAAGCAGAAGACGGCATACGAGAT [12-nucleotide index] GTGACTGGAGTTCAGACGTGTGCTC | PCR 2 |

**Supplementary References:**

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3. Caporaso JG, Lauber CL, Walters WA, Berg-Lyons D, Huntley J, Fierer N, et al. Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms. ISME J. 2012;6(8):1621-4. doi: 10.1038/ismej.2012.8. PubMed PMID: 22402401; PubMed Central PMCID: PMCPMC3400413.

4. Callahan BJ, McMurdie PJ, Rosen MJ, Han AW, Johnson AJ, Holmes SP. DADA2: High-resolution sample inference from Illumina amplicon data. Nat Methods. 2016;13(7):581-3. doi: 10.1038/nmeth.3869. PubMed PMID: 27214047; PubMed Central PMCID: PMCPMC4927377.

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