**SUPPLEMENTAL METHODS**

**Clinical data**

The sequential organ failure assessment (SOFA) score was used to evaluate acute severity of illness at the time of ICU admission, and to determine the effectiveness of randomization. SOFA score was formulated as has been previously described, using the worst values within the preceding 24 hour period. Individual SOFA categories are compared as tertiles in Table 1; to formulate the summary SOFA score, standard SOFA cut-offs were used and then the summary score was again divided into tertiles. ICU interventions were classified categorically based on whether they had been received within the 24 hour period preceding study enrollment.

**16S rRNA gene sequencing**

16S rRNA gene sequencing was performed by Corebiome (St. Paul, MN). The V4 region of the 16S gene was sequenced using the 515F/806R primers from the Human Microbiome Project to produce an amplicon of ~290bp.1 DNA was extracted with Qiagen’s DNeasy PowerSoil Pro Kit automated for high throughput on QiaCube, with bead beating in Qiagen Powerbead Pro plates (Cat No. 19311). Samples were quantified using qPCR and then prepared with a protocol derived from Gohl *et al*., using KAPA HiFi Polymerase.2 Libraries were sequenced on an Illumina MiSeq using paired-end 2 x 250 reads and the MiSeq Reagent Kit v3. Complete sequencing data has been uploaded under BioProject PRJNA603980.

**Analysis of 16S rRNA sequencing data**

Raw fastq files were processed using the DADA2 pipeline in R version 3.6.1 and Rstudio version 1.2.1335.3 The complete code for the sequence reads processing is provided in **Supplementary Data file 1**. Briefly, the reads were trimmed, quality filtered, merged, error corrected and chimer filtered. Taxonomy was assigned using the Ribosomal Database Project (RDP) classifier with the SILVA reference database training set version 132,4 formatted for the DADA2 pipeline (silva\_nr\_v132\_train\_set.fa).5 Alpha diversity estimates were calculated using the Phyloseq R package.6 Change in the differential abundance of the prespecified short-chain fatty acid (SCFA) producers was calculated based on relative abundance after sampling to an even depth of 20,000 reads per sample. This subsampling led to the loss of three samples from patient 11 (12,800, 5,396 and 2,715 reads, respectively). The prespecified SCFA-producing taxa were; Odoribacter, Eubacterium, Butyrivibrio, Clostridium, Coprococcus, Butyricicoccus, Pseudoflavonifractor, Flavonifractor, Roseburia, Anaerostipes, Oscillibacter, Faecalibacterium, Alistipes. The abundance table was subsetted to these taxa and the within-patient change in relative abundance relative to baseline or Day 0 was calculated as [(Day X – Day 0) / Day 0]. The primary outcome of within-individual change from baseline to Day 3 was assessed as an intent-to-treat Wilcox rank-sum test, comparing the fiber versus no fiber groups based on the initial treatment assignment (i.e., intent-to-treat). Hypothesis-free exploration of differential abundances was performed usingt the DESeq2 statistical framework7 as implemented in the Phyloseq package. The following comparisons were made: (1) Day 0 versus Day 3 within the fiber group, (2) Day 0 versus Day 3 within the no fiber group, and (3) Day 3 for the fiber versus no fiber groups. Only OTUs that were present in at least 50% of the samples were included in these analyses.

**SCFA levels**

Levels of short-chain fatty acids (SCFAs) were analyzed by Metabolon (Morrisville, NC). Human stool samples were spiked with stable labelled internal standards and homogenized and subjected to protein precipitation with an organic solvent. After centrifugation, an aliquot of the supernatant was derivatized. The reaction mixture was diluted, and an aliquot injected onto an Agilent 1290/AB Sciex QTrap 5500 LC MS/MS system equipped with a C18 reversed phase UHPLC column. The mass spectrometer was operated in negative mode using electrospray ionization (ESI). The peak area of the individual analyte product ions was measured against the peak area of the product ions of the corresponding internal standards.  Quantitation was performed using a weighted linear least squares regression analysis generated from fortified calibration standards prepared immediately prior to each run. LC-MS/MS raw data were collected and processed using AB SCIEX software Analyst 1.6.2. The endogenous quality control (QC) was prepared from a single lot of human stool. All analytes were at the endogenous level except hexanoate, which was spiked in due to low levels. The other three levels of QC were prepared by spiking phosphate buffered saline (PBS) with all analytes in the appropriate concentrations for each level. Sample analysis was carried out in a 96-well plate format containing two calibration curves and eight QC samples per plate to monitor assay performance. A single batch was prepared and analyzed. Precision was evaluated using the corresponding QC replicates in the sample runs. QCs were acceptable for all analytes based on the criteria that at least 50% of QC samples at each concentration level per analyte should be within ±20.0% of the running mean, and at least 2/3 of all QC samples per analyte should fall within ±20.0% of the corresponding running mean. For the final analysis, the sum total of 9 SCFAs were combined for each sample: 2-methylbutyrate, acetate, butyrate, hexanoate, isobutyrate, isovalerate, propionate, and valerate.

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