

**Supplementary Material for**

**Minimal variations of human oral virome and  
microbiome in human IgA deficiency**

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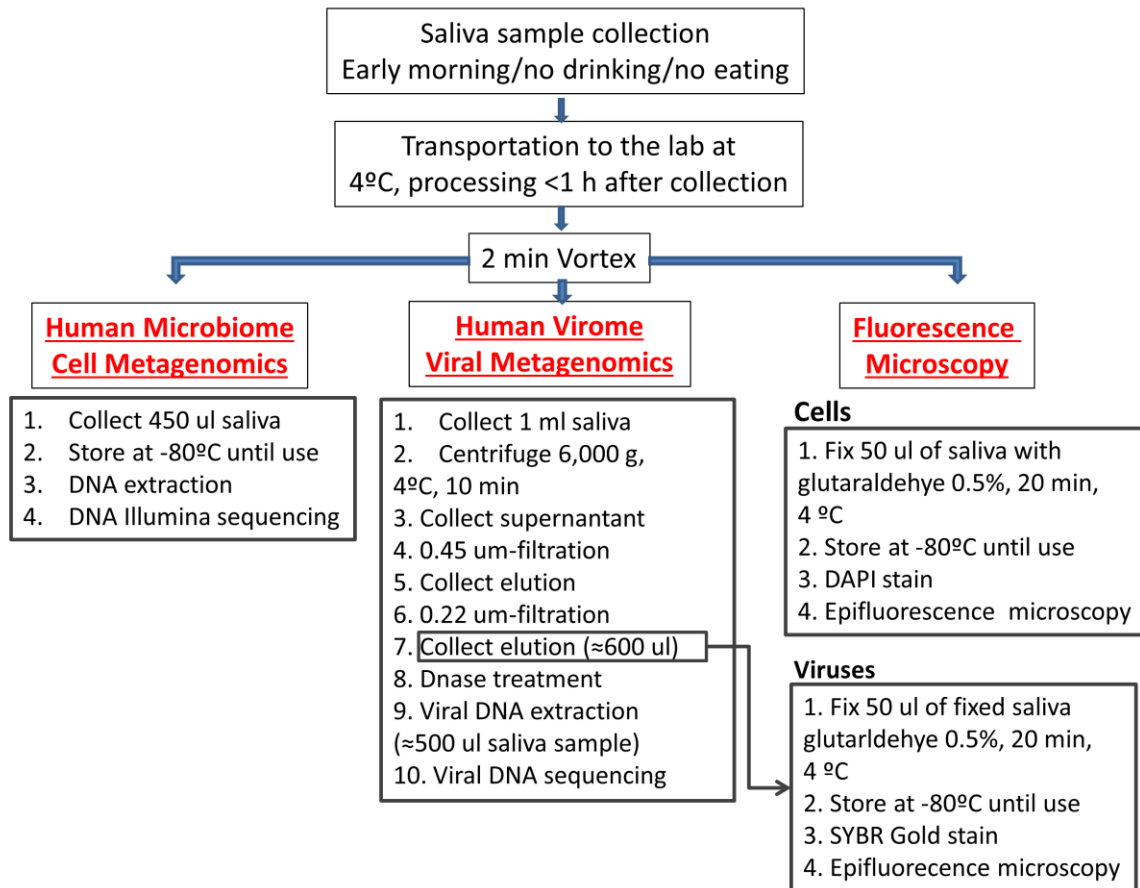
## Public access to metagenomic data and 16S rRNA gene sequences

Viral and microbial assembled metagenomes generated in this study are publicly available at IMG-JGI (23) database under the following identification numbers indicated in the table as **IMG genome ID** that can be used for searching in that database. **Red colour** indicate that these correspond to **CVID samples**

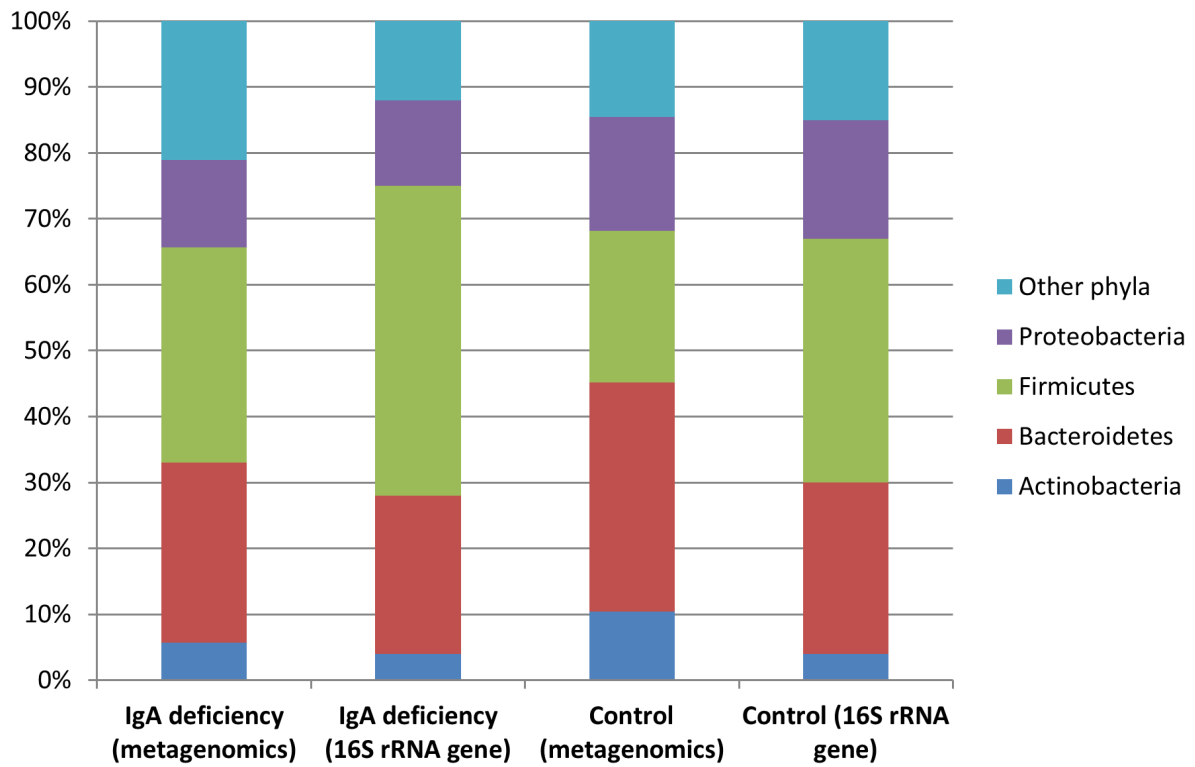
<b>IMG Genome ID</b>	<b>Genome Name / Sample Name (MICROBIAL METAGENOMES)</b>	<b>Genome Size assembled</b>	<b>Gene Count assembled</b>
3300022491	Human saliva microbial communities from oral cavities of healthy adults from Alicante, Spain - individual 1	29111330	35157
3300022479	Human saliva microbial communities from oral cavities of healthy adults from Alicante, Spain - individual 10	14084879	17378
3300022480	Human saliva microbial communities from oral cavities of healthy adults from Alicante, Spain - individual 11	5085306	7156
3300022482	Human saliva microbial communities from oral cavities of healthy adults from Alicante, Spain - individual 12	14438064	19279
3300022477	Human saliva microbial communities from oral cavities of healthy adults from Alicante, Spain - individual 14	330036	474
3300022488	Human saliva microbial communities from oral cavities of healthy adults from Alicante, Spain - individual 15	20290665	25879
3300022489	Human saliva microbial communities from oral cavities of healthy adults from Alicante, Spain - individual 16	30886265	38153
3300022493	Human saliva microbial communities from oral cavities of healthy adults from Alicante, Spain - individual 17	52354973	61599
3300022473	Human saliva microbial communities from oral cavities of healthy adults from Alicante, Spain - individual 2	14268001	17389
3300022484	Human saliva microbial communities from oral cavities of healthy adults from Alicante, Spain - individual 3	19175940	23458
3300022485	Human saliva microbial communities from oral cavities of healthy adults from Alicante, Spain - individual 4	17441767	22924
3300022474	Human saliva microbial communities from oral cavities of healthy adults from Alicante, Spain - individual 6	3712523	5230
3300022486	Human saliva microbial communities from oral cavities of healthy adults from Alicante, Spain - individual 7	23689678	28123
3300022472	Human saliva microbial communities from oral cavities of healthy adults from Alicante, Spain - individual 8	9671306	11789
<b>3300022476</b>	<b>Human saliva microbial communities from oral cavities of IgA immunodeficiency people from Alicante, Spain - individual 1</b>	4304770	5960
3300022478	Human saliva microbial communities from oral cavities of IgA immunodeficiency people from Alicante, Spain - individual 10	6134852	8428
<b>3300022475</b>	<b>Human saliva microbial communities from oral cavities of IgA immunodeficiency people from Alicante, Spain - individual 2</b>	5166800	6716
<b>3300022490</b>	<b>Human saliva microbial communities from oral cavities of IgA immunodeficiency people from Alicante, Spain - individual 3</b>	33915936	38921
3300022483	Human saliva microbial communities from oral cavities of IgA immunodeficiency people from Alicante, Spain - individual 4	19339156	24447
3300022487	Human saliva microbial communities from oral cavities of IgA immunodeficiency people from Alicante, Spain - individual 5	25053798	29360
3300022590	Human saliva microbial communities from oral cavities of IgA immunodeficiency people from Alicante, Spain - individual 6	71923080	85731
3300022495	Human saliva microbial communities from oral cavities of IgA immunodeficiency people from Alicante, Spain - individual 7	58991602	74509
3300022496	Human saliva microbial communities from oral cavities of IgA immunodeficiency people from Alicante, Spain - individual 8	15318436	20256
3300022494	Human saliva microbial communities from oral cavities of IgA immunodeficiency people from Alicante, Spain - individual 9	57308440	68268

IMG Genome ID	Genome Name / Sample Name ( <u>VIRAL METAGENOMES</u> )	Genome Size assembled	Gene Count assembled
3300028515	Human saliva viral communities from oral cavities of healthy adults from Alicante,Spain - individual 1	1702328	2505
3300028504	Human saliva viral communities from oral cavities of healthy adults from Alicante,Spain - individual 12	267982	401
3300028513	Human saliva viral communities from oral cavities of healthy adults from Alicante,Spain - individual 13	1323485	1985
3300028516	Human saliva viral communities from oral cavities of healthy adults from Alicante,Spain - individual 14	1819158	2617
3300028509	Human saliva viral communities from oral cavities of healthy adults from Alicante,Spain - individual 15	1232109	1874
3300028541	Human saliva viral communities from oral cavities of healthy adults from Alicante,Spain - individual 17	1699083	2464
3300028537	Human saliva viral communities from oral cavities of healthy adults from Alicante,Spain - individual 18	1098202	1714
3300028503	Human saliva viral communities from oral cavities of healthy adults from Alicante,Spain - individual 3	698838	1014
3300028511	Human saliva viral communities from oral cavities of healthy adults from Alicante,Spain - individual 4	1359060	1870
3300028519	Human saliva viral communities from oral cavities of healthy adults from Alicante,Spain - individual 5	2863798	4137
3300028514	Human saliva viral communities from oral cavities of healthy adults from Alicante,Spain - individual 6	1492463	2160
3300028542	Human saliva viral communities from oral cavities of healthy adults from Alicante,Spain - individual 7	4173712	5869
3300028538	Human saliva viral communities from oral cavities of healthy adults from Alicante,Spain - individual 8	2141600	2989
3300028520	Human saliva viral communities from oral cavities of healthy adults from Alicante,Spain - individual 9	2287909	3239
3300028507	Human saliva viral communities from oral cavities of IgA immunodeficiency people from Alicante,Spain - individual 1	889371	1414
3300028505	Human saliva viral communities from oral cavities of IgA immunodeficiency people from Alicante,Spain - individual 10	276922	461
3300028508	Human saliva viral communities from oral cavities of IgA immunodeficiency people from Alicante,Spain - individual 2	1024537	1419
3300028539	Human saliva viral communities from oral cavities of IgA immunodeficiency people from Alicante,Spain - individual 3	953530	1412
3300028517	Human saliva viral communities from oral cavities of IgA immunodeficiency people from Alicante,Spain - individual 4	1684016	2537
3300028506	Human saliva viral communities from oral cavities of IgA immunodeficiency people from Alicante,Spain - individual 5	1152454	1627
3300028512	Human saliva viral communities from oral cavities of IgA immunodeficiency people from Alicante,Spain - individual 6	1492463	2160
3300028510	Human saliva viral communities from oral cavities of IgA immunodeficiency people from Alicante,Spain - individual 7	1236571	1855
3300028518	Human saliva viral communities from oral cavities of IgA immunodeficiency people from Alicante,Spain - individual 8	2141600	2989
3300028544	Human saliva viral communities from oral cavities of IgA immunodeficiency people from Alicante,Spain - individual 9	1207203	1877

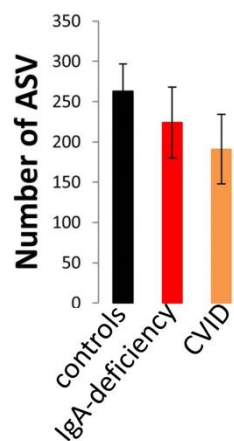
**16S rRNA gene sequences are available at NCBI with the following Bioproject ID number PRJNA682933**  
**Raw metagenomic reads are available from our bioinformatic server upon request (please email to the corresponding author m.martinez@ua.es)**



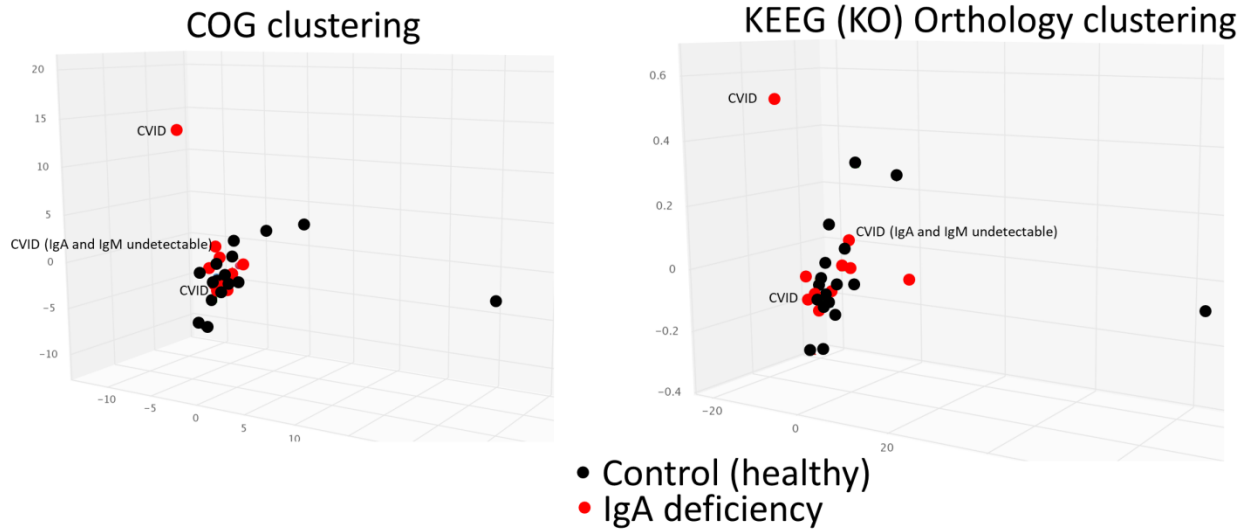
**Fig. S1.** Schematic diagram of saliva sampling and processing



**Fig. S2.** Taxonomic assignment of oral microbiome obtained by metagenomics and 16S rRNA gene analysis. See methods for details.



**Fig. S3.** Number of ASV found by Qiime 2 (see method for details) in the analyzed samples. Estimation of difference in alpha richness was then calculated (Fig. 1B).



**Fig. S4.** Metagenomic analysis of clustering of samples based on genetic content. ORFs were predicted with Prodigal program at the JGI-IMG platform. Annotation was performed with COG, pfam and KO. All three PCA analyses showed very similar clustering and relatedness between samples. For convenience, pfam clustering is omitted. Note that although two of the analyzed CVID samples were more scattered in the plot, these differences were also observed for some healthy control samples which suggest that natural intrinsic interpersonal variability of our microbiome might lead these differences.

**Table S1: 16S rRNA gene sequences obtained from samples**

<b>Sample</b>	<b>N of reads obtained from Miseq</b>	<b>N of reads afer QC</b>	<b>N of joined sequences</b>	<b>N q-score filtered sequences</b>	<b>N sequences after Deblur Denoising</b>
<b>Control 1</b>	633464	623244	294723	142775	3018
<b>Control 2</b>	396814	389914	184856	86364	2077
<b>Control 3</b>	348850	342288	161210	68299	1793
<b>Control 4</b>	477894	469754	222635	102616	2447
<b>Control 6</b>	345280	339410	160122	74284	2313
<b>Control 7</b>	452960	444614	210558	94091	2295
<b>Control 8</b>	433138	425914	201444	93809	2715
<b>Control 10</b>	430134	422678	200224	94355	2079
<b>Control 11</b>	510352	500930	236312	103215	2688
<b>Control 12</b>	445358	437640	207009	96575	2572
<b>Control 13</b>	510566	502252	237211	112758	252
<b>Control 14</b>	579006	569102	269708	129915	3329
<b>Control 15</b>	464716	457618	215998	92419	2281
<b>Control 16</b>	383942	378324	179562	76090	1803
<b>Control 17</b>	483166	475802	225737	96942	2534
<b>Control 18</b>	477880	470934	223912	96902	2738
<b>IgA1P (CVID)</b>	441208	434586	206552	89069	2382
<b>IgA2P (CVID)</b>	492388	484068	229767	93570	2356
<b>IgA3P (CVID)</b>	466550	459434	218362	95370	2817
<b>IgA4P</b>	437314	430406	204260	84459	2247
<b>IgA 5P</b>	526896	517578	244959	101682	2324
<b>IgA 6P</b>	490422	482408	228592	97855	2286
<b>IgA 7P</b>	496122	488670	231418	101961	2427
<b>IgA 8P</b>	479434	472294	224260	97478	2410
<b>IgA 9P</b>	739212	732312	350874	84839	2124
<b>IgA 10P</b>	495638	488922	233426	104812	2690

**Table S2.** Unique ASV found only in each one of the group. Note that relative abundance for those ASV is extremely low representing thus rare ASV. Taxonomic assignment was done with SILVA database implemented in Qiime2.

ASV FOUND ONLY IN IgA patients	Mean relative abundance
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas	0,04797593
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Leptotrichiaceae; g__Leptotrichia; s__Leptotrichia_sp_oral_clone_EI013	0,05686789
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Weeksellaceae; g__Bergeyella; s__uncultured_bacterium	0,05947955
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Leptotrichiaceae; g__Leptotrichia; s__Leptotrichia_sp_oral_clone_EI013	0,0743657
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Leptotrichiaceae; g__Streptobacillus; s__Streptobacillus_hongkongensis	0,05576208
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella	0,06899409
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Neisseriaceae; g__Neisseria	0,07209778
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp_oral_taxon_299_str_F0039	0,04250356
d__Bacteria; p__Firmicutes; c__Clostridia; o__Peptostreptococcales-Tissierellales; f__Peptostreptococcales-Tissierellales; g__Parvimonas	0,05037783
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium	0,04622103
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas	0,10828625
d__Bacteria; p__Patescibacteria; c__Gracilibacteria; o__Absconditabacteriales_(SR1); f__Absconditabacteriales_(SR1); g__Absconditabacteriales_(SR1)	0,05873396
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Leptotrichiaceae; g__Leptotrichia	0,05204028
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Leptotrichiaceae; g__Streptobacillus; s__uncultured_bacterium	0,04089219
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas	0,05249344
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella	0,04783288
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae; g__Haemophilus	0,12274643
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas; s__Porphyromonas_sp_oral_clone_DP023	0,05024276
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella	0,0813365
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Leptotrichiaceae; g__Leptotrichia; s__Leptotrichia_sp_oral_clone_EI013	0,19247594
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella	0,09888752
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales	0,03717472
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_pleuritidis	0,04198153
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae; g__Actinobacillus	0,13796173
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales	0,04730384
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae	0,03717472



d_Bacteria; p_Fusobacteriota; c_Fusobacteriia; o_Fusobacteriales; f_Leptotrichiaceae; g_Streptobacillus; s_uncultured_bacterium	0,06609556
d_Bacteria; p_Firmicutes; c_Bacilli; o_Lactobacillales	0,04855155
d_Bacteria; p_Patescibacteria; c_Gracilibacteria; o_Absconditabacteriales_(SR1); f_Absconditabacteriales_(SR1); g_Absconditabacteriales_(SR1)	0,03717472
d_Bacteria; p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; f_Prevotellaceae; g_Prevotella	0,0713686
d_Bacteria; p_Patescibacteria; c_Gracilibacteria; o_Absconditabacteriales_(SR1); f_Absconditabacteriales_(SR1); g_Absconditabacteriales_(SR1)	0,04460967
d_Bacteria; p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; f_Prevotellaceae; g_Prevotella; s_Prevotella_sp._HJM029	0,0521358
d_Bacteria; p_Bacteroidota; c_Bacteroidia; o_Flavobacteriales; f_Weeksellaceae; g_Bergeyella; s_uncultured_bacterium	0,03717472
d_Bacteria; p_Actinobacteriota; c_Actinobacteria; o_Micrococcales; f_Micrococcaceae; g_Rothia; s_uncultured_organism	0,03904863
d_Bacteria; p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; f_Porphyromonadaceae; g_Porphyromonas	0,12141992
d_Bacteria; p_Firmicutes; c_Negativicutes; o_Veillonellales-Selenomonadales; f_Veillonellaceae; g_Veillonella	0,07428563
d_Bacteria; p_Fusobacteriota; c_Fusobacteriia; o_Fusobacteriales; f_Leptotrichiaceae; g_Leptotrichia; s_Leptotrichia_sp._oral_clone_EI013	0,04804746
d_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Pasteurellales; f_Pasteurellaceae; g_Haemophilus	0,05785295
d_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Pasteurellales; f_Pasteurellaceae; g_Haemophilus	0,04978711
d_Bacteria; p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; f_Prevotellaceae; g_Prevotella; s_Prevotella_sp._GEJ23	0,04733219
d_Bacteria; p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; f_Prevotellaceae; g_Prevotella	0,18272081
d_Bacteria; p_Fusobacteriota; c_Fusobacteriia; o_Fusobacteriales; f_Leptotrichiaceae; g_Streptobacillus; s_uncultured_bacterium	0,04129503
d_Bacteria; p_Firmicutes; c_Negativicutes; o_Veillonellales-Selenomonadales; f_Veillonellaceae; g_Veillonella	0,12911846
d_Bacteria; p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; f_Prevotellaceae; g_Alloprevotella	0,04532344
d_Bacteria; p_Patescibacteria; c_Gracilibacteria; o_Absconditabacteriales_(SR1); f_Absconditabacteriales_(SR1); g_Absconditabacteriales_(SR1)	0,04089219
d_Bacteria; p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; f_Porphyromonadaceae; g_Porphyromonas	0,04305868
d_Bacteria; p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; f_Prevotellaceae; g_Prevotella; s_Prevotella_pleuritidis	0,07990389
d_Bacteria; p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; f_Prevotellaceae; g_Prevotella; s_Prevotella_pleuritidis	0,04641133
d_Bacteria; p_Actinobacteriota; c_Actinobacteria; o_Micrococcales; f_Micrococcaceae; g_Rothia; s_uncultured_organism	0,03904863
d_Bacteria; p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; f_Prevotellaceae; g_Prevotella	0,06024096
d_Bacteria; p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; f_Porphyromonadaceae; g_Porphyromonas	0,12183483
d_Bacteria; p_Fusobacteriota; c_Fusobacteriia; o_Fusobacteriales; f_Fusobacteriaceae; g_Fusobacterium	0,05517827
d_Bacteria; p_Fusobacteriota; c_Fusobacteriia; o_Fusobacteriales; f_Leptotrichiaceae; g_Leptotrichia; s_Leptotrichia_sp._oral_clone_EI013	0,15310586
d_Bacteria; p_Firmicutes; c_Bacilli; o_Staphylococcales; f_Gemellaceae; g_Gemella	0,04115793
d_Bacteria; p_Fusobacteriota; c_Fusobacteriia; o_Fusobacteriales; f_Leptotrichiaceae; g_Leptotrichia; s_Leptotrichia_sp._oral_clone_EI013	0,31496063
d_Bacteria; p_Fusobacteriota; c_Fusobacteriia; o_Fusobacteriales; f_Fusobacteriaceae; g_Fusobacterium	0,0466893

d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae; g__Haemophilus	0,04270476
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Leptotrichiaceae; g__Streptobacillus; s__uncultured_bacterium	0,07724167
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella	0,09064689
d__Bacteria; p__Patascibacteria; c__Gracilibacteria; o__Absconditabacteriales (SR1); f__Absconditabacteriales (SR1); g__Absconditabacteriales (SR1)	0,07806691
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Leptotrichiaceae; g__Streptobacillus; s__uncultured_bacterium	0,05178439
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus	0,04259851
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium	0,05897546
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus	0,19426314
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella; s__Prevotella_sp.	0,04360078

**Mean  
relative  
abundance**

**ASV FOUND ONLY IN COTROLS**

d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Leptotrichiaceae; g__uncultured; Ambiguous_taxa	0,01877441
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium	0,01959908
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae	0,02065185
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_veroralis	0,02070908
d__Bacteria; p__Actinobacteriota; c__Coriobacteriia; o__Coriobacteriales; f__Atopobiaceae; g__Atopobium; s__uncultured_organism	0,02070908
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae	0,02252929
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae	0,02282688
d__Bacteria; p__Firmicutes; c__Bacilli; o__Erysipelotrichales; f__Erysipelotrichaceae; g__Solobacterium; s__Solobacterium_moorei	0,02290685
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella; s__Prevotella_sp.	0,02302026
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus	0,02302026
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp._oral_taxon_299_str._F0039	0,02302026
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales	0,02316272
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella; s__Prevotella_sp.	0,02351355
d__Bacteria; p__Firmicutes; c__Clostridia; o__Peptococcales; f__Peptococcaceae; g__Peptococcus; Ambiguous_taxa	0,02382984
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp._oral_taxon_299_str._F0039	0,02389626
d__Bacteria; p__Campilobacterota; c__Campylobacteria; o__Campylobacterales; f__Campylobacteraceae; g__Campylobacter	0,02393549
d__Bacteria; p__Firmicutes; c__Clostridia; o__Lachnospirales; f__Lachnospiraceae; g__Oribacterium	0,0239499

d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas; s__unidentified	0,02424084
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,02448236
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_nigrescens	0,02455106
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_pallens	0,02466456
d__Bacteria; p__Patescibacteria; c__Gracilibacteria; o__Absconditabacteriales_(SR1); f__Absconditabacteriales_(SR1); g__Absconditabacteriales_(SR1); s__SR1_bacterium_oral_taxon_875	0,02466456
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus	0,02485089
d__Bacteria; p__Firmicutes; c__Bacilli; o__Staphylococcales; f__Gemellaceae; g__Gemella	0,02494957
d__Bacteria; p__Firmicutes; c__Clostridia; o__Lachnospirales; f__Lachnospiraceae; g__Oribacterium	0,0253033
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,02554148
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Neisseriaceae	0,02554148
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae	0,02556973
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales	0,02559423
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,02566074
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Weeksellaceae; g__Bergeyella; s__uncultured_Bergeyella_sp.	0,02569897
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella; s__Prevotella_sp.	0,02588666
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_nigrescens	0,02596609
d__Bacteria; p__Actinobacteriota; c__Coriobacteriia; o__Coriobacteriales; f__Atopobiaceae; g__Atopobium	0,02611709
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,02617574
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Leptotrichiaceae; g__uncultured; Ambiguous_taxa	0,02628417
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium	0,02629264
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella	0,02649186
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Selenomonadaceae; g__Selenomonas	0,02649418
d__Bacteria; p__Firmicutes; c__Clostridia; o__Peptostreptococcales-Tissierellales; f__Anaerovoracaceae; g__[Eubacterium]_nodatum_group; s__[Eubacterium]_infirmum	0,02655637
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,02657151
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Leptotrichiaceae; g__Leptotrichia	0,02665675
d__Bacteria; p__Campilobacterota; c__Campylobacteriia; o__Campylobacteriales; f__Campylobacteraceae; g__Campylobacter; s__uncultured_organism	0,02666382
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Neisseriaceae; g__Neisseria; s__Neisseria_flavescens	0,02673017
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium	0,0268634
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Weeksellaceae; g__Bergeyella; s__uncultured_Bergeyella_sp.	0,02698296

d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas; s__Porphyromonas_gingivalis	0,02702118
d__Bacteria; p__Firmicutes; c__Bacilli; o__Mycoplasmatales; f__Mycoplasmataceae; g__Mycoplasma	0,02702118
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium	0,02705005
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium	0,02705918
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,02728175
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_veroralis	0,02734681
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp._GEJ23	0,02735181
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas; s__Porphyromonas_sp._oral_clone_DP023	0,02743376
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Weeksellaceae; g__Bergeyella; s__uncultured_Bergeyella_sp.	0,02754276
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella; s__Prevotella_sp.	0,02755977
d__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Micrococcales; f__Micrococcaceae; g__Rothia; s__uncultured_bacterium	0,02763431
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp._oral_taxon_299_str._F0039	0,02763758
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium	0,02767008
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,02790179
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas	0,02805921
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae; g__Actinobacillus	0,02809563
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_pallens	0,02859687
d__Bacteria; p__Firmicutes; c__Bacilli; o__Staphylococcales; f__Gemellaceae; g__Gemella	0,02878364
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_pallens	0,02922248
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae	0,02938146
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Leptotrichiaceae; g__uncultured; Ambiguous_taxa	0,02946218
d__Bacteria; p__Campilobacterota; c__Campylobacteria; o__Campylobacterales; f__Campylobacteraceae; g__Campylobacter	0,02959747
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Megasphaera; s__Megasphaera_micronuciformis	0,02963785
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae	0,02971288
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,02971327
d__Bacteria; p__Firmicutes; c__Clostridia; o__Peptostreptococcales-Tissierellales; f__Anaerovoracaceae; g__[Eubacterium]_nodatum_group; s__[Eubacterium]_infirmum	0,02975154
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus	0,0299263
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus	0,02995643
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_veroralis	0,03005161

d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp._GEJ23	0,03006253
d__Bacteria; p__Firmicutes; c__Clostridia; o__Peptostreptococcales-Tissierellales; f__Peptostreptococcaceae; g__Filifactor; Ambiguous_taxa	0,03006253
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,03008279
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella; s__Prevotella_sp._oral_clone_BU035	0,03009148
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella; s__Prevotella_sp._oral_clone_BU035	0,03009148
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella; s__Prevotella_sp._oral_clone_BU035	0,03009148
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus	0,03014029
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus	0,03014029
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales	0,03020531
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Weeksellaceae; g__Bergeyella; s__uncultured_bacterium	0,03023354
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium	0,03030594
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_pallens	0,03040758
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp._oral_taxon_299_str._F0039	0,03046297
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella; s__Alloprevotella_tanneriae	0,0307384
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Leptotrichiaceae; g__Leptotrichia	0,03109264
d__Bacteria; p__Campilobacterota; c__Campylobacteria; o__Campylobacterales; f__Campylobacteraceae; g__Campylobacter; s__uncultured_organism	0,03110608
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae	0,03133479
d__Bacteria; p__Firmicutes; c__Clostridia; o__Lachnospirales; f__Lachnospiraceae; g__Lachnoanaerobaculum	0,03150786
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Leptotrichiaceae; g__Leptotrichia	0,03154387
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas; s__unidentified	0,03158753
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella	0,03160641
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella	0,03162344
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium	0,03162393
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas; s__unidentified	0,03170422
d__Bacteria; p__Firmicutes; c__Bacilli; o__Erysipelotrichales; f__Erysipelotrichaceae; g__Solobacterium; s__Solobacterium_moorei	0,03192926
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp._GEJ23	0,03195763
d__Bacteria; p__Patescibacteria; c__Gracilibacteria; o__Absconditabacteriales_(SR1); f__Absconditabacteriales_(SR1); g__Absconditabacteriales_(SR1); s__SR1_bacterium_oral_taxon_875	0,03206393
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Paludibacteraceae; g__F0058; Ambiguous_taxa	0,03213637
d__Bacteria; p__Campilobacterota; c__Campylobacteria; o__Campylobacterales; f__Campylobacteraceae; g__Campylobacter	0,03221343

d__Bacteria; p__Firmicutes; c__Bacilli; o__Mycoplasmatales; f__Mycoplasmataceae; g__Mycoplasma	0,03222192
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,03224206
d__Bacteria; p__Campilobacterota; c__Campylobacteria; o__Campylobacterales; f__Campylobacteraceae; g__Campylobacter; s__unidentified	0,03228583
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,03236928
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium	0,03260373
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium	0,03262663
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_veroralis	0,03267974
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas; s__Porphyromonas_sp._oral_clone_DP023	0,03293872
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium; s__Fusobacterium_sp._Marseille-P2749	0,03306878
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium	0,03313453
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_veroralis	0,03322622
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Neisseriaceae; g__Neisseria	0,03342698
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas	0,03389701
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,03393039
d__Bacteria; p__Campilobacterota; c__Campylobacteria; o__Campylobacterales; f__Campylobacteraceae; g__Campylobacter	0,03398917
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Neisseriaceae; g__Neisseria	0,03402022
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,03413094
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas; s__Porphyromonas_gingivalis	0,03425023
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp._GEJ23	0,03453039
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp._oral_taxon_299_str._F0039	0,03456547
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella	0,03474434
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Neisseriaceae; g__Neisseria	0,03485778
d__Bacteria; p__Campilobacterota; c__Campylobacteria; o__Campylobacterales; f__Campylobacteraceae; g__Campylobacter; s__uncultured_organism	0,03507833
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae	0,03517269
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp._oral_taxon_299_str._F0039	0,03520543
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,03525023
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella	0,03530095
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium	0,03535147
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp._oral_taxon_299_str._F0039	0,0354188
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Megasphaera; s__Megasphaera_micronuciformis	0,03562034

d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus	0,0357296
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella; s__Prevotella_sp.	0,03574713
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae; g__Actinobacillus	0,03575807
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae; g__Actinobacillus	0,03575807
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Neisseriaceae; g__Neisseria	0,03590205
d__Bacteria; p__Firmicutes; c__Clostridia; o__Peptostreptococcales-Tissierellales; f__Peptostreptococcaceae; g__Peptostreptococcus	0,03604943
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas; s__Porphyromonas_sp._oral_clone_DP023	0,03605803
d__Bacteria; p__Campilobacterota; c__Campylobacteria; o__Campylobacterales; f__Campylobacteraceae; g__Campylobacter; s__unidentified	0,03619019
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas; s__Porphyromonas_sp._oral_clone_DP023	0,03624017
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella; s__Prevotella_sp._oral_clone_BU035	0,03644122
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Neisseriaceae	0,03649525
d__Bacteria; p__Firmicutes; c__Clostridia; o__Lachnospirales; f__Lachnospiraceae; g__Stomatobaculum	0,0366426
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella	0,03667755
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Leptotrichiaceae; g__Leptotrichia; s__Leptotrichia_sp._oral_clone_FP036	0,03669053
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,03677652
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae; g__Haemophilus	0,03717267
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,03718017
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium	0,03718682
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_pallens	0,03748437
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp._oral_taxon_299_str._F0039	0,03793645
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella; s__Prevotella_sp.	0,03828275
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus	0,03851577
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp._oral_taxon_299_str._F0039	0,03866618
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Neisseriaceae; g__Neisseria	0,0387807
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,03879835
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas; s__Porphyromonas_sp._oral_clone_DP023	0,03894593
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Megasphaera; s__Megasphaera_micronuciformis	0,03932313
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella; s__Prevotella_sp.	0,03945707
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium	0,04028449
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium	0,04049081

d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae; g__Actinobacillus	0,04086637
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Neisseriaceae; g__Neisseria	0,04131026
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus	0,04167411
d__Bacteria; p__Firmicutes; c__Clostridia; o__Peptostreptococcales-Tissierellales; f__Peptostreptococcaceae; g__Filifactor; Ambiguous_taxa	0,04171339
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp._oral_taxon_299_str._F0039	0,0418046
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus	0,04187209
d__Bacteria; p__Patescibacteria; c__Gracilibacteria; o__Absconditabacteriales_(SR1); f__Absconditabacteriales_(SR1); g__Absconditabacteriales_(SR1); s__SR1_bacterium_oral_taxon_875	0,04192976
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Megasphaera; s__Megasphaera_micronuciformis	0,04225621
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Megasphaera; s__Megasphaera_micronuciformis	0,04230329
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae	0,0428791
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella	0,04335862
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas; s__Porphyromonas_sp._oral_clone_DP023	0,04368534
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella; s__Prevotella_sp.	0,04375866
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_pallens	0,04385897
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp._GEJ23	0,044475
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,04464286
d__Bacteria; p__Firmicutes; c__Clostridia; o__Lachnospirales; f__Lachnospiraceae; g__Lachnoanaerobaculum; s__uncultured_organism	0,04466035
d__Bacteria; p__Firmicutes; c__Clostridia; o__Peptostreptococcales-Tissierellales; f__Peptostreptococcales-Tissierellales; g__Parvimonas	0,04482621
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas; s__unidentified	0,04523411
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella; s__Prevotella_sp.	0,04531511
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp._oral_taxon_299_str._F0039	0,0457264
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella	0,04575555
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae	0,04585674
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae	0,04603591
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_pallens	0,0462963
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_pallens	0,04690699
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,04749845
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae	0,04808585
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium	0,04824212



d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella	0,04870998
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_intermedia	0,04887762
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium	0,04919849
d__Bacteria; p__Patescibacteria; c__Gracilibacteria; o__Absconditabacteriales_(SR1); f__Absconditabacteriales_(SR1); g__Absconditabacteriales_(SR1); s__SR1_bacterium_oral_taxon_875	0,04932912
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella; s__Prevotella_sp.	0,04995264
d__Bacteria; p__Firmicutes; c__Bacilli; o__Erysipelotrichales; f__Erysipelotrichaceae; g__Solobacterium; s__Solobacterium_moorei	0,05012326
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,05065513
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp_oral_taxon_299_str_F0039	0,05066123
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_intermedia	0,05112946
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_intermedia	0,05128314
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_pallens	0,05163563
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Leptotrichiaceae; g__Leptotrichia	0,05200886
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas; s__Porphyromonas_sp_oral_clone_DP023	0,05279497
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas; s__Porphyromonas_sp_oral_clone_DP023	0,05299531
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella; s__Prevotella_sp_oral_clone_BU035	0,05419486
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp_oral_taxon_299_str_F0039	0,05455564
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus	0,05545973
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae; g__Actinobacillus	0,05619125
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus	0,05653501
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp_oral_taxon_299_str_F0039	0,05721818
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,05722814
d__Bacteria; p__Firmicutes; c__Clostridia; o__Peptostreptococcales-Tissierellales; f__Peptostreptococcaceae; g__Peptostreptococcus	0,0576293
d__Bacteria; p__Firmicutes; c__Clostridia; o__Peptostreptococcales-Tissierellales; f__Peptostreptococcaceae; g__Peptostreptococcus	0,05810097
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp_oral_taxon_299_str_F0039	0,05814594
d__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Micrococcales; f__Micrococcaceae; g__Rothia	0,0585921
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp_oral_taxon_299_str_F0039	0,05859563
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp_GEJ23	0,05883254
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp_GEJ23	0,05966556
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella; s__Prevotella_sp.	0,06202545

d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella	0,06217222
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus	0,06401902
d__Bacteria; p__Patescibacteria; c__Gracilibacteria; o__Absconditabacteriales_(SR1); f__Absconditabacteriales_(SR1); g__Absconditabacteriales_(SR1); s__SR1_bacterium_oral_taxon_875	0,06412786
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_pallens	0,06432602
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_veroralis	0,06570057
d__Bacteria; p__Patescibacteria; c__Gracilibacteria; o__Absconditabacteriales_(SR1); f__Absconditabacteriales_(SR1); g__Absconditabacteriales_(SR1); s__SR1_bacterium_oral_taxon_875	0,06659432
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus	0,06673129
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp._oral_taxon_299_str._F0039	0,06699718
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae	0,06731075
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,07066055
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Neisseriaceae; g__Neisseria	0,07078695
d__Bacteria; p__Firmicutes; c__Bacilli; o__Staphylococcales; f__Gemellaceae; g__Gemella	0,0720826
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium	0,07535288
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella; s__Alloprevotella_tannerae	0,07592131
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae	0,07700344
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella; s__Prevotella_sp.	0,0782809
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_pallens	0,07908949
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,08031081
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella; s__Prevotella_sp.	0,08122962
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas; s__unidentified	0,08210847
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,08220818
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,08246181
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_intermedia	0,08459163
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae	0,08540416
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Alloprevotella	0,08670935
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus	0,08798677
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Neisseriaceae; g__Neisseria; s__Neisseria_flavescens	0,08991058
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp._oral_taxon_299_str._F0039	0,09202429
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Neisseriaceae; g__Neisseria	0,10102208

d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Neisseriaceae; g__Neisseria	0,10380038
d__Bacteria; p__Fusobacteriota; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium	0,1076125
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,11269848
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_sp._oral_taxon_299_str._F0039	0,11381797
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Neisseriaceae; g__Neisseria	0,11708333
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae; g__Actinobacillus	0,11749081
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,12165745
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__Prevotella_veroralis	0,14272838
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Porphyromonas; s__Porphyromonas_sp._oral_clone_DP023	0,15123525
d__Bacteria; p__Firmicutes; c__Negativicutes; o__Veillonellales-Selenomonadales; f__Veillonellaceae; g__Veillonella	0,17451165
<u>d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Neisseriaceae; g__Neisseria</u>	<u>0,17724353</u>

<b>Table S3. Sequencing data from viral and microbial metagenomes (raw sequencing data)</b>	
Sample group	Total No. of sequenced nucleotides (Mb)
viral metagenomes (Controls)	6704
viral metagenomes (IgA deficiency)	5900
cell metagenomes (Controls)	44672
cell metagenomes (IgA deficiency)	50164