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SUPPLEMENTAL TABLE 1 Reaction mixture for amplicon PCR during library preparation for gene sequencing of 16S rRNA

Component	Per reaction (μL)
5x HOT FIREPol® Blend Master Mix Ready to Load (Solis BioDyne)	5
Forward primer [1], PRK341F (10 μM)	0.5
Reverse primer [1], PRK806R (10 μM)	0.5
Nuclease-free water	17
Template DNA	2

[1]Forward 5'- CCTACGGGRBGCASCAG-3', reverse 5'- GGACTACYVGGGTATCTAAT-3' (1).

SUPPLEMENTAL TABLE 2 Temperature cycles used for amplicon PCR during library preparation for gene sequencing of 16S rRNA

Operation	Temperature (°C)	Duration	Number of cycles
Initial activation	95	15 min	1
Denaturation	95	30 sec	
Annealing	55	30 sec	25
Elongation	72	45 sec	
Final elongation	72	7 min	1
-	4	∞	-

SUPPLEMENTAL TABLE 3 Reaction mixture for index PCR during library preparation for gene sequencing of 16S rRNA

Component	Per reaction (μL)
5x FIREPol® Master Mix Ready to Load (Solis BioDyne)	5
Forward primer [1] (1 μM)	5
Reverse primer [1] (1 μM)	5
Nuclease-free water	8
Template DNA	2

[1]See Supplemental Table 5.

SUPPLEMENTAL TABLE 4 Temperature cycles used for index PCR during library preparation for gene sequencing of 16S rRNA

Operation	Temperature (°C)	Duration	Number of cycles
Initial activation	95	5 min	1
Denaturation	95	30 sec	
Annealing	55	1 min	10
Elongation	72	45 sec	
Final elongation	72	7 min	1
-	4	∞	-

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SUPPLEMENTAL TABLE 5 Primers modified with Illumina adapters used for index PCR during library preparation for gene sequencing of 16S rRNA (2). Unique combination of forward and reverse primer was used for each sample

Primer name	Sequence, 5' → 3'	Target gene (region)	Direction
F1	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttc cgatctagtcaaCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F2	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttc cgatctagttccCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F3	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttc cgatctatgtcaCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F4	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttc cgatctccgtccCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F5	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttc cgatctgtagagCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F6	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttc cgatctgtccgcCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F7	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttc cgatctgtgaaaCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F9	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttc cgatctgtttcgCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F10	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttc cgatctcgtacgCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F11	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttc cgatctgagtggCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F12	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttc cgatctggtagcCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F13	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttc cgatctactgatCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F14	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttc cgatctatgagcCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F15	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttc cgatctattcctCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F16	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttc cgatctcaaaagCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
R1	caagcagaagacggcatacgagatCGTGATgtgactggagttcaga cgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R2	caagcagaagacggcatacgagatACATCGgtgactggagttcaga cgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R3	caagcagaagacggcatacgagatGCCTAAgtgactggagttcaga cgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R4	caagcagaagacggcatacgagatTGGTCAgtgactggagttcaga cgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R5	caagcagaagacggcatacgagatCACTCTgtgactggagttcaga cgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R6	caagcagaagacggcatacgagatATTGGCgtgactggagttcaga cgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R7	caagcagaagacggcatacgagatGATCTGgtgactggagttcaga cgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R8	caagcagaagacggcatacgagatTCAAGTgtgactggagttcaga cgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R9	caagcagaagacggcatacgagatCTGATCgtgactggagttcaga cgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse

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R10	caagcagaagacggcatacgagatAAGCTAgtgactggagttcagacgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R11	caagcagaagacggcatacgagatGTAGCCgtgactggagttcagacgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R12	caagcagaagacggcatacgagatTACAAGgtgactggagttcagacgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R13	caagcagaagacggcatacgagatTTGACTgtgactggagttcagacgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R14	caagcagaagacggcatacgagatGGAACTgtgactggagttcagacgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R15	caagcagaagacggcatacgagatTGACATgtgactggagttcagacgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R16	caagcagaagacggcatacgagatGGACGGgtgactggagttcagacgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R17	caagcagaagacggcatacgagatCTCTACgtgactggagttcagacgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R18	caagcagaagacggcatacgagatGCGGACgtgactggagttcagacgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R19	caagcagaagacggcatacgagatTTTCACgtgactggagttcagacgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R20	caagcagaagacggcatacgagatGGCCACgtgactggagttcagacgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R21	caagcagaagacggcatacgagatCGAAACgtgactggagttcagacgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R22	caagcagaagacggcatacgagatCGTACGgtgactggagttcagacgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R23	caagcagaagacggcatacgagatCCACTCgtgactggagttcagacgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R24	caagcagaagacggcatacgagatGCTACCgtgactggagttcagacgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R25	caagcagaagacggcatacgagatATCAGTgtgactggagttcagacgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R26	caagcagaagacggcatacgagatGCTCATgtgactggagttcagacgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R27	caagcagaagacggcatacgagatAGGAATgtgactggagttcagacgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R28	caagcagaagacggcatacgagatCTTTTGgtgactggagttcagacgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R29	caagcagaagacggcatacgagatTAGTTGgtgactggagttcagacgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R30	caagcagaagacggcatacgagatCCGGTGgtgactggagttcagacgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R31	caagcagaagacggcatacgagatATCGTGgtgactggagttcagacgtgtgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse

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SUPPLEMENTAL TABLE 6 Within- and between-group comparisons of fecal bacterial abundances at baseline and 4-week follow-up in the control and LFD group (all taxa included)[1]

Taxon	Control group (*n* = 36)				LFD group (*n* = 33)			
	Baseline	Follow-up	*P* value [2]	*P* value adj [3]	Baseline	Follow-up	*P* value [2]	*P* value adj [3]
p_Actinobacteria	1.09 [0.42,1.84]	1.10 [0.61,1.54]	0.8123	0.9138	1.03 [0.74,2.13]	1.00 [0.51,1.64]	0.4688	0.8439
c_Actinobacteria	0.52 [0.02,1.07]	0.41 [0.04,0.97]	0.9478	1.0000	0.29 [0.13,1.05]	0.16 [0.04,0.57]	0.0485 *	0.3881
o_Bifidobacteriales	0.52 [0.02,1.07]	0.40 [0.04,0.97]	1.0000	1.0000	0.28 [0.13,1.05]	0.16 [0.04,0.57]	0.0518	0.4920
f_Bifidobacteriaceae	0.52 [0.02,1.07]	0.40 [0.04,0.97]	1.0000	1.0000	0.28 [0.13,1.05]	0.16 [0.04,0.57]	0.0518	0.5869
g_Bifidobacterium	0.52 [0.02,1.07]	0.40 [0.04,0.97]	1.0000	1.0000	0.28 [0.13,1.05]	0.16 [0.04,0.57]	0.0518	0.7218
c_Coriobacteriia	0.59 [0.24,0.89]	0.51 [0.24,0.78]	0.9311	1.0000	0.61 [0.37,1.10]	0.65 [0.33,1.08]	0.9578	1.0000
o_Coriobacteriales	0.59 [0.24,0.89]	0.51 [0.24,0.78]	0.9311	1.0000	0.61 [0.37,1.10]	0.65 [0.33,1.08]	0.9578	1.0000
f_Coriobacteriaceae	0.59 [0.24,0.89]	0.51 [0.24,0.78]	0.9311	1.0000	0.61 [0.37,1.10]	0.65 [0.33,1.08]	0.9578	0.9881
g_Collinsella	0.12 [0.02,0.30]	0.12 [0.02,0.24]	0.8110	1.0000	0.12 [0.02,0.35]	0.08 [0.01,0.33]	0.5165	0.8688
g_Eggerthella	0.01 [0.00,0.03]	0.00 [0.00,0.03]	0.5986	0.9694	0.00 [0.00,0.02]	0.00 [0.00,0.02]	0.3359	0.7886
g_Enterorhabdus	0.09 [0.01,0.25]	0.12 [0.02,0.20]	0.5066	0.9600	0.12 [0.03,0.17]	0.13 [0.04,0.20]	0.8789	0.9774
g_Gordonibacter	0.00 [0.00,0.00]	0.00 [0.00,0.01]	0.0965	0.6232	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.8542	0.9640
g_Senegalimassilia	0.00 [0.00,0.02]	0.00 [0.00,0.01]	0.2546	0.8795	0.01 [0.00,0.04]	0.01 [0.00,0.04]	0.9721	1.0000
g_unknown_ Coriobacteriaceae	0.14 [0.00,0.32]	0.09 [0.00,0.29]	0.3684	0.8795	0.18 [0.05,0.53]	0.25 [0.05,0.54]	0.8936	0.9811
p_Bacteroidetes	29.44 [24.65,37.60]	32.30 [25.05,37.90]	0.5497	0.7067	29.33 [21.84,35.63]	29.82 [24.03,35.10]	0.4264	0.8439

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c_Bacteroidia	29.44 [24.65,37.60]	32.30 [24.88,37.90]	0.5497	0.9981	29.33 [21.84,35.63]	29.82 [24.03,35.10]	0.4264	0.7168
o_Bacteroidales	29.44 [24.65,37.60]	32.30 [24.88,37.90]	0.5497	0.9877	29.33 [21.84,35.63]	29.82 [24.03,35.10]	0.4264	0.7803
f_Bacteroidaceae	19.39 [12.51,25.91]	19.04 [14.13,27.41]	0.2325	0.8390	18.48 [9.98,23.08]	18.89 [13.18,25.01]	0.4060	0.8993
g_Bacteroides	19.39 [12.51,25.91]	19.04 [14.13,27.41]	0.2325	0.8760	18.48 [9.98,23.08]	18.89 [13.18,25.01]	0.4060	0.7920
f_BacteroidalesS24-7group	0.00 [0.00,0.02]	0.01 [0.00,0.06]	0.1866	0.8390	0.01 [0.00,0.01]	0.00 [0.00,0.01]	0.3446	0.8993
g_unknown_ BacteroidalesS24-7group	0.00 [0.00,0.02]	0.01 [0.00,0.06]	0.1866	0.8223	0.01 [0.00,0.01]	0.00 [0.00,0.01]	0.3446	0.7886
f_Porphyromonadaceae	3.37 [1.86,6.10]	4.60 [2.56,5.60]	0.2714	0.8390	4.31 [2.08,7.18]	3.10 [2.34,6.07]	0.6359	0.9008
g_Barnesiella	0.42 [0.01,1.28]	0.54 [0.01,1.33]	0.0940	0.6232	0.71 [0.07,1.12]	0.57 [0.10,1.24]	0.8541	0.9640
g_Butyricimonas	0.01 [0.00,0.29]	0.01 [0.00,0.35]	0.0209 *	0.5801	0.10 [0.00,0.33]	0.06 [0.00,0.35]	0.7087	0.9370
g_Coprobacter	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.0914	0.6232	0.00 [0.00,0.04]	0.00 [0.00,0.03]	0.6245	0.9063
g_Odoribacter	0.29 [0.14,0.44]	0.36 [0.15,0.52]	0.6877	1.0000	0.34 [0.08,0.51]	0.35 [0.10,0.65]	0.3037	0.7886
g_Parabacteroides	1.85 [0.69,4.92]	2.28 [0.99,4.48]	0.3789	0.8795	2.55 [1.08,4.93]	1.94 [0.95,3.88]	0.5941	0.9063
f_Prevotellaceae	0.03 [0.01,1.55]	0.02 [0.00,1.42]	0.0909	0.6181	0.02 [0.01,1.99]	0.03 [0.00,1.92]	0.1530	0.8993
g_Paraprevotella	0.00 [0.00,0.05]	0.00 [0.00,0.01]	0.0604	0.6232	0.01 [0.00,0.03]	0.00 [0.00,0.03]	0.9348	0.9977
g_Prevotella9	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.0995	0.6232	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.2559	0.7886
f_Rikenellaceae	3.36 [2.58,5.87]	3.70 [2.93,6.05]	0.6028	0.9728	3.62 [2.49,6.04]	4.15 [2.63,6.64]	0.0464 *	0.5869
g_Alistipes	3.25 [2.41,5.87]	3.70 [2.93,5.70]	0.6028	0.9694	3.62 [2.40,6.04]	4.15 [2.63,6.64]	0.0443 *	0.7218
p_Cyanobacteria	0.00 [0.00,0.01]	0.00 [0.00,0.03]	1.0000	1.0000	0.00 [0.00,0.10]	0.02 [0.00,0.06]	0.2625	0.8439
c_Melainabacteria	0.00 [0.00,0.01]	0.00 [0.00,0.03]	1.0000	1.0000	0.00 [0.00,0.09]	0.01 [0.00,0.06]	0.2513	0.7168

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o_Gastranaerophilales	0.00 [0.00,0.01]	0.00 [0.00,0.03]	1.0000	1.0000	0.00 [0.00,0.09]	0.01 [0.00,0.06]	0.2513	0.7803
g_unknown_ Gastranaerophilales	0.00 [0.00,0.01]	0.00 [0.00,0.03]	1.0000	1.0000	0.00 [0.00,0.09]	0.01 [0.00,0.06]	0.2513	0.7886
f_unknown_ Gastranaerophilales	0.00 [0.00,0.01]	0.00 [0.00,0.03]	1.0000	1.0000	0.00 [0.00,0.09]	0.01 [0.00,0.06]	0.2513	0.8993
p_Euryarchaeota	0.00 [0.00,0.04]	0.00 [0.00,0.14]	0.0318 *	0.1223	0.00 [0.00,0.04]	0.00 [0.00,0.09]	0.8445	0.9500
c_Methanobacteria	0.00 [0.00,0.04]	0.00 [0.00,0.14]	0.0318 *	0.2175	0.00 [0.00,0.04]	0.00 [0.00,0.09]	0.8445	1.0000
o_Methanobacteriales	0.00 [0.00,0.04]	0.00 [0.00,0.14]	0.0318 *	0.3018	0.00 [0.00,0.04]	0.00 [0.00,0.09]	0.8445	0.9597
f_Methanobacteriaceae	0.00 [0.00,0.04]	0.00 [0.00,0.14]	0.0318 *	0.5137	0.00 [0.00,0.04]	0.00 [0.00,0.09]	0.8445	0.9418
g_Methanobrevibacter	0.00 [0.00,0.04]	0.00 [0.00,0.13]	0.0244 *	0.5801	0.00 [0.00,0.04]	0.00 [0.00,0.07]	0.8240	0.9640
p_Firmicutes	66.09 [56.05,71.20]	61.64 [54.45,70.50]	0.1975	0.3554	64.58 [55.94,73.51]	65.98 [59.91,70.26]	0.3669	0.8439
c_Bacilli	0.22 [0.11,0.52]	0.24 [0.10,0.68]	1.0000	1.0000	0.23 [0.07,0.43]	0.30 [0.14,0.57]	0.3764	0.7168
o_Lactobacillales	0.22 [0.11,0.52]	0.24 [0.09,0.68]	1.0000	1.0000	0.23 [0.07,0.43]	0.30 [0.14,0.57]	0.3035	0.7803
f_Carnobacteriaceae	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.5027	0.9728	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.8400	0.9418
g_unknown_ Carnobacteriaceae	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.5027	0.9600	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.8232	0.9640
f_Lactobacillaceae	0.00 [0.00,0.02]	0.00 [0.00,0.02]	0.9091	1.0000	0.01 [0.00,0.03]	0.01 [0.00,0.06]	0.4018	0.8993
g_Lactobacillus	0.00 [0.00,0.02]	0.00 [0.00,0.02]	0.9091	1.0000	0.01 [0.00,0.03]	0.01 [0.00,0.06]	0.4018	0.7920
f_Streptococcaceae	0.20 [0.09,0.39]	0.20 [0.08,0.58]	0.7818	1.0000	0.16 [0.06,0.36]	0.27 [0.08,0.37]	0.3644	0.8993
g_Lactococcus	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.7740	1.0000	0.00 [0.00,0.01]	0.00 [0.00,0.01]	1.0000	1.0000
g_Streptococcus	0.18 [0.08,0.39]	0.19 [0.06,0.49]	0.8186	1.0000	0.11 [0.05,0.30]	0.18 [0.06,0.36]	0.3419	0.7886
c_Clostridia	62.75 [52.02,69.00]	60.30 [52.11,67.50]	0.1484	0.4098	62.61 [54.88,69.68]	62.30 [56.53,67.38]	0.3528	0.7168

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o_Clostridiales	62.75 [52.02,69.00]	60.30 [52.11,67.50]	0.1484	0.5840	62.61 [54.88,69.68]	62.30 [56.49,67.37]	0.3576	0.7803
f_Christensenellaceae	0.91 [0.37,1.53]	0.84 [0.32,2.12]	0.5452	0.9728	0.71 [0.31,2.01]	0.86 [0.36,1.96]	0.6136	0.9008
g_ChristensenellaceaeR-7group	0.87 [0.36,1.37]	0.84 [0.32,2.09]	0.4761	0.9444	0.69 [0.28,2.00]	0.84 [0.34,1.94]	0.6173	0.9063
g_unknown_ Christensenellaceae	0.02 [0.00,0.04]	0.01 [0.00,0.04]	0.6844	1.0000	0.02 [0.01,0.04]	0.01 [0.00,0.03]	0.3527	0.7919
f_Clostridiaceae1	0.04 [0.01,0.15]	0.04 [0.00,0.10]	0.3873	0.9728	0.10 [0.02,0.28]	0.08 [0.03,0.25]	0.9590	0.9881
g_Clostridiumsensustricto1	0.04 [0.01,0.15]	0.04 [0.00,0.10]	0.3873	0.8795	0.10 [0.02,0.28]	0.08 [0.03,0.23]	0.9918	1.0000
f_ClostridialesvadinBB60group	0.04 [0.01,0.18]	0.06 [0.02,0.36]	0.1646	0.8390	0.07 [0.02,0.31]	0.06 [0.02,0.26]	0.5025	0.8993
g_unknown_ ClostridialesvadinBB60group	0.04 [0.01,0.18]	0.06 [0.02,0.36]	0.1646	0.7616	0.07 [0.02,0.31]	0.06 [0.02,0.26]	0.5025	0.8667
f_Defluviitaleaceae	0.01 [0.00,0.04]	0.01 [0.00,0.03]	0.6280	0.9728	0.01 [0.00,0.02]	0.01 [0.00,0.03]	1.0000	1.0000
g_DefluviitaleaceaeUCG-011	0.01 [0.00,0.04]	0.01 [0.00,0.03]	0.6280	0.9773	0.01 [0.00,0.02]	0.01 [0.00,0.03]	1.0000	1.0000
f_FamilyXIII	0.14 [0.10,0.27]	0.12 [0.07,0.20]	0.2700	0.8390	0.13 [0.06,0.21]	0.15 [0.08,0.23]	0.3910	0.8993
g_FamilyXIIIAD3011group	0.08 [0.04,0.15]	0.07 [0.03,0.14]	0.7014	1.0000	0.07 [0.02,0.14]	0.08 [0.04,0.16]	0.6806	0.9310
g_FamilyXIIIUCG-001	0.06 [0.01,0.09]	0.03 [0.02,0.06]	0.0447 *	0.6232	0.04 [0.01,0.07]	0.04 [0.01,0.09]	0.4049	0.7920
g_[Eubacterium]brachygroup	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.9849	1.0000	0.00 [0.00,0.01]	0.00 [0.00,0.02]	0.1423	0.7761
f_Lachnospiraceae	29.12 [25.39,33.94]	28.03 [23.12,31.17]	0.0599	0.5137	30.95 [26.18,34.17]	29.23 [24.09,33.65]	0.5602	0.9008
g_Anaerosporobacter	0.00 [0.00,0.04]	0.00 [0.00,0.03]	0.1241	0.7032	0.00 [0.00,0.03]	0.00 [0.00,0.05]	0.7757	0.9640
g_Anaerostipes	0.86 [0.45,2.00]	1.14 [0.65,1.43]	0.2928	0.8795	1.01 [0.41,1.90]	0.36 [0.18,0.73]	0.0002 *	0.0194 *
g_Blautia	3.43 [2.53,4.93]	2.92 [2.23,4.73]	0.2146	0.8510	3.22 [2.61,4.05]	3.86 [2.21,4.74]	0.3862	0.7920
g_Butyrivibrio	0.00 [0.00,0.00]	0.00 [0.00,0.01]	0.3765	0.8795	0.00 [0.00,0.01]	0.00 [0.00,0.00]	0.1217	0.7623

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g_Coprococcus1	0.22 [0.15,0.33]	0.26 [0.17,0.37]	0.5556	0.9694	0.26 [0.15,0.34]	0.23 [0.12,0.33]	0.4970	0.8667
g_Coprococcus2	0.01 [0.00,0.51]	0.02 [0.00,0.87]	0.8044	1.0000	0.04 [0.01,1.66]	0.07 [0.01,2.41]	0.3394	0.7886
g_Eisenbergiella	0.12 [0.08,0.22]	0.11 [0.05,0.23]	0.6019	0.9694	0.07 [0.03,0.15]	0.08 [0.05,0.16]	0.3300	0.7886
g_Fusicatenibacter	1.52 [0.82,2.42]	1.39 [0.92,2.02]	0.1975	0.8223	1.45 [0.82,2.13]	1.37 [0.90,2.14]	0.8512	0.9640
g_Lachnoclostridium	1.43 [0.89,2.42]	1.17 [0.94,1.91]	0.0396 *	0.6232	1.38 [1.03,1.89]	1.48 [0.94,1.92]	0.9929	1.0000
g_Lachnospira	1.49 [0.53,2.21]	1.00 [0.51,1.73]	0.2004	0.8223	1.11 [0.55,1.80]	0.78 [0.39,1.62]	0.5735	0.9063
g_LachnospiraceaeFCS020group	0.17 [0.08,0.27]	0.14 [0.11,0.22]	0.5667	0.9694	0.15 [0.10,0.24]	0.17 [0.09,0.26]	0.9404	0.9977
g_LachnospiraceaeFE2018group	0.01 [0.00,0.04]	0.01 [0.00,0.03]	0.7263	1.0000	0.00 [0.00,0.02]	0.00 [0.00,0.02]	0.4292	0.8115
g_LachnospiraceaeNC2004group	0.08 [0.02,0.64]	0.19 [0.04,0.51]	0.7648	1.0000	0.14 [0.03,0.64]	0.35 [0.07,0.89]	0.2347	0.7886
g_LachnospiraceaeND3007group	0.43 [0.28,0.55]	0.49 [0.25,0.71]	0.0990	0.6232	0.47 [0.24,0.78]	0.59 [0.31,0.95]	0.1184	0.7623
g_LachnospiraceaeNK4A136group	0.84 [0.50,1.26]	0.98 [0.51,1.23]	0.3747	0.8795	0.95 [0.56,1.94]	1.12 [0.45,1.90]	0.9715	1.0000
g_LachnospiraceaeUCG-001	0.21 [0.04,0.93]	0.30 [0.07,1.01]	0.7613	1.0000	0.52 [0.23,0.90]	0.54 [0.20,1.06]	0.4433	0.8115
g_LachnospiraceaeUCG-004	0.32 [0.16,0.55]	0.44 [0.18,0.61]	0.0846	0.6232	0.44 [0.25,0.72]	0.32 [0.13,0.61]	0.1141	0.7623
g_LachnospiraceaeUCG-008	0.01 [0.00,0.03]	0.03 [0.01,0.04]	0.1322	0.7153	0.02 [0.01,0.04]	0.03 [0.01,0.06]	0.0126 *	0.6182
g_LachnospiraceaeUCG-010	0.01 [0.00,0.02]	0.01 [0.00,0.02]	0.3266	0.8795	0.01 [0.00,0.02]	0.02 [0.00,0.04]	0.0305 *	0.7218
g_Marvinbryantia	0.04 [0.02,0.12]	0.05 [0.01,0.15]	0.8863	1.0000	0.08 [0.03,0.14]	0.08 [0.02,0.19]	0.2177	0.7886
g_Oribacterium	0.00 [0.00,0.01]	0.01 [0.00,0.02]	0.0649	0.6232	0.01 [0.00,0.02]	0.01 [0.00,0.02]	0.3627	0.7920
g_Pseudobutyrivibrio	0.00 [0.00,0.04]	0.00 [0.00,0.03]	0.9749	1.0000	0.00 [0.00,0.03]	0.00 [0.00,0.05]	0.1957	0.7761
g_Roseburia	0.72 [0.32,1.51]	1.01 [0.46,1.95]	0.3339	0.8795	1.40 [0.71,2.77]	0.92 [0.29,2.26]	0.2679	0.7886

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g_Sellimonas	0.00 [0.00,0.03]	0.00 [0.00,0.03]	0.0946	0.6232	0.00 [0.00,0.03]	0.01 [0.00,0.03]	0.0546	0.7218
g_Tyzzerella	0.00 [0.00,0.00]	0.00 [0.00,0.01]	1.0000	1.0000	0.00 [0.00,0.01]	0.00 [0.00,0.00]	0.0704	0.7620
g_Tyzzerella3	0.01 [0.00,0.06]	0.00 [0.00,0.07]	0.2962	0.8795	0.01 [0.00,0.12]	0.00 [0.00,0.07]	0.0397 *	0.7218
g_Tyzzerella4	0.38 [0.17,0.66]	0.37 [0.27,0.51]	0.8777	1.0000	0.27 [0.16,0.38]	0.26 [0.09,0.47]	0.6104	0.9063
g_[Eubacterium]halliigroup	1.22 [0.75,1.92]	1.33 [0.77,1.71]	0.9436	1.0000	1.20 [0.65,2.03]	1.09 [0.87,1.66]	0.8217	0.9640
g_[Eubacterium]rectalegroup	4.72 [1.97,9.47]	3.65 [2.01,7.94]	0.4140	0.8891	4.81 [2.53,8.05]	3.55 [1.70,5.96]	0.1445	0.7761
g_[Eubacterium]ruminantiumgroup	0.00 [0.00,0.00]	0.00 [0.00,0.00]	0.1597	0.7616	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.3988	0.7920
g_[Eubacterium]ventriosumgroup	0.21 [0.08,0.47]	0.27 [0.12,0.53]	0.1664	0.7616	0.24 [0.15,0.53]	0.22 [0.13,0.61]	0.8986	0.9811
g_[Eubacterium]xylanophilumgroup	0.10 [0.00,0.50]	0.08 [0.00,0.43]	0.5455	0.9694	0.13 [0.00,0.42]	0.14 [0.01,0.41]	0.1790	0.7761
g_[Ruminococcus]torquesgroup	1.21 [0.81,2.37]	1.23 [0.67,1.89]	0.9562	1.0000	1.25 [0.83,1.60]	1.12 [0.72,1.71]	0.4368	0.8115
g_unknown_ Lachnospiraceae	2.59 [1.79,3.98]	2.46 [1.48,4.69]	0.8382	1.0000	2.87 [1.54,4.15]	3.07 [1.92,5.24]	0.4580	0.8258
f_Peptococcaceae	0.06 [0.00,0.14]	0.05 [0.01,0.16]	0.5480	0.9728	0.04 [0.00,0.08]	0.04 [0.00,0.11]	0.5419	0.9008
g_Peptococcus	0.00 [0.00,0.03]	0.00 [0.00,0.02]	0.3127	0.8795	0.00 [0.00,0.03]	0.00 [0.00,0.02]	0.8360	0.9640
g_unknown_ Peptococcaceae	0.02 [0.00,0.08]	0.04 [0.00,0.13]	0.8611	1.0000	0.01 [0.00,0.07]	0.01 [0.00,0.08]	0.3713	0.7920
f_Peptostreptococcaceae	0.06 [0.02,0.18]	0.11 [0.01,0.25]	0.6497	0.9728	0.09 [0.02,0.28]	0.11 [0.03,0.67]	0.1891	0.8993
g_Intestinibacter	0.02 [0.01,0.08]	0.03 [0.00,0.10]	0.6573	1.0000	0.03 [0.00,0.14]	0.07 [0.01,0.24]	0.0940	0.7623
g_Peptoclostridium	0.04 [0.00,0.11]	0.06 [0.00,0.13]	0.9191	1.0000	0.03 [0.00,0.12]	0.03 [0.01,0.23]	0.8035	0.9640
f_Ruminococcaceae	29.97 [24.13,34.80]	29.32 [24.31,33.82]	0.6581	0.9728	30.08 [25.48,34.81]	30.80 [27.54,34.88]	0.8462	0.9418
g_Anaerofilum	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.1562	0.7616	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.5210	0.8688

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g_Anaerotruncus	0.15 [0.07,0.33]	0.19 [0.07,0.38]	0.4510	0.9254	0.17 [0.08,0.39]	0.22 [0.14,0.61]	0.1184	0.7623
g_Butyricicoccus	0.48 [0.32,0.83]	0.44 [0.25,0.72]	0.4184	0.8891	0.56 [0.36,0.91]	0.69 [0.35,0.88]	0.6616	0.9262
g_CandidatusSoleaferrea	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.0589	0.6232	0.00 [0.00,0.01]	0.00 [0.00,0.02]	0.0208 *	0.6182
g_Faecalibacterium	13.89 [9.89,17.95]	13.44 [7.22,17.49]	0.0743	0.6232	14.57 [10.77,18.05]	13.37 [10.27,16.78]	0.1334	0.7761
g_Flavonifractor	0.03 [0.02,0.08]	0.03 [0.01,0.08]	0.3989	0.8795	0.03 [0.01,0.06]	0.01 [0.01,0.05]	0.0204 *	0.6182
g_Hydrogenoanaerobacterium	0.00 [0.00,0.01]	0.00 [0.00,0.01]	1.0000	1.0000	0.00 [0.00,0.00]	0.00 [0.00,0.01]	0.6727	0.9308
g_Intestinimonas	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.7486	1.0000	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.3204	0.7886
g_Oscillibacter	0.01 [0.00,0.03]	0.02 [0.00,0.03]	0.8197	1.0000	0.01 [0.00,0.03]	0.01 [0.00,0.04]	0.6137	0.9063
g_Oscillospira	0.00 [0.00,0.00]	0.00 [0.00,0.00]	0.3162	0.8795	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.1208	0.7623
g_Ruminiclostridium	0.00 [0.00,0.00]	0.00 [0.00,0.01]	0.0021 *	0.2442	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.1936	0.7761
g_Ruminiclostridium5	0.23 [0.13,0.49]	0.36 [0.18,0.75]	0.0072 *	0.4298	0.37 [0.14,0.74]	0.40 [0.19,0.63]	0.4344	0.8115
g_Ruminiclostridium6	0.01 [0.00,0.65]	0.02 [0.00,0.50]	0.4300	0.8978	0.01 [0.00,0.28]	0.01 [0.00,0.39]	0.2636	0.7886
g_Ruminiclostridium9	0.14 [0.07,0.20]	0.10 [0.07,0.18]	0.9124	1.0000	0.13 [0.07,0.23]	0.12 [0.07,0.19]	0.4052	0.7920
g_RuminococcaceaeNK4A214group	0.25 [0.11,0.40]	0.19 [0.08,0.57]	0.5901	0.9694	0.33 [0.06,1.04]	0.50 [0.08,1.41]	0.1751	0.7761
g_RuminococcaceaeUCG-002	1.09 [0.57,1.75]	1.14 [0.59,1.93]	0.8250	1.0000	1.09 [0.42,1.60]	0.97 [0.64,2.14]	0.0961	0.7623
g_RuminococcaceaeUCG-003	0.25 [0.12,0.50]	0.23 [0.13,0.34]	0.3716	0.8795	0.20 [0.09,0.38]	0.27 [0.15,0.51]	0.1619	0.7761
g_RuminococcaceaeUCG-004	0.03 [0.00,0.19]	0.03 [0.00,0.15]	0.3380	0.8795	0.01 [0.00,0.15]	0.01 [0.00,0.16]	0.3355	0.7886
g_RuminococcaceaeUCG-005	0.12 [0.03,0.39]	0.15 [0.03,0.39]	0.3794	0.8795	0.17 [0.06,0.43]	0.23 [0.05,0.50]	0.1892	0.7761
g_RuminococcaceaeUCG-009	0.01 [0.00,0.02]	0.00 [0.00,0.02]	0.9826	1.0000	0.01 [0.00,0.01]	0.01 [0.00,0.02]	0.9474	0.9977

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g_RuminococcaceaeUCG-010	0.11 [0.04,0.42]	0.17 [0.02,0.43]	0.7375	1.0000	0.15 [0.01,0.45]	0.17 [0.03,0.44]	0.7891	0.9640
g_RuminococcaceaeUCG-013	0.51 [0.21,0.78]	0.58 [0.22,1.21]	0.3109	0.8795	0.45 [0.21,0.98]	0.46 [0.21,1.03]	0.8302	0.9640
g_RuminococcaceaeUCG-014	0.71 [0.03,1.81]	0.83 [0.02,1.70]	0.8241	1.0000	0.61 [0.08,2.74]	1.17 [0.14,2.21]	0.6451	0.9250
g_Ruminococcus1	0.38 [0.02,0.69]	0.26 [0.01,0.82]	0.5083	0.9600	0.37 [0.04,1.10]	0.55 [0.08,1.52]	0.3441	0.7886
g_Subdoligranulum	2.22 [1.58,3.73]	1.94 [1.18,3.37]	0.2356	0.8760	1.76 [1.09,3.62]	1.97 [1.18,3.33]	0.7084	0.9370
g_[Eubacterium]coprostanoligenesgroup	0.58 [0.38,1.11]	0.55 [0.25,1.26]	0.8442	1.0000	0.82 [0.43,1.60]	0.90 [0.47,1.63]	0.3215	0.7886
g_unknown_ Ruminococcaceae	2.85 [1.09,4.30]	3.06 [1.17,5.36]	0.1152	0.6852	2.66 [1.74,4.25]	2.74 [1.74,5.54]	0.2797	0.7886
c_Erysipelotrichia	0.39 [0.24,0.58]	0.40 [0.24,0.69]	0.8122	1.0000	0.48 [0.30,0.82]	0.80 [0.35,1.16]	0.0456 *	0.3881
o_Erysipelotrichales	0.39 [0.24,0.58]	0.40 [0.24,0.69]	0.8122	1.0000	0.48 [0.30,0.82]	0.80 [0.35,1.16]	0.0456 *	0.4920
f_Erysipelotrichaceae	0.39 [0.24,0.58]	0.40 [0.24,0.69]	0.8122	1.0000	0.48 [0.30,0.82]	0.80 [0.35,1.16]	0.0456 *	0.5869
g_Erysipelatoclostridium	0.01 [0.00,0.03]	0.01 [0.00,0.04]	0.5520	0.9694	0.01 [0.00,0.02]	0.01 [0.00,0.03]	0.5723	0.9063
g_ErysipelotrichaceaeUCG-003	0.15 [0.01,0.44]	0.19 [0.02,0.41]	0.7653	1.0000	0.25 [0.11,0.44]	0.31 [0.12,0.74]	0.1607	0.7761
g_Faecalitalea	0.00 [0.00,0.00]	0.00 [0.00,0.01]	0.2430	0.8764	0.00 [0.00,0.01]	0.00 [0.00,0.03]	0.5749	0.9063
g_Holdemanella	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.8736	1.0000	0.00 [0.00,0.10]	0.00 [0.00,0.09]	0.1837	0.7761
g_Holdemania	0.01 [0.00,0.02]	0.01 [0.00,0.03]	0.5507	0.9694	0.00 [0.00,0.01]	0.01 [0.00,0.02]	0.2307	0.7886
g_Turicibacter	0.01 [0.00,0.09]	0.01 [0.00,0.07]	0.3281	0.8795	0.02 [0.00,0.12]	0.03 [0.01,0.14]	0.7757	0.9640
g_[Clostridium]innocuumgroup	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.8854	1.0000	0.00 [0.00,0.01]	0.00 [0.00,0.02]	0.9429	0.9977
g_unknown_ Erysipelotrichaceae	0.00 [0.00,0.00]	0.00 [0.00,0.01]	0.4680	0.9440	0.00 [0.00,0.00]	0.00 [0.00,0.01]	0.1094	0.7623
c_Negativicutes	1.35 [0.72,2.55]	1.33 [0.61,2.68]	0.4989	0.9981	1.20 [0.50,2.59]	0.89 [0.50,2.30]	0.3042	0.7168

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o_Selenomonadales	1.35 [0.72,2.55]	1.33 [0.61,2.68]	0.4989	0.9877	1.20 [0.50,2.59]	0.89 [0.50,2.30]	0.3042	0.7803
f_Acidaminococcaceae	0.13 [0.00,0.55]	0.19 [0.01,0.57]	0.9002	1.0000	0.31 [0.00,0.56]	0.23 [0.00,0.49]	0.2293	0.8993
g_Phascolarctobacterium	0.13 [0.00,0.55]	0.19 [0.00,0.53]	0.6738	1.0000	0.15 [0.00,0.44]	0.21 [0.00,0.44]	0.6607	0.9262
f_Veillonellaceae	0.93 [0.02,2.55]	0.78 [0.06,2.36]	0.9249	1.0000	0.52 [0.03,2.58]	0.75 [0.02,1.89]	0.3145	0.8993
g_Dialister	0.60 [0.00,2.06]	0.61 [0.00,1.74]	0.5924	0.9694	0.04 [0.01,2.44]	0.02 [0.00,1.84]	0.5840	0.9063
g_Veillonella	0.01 [0.00,0.04]	0.01 [0.00,0.04]	0.2722	0.8795	0.01 [0.00,0.04]	0.00 [0.00,0.02]	0.0660	0.7620
p_Lentisphaerae	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.1537	0.3458	0.00 [0.00,0.02]	0.00 [0.00,0.02]	1.0000	1.0000
c_Lentisphaeria	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.1537	0.4098	0.00 [0.00,0.02]	0.00 [0.00,0.02]	1.0000	1.0000
o_Victivallales	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.1537	0.5840	0.00 [0.00,0.02]	0.00 [0.00,0.02]	1.0000	1.0000
p_Proteobacteria	2.31 [1.26,4.78]	2.46 [1.78,4.89]	0.3035	0.4552	2.73 [0.75,3.86]	1.72 [0.96,5.08]	0.7863	0.9500
c_Alphaproteobacteria	0.04 [0.00,0.62]	0.04 [0.00,0.63]	0.6238	0.9981	0.04 [0.01,0.77]	0.14 [0.01,0.50]	0.8289	1.0000
o_Rhodospirillales	0.04 [0.00,0.62]	0.04 [0.00,0.63]	0.6238	0.9877	0.04 [0.00,0.77]	0.14 [0.01,0.50]	0.8587	0.9597
f_Rhodospirillaceae	0.04 [0.00,0.62]	0.04 [0.00,0.63]	0.6238	0.9728	0.04 [0.00,0.77]	0.14 [0.01,0.50]	0.8587	0.9418
g_unknown_ Rhodospirillaceae	0.04 [0.00,0.62]	0.04 [0.00,0.63]	0.6238	0.9773	0.04 [0.00,0.77]	0.14 [0.01,0.50]	0.8587	0.9640
c_Betaproteobacteria	1.20 [0.34,2.41]	1.29 [0.39,2.13]	0.9624	1.0000	1.19 [0.39,2.27]	0.75 [0.39,1.66]	0.4061	0.7168
o_Burkholderiales	1.20 [0.34,2.41]	1.29 [0.39,2.13]	0.9624	1.0000	1.19 [0.39,2.27]	0.75 [0.39,1.66]	0.4061	0.7803
f_Alcaligenaceae	1.20 [0.32,2.30]	1.26 [0.37,2.12]	0.9499	1.0000	1.19 [0.39,2.26]	0.74 [0.39,1.65]	0.4318	0.8993
g_Parasutterella	0.07 [0.00,0.35]	0.06 [0.01,0.33]	0.6324	0.9773	0.05 [0.01,0.22]	0.11 [0.02,0.33]	0.3424	0.7886
g_Sutterella	0.59 [0.01,1.41]	0.52 [0.02,1.63]	0.9828	1.0000	0.44 [0.02,1.47]	0.38 [0.01,1.31]	0.6891	0.9319

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f_Oxalobacteraceae	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.9773	1.0000	0.00 [0.00,0.02]	0.00 [0.00,0.02]	0.7772	0.9418
g_Oxalobacter	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.9720	1.0000	0.00 [0.00,0.01]	0.00 [0.00,0.01]	0.8585	0.9640
c_Deltaproteobacteria	0.15 [0.02,0.51]	0.18 [0.04,0.39]	0.5813	0.9981	0.19 [0.04,0.39]	0.20 [0.04,0.55]	0.4754	0.7168
o_Desulfovibrionales	0.15 [0.02,0.51]	0.18 [0.04,0.39]	0.5813	0.9877	0.19 [0.04,0.39]	0.20 [0.04,0.55]	0.4754	0.7803
f_Desulfovibrionaceae	0.15 [0.02,0.51]	0.18 [0.04,0.39]	0.5813	0.9728	0.19 [0.04,0.39]	0.20 [0.04,0.55]	0.4754	0.8993
g_Bilophila	0.09 [0.01,0.22]	0.12 [0.02,0.25]	0.9044	1.0000	0.12 [0.02,0.18]	0.10 [0.03,0.22]	0.3108	0.7886
g_Desulfovibrio	0.00 [0.00,0.05]	0.00 [0.00,0.06]	0.7543	1.0000	0.01 [0.00,0.16]	0.01 [0.00,0.31]	0.5256	0.8688
c_Gammaproteobacteria	0.12 [0.05,0.18]	0.15 [0.03,0.46]	0.0769	0.3074	0.09 [0.03,0.44]	0.16 [0.02,0.55]	0.9478	1.0000
o_Enterobacteriales	0.04 [0.00,0.10]	0.02 [0.01,0.16]	0.2226	0.7048	0.02 [0.00,0.28]	0.02 [0.01,0.16]	0.7982	0.9597
f_Enterobacteriaceae	0.04 [0.00,0.10]	0.02 [0.01,0.16]	0.2226	0.8390	0.02 [0.00,0.28]	0.02 [0.01,0.16]	0.7982	0.9418
g_Escherichia-Shigella	0.03 [0.00,0.10]	0.02 [0.00,0.15]	0.2756	0.8795	0.01 [0.00,0.05]	0.01 [0.00,0.10]	0.7949	0.9640
o_Pasteurellales	0.03 [0.01,0.09]	0.04 [0.00,0.14]	0.4046	0.9877	0.03 [0.00,0.07]	0.03 [0.00,0.18]	0.3424	0.7803
f_Pasteurellaceae	0.03 [0.01,0.09]	0.04 [0.00,0.14]	0.4046	0.9728	0.03 [0.00,0.07]	0.03 [0.00,0.18]	0.3424	0.8993
g_Haemophilus	0.03 [0.01,0.08]	0.04 [0.00,0.14]	0.3991	0.8795	0.03 [0.00,0.07]	0.03 [0.00,0.18]	0.3363	0.7886
p_Tenericutes	0.03 [0.00,0.25]	0.09 [0.00,0.31]	0.0408 *	0.1223	0.07 [0.01,1.24]	0.04 [0.00,0.59]	0.1699	0.8439
c_Mollicutes	0.03 [0.00,0.25]	0.09 [0.00,0.31]	0.0408 *	0.2175	0.07 [0.01,1.24]	0.04 [0.00,0.59]	0.1699	0.7168
o_Anaeroplasmatales	0.00 [0.00,0.00]	0.00 [0.00,0.00]	0.5248	0.9877	0.00 [0.00,0.45]	0.00 [0.00,0.09]	0.3066	0.7803
f_Anaeroplasmataceae	0.00 [0.00,0.00]	0.00 [0.00,0.00]	0.5248	0.9728	0.00 [0.00,0.45]	0.00 [0.00,0.09]	0.3066	0.8993
g_Anaeroplasma	0.00 [0.00,0.00]	0.00 [0.00,0.00]	0.5248	0.9694	0.00 [0.00,0.45]	0.00 [0.00,0.09]	0.3066	0.7886

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o_MollicutesRF9	0.00 [0.00,0.05]	0.01 [0.00,0.17]	0.0604	0.3827	0.02 [0.00,0.08]	0.00 [0.00,0.09]	0.6145	0.8982
g_unknown_ MollicutesRF9	0.00 [0.00,0.05]	0.01 [0.00,0.17]	0.0604	0.6232	0.02 [0.00,0.08]	0.00 [0.00,0.09]	0.6145	0.9063
f_unknown_ MollicutesRF9	0.00 [0.00,0.05]	0.01 [0.00,0.17]	0.0604	0.5137	0.02 [0.00,0.08]	0.00 [0.00,0.09]	0.6145	0.9008
o_NB1-n	0.00 [0.00,0.05]	0.00 [0.00,0.14]	0.9826	1.0000	0.00 [0.00,0.04]	0.00 [0.00,0.10]	0.8503	0.9597
g_unknown_ NB1-n	0.00 [0.00,0.05]	0.00 [0.00,0.14]	0.9826	1.0000	0.00 [0.00,0.04]	0.00 [0.00,0.10]	0.8503	0.9640
f_unknown_ NB1-n	0.00 [0.00,0.05]	0.00 [0.00,0.14]	0.9826	1.0000	0.00 [0.00,0.04]	0.00 [0.00,0.10]	0.8503	0.9418
p_Verrucomicrobia	0.01 [0.00,0.08]	0.04 [0.00,0.20]	0.0051 *	0.0459 *	0.02 [0.00,0.18]	0.07 [0.00,0.22]	0.5628	0.8442
c_Verrucomicrobiae	0.01 [0.00,0.08]	0.04 [0.00,0.18]	0.0114 *	0.1829	0.02 [0.00,0.16]	0.07 [0.00,0.22]	0.4928	0.7168
o_Verrucomicrobiales	0.01 [0.00,0.08]	0.04 [0.00,0.18]	0.0114 *	0.2172	0.02 [0.00,0.16]	0.07 [0.00,0.22]	0.4928	0.7803
f_Verrucomicrobiaceae	0.01 [0.00,0.08]	0.04 [0.00,0.18]	0.0114 *	0.3887	0.02 [0.00,0.16]	0.07 [0.00,0.22]	0.4928	0.8993
g_Akkermansia	0.01 [0.00,0.08]	0.04 [0.00,0.18]	0.0114 *	0.4535	0.02 [0.00,0.16]	0.07 [0.00,0.22]	0.4928	0.8667

[1]Bacterial abundances (%) are presented as median [25th ,75th percentile]. FODMAP, fermentable oligosaccharides, disaccharides, monosaccharides, and polyols; LFD, low FODMAP diet.

[2]Within-group analysis: Wilcoxon signed-rank test between baseline and follow-up.

[3]Benjamini-Hochberg adjusted *P* values. Adjustments were performed separately for each taxonomic level.

*: $P < 0.05$.

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SUPPLEMENTAL TABLE 7 Correlation between within-subject Bray-Curtis distances and changes in GSRS-IBS scores[1]

Within-subject Bray-Curtis	GSRS-IBS					
	Total	**Pain**	**Bloating**	**Constipation**	**Diarrhea**	**Satiety**
All	*P*= 0.4717 Rho= -0.09	*P*= 0.1388 Rho= -0.18	*P*= 0.1120 Rho= -0.19	*P*= 0.5431 Rho= -0.07	*P*= 0.7021 Rho= 0.05	*P*= 0.7591 Rho= 0.04
Control group	*P*= 0.2395 Rho= 0.20	*P*= 0.3556 Rho= -0.16	*P*= 0.4597 Rho= 0.13	*P*= 0.0144 * Rho= 0.40	*P*= 0.8960 Rho= -0.02	*P*= 0.0991 Rho= 0.28
LFD group	*P*= 0.3319 Rho= 0.17	*P*= 0.3244 Rho= 0.18	*P*= 0.8222 Rho= 0.04	*P*= 0.0618 Rho= -0.33	*P*= 0.0099 * Rho= 0.44	*P*= 0.2512 Rho= 0.21

[1]Spearman's rank correlation coefficients (Rho) with corresponding *P* values are presented for the total population (*n* = 69) and separately for the control (*n* = 36) and low FODMAP diet (LFD, *n* = 33) group. Change is defined as 4-week follow-up minus baseline value. Within-subject Bray-Curtis distance is defined as the Bray-Curtis distance of the baseline and follow-up sample from the same participant. Positive correlation indicates that smaller within-subject Bray-Curtis distances are associated with reduced GSRS-IBS scores, while negative correlation indicates that larger within-subject Bray-Curtis distances are associated with reduced GSRS-IBS scores. FODMAP, fermentable oligosaccharides, disaccharides, monosaccharides, and polyols; GSRS-IBS, Gastrointestinal Symptom Rating Scale IBS version; IBS, irritable bowel syndrome; LFD, low FODMAP diet.

*: *P* < 0.05.

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SUPPLEMENTAL TABLE 8 Correlation between changes in bacterial abundances and changes in GSRS-IBS scores (total population)[1]

Taxon	GSRS-IBS					
	Total	**Pain**	**Bloating**	**Constipation**	**Diarrhea**	**Satiety**
g_Anaerostipes	*P*= 0.0346 * Rho= 0.26	*P*= 0.1078 Rho= 0.20	*P*= 0.0107 * Rho= 0.31	*P*= 0.6108 Rho= 0.06	*P*= 0.8095 Rho= 0.03	*P*= 0.0132 * Rho= 0.30
c_Actinobacteria	*P*= 0.0367 * Rho= 0.25	*P*= 0.1353 Rho= 0.18	*P*= 0.0427 * Rho= 0.25	*P*= 0.2970 Rho= -0.13	*P*= 0.0166 * Rho= 0.29	*P*= 0.3346 Rho= 0.12
g_Flavonifractor	*P*= 0.2972 Rho= 0.13	*P*= 0.5765 Rho= 0.07	*P*= 0.9828 Rho= -0.00	*P*= 0.0992 Rho= 0.20	*P*= 0.5083 Rho= 0.08	*P*= 0.6687 Rho= 0.05
g_Tyzzerella3	*P*= 0.8799 Rho= -0.02	*P*= 0.8504 Rho= -0.02	*P*= 0.6257 Rho= 0.06	*P*= 0.3564 Rho= -0.11	*P*= 0.9658 Rho= -0.01	*P*= 0.3588 Rho= 0.11
c_Erysipelotrichia[2]	*P*= 0.7761 Rho= -0.04	*P*= 0.3968 Rho= -0.10	*P*= 0.0865 Rho= -0.21	*P*= 0.5929 Rho= -0.07	*P*= 0.7559 Rho= 0.04	*P*= 0.5470 Rho= 0.07
g_Alistipes	*P*= 0.2307 Rho= -0.15	*P*= 0.2900 Rho= -0.13	*P*= 0.6669 Rho= -0.05	*P*= 0.6441 Rho= 0.06	*P*= 0.1748 Rho= -0.17	*P*= 0.7528 Rho= -0.04
f_Rikenellaceae	*P*= 0.2119 Rho= -0.15	*P*= 0.2758 Rho= -0.13	*P*= 0.6432 Rho= -0.06	*P*= 0.6354 Rho= 0.06	*P*= 0.1614 Rho= -0.17	*P*= 0.7188 Rho= -0.04
g_Lachnospiraceae UCG-008	*P*= 0.1479 Rho= -0.18	*P*= 0.1613 Rho= -0.17	*P*= 0.3843 Rho= -0.11	*P*= 0.5095 Rho= -0.08	*P*= 0.6403 Rho= -0.06	*P*= 0.7631 Rho= -0.04
g_CandidatusSoleaferrea	*P*= 0.1146 Rho= -0.19	*P*= 0.3708 Rho= -0.11	*P*= 0.0232 * Rho= -0.27	*P*= 0.4200 Rho= -0.10	*P*= 0.1940 Rho= -0.16	*P*= 0.6797 Rho= -0.05
g_Lachnospiraceae UCG-010	*P*= 0.0380 * Rho= -0.25	*P*= 0.6044 Rho= -0.06	*P*= 0.0028 * Rho= -0.36	*P*= 0.9655 Rho= -0.01	*P*= 0.1082 Rho= -0.20	*P*= 0.1885 Rho= -0.16

[1]Spearman's rank correlation coefficients (Rho) with corresponding *P* values are presented for the total population (n = 69). Change is defined as 4-week follow-up minus baseline value. Only the taxa which changed or tended to change in abundance from baseline to follow-up in the low FODMAP diet group are included (see Table 2). Positive correlation indicates that reduced bacterial abundances are associated with reduced GSRS-IBS scores, while negative correlation indicates that increased abundances are associated with reduced GSRS-IBS scores. FODMAP, fermentable oligosaccharides, disaccharides, monosaccharides, and polyols; GSRS-IBS, Gastrointestinal Symptom Rating Scale IBS version; IBS, irritable bowel syndrome.

[2]Completely dominated by family *Erysipelotrichaceae*.

*: $P < 0.05$.

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SUPPLEMENTAL TABLE 9 Correlation between changes in bacterial abundances and changes in GSRS-IBS scores (control group only)[1]

Taxon	GSRS-IBS					
	Total	**Pain**	**Bloating**	**Constipation**	**Diarrhea**	**Satiety**
g_Anaerostipes	*P*= 0.3952 Rho= 0.15	*P*= 0.8981 Rho= 0.02	*P*= 0.7063 Rho= 0.07	*P*= 0.9326 Rho= -0.02	*P*= 0.5810 Rho= -0.10	*P*= 0.0659 Rho= 0.31
c_Actinobacteria	*P*= 0.0691 Rho= 0.31	*P*= 0.5946 Rho= 0.09	*P*= 0.0912 Rho= 0.29	*P*= 0.6364 Rho= -0.08	*P*= 0.2631 Rho= 0.19	*P*= 0.0948 Rho= 0.28
g_Flavonifractor	*P*= 0.2304 Rho= 0.21	*P*= 0.7040 Rho= 0.07	*P*= 0.3566 Rho= 0.16	*P*= 0.1331 Rho= 0.26	*P*= 0.6641 Rho= 0.08	*P*= 0.8876 Rho= -0.02
g_Tyzzerella3	*P*= 0.9096 Rho= -0.02	*P*= 0.6125 Rho= -0.09	*P*= 0.7024 Rho= -0.07	*P*= 0.5584 Rho= -0.10	*P*= 0.8388 Rho= 0.04	*P*= 0.2700 Rho= 0.19
c_Erysipelotrichia[2]	*P*= 0.5948 Rho= 0.09	*P*= 0.5357 Rho= 0.11	*P*= 0.4381 Rho= -0.13	*P*= 0.3950 Rho= 0.15	*P*= 0.7973 Rho= 0.04	*P*= 0.5037 Rho= 0.12
g_Alistipes	*P*= 0.6995 Rho= -0.07	*P*= 0.3262 Rho= -0.17	*P*= 0.9311 Rho= -0.02	*P*= 0.0766 Rho= 0.30	*P*= 0.3887 Rho= -0.15	*P*= 0.4040 Rho= -0.14
f_Rikenellaceae	*P*= 0.6846 Rho= -0.07	*P*= 0.3205 Rho= -0.17	*P*= 0.9085 Rho= -0.02	*P*= 0.0766 Rho= 0.30	*P*= 0.3828 Rho= -0.15	*P*= 0.3937 Rho= -0.15
g_Lachnospiraceae UCG-008	*P*= 0.3214 Rho= -0.17	*P*= 0.2783 Rho= -0.19	*P*= 0.9888 Rho= -0.00	*P*= 0.7922 Rho= -0.05	*P*= 0.1677 Rho= -0.24	*P*= 0.8439 Rho= 0.03
g_CandidatusSoleaferrea	*P*= 0.9744 Rho= -0.01	*P*= 0.7195 Rho= 0.06	*P*= 0.6632 Rho= -0.08	*P*= 0.0435 * Rho= 0.34	*P*= 0.1558 Rho= -0.24	*P*= 0.5936 Rho= 0.09
g_Lachnospiraceae UCG-010	*P*= 0.9541 Rho= 0.01	*P*= 0.2197 Rho= 0.21	*P*= 0.8030 Rho= 0.04	*P*= 0.7715 Rho= -0.05	*P*= 0.6759 Rho= 0.07	*P*= 0.6872 Rho= 0.07

[1]Spearman's rank correlation coefficients (Rho) with corresponding *P* values are presented for the control group (*n* = 36). Change is defined as 4-week follow-up minus baseline value. Only the taxa which changed or tended to change in abundance from baseline to follow-up in the low FODMAP diet group are included (see Table 2). Positive correlation indicates that reduced bacterial abundances are associated with reduced GSRS-IBS scores, while negative correlation indicates that increased abundances are associated with reduced GSRS-IBS scores. FODMAP, fermentable oligosaccharides, disaccharides, monosaccharides, and polyols; GSRS-IBS, Gastrointestinal Symptom Rating Scale IBS version; IBS, irritable bowel syndrome.

[2]Completely dominated by family *Erysipelotrichaceae*.

*: $P < 0.05$.

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SUPPLEMENTAL TABLE 10 Correlation between change in bacterial abundance and change in GSRS-IBS score (LFD group only)[1]

Taxon	GSRS-IBS					
	Total	**Pain**	**Bloating**	**Constipation**	**Diarrhea**	**Satiety**
g_Anaerostipes	*P*= 0.4097 Rho= 0.15	*P*= 0.5544 Rho= 0.11	*P*= 0.1230 Rho= 0.27	*P*= 0.4173 Rho= -0.15	*P*= 0.5894 Rho= 0.10	*P*= 0.9578 Rho= -0.01
c_Actinobacteria	*P*= 0.4358 Rho= 0.14	*P*= 0.3352 Rho= 0.17	*P*= 0.6055 Rho= 0.09	*P*= 0.1536 Rho= -0.25	*P*= 0.0519 Rho= 0.34	*P*= 0.3442 Rho= -0.17
g_Flavonifractor	*P*= 0.8862 Rho= 0.03	*P*= 0.9154 Rho= 0.02	*P*= 0.0944 Rho= -0.30	*P*= 0.5888 Rho= 0.10	*P*= 0.7916 Rho= 0.05	*P*= 0.7276 Rho= 0.06
g_Tyzzerella3	*P*= 0.6735 Rho= -0.08	*P*= 0.9877 Rho= -0.00	*P*= 0.5140 Rho= 0.12	*P*= 0.3934 Rho= -0.15	*P*= 0.7828 Rho= -0.05	*P*= 0.9762 Rho= 0.01
c_Erysipelotrichia[2]	*P*= 0.5006 Rho= 0.12	*P*= 0.7702 Rho= -0.05	*P*= 0.8366 Rho= -0.04	*P*= 0.6775 Rho= -0.08	*P*= 0.2413 Rho= 0.21	*P*= 0.1854 Rho= 0.24
g_Alistipes	*P*= 0.4342 Rho= -0.14	*P*= 0.6403 Rho= -0.08	*P*= 0.9822 Rho= 0.00	*P*= 0.3172 Rho= -0.18	*P*= 0.4032 Rho= -0.15	*P*= 0.8730 Rho= 0.03
f_Rikenellaceae	*P*= 0.4045 Rho= -0.15	*P*= 0.6006 Rho= -0.10	*P*= 0.9970 Rho= -0.00	*P*= 0.3154 Rho= -0.18	*P*= 0.3848 Rho= -0.16	*P*= 0.8812 Rho= 0.03
g_Lachnospiraceae UCG-008	*P*= 0.9195 Rho= -0.02	*P*= 0.7320 Rho= -0.06	*P*= 0.8848 Rho= -0.03	*P*= 0.6715 Rho= -0.08	*P*= 0.3976 Rho= 0.15	*P*= 0.8389 Rho= 0.04
g_CandidatusSoleaferrea	*P*= 0.9805 Rho= 0.00	*P*= 0.8178 Rho= 0.04	*P*= 0.6329 Rho= -0.09	*P*= 0.0982 Rho= -0.29	*P*= 0.5514 Rho= 0.11	*P*= 0.4182 Rho= 0.15
g_Lachnospiraceae UCG-010	*P*= 0.0952 Rho= -0.30	*P*= 0.5020 Rho= -0.12	*P*= 0.0041 * Rho= -0.49	*P*= 0.4190 Rho= 0.15	*P*= 0.1539 Rho= -0.25	*P*= 0.2699 Rho= -0.20

[1]Spearman's rank correlation coefficients (Rho) with corresponding *P* values are presented for the LFD group (*n* = 33). Change is defined as 4-week follow-up minus baseline value. Only the taxa which changed or tended to change in abundance from baseline to follow-up in the low FODMAP diet group are included (see Table 2). Positive correlation indicates that reduced bacterial abundances are associated with reduced GSRS-IBS scores, while negative correlation indicates that increased abundances are associated with reduced GSRS-IBS scores. FODMAP, fermentable oligosaccharides, disaccharides, monosaccharides, and polyols; GSRS-IBS, Gastrointestinal Symptom Rating Scale IBS version; IBS, irritable bowel syndrome; LFD, low FODMAP diet.

[2]Completely dominated by family *Erysipelotrichaceae*.

*: $P < 0.05$.

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SUPPLEMENTAL TABLE 11 Correlation between changes in propionic and valeric acid fecal concentrations and changes in GSRS-IBS scores[1]

GSRS-IBS	Propionic acid, mmol/kg feces			Valeric acid, mmol/kg feces		
	All	**Control group**	**LFD group**	**All**	**Control group**	**LFD group**
Total	*P*= 0.7288 Rho= -0.04	*P*= 0.5369 Rho= -0.11	*P*= 0.8764 Rho= -0.03	*P*= 0.8880 Rho= 0.02	*P*= 0.5515 Rho= 0.11	*P*= 0.2370 Rho= -0.22
Pain	*P*= 0.6898 Rho= -0.05	*P*= 0.3411 Rho= -0.17	*P*= 0.8148 Rho= 0.04	*P*= 0.4217 Rho= -0.10	*P*= 0.6409 Rho= -0.08	*P*= 0.3208 Rho= -0.18
Bloating	*P*= 0.6045 Rho= 0.07	*P*= 0.5445 Rho= 0.11	*P*= 0.9361 Rho= -0.02	*P*= 0.2817 Rho= 0.13	*P*= 0.2298 Rho= 0.21	*P*= 0.5311 Rho= -0.12
Constipation	*P*= 0.4154 Rho= 0.10	*P*= 0.4127 Rho= 0.15	*P*= 0.9225 Rho= -0.02	*P*= 0.4026 Rho= 0.11	*P*= 0.5693 Rho= 0.10	*P*= 0.8246 Rho= -0.04
Diarrhea	*P*= 0.7195 Rho= -0.05	*P*= 0.5293 Rho= -0.11	*P*= 0.9936 Rho= 0.00	*P*= 0.9893 Rho= 0.00	*P*= 0.4343 Rho= 0.14	*P*= 0.5003 Rho= -0.12
Satiety	*P*= 0.0438 * Rho= -0.25	*P*= 0.0761 Rho= -0.31	*P*= 0.0908 Rho= -0.30	*P*= 0.9011 Rho= -0.02	*P*= 0.8014 Rho= -0.05	*P*= 0.3497 Rho= -0.17

[1]Spearman's rank correlation coefficients (Rho) with corresponding *P* values are presented for the total population ($n = 66$) and separately for the control ($n = 34$) and low FODMAP diet ($n = 32$) group. Change is defined as 4-week follow-up minus baseline value. Positive correlation indicates that reduced SCFA concentrations are associated with reduced GSRS-IBS scores, while negative correlation indicates that increased SCFA concentrations are associated with reduced GSRS-IBS scores. FODMAP, fermentable oligosaccharides, disaccharides, monosaccharides, and polyols; GSRS-IBS, Gastrointestinal Symptom Rating Scale IBS version; IBS, irritable bowel syndrome; LFD, low FODMAP diet.

*: $P < 0.05$.

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SUPPLEMENTAL TABLE 12 Correlation between fecal relative abundances of bacterial taxa (%) at baseline and changes in GSRS-IBS total scores[1]

Taxon	All	Control group	LFD group
f_Bacteroidaceae[2]	P= 0.0417 * Rho= 0.25	P= 0.7252 Rho= 0.06	P= 0.0148 * Rho= 0.42
f_Clostridiaceae1	P= 0.8110 Rho= 0.03	P= 0.0492 * Rho= 0.33	P= 0.8269 Rho= -0.04
g_Clostridiumsensustricto1	P= 0.8110 Rho= 0.03	P= 0.0492 * Rho= 0.33	P= 0.8269 Rho= -0.04
g_LachnospiraceaeND3007group	P= 0.1429 Rho= -0.18	P= 0.3469 Rho= 0.16	P= 0.0464 * Rho= -0.35
f_Ruminococcaceae	P= 0.2113 Rho= -0.15	P= 0.6503 Rho= 0.08	P= 0.0372 * Rho= -0.36
g_RuminococcaceaeUCG-010	P= 0.4018 Rho= 0.10	P= 0.6432 Rho= -0.08	P= 0.0288 * Rho= 0.38
g_RuminococcaceaeUCG-013	P= 0.3801 Rho= -0.11	P= 0.6076 Rho= 0.09	P= 0.0287 * Rho= -0.38
g_ErysipelotrichaceaeUCG-003	P= 0.0150 * Rho= -0.29	P= 0.1323 Rho= -0.26	P= 0.2935 Rho= -0.19
c_Negativicutes[3]	P= 0.0303 * Rho= 0.26	P= 0.4322 Rho= 0.14	P= 0.0412 * Rho= 0.36
f_Veillonellaceae	P= 0.1313 Rho= 0.18	P= 0.9714 Rho= -0.01	P= 0.0114 * Rho= 0.43
c_Gammaproteobacteria	P= 0.1045 Rho= 0.20	P= 0.4949 Rho= 0.12	P= 0.0169 * Rho= 0.41
o_Enterobacteriales[4]	P= 0.0507 Rho= 0.24	P= 0.1564 Rho= 0.24	P= 0.0337 * Rho= 0.37
g_Escherichia-Shigella	P= 0.0187 * Rho= 0.28	P= 0.0888 Rho= 0.29	P= 0.1329 Rho= 0.27

[1]Spearman's rank correlation coefficients (Rho) with corresponding *P* values are presented for the total population ($n = 69$) and separately for the control ($n = 36$) and LFD ($n = 33$) group. Change is defined as 4-week follow-up minus baseline value. Only taxa with unadjusted $P < 0.05$ are reported. No correlations were significant after Benjamini-Hochberg (BH) adjustment (performed separately for each taxonomic level). Positive correlation indicates that lower baseline values are associated with reduced GSRS-IBS scores, while negative correlation indicates that higher baseline values are associated with reduced GSRS-IBS scores. FODMAP, fermentable oligosaccharides, disaccharides, monosaccharides, and polyols; GSRS-IBS, Gastrointestinal Symptom Rating Scale IBS version; IBS, irritable bowel syndrome; LFD, low FODMAP diet.

[2]Completely dominated by genus *Bacteroides*.

[3]Completely dominated by order Selenomonadales.

[4]Completely dominated by family *Enterobacteriaceae*.

*: Unadjusted $P < 0.05$, Benjamini-Hochberg adjusted $P > 0.05$.

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SUPPLEMENTAL TABLE 13 Correlation between fecal SCFAs concentrations ("conc", mmol/kg feces) and percentages ("%", of total SCFAs) at baseline and changes in GSRS-IBS total scores[1]

SCFA	All	Control group	LFD group
Total SCFAs, conc	*P*= 0.9313 Rho= -0.01	*P*= 0.4647 Rho= -0.13	*P*= 0.7194 Rho= 0.07
Acetic acid, conc	*P*= 0.9138 Rho= 0.01	*P*= 0.5438 Rho= -0.11	*P*= 0.5378 Rho= 0.11
Butyric acid, conc	*P*= 0.8718 Rho= -0.02	*P*= 0.3523 Rho= -0.16	*P*= 0.4428 Rho= 0.14
Propionic acid, conc	*P*= 0.7874 Rho= -0.03	*P*= 0.4043 Rho= -0.15	*P*= 0.8681 Rho= 0.03
Iso-valeric acid, conc	*P*= 0.9030 Rho= 0.02	*P*= 0.2760 Rho= -0.19	*P*= 0.6662 Rho= 0.08
Valeric acid, conc	*P*= 0.4468 Rho= 0.10	*P*= 0.6694 Rho= -0.08	*P*= 0.0671 Rho= 0.33
Iso-butyric acid, conc	*P*= 0.8964 Rho= -0.02	*P*= 0.1678 Rho= -0.24	*P*= 0.8528 Rho= 0.03
Caproic acid, conc	*P*= 0.0285 * Rho= 0.27	*P*= 0.6439 Rho= 0.08	*P*= 0.0327 * Rho= 0.38
Acetic acid, %	*P*= 0.7053 Rho= 0.05	*P*= 0.4754 Rho= 0.13	*P*= 0.6589 Rho= 0.08
Butyric acid, %	*P*= 0.4420 Rho= -0.10	*P*= 0.3686 Rho= -0.16	*P*= 0.7571 Rho= -0.06
Propionic acid, %	*P*= 0.6505 Rho= -0.06	*P*= 0.5641 Rho= 0.10	*P*= 0.1866 Rho= -0.24
Iso-valeric acid, %	*P*= 0.9793 Rho= 0.00	*P*= 0.7117 Rho= -0.07	*P*= 0.5289 Rho= -0.12
Valeric acid, %	*P*= 0.4581 Rho= 0.09	*P*= 0.3457 Rho= 0.17	*P*= 0.4545 Rho= 0.14
Iso-butyric acid, %	*P*= 0.9703 Rho= 0.00	*P*= 0.7479 Rho= -0.06	*P*= 0.3025 Rho= -0.19
Caproic acid, %	*P*= 0.0264 * Rho= 0.27	*P*= 0.4815 Rho= 0.12	*P*= 0.0337 * Rho= 0.38

[1]Spearman's rank correlation coefficients (Rho) with corresponding *P* values are presented for the total population ($n = 66$) and separately for the control ($n = 34$) and low FODMAP diet ($n = 32$) group. Change is defined as 4-wk follow-up minus baseline value. Positive correlation indicates that lower baseline SCFA are associated with reduced GSRS-IBS scores, while negative correlation indicates that higher baseline SCFA are associated with reduced GSRS-IBS scores. FODMAP, fermentable oligosaccharides, disaccharides, monosaccharides, and polyols; GSRS-IBS, Gastrointestinal Symptom Rating Scale IBS version; IBS, irritable bowel syndrome; LFD, low FODMAP diet.

*: $P < 0.05$.

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References

1. Yu Y, Lee C, Kim J, Hwang S. Group-specific primer and probe sets to detect methanogenic communities using quantitative real-time polymerase chain reaction. Biotechnol Bioeng 2005;89(6):670-9. doi: 10.1002/bit.20347.
2. Avershina E, Lundgard K, Sekelja M, Dotterud C, Storro O, Oien T, Johnsen R, Rudi K. Transition from infant- to adult-like gut microbiota. Environ Microbiol 2016;18(7):2226-36. doi: 10.1111/1462-2920.13248.