Figure S1

Analysis of the dynamics of the gut microbiota. A: Principal component analysis of square-root transformed relative abundances. **B:** Network analysis using Spearman (left) and Pearson (right) correlations.

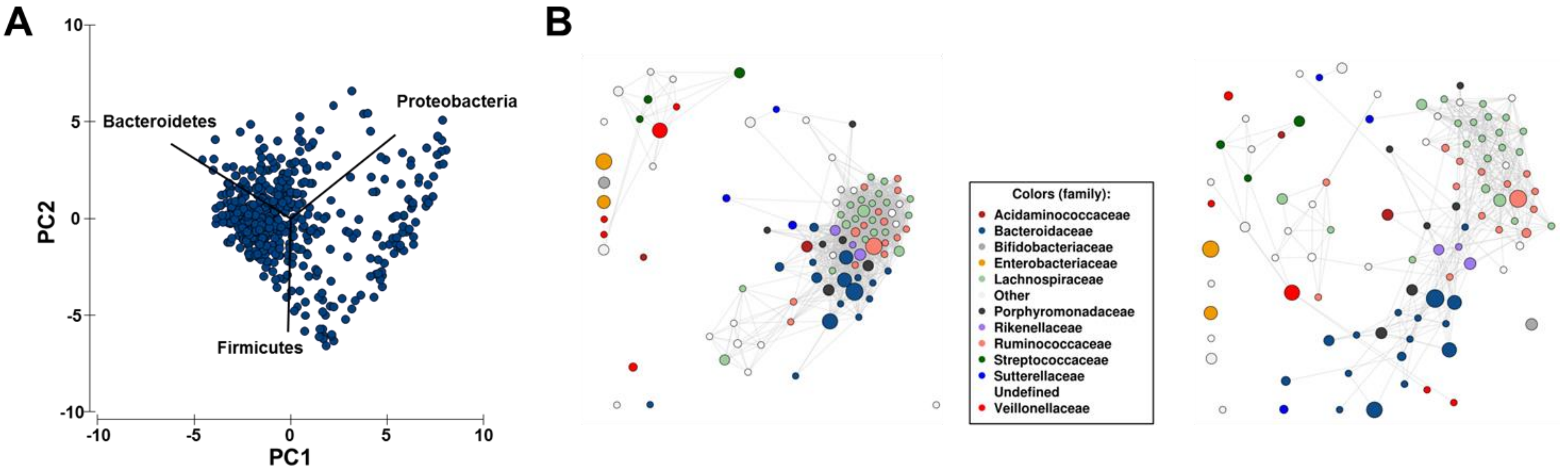

Figure S2

Dynamics of the gut microbiota in healthy individuals. Principal component analysis of square-root transformed relative abundances shows samples from Australia, France, Chile and Japan (n= 688 samples from 590 individuals) clustering into enterotypes dominated by *Bacteroides*, *Prevotella*, *Akkermansia* or *Faecalibacterium*.

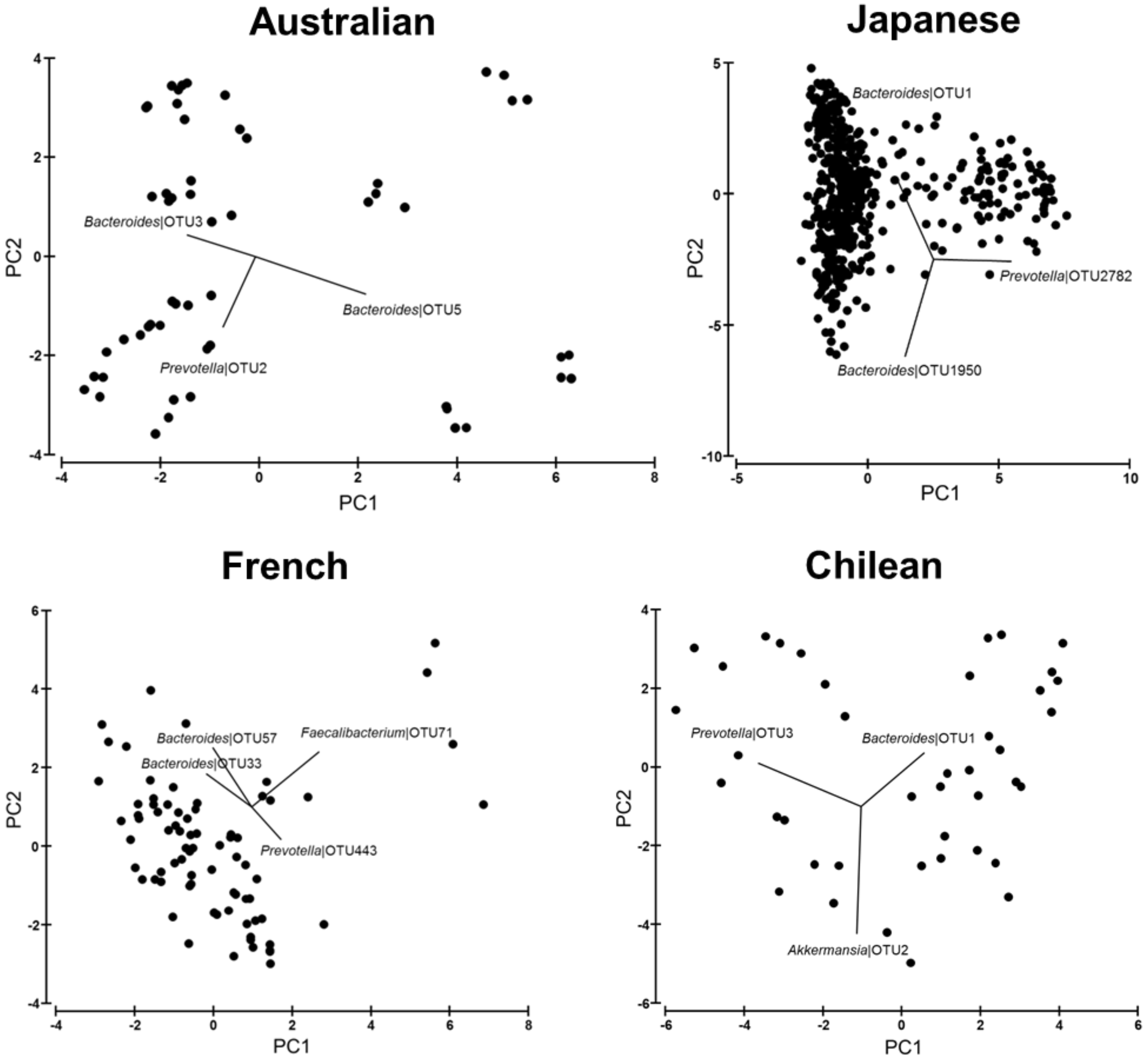

Figure S3

Analysis of patient microbiome enterotypes. Plots are non-metric multidimensional scaling plots on Bray-Curtis resemblance of square-root transformed relative abundances. **A:** Samples were separated into two groups according to their levels of Proteobacteria, with a relative abundance of 25% used as a cut-off (Yes: High Proteobacteria; No: Low Proteobacteria). **B:** Dirichlet multinomial mixtures partitioned patient microbiomes into two groups dominated by *Bacteroides* (partition 2) or *Escherichia/Shigella* (partition 1). Partition 1 had an average relative abundance of *Bacteroides* OTU0001=21.4%, *Escherichia*/*Shigella* OTU0002=28.8%, while partition 2 contained *Bacteroides* OTU0001=44.5%, *Escherichia*/*Shigella* OTU0002=7.3%. 88% of samples classified to *Escherichia*/*Shigella*-dominated enterotype (Panel A, blue) were classified into partition 1 (blue).

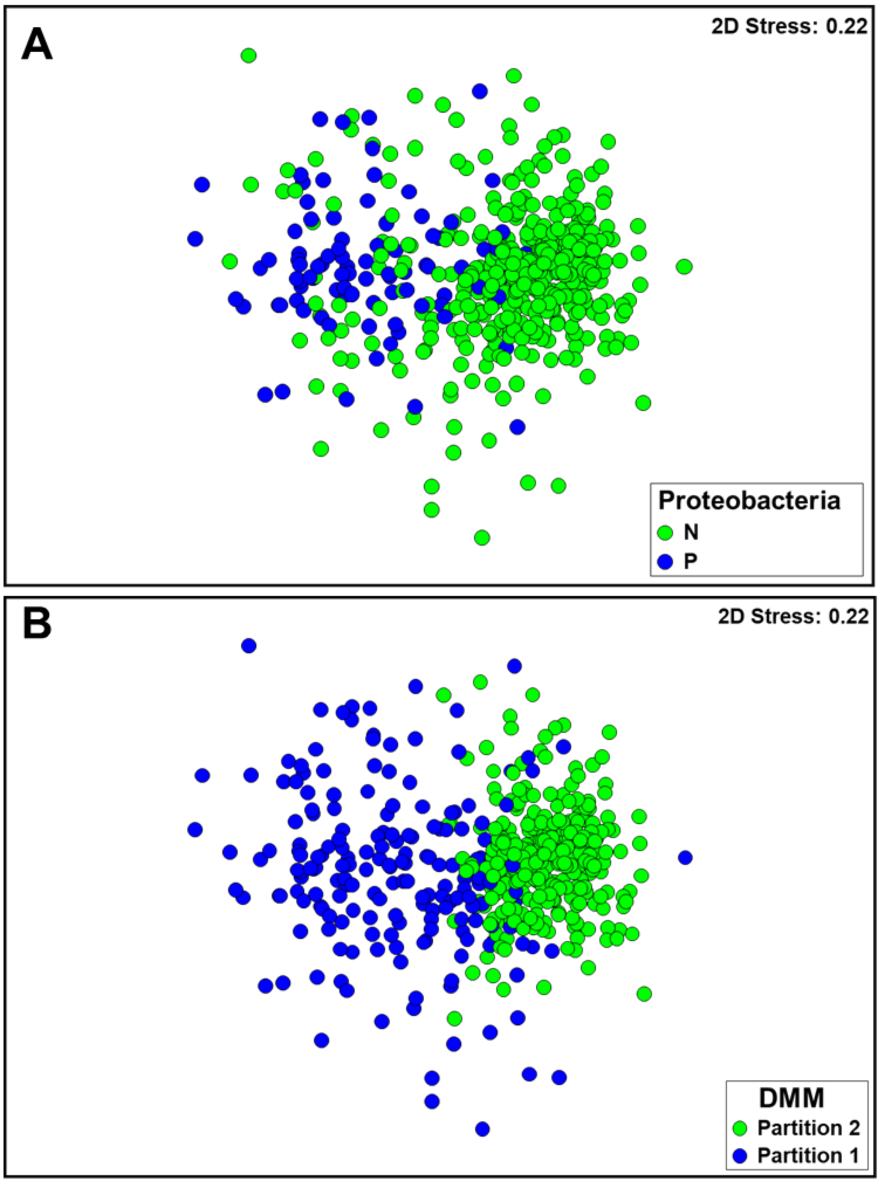

Figure S4

Microbial diversity across colour and consistency of faecal samples. Evenness (**A**) and Shannon's diversity (**B)** analysed across sample colour. Evenness (**C**) and Shannon's diversity (**D)** analysed across sample consistency. **E:** Hierarchal clustering of OTUs across colour and consistency. **F:** Hierarchal clustering of sample distribution across colour and consistency. Red bar indicate an enrichment of liquid and colours other than brown.

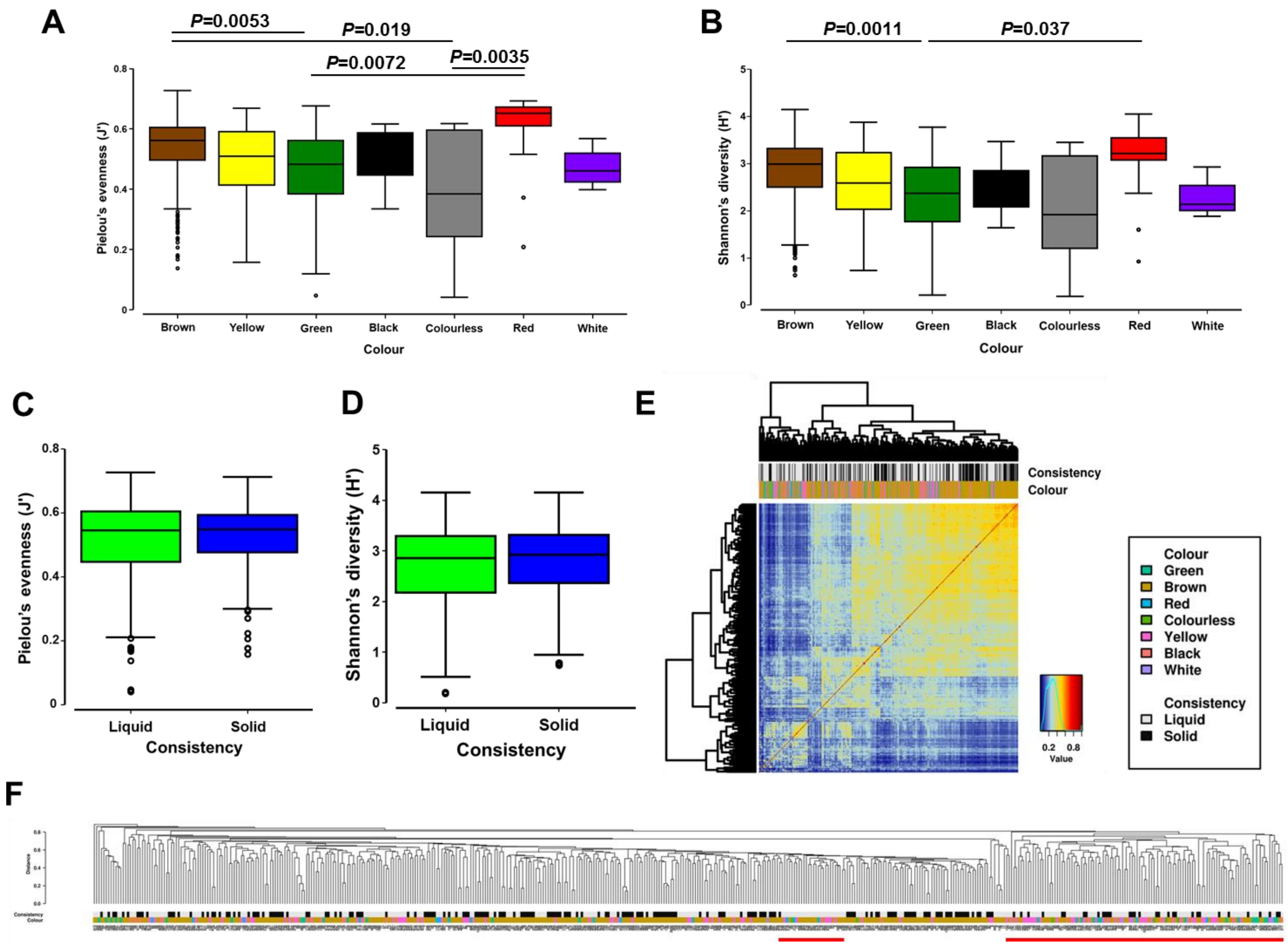

Figure S5

Krona plots of average relative abundance across colour and consistency.

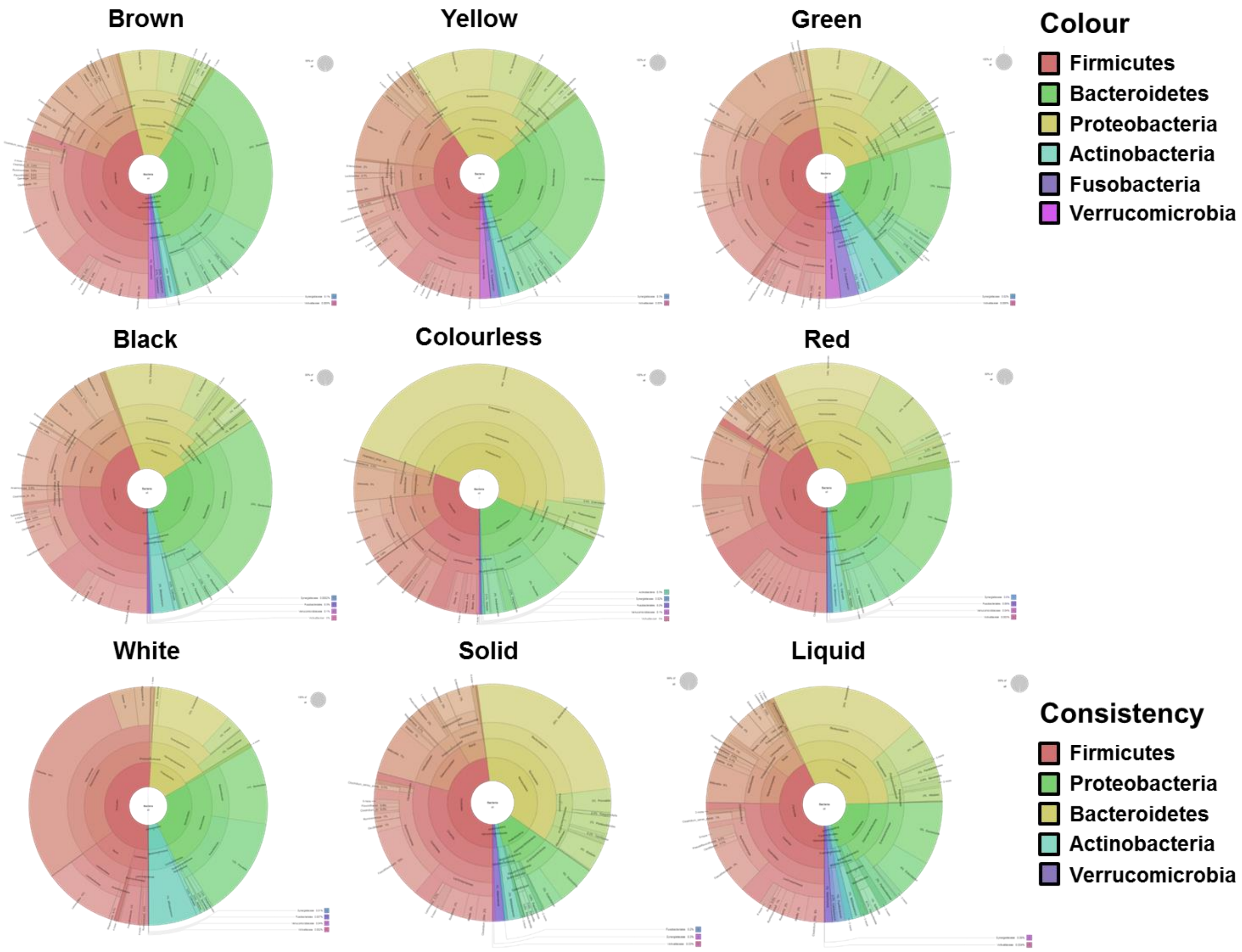

Figure S6

Boxplot of relative abundance of microbial taxa of interest across colour and consistency. A: *Bacteroides*, **B:** *Faecalibacterium*, **C:** *Bacteroides*, **D:** *Escherichia/Shigella*, **E:** *Faecalibacterium*.

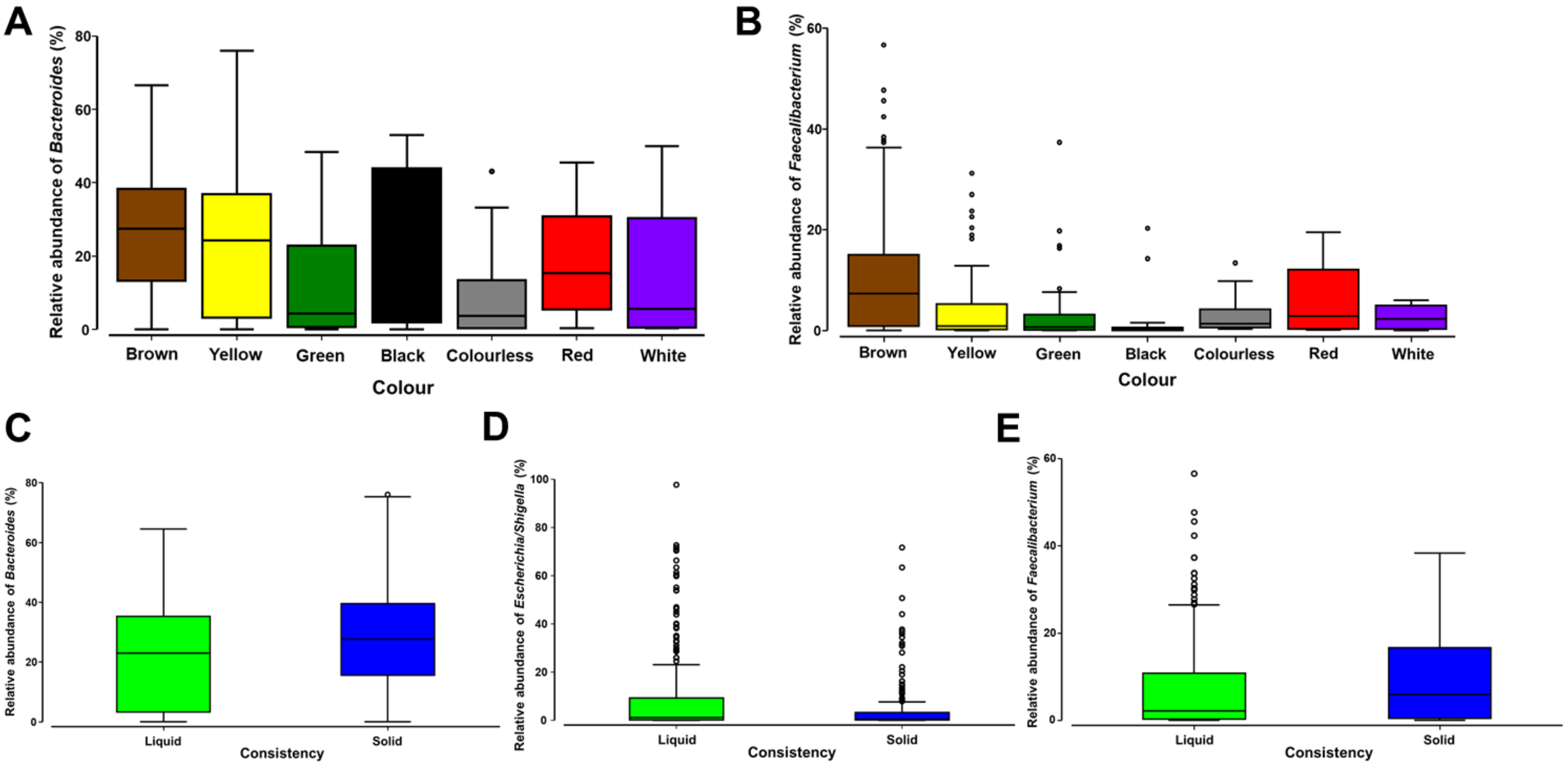

Figure S7

Data distribution and reproducibility. A: Square-root transformation shows a marked improvement in distribution of data. **B:** Cluster analysis of replicates following Bray-Curtis resemblance shows highly reproducible results.

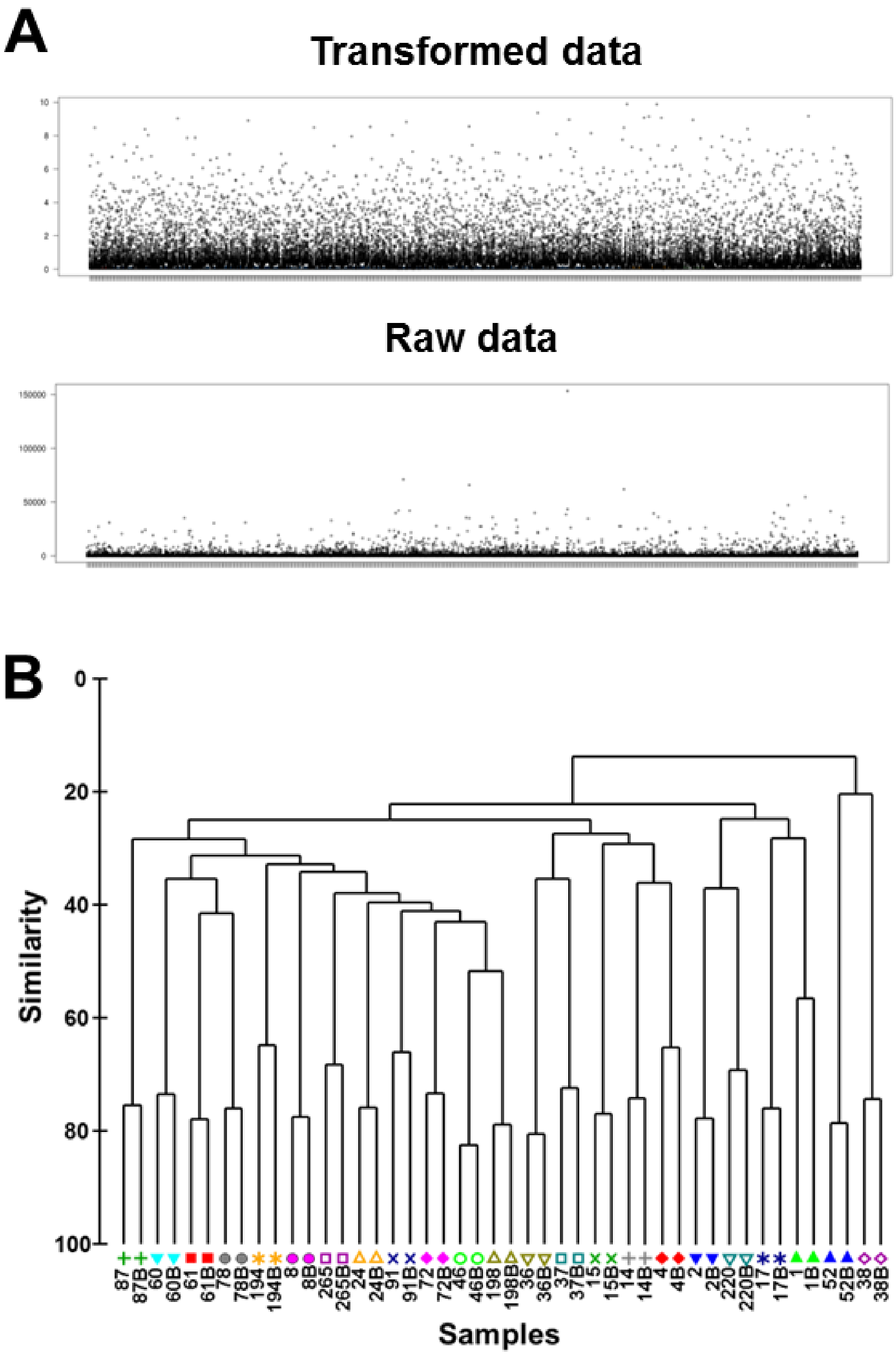

Table S1

Microbial taxa enriched in samples within the *Escherichia/Shigella* enterotype. Analysis was performed using LEfSe. N: Not enriched with Proteobacteria; P: Enriched with Proteobacteria.

Taxa	Group	LDA Score	P-value
Actinobacteria.Actinobacteria.Actinomycetales	P	3.336211	4.4E-12
Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae	P	3.146894	1.82E-06
Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Actinomyces	P	3.135554	2.41E-06
Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Actinomyces.Otu0094	P	2.872944	9.09E-05
Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Actinomyces.Otu0151	P	2.691813	0.001029
Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Actinomyces.Otu0861	P	2.120078	0.015802
Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Actinomyces.Otu4345	P	2.283646	0.000264
Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Actinomyces.Otu4436	P	2.286324	0.03557
Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Actinomyces.Otu4923	P	2.544935	0.03557
Actinobacteria.Actinobacteria.Actinomycetales.Corynebacteriaceae.Corynebacterium.Otu4742	P	2.502213	0.03557
Actinobacteria.Actinobacteria.Actinomycetales.Dermabacteraceae	P	2.548915	0.03557
Actinobacteria.Actinobacteria.Actinomycetales.Dermabacteraceae.Dermabacter	P	2.548293	0.03557
Actinobacteria.Actinobacteria.Actinomycetales.Dermabacteraceae.Dermabacter.Otu6721	P	2.474229	0.03557
Actinobacteria.Actinobacteria.Actinomycetales.Dermacoccaceae	P	2.478681	0.03557
Actinobacteria.Actinobacteria.Actinomycetales.Dermacoccaceae.Dermacoccus	P	2.608146	0.03557
Actinobacteria.Actinobacteria.Actinomycetales.Dermacoccaceae.Dermacoccus.Otu2261	P	2.430589	0.03557
Actinobacteria.Actinobacteria.Actinomycetales.Microbacteriaceae.Cryobacterium	P	2.305918	0.002926
Actinobacteria.Actinobacteria.Actinomycetales.Microbacteriaceae.Cryobacterium.Otu6532	P	2.265789	0.002926
Actinobacteria.Actinobacteria.Actinomycetales.Microbacteriaceae.Leucobacter	P	2.497168	0.03557
Actinobacteria.Actinobacteria.Actinomycetales.Microbacteriaceae.Leucobacter.Otu5265	P	2.340917	0.03557
Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae	P	2.862467	1.37E-10
Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Rothia	P	2.82767	8.58E-10
Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Rothia.Otu0163	P	2.820782	7.56E-10
Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Rothia.Otu5549	P	2.426356	0.03557
Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Rothia.Otu6730	P	2.063287	0.03557

Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae.Bifidobacteriaceae_unclassified.Otu6904	P	2.596543	0.03557
Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae.Bifidobacterium	P	3.388466	0.031407
Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae.Bifidobacterium.Otu0013	P	3.391552	0.024476
Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae.Bifidobacterium.Otu3821	P	2.298118	0.03557
Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae.Bifidobacterium.Otu4403	P	2.380748	0.03557
Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae.Bifidobacterium.Otu7145	P	2.241055	0.03557
Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae.Scardovia.Otu4506	P	2.535713	0.03557
Actinobacteria.Actinobacteria.Coriobacteriales	N	3.295671	4.22E-10
Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae	N	3.295671	4.22E-10
Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.Asaccharobacter.Otu5498	P	2.406852	0.03557
Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.Atopobium	N	2.648583	0.001108
Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.Atopobium.Otu0119	N	2.669449	0.00102
Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.Collinsella	N	2.971856	7.37E-08
Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.Collinsella.Otu0088	N	2.94087	1.43E-06
Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.Eggerthella	N	2.146191	3.48E-06
Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.Eggerthella.Otu0261	N	2.126866	4.89E-06
Armatimonadetes	P	2.260325	0.03557
Armatimonadetes.Armatimonadetes_gp5	P	2.360245	0.03557
Armatimonadetes.Armatimonadetes_gp5.Armatimonadetes_gp5_unclassified	P	2.467773	0.03557
Armatimonadetes.Armatimonadetes_gp5.Armatimonadetes_gp5_unclassified.Armatimonadetes_gp5_unclassified	P	2.557918	0.03557
Armatimonadetes.Armatimonadetes_gp5.Armatimonadetes_gp5_unclassified.Armatimonadetes_gp5_unclassified.Armatimonadetes_gp5_unclassified	P	2.428138	0.03557
Armatimonadetes.Armatimonadetes_gp5.Armatimonadetes_gp5_unclassified.Armatimonadetes_gp5_unclassified.Armatimonadetes_gp5_unclassified.Otu4094	P	2.373758	0.03557
Bacteria_unclassified	N	3.50565	3.94E-07
Bacteria_unclassified.Bacteria_unclassified	N	3.50565	3.94E-07
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Bacteria_unclassified.Bacteria_unclassified.Bacteria_unclassified.Bacteria_unclassified.Bacteria_unclassified	N	3.50565	3.94E-07
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Bacteria_unclassified.Bacteria_unclassified.Bacteria_unclassified.Bacteria_unclassified.Bacteria_unclassified.Otu6279	P	2.554252	0.03557
Bacteria_unclassified.Bacteria_unclassified.Bacteria_unclassified.Bacteria_unclassified.Bacteria_unclassified.Otu7208	P	2.395096	0.03557
Bacteroidetes	N	5.154918	1.04E-24
Bacteroidetes.Bacteroidetes_unclassified	P	2.478865	0.028463
Bacteroidetes.Bacteroidetes_unclassified.Bacteroidetes_unclassified	P	2.476008	0.028463
Bacteroidetes.Bacteroidetes_unclassified.Bacteroidetes_unclassified.Bacteroidetes_unclassified	P	2.482058	0.028463
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Bacteroidetes.Bacteroidia	N	5.155169	5.01E-25
Bacteroidetes.Bacteroidia.Bacteroidales	N	5.155169	5.01E-25
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae	N	4.951704	3.23E-18
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides	N	4.951493	3.33E-18
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0001	N	4.595841	5.49E-18
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0005	N	3.775714	1.28E-08
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0008	N	4.052277	1.46E-14
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0010	N	4.074887	2.56E-15
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0018	N	3.526821	4.52E-07
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Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu3861	P	2.709121	0.03557
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Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu6827	P	2.497068	0.03557
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Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae	N	4.226732	3.47E-14
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Barnesiella	N	3.643141	4.83E-08

Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Barnesiella.Otu0047	N	3.259838	0.000164
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Barnesiella.Otu0080	N	3.186307	0.018283
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Barnesiella.Otu0381	N	2.152433	0.018033
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Barnesiella.Otu4363	P	2.186907	0.03557
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Butyricimonas	N	3.164535	3.73E-06
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Butyricimonas.Otu0070	N	3.112303	9.48E-07
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Butyricimonas.Otu6232	P	2.378024	0.03557
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Dysgonomonas.Otu3108	P	2.426136	0.03557
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Dysgonomonas.Otu3809	P	2.545765	0.03557
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Dysgonomonas.Otu4339	P	2.552855	0.03557
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Odoribacter	N	3.40448	3.16E-10
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Odoribacter.Otu0043	N	3.32795	6.02E-11
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Odoribacter.Otu7078	P	2.62244	0.03557
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Paludibacter	P	2.148963	0.03557
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Paludibacter.Otu4473	P	2.575393	0.03557
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Parabacteroides	N	3.837384	3.04E-11
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Parabacteroides.Otu0019	N	3.447834	6.12E-09
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Parabacteroides.Otu0022	N	3.53338	4.72E-06
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Porphyromonadaceae_unclassified	N	3.215596	7.41E-05
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Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Porphyromonadaceae_unclassified.Otu5010	P	2.598425	0.03557
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Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Paraprevotella.Otu0092	N	3.029421	0.015661
Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Prevotella.Otu0137	N	2.444765	0.028273
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Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Prevotella.Otu4203	P	2.5659	0.03557

Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Prevotella.Otu4451	P	2.437731	0.03557
Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae	N	4.2018	7.28E-19
Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Alistipes	N	4.196689	7.76E-19
Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Alistipes.Otu0015	N	3.825156	7.55E-13
Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Alistipes.Otu0025	N	3.69254	2.63E-09
Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Alistipes.Otu0075	N	3.11218	8.05E-10
Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Alistipes.Otu0189	N	2.353947	0.014062
Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Alistipes.Otu0197	N	2.541874	2.7E-05
Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Alistipes.Otu0237	N	2.736512	0.016289
Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Alistipes.Otu0278	N	2.175896	0.046153
Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Alistipes.Otu0289	N	2.169957	2.23E-05
Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Alistipes.Otu0308	N	2.136461	8.61E-05
Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Rikenellaceae_unclassified	N	2.569783	0.037714
Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Rikenellaceae_unclassified.Otu0192	N	2.57098	0.041639
Bacteroidetes.Cytophagia	P	2.190256	0.03557
Bacteroidetes.Cytophagia.Cytophagales	P	2.315359	0.03557
Bacteroidetes.Cytophagia.Cytophagales.Cytophagaceae	P	2.543009	0.03557
Bacteroidetes.Cytophagia.Cytophagales.Cytophagaceae.Dyadobacter	P	2.229669	0.03557
Bacteroidetes.Cytophagia.Cytophagales.Cytophagaceae.Dyadobacter.Otu6477	P	2.48076	0.03557
Bacteroidetes.Flavobacteriia	P	2.142346	4.76E-08
Bacteroidetes.Flavobacteriia.Flavobacteriales	P	2.139798	4.76E-08
Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae	P	2.122931	4.76E-08
Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae.Capnocytophaga.Otu1633	P	2.416672	0.03557
Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae.Chryseobacterium.Otu2583	P	2.634684	0.03557
Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae.Chryseobacterium.Otu6614	P	2.331824	0.03557
Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae.Elizabethkingia	P	2.479863	0.03557
Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae.Elizabethkingia.Otu4881	P	2.759111	0.03557
Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae.Wautersiella	P	2.034767	0.03557
Bacteroidetes.Flavobacteriia.Flavobacteriales.Flavobacteriaceae.Wautersiella.Otu5019	P	2.472909	0.03557
Bacteroidetes.Sphingobacteriia.Sphingobacteriales.Sphingobacteriaceae.Pedobacter.Otu2389	P	2.208569	0.03557
Candidatus_Saccharibacteria.Candidatus_Saccharibacteria_unclassified.Candidatus_Saccharibacteria_unclassified.Candidatus_Saccharibacteria_unclassified.Candidatus_Saccharibacteria_unclassified.Otu6620	P	2.220186	0.03557

Deinococcus_Thermus	P	2.507687	0.03557
Deinococcus_Thermus.Deinococci	P	2.463411	0.03557
Deinococcus_Thermus.Deinococci.Deinococcales	P	2.411899	0.03557
Deinococcus_Thermus.Deinococci.Deinococcales.Deinococcaceae	P	2.466983	0.03557
Deinococcus_Thermus.Deinococci.Deinococcales.Deinococcaceae.Deinococcus	P	2.338567	0.03557
Deinococcus_Thermus.Deinococci.Deinococcales.Deinococcaceae.Deinococcus.Otu3834	P	2.380863	0.03557
Firmicutes	N	4.90129	3.9E-11
Firmicutes.Bacilli	P	4.591413	3.53E-16
Firmicutes.Bacilli.Bacillales	P	3.310666	1.41E-11
Firmicutes.Bacilli.Bacillales.Bacillales_Incertae_Sedis_XI	P	3.303465	6.52E-10
Firmicutes.Bacilli.Bacillales.Bacillales_Incertae_Sedis_XI.Gemella	P	3.303278	6.52E-10
Firmicutes.Bacilli.Bacillales.Bacillales_Incertae_Sedis_XI.Gemella.Otu0205	P	3.304242	9.15E-09
Firmicutes.Bacilli.Bacillales.Bacillales_Incertae_Sedis_XI.Gemella.Otu4519	P	2.57082	0.03557
Firmicutes.Bacilli.Bacillales.Bacillales_unclassified.Bacillales_unclassified.Otu2650	P	2.217784	0.03557
Firmicutes.Bacilli.Bacillales.Bacillales_unclassified.Bacillales_unclassified.Otu4468	P	2.228675	0.03557
Firmicutes.Bacilli.Bacillales.Bacillales_unclassified.Bacillales_unclassified.Otu5063	P	2.4738	0.03557
Firmicutes.Bacilli.Bacillales.Paenibacillaceae_1.Paenibacillus.Otu2032	P	2.716555	0.03557
Firmicutes.Bacilli.Bacillales.Paenibacillaceae_1.Paenibacillus.Otu2911	P	2.183247	0.03557
Firmicutes.Bacilli.Bacillales.Paenibacillaceae_1.Paenibacillus.Otu6069	P	2.536552	0.03557
Firmicutes.Bacilli.Bacillales.Planococcaceae	P	2.585214	0.03557
Firmicutes.Bacilli.Bacillales.Planococcaceae.Planococcaceae_unclassified	P	2.140699	0.03557
Firmicutes.Bacilli.Bacillales.Planococcaceae.Planococcaceae_unclassified.Otu6612	P	2.208758	0.03557
Firmicutes.Bacilli.Bacillales.Staphylococcaceae	N	2.966184	1.54E-05
Firmicutes.Bacilli.Bacillales.Staphylococcaceae.Staphylococcus	N	2.991895	9.56E-06
Firmicutes.Bacilli.Bacillales.Staphylococcaceae.Staphylococcus.Otu0071	N	3.001252	7.91E-06
Firmicutes.Bacilli.Bacilli_unclassified.Bacilli_unclassified.Bacilli_unclassified.Otu5891	P	2.398872	0.03557
Firmicutes.Bacilli.Bacilli_unclassified.Bacilli_unclassified.Bacilli_unclassified.Otu6338	P	2.075307	0.03557
Firmicutes.Bacilli.Lactobacillales	P	4.569979	1.84E-15
Firmicutes.Bacilli.Lactobacillales.Aerococcaceae	P	2.68836	0.001361
Firmicutes.Bacilli.Lactobacillales.Aerococcaceae.Abiotrophia	P	2.715936	0.00107
Firmicutes.Bacilli.Lactobacillales.Aerococcaceae.Abiotrophia.Otu0171	P	2.653948	0.00107
Firmicutes.Bacilli.Lactobacillales.Aerococcaceae.Facklamia	P	2.356411	0.03557

Firmicutes.Bacilli.Lactobacillales.Aerococcaceae.Facklamia.Otu6756	P	2.26824	0.03557
Firmicutes.Bacilli.Lactobacillales.Carnobacteriaceae	P	3.098486	6.65E-07
Firmicutes.Bacilli.Lactobacillales.Carnobacteriaceae.Carnobacteriaceae_unclassified.Otu3857	P	2.34924	0.03557
Firmicutes.Bacilli.Lactobacillales.Carnobacteriaceae.Carnobacteriaceae_unclassified.Otu4706	P	2.278495	0.03557
Firmicutes.Bacilli.Lactobacillales.Carnobacteriaceae.Carnobacteriaceae_unclassified.Otu5346	P	2.219158	0.03557
Firmicutes.Bacilli.Lactobacillales.Carnobacteriaceae.Carnobacteriaceae_unclassified.Otu6388	P	2.411851	0.03557
Firmicutes.Bacilli.Lactobacillales.Carnobacteriaceae.Granulicatella	P	3.094914	8.95E-07
Firmicutes.Bacilli.Lactobacillales.Carnobacteriaceae.Granulicatella.Otu0065	P	3.050196	5.51E-06
Firmicutes.Bacilli.Lactobacillales.Carnobacteriaceae.Granulicatella.Otu0465	P	2.181621	0.000289
Firmicutes.Bacilli.Lactobacillales.Carnobacteriaceae.Granulicatella.Otu3555	P	2.233088	0.002926
Firmicutes.Bacilli.Lactobacillales.Carnobacteriaceae.Granulicatella.Otu5663	P	2.312998	0.03557
Firmicutes.Bacilli.Lactobacillales.Carnobacteriaceae.Granulicatella.Otu7230	P	2.525407	0.03557
Firmicutes.Bacilli.Lactobacillales.Enterococcaceae	P	3.822466	9.54E-10
Firmicutes.Bacilli.Lactobacillales.Enterococcaceae.Enterococcaceae_unclassified	P	2.02286	1.56E-08
Firmicutes.Bacilli.Lactobacillales.Enterococcaceae.Enterococcus	P	3.817141	2.47E-09
Firmicutes.Bacilli.Lactobacillales.Enterococcaceae.Enterococcus.Otu0009	P	3.816529	1.9E-09
Firmicutes.Bacilli.Lactobacillales.Enterococcaceae.Enterococcus.Otu3778	P	2.274381	0.002926
Firmicutes.Bacilli.Lactobacillales.Enterococcaceae.Enterococcus.Otu5768	P	2.374369	0.03557
Firmicutes.Bacilli.Lactobacillales.Enterococcaceae.Enterococcus.Otu6117	P	2.255227	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae	P	3.653504	0.001854
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillaceae_unclassified.Otu2955	P	2.574822	0.002926
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillaceae_unclassified.Otu3090	P	2.315695	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillaceae_unclassified.Otu6975	P	2.493452	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus	P	3.647765	0.001559
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu0140	P	3.064074	0.003407
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu0234	P	2.765007	0.008071
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu0554	P	2.458851	0.002926
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu2052	P	2.190196	0.002926
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu2077	P	2.16049	0.002926
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu2346	P	2.518956	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu2507	P	2.537502	0.002926
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu3124	P	2.515643	0.03557

Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu3223	P	2.47049	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu3402	P	2.641229	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu3709	P	2.555341	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu3806	P	2.497028	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu3985	P	2.414209	0.002926
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu4418	P	2.228386	0.002926
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu4543	P	2.617563	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu4783	P	2.234484	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu4955	P	2.572039	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu5302	P	2.506517	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu5812	P	2.584261	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu5847	P	2.419361	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu5853	P	2.475718	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu6042	P	2.370056	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu6063	P	2.310771	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus.Otu6083	P	2.465124	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillales_unclassified.Lactobacillales_unclassified.Otu3456	P	2.439411	0.002926
Firmicutes.Bacilli.Lactobacillales.Lactobacillales_unclassified.Lactobacillales_unclassified.Otu3486	P	2.341646	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillales_unclassified.Lactobacillales_unclassified.Otu4110	P	2.665203	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillales_unclassified.Lactobacillales_unclassified.Otu4394	P	2.741041	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillales_unclassified.Lactobacillales_unclassified.Otu4401	P	2.356607	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillales_unclassified.Lactobacillales_unclassified.Otu4408	P	2.51447	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillales_unclassified.Lactobacillales_unclassified.Otu4426	P	2.232644	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillales_unclassified.Lactobacillales_unclassified.Otu4659	P	2.294812	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillales_unclassified.Lactobacillales_unclassified.Otu6691	P	2.776496	0.03557
Firmicutes.Bacilli.Lactobacillales.Lactobacillales_unclassified.Lactobacillales_unclassified.Otu7041	P	2.354363	0.03557
Firmicutes.Bacilli.Lactobacillales.Leuconostocaceae.Weissella.Otu5629	P	2.644177	0.03557
Firmicutes.Bacilli.Lactobacillales.Leuconostocaceae.Weissella.Otu6049	P	2.623089	0.03557
Firmicutes.Bacilli.Lactobacillales.Leuconostocaceae.Weissella.Otu6892	P	2.691752	0.03557
Firmicutes.Bacilli.Lactobacillales.Leuconostocaceae.Weissella.Otu6968	P	2.427023	0.03557
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae	P	4.380059	1.79E-11
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Lactococcus	P	2.456788	0.004007

Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Lactococcus.Otu0282	P	2.36071	0.001874
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Lactococcus.Otu6430	P	2.558133	0.03557
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus	P	4.375313	2.48E-11
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Otu0023	P	3.835113	5.8E-12
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Otu0036	P	3.821664	8.62E-05
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Otu0041	P	3.01189	0.000229
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Otu0241	P	2.104167	0.013116
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Otu0405	P	2.218765	0.002202
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Otu1699	P	2.282841	0.002926
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Otu3306	P	2.338579	0.03557
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Otu3364	P	2.407414	0.03557
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Otu3605	P	2.11557	0.002926
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Otu3786	P	2.33567	0.03557
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Otu3848	P	2.412641	0.03557
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Otu4102	P	2.647784	0.03557
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Otu4797	P	2.054663	0.03557
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Otu4880	P	2.227093	0.03557
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Otu4903	P	2.367804	0.03557
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Otu5713	P	2.183793	0.03557
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Otu5843	P	2.556655	0.03557
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Otu6206	P	2.50191	0.03557
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Otu6874	P	2.484447	0.03557
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Otu6977	P	2.412641	0.03557
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Otu7286	P	2.505688	0.03557
Firmicutes.Clostridia	N	5.012388	9.5E-24
Firmicutes.Clostridia.Clostridia_unclassified	N	2.078326	0.005758
Firmicutes.Clostridia.Clostridia_unclassified.Clostridia_unclassified	N	2.112451	0.005758
Firmicutes.Clostridia.Clostridia_unclassified.Clostridia_unclassified.Clostridia_unclassified	N	2.12958	0.005758
Firmicutes.Clostridia.Clostridia_unclassified.Clostridia_unclassified.Clostridia_unclassified.Otu5360	P	2.112341	0.03557
Firmicutes.Clostridia.Clostridiales	N	5.011841	9.82E-24
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1	P	3.75565	0.015091
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1.Anaerosporobacter.Otu5974	P	2.574851	0.03557

Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1.Clostridiaceae_1_unclassified	N	2.800774	0.004493
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1.Clostridiaceae_1_unclassified.Otu3933	P	2.370285	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1.Clostridiaceae_1_unclassified.Otu4741	P	2.164347	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1.Clostridiaceae_1_unclassified.Otu5098	P	2.627598	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1.Clostridiaceae_1_unclassified.Otu5145	P	2.585374	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1.Clostridiaceae_1_unclassified.Otu6108	P	2.531976	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1.Clostridiaceae_1_unclassified.Otu6643	P	2.221352	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1.Clostridiaceae_1_unclassified.Otu7219	P	2.609005	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1.Clostridiaceae_1_unclassified.Otu7268	P	2.412568	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1.Clostridium_sensu_stricto	P	3.805337	0.045047
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1.Clostridium_sensu_stricto.Otu0087	N	2.606977	0.002455
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1.Clostridium_sensu_stricto.Otu0304	N	2.162546	0.001885
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1.Clostridium_sensu_stricto.Otu3259	P	2.379289	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1.Clostridium_sensu_stricto.Otu3800	P	2.751606	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1.Clostridium_sensu_stricto.Otu4350	P	2.58051	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1.Clostridium_sensu_stricto.Otu5731	P	2.58651	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1.Clostridium_sensu_stricto.Otu6637	P	2.419227	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1.Sarcina	N	2.207651	0.025861
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1.Sarcina.Otu0267	N	2.189007	0.025861
Firmicutes.Clostridia.Clostridiales.Clostridiales_Incertae_Sedis_XI	P	2.414147	0.003819
Firmicutes.Clostridia.Clostridiales.Clostridiales_Incertae_Sedis_XI.Parvimonas.Otu3096	P	2.331678	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiales_Incertae_Sedis_XI.Parvimonas.Otu6133	P	2.621473	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiales_Incertae_Sedis_XI.Parvimonas.Otu6550	P	2.291493	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiales_Incertae_Sedis_XI.Peptoniphilus.Otu4479	P	2.409788	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiales_Incertae_Sedis_XIII	N	2.088899	0.006143
Firmicutes.Clostridia.Clostridiales.Clostridiales_Incertae_Sedis_XIII.Anaerovorax.Otu5385	P	2.422925	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiales_Incertae_Sedis_XIII.Clostridiales_Incertae_Sedis_XIII_unclassified	N	2.045885	3.59E-05
Firmicutes.Clostridia.Clostridiales.Clostridiales_unclassified	N	3.752017	4.88E-14
Firmicutes.Clostridia.Clostridiales.Clostridiales_unclassified.Clostridiales_unclassified	N	3.752017	4.88E-14
Firmicutes.Clostridia.Clostridiales.Clostridiales_unclassified.Clostridiales_unclassified.Otu0099	N	2.867714	9.53E-06
Firmicutes.Clostridia.Clostridiales.Clostridiales_unclassified.Clostridiales_unclassified.Otu0155	N	2.655109	0.00368
Firmicutes.Clostridia.Clostridiales.Clostridiales_unclassified.Clostridiales_unclassified.Otu0324	N	2.092924	2.07E-09

Firmicutes.Clostridia.Clostridiales.Clostridiales_unclassified.Clostridiales_unclassified.Otu0326	N	2.126176	0.034542
Firmicutes.Clostridia.Clostridiales.Clostridiales_unclassified.Clostridiales_unclassified.Otu0349	N	2.142648	0.009157
Firmicutes.Clostridia.Clostridiales.Clostridiales_unclassified.Clostridiales_unclassified.Otu2895	P	2.144008	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiales_unclassified.Clostridiales_unclassified.Otu4557	P	2.559544	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiales_unclassified.Clostridiales_unclassified.Otu4846	P	2.474725	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiales_unclassified.Clostridiales_unclassified.Otu5107	P	2.5834	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiales_unclassified.Clostridiales_unclassified.Otu6380	P	2.758641	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiales_unclassified.Clostridiales_unclassified.Otu6406	P	2.386453	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiales_unclassified.Clostridiales_unclassified.Otu6535	P	2.527102	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiales_unclassified.Clostridiales_unclassified.Otu6712	P	2.078897	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiales_unclassified.Clostridiales_unclassified.Otu7068	P	2.518751	0.03557
Firmicutes.Clostridia.Clostridiales.Clostridiales_unclassified.Clostridiales_unclassified.Otu7257	P	2.290015	0.03557
Firmicutes.Clostridia.Clostridiales.Eubacteriaceae	N	2.016888	3.58E-05
Firmicutes.Clostridia.Clostridiales.Eubacteriaceae.Eubacterium.Otu7178	P	2.433514	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae	N	4.623296	8.59E-20
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Anaerostipes	N	3.015136	2.84E-13
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Anaerostipes.Otu0060	N	2.96307	8.15E-09
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Anaerostipes.Otu0302	N	2.024256	0.000531
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blautia	N	3.794083	6.99E-21
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blautia.Otu0021	N	3.260295	8.14E-14
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blautia.Otu0046	N	3.206015	2.27E-12
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blautia.Otu0049	N	2.845721	8.55E-08
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blautia.Otu0103	N	2.742976	4.91E-10
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blautia.Otu0104	N	2.631882	8.69E-05
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blautia.Otu0146	N	2.436371	2.78E-05
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blautia.Otu0161	N	2.656631	0.000396
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blautia.Otu3872	P	2.48613	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blautia.Otu4054	P	2.624601	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blautia.Otu4287	P	2.513707	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blautia.Otu4856	P	2.31258	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blautia.Otu4962	P	2.379538	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blautia.Otu5061	P	2.163697	0.03557

Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blautia.Otu5297	P	2.850238	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blautia.Otu6178	P	2.341916	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blautia.Otu6332	P	2.590682	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blautia.Otu6603	P	2.410077	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blautia.Otu6860	P	2.425957	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa	N	3.92768	2.44E-15
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu0026	N	3.104339	5.96E-06
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu0035	N	3.37782	3.9E-10
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu0056	N	2.801183	0.000441
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu0085	N	3.02477	6.89E-09
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu0107	N	2.710704	9.25E-07
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu0115	N	2.653232	0.000532
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu0131	N	2.671782	2.59E-07
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu0165	N	2.6047	7.52E-11
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu0182	N	2.437816	8.14E-08
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu0199	N	2.002441	9.04E-05
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu0215	N	2.464263	1.16E-05
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu0223	P	2.049206	0.008401
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu0226	N	2.302154	0.026758
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu0247	N	2.007251	0.000564
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu0285	N	2.091999	2.72E-06
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu3339	P	2.535425	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu3589	P	2.546203	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu4936	P	2.653628	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu5869	P	2.637773	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu5979	P	2.366206	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu6030	P	2.376933	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu6139	P	2.534585	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu6187	P	2.658861	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu6434	P	2.597782	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu6711	P	2.461405	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu6778	P	2.827516	0.03557

Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu6832	P	2.342851	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVb	N	3.05561	7.22E-10
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVb.Otu0116	N	2.899211	0.023803
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVb.Otu0235	N	2.279095	0.044843
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVb.Otu7213	P	2.778884	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Coprococcus	N	3.201786	5.33E-15
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Coprococcus.Otu0125	N	2.762899	9.11E-10
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Coprococcus.Otu0147	N	2.699896	8.97E-07
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Coprococcus.Otu0239	N	2.33967	0.025864
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Dorea	N	3.102855	3.41E-13
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Dorea.Otu0098	N	2.93088	4.65E-09
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Dorea.Otu0111	P	2.224366	0.044742
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Dorea.Otu0122	N	2.566487	4.05E-11
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Dorea.Otu4359	P	2.173671	0.031034
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Dorea.Otu4822	P	2.431295	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Dorea.Otu6399	P	2.530148	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnoanaerobaculum	P	2.703109	0.000151
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnoanaerobaculum.Otu0348	P	2.292928	0.040755
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnoanaerobaculum.Otu0437	P	2.497103	3.32E-07
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospira	N	3.141229	2.71E-07
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospira.Otu0059	N	3.138507	2.84E-07
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified	N	3.862523	3.86E-15
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0016	N	3.146678	0.005326
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0063	N	3.036323	2.89E-09
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0066	N	2.811653	1.02E-08
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0126	N	2.546735	0.000361
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0129	N	2.519507	9.4E-09
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0136	N	2.625379	0.000116
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Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0153	N	2.66901	2.93E-07
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Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0185	N	2.576654	6.83E-08

Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0209	N	2.399444	9.82E-05
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Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0259	N	2.165388	0.000132
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0264	N	2.275153	3.52E-05
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0268	N	2.179496	4.32E-05
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0276	N	2.21373	6.91E-06
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Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu2715	P	2.648414	0.03557
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Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu4064	P	2.23846	0.002926
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu4084	P	2.15841	0.03557
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Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu4260	P	2.439087	0.03557
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Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu4487	P	2.168201	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu4648	P	2.631243	0.03557
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Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu5441	P	2.267822	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu5651	P	2.592784	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu5839	P	2.575576	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu5866	P	2.402546	0.03557

Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu5870	P	2.348388	0.03557
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Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu6200	P	2.290854	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu6358	P	2.473994	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu6427	P	2.50262	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu6486	P	2.461423	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu6526	P	2.288605	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu6633	P	2.358278	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu6645	P	2.464947	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu6664	P	2.208204	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu6702	P	2.223631	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu6713	P	2.373804	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu6717	P	2.49197	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu6866	P	2.061392	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu6879	P	2.385906	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu7032	P	2.426947	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu7033	P	2.599872	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu7062	P	2.230711	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu7122	P	2.512657	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu7144	P	2.102984	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu7246	P	2.443154	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu7327	P	2.308125	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Moryella	P	2.370568	0.005783
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Moryella.Otu0426	P	2.386594	0.001713
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Oribacterium.Otu4450	P	2.228104	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Oribacterium.Otu6669	P	2.010754	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Roseburia	N	4.05566	1.03E-14
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Roseburia.Otu0012	N	3.857048	9.4E-12
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Roseburia.Otu0034	N	3.466419	3.47E-10
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Roseburia.Otu0169	N	2.552445	7.9E-08
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Roseburia.Otu0227	N	2.439768	0.002522
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Roseburia.Otu0299	N	2.199818	9.32E-11

Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Roseburia.Otu0340	N	2.03786	2.01E-06
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Roseburia.Otu4298	P	2.573373	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Roseburia.Otu4554	P	2.593251	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Roseburia.Otu4665	P	2.670395	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Roseburia.Otu6467	P	2.441235	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Roseburia.Otu6520	P	2.350847	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Roseburia.Otu6896	P	2.161745	0.03557
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Ruminococcus2	N	3.515501	5.04E-14
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Ruminococcus2.Otu0051	N	3.188693	1.77E-10
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Ruminococcus2.Otu0052	N	3.075256	4.87E-05
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Ruminococcus2.Otu0152	N	2.340302	2.77E-05
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Ruminococcus2.Otu0213	N	2.349315	1.76E-05
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Ruminococcus2.Otu4786	P	2.465472	0.03557
Firmicutes.Clostridia.Clostridiales.Peptococcaceae_1.Peptococcus.Otu2327	P	2.415132	0.03557
Firmicutes.Clostridia.Clostridiales.Peptostreptococcaceae	P	2.995383	0.007626
Firmicutes.Clostridia.Clostridiales.Peptostreptococcaceae.Clostridium_XI	P	2.981835	5.94E-05
Firmicutes.Clostridia.Clostridiales.Peptostreptococcaceae.Clostridium_XI.Otu0145	P	2.725991	8.12E-06
Firmicutes.Clostridia.Clostridiales.Peptostreptococcaceae.Clostridium_XI.Otu0157	N	2.448942	1.21E-06
Firmicutes.Clostridia.Clostridiales.Peptostreptococcaceae.Clostridium_XI.Otu4494	P	2.496024	0.03557
Firmicutes.Clostridia.Clostridiales.Peptostreptococcaceae.Clostridium_XI.Otu5426	P	2.483986	0.03557
Firmicutes.Clostridia.Clostridiales.Peptostreptococcaceae.Clostridium_XI.Otu6352	P	2.831425	0.03557
Firmicutes.Clostridia.Clostridiales.Peptostreptococcaceae.Peptostreptococcus	P	2.131364	0.047713
Firmicutes.Clostridia.Clostridiales.Peptostreptococcaceae.Peptostreptococcus.Otu0283	P	2.150713	0.047455
Firmicutes.Clostridia.Clostridiales.Peptostreptococcaceae.Peptostreptococcus.Otu4294	P	2.248459	0.03557
Firmicutes.Clostridia.Clostridiales.Peptostreptococcaceae.Peptostreptococcus.Otu5198	P	2.611432	0.03557
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae	N	4.784961	3.63E-27
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Butyricicoccus	N	2.489513	8.71E-12
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Butyricicoccus.Otu0255	N	2.283081	1.67E-10
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Butyricicoccus.Otu4597	P	2.360366	0.03557
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Clostridium_IV	N	3.392065	1.24E-17
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Clostridium_IV.Otu0123	N	2.765504	3.05E-06
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Clostridium_IV.Otu0134	N	2.842239	0.008873

Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Clostridium_IV.Otu0333	N	2.083479	5.93E-05
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Clostridium_IV.Otu6867	P	2.483621	0.03557
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Faecalibacterium	N	4.599637	5.85E-20
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Faecalibacterium.Otu0003	N	4.547242	6.6E-19
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Faecalibacterium.Otu0024	N	3.468084	3.3E-08
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Faecalibacterium.Otu0191	N	2.470491	6.56E-11
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Faecalibacterium.Otu0338	N	2.033452	1.35E-13
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Faecalibacterium.Otu3489	P	2.433477	0.03557
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Faecalibacterium.Otu3998	P	2.021437	0.002926
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Faecalibacterium.Otu5055	P	2.607884	0.03557
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Faecalibacterium.Otu5116	P	2.370749	0.03557
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Faecalibacterium.Otu5647	P	2.62766	0.03557
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Faecalibacterium.Otu5828	P	2.343784	0.03557
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Flavonifractor	N	3.293399	8.68E-23
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Flavonifractor.Otu0055	N	3.174505	2.61E-19
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Flavonifractor.Otu0232	N	2.469019	0.006745
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Flavonifractor.Otu0296	N	2.144891	2.96E-09
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Flavonifractor.Otu7022	P	2.685374	0.03557
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Gemmiger	N	3.202421	5.5E-08
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Gemmiger.Otu0048	N	3.200677	5.35E-08
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Gemmiger.Otu5923	P	2.337617	0.03557
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Gemmiger.Otu7165	P	2.482002	0.03557
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Oscillibacter	N	3.778178	1.09E-20
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Oscillibacter.Otu0032	N	3.534052	1.54E-10
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Oscillibacter.Otu0084	N	3.098075	1.02E-06
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Oscillibacter.Otu0101	N	2.956057	5.61E-16
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Oscillibacter.Otu0271	N	2.22955	0.004887
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Pseudoflavonifractor	P	3.594009	1.34E-13
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Pseudoflavonifractor.Otu0057	P	3.602119	8.09E-06
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Pseudoflavonifractor.Otu0218	N	2.423235	1.42E-11
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Pseudoflavonifractor.Otu5091	P	2.540533	0.03557
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Pseudoflavonifractor.Otu6831	P	2.871587	0.03557

Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified	N	3.854641	1.11E-22
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu0062	N	3.177166	1.77E-05
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu0082	N	3.159992	0.000347
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu0177	N	2.62794	3.22E-06
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu0180	N	2.505808	4.98E-13
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu0194	N	2.632559	0.000995
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu0221	N	2.232862	1.56E-06
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu0233	N	2.377574	0.000141
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu0281	N	2.160321	0.00089
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu0312	N	2.12714	0.001273
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu0317	N	2.03109	7.82E-05
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu0332	N	2.091857	2.4E-08
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu0356	N	2.029981	1.46E-05
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu2266	P	2.341938	0.03557
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu4650	P	2.306489	0.03557
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu7067	P	2.448556	0.03557
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu7079	P	2.233461	0.03557
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcus	N	3.547932	4E-13
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcus.Otu0045	N	3.311856	5.46E-08
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcus.Otu0113	N	2.822791	8.93E-05
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcus.Otu0270	N	2.267079	0.000684
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Sporobacter	N	2.902963	7.68E-09
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Sporobacter.Otu0159	N	2.692154	0.000123
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Sporobacter.Otu0202	N	2.35372	5.3E-05
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Subdoligranulum	N	2.900058	1.35E-11
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Subdoligranulum.Otu0093	N	2.936091	1.07E-11
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Subdoligranulum.Otu0204	N	2.240291	0.00186
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Subdoligranulum.Otu1818	P	2.5869	0.03557
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Subdoligranulum.Otu6745	P	2.498552	0.03557
Firmicutes.Erysipelotrichia	P	2.949362	2.39E-05
Firmicutes.Erysipelotrichia.Erysipelotrichales	P	2.949362	2.39E-05
Firmicutes.Erysipelotrichia.Erysipelotrichales.Erysipelotrichaceae	P	2.949362	2.39E-05

Firmicutes.Erysipelotrichia.Erysipelotrichales.Erysipelotrichaceae.Clostridium_XVIII	N	2.79156	0.000116
Firmicutes.Erysipelotrichia.Erysipelotrichales.Erysipelotrichaceae.Clostridium_XVIII.Otu0109	P	2.741841	0.002632
Firmicutes.Erysipelotrichia.Erysipelotrichales.Erysipelotrichaceae.Clostridium_XVIII.Otu5774	P	2.276232	0.03557
Firmicutes.Erysipelotrichia.Erysipelotrichales.Erysipelotrichaceae.Clostridium_XVIII.Otu7106	P	2.499812	0.03557
Firmicutes.Erysipelotrichia.Erysipelotrichales.Erysipelotrichaceae.Erysipelotrichaceae_unclassified	N	2.520372	0.031372
Firmicutes.Erysipelotrichia.Erysipelotrichales.Erysipelotrichaceae.Holdemania.Otu6413	P	2.36281	0.03557
Firmicutes.Erysipelotrichia.Erysipelotrichales.Erysipelotrichaceae.Solobacterium	P	2.121571	0.039734
Firmicutes.Erysipelotrichia.Erysipelotrichales.Erysipelotrichaceae.Solobacterium.Otu0391	P	2.137067	0.034531
Firmicutes.Erysipelotrichia.Erysipelotrichales.Erysipelotrichaceae.Solobacterium.Otu5546	P	2.285387	0.03557
Firmicutes.Erysipelotrichia.Erysipelotrichales.Erysipelotrichaceae.Turicibacter	P	2.902539	0.003408
Firmicutes.Erysipelotrichia.Erysipelotrichales.Erysipelotrichaceae.Turicibacter.Otu0203	P	2.889647	0.003354
Firmicutes.Firmicutes_unclassified	N	3.029602	3.14E-10
Firmicutes.Firmicutes_unclassified.Firmicutes_unclassified	N	3.030354	3.14E-10
Firmicutes.Firmicutes_unclassified.Firmicutes_unclassified.Firmicutes_unclassified	N	3.029675	3.14E-10
Firmicutes.Firmicutes_unclassified.Firmicutes_unclassified.Firmicutes_unclassified.Firmicutes_unclassified	N	3.028809	3.14E-10
Firmicutes.Firmicutes_unclassified.Firmicutes_unclassified.Firmicutes_unclassified.Firmicutes_unclassified.Otu0170	N	2.599059	0.00021
Firmicutes.Firmicutes_unclassified.Firmicutes_unclassified.Firmicutes_unclassified.Firmicutes_unclassified.Otu0229	N	2.35898	6.25E-06
Firmicutes.Firmicutes_unclassified.Firmicutes_unclassified.Firmicutes_unclassified.Firmicutes_unclassified.Otu5031	P	2.650115	0.03557
Firmicutes.Firmicutes_unclassified.Firmicutes_unclassified.Firmicutes_unclassified.Firmicutes_unclassified.Otu5248	P	2.585531	0.03557
Firmicutes.Firmicutes_unclassified.Firmicutes_unclassified.Firmicutes_unclassified.Firmicutes_unclassified.Otu6006	P	2.530373	0.03557
Firmicutes.Firmicutes_unclassified.Firmicutes_unclassified.Firmicutes_unclassified.Firmicutes_unclassified.Otu6657	P	2.500888	0.03557
Firmicutes.Firmicutes_unclassified.Firmicutes_unclassified.Firmicutes_unclassified.Firmicutes_unclassified.Otu6704	P	2.637284	0.03557
Firmicutes.Negativicutes	N	4.170994	3.64E-05
Firmicutes.Negativicutes.Selenomonadales	N	4.170994	3.64E-05
Firmicutes.Negativicutes.Selenomonadales.Acidaminococcaceae	N	4.054151	1.32E-08
Firmicutes.Negativicutes.Selenomonadales.Acidaminococcaceae.Acidaminococcaceae_unclassified.Otu0053	N	3.225977	0.046195
Firmicutes.Negativicutes.Selenomonadales.Acidaminococcaceae.Acidaminococcus.Otu3080	P	2.594685	0.03557
Firmicutes.Negativicutes.Selenomonadales.Acidaminococcaceae.Acidaminococcus.Otu5323	P	2.619894	0.03557
Firmicutes.Negativicutes.Selenomonadales.Acidaminococcaceae.Acidaminococcus.Otu6266	P	2.490171	0.03557
Firmicutes.Negativicutes.Selenomonadales.Acidaminococcaceae.Phascolarctobacterium	N	3.928497	9.52E-06
Firmicutes.Negativicutes.Selenomonadales.Acidaminococcaceae.Phascolarctobacterium.Otu0011	N	3.917668	6.93E-06
Firmicutes.Negativicutes.Selenomonadales.Acidaminococcaceae.Phascolarctobacterium.Otu3585	P	2.396318	0.03557

Firmicutes.Negativicutes.Selenomonadales.Acidaminococcaceae.Phascolarctobacterium.Otu6642	P	2.230598	0.03557
Firmicutes.Negativicutes.Selenomonadales.Veillonellaceae.Centipeda.Otu5202	P	2.190794	0.03557
Firmicutes.Negativicutes.Selenomonadales.Veillonellaceae.Dialister	N	3.596465	0.012663
Firmicutes.Negativicutes.Selenomonadales.Veillonellaceae.Dialister.Otu0027	N	3.570475	0.005674
Firmicutes.Negativicutes.Selenomonadales.Veillonellaceae.Dialister.Otu4028	P	2.056177	0.03557
Firmicutes.Negativicutes.Selenomonadales.Veillonellaceae.Dialister.Otu5723	P	2.551057	0.03557
Firmicutes.Negativicutes.Selenomonadales.Veillonellaceae.Dialister.Otu7200	P	2.189638	0.03557
Firmicutes.Negativicutes.Selenomonadales.Veillonellaceae.Dialister.Otu7264	P	2.769259	0.03557
Firmicutes.Negativicutes.Selenomonadales.Veillonellaceae.Megamonas	N	3.364104	0.046939
Firmicutes.Negativicutes.Selenomonadales.Veillonellaceae.Megamonas.Otu0033	N	3.363306	0.046212
Firmicutes.Negativicutes.Selenomonadales.Veillonellaceae.Veillonella.Otu1529	P	2.640799	0.03557
Firmicutes.Negativicutes.Selenomonadales.Veillonellaceae.Veillonella.Otu5737	P	2.539543	0.03557
Firmicutes.Negativicutes.Selenomonadales.Veillonellaceae.Veillonella.Otu6162	P	2.318364	0.03557
Firmicutes.Negativicutes.Selenomonadales.Veillonellaceae.Veillonella.Otu6364	P	2.350364	0.03557
Firmicutes.Negativicutes.Selenomonadales.Veillonellaceae.Veillonella.Otu7097	P	2.52606	0.03557
Firmicutes.Negativicutes.Selenomonadales.Veillonellaceae.Veillonellaceae_unclassified.Otu2178	P	2.588507	0.03557
Firmicutes.Negativicutes.Selenomonadales.Veillonellaceae.Veillonellaceae_unclassified.Otu4355	P	2.477507	0.03557
Firmicutes.Negativicutes.Selenomonadales.Veillonellaceae.Veillonellaceae_unclassified.Otu5240	P	2.340486	0.03557
Firmicutes.Negativicutes.Selenomonadales.Veillonellaceae.Veillonellaceae_unclassified.Otu7087	P	2.504454	0.03557
Firmicutes.Negativicutes.Selenomonadales.Veillonellaceae.Veillonellaceae_unclassified.Otu7273	P	2.54682	0.03557
Fusobacteria	P	3.785157	0.034539
Fusobacteria.Fusobacteriia	P	3.785157	0.034539
Fusobacteria.Fusobacteriia.Fusobacteriales	P	3.785157	0.034539
Fusobacteria.Fusobacteriia.Fusobacteriales.Fusobacteriaceae.Cetobacterium.Otu4232	P	2.502359	0.03557
Fusobacteria.Fusobacteriia.Fusobacteriales.Fusobacteriaceae.Cetobacterium.Otu6045	P	2.667195	0.03557
Fusobacteria.Fusobacteriia.Fusobacteriales.Fusobacteriaceae.Fusobacterium.Otu3413	P	2.414368	0.03557
Fusobacteria.Fusobacteriia.Fusobacteriales.Fusobacteriaceae.Fusobacterium.Otu3825	P	2.161426	0.000264
Fusobacteria.Fusobacteriia.Fusobacteriales.Fusobacteriaceae.Fusobacterium.Otu3876	P	2.640737	0.03557
Fusobacteria.Fusobacteriia.Fusobacteriales.Fusobacteriaceae.Fusobacterium.Otu4319	P	2.226656	0.03557
Fusobacteria.Fusobacteriia.Fusobacteriales.Leptotrichiaceae	P	2.527169	0.003093
Fusobacteria.Fusobacteriia.Fusobacteriales.Leptotrichiaceae.Leptotrichia	P	2.515438	0.014068
Fusobacteria.Fusobacteriia.Fusobacteriales.Leptotrichiaceae.Leptotrichia.Otu4517	P	2.700435	0.03557

Fusobacteria.Fusobacteriia.Fusobacteriales.Leptotrichiaceae.Leptotrichia.Otu7292	P	2.328657	0.03557
Fusobacteria.Fusobacteriia.Fusobacteriales.Leptotrichiaceae.Sneathia.Otu1524	P	2.502713	0.03557
Lentisphaerae	N	2.287408	0.013166
Lentisphaerae.Lentisphaeria	N	2.087376	0.018112
Lentisphaerae.Lentisphaeria.Victivallales	N	2.087601	0.018112
Lentisphaerae.Lentisphaeria.Victivallales.Victivallaceae	N	2.078661	0.018112
Lentisphaerae.Lentisphaeria.Victivallales.Victivallaceae.Victivallis	N	2.086662	0.018112
Planctomycetes	P	2.486531	0.03557
Planctomycetes.Planctomycetia	P	2.122229	0.03557
Planctomycetes.Planctomycetia.Planctomycetales	P	2.551204	0.03557
Planctomycetes.Planctomycetia.Planctomycetales.Planctomycetaceae	P	2.142176	0.03557
Planctomycetes.Planctomycetia.Planctomycetales.Planctomycetaceae.Planctomycetaceae_unclassified	P	2.071026	0.03557
Planctomycetes.Planctomycetia.Planctomycetales.Planctomycetaceae.Planctomycetaceae_unclassified.Otu4838	P	2.248324	0.03557
Proteobacteria	P	5.353459	3.06E-50
Proteobacteria.Alphaproteobacteria.Alphaproteobacteria_unclassified	N	3.087503	8.74E-05
Proteobacteria.Alphaproteobacteria.Alphaproteobacteria_unclassified.Alphaproteobacteria_unclassified	N	3.096964	8.74E-05
Proteobacteria.Alphaproteobacteria.Alphaproteobacteria_unclassified.Alphaproteobacteria_unclassified.Alphaproteobacteria_unclassified	N	3.093232	8.74E-05
Proteobacteria.Alphaproteobacteria.Alphaproteobacteria_unclassified.Alphaproteobacteria_unclassified.Alphaproteobacteria_unclassified.Otu0252	N	2.336322	0.008009
Proteobacteria.Alphaproteobacteria.Alphaproteobacteria_unclassified.Alphaproteobacteria_unclassified.Alphaproteobacteria_unclassified.Otu6041	P	2.094031	0.03557
Proteobacteria.Alphaproteobacteria.Caulobacterales.Caulobacteraceae.Brevundimonas.Otu1675	P	2.053016	0.000264
Proteobacteria.Alphaproteobacteria.Rhizobiales	P	2.162724	0.000192
Proteobacteria.Alphaproteobacteria.Rhizobiales.Brucellaceae.Brucella	P	2.263601	0.03557
Proteobacteria.Alphaproteobacteria.Rhizobiales.Brucellaceae.Brucella.Otu5504	P	2.450309	0.03557
Proteobacteria.Alphaproteobacteria.Rhizobiales.Rhizobiales_unclassified.Rhizobiales_unclassified.Otu5182	P	2.189782	0.03557
Proteobacteria.Alphaproteobacteria.Rhodospirillales.Acetobacteraceae.Roseomonas	P	2.432543	0.03557
Proteobacteria.Alphaproteobacteria.Rhodospirillales.Acetobacteraceae.Roseomonas.Otu3481	P	2.253588	0.03557
Proteobacteria.Alphaproteobacteria.Sphingomonadales	P	2.378022	0.000284
Proteobacteria.Alphaproteobacteria.Sphingomonadales.Sphingomonadaceae	P	2.393832	0.000284
Proteobacteria.Alphaproteobacteria.Sphingomonadales.Sphingomonadaceae.Sphingomonas	P	2.398419	3.14E-05
Proteobacteria.Alphaproteobacteria.Sphingomonadales.Sphingomonadaceae.Sphingomonas.Otu0411	P	2.393717	0.000101
Proteobacteria.Betaproteobacteria	N	3.533047	2.13E-06
Proteobacteria.Betaproteobacteria.Burkholderiales	N	3.688472	1.96E-10

Proteobacteria.Betaproteobacteria.Burkholderiales.Alcaligenaceae.Alcaligenaceae_unclassified	P	2.36543	0.039978
Proteobacteria.Betaproteobacteria.Burkholderiales.Alcaligenaceae.Alcaligenaceae_unclassified.Otu0320	P	2.392006	0.039978
Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae.Burkholderia	P	2.352729	0.03557
Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae.Burkholderia.Otu5475	P	2.558869	0.03557
Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiales_incertae_sedis	N	2.211224	0.031509
Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiales_incertae_sedis.Tepidimonas.Otu1749	N	2.135362	0.031509
Proteobacteria.Betaproteobacteria.Burkholderiales.Comamonadaceae.Comamonadaceae_unclassified	P	2.561033	0.03557
Proteobacteria.Betaproteobacteria.Burkholderiales.Comamonadaceae.Comamonadaceae_unclassified.Otu4603	P	2.439334	0.03557
Proteobacteria.Betaproteobacteria.Burkholderiales.Oxalobacteraceae	P	2.314787	0.00341
Proteobacteria.Betaproteobacteria.Burkholderiales.Oxalobacteraceae.Oxalobacter	P	2.288228	0.002013
Proteobacteria.Betaproteobacteria.Burkholderiales.Oxalobacteraceae.Oxalobacter.Otu0712	P	2.327092	0.002013
Proteobacteria.Betaproteobacteria.Burkholderiales.Sutterellaceae	N	3.6902	2.19E-10
Proteobacteria.Betaproteobacteria.Burkholderiales.Sutterellaceae.Parasutterella	N	3.269824	1.87E-09
Proteobacteria.Betaproteobacteria.Burkholderiales.Sutterellaceae.Parasutterella.Otu0028	N	3.243129	2.29E-09
Proteobacteria.Betaproteobacteria.Burkholderiales.Sutterellaceae.Sutterella	N	3.427336	0.02067
Proteobacteria.Betaproteobacteria.Burkholderiales.Sutterellaceae.Sutterella.Otu4467	P	2.407859	0.03557
Proteobacteria.Betaproteobacteria.Burkholderiales.Sutterellaceae.Sutterella.Otu4934	P	2.146876	0.03557
Proteobacteria.Betaproteobacteria.Burkholderiales.Sutterellaceae.Sutterella.Otu5110	P	2.637208	0.03557
Proteobacteria.Betaproteobacteria.Burkholderiales.Sutterellaceae.Sutterella.Otu5804	P	2.536346	0.03557
Proteobacteria.Betaproteobacteria.Burkholderiales.Sutterellaceae.Sutterella.Otu6629	P	2.549275	0.03557
Proteobacteria.Betaproteobacteria.Burkholderiales.Sutterellaceae.Sutterella.Otu6969	P	2.111905	0.002926
Proteobacteria.Betaproteobacteria.Burkholderiales.Sutterellaceae.Sutterella.Otu7216	P	2.596655	0.03557
Proteobacteria.Betaproteobacteria.Methylophilales	P	2.167405	0.03557
Proteobacteria.Betaproteobacteria.Methylophilales.Methylophilaceae	P	2.380935	0.03557
Proteobacteria.Betaproteobacteria.Methylophilales.Methylophilaceae.Methylophilus	P	2.406777	0.03557
Proteobacteria.Betaproteobacteria.Methylophilales.Methylophilaceae.Methylophilus.Otu7233	P	2.510542	0.03557
Proteobacteria.Betaproteobacteria.Neisseriales	P	3.177386	0.003012
Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae	P	3.159134	0.003012
Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Eikenella	P	2.628969	0.002793
Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Eikenella.Otu0288	P	2.615909	0.002793
Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Eikenella.Otu6140	P	2.610457	0.03557
Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Eikenella.Otu6568	P	2.333256	0.03557

Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria	P	3.037947	0.017965
Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria.Otu0162	P	3.016513	0.021823
Proteobacteria.Deltaproteobacteria	N	2.825968	1.41E-10
Proteobacteria.Deltaproteobacteria.Bdellovibrionales.Bacteriovoracaceae	P	2.301322	0.03557
Proteobacteria.Deltaproteobacteria.Bdellovibrionales.Bacteriovoracaceae.Peredibacter	P	2.617674	0.03557
Proteobacteria.Deltaproteobacteria.Bdellovibrionales.Bacteriovoracaceae.Peredibacter.Otu4697	P	2.288183	0.03557
Proteobacteria.Deltaproteobacteria.Desulfovibrionales	N	2.796063	7.44E-11
Proteobacteria.Deltaproteobacteria.Desulfovibrionales.Desulfovibrionaceae	N	2.749284	2.62E-10
Proteobacteria.Deltaproteobacteria.Desulfovibrionales.Desulfovibrionaceae.Bilophila	N	2.654933	1.27E-09
Proteobacteria.Deltaproteobacteria.Desulfovibrionales.Desulfovibrionaceae.Bilophila.Otu0097	N	2.644006	2.29E-09
Proteobacteria.Deltaproteobacteria.Desulfovibrionales.Desulfovibrionaceae.Bilophila.Otu6025	P	2.422381	0.03557
Proteobacteria.Deltaproteobacteria.Desulfovibrionales.Desulfovibrionaceae.Desulfovibrio	N	2.079726	0.000566
Proteobacteria.Deltaproteobacteria.Desulfovibrionales.Desulfovibrionaceae.Desulfovibrio.Otu0309	N	2.048282	0.000193
Proteobacteria.Epsilonproteobacteria.Campylobacterales.Campylobacteraceae.Campylobacter.Otu3615	P	2.32394	0.03557
Proteobacteria.Epsilonproteobacteria.Campylobacterales.Campylobacteraceae.Campylobacter.Otu4138	P	2.294081	0.03557
Proteobacteria.Epsilonproteobacteria.Campylobacterales.Campylobacteraceae.Campylobacter.Otu4984	P	2.464109	0.03557
Proteobacteria.Gammaproteobacteria	P	5.359334	3.27E-48
Proteobacteria.Gammaproteobacteria.Aeromonadales.Aeromonadaceae.Aeromonas.Otu1240	P	2.001431	0.002926
Proteobacteria.Gammaproteobacteria.Aeromonadales.Aeromonadaceae.Aeromonas.Otu4542	P	2.525496	0.03557
Proteobacteria.Gammaproteobacteria.Aeromonadales.Aeromonadaceae.Aeromonas.Otu5797	P	2.539359	0.03557
Proteobacteria.Gammaproteobacteria.Aeromonadales.Succinivibrionaceae.Succinatimonas.Otu4172	P	2.323722	0.03557
Proteobacteria.Gammaproteobacteria.Aeromonadales.Succinivibrionaceae.Succinatimonas.Otu5859	P	2.495797	0.03557
Proteobacteria.Gammaproteobacteria.Aeromonadales.Succinivibrionaceae.Succinatimonas.Otu6280	P	2.334621	0.03557
Proteobacteria.Gammaproteobacteria.Alteromonadales.Alteromonadaceae.Alishewanella	P	2.303936	0.03557
Proteobacteria.Gammaproteobacteria.Alteromonadales.Alteromonadaceae.Alishewanella.Otu2203	P	2.395861	0.03557
Proteobacteria.Gammaproteobacteria.Chromatiales	P	2.483574	0.03557
Proteobacteria.Gammaproteobacteria.Chromatiales.Chromatiaceae	P	2.516479	0.03557
Proteobacteria.Gammaproteobacteria.Chromatiales.Chromatiaceae.Rheinheimera	P	2.270244	0.03557
Proteobacteria.Gammaproteobacteria.Chromatiales.Chromatiaceae.Rheinheimera.Otu4540	P	2.327604	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales	P	5.301362	1.14E-38
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae	P	5.301362	1.14E-38
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacter	P	4.817627	3.4E-16

Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacter.Otu0006	P	4.816932	2.91E-16
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified	P	3.294698	4.36E-24
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu0253	P	2.90962	1.5E-24
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu0372	P	3.004201	0.039891
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu2850	P	2.188071	0.002926
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu3084	P	2.250869	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu3649	P	2.587261	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu3661	P	2.407781	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu3805	P	2.060686	0.002926
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu3997	P	2.718547	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu4088	P	2.154319	0.002926
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu4123	P	2.643966	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu4347	P	2.612567	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu4482	P	2.430658	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu4628	P	2.787841	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu4728	P	2.365449	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu4795	P	2.550235	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu5039	P	2.252896	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu5139	P	2.264045	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu5382	P	2.370363	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu5476	P	2.183803	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu6015	P	2.453535	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu6255	P	2.358716	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu6362	P	2.389493	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu6393	P	2.267087	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu6412	P	2.409003	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu6796	P	2.43401	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu6852	P	2.411768	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu6930	P	2.176371	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Escherichia_Shigella	P	5.103562	2.57E-23
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Escherichia_Shigella.Otu0002	P	5.102709	2.29E-23
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Escherichia_Shigella.Otu0228	P	2.239215	0.00265

Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Escherichia_Shigella.Otu2853	P	2.42877	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Escherichia_Shigella.Otu4490	P	2.428513	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Escherichia_Shigella.Otu4876	P	2.556689	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Escherichia_Shigella.Otu5223	P	2.628083	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Escherichia_Shigella.Otu5257	P	2.318015	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Escherichia_Shigella.Otu5474	P	2.641203	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Escherichia_Shigella.Otu5700	P	2.465324	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Escherichia_Shigella.Otu6400	P	2.173159	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Escherichia_Shigella.Otu6405	P	2.52552	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Escherichia_Shigella.Otu6699	P	2.65307	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Morganella	P	3.422344	0.008104
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Morganella.Otu0086	P	3.427451	0.008104
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Morganella.Otu7234	P	2.490169	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Proteus	P	3.422889	0.000303
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Proteus.Otu0058	P	3.418936	0.000303
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Proteus.Otu1884	P	2.393037	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Proteus.Otu2417	P	2.04295	0.030565
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Proteus.Otu3763	P	2.398993	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Proteus.Otu4477	P	2.494135	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Proteus.Otu5809	P	2.599233	0.03557
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Proteus.Otu5959	P	2.549232	0.03557
Proteobacteria.Gammaproteobacteria.Gammaproteobacteria_unclassified.Gammaproteobacteria_unclassified.Gammaproteobacteria_unclassified.Otu3465	P	2.518888	0.03557
Proteobacteria.Gammaproteobacteria.Gammaproteobacteria_unclassified.Gammaproteobacteria_unclassified.Gammaproteobacteria_unclassified.Otu4197	P	2.549641	0.03557
Proteobacteria.Gammaproteobacteria.Gammaproteobacteria_unclassified.Gammaproteobacteria_unclassified.Gammaproteobacteria_unclassified.Otu4579	P	2.035739	0.03557
Proteobacteria.Gammaproteobacteria.Gammaproteobacteria_unclassified.Gammaproteobacteria_unclassified.Gammaproteobacteria_unclassified.Otu4767	P	2.755648	0.03557
Proteobacteria.Gammaproteobacteria.Gammaproteobacteria_unclassified.Gammaproteobacteria_unclassified.Gammaproteobacteria_unclassified.Otu4895	P	2.46481	0.03557
Proteobacteria.Gammaproteobacteria.Gammaproteobacteria_unclassified.Gammaproteobacteria_unclassified.Gammaproteobacteria_unclassified.Otu6093	P	2.527669	0.03557
Proteobacteria.Gammaproteobacteria.Pasteurellales	P	4.085783	0.026586
Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae	P	4.085783	0.026586
Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Haemophilus	P	3.314158	0.00061
Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Haemophilus.Otu0130	P	3.320212	0.000796
Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Haemophilus.Otu3221	P	2.275693	0.031509

Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Haemophilus.Otu3767	P	2.866418	0.03557
Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Haemophilus.Otu4307	P	2.31283	0.03557
Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Haemophilus.Otu6077	P	2.538376	0.03557
Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Haemophilus.Otu6659	P	2.402792	0.03557
Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Pasteurellaceae_unclassified.Otu4565	P	2.567659	0.03557
Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Pasteurellaceae_unclassified.Otu5017	P	2.372498	0.03557
Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Pasteurellaceae_unclassified.Otu5992	P	2.440301	0.03557
Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Pasteurellaceae_unclassified.Otu6582	P	2.130649	0.03557
Proteobacteria.Gammaproteobacteria.Pseudomonadales	P	3.858651	0.003651
Proteobacteria.Gammaproteobacteria.Pseudomonadales.Moraxellaceae	P	2.494967	0.000592
Proteobacteria.Gammaproteobacteria.Pseudomonadales.Moraxellaceae.Acinetobacter	P	2.437651	0.003512
Proteobacteria.Gammaproteobacteria.Pseudomonadales.Moraxellaceae.Acinetobacter.Otu0620	P	2.449528	0.000192
Proteobacteria.Gammaproteobacteria.Pseudomonadales.Pseudomonadaceae	P	3.89146	0.019706
Proteobacteria.Gammaproteobacteria.Pseudomonadales.Pseudomonadaceae.Pseudomonadaceae_unclassified.Otu4469	P	2.293922	0.03557
Proteobacteria.Gammaproteobacteria.Pseudomonadales.Pseudomonadaceae.Pseudomonadaceae_unclassified.Otu6501	P	2.360873	0.03557
Proteobacteria.Gammaproteobacteria.Pseudomonadales.Pseudomonadaceae.Pseudomonas	P	3.884915	0.014036
Proteobacteria.Gammaproteobacteria.Pseudomonadales.Pseudomonadaceae.Pseudomonas.Otu0455	P	2.260235	0.004047
Proteobacteria.Gammaproteobacteria.Pseudomonadales.Pseudomonadaceae.Pseudomonas.Otu4633	P	2.357126	0.002926
Proteobacteria.Gammaproteobacteria.Vibrionales.Vibrionaceae.Photobacterium.Otu3910	P	2.348619	0.03557
Proteobacteria.Gammaproteobacteria.Xanthomonadales.Xanthomonadaceae.Luteimonas.Otu5006	P	2.535717	0.03557
Proteobacteria.Gammaproteobacteria.Xanthomonadales.Xanthomonadaceae.Stenotrophomonas.Otu3493	P	2.69631	0.03557
Proteobacteria.Gammaproteobacteria.Xanthomonadales.Xanthomonadaceae.Stenotrophomonas.Otu5592	P	2.502213	0.03557
Tenericutes.Mollicutes.Mycoplasmatales.Mycoplasmataceae.Mycoplasma.Otu5320	P	2.431214	0.03557
Verrucomicrobia	N	3.826575	2.51E-05
Verrucomicrobia.Verrucomicrobiae	N	3.823555	8.84E-05
Verrucomicrobia.Verrucomicrobiae.Verrucomicrobiales	N	3.823555	8.84E-05
Verrucomicrobia.Verrucomicrobiae.Verrucomicrobiales.Verrucomicrobiaceae	N	3.823555	8.84E-05
Verrucomicrobia.Verrucomicrobiae.Verrucomicrobiales.Verrucomicrobiaceae.Akkermansia	N	3.823555	8.84E-05
Verrucomicrobia.Verrucomicrobiae.Verrucomicrobiales.Verrucomicrobiaceae.Akkermansia.Otu0031	N	3.539659	0.026002

Table S2

PICRUSt-predicted pathways (KEGG Level 3) found to be uniquely enriched in microbiota data for specific stool colour following comparison with brown faecal samples. A range of other pathways were found to be commonly enriched when different stool colours were compared to brown stool.

Stool colour	**KEGG Pathway**
Black	Lipid biosynthesis proteins
Yellow	Cell cycle: Caulobacter DNA replication proteins Glycolysis / Gluconeogenesis Lipopolysaccharide biosynthesis proteins Geraniol degradation Membrane and intracellular structural molecules Other ion coupled transporters Pores ion channels
White	DNA replication Cysteine and methionine metabolism Flavone and flavonol biosynthesis Stilbenoid diarylheptanoid and gingerol biosynthesis Biosynthesis of ansamycins Ethylbenzene degradation Translation proteins
Red	Notch signaling pathway Wnt signaling pathway Base excision repair Glycine serine and threonine metabolism Glycerolipid metabolism
Colourless	Bacterial invasion of epithelial cells C5 Branched dibasic acid metabolism Pentose phosphate pathway Steroid hormone biosynthesis

	Biosynthesis of vancomycin group antibiotics Carotenoid biosynthesis Polycyclic aromatic hydrocarbon degradation Digestive System PPAR signaling pathway Biosynthesis and biodegradation of secondary metabolites
Green	Phenylalanine metabolism Glyoxylate and dicarboxylate metabolism Pyruvate metabolism Nitrogen metabolism Fatty acid biosynthesis Porphyrin and chlorophyll metabolism Retinol metabolism Vitamin B6 metabolism D-Alanine metabolism Tetracycline biosynthesis Aminobenzoate degradation Drug metabolism cytochrome P450 Drug metabolism other enzymes Metabolism of xenobiotics by cytochrome P450 NOD like receptor signaling pathway Carbohydrate metabolism

Table S3

Bacterial taxa enriched in bacterial or viral acute gastroenteritis cases. Analysis was performed using LEfSe. BAC: enriched in bacterial acute gastroenteritis; VIR: enriched in viral acute gastroenteritis.

Microbial Taxa	**Group**	**LDA Score**	**P-value**
Actinobacteria	VIR	3.819957	0.042385
Actinobacteria.Actinobacteria	VIR	3.819957	0.042385
Actinobacteria.Actinobacteria.Actinomycetales	BAC	3.086093	0.049478
Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae	BAC	2.962643	0.019651
Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Actinomyces	BAC	2.952841	0.026711
Actinobacteria.Actinobacteria.Bifidobacteriales	VIR	3.790115	0.017854
Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae	VIR	3.790115	0.017854
Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae.Bifidobacterium	VIR	3.789649	0.016236
Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae.Bifidobacterium.Otu0013	VIR	3.779967	0.014218
Actinobacteria.Actinobacteria.Coriobacteriales	VIR	3.181984	0.024339
Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae	VIR	3.181984	0.024339
Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.Asaccharobacter	VIR	2.15698	0.021881
Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.Asaccharobacter.Otu0589	VIR	2.107921	0.04772
Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.Collinsella	VIR	3.227099	0.000196
Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.Collinsella.Otu0088	VIR	3.223773	0.000185
Bacteria_unclassified	BAC	3.097851	0.032611
Bacteria_unclassified.Bacteria_unclassified	BAC	3.097851	0.032611
Bacteria_unclassified.Bacteria_unclassified.Bacteria_unclassified	BAC	3.097851	0.032611
Bacteria_unclassified.Bacteria_unclassified.Bacteria_unclassified.Bacteria_unclassified	BAC	3.097851	0.032611
Bacteria_unclassified.Bacteria_unclassified.Bacteria_unclassified.Bacteria_unclassified.Bacteria_unclassified	BAC	3.097851	0.032611
Bacteria_unclassified.Bacteria_unclassified.Bacteria_unclassified.Bacteria_unclassified.Bacteria_unclassified.Otu0073	BAC	2.992939	0.000345
Bacteria_unclassified.Bacteria_unclassified.Bacteria_unclassified.Bacteria_unclassified.Bacteria_unclassified.Otu0096	VIR	2.098758	0.009545
Bacteroidetes	VIR	4.673476	0.03476
Bacteroidetes.Bacteroidia	VIR	4.691831	0.027511
Bacteroidetes.Bacteroidia.Bacteroidales	VIR	4.691831	0.027511

Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0001	VIR	4.383742	0.008424
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0010	VIR	3.898617	0.022255
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0020	VIR	3.78897	0.01851
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0030	VIR	3.490538	0.002154
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0158	VIR	2.696595	0.000914
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0193	VIR	2.539525	0.014982
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0201	VIR	2.126747	0.049803
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0210	VIR	2.525164	0.027231
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0214	VIR	2.253262	0.03293
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0242	VIR	2.344592	0.001563
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0243	VIR	2.544283	0.004986
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0300	VIR	2.208003	0.015586
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0322	VIR	2.527519	0.00195
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0378	VIR	2.121595	0.006958
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0404	VIR	2.476947	0.023733
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0420	VIR	2.084469	0.0107
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0445	VIR	2.304637	0.000203
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0538	BAC	2.131119	0.022546
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0649	VIR	2.219085	0.011817
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0653	BAC	3.062748	0.013905
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0731	VIR	2.103121	0.046143
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0789	VIR	2.033064	0.006472
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0838	VIR	2.24246	0.04772
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0857	VIR	2.622492	0.008365
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu0930	VIR	2.337439	0.016957
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu1029	VIR	2.847424	0.023351
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu1046	VIR	2.519428	0.04081
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu1192	VIR	2.462371	0.023351
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu1273	VIR	2.486582	0.023351
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides.Otu1941	VIR	2.992537	0.023351
Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidales_unclassified.Bacteroidales_unclassified.Otu0884	VIR	2.261603	0.028114
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae	VIR	4.179259	0.001466

Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Barnesiella	VIR	3.958317	0.005016
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Butyricimonas.Otu0070	VIR	3.190242	0.048783
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Odoribacter	VIR	3.418337	0.031845
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Odoribacter.Otu0043	VIR	3.428519	0.013421
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Parabacteroides	VIR	3.60135	0.007061
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Parabacteroides.Otu0019	VIR	3.420619	0.000773
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Parabacteroides.Otu0022	VIR	3.313753	0.016722
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Parabacteroides.Otu0492	VIR	2.446295	0.023351
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Porphyromonadaceae_unclassified.Otu0150	VIR	3.092866	0.01148
Bacteroidetes.Bacteroidia.Bacteroidales.Porphyromonadaceae.Porphyromonadaceae_unclassified.Otu0696	VIR	2.185798	0.01576
Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Prevotella.Otu0316	BAC	2.557841	0.021315
Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae	VIR	4.260758	0.000378
Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Alistipes	VIR	4.262887	0.000302
Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Alistipes.Otu0015	VIR	3.987898	0.001527
Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Alistipes.Otu0025	VIR	3.854689	0.02626
Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Alistipes.Otu0075	VIR	2.945027	2.94E-05
Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Alistipes.Otu0197	VIR	2.191886	0.006474
Bacteroidetes.Bacteroidia.Bacteroidales.Rikenellaceae.Alistipes.Otu0508	VIR	2.119191	0.001046
Firmicutes.Bacilli.Lactobacillales.Enterococcaceae	BAC	3.367762	0.000146
Firmicutes.Bacilli.Lactobacillales.Enterococcaceae.Enterococcus	BAC	3.364261	0.000153
Firmicutes.Bacilli.Lactobacillales.Enterococcaceae.Enterococcus.Otu0009	BAC	3.359233	0.000168
Firmicutes.Bacilli.Lactobacillales.Enterococcaceae.Enterococcus.Otu0473	BAC	2.537811	0.049355
Firmicutes.Bacilli.Lactobacillales.Leuconostocaceae.Weissella	BAC	2.310907	0.049355
Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus.Otu1753	BAC	3.465571	0.047379
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1	BAC	3.538807	0.028311
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1.Clostridium_sensu_stricto	BAC	3.541443	0.020893
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1.Clostridium_sensu_stricto.Otu0087	BAC	2.609544	0.042053
Firmicutes.Clostridia.Clostridiales.Clostridiaceae_1.Clostridium_sensu_stricto.Otu0154	BAC	2.736277	0.02898
Firmicutes.Clostridia.Clostridiales.Clostridiales_Incertae_Sedis_XI.Anaerococcus	BAC	2.922977	0.011621
Firmicutes.Clostridia.Clostridiales.Clostridiales_Incertae_Sedis_XI.Anaerococcus.Otu0290	BAC	2.921711	0.018453
Firmicutes.Clostridia.Clostridiales.Clostridiales_Incertae_Sedis_XI.Peptoniphilus.Otu0584	BAC	2.564394	0.013905
Firmicutes.Clostridia.Clostridiales.Clostridiales_Incertae_Sedis_XIII.Mogibacterium	BAC	2.445442	0.009312

Firmicutes.Clostridia.Clostridiales.Clostridiales_unclassified.Clostridiales_unclassified.Otu0295	BAC	2.335734	0.049355
Firmicutes.Clostridia.Clostridiales.Clostridiales_unclassified.Clostridiales_unclassified.Otu0324	VIR	2.075075	0.036319
Firmicutes.Clostridia.Clostridiales.Clostridiales_unclassified.Clostridiales_unclassified.Otu0618	VIR	2.255882	0.016434
Firmicutes.Clostridia.Clostridiales.Clostridiales_unclassified.Clostridiales_unclassified.Otu0895	VIR	2.377217	0.023351
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Anaerostipes.Otu0060	BAC	2.974879	0.006641
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Anaerostipes.Otu0302	BAC	2.620615	0.032663
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blautia.Otu0021	VIR	3.313928	0.00246
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blautia.Otu0103	VIR	2.88622	0.000567
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Blautia.Otu0280	BAC	2.115455	0.025897
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu0035	VIR	2.847164	0.010014
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu0085	VIR	3.430168	0.002193
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu0107	BAC	3.247237	0.00321
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu0165	VIR	2.696802	0.013648
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu0182	VIR	2.379707	0.04407
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu0307	VIR	2.170673	0.023351
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVa.Otu0503	VIR	2.236775	0.01378
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVb	VIR	3.643937	0.000133
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVb.Otu0116	VIR	3.548322	0.007055
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVb.Otu0235	VIR	2.860733	0.001799
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVb.Otu0376	VIR	2.081809	0.004266
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Clostridium_XlVb.Otu0729	VIR	2.089294	0.017966
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Coprococcus	VIR	3.129715	0.023596
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Coprococcus.Otu0125	VIR	2.610679	0.014618
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Coprococcus.Otu0239	VIR	2.557179	7.99E-05
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Coprococcus.Otu1504	VIR	2.68431	0.023351
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Dorea	VIR	3.209513	0.037686
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Dorea.Otu0098	VIR	3.079587	0.000324
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Dorea.Otu0122	VIR	3.093075	2.53E-05
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Dorea.Otu0257	BAC	2.70052	0.035618
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Dorea.Otu1097	BAC	2.95365	0.032497
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Dorea.Otu1227	VIR	2.691266	0.038279
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Hespellia	VIR	2.195289	0.014692

Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Hespellia.Otu0362	VIR	2.182173	0.014692
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0016	BAC	4.131791	0.041327
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0063	VIR	3.330634	0.000976
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0066	BAC	3.056326	0.005601
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0129	BAC	2.687995	0.000354
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0136	BAC	2.678367	0.030924
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0144	BAC	2.933557	6.76E-05
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0153	VIR	2.735008	0.001436
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0209	BAC	2.84408	0.001113
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0268	VIR	2.188441	0.033839
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0276	VIR	2.309281	2.72E-05
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0298	VIR	2.219332	0.003703
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0468	VIR	2.167442	0.039897
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0472	VIR	2.030349	0.04381
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0489	BAC	2.642153	0.049355
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0511	VIR	2.085334	0.00179
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu0806	VIR	2.592774	0.023351
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu1115	VIR	2.318282	0.008365
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Lachnospiraceae_unclassified.Otu1450	VIR	2.67339	0.046297
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Oribacterium.Otu0337	BAC	2.466759	0.005796
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Roseburia	VIR	3.681243	0.031754
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Roseburia.Otu0034	VIR	3.552313	0.00073
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Roseburia.Otu0340	VIR	2.388698	0.001352
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Roseburia.Otu0351	VIR	2.190834	0.001429
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Roseburia.Otu0433	VIR	2.06012	0.025458
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Roseburia.Otu1372	VIR	2.733437	0.023351
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Roseburia.Otu1528	VIR	2.377559	0.038279
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Ruminococcus2	VIR	3.206984	0.005185
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Ruminococcus2.Otu0051	VIR	2.983026	0.023217
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Ruminococcus2.Otu0213	VIR	2.030617	0.017202
Firmicutes.Clostridia.Clostridiales.Lachnospiraceae.Ruminococcus2.Otu1764	VIR	2.586018	0.023351
Firmicutes.Clostridia.Clostridiales.Peptostreptococcaceae	BAC	3.628959	2.74E-07

Firmicutes.Clostridia.Clostridiales.Peptostreptococcaceae.Clostridium_XI	BAC	3.590344	3.53E-06
Firmicutes.Clostridia.Clostridiales.Peptostreptococcaceae.Clostridium_XI.Otu0114	BAC	3.497929	8.18E-07
Firmicutes.Clostridia.Clostridiales.Peptostreptococcaceae.Clostridium_XI.Otu1268	BAC	2.517768	0.032497
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Clostridium_IV.Otu0134	VIR	2.880988	0.013597
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Clostridium_IV.Otu0834	VIR	3.105283	0.023351
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Clostridium_IV.Otu0871	VIR	2.349559	0.046297
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Faecalibacterium.Otu0659	VIR	2.07379	0.000366
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Faecalibacterium.Otu0819	VIR	2.769859	0.006065
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Faecalibacterium.Otu1329	VIR	2.954595	0.023351
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Flavonifractor.Otu0232	VIR	2.644705	0.002717
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Flavonifractor.Otu0296	VIR	2.089906	0.004032
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Gemmiger	VIR	2.753158	1.44E-05
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Gemmiger.Otu0048	VIR	2.752501	1.61E-05
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Oscillibacter	VIR	3.255863	0.024957
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Oscillibacter.Otu0084	VIR	2.994957	0.013955
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Oscillibacter.Otu0101	VIR	2.782931	0.006979
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Oscillibacter.Otu0271	VIR	2.7094	0.000203
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Oscillibacter.Otu0336	BAC	2.591076	0.049582
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Oscillibacter.Otu0419	VIR	2.042714	0.015693
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Oscillibacter.Otu0673	VIR	2.152622	0.023351
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Pseudoflavonifractor.Otu0218	BAC	2.111688	0.048295
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified	VIR	3.354006	0.021478
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu0062	VIR	2.846266	0.014162
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu0180	VIR	2.585229	0.000627
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu0194	BAC	2.143786	0.029271
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu0221	VIR	2.409728	0.001294
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu0306	VIR	2.904084	0.039897
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu0321	VIR	2.729968	0.023351
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu0330	VIR	2.26547	0.009614
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu0385	VIR	2.33262	0.001558
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu0616	VIR	2.854242	0.023351
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu0793	VIR	2.530617	0.00875

Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcaceae_unclassified.Otu0880	VIR	2.195379	0.016841
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcus.Otu0113	VIR	3.340934	0.049914
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Ruminococcus.Otu0270	VIR	2.54097	0.03974
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Sporobacter	VIR	2.167491	0.048037
Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Sporobacter.Otu0202	VIR	2.277028	0.007728
Firmicutes.Erysipelotrichia.Erysipelotrichales.Erysipelotrichaceae.Clostridium_XVIII.Otu0109	VIR	3.079288	0.014651
Firmicutes.Erysipelotrichia.Erysipelotrichales.Erysipelotrichaceae.Erysipelotrichaceae_unclassified.Otu0206	VIR	2.684436	0.017798
Firmicutes.Firmicutes_unclassified.Firmicutes_unclassified.Firmicutes_unclassified.Firmicutes_unclassified.Otu0170	VIR	2.017515	0.000878
Firmicutes.Firmicutes_unclassified.Firmicutes_unclassified.Firmicutes_unclassified.Firmicutes_unclassified.Otu0229	VIR	2.025081	0.042849
Firmicutes.Negativicutes.Selenomonadales.Acidaminococcaceae	VIR	4.195698	0.00467
Firmicutes.Negativicutes.Selenomonadales.Acidaminococcaceae.Phascolarctobacterium.Otu0611	VIR	2.271596	0.01875
Firmicutes.Negativicutes.Selenomonadales.Veillonellaceae.Megasphaera.Otu0089	BAC	2.22112	0.04381
Firmicutes.Negativicutes.Selenomonadales.Veillonellaceae.Veillonella.Otu0555	BAC	2.31581	0.032414
Fusobacteria.Fusobacteriia.Fusobacteriales.Fusobacteriaceae.Fusobacterium.Otu0078	BAC	3.32888	0.049355
Fusobacteria.Fusobacteriia.Fusobacteriales.Fusobacteriaceae.Fusobacterium.Otu0422	BAC	2.417381	0.047379
Fusobacteria.Fusobacteriia.Fusobacteriales.Leptotrichiaceae.Leptotrichia.Otu0780	VIR	2.580063	0.005975
Lentisphaerae	VIR	2.535665	0.041072
Lentisphaerae.Lentisphaeria	VIR	2.626109	0.006853
Lentisphaerae.Lentisphaeria.Victivallales	VIR	2.583593	0.006853
Lentisphaerae.Lentisphaeria.Victivallales.Victivallaceae	VIR	2.586756	0.006853
Lentisphaerae.Lentisphaeria.Victivallales.Victivallaceae.Victivallis	VIR	2.628206	0.006853
Proteobacteria.Alphaproteobacteria.Alphaproteobacteria_unclassified.Alphaproteobacteria_unclassified.Alphaproteobacteria_unclassified.Otu1003	VIR	2.459322	0.023351
Proteobacteria.Betaproteobacteria.Burkholderiales.Sutterellaceae.Sutterella	VIR	3.784127	0.038352
Proteobacteria.Betaproteobacteria.Burkholderiales.Sutterellaceae.Sutterella.Otu0029	VIR	3.714506	0.038267
Proteobacteria.Deltaproteobacteria	VIR	2.545365	0.003479
Proteobacteria.Deltaproteobacteria.Desulfovibrionales	VIR	2.46861	0.001036
Proteobacteria.Deltaproteobacteria.Desulfovibrionales.Desulfovibrionaceae	VIR	2.469039	0.000249
Proteobacteria.Deltaproteobacteria.Desulfovibrionales.Desulfovibrionaceae.Bilophila	VIR	2.436349	0.000235
Proteobacteria.Deltaproteobacteria.Desulfovibrionales.Desulfovibrionaceae.Bilophila.Otu0097	VIR	2.421728	0.000194
Proteobacteria.Epsilonproteobacteria.Campylobacterales.Campylobacteraceae.Campylobacter.Otu0318	BAC	2.699616	0.025236
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacter	BAC	4.145008	0.010746
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacter.Otu0006	BAC	4.136803	0.012274

Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacter.Otu0297	BAC	2.451644	0.006602
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacter.Otu1530	BAC	2.825633	0.049355
Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacteriaceae_unclassified.Otu0777	BAC	2.619186	0.021315