Supplemental Table 1. Comparison of the 50 types of gut microbiota genera present in more than 10% of participants.

OTU.ID	Lactulose[1]	Placebo[1]	effect size[2]	expected p value[3]	expected q value[4]
d__Bacteria|p__Bacillota_C|c__Negativicutes|o__Veillonellales|f__Megasphaeraceae|g__Megasphaera_A_38685	-1.94	-2.36	-0.13	0.06	0.94
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Oscillospirales|f__Ruminococcaceae|g__Hominimerdicol	-1.98	-2.35	-0.10	0.14	0.95
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Lachnospirales|f__Lachnospiraceae|g__Blautia_A_14178	5.07	5.28	0.10	0.37	0.95
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Lachnospirales|f__Lachnospiraceae|g__Fusicatenibacter	3.10	3.31	0.04	0.65	0.95
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Lachnospirales|f__Lachnospiraceae|g__Agathobacter_16	2.04	2.38	0.03	0.84	0.96
d__Bacteria|p__Bacteroidota|c__Bacteroidia|o__Bacteroidales|f__Bacteroidaceae|g__Phocaeicola_A	4.79	4.98	0.06	0.57	0.95
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Oscillospirales|f__Ruminococcaceae|g__Faecalibacterium	4.87	4.92	0.03	0.78	0.95
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Oscillospirales|f__Ruminococcaceae|g__Gemmiger_A_7	2.66	2.85	-0.03	0.81	0.96
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Lachnospirales|f__Lachnospiraceae|g__Ruminococcus_B	0.74	0.92	0.05	0.57	0.95
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Lachnospirales|f__Lachnospiraceae|g__Mediterraneibacte	2.63	2.83	0.05	0.60	0.95
d__Bacteria|p__Actinomycetota|c__Coriobacteriia|o__Coriobacteriales|f__Coriobacteriaceae|g__Collinsella	1.83	1.83	-0.01	0.82	0.96
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Lachnospirales|f__Lachnospiraceae|g__Anaerostipes	2.26	2.53	0.04	0.72	0.95
d__Bacteria|p__Bacteroidota|c__Bacteroidia|o__Bacteroidales|f__Tannerellaceae|g__Parabacteroides_B_862066	2.30	2.56	0.06	0.49	0.95
d__Bacteria|p__Bacillota_I|c__Bacilli_A|o__Erysipelotrichales|f__Coprobacillaceae|g__Faecalibacillus	-1.25	-1.17	0.05	0.58	0.95
d__Bacteria|p__Bacteroidota|c__Bacteroidia|o__Bacteroidales|f__Bacteroidaceae|g__Bacteroides_H_857956	4.38	4.05	-0.04	0.73	0.95
d__Bacteria|p__Bacillota_I|c__Bacilli_A|o__Erysipelotrichales|f__Erysipelotrichaceae|g__Holdemanella	-1.25	-1.04	0.03	0.61	0.95
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Lachnospirales|f__Lachnospiraceae|g__Anaerobutyricum	2.20	2.35	0.06	0.53	0.95
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Lachnospirales|f__Lachnospiraceae|__	2.35	2.32	0.01	0.79	0.95
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Peptostreptococcales|f__Peptostreptococcaceae_256921|_	-0.04	0.38	0.12	0.26	0.95
d__Bacteria|p__Bacillota_I|c__Bacilli_A|o__Lactobacillales|f__Streptococcaceae|g__Streptococcus	1.21	1.60	0.05	0.59	0.95
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Lachnospirales|f__Lachnospiraceae|g__Enterocloster	1.53	1.39	-0.07	0.42	0.95
d__Bacteria|p__Bacteroidota|c__Bacteroidia|o__Bacteroidales|f__Muribaculaceae|g__Paramuribaculum	-2.33	-2.29	-0.04	0.56	0.95
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Oscillospirales|f__Acutalibacteraceae|g__Hominenteromi	-1.39	-1.53	-0.05	0.56	0.95
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Oscillospirales|f__Butyricicoccaceae|g__Agathobaculum	0.36	0.65	0.08	0.43	0.95
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Lachnospirales|f__Lachnospiraceae|g__Acetatifactor	-1.47	-1.64	-0.04	0.54	0.95
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Oscillospirales|f__Ruminococcaceae|g__Ruminococcus_(	-3.03	-3.25	-0.04	0.66	0.95
d__Bacteria|p__Fusobacteriota|c__Fusobacteriia|o__Fusobacteriales|f__Fusobacteriaceae|g__Cetobacterium_A	-8.18	-7.91	0.04	0.55	0.95
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Peptostreptococcales|f__Peptostreptococcaceae_256921|g	-1.82	-1.39	0.06	0.43	0.95
d__Bacteria|p__Bacillota_C|c__Negativicutes|o__Acidaminococcales|f__Acidaminococcaceae|g__URXU01	-2.49	-3.05	-0.06	0.49	0.95
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Lachnospirales|f__Lachnospiraceae|g__Dorea_A	2.18	2.35	0.04	0.68	0.95
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Lachnospirales|f__Lachnospiraceae|g__Faecalimonas	-2.77	-2.87	-0.02	0.83	0.96
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Lachnospirales|f__Lachnospiraceae|g__Blautia_A_14178	-1.35	-0.87	0.03	0.63	0.95
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Clostridiales|f__Clostridiaceae_222000|g__Clostridium_T	-1.94	-1.69	0.05	0.59	0.95
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__UBA1381|f__UBA1381|g__Hominilimicola	0.21	0.07	-0.00	0.85	0.96
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Oscillospirales|f__Oscillospiraceae_88309|g__Lawsoniba	0.10	0.32	0.02	0.76	0.95
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Lachnospirales|f__Lachnospiraceae|g__	0.04	0.04	0.05	0.63	0.95
d__Bacteria|p__Bacillota_I|c__Bacilli_A|o__Erysipelotrichales|f__Coprobacillaceae|g__Catenibacterium	-1.75	-1.62	0.01	0.81	0.96
d__Bacteria|p__Bacillota_C|c__Negativicutes|o__Veillonellales|f__Dialisteraceae|g__Dialister_37762	-2.07	-2.15	-0.03	0.76	0.96
d__Bacteria|p__Fusobacteriota|c__Fusobacteriia|o__Fusobacteriales|f__Fusobacteriaceae|g__Fusobacterium_A	-1.61	-1.64	0.00	0.90	0.96
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Lachnospirales|f__Lachnospiraceae|g__Lachnospira	1.18	1.25	0.06	0.51	0.95
d__Bacteria|p__Bacillota_C|c__Negativicutes|__|__|__	-1.82	-1.89	-0.03	0.74	0.96
d__Bacteria|__|__|__|__|__	-0.68	-0.42	0.03	0.76	0.96
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Lachnospirales|f__Lachnospiraceae|g__Eubacterium_G_1	0.22	0.47	0.04	0.59	0.95
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Lachnospirales|f__Lachnospiraceae|g__Bariatricus	-2.23	-2.50	-0.00	0.88	0.96
d__Bacteria|p__Pseudomonadota|c__Gammaproteobacteria|o__Burkholderiales|f__Burkholderiaceae_A_595427|g__Sutt	0.97	1.20	0.02	0.76	0.95
d__Bacteria|p__Bacillota_C|c__Negativicutes|o__Selenomonadales|f__Selenomonadaceae_42771|g__Mitsuokella	-3.12	-3.32	-0.01	0.81	0.96
d__Bacteria|p__Bacteroidota|c__Bacteroidia|o__Bacteroidales|f__Bacteroidaceae|g__Alloprevotella	-2.25	-2.33	-0.01	0.74	0.96
d__Bacteria|p__Bacteroidota|c__Bacteroidia|o__Bacteroidales|f__Bacteroidaceae|g__Prevotella	1.87	1.62	-0.01	0.92	0.97
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Lachnospirales|f__Lachnospiraceae|g__Roseburia_A_16	0.19	0.65	0.05	0.60	0.95
d__Bacteria|p__Bacillota_A_368345|c__Clostridia_258483|o__Oscillospirales|f__Acutalibacteraceae|g__Ruminococcus_	0.49	0.26	-0.02	0.74	0.96

1 CLR-transformed values

2 The negative effect size indicates taxa that were more abundant in lactulose intake than in placebo intake, and the positive values indicate taxa that were less abundant.

3 Expected p value of Wilcoxon rank test. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$

4 Expected Benjamini-Hochberg corrected p value of Wilcoxon test. * $q < 0.05$, ** $q < 0.01$, *** $q < 0.001$