

Supplementary Table 1: Retain-resolved taxa full taxonomy and resolution reference key with population statistics. Each taxa is assigned a unique ID (spID) To differentiate unique ASVs or agglomerated genus-level taxa with equivalent taxonomy..

Taxa Full Label	Level	Statistics		spID	Taxonomy					
		Prevalence	Mean Relative Abundance		Kingdom	Phylum	Class	Order	Family	Genus
sp1_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Blautia	ASV	0.96	5.2E-02	sp1	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
sp2_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Agathobacter	ASV	0.79	3.9E-02	sp2	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Agathobacter
sp3_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.78	2.1E-02	sp3	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
sp4_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Faecalibacterium	ASV	0.75	1.7E-02	sp4	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
sp5_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Faecalibacterium	ASV	0.75	1.5E-02	sp5	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
sp6_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_NA	ASV	0.80	1.6E-02	sp6	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	NA
sp7_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.50	9.6E-03	sp7	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
sp8_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.56	1.2E-02	sp8	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
sp9_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.49	1.1E-02	sp9	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
sp10_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Fusicatenibacter	ASV	0.85	1.3E-02	sp10	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Fusicatenibacter
sp11_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Subdoligranulum	ASV	0.72	1.7E-02	sp11	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Subdoligranulum
sp12_Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Escherichia/Shigella	ASV	0.71	9.4E-03	sp12	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Escherichia/Shigella
sp13_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Dorea	ASV	0.65	1.3E-02	sp13	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea
sp14_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.39	1.1E-02	sp14	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
sp15_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Faecalibacterium	ASV	0.56	9.9E-03	sp15	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
sp16_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Anaerostipes	ASV	0.87	1.0E-02	sp16	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Anaerostipes
sp17_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.29	1.1E-02	sp17	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
sp18_Bacteria_Verrucomicrobia_Verrucomicrobiae_Verrucomicrobiales_Akkermansia_Akkermansia	ASV	0.30	9.6E-03	sp18	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Akkermansia	Akkermansia
sp19_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Blautia	ASV	0.78	7.9E-03	sp19	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
sp20_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Subdoligranulum	ASV	0.66	9.2E-03	sp20	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Subdoligranulum
sp21_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Blautia	ASV	0.77	9.8E-03	sp21	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
sp22_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Blautia	ASV	0.83	9.0E-03	sp22	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
sp23_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Tannerellaceae_Parabacteroides	ASV	0.66	7.5E-03	sp23	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Tannerellaceae	Parabacteroides
sp24_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_NA	ASV	0.63	9.3E-03	sp24	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	NA
sp25_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Faecalibacterium	ASV	0.48	9.1E-03	sp25	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
sp26_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Roseburia	ASV	0.34	7.5E-03	sp26	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
sp27_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Rikenellaceae_Alistipes	ASV	0.52	5.6E-03	sp27	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
sp28_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_NA	ASV	0.53	7.0E-03	sp28	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	NA
sp29_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_NA	ASV	0.74	6.8E-03	sp29	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	NA
sp30_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Rikenellaceae_Alistipes	ASV	0.59	6.4E-03	sp30	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
sp31_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.66	6.7E-03	sp31	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
sp32_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.27	4.0E-03	sp32	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
sp33_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcus_2	ASV	0.23	5.6E-03	sp33	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus_2
sp34_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Blautia	ASV	0.53	6.7E-03	sp34	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
sp35_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.30	6.2E-03	sp35	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
sp36_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.45	4.3E-03	sp36	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
sp37_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_UCG-003	ASV	0.44	6.1E-03	sp37	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Erysipelotrichaceae_UCG-003
sp38_Bacteria_Firmicutes_Negativicutes_Selenomonadales_Veillonellaceae_Dialister	ASV	0.41	5.1E-03	sp38	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Dialister
sp39_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcus_2	ASV	0.21	5.9E-03	sp39	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus_2
sp40_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_NA	ASV	0.50	4.9E-03	sp40	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	NA
sp41_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.26	4.6E-03	sp41	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
sp42_Bacteria_Firmicutes_Bacilli_Lactobacillales_Streptococcaceae_Streptococcus	ASV	0.69	3.7E-03	sp42	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
sp43_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Anaerostipes	ASV	0.68	5.3E-03	sp43	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Anaerostipes
sp44_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-002	ASV	0.39	4.3E-03	sp44	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_UCG-002
sp45_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Roseburia	ASV	0.39	4.3E-03	sp45	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
sp46_Bacteria_Firmicutes_Clostridia_Clostridiales_Peptostreptococcaceae_Intestinibacter	ASV	0.58	4.7E-03	sp46	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Intestinibacter
sp47_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_NK4A136_group	ASV	0.40	3.1E-03	sp47	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_NK4A136_group
sp48_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminiclostridium_5	ASV	0.57	4.7E-03	sp48	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminiclostridium_5
sp49_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.28	2.9E-03	sp49	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
sp50_Bacteria_Verrucomicrobia_Verrucomicrobiae_Verrucomicrobiales_Akkermansia_Akkermansia	ASV	0.17	3.8E-03	sp50	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Akkermansia	Akkermansia
sp51_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Roseburia	ASV	0.33	3.7E-03	sp51	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
sp52_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Coprococcus_3	ASV	0.42	3.4E-03	sp52	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus_3
sp53_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnoclostridium	ASV	0.72	2.7E-03	sp53	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnoclostridium
sp54_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_NA	ASV	0.45	3.7E-03	sp54	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	NA
sp55_Bacteria_Actinobacteria_Actinobacteria_Bifidobacteriales_Bifidobacteriaceae_Bifidobacterium	ASV	0.26	5.4E-03	sp55	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium
sp56_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Agathobacter	ASV	0.34	4.2E-03	sp56	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Agathobacter
sp57_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.49	3.0E-03	sp57	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
sp58_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.21	3.5E-03	sp58	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
sp59_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.42	3.0E-03	sp59	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
sp60_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.11	1.5E-03	sp60	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
sp61_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Dorea	ASV	0.68	3.6E-03	sp61	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea
sp62_Bacteria_Actinobacteria_Actinobacteria_Bifidobacteriales_Bifidobacteriaceae_Bifidobacterium	ASV	0.47	3.8E-03	sp62	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium
sp63_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcus_2	ASV	0.14	3.2E-03	sp63	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus_2
sp64_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_UCG-003	ASV	0.17	3.3E-03	sp64	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Erysipelotrichaceae_UCG-003
sp65_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.19	4.8E-03	sp65	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
sp66_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Blautia	ASV	0.46	3.4E-03	sp66	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
sp69_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.25	2.4E-03	sp69	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
sp70_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_NK4A136_group	ASV	0.51	2.4E-03	sp70	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_NK4A136_group
sp71_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Roseburia	ASV	0.58	3.6E-03	sp71	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
sp72_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.15	3.0E-03	sp72	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
sp73_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_UBA1819	ASV	0.94	3.6E-03	sp73	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	UBA1819

sp74_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_NA	ASV	0.30	2.8E-03	sp74_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_NA	ASV	0.30	2.8E-03
sp75_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-013	ASV	0.77	2.7E-03	sp75_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-013	ASV	0.77	2.7E-03
sp76_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Catenibacterium	ASV	0.13	3.5E-03	sp76_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Catenibacterium	ASV	0.13	3.5E-03
sp77_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_NA	ASV	0.18	2.8E-03	sp77_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_NA	ASV	0.18	2.8E-03
sp78_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcus_2	ASV	0.12	3.1E-03	sp78_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcus_2	ASV	0.12	3.1E-03
sp79_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-002	ASV	0.21	2.3E-03	sp79_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-002	ASV	0.21	2.3E-03
sp80_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Tannerellaceae_Parabacteroides	ASV	0.27	1.8E-03	sp80_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Tannerellaceae_Parabacteroides	ASV	0.27	1.8E-03
sp81_Bacteria_Firmicutes_Clostridia_Clostridiales_Clostridiaceae_1_Clostridium_sensu_stricto_1	ASV	0.43	2.8E-03	sp81_Bacteria_Firmicutes_Clostridia_Clostridiales_Clostridiaceae_1_Clostridium_sensu_stricto_1	ASV	0.43	2.8E-03
sp82_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_NA	ASV	0.16	2.1E-03	sp82_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_NA	ASV	0.16	2.1E-03
sp83_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Faecalibacterium	ASV	0.29	2.1E-03	sp83_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Faecalibacterium	ASV	0.29	2.1E-03
sp84_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Tyzzerella	ASV	0.26	2.1E-03	sp84_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Tyzzerella	ASV	0.26	2.1E-03
sp85_Bacteria_Firmicutes_Bacilli_Lactobacillales_Streptococcaceae_Streptococcus	ASV	0.65	1.4E-03	sp85_Bacteria_Firmicutes_Bacilli_Lactobacillales_Streptococcaceae_Streptococcus	ASV	0.65	1.4E-03
sp86_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_NK4A136_group	ASV	0.45	2.2E-03	sp86_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_NK4A136_group	ASV	0.45	2.2E-03
sp87_Bacteria_Actinobacteria_Coriobacteriia_Coriobacteriales_Coriobacteriaceae_Collinsella	ASV	0.62	3.1E-03	sp87_Bacteria_Actinobacteria_Coriobacteriia_Coriobacteriales_Coriobacteriaceae_Collinsella	ASV	0.62	3.1E-03
sp88_Bacteria_Verrucomicrobia_Verrucomicrobiae_Verrucomicrobiales_Akkermansiaceae_Akkermansia	ASV	0.13	3.7E-03	sp88_Bacteria_Verrucomicrobia_Verrucomicrobiae_Verrucomicrobiales_Akkermansiaceae_Akkermansia	ASV	0.13	3.7E-03
sp89_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.19	2.1E-03	sp89_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.19	2.1E-03
sp90_Bacteria_Firmicutes_Clostridia_Clostridiales_Peptostreptococcaceae_Romboutsia	ASV	0.61	3.1E-03	sp90_Bacteria_Firmicutes_Clostridia_Clostridiales_Peptostreptococcaceae_Romboutsia	ASV	0.61	3.1E-03
sp91_Bacteria_Actinobacteria_Actinobacteria_Bifidobacteriales_Bifidobacteriaceae_Bifidobacterium	ASV	0.30	2.8E-03	sp91_Bacteria_Actinobacteria_Actinobacteria_Bifidobacteriales_Bifidobacteriaceae_Bifidobacterium	ASV	0.30	2.8E-03
sp93_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_NA	ASV	0.36	2.5E-03	sp93_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_NA	ASV	0.36	2.5E-03
sp94_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminiclostridium_6	ASV	0.40	2.7E-03	sp94_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminiclostridium_6	ASV	0.40	2.7E-03
sp95_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.11	1.7E-03	sp95_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.11	1.7E-03
sp96_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminiclostridium_5	ASV	0.85	2.3E-03	sp96_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminiclostridium_5	ASV	0.85	2.3E-03
sp97_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.36	1.8E-03	sp97_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.36	1.8E-03
sp98_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.22	2.0E-03	sp98_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.22	2.0E-03
sp100_Bacteria_Firmicutes_Negativicutes_Selenomonadales_Acidaminococcaceae_Acidaminococcus	ASV	0.21	1.7E-03	sp100_Bacteria_Firmicutes_Negativicutes_Selenomonadales_Acidaminococcaceae_Acidaminococcus	ASV	0.21	1.7E-03
sp101_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_NK4A136_group	ASV	0.45	1.2E-03	sp101_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_NK4A136_group	ASV	0.45	1.2E-03
sp102_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_NA	ASV	0.34	2.2E-03	sp102_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_NA	ASV	0.34	2.2E-03
sp103_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Rikenellaceae_Alistipes	ASV	0.31	1.6E-03	sp103_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Rikenellaceae_Alistipes	ASV	0.31	1.6E-03
sp104_Bacteria_Firmicutes_Bacilli_Lactobacillales_Streptococcaceae_Streptococcus	ASV	0.39	1.5E-03	sp104_Bacteria_Firmicutes_Bacilli_Lactobacillales_Streptococcaceae_Streptococcus	ASV	0.39	1.5E-03
sp105_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-005	ASV	0.36	2.3E-03	sp105_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-005	ASV	0.36	2.3E-03
sp106_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Faecalibacterium	ASV	0.31	2.0E-03	sp106_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Faecalibacterium	ASV	0.31	2.0E-03
sp107_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-002	ASV	0.27	1.5E-03	sp107_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-002	ASV	0.27	1.5E-03
sp109_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Faecalitalea	ASV	0.36	2.2E-03	sp109_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Faecalitalea	ASV	0.36	2.2E-03
sp110_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Erysipelatoclostridium	ASV	0.58	1.5E-03	sp110_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Erysipelatoclostridium	ASV	0.58	1.5E-03
sp111_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcus_1	ASV	0.21	1.2E-03	sp111_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcus_1	ASV	0.21	1.2E-03
sp112_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_NK4A214_group	ASV	0.33	1.6E-03	sp112_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_NK4A214_group	ASV	0.33	1.6E-03
sp114_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.26	1.6E-03	sp114_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.26	1.6E-03
sp115_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-004	ASV	0.63	1.7E-03	sp115_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-004	ASV	0.63	1.7E-03
sp116_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Negativibacillus	ASV	0.36	1.5E-03	sp116_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Negativibacillus	ASV	0.36	1.5E-03
sp118_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.15	1.3E-03	sp118_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.15	1.3E-03
sp119_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Agathobacter	ASV	0.40	1.4E-03	sp119_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Agathobacter	ASV	0.40	1.4E-03
sp120_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Roseburia	ASV	0.17	1.3E-03	sp120_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Roseburia	ASV	0.17	1.3E-03
sp121_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Coprococcus_1	ASV	0.53	1.7E-03	sp121_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Coprococcus_1	ASV	0.53	1.7E-03
sp122_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnoclostridium	ASV	0.42	1.3E-03	sp122_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnoclostridium	ASV	0.42	1.3E-03
sp123_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-002	ASV	0.42	1.4E-03	sp123_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-002	ASV	0.42	1.4E-03
sp124_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnoclostridium	ASV	0.26	1.7E-03	sp124_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnoclostridium	ASV	0.26	1.7E-03
sp125_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Tannerellaceae_Parabacteroides	ASV	0.17	1.3E-03	sp125_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Tannerellaceae_Parabacteroides	ASV	0.17	1.3E-03
sp126_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_NA	ASV	0.14	1.4E-03	sp126_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_NA	ASV	0.14	1.4E-03
sp127_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-013	ASV	0.40	1.7E-03	sp127_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-013	ASV	0.40	1.7E-03
sp128_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Rikenellaceae_Alistipes	ASV	0.28	1.8E-03	sp128_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Rikenellaceae_Alistipes	ASV	0.28	1.8E-03
sp129_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnoclostridium	ASV	0.47	1.1E-03	sp129_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnoclostridium	ASV	0.47	1.1E-03
sp131_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Anaerostipes	ASV	0.50	1.8E-03	sp131_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Anaerostipes	ASV	0.50	1.8E-03
sp134_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_NA	ASV	0.36	1.2E-03	sp134_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_NA	ASV	0.36	1.2E-03
sp136_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Anaerostipes	ASV	0.31	2.1E-03	sp136_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Anaerostipes	ASV	0.31	2.1E-03
sp137_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Oscillibacter	ASV	0.70	1.5E-03	sp137_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Oscillibacter	ASV	0.70	1.5E-03
sp139_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospira	ASV	0.41	1.2E-03	sp139_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospira	ASV	0.41	1.2E-03
sp140_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Turcibacter	ASV	0.44	1.5E-03	sp140_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Turcibacter	ASV	0.44	1.5E-03
sp141_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.16	2.0E-03	sp141_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.16	2.0E-03
sp142_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Blautia	ASV	0.18	1.3E-03	sp142_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Blautia	ASV	0.18	1.3E-03
sp146_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Butyricicoccus	ASV	0.58	1.4E-03	sp146_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Butyricicoccus	ASV	0.58	1.4E-03
sp149_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Flavonifractor	ASV	0.68	1.4E-03	sp149_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Flavonifractor	ASV	0.68	1.4E-03
sp150_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnoclostridium	ASV	0.20	1.2E-03	sp150_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnoclostridium	ASV	0.20	1.2E-03
sp152_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Blautia	ASV	0.20	1.6E-03	sp152_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Blautia	ASV	0.20	1.6E-03
sp153_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Tannerellaceae_Parabacteroides	ASV	0.17	1.1E-03	sp153_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Tannerellaceae_Parabacteroides	ASV	0.17	1.1E-03
sp154_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Blautia	ASV	0.25	1.5E-03	sp154_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Blautia	ASV	0.25	1.5E-03
sp155_Bacteria_Firmicutes_Clostridia_Clostridiales_Christensenellaceae_Christensenellaceae_R-7_group	ASV	0.15	2.0E-03	sp155_Bacteria_Firmicutes_Clostridia_Clostridiales_Christensenellaceae_Christensenellaceae_R-7_group	ASV	0.15	2.0E-03
sp156_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_NK4A214_group	ASV	0.23	1.6E-03	sp156_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_NK4A214_group	ASV	0.23	1.6E-03
sp158_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_NA	ASV	0.13	1.1E-03	sp158_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_NA	ASV	0.13	1.1E-03
sp162_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospira	ASV	0.39	1.2E-03	sp162_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospira	ASV	0.39	1.2E-03
sp163_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_NK4A214_group	ASV	0.23	1.2E-03	sp163_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_NK4A214_group	ASV	0.23	1.2E-03
sp168_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Tyzzerella	ASV	0.11	1.1E-03	sp168_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Tyzzerella	ASV	0.11	1.1E-03
sp169_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Blautia	ASV	0.24	1.2E-03	sp169_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Blautia	ASV	0.24	1.2E-03
sp171_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospira	ASV	0.37	1.2E-03	sp171_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospira	ASV	0.37	1.2E-03
sp172_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Blautia	ASV	0.47	1.2E-03	sp172_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Blautia	ASV	0.47	1.2E-03
sp173_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcus_1	ASV	0.10	1.0E-03	sp173_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcus_1	ASV	0.10	1.0E-03
sp174_Bacteria_Proteobacteria_Gammaproteobacteria_Betaproteobacteriales_Burkholderiaceae_Parautterella	ASV	0.33	1.2E-03	sp174_Bacteria_Proteobacteria_Gammaproteobacteria_Betaproteobacteriales_Burkholderiaceae_Parautterella	ASV	0.33	1.2E-03
sp175_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Roseburia	ASV	0.20	1.2E-03	sp175_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Roseburia	ASV	0.20	1.2E-03
sp177_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminiclostridium_5	ASV	0.66	1.0E-03	sp177_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminiclostridium_5	ASV	0.66	1.0E-03

sp179_Bacteria_Firmicutes_Clostridia_Clostridiales_Christensenellaceae_Christensenellaceae_R-7_group	ASV	0.41	1.0E-03	sp179_Bacteria_Firmicutes_Clostridia_Clostridiales_Christensenellaceae_Christensenellaceae_R-7_group	ASV	0.41	1.0E-03
sp180_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Roseburia	ASV	0.10	1.3E-03	sp180_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Roseburia	ASV	0.10	1.3E-03
sp185_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Rikenellaceae_Alistipes	ASV	0.11	1.1E-03	sp185_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Rikenellaceae_Alistipes	ASV	0.11	1.1E-03
sp194_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.13	1.0E-03	sp194_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	ASV	0.13	1.0E-03
sp196_Bacteria_Firmicutes_Clostridia_Clostridiales_Clostridiaceae_1_Clostridium_sensu_stricto_1	ASV	0.23	1.1E-03	sp196_Bacteria_Firmicutes_Clostridia_Clostridiales_Clostridiaceae_1_Clostridium_sensu_stricto_1	ASV	0.23	1.1E-03
sp197_Bacteria_Firmicutes_Clostridia_Clostridiales_Peptostreptococcaceae_Terrisporobacter	ASV	0.15	1.1E-03	sp197_Bacteria_Firmicutes_Clostridia_Clostridiales_Peptostreptococcaceae_Terrisporobacter	ASV	0.15	1.1E-03
sp200_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_LND3007_group	ASV	0.54	8.9E-04	sp200_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_LND3007_group	ASV	0.54	8.9E-04
sp201_Bacteria_Firmicutes_Clostridia_Clostridiales_Christensenellaceae_Christensenellaceae_R-7_group	ASV	0.14	1.0E-03	sp201_Bacteria_Firmicutes_Clostridia_Clostridiales_Christensenellaceae_Christensenellaceae_R-7_group	ASV	0.14	1.0E-03
sp208_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-002	ASV	0.15	1.2E-03	sp208_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-002	ASV	0.15	1.2E-03
sp217_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Blautia	ASV	0.15	1.3E-03	sp217_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Blautia	ASV	0.15	1.3E-03
sp221_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-002	ASV	0.10	1.1E-03	sp221_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-002	ASV	0.10	1.1E-03
sp231_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Blautia	ASV	0.11	1.0E-03	sp231_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Blautia	ASV	0.11	1.0E-03
sp236_Bacteria_Proteobacteria_Deltaproteobacteria_Desulfowibrionales_Desulfowibrionaceae_Bilophila	ASV	0.57	6.4E-04	sp236_Bacteria_Proteobacteria_Deltaproteobacteria_Desulfowibrionales_Desulfowibrionaceae_Bilophila	ASV	0.57	6.4E-04
sp240_Bacteria_Firmicutes_Clostridia_Clostridiales_Christensenellaceae_Christensenellaceae_R-7_group	ASV	0.26	1.0E-03	sp240_Bacteria_Firmicutes_Clostridia_Clostridiales_Christensenellaceae_Christensenellaceae_R-7_group	ASV	0.26	1.0E-03
sp254_Bacteria_Firmicutes_Clostridia_Clostridiales_Family_XIII_Family_XIII_AD3011_group	ASV	0.50	5.7E-04	sp254_Bacteria_Firmicutes_Clostridia_Clostridiales_Family_XIII_Family_XIII_AD3011_group	ASV	0.50	5.7E-04
sp375_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Holdemania	ASV	0.52	3.6E-04	sp375_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Holdemania	ASV	0.52	3.6E-04
sp67_Bacteria_Firmicutes_Bacilli_Lactobacillales_Streptococcaceae_Streptococcus	genus	0.79	8.2E-03	sp67_Bacteria_Firmicutes_Bacilli_Lactobacillales_Streptococcaceae_Streptococcus	genus	0.79	8.2E-03
sp68_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	genus	0.95	4.0E-02	sp68_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Bacteroidaceae_Bacteroides	genus	0.95	4.0E-02
sp108_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Holdemania	genus	0.15	3.6E-03	sp108_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Holdemania	genus	0.15	3.6E-03
sp132_Bacteria_Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae_Lactobacillus	genus	0.39	1.7E-03	sp132_Bacteria_Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae_Lactobacillus	genus	0.39	1.7E-03
sp135_Bacteria_Proteobacteria_Gammaproteobacteria_Betaproteobacteriales_Burkholderiaceae_Parasutterella	genus	0.39	1.4E-03	sp135_Bacteria_Proteobacteria_Gammaproteobacteria_Betaproteobacteriales_Burkholderiaceae_Parasutterella	genus	0.39	1.4E-03
sp145_Bacteria_Firmicutes_Bacilli_Lactobacillales_Enterococcaceae_Enterococcus	genus	0.18	3.4E-04	sp145_Bacteria_Firmicutes_Bacilli_Lactobacillales_Enterococcaceae_Enterococcus	genus	0.18	3.4E-04
sp148_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Rikenellaceae_Alistipes	genus	0.73	6.5E-03	sp148_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Rikenellaceae_Alistipes	genus	0.73	6.5E-03
sp151_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Catenibacterium	genus	0.13	2.5E-03	sp151_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Catenibacterium	genus	0.13	2.5E-03
sp161_Bacteria_Firmicutes_Clostridia_Clostridiales_Christensenellaceae_Christensenellaceae_R-7_group	genus	0.61	8.7E-03	sp161_Bacteria_Firmicutes_Clostridia_Clostridiales_Christensenellaceae_Christensenellaceae_R-7_group	genus	0.61	8.7E-03
sp165_Bacteria_Firmicutes_Negativicutes_Selenomonadales_Veillonellaceae_Dialister	genus	0.39	3.0E-03	sp165_Bacteria_Firmicutes_Negativicutes_Selenomonadales_Veillonellaceae_Dialister	genus	0.39	3.0E-03
sp166_Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Klebsiella	genus	0.17	2.9E-03	sp166_Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Klebsiella	genus	0.17	2.9E-03
sp170_Bacteria_Firmicutes_Negativicutes_Selenomonadales_Acidaminocaccaceae_Phascolarctobacterium	genus	0.51	1.7E-03	sp170_Bacteria_Firmicutes_Negativicutes_Selenomonadales_Acidaminocaccaceae_Phascolarctobacterium	genus	0.51	1.7E-03
sp176_Bacteria_Fusobacteria_Fusobacterii_Fusobacteriales_Fusobacteriaceae_Fusobacterium	genus	0.17	2.5E-03	sp176_Bacteria_Fusobacteria_Fusobacterii_Fusobacteriales_Fusobacteriaceae_Fusobacterium	genus	0.17	2.5E-03
sp178_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_NA	genus	0.99	2.0E-02	sp178_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_NA	genus	0.99	2.0E-02
sp182_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_UCG-001	genus	0.47	1.3E-03	sp182_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_UCG-001	genus	0.47	1.3E-03
sp183_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_CAG-56	genus	0.34	1.1E-03	sp183_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_CAG-56	genus	0.34	1.1E-03
sp187_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Erysipelatoclostridium	genus	0.72	1.6E-03	sp187_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Erysipelatoclostridium	genus	0.72	1.6E-03
sp189_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Roseburia	genus	0.73	4.5E-03	sp189_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Roseburia	genus	0.73	4.5E-03
sp190_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Blautia	genus	0.93	1.3E-02	sp190_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Blautia	genus	0.93	1.3E-02
sp191_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Prevotellaceae_Prevotella_9	genus	0.20	7.8E-03	sp191_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Prevotellaceae_Prevotella_9	genus	0.20	7.8E-03
sp193_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-014	genus	0.42	7.0E-03	sp193_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-014	genus	0.42	7.0E-03
sp195_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnoclostridium	genus	0.98	9.7E-03	sp195_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnoclostridium	genus	0.98	9.7E-03
sp198_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Muribaculaceae_NA	genus	0.14	2.3E-03	sp198_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Muribaculaceae_NA	genus	0.14	2.3E-03
sp199_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminiclostridium_9	genus	0.85	1.7E-03	sp199_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminiclostridium_9	genus	0.85	1.7E-03
sp204_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcus_1	genus	0.58	4.5E-03	sp204_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcus_1	genus	0.58	4.5E-03
sp205_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Anaerostipes	genus	0.75	3.8E-03	sp205_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Anaerostipes	genus	0.75	3.8E-03
sp206_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcus_2	genus	0.19	4.0E-03	sp206_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcus_2	genus	0.19	4.0E-03
sp209_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Faecalibacterium	genus	0.60	5.9E-03	sp209_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Faecalibacterium	genus	0.60	5.9E-03
sp211_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminiclostridium_5	genus	0.80	2.8E-03	sp211_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminiclostridium_5	genus	0.80	2.8E-03
sp213_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Coprococcus_3	genus	0.43	1.8E-03	sp213_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Coprococcus_3	genus	0.43	1.8E-03
sp219_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Tannerellaceae_Parabacteroides	genus	0.73	6.5E-03	sp219_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Tannerellaceae_Parabacteroides	genus	0.73	6.5E-03
sp223_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Anaerofilum	genus	0.48	8.5E-04	sp223_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Anaerofilum	genus	0.48	8.5E-04
sp224_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-005	genus	0.74	2.4E-03	sp224_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-005	genus	0.74	2.4E-03
sp226_Bacteria_Firmicutes_Clostridia_Clostridiales_Family_XIII_Family_XIII_AD3011_group	genus	0.78	2.2E-03	sp226_Bacteria_Firmicutes_Clostridia_Clostridiales_Family_XIII_Family_XIII_AD3011_group	genus	0.78	2.2E-03
sp238_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_DTU089	genus	0.79	1.2E-03	sp238_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_DTU089	genus	0.79	1.2E-03
sp244_Bacteria_Actinobacteria_Actinobacterii_Bifidobacteriales_Bifidobacteriaceae_Bifidobacterium	genus	0.53	2.0E-03	sp244_Bacteria_Actinobacteria_Actinobacterii_Bifidobacteriales_Bifidobacteriaceae_Bifidobacterium	genus	0.53	2.0E-03
sp251_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Coprococcus_2	genus	0.16	1.3E-03	sp251_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Coprococcus_2	genus	0.16	1.3E-03
sp255_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_NA	genus	0.94	8.5E-03	sp255_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_NA	genus	0.94	8.5E-03
sp258_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_UCG-010	genus	0.83	1.7E-03	sp258_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_UCG-010	genus	0.83	1.7E-03
sp259_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-003	genus	0.47	8.2E-04	sp259_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-003	genus	0.47	8.2E-04
sp261_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Tyzzereella_4	genus	0.25	2.0E-03	sp261_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Tyzzereella_4	genus	0.25	2.0E-03
sp262_Bacteria_Firmicutes_Clostridia_Clostridiales_Family_XIII_Family_XIII_UCG-001	genus	0.60	6.4E-04	sp262_Bacteria_Firmicutes_Clostridia_Clostridiales_Family_XIII_Family_XIII_UCG-001	genus	0.60	6.4E-04
sp263_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Candidatus_Stoquefichus	genus	0.33	4.4E-04	sp263_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Candidatus_Stoquefichus	genus	0.33	4.4E-04
sp264_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Flavonifractor	genus	0.62	9.1E-04	sp264_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Flavonifractor	genus	0.62	9.1E-04
sp266_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospira	genus	0.56	1.6E-03	sp266_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospira	genus	0.56	1.6E-03
sp267_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Sellimonas	genus	0.50	2.0E-03	sp267_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Sellimonas	genus	0.50	2.0E-03
sp268_Bacteria_Proteobacteria_Deltaproteobacteria_Desulfowibrionales_Desulfowibrionaceae_Desulfowibrio	genus	0.35	1.9E-03	sp268_Bacteria_Proteobacteria_Deltaproteobacteria_Desulfowibrionales_Desulfowibrionaceae_Desulfowibrio	genus	0.35	1.9E-03
sp270_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_UCG-004	genus	0.41	7.4E-04	sp270_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_UCG-004	genus	0.41	7.4E-04
sp278_Bacteria_Firmicutes_Clostridia_Clostridiales_Family_XIII_Mogibacterium	genus	0.13	5.2E-04	sp278_Bacteria_Firmicutes_Clostridia_Clostridiales_Family_XIII_Mogibacterium	genus	0.13	5.2E-04
sp279_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Prevotellaceae_Paraprevotella	genus	0.18	1.0E-03	sp279_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Prevotellaceae_Paraprevotella	genus	0.18	1.0E-03
sp280_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_NK4A214_group	genus	0.36	2.6E-03	sp280_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_NK4A214_group	genus	0.36	2.6E-03
sp286_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Pygmaibacter	genus	0.48	5.2E-04	sp286_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Pygmaibacter	genus	0.48	5.2E-04
sp288_Bacteria_Firmicutes_Negativicutes_Selenomonadales_Veillonellaceae_Megaspheara	genus	0.18	1.4E-03	sp288_Bacteria_Firmicutes_Negativicutes_Selenomonadales_Veillonellaceae_Megaspheara	genus	0.18	1.4E-03
sp294_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Butyricoccus	genus	0.84	1.5E-03	sp294_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Butyricoccus	genus	0.84	1.5E-03
sp297_Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Escherichia/Shigella	genus	0.16	2.4E-03	sp297_Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Escherichia/Shigella	genus	0.16	2.4E-03
sp299_Bacteria_Proteobacteria_Gammaproteobacteria_Betaproteobacteriales_Burkholderiaceae_Sutterella	genus	0.38	9.0E-04	sp299_Bacteria_Proteobacteria_Gammaproteobacteria_Betaproteobacteriales_Burkholderiaceae_Sutterella	genus	0.38	9.0E-04
sp305_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Subdoligranulum	genus	0.45	2.0E-03	sp305_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Subdoligranulum	genus	0.45	2.0E-03
sp310_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Eisenbergiella	genus	0.56	1.3E-03	sp310_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Eisenbergiella	genus	0.56	1.3E-03
sp311_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Anaerotruncus	genus	0.70	9.7E-04	sp311_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Anaerotruncus	genus	0.70	9.7E-04
sp329_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Dorea	genus	0.42	1.4E-03	sp329_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Dorea	genus	0.42	1.4E-03
sp338_Bacteria_Actinobacteria_Coriorbacterii_Coriorbacteriales_Coriorbacteriaceae_Collinsella	genus	0.27	5.0E-04	sp338_Bacteria_Actinobacteria_Coriorbacterii_Coriorbacteriales_Coriorbacteriaceae_Collinsella	genus	0.27	5.0E-04
sp343_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Turicibacter	genus	0.23	3.5E-04	sp343_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Turicibacter	genus	0.23	3.5E-04

sp343_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Intestinimonas	genus	0.79	1.9E-03	sp343_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Intestinimonas	genus	0.79	1.9E-03
sp344_Bacteria_Firmicutes_Bacilli_Lactobacillales_Streptococcaceae_Lactococcus	genus	0.47	4.7E-04	sp344_Bacteria_Firmicutes_Bacilli_Lactobacillales_Streptococcaceae_Lactococcus	genus	0.47	4.7E-04
sp345_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Marinifilaceae_Odoribacter	genus	0.50	1.1E-03	sp345_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Marinifilaceae_Odoribacter	genus	0.50	1.1E-03
sp353_Bacteria_Cyanobacteria_Oxyphotobacteria_Chloroplast_NA_NA	genus	0.24	7.0E-04	sp353_Bacteria_Cyanobacteria_Oxyphotobacteria_Chloroplast_NA_NA	genus	0.24	7.0E-04
sp355_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_UCG-002	genus	0.36	2.4E-03	sp355_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_UCG-002	genus	0.36	2.4E-03
sp357_Bacteria_Firmicutes_Clostridia_Clostridiales_Peptostreptococcaceae_Intestinibacter	genus	0.12	7.7E-04	sp357_Bacteria_Firmicutes_Clostridia_Clostridiales_Peptostreptococcaceae_Intestinibacter	genus	0.12	7.7E-04
sp361_Bacteria_Actinobacteria_Coribacteriales_Coribacteriales_Incertae_Sedis_NA	genus	0.41	5.9E-04	sp361_Bacteria_Actinobacteria_Coribacteriales_Coribacteriales_Incertae_Sedis_NA	genus	0.41	5.9E-04
sp371_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_NK4A136_group	genus	0.52	2.4E-03	sp371_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_NK4A136_group	genus	0.52	2.4E-03
sp372_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Faecalitalea	genus	0.52	1.1E-03	sp372_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Faecalitalea	genus	0.52	1.1E-03
sp374_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Marvinbryantia	genus	0.60	1.0E-03	sp374_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Marvinbryantia	genus	0.60	1.0E-03
sp379_Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacter	genus	0.10	2.9E-04	sp379_Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacter	genus	0.10	2.9E-04
sp380_Bacteria_Firmicutes_Clostridia_Clostridiales_Peptostreptococcaceae_Romboutsia	genus	0.16	4.0E-04	sp380_Bacteria_Firmicutes_Clostridia_Clostridiales_Peptostreptococcaceae_Romboutsia	genus	0.16	4.0E-04
sp389_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Hungatella	genus	0.48	6.8E-04	sp389_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Hungatella	genus	0.48	6.8E-04
sp403_Bacteria_Firmicutes_Clostridia_Clostridiales_Clostridiaceae_1_Clostridium_sensu_stricto_1	genus	0.30	1.1E-03	sp403_Bacteria_Firmicutes_Clostridia_Clostridiales_Clostridiaceae_1_Clostridium_sensu_stricto_1	genus	0.30	1.1E-03
sp406_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_UCS-1-2E3	genus	0.22	2.3E-04	sp406_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_UCS-1-2E3	genus	0.22	2.3E-04
sp407_Bacteria_Proteobacteria_Gammaproteobacteria_Pasteurellales_Pasteurellaceae_Haemophilus	genus	0.28	5.6E-04	sp407_Bacteria_Proteobacteria_Gammaproteobacteria_Pasteurellales_Pasteurellaceae_Haemophilus	genus	0.28	5.6E-04
sp413_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Negativibacillus	genus	0.41	9.3E-04	sp413_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Negativibacillus	genus	0.41	9.3E-04
sp440_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminiclostridium_6	genus	0.17	7.7E-04	sp440_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminiclostridium_6	genus	0.17	7.7E-04
sp452_Bacteria_Firmicutes_Clostridia_Clostridiales_Family_XIII_NA	genus	0.74	1.1E-03	sp452_Bacteria_Firmicutes_Clostridia_Clostridiales_Family_XIII_NA	genus	0.74	1.1E-03
sp454_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Barnesiellaceae_Barnesiella	genus	0.28	2.1E-03	sp454_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Barnesiellaceae_Barnesiella	genus	0.28	2.1E-03
sp468_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Tyzzzeria_3	genus	0.15	2.9E-04	sp468_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Tyzzzeria_3	genus	0.15	2.9E-04
sp471_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Agathobacter	genus	0.60	4.8E-03	sp471_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Agathobacter	genus	0.60	4.8E-03
sp497_Bacteria_Actinobacteria_Coribacteriales_Coribacteriales_Eggerthellaceae_Eggerthella	genus	0.51	4.1E-04	sp497_Bacteria_Actinobacteria_Coribacteriales_Coribacteriales_Eggerthellaceae_Eggerthella	genus	0.51	4.1E-04
sp507_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Shuttleworthia	genus	0.37	8.3E-04	sp507_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Shuttleworthia	genus	0.37	8.3E-04
sp524_Bacteria_Firmicutes_Clostridia_Clostridiales_Christensenellaceae_NA	genus	0.68	6.0E-04	sp524_Bacteria_Firmicutes_Clostridia_Clostridiales_Christensenellaceae_NA	genus	0.68	6.0E-04
sp531_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_FCS020_group	genus	0.58	5.3E-04	sp531_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_FCS020_group	genus	0.58	5.3E-04
sp567_Bacteria_Actinobacteria_Coribacteriales_Coribacteriales_Eggerthellaceae_NA	genus	0.18	2.4E-04	sp567_Bacteria_Actinobacteria_Coribacteriales_Coribacteriales_Eggerthellaceae_NA	genus	0.18	2.4E-04
sp576_Bacteria_Firmicutes_Clostridia_Clostridiales_Clostridiaceae_vadinBB60_group_NA	genus	0.34	8.3E-04	sp576_Bacteria_Firmicutes_Clostridia_Clostridiales_Clostridiaceae_vadinBB60_group_NA	genus	0.34	8.3E-04
sp598_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_NA	genus	0.54	8.5E-04	sp598_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_NA	genus	0.54	8.5E-04
sp604_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Barnesiellaceae_NA	genus	0.12	2.4E-04	sp604_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Barnesiellaceae_NA	genus	0.12	2.4E-04
sp629_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Oscillospira	genus	0.26	1.9E-04	sp629_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Oscillospira	genus	0.26	1.9E-04
sp633_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Erysipelotrichaceae_UCG-003	genus	0.20	7.0E-04	sp633_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Erysipelotrichaceae_UCG-003	genus	0.20	7.0E-04
sp652_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_GCA-900066575	genus	0.58	5.0E-04	sp652_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_GCA-900066575	genus	0.58	5.0E-04
sp666_Bacteria_Synergistetes_Synergistia_Synergistales_Synergistaceae_Cloacibacillus	genus	0.16	6.0E-04	sp666_Bacteria_Synergistetes_Synergistia_Synergistales_Synergistaceae_Cloacibacillus	genus	0.16	6.0E-04
sp683_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Oscillibacter	genus	0.68	5.1E-04	sp683_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Oscillibacter	genus	0.68	5.1E-04
sp685_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Hydrogenoanaerobacterium	genus	0.26	2.5E-04	sp685_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Hydrogenoanaerobacterium	genus	0.26	2.5E-04
sp691_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Holdemania	genus	0.44	2.7E-04	sp691_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Holdemania	genus	0.44	2.7E-04
sp731_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Fuscatenibacter	genus	0.28	1.2E-03	sp731_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Fuscatenibacter	genus	0.28	1.2E-03
sp733_Bacteria_Actinobacteria_Coribacteriales_Coribacteriales_Eggerthellaceae_Adlercreutzia	genus	0.52	3.7E-04	sp733_Bacteria_Actinobacteria_Coribacteriales_Coribacteriales_Eggerthellaceae_Adlercreutzia	genus	0.52	3.7E-04
sp749_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_UBA1819	genus	0.32	5.2E-04	sp749_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_UBA1819	genus	0.32	5.2E-04
sp753_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Coprobacillus	genus	0.22	1.7E-04	sp753_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Coprobacillus	genus	0.22	1.7E-04
sp772_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Dielma	genus	0.39	1.8E-04	sp772_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Dielma	genus	0.39	1.8E-04
sp789_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminiclostridium	genus	0.11	3.2E-04	sp789_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminiclostridium	genus	0.11	3.2E-04
sp796_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Caproiciproducens	genus	0.44	2.2E-04	sp796_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Caproiciproducens	genus	0.44	2.2E-04
sp800_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_GCA-900066755	genus	0.32	1.2E-04	sp800_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_GCA-900066755	genus	0.32	1.2E-04
sp809_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_UCG-004	genus	0.21	3.9E-04	sp809_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_UCG-004	genus	0.21	3.9E-04
sp817_Bacteria_Actinobacteria_Coribacteriales_Coribacteriales_Eggerthellaceae_Senegalimassilia	genus	0.16	2.1E-04	sp817_Bacteria_Actinobacteria_Coribacteriales_Coribacteriales_Eggerthellaceae_Senegalimassilia	genus	0.16	2.1E-04
sp818_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Phocaea	genus	0.42	1.1E-04	sp818_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Phocaea	genus	0.42	1.1E-04
sp826_Bacteria_Firmicutes_Negativicutes_Selenomonadales_Veillonellaceae_Veillonella	genus	0.24	3.9E-04	sp826_Bacteria_Firmicutes_Negativicutes_Selenomonadales_Veillonellaceae_Veillonella	genus	0.24	3.9E-04
sp836_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Anaerospobacter	genus	0.11	1.6E-04	sp836_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Anaerospobacter	genus	0.11	1.6E-04
sp858_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_GCA-900066225	genus	0.59	5.8E-04	sp858_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_GCA-900066225	genus	0.59	5.8E-04
sp908_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Solobacterium	genus	0.13	1.1E-04	sp908_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Solobacterium	genus	0.13	1.1E-04
sp959_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Prevotellaceae_Prevotella_7	genus	0.15	1.3E-04	sp959_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Prevotellaceae_Prevotella_7	genus	0.15	1.3E-04
sp963_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Candidatus_Soleaferrea	genus	0.67	2.1E-04	sp963_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Candidatus_Soleaferrea	genus	0.67	2.1E-04
sp978_Bacteria_Tenericutes_Mollicutes_Mollicutes_RF39_NA_NA	genus	0.21	1.6E-03	sp978_Bacteria_Tenericutes_Mollicutes_Mollicutes_RF39_NA_NA	genus	0.21	1.6E-03
sp982_Bacteria_Actinobacteria_Coribacteriales_Coribacteriales_Eggerthellaceae_Slackia	genus	0.27	1.5E-04	sp982_Bacteria_Actinobacteria_Coribacteriales_Coribacteriales_Eggerthellaceae_Slackia	genus	0.27	1.5E-04
sp1020_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Merdbacter	genus	0.23	2.3E-04	sp1020_Bacteria_Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Merdbacter	genus	0.23	2.3E-04
sp1048_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Marinifilaceae_Butyricimonas	genus	0.33	4.5E-04	sp1048_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Marinifilaceae_Butyricimonas	genus	0.33	4.5E-04
sp1132_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminiclostridium_1	genus	0.21	2.5E-04	sp1132_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminiclostridium_1	genus	0.21	2.5E-04
sp1138_Bacteria_Firmicutes_Negativicutes_Selenomonadales_Veillonellaceae_Allisonella	genus	0.11	1.2E-04	sp1138_Bacteria_Firmicutes_Negativicutes_Selenomonadales_Veillonellaceae_Allisonella	genus	0.11	1.2E-04
sp1198_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-010	genus	0.48	1.1E-03	sp1198_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-010	genus	0.48	1.1E-03
sp1213_Bacteria_Firmicutes_Clostridia_Clostridiales_Peptococcaceae_Peptococcus	genus	0.21	1.7E-04	sp1213_Bacteria_Firmicutes_Clostridia_Clostridiales_Peptococcaceae_Peptococcus	genus	0.21	1.7E-04
sp1254_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Tyzzzeria	genus	0.15	2.0E-04	sp1254_Bacteria_Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Tyzzzeria	genus	0.15	2.0E-04
sp1261_Bacteria_Proteobacteria_Gammaproteobacteria_Betaproteobacteriales_Burkholderiaceae_Oxalobacter	genus	0.24	1.0E-04	sp1261_Bacteria_Proteobacteria_Gammaproteobacteria_Betaproteobacteriales_Burkholderiaceae_Oxalobacter	genus	0.24	1.0E-04
sp1325_Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_NA	genus	0.17	1.6E-04	sp1325_Bacteria_Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_NA	genus	0.17	1.6E-04
sp1361_Bacteria_Firmicutes_Clostridia_Clostridiales_Peptococcaceae_NA	genus	0.44	2.3E-04	sp1361_Bacteria_Firmicutes_Clostridia_Clostridiales_Peptococcaceae_NA	genus	0.44	2.3E-04
sp1399_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-013	genus	0.43	4.4E-04	sp1399_Bacteria_Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-013	genus	0.43	4.4E-04
sp1434_Bacteria_Proteobacteria_Alphaproteobacteria_Rhodospirillales_NA_NA	genus	0.16	2.4E-04	sp1434_Bacteria_Proteobacteria_Alphaproteobacteria_Rhodospirillales_NA_NA	genus	0.16	2.4E-04
sp1500_Bacteria_Actinobacteria_Coribacteriales_Coribacteriales_Eggerthellaceae_Gordonibacter	genus	0.26	1.1E-04	sp1500_Bacteria_Actinobacteria_Coribacteriales_Coribacteriales_Eggerthellaceae_Gordonibacter	genus	0.26	1.1E-04
sp1737_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Prevotellaceae_Prevotella	genus	0.13	1.0E-04	sp1737_Bacteria_Bacteroidetes_Bacteroidia_Bacteroidales_Prevotellaceae_Prevotella	genus	0.13	1.0E-04
sp1802_Bacteria_Firmicutes_Clostridia_Clostridiales_Defluviitaleaceae_Defluviitaleaceae_UCG-011	genus	0.47	2.6E-04	sp1802_Bacteria_Firmicutes_Clostridia_Clostridiales_Defluviitaleaceae_Defluviitaleaceae_UCG-011	genus	0.47	2.6E-04
sp2043_Bacteria_Firmicutes_Clostridia_Clostridiales_NA_NA	genus	0.25	1.5E-04	sp2043_Bacteria_Firmicutes_Clostridia_Clostridiales_NA_NA	genus	0.25	1.5E-04
sp2094_Bacteria_Proteobacteria_Deltaproteobacteria_Desulfowibrionales_Desulfowibrionaceae_Bilophila	genus	0.13	1.2E-04	sp2094_Bacteria_Proteobacteria_Deltaproteobacteria_Desulfowibrionales_Desulfowibrionaceae_Bilophila	genus	0.13	1.2E-04

Supplementary Table 2: Brown taxa module membership and taxa significance for clinical traits correlated with the covariate adjusted brown module (GAD7, PHQ9, DARS). Taxa significance is measured by the correlation (Pearson) between each taxon and clinical trait. Brown module membership is the correlation between the individual taxon and the brown module eigentaxon. High module membership is a proxy measurement for highly connected taxa and therefore module hub taxa are defined by high module membership.

	Brown Module	GAD7				PHQ9			DARS			
	Membership	r	p	p.BH		r	p	p.BH		r	p	p.BH
sp1198_Ruminococcaceae_UCG-010	0.81	-0.3	8.13E-05	0.005	**	-0.23	3.68E-03	0.053	.	0.12	1.17E-01	0.366
sp161_Christensenellaceae_R-7_group	0.72	-0.21	8.16E-03	0.057	.	-0.17	2.78E-02	0.216		0.15	5.63E-02	0.292
sp576_Clostridiales_vadinBB60_group_NA	0.69	-0.25	1.54E-03	0.027	*	-0.11	1.64E-01	0.485		0.14	7.68E-02	0.292
sp105_Ruminococcaceae_UCG-005	0.68	-0.2	1.02E-02	0.057	.	-0.07	3.47E-01	0.58		0.05	5.08E-01	0.813
sp1132_Ruminiclostridium_1	0.64	-0.24	1.90E-03	0.027	*	-0.19	1.32E-02	0.158		0.12	1.36E-01	0.402
sp280_Ruminococcaceae_NK4A214_group	0.64	-0.3	1.30E-04	0.005	**	-0.19	1.67E-02	0.172		0.17	3.10E-02	0.292
sp107_Ruminococcaceae_UCG-002	0.63	-0.16	3.55E-02	0.111	.	-0.11	1.71E-01	0.485		0.02	8.28E-01	0.885
sp1361_Peptococcaceae_NA	0.63	-0.25	1.19E-03	0.027	*	-0.27	4.63E-04	0.017	*	0.16	4.19E-02	0.292
sp240_Christensenellaceae_R-7_group	0.6	-0.17	2.98E-02	0.103	.	-0.09	2.36E-01	0.548		0.11	1.67E-01	0.43
sp155_Christensenellaceae_R-7_group	0.6	-0.2	1.02E-02	0.057	.	-0.15	6.47E-02	0.262		0.09	2.68E-01	0.568
sp224_Ruminococcaceae_UCG-005	0.6	-0.21	7.03E-03	0.057	.	-0.16	4.24E-02	0.235		0.1	1.97E-01	0.443
sp79_Ruminococcaceae_UCG-002	0.59	-0.15	5.45E-02	0.157	.	-0.01	8.59E-01	0.884		0.05	5.20E-01	0.814
sp2043_NA_NA	0.54	-0.2	1.11E-02	0.057	.	-0.16	4.60E-02	0.237		0.2	8.83E-03	0.194
sp156_Ruminococcaceae_NK4A214_group	0.52	-0.21	7.76E-03	0.057	.	-0.24	2.04E-03	0.037	*	0.2	1.08E-02	0.194
sp268_Desulfovibrio	0.51	0.04	6.44E-01	0.773	.	0.05	5.06E-01	0.637		-0.02	7.73E-01	0.864
sp355_Ruminococcaceae_UCG-002	0.51	-0.17	2.99E-02	0.103	.	-0.17	3.00E-02	0.216		0.14	6.86E-02	0.292
sp345_Odoribacter	0.5	-0.1	2.16E-01	0.409	.	-0.05	5.13E-01	0.637		0.07	3.71E-01	0.652
sp978_NA_NA	0.47	-0.12	1.19E-01	0.275	.	-0.08	3.11E-01	0.58		0.05	5.59E-01	0.834
sp1399_Ruminococcaceae_UCG-013	0.46	-0.13	1.07E-01	0.262	.	-0.07	3.74E-01	0.58		0.04	6.03E-01	0.834
sp193_Ruminococcaceae_UCG-014	0.46	-0.2	9.98E-03	0.057	.	-0.14	7.56E-02	0.287		-0.02	7.68E-01	0.864
sp666_Cloacibacillus	0.45	-0.09	2.56E-01	0.46	.	-0.05	5.13E-01	0.637		0.16	4.64E-02	0.292
sp208_Ruminococcaceae_UCG-002	0.44	-0.12	1.33E-01	0.291	.	-0.02	8.22E-01	0.869		0.13	9.31E-02	0.319
sp201_Christensenellaceae_R-7_group	0.43	-0.12	1.32E-01	0.291	.	-0.1	2.03E-01	0.517		0.03	7.32E-01	0.864
sp148_Alistipes	0.38	-0.19	1.45E-02	0.065	.	-0.16	3.79E-02	0.228		0.14	7.05E-02	0.292
sp1048_Butyricimonas	0.38	-0.08	3.13E-01	0.513	.	-0.07	3.47E-01	0.58		0.01	8.56E-01	0.893
sp1261_Oxalobacter	0.38	-0.05	5.32E-01	0.672	.	-0.07	3.87E-01	0.581		0.02	8.36E-01	0.885
sp94_Ruminiclostridium_6	0.37	-0.19	1.39E-02	0.065	.	-0.1	2.10E-01	0.517		0.04	6.53E-01	0.855
sp226_Family_XIII_AD3011_group	0.37	-0.11	1.57E-01	0.322	.	-0.06	4.18E-01	0.614		0.13	8.81E-02	0.317
sp1802_Defluviitaleaceae_UCG-011	0.35	-0.19	1.67E-02	0.071	.	-0.26	8.61E-04	0.021	*	0.12	1.40E-01	0.402
sp440_Ruminiclostridium_6	0.34	-0.09	2.41E-01	0.445	.	0.02	8.33E-01	0.869		0.14	7.35E-02	0.292
sp454_Barnesiella	0.34	-0.07	4.08E-01	0.576	.	0.05	4.87E-01	0.637		0.03	7.44E-01	0.864
sp97_Bacteroides	0.31	-0.19	1.76E-02	0.071	.	-0.07	3.79E-01	0.58		0.08	3.39E-01	0.626
sp30_Alistipes	0.3	-0.13	1.02E-01	0.262	.	-0.1	1.97E-01	0.517		0.04	6.01E-01	0.834
sp173_Ruminococcus_1	0.29	-0.07	3.91E-01	0.57	.	-0.09	2.59E-01	0.58		0.06	4.19E-01	0.702
sp255_Ruminococcaceae_NA	0.29	-0.13	1.09E-01	0.262	.	-0.05	5.43E-01	0.641		0.07	3.71E-01	0.652
sp361_Coriobacteriales_Incertae_Sedis_NA	0.28	-0.14	8.41E-02	0.224	.	-0.12	1.35E-01	0.44		0.07	4.09E-01	0.7
sp27_Alistipes	0.28	-0.14	8.22E-02	0.224	.	-0.11	1.45E-01	0.454		0.1	1.95E-01	0.443
sp219_Parabacteroides	0.26	-0.1	2.00E-01	0.399	.	-0.08	2.86E-01	0.58		0.15	5.30E-02	0.292
sp51_Roseburia	0.25	-0.15	5.42E-02	0.157	.	-0.15	6.15E-02	0.262		0.01	8.82E-01	0.907
sp262_Family_XIII_UCG-001	0.24	-0.05	5.13E-01	0.666	.	-0.11	1.75E-01	0.485		-0.02	7.78E-01	0.864
sp817_Senegalimassilia	0.24	-0.01	8.72E-01	0.924	.	0.02	8.28E-01	0.869		0	9.91E-01	0.991
sp128_Alistipes	0.23	-0.01	8.51E-01	0.915	.	0.1	2.16E-01	0.517		0.11	1.82E-01	0.437
sp82_Ruminococcaceae_NA	0.23	0.07	3.51E-01	0.562	.	0.07	3.60E-01	0.58		-0.01	9.08E-01	0.921
sp139_Lachnospira	0.21	-0.09	2.64E-01	0.464	.	-0.06	4.73E-01	0.637		0.03	7.29E-01	0.864
sp23_Parabacteroides	0.2	-0.11	1.54E-01	0.322	.	-0.12	1.14E-01	0.393		0.02	7.56E-01	0.864
sp567_Eggerthellaceae_NA	0.19	-0.02	8.09E-01	0.911	.	-0.04	6.10E-01	0.709		-0.13	1.06E-01	0.348
sp185_Alistipes	0.19	0	9.83E-01	0.985	.	0.06	4.27E-01	0.615		-0.08	3.12E-01	0.592
sp1434_NA_NA	0.18	-0.05	5.18E-01	0.666	.	-0.07	3.64E-01	0.58		0.11	1.49E-01	0.402
sp175_Roseburia	0.16	0.06	4.31E-01	0.596	.	0	9.61E-01	0.961		-0.04	6.33E-01	0.855
sp191_Prevotella_9	0.16	0.1	2.05E-01	0.399	.	0.14	6.56E-02	0.262		-0.15	5.95E-02	0.292
sp7_Bacteroides	0.16	-0.22	4.34E-03	0.052	.	-0.13	1.05E-01	0.377		0.03	7.17E-01	0.864
sp71_Roseburia	0.15	-0.21	8.20E-03	0.057	.	-0.16	3.54E-02	0.228		0.06	4.41E-01	0.721
sp17_Bacteroides	0.15	-0.08	3.13E-01	0.513	.	-0.01	9.38E-01	0.951		0.17	2.58E-02	0.292
sp103_Alistipes	0.14	0.07	3.86E-01	0.57	.	0.02	7.61E-01	0.856		0.02	7.92E-01	0.864
sp77_Ruminococcaceae_NA	0.14	-0.03	7.15E-01	0.818	.	-0.02	8.30E-01	0.869		0.09	2.30E-01	0.502
sp171_Lachnospira	0.14	-0.18	2.44E-02	0.092	.	-0.15	6.18E-02	0.262		0.02	7.91E-01	0.864
sp120_Roseburia	0.13	-0.07	3.65E-01	0.57	.	-0.08	3.24E-01	0.58		0.15	5.46E-02	0.292
sp58_Bacteroides	0.12	-0.04	5.88E-01	0.718	.	0.05	5.42E-01	0.641		0.03	6.92E-01	0.864
sp278_Mogibacterium	0.12	0.07	3.96E-01	0.57	.	0.08	3.05E-01	0.58		-0.08	2.86E-01	0.578
sp221_Ruminococcaceae_UCG-002	0.11	0.02	8.36E-01	0.915	.	0.02	7.87E-01	0.869		-0.04	5.96E-01	0.834
sp198_Muribaculaceae_NA	0.11	0.03	7.16E-01	0.818	.	0.08	3.34E-01	0.58		-0.08	3.02E-01	0.587
sp1213_Peptococcus	0.11	-0.05	5.12E-01	0.666	.	-0.08	3.08E-01	0.58		0.04	6.45E-01	0.855
sp76_Catenibacterium	0.1	-0.07	3.85E-01	0.57	.	-0.08	3.26E-01	0.58		0.05	5.46E-01	0.834
sp151_Catenibacterium	0.1	-0.04	5.78E-01	0.717	.	-0.07	3.63E-01	0.58		-0.04	5.75E-01	0.834
sp279_Paraprevotella	0.09	0	9.65E-01	0.985	.	0.05	5.06E-01	0.637		-0.11	1.76E-01	0.437
sp108_Holdemanela	0.07	-0.03	6.82E-01	0.805	.	0.03	6.83E-01	0.78		-0.16	4.33E-02	0.292
sp158_Lachnospiraceae_NA	0.03	0	9.85E-01	0.985	.	0.05	4.93E-01	0.637		-0.11	1.51E-01	0.402
sp959_Prevotella_7	0.03	0.17	3.36E-02	0.11	.	0.28	3.70E-04	0.017	*	-0.18	2.12E-02	0.292
sp64_Erysipelotrichaceae_UCG-003	0.03	-0.08	3.04E-01	0.513	.	0.05	5.22E-01	0.637		-0.08	2.89E-01	0.578
sp126_Ruminococcaceae_NA	0.02	-0.01	8.51E-01	0.915	.	0.06	4.47E-01	0.632		-0.14	7.70E-02	0.292
sp299_Sutterella	0	0	9.83E-01	0.985	.	0.17	2.67E-02	0.216		-0.24	2.11E-03	0.102
sp982_Slackia	0	0.06	4.63E-01	0.629	.	0.09	2.70E-01	0.58		-0.23	2.83E-03	0.102

Supplementary Table S3: Module membership of unadjusted brown module taxa, generated from

Taxa	Brown Module Membership
sp1198_ruminococcaceae_ruminococcaceae_ucg_010	0.80
sp161_christensenellaceae_christensenellaceae_r_7_group	0.75
sp576_clostridiales_vadin_bb60_group_na	0.70
sp1361_peptococcaceae_na	0.69
sp224_ruminococcaceae_ruminococcaceae_ucg_005	0.68
sp280_ruminococcaceae_ruminococcaceae_nk4a214_group	0.67
sp105_ruminococcaceae_ruminococcaceae_ucg_005	0.66
sp1132_ruminococcaceae_ruminiclostridium_1	0.63
sp156_ruminococcaceae_ruminococcaceae_nk4a214_group	0.61
sp107_ruminococcaceae_ruminococcaceae_ucg_002	0.58
sp240_christensenellaceae_christensenellaceae_r_7_group	0.57
sp2043_na_na	0.55
sp79_ruminococcaceae_ruminococcaceae_ucg_002	0.53
sp193_ruminococcaceae_ruminococcaceae_ucg_014	0.53
sp155_christensenellaceae_christensenellaceae_r_7_group	0.53
sp685_ruminococcaceae_hydrogenoanaerobacterium	0.52
sp1399_ruminococcaceae_ruminococcaceae_ucg_013	0.51
sp343_ruminococcaceae_intestinimonas	0.49
sp858_ruminococcaceae_gca_900066225	0.49
sp201_christensenellaceae_christensenellaceae_r_7_group	0.48
sp1802_defluviitaleaceae_defluviitaleaceae_ucg_011	0.48
sp355_ruminococcaceae_ruminococcaceae_ucg_002	0.47
sp148_rikenellaceae_alistipes	0.46
sp666_synergistaceae_cloacibacillus	0.45
sp978_na_na	0.45
sp226_family_xiii_family_xiii_ad3011_group	0.44
sp94_ruminococcaceae_ruminiclostridium_6	0.44
sp255_ruminococcaceae_na	0.43
sp345_marinifilaceae_odoribacter	0.42
sp524_christensenellaceae_na	0.42
sp1261_burkholderiaceae_oxalobacter	0.39
sp268_desulfovibrionaceae_desulfovibrio	0.39
sp208_ruminococcaceae_ruminococcaceae_ucg_002	0.39
sp1048_marinifilaceae_butyricimonas	0.39
sp97_bacteroidaceae_bacteroides	0.36
sp311_ruminococcaceae_anaerotruncus	0.36
sp683_ruminococcaceae_oscillibacter	0.35
sp262_family_xiii_family_xiii_ucg_001	0.34
sp749_ruminococcaceae_uba1819	0.33
sp361_coriobacteriales_incertae_sedis_na	0.33
sp223_ruminococcaceae_anaerofilum	0.33
sp27_rikenellaceae_alistipes	0.32

sp173_ruminococcaceae_ruminococcus_1	0.32
sp30_rikenellaceae_alistipes	0.32
sp454_barnesiellaceae_barnesiella	0.31
sp139_lachnospiraceae_lachnospira	0.30
sp440_ruminococcaceae_ruminiclostridium_6	0.30
sp71_lachnospiraceae_roseburia	0.29
sp219_tannerellaceae_parabacteroides	0.27
sp1434_na_na	0.26
sp17_bacteroidaceae_bacteroides	0.25
sp128_rikenellaceae_alistipes	0.23
sp199_ruminococcaceae_ruminiclostridium_9	0.21
sp171_lachnospiraceae_lachnospira	0.20
sp371_lachnospiraceae_lachnospiraceae_nk4a136_group	0.19
sp51_lachnospiraceae_roseburia	0.18
sp7_bacteroidaceae_bacteroides	0.17
sp23_tannerellaceae_parabacteroides	0.17
sp185_rikenellaceae_alistipes	0.16
sp170_acidaminococcaceae_phascolarctobacterium	0.14
sp652_lachnospiraceae_gca_900066575	0.12
sp836_lachnospiraceae_anaerosporobacter	0.11
sp18_akermansiaceae_akermansia	0.10
sp733_eggerthellaceae_adlercreutzia	0.10
sp77_ruminococcaceae_na	0.10
sp120_lachnospiraceae_roseburia	0.09
sp103_rikenellaceae_alistipes	0.09
sp47_lachnospiraceae_lachnospiraceae_nk4a136_group	0.08
sp64_erysipelotrichaceae_erysipelotrichaceae_ucg_003	0.08
sp175_lachnospiraceae_roseburia	0.08
sp206_ruminococcaceae_ruminococcus_2	0.07
sp58_bacteroidaceae_bacteroides	0.07
sp221_ruminococcaceae_ruminococcaceae_ucg_002	0.07
sp65_bacteroidaceae_bacteroides	0.04
sp93_lachnospiraceae_na	0.02
sp39_ruminococcaceae_ruminococcus_2	0.02
sp3_bacteroidaceae_bacteroides	-0.01
sp69_bacteroidaceae_bacteroides	-0.02
sp116_ruminococcaceae_negativibacillus	-0.04
sp14_bacteroidaceae_bacteroides	-0.05
sp9_bacteroidaceae_bacteroides	-0.05

Supplementary Table 4: Taxa significantly associated with a clinical trait before correction. Association between CLR transformed taxon abundance and clinical scores calculated ALDEx2 glm function.

clinical trait	taxa	β	X Intercept	p	p.BH
GAD7	sp7_Bacteroides	-0.22	3.4	0.013	0.898
GAD7	sp28_Lachnospiraceae_NA	0.28	-0.4	0.001	0.354
GAD7	sp45_Roseburia	0.17	-0.9	0.04	0.996
GAD7	sp71_Roseburia	-0.2	3.5	0.01	0.790
GAD7	sp94_Ruminiclostridium_6	-0.17	1.3	0.025	0.951
GAD7	sp109_Faecalitalea	0.17	-1.9	0.035	0.963
GAD7	sp122_Lachnoclostridium	0.16	-1.4	0.034	0.978
GAD7	sp152_Blautia	0.19	-3.4	0.021	0.769
GAD7	sp148_Alistipes	-0.15	5.0	0.029	0.985
GAD7	sp161_Christensenellaceae_R-7_group	-0.16	3.6	0.031	0.972
GAD7	sp193_Ruminococcaceae_UCG-014	-0.19	2.2	0.02	0.917
GAD7	sp195_Lachnoclostridium	0.1	5.8	0.008	0.953
GAD7	sp224_Ruminococcaceae_UCG-005	-0.15	3.9	0.015	0.879
GAD7	sp244_Bifidobacterium	0.22	-0.9	0.003	0.556
GAD7	sp280_Ruminococcaceae_NK4A214_group	-0.22	1.4	0.004	0.503
GAD7	sp343_Intestinimonas	-0.12	3.8	0.039	0.975
GAD7	sp372_Faecalitalea	0.19	-1.3	0.01	0.777
GAD7	sp380_Romboutsia	0.17	-3.8	0.015	0.695
GAD7	sp524_Christensenellaceae_NA	-0.18	2.5	0.001	0.243
GAD7	sp1198_Ruminococcaceae_UCG-010	-0.22	2.0	<0.001	0.195
GAD7	sp1361_Peptococcaceae_NA	-0.14	0.2	0.027	0.777
PHQ-9	sp19_Blautia	0.12	3.6	0.039	0.998
PHQ-9	sp28_Lachnospiraceae_NA	0.17	0.0	0.03	0.991
PHQ-9	sp71_Roseburia	-0.15	3.4	0.02	0.950
PHQ-9	sp109_Faecalitalea	0.15	-2.3	0.026	0.907
PHQ-9	sp129_Lachnoclostridium	0.15	-1.1	0.013	0.864
PHQ-9	sp152_Blautia	0.13	-3.2	0.045	0.944
PHQ-9	sp195_Lachnoclostridium	0.08	5.8	0.014	1.000
PHQ-9	sp224_Ruminococcaceae_UCG-005	-0.1	3.8	0.046	0.993
PHQ-9	sp244_Bifidobacterium	0.15	-0.7	0.017	0.948
PHQ-9	sp280_Ruminococcaceae_NK4A214_group	-0.15	1.1	0.029	0.901
PHQ-9	sp288_Megasphaera	0.15	-3.6	0.022	0.815
PHQ-9	sp299_Sutterella	0.12	-1.9	0.048	0.966
PHQ-9	sp343_Intestinimonas	-0.13	4.2	0.007	0.759
PHQ-9	sp372_Faecalitalea	0.13	-1.2	0.04	0.973
PHQ-9	sp380_Romboutsia	0.12	-3.7	0.039	0.874
PHQ-9	sp524_Christensenellaceae_NA	-0.15	2.6	0.002	0.294
PHQ-9	sp1198_Ruminococcaceae_UCG-010	-0.14	1.7	0.013	0.792
PHQ-9	sp1361_Peptococcaceae_NA	-0.13	0.5	0.008	0.673
PHQ-9	sp1802_Defluviitaleaceae_UCG-011	-0.12	0.6	0.019	0.769
DARS	sp55_Bifidobacterium	-0.09	3.5	0.015	0.873
DARS	sp104_Streptococcus	0.08	-4.2	0.022	0.850
DARS	sp299_Sutterella	-0.07	2.6	0.023	0.832