

355 **SUPPLEMENTAL METHODS:**

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357 **Sample processing and next generation sequencing**

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359 For DNA extraction, 0.3g of stool were added to Mo Bio Powersoil[®] (Mo Bio, Carlsbad,
360 CA) power bead tubes, vortexed for 10 minutes, centrifuged at 10,000 x g for 30 seconds; 200
361 µL of supernatant were processed using a bacterial card on the EZ1 Advanced XL automated
362 extraction system (Qiagen, Valencia, CA). DNA was eluted in 50 µL and stored at -20°C.

363 In preparation for next generation sequencing, the V1-V2 hypervariable regions of the
364 16S ribosomal genes were amplified by PCR in a 25µL reaction that included 2µL of microbiome
365 DNA and primers 8F (5'-AGAGTTTGA TCCTGGCTCAG) and 338R (5'-TGCTGCCTCCCGTAGGAGT),
366 using the FastStart High Fidelity PCR System (Roche, Indianapolis, IN). Thermocycler conditions
367 were 95°C for 15 minutes; 30 cycles of 94°C for 30 sec, 57°C for 30 sec, 72°C for 30 sec; 7
368 minute hold at 72°C, and a final hold at 4°C. PCR was performed in triplicate and products were
369 pooled. PCR products were subsequently amplified following an Illumina procedure

370 (http://res.illumina.com/documents/products%5Cappnotes%5Cappnote_16s_sequencing.pdf),

371 using primers that include 5' overhang adapter sequences. Products were cleaned using the

372 QIAquick PCR Purification Kit (Qiagen, Valencia, CA). Library preparation and sequencing was

373 performed by the CDC Biotechnology Core using the Nextera XT Sample Preparation Kit and an

374 Illumina MiSeq instrument (Illumina, San Diego, CA).]

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376 **Next generation sequencing analysis**

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378 Sequencing generated 7.1 gigabases of 250 bp paired-end reads. Raw sequencing reads
379 were assembled into 16S rRNA V1-V2 contigs using PANDAseq 2.6 (default settings),³⁵ which
380 corrects for base-call errors in the overlap region and discards low quality assemblies. Next
381 generation sequencing yielded 1,008,018 (Range: 584,059-1,656,961) 16S V1-V2 contigs per
382 sample with an average sequence length of 369 bp. Assembled DNA sequence data were
383 processed using QIIME 1.8 suite scripts.³⁶ DNA sequences sharing $\geq 97\%$ similarity were
384 clustered into OTUs using the UCLUST algorithm.¹⁹ The centroid sequence was selected as the
385 representative sequence for all members within a single OTU. OTUs containing only one
386 sequence (singletons) were discarded from the dataset. The centroid sequence of each
387 accepted OTU was assigned to known taxa using the Greengenes database (v. 13-8),³⁷ by means
388 of the USEARCH component of UCLUST. Additionally, KRAKEN³⁸ was used to align all sequences
389 to the NCBI RefSeq database. KRONA³⁹ and QIIME scripts were used to generate taxonomic
390 distribution plots, for KRAKEN alignments and UCLUST clustering, respectively.

391 Using the QIIME 1.8 suite, all sequence data were rarefied (randomly selected) to 5,000
392 sequences per sample. Shannon Diversity Index⁹ and Observed Species were selected for alpha
393 diversity analyses. Centroid sequences of each OTU were aligned with each other using
394 PyNAST⁴⁰ and these alignments were turned into an OTU phylogenetic tree using FastTree
395 software.⁴¹ The inferred tree was utilized for beta-diversity community analyses (weighted
396 UniFrac distance²⁰). Beta-diversity analyses were visualized by principal coordinates plots using
397 the cmdscale function in R statistical software (v. 3.0.2).

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522 Source files

523 Figure 2

Family	D01	D02	L04	L05	L06	L07	L08	L09	L10	L11
Bacteroidetes:Bacteroidaceae	0.41627145	0.39826186	0.59630411	0.08657501	0.00019576	7.1415E-05	0.00017209	0.0001938	1.3407E-06	4.8142E-06
Bacteroidetes:Rikenellaceae	0.00559361	0.00298862	0.00469674	0.06041152	0.00017892	0.94705409	0.00013828	1.2548E-05	6.7035E-07	1.3755E-06
Firmicutes:Alcaligenaceae	0.11350382	2.0161E-05	0.21971527	0.00015758	4.6309E-05	1.843E-05	0.00311817	4.1827E-05	2.6814E-06	2.0632E-06
Firmicutes:Erysipelotrichaceae	0.00113307	0.00073767	0.00215255	0.10086515	2.5259E-05	0.01690339	0.25448736	0	7.1728E-05	8.1842E-05
Firmicutes:Lachnospiraceae	0.0671562	0.13381064	0.03031846	0.1424167	7.4726E-05	0.00072336	0.13844893	4.601E-05	4.8936E-05	5.1581E-05
Firmicutes:Enterococcaceae	6.0787E-05	6.76E-05	0.0033028	2.398E-05	1.4735E-05	0.01250563	0.00053982	0.70683634	0.97512462	0.00089269
Firmicutes:Ruminococcaceae	0.13509656	0.14756066	0.11601575	0.17368613	9.2618E-05	0.00884275	0.48213028	5.2981E-05	9.8542E-05	0.00012448
Firmicutes:Lactobacillaceae	2.1883E-05	2.3719E-06	0.00022773	2.398E-05	0.10875123	0.00043425	0.00151259	0.0021513	0.00019306	0.97933948
Proteobacteria:Pseudomonadaceae	1.2157E-06	3.4393E-05	0.00025529	0.00015587	0.87946947	8.1781E-05	0	1.2548E-05	6.7035E-07	2.0632E-06
Proteobacteria:Enterobacteriaceae	3.4041E-05	3.2021E-05	0.00101825	0.08660413	2.2102E-05	3.4555E-06	0.00016424	0.23252017	1.5418E-05	3.2324E-05
Others	0.27	0.32	0.03	0.35	0.01	0.01	0.12	0.06	0.03	0.02

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525 Figure 2

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	L08	L09	L11	L05	D02	L04	D01	L06	L10	L07
L08	0	0.856339506	1.15486735	0.941269993	1.054084867	1.12876338	1.167102987	1.141755564	0.827891939	1.146248375
L09	0.856339506	0	0.677130872	0.819648544	0.960095228	0.966079027	0.989132083	0.92539822	0.264353894	0.918681711
L11	1.15486735	0.677130872	0	1.203977063	1.253034282	1.256379581	1.282570707	1.112168257	0.535575446	1.239526006
L05	0.941269993	0.819648544	1.203977063	0	1.023247526	1.087534203	0.976315994	1.222748291	0.877773745	1.23547533
D02	1.054084867	0.960095228	1.253034282	1.023247526	0	0.81415079	0.653089712	1.252881341	0.926340855	1.246550162
L04	1.12876338	0.966079027	1.256379581	1.087534203	0.81415079	0	0.811531362	1.167959823	0.929886708	1.264520656
D01	1.167102987	0.989132083	1.282570707	0.976315994	0.653089712	0.811531362	0	1.292265776	0.944617567	1.3081192
L06	1.141755564	0.92539822	1.112168257	1.222748291	1.252881341	1.167959823	1.292265776	0	0.885649096	1.165524797
L10	0.827891939	0.264353894	0.535575446	0.877773745	0.926340855	0.929886708	0.944617567	0.885649096	0	0.911633641
L07	1.146248375	0.918681711	1.239526006	1.23547533	1.246550162	1.264520656	1.3081192	1.165524797	0.911633641	0