

**Supplementary Table S5. ASVs mapping to the reference genomes and the corresponding absolute and relative abundances.** Parameters considered: query coverage  $\geq 90\%$  and similarity  $\geq 97\%$ . “Genome” represents the contig where the ASVs align and “sstart” / “send” the location coordinates; “pident” is the % of similarity. “Method” refers to the sequencing approach. “Genome Name” is the name of the species of the mock. whereas “Assigned Species” and “Assigned Genus” correspond to the classification obtained at species and genus level, respectively. “Expected” shows whether the region of the match is annotated as the 16S rRNA gene.

ASV	Genome	pident	sstart	send	Method	Genome Name	Expected	Assigned Species	Assigned Genus	abs	rel
116988315318af8 14daac19fb60efb 18					V3V4				d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Streptococcace ae;g__Streptococcus	2	0.00
ddd048fa84342d 57fc92066835939 98c					V3V4				d__Bacteria;p__Firmicutes;c__Bacilli; o__Staphylococcales;f__Staphylococ caceae;g__Staphylococcus	1.00E +00	0.00
0af0987236663cf 1a404ee8f8d0d9 ef4					V3V4				d__Bacteria;p__Bacteroidota;c__Bact eroidia;o__Bacteroidales;f__Bacteroi daceae;g__Bacteroides	4	0.00
c84fc45ac0df1b3 6f969d4b7d4b4d 76a					V3V4				d__Bacteria;p__Actinobacteriota;c__ Actinobacteria;o__Bifidobacteriales;f__ Bifidobacteriaceae;g__Bifidobacter ium	1	0.00
2fd84e313a8e8a4 5246db82a092a0 3c1					V3V4			d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Enterobacter ales;f__Enterobacteriaceae;g__Escher ichia-Shigella; s__uncultured_Pantoea	d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Enterobacter ales;f__Enterobacteriaceae;g__Escher ichia-Shigella	1	0.00
9d3843fd30f6e58 82ad76d87bf912 be1					V3V4			d__Bacteria;p__Actinobacteriota;c__ Actinobacteria;o__Bifidobacteriales;f__ Bifidobacteriaceae;g__Bifidobacter ium;s__Bifidobacterium_faecale	d__Bacteria;p__Actinobacteriota;c__ Actinobacteria;o__Bifidobacteriales;f__ Bifidobacteriaceae;g__Bifidobacter ium	2	0.00
80b9934b6e140e 0309d745b33db8 da19					V3V4				d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Enterococcacea e;g__Enterococcus	3	0.00
b347624d5c5225 ccf4cd38d7a0dcc 598					V3V4				d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Enterobacter ales;f__Enterobacteriaceae;g__Escher ichia-Shigella	2	0.00
f9aa8d0e7ab74d d5b1c80f4e823b6 886					V3V4				d__Bacteria;p__Actinobacteriota;c__ Actinobacteria;o__Bifidobacteriales;f__	4	0.00

			__Bifidobacteriaceae;g__Bifidobacterium		
456726fcb18558bdbc6377e38896547e	V3V4		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	19	0.02
6a0eae87b93fd07ad46db3b1eaabd43	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	2	0.00
1c98130024b2622235bedbaf30c690d9	V3V4		d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	1.00E+00	0.00
e22ead36335328e214f9b66dfb1b30d1	V3V4		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	3	0.00
ac2d45456f92a5bc851ac12762130a96	V3V4			5	0.01
1c02778d589eec0fecf00d976b50fec8	V3V4		d__Bacteria;p__Campilobacterota;c__Campylobacteria;o__Campylobacterales;f__Helicobacteraceae;g__Helicobacter	2	0.00
ab86e2b48526034e6f335615a043d483	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1	0.00
b0a2169e2a052ead8185d4ac9668ede5	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	2	0.00
245ba600e28a95b9df533245cb5a222d	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	25	0.03
4dbd2311865e718e629475768ec56594	V3V4			4	0.00
5a92b2a407a87bb5d987cec082ef10db	V3V4		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	4	0.00
ae8c26f926b77ff67bb2949dbc67be3	V3V4		d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	1	0.00

3871f21058d3b1 9c17520843acb6e 109	V3V4	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__uncultured_Marinobacter	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	2	0.00
e9970500442b31 68e1d6522bb65e 33f3	V3V4		d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Actinomyces	3	0.00
b154827d580ab4 4bf2c451c4f9e74 a60	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	3	0.00
052f8d7804cf053 a144f4474566d4f d0	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_troglodytae	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	5	0.01
d86828b11a697d 3aee5c4d466b98 8380	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	18	0.02
2f11acb78d09ec9 436a120ef712836 de	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	3	0.00
80dbafcfb4b1f68 4d52673147ac8d 308	V3V4	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_thetaiotaomicron	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	5	0.01
901163b6f627002 d8cbc1afae9f4f4 05	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1	0.00
2c5c63739b3f140 a688647b359e29 0c1	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_troglodytae	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	1	0.00
7ffac11a381face9 86d02ca535d4ac b4	V3V4		d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Actinomyces	1	0.00
063506beba6c1fb b0929c8d0e8a3ff 81	V3V4	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Actinomyces;s__Mycobacterium_tuberculosis	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Actinomyces	1	0.00

66fc81d0779ee35 43c336e55f997ff1 8	V3V4		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter	1	0.00
33bc5391ced327 08caab9eeee2f6d 17a	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_troglodytae	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	7	0.01
e8119a79e6d3fd 00d40d024ec7db 9280	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	1	0.00
847571fab7d7e46 326f4d957421d5 5f4	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	2	0.00
e61cd640ab153c 0aa0eb50ef858c4 762	V3V4		d__Bacteria;p__Deinococcota;c__Deinococci;o__Deinococcales;f__Deinococcaceae;g__Deinococcus	2	0.00
3ca103332462a6f 22bc3f3a71e1928 61	V3V4			4	0.00
c66358457390ce9 93711d5e370a5f2 86	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1	0.00
6076e162d2870c ad4ff4cccf66bea5 62	V3V4			1	0.00
07a15062be8ee3 0ddc3329c1e787 68dc	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	4.00E+00	0.00
edd5425137c3ff7 76e8e9bc317afb5 8b	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_troglodytae	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	4	0.00
905130d5a231d4 3581bea3477d95 3f09	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1	0.00
b527ff38a17f5fd b76c2636c890e15 ce	V3V4		d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	1	0.00
b0cc6e3b244191a b1357fe19e1fc9a 2e	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	1	0.00

492ed26e8fe4359 d9dd1c133c3e7b 3cb	V3V4			1	0.00
cb93c047af2ba2e 33389d8b998a28 150	V3V4		d__Bacteria;p__Actinobacteriota;c__ Actinobacteria;o__Actinomycetales;f__ Actinomycetaceae;g__Actinomyces	10	0.01
5283f476090a024 8b7f6fffc1348a8e 8	V3V4		d__Bacteria;p__Actinobacteriota;c__ Actinobacteria;o__Bifidobacteriales;f__ Bifidobacteriaceae;g__Bifidobacterium	40	0.04
90a6a6f14d4d80 c00fa17c150ca9e bce	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Lactobacillacea e;g__Lactobacillus;s__mouse_gut	d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Lactobacillacea e;g__Lactobacillus	2	0.00
fa7f3fe11e36c4b6 d30ae148713ff05 f	V3V4		d__Bacteria;p__Firmicutes;c__Clostridia;o__ Peptostreptococcales-Tissierellales;f__ Peptostreptococcaceae;g__Romboutsia	9	0.01
f74124cf2698857f 11924bc4cc47b6c 2	V3V4	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__ Enterobacterales;f__Enterobacteriaceae;g__ Escherichia-Shigella;s__uncultured_Escherichia	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__ Enterobacterales;f__Enterobacteriaceae;g__ Escherichia-Shigella	9	0.01
44163af77873c2c 3b907dd79b05e2 f0f	V3V4		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__ Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	10	0.01
397d12199a2dee 22c6c3cb0607d4 b244	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__ Lactobacillales;f__Lactobacillacea e;g__Lactobacillus	1	0.00
ee63c66fa9845ff0 18f2385400ffac1c	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli;o__ Lactobacillales;f__Streptococcaceae;g__ Streptococcus;s__Streptococcus_trogloodytae	d__Bacteria;p__Firmicutes;c__Bacilli;o__ Lactobacillales;f__Streptococcaceae;g__ Streptococcus	2	0.00
4498526ac722cce 4d07cae5cbaca12 24	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__ Lactobacillales;f__Enterococcaceae;g__ Enterococcus	2	0.00
30552d6e490547 2fe90f1d1ea2584 c57	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__ Lactobacillales;f__Streptococcaceae;g__ Streptococcus	4	0.00
2e081b7ff660c34 d0503c723de0faa b3	V3V4		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__ Pseudomonadales;f__Moraxellaceae;g__Acinetobacter	3	0.00

abce05ed9ee1d3 89232f2a3ea3bc9 657	V3V4		d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	2	0.00
7be95baaddca16 3f1c6b316ba8621 9ee	V3V4		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	2	0.00
7dd0c4a5fa6311 8d9da0fe733dbe 7f5c	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1	0.00
3f012a293d1c7f7 075486004465ca1 56	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1	0.00
b348310b9ad541 3880fcab00d56e2 494	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__mouse_gut	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	2	0.00
c92d34b04f93ee7 6340cf1dfd390ca d3	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	2	0.00
8176a592411252 53f19efb1a2a102 5a7	V3V4		d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	1	0.00
f32c3098ccb00b2 74be15992dbf7c1 e3	V3V4			1	0.00
1cfaf7686133c22 ec3308efb96e0a2 2a	V3V4			2	0.00
3829fc0b69d7943 9dc17485f0ec03ff f	V3V4		d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	1	0.00
5c666123cdf2417 dcff3c0ce45e894 36	V3V4		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Neisseriaceae;g__Neisseria	1	0.00
381b667dc5dd68 c1fbe51b785562c 860	V3V4		d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	5	0.01
e7988e34895ba1 648612e0e677fc9 e4e	V3V4			1	0.00
0e157a51af08007 fc87a7c2925c674 f1	V3V4	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escher	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacter	1	0.00

		ichia-Shigella;s__uncultured_Pantoea	ales;f__Enterobacteriaceae;g__Escherichia-Shigella		
76444b43bd86d5ee5f46904d49c9754d	V3V4		d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	19	0.02
78964bebb9fd2e86a40c9ed3585969a6	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1	0.00
e07ea05065633374ef3159033952de15	V3V4			2	0.00
c1a575ede20550366883decab3d0b7e1	V3V4			16	0.02
5848a447494c6f23aa875baa5de5a8da	V3V4		d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	2	0.00
1d927a61fda6a288d40c2479c1da7b53	V3V4		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia-Shigella	3	0.00
699e0f7469c165b701834385f9a13ed7	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	1	0.00
b468694797c5990818fe1cf509f2f807	V3V4		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	4	0.00
08bc05c4756c28aca9d5e9f1dc5901ad	V3V4			1	0.00
04a6e1bfd2e94a99f1bd4c7f4f5b7017	V3V4			3	0.00
4c7b75d43255eed2661601ed23c87123	V3V4			3	0.00
b96951bab7f5282a3531696b0e3ec620	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1	0.00

278f5855ed26318 212ca668522a925 c0	V3V4		d__Bacteria;p__Actinobacteriota;c__ Actinobacteria;o__Actinomycetales;f__ Actinomycetaceae;g__Actinomyces	7	0.01
1070c4298b1ec67 0ca36faf1e6acca4 0	V3V4		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Neisseriaceae;g__Neisseria	1	0.00
1f68bc4e3aeeb65 d48f63fbef319adae	V3V4		d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	1	0.00
41fc41da8fe491d 0ab4515cc43afd5 8e	V3V4		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	15	0.02
bd2bc954f821d9 8b470847b8a594 78b0	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1	0.00
a1d3cc08120790 0015d39f5b81ecd35	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_trogodytae	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	1	0.00
7129605bb839e8 e5c432cf15aa68c 864	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	1	0.00
b3289bc3fc34222 3a3882db9a80d8 8c6	V3V4		d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	14	0.01
fd63fd7ea904a2c 74a93909008964 afb	V3V4			1	0.00
0aaa2ce281156ce dcc1dba12c7fb0 b43	V3V4		d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Actinomyces	4	0.00
656a3f9265f027e edeae38b5a655f0 57	V3V4	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_vulgatus	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	1	0.00
bcc1f1c4c18982e 2887807cbe6e1b 0fc	V3V4			2	0.00



26055d990cb566 310cc60ca222661 e9c	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Streptococcace ae;g__Streptococcus	1	0.00
8b1242f5d16dcc a61bf8d5c4ce68b 69c	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli; o__Staphylococcales;f__Staphylococ caceae;g__Staphylococcus	3	0.00
40c09ab1cbda98 0dbfdbaeff778e1 cc1	V3V4	d__Bacteria;p__Firmicutes;c__Clostr idia;o__Peptostreptococcales- Tissierellales;f__Anaerovoracaceae;g __Mogibacterium;s__uncultured_ba cterium	d__Bacteria;p__Firmicutes;c__Clostr idia;o__Peptostreptococcales- Tissierellales;f__Anaerovoracaceae;g __Mogibacterium	4	0.00
a17b3f33f0dd27 b289b0f9ef201f5 3c5	V3V4		d__Bacteria;p__Deinococcota;c__Dei nococci;o__Deinococcales;f__Deinoc occaceae;g__Deinococcus	2	0.00
68ffc7181ac528d 49f7458b4547eb4 7b	V3V4			5	0.01
f91f431a88c3772 30dd1c8bb79703 853	V3V4		d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Burkholderia les;f__Neisseriaceae;g__Neisseria	1	0.00
b0060cc6b7ce620 870420f8b3fa3b6 c1	V3V4		d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Enterobacter ales;f__Enterobacteriaceae;g__Escher ichia-Shigella	1	0.00
08dfad997477a5 742bc80007f5277 ef8	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Streptococcace ae;g__Streptococcus	4	0.00
4a8f3208e638a1c 148bb51ecbb6ef1 8d	V3V4			4	0.00
9089af94287bb71 026b03ad629aac 9a0	V3V4	d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Pseudomona dales;f__Pseudomonadaceae;g__Pse udomonas;s__uncultured_Marinoba cter	d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Pseudomona dales;f__Pseudomonadaceae;g__Pse udomonas	2	0.00
7d0c9763930875 4ea15f6592b87cb 884	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli; o__Bacillales;f__Bacillaceae;g__Bacill us	4	0.00
52f955461f86ad8 83c55d8a3e8202 279	V3V4		d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Pseudomona dales;f__Moraxellaceae;g__Acinetob acter	5	0.01

c2b613466af9051a1e76bf383e85e2cf	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	3	0.00
c646867128acf18b40a0553724e2d3d9	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1	0.00
c2e4ed60db611124a48fcec819041b	V3V4	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	16	0.02
edd03326781345dce17c282af79662d9	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1	0.00
03359371173b50f5325d305f0cf4ac20	V3V4	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Propionibacteriales;f__Propionibacteriaceae;g__Cutibacterium	4	0.00
11e8bc474b260bc0d712df6ea46b5199	V3V4		4	0.00
090b5dca9050c83d67c1b7482f9ec905	V3V4	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	4	0.00
9713c18671402dea22a8cf2aaf4d75b7	V3V4	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Actinomyces	9	0.01
e63f1461c4c56b18a07fbf6cd5b09142	V3V4	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella;s__Malaclemys_terrapi	1	0.00
44fe027804a633841108da2a936cf813	V3V4		1	0.00
f16b81eedac66ac1b68662de35eb5f5a	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_troglyodytae	2	0.00
7132ebbc3bfce41e701cfe1f86ed45dd	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__uncultured_bacterium	1	0.00

dc2ae076f875112 08642bf8508d3e9 04	V3V4			1	0.00
d9a9cba2990f6a6 c154303d3ec7092 05	V3V4		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	1	0.00
f2ed2c40a65cdcd 33edffde8adbea b62	V3V4		d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	5	0.01
52f23ca04c38e4e 75a6c8391c1a5cc 57	V3V4		d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Rhodobacter	2	0.00
88a0532c9cd77a 5109be4a3c8136 d363	V3V4	d__Bacteria;p__Deinococcota;c__Deinococci;o__Deinococcales;f__Deinococcaceae;g__Deinococcus;s__Deinococcus_radiodurans	d__Bacteria;p__Deinococcota;c__Deinococci;o__Deinococcales;f__Deinococcaceae;g__Deinococcus	7	0.01
c07ec260b3193f7 708e297285494e5 49	V3V4		d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	1	0.00
fd6d065f1839c95 af0c64f26f383a16 c	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__mouse_gut	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	2	0.00
50fdd882f9a2f68 6b0bb371512ce5 c56	V3V4			9	0.01
183d55896ac0ec4 15369542ee7bc7 d09	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_trogodytae	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	3	0.00
b1c1e045e4aa3c0 70d1ca97bb34c3 77f	V3V4			1	0.00
f3f6af8f3182835c 90c5712e22748cc b	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	4	0.00
b0f8cd8129d46e d63ef0548638543 eaf	V3V4		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter	1	0.00

84d98d85677eba c820163018f3b58 4b0	V3V4		d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Propionibacteriales;f__Propionibacteriaceae;g__Cutibacterium	1	0.00
532b8c57ef37371 3b169f64953ceb7 eb	V3V4		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	1	0.00
4a8150ec3ef5381 fe77e67c074d9d9 6f	V3V4	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__uncultured_Marinobacter	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	25	0.03
9246824a9517e9 d0ff9477deab0a7 ac7	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus	2	0.00
314a64ec81e0374 28ef7102a4eb0b8 da	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	2	0.00
a1cc90a21c23d21 37d56bb6dc2921 c4f	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	3	0.00
ec9e6cc25798a85 f930369b2d00d8 2fd	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	3	0.00
1168280d13dbc6 51e68f5caf1d7bc e82	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1	0.00
71ae4c3f71b0940 1305f029a0f7d46 43	V3V4			2	0.00
a9434f8c6924d89 46a7a9f473c1780 38	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	2	0.00
293a8d61d2ae49 3e6eaf6996542ef 8a6	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	2	0.00
988117d050ad20 3b779ce3d394bf8 9a2	V3V4			3	0.00
f05922e3d687273 e586590a7e83a10 a3	V3V4			2	0.00

967eff4d421800 813303a3b0a03a 194	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli; o__Erysipelotrichales;f__Erysipelotri chaceae;g__Holdemanella	3	0.00
f12f13f1a547f87a b5808f9626d2f21 6	V3V4	d__Bacteria;p__Firmicutes;c__Clostr idia;o__Lachnospirales;f__Lachnosp iraceae;g__Blautia	12	0.01
3040e0c8ab58060 a4e34cc39ef03da 52	V3V4	d__Bacteria;p__Actinobacteriota;c__ Actinobacteria;o__Actinomycetales;f__ Actinomycetaceae;g__Actinomyce s	1	0.00
8454e15db29796 8395307aef9bf3f de4	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli; o__Staphylococcales;f__Staphylococ caceae;g__Staphylococcus	1	0.00
17ca9aee028bd1 0cc2bd929cbd0c 54fb	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Lactobacillacea e;g__Lactobacillus	1	0.00
233af22eb710eb9 ddd3e0c2178da7 f39	V3V4	d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Enterobacter iales;f__Enterobacteriaceae;g__Escher ichia-Shigella	3	0.00
9c1d5c5045803e1 5a96a235f8de9dc 24	V3V4	d__Bacteria;p__Actinobacteriota;c__ Actinobacteria;o__Propionibacteriale s;f__Propionibacteriaceae;g__Cutiba cterium	3	0.00
55ecec4f9cd6b3f 10605efc76a6823 dc	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Enterococcacea e;g__Enterococcus	2	0.00
488a8665cc64ed5 fba5a8685d8df50 7a	V3V4		4	0.00
6023071f6f9e948 bed1c969f0601d 684	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Enterococcacea e;g__Enterococcus	4	0.00
4be7df120f0d1c5 c7c0e6079210d60 42	V3V4	d__Bacteria;p__Proteobacteria;c__Al phaproteobacteria;o__Rhodobacteral es;f__Rhodobacteraceae;g__Rhodoba cter	1	0.00
3a493d430b6c9e bfc351bdf059799 e78	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Lactobacillacea e;g__Lactobacillus	2	0.00
ce388ec374f5d25 2945e6b8743ee9 0c0	V3V4	d__Bacteria;p__Deinococcota;c__Dei nococci;o__Deinococcales;f__Deinoc occaceae;g__Deinococcus	5	0.01

fa91d0754e33b45 a3cda25ae630c7e b1	V3V4		d__Bacteria;p__Actinobacteriota;c__ Actinobacteria;o__Propionibacteriale s;f__Propionibacteriaceae;g__Cutiba cterium	1	0.00
5ef26d58b743e2c 2b49b51badcbf8 900	V3V4			4	0.00
9e10aab3874583 d56021f515a5c4c bf4	V3V4		d__Bacteria;p__Firmicutes;c__Clostr idia;o__Clostridiales;f__Clostridiace ae;g__Clostridium_sensu_stricto_1	1	0.00
0253bd5f7388df3 5c5f43b2d85b26 7fa	V3V4			1	0.00
3942209bbeeb67 2021ff36f82794ae 6e	V3V4	d__Bacteria;p__Campilobacterota;c__ _Campylobacteria;o__Campylobacte rales;f__Helicobacteraceae;g__Helico bacter;s__uncultured_Helicobacter	d__Bacteria;p__Campilobacterota;c__ _Campylobacteria;o__Campylobacte rales;f__Helicobacteraceae;g__Helico bacter	4	0.00
e0c987cbfa9d14a e13e9cf00023dd2 3b	V3V4			6	0.01
cb81aae5ff4960b 2c64970d7c8ef0c b1	V3V4			2	0.00
1f9d41814f8c483 2104632e6be3ad d7d	V3V4		d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Enterobacter ales;f__Enterobacteriaceae;g__Escher ichia-Shigella	12	0.01
de6c5767675dae a2809d212ff3e6d b03	V3V4			2	0.00
acab893a2330eff acc9f74ae5a5994 4f	V3V4		d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Burkholderia les;f__Neisseriaceae;g__Neisseria	3	0.00
b4393dd2898000 d8bf94ad374a84 e508	V3V4		d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Lactobacillacea e;g__Lactobacillus	1	0.00
3534d05428b2f9 d14741eb884c9a 3144	V3V4		d__Bacteria;p__Actinobacteriota;c__ Actinobacteria;o__Propionibacteriale s;f__Propionibacteriaceae;g__Cutiba cterium	1	0.00
6b1e9704d9c7b3 dcfcfdb6c995e6 4d8	V3V4	d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Enterobacter ales;f__Enterobacteriaceae;g__Escher ichia-Shigella;s__Streptomyces_sp.	d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Enterobacter ales;f__Enterobacteriaceae;g__Escher ichia-Shigella	4	0.00

36b49d1cdea366 09242c463e217b7 880	V3V4	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Propionibacteriales;f__Propionibacteriaceae;g__Cutibacterium	7	0.01
03b94133f169109 cf1d00b403c5f09 89	V3V4	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	7	0.01
9674fc3295b7329 cfd903d5da7838 ee	V3V4	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	1	0.00
1face95889737ae c126a40991f8032 ef	V3V4	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	1	0.00
06ec07e2478fcd1 a6a1420ba11e83 e3c	V3V4	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	4	0.00
63c4d6d4257da3 014c495f2543005 3a5	V3V4	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	2	0.00
8fafdc7828b7257 1545121e1f3d36a 36	V3V4	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	10	0.01
9fbc75ff0f6bf962 fdbf13b85550324 1	V3V4	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	3	0.00
007a2dac44d387 9720067e0521158 cf0	V3V4	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	3	0.00
27ed56bde0d423 5bf1f6a57e9da3e 72c	V3V4	d__Bacteria;p__Deinococcota;c__Deinococchi;o__Deinococcales;f__Deinococcaceae;g__Deinococcus	3	0.00
70e63d68330c32 81404f22001f081 c99	V3V4	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	6	0.01

b1b42f4f1c0d778afcd2ceebbbaf5dbc					V3V4			d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	3	0.00	
33aea641c7dd0a325acf8de4e821c12d					V3V4				2	0.00	
b7756945b974867c86021564547c2a6d					V3V4				3	0.00	
48705a13153b62ac0af4ab27b73192e3					V3V4		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__uncultured_prokaryote	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	6	0.01	
1b5ca727a776fec4cc49a2e3388a7bd5					V3V4				2	0.00	
a47fbbed7375d0d17895e59409f03a53					V3V4			d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	1	0.00	
da79262b440ec0361d03c434e6dd7956					V3V4			d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	1	0.00	
362e0b0c0223e3f1e0f39abb4f87eb					V3V4			d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Rhodobacter	1	0.00	
d285d1af9dd4fe2762db30c758452a4c					V3V4				2	0.00	
e202f18d818883a9a0e8a8019c46d960	1eb3021faaec49c2_1	97.196	455325	455751	V3V4	Escherichia_coli_ATCC_700926	True	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	1	0.00	
5497318e515a8c328a68f95975d9c7d4	f5bcb58692924cb7_1	100	1597643	1597217	V3V4	Staphylococcus_epidermidis_ATCC_12228	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	5.15E+03	5.17	
2daa31dbdedabfa287858d52c4ade4d7	f5bcb58692924cb7_1	99.063	1597643	1597217	V3V4	Staphylococcus_epidermidis_ATCC_12228	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	10	0.01	



d33a6211611cad a51a0eda6d00b3 f45f	c45a1c5 7adf446 0e_2	100	23603	23859	V3V4	Bifidobact erium_ado lescentis_ ATCC_157 03	True		d__Bacteria;p__Actinobacteriota;c__ Actinobacteria;o__Bifidobacteriales;f __Bifidobacteriaceae;g__Bifidobacter ium	31	0.03
9a004eaacc9a867 ffef598974a724e2 4	f5bcb58 692924c b7_1	98.364	15976 43	15972 17	V3V4	Staphyloc occus_epi dermidis_ ATCC_122 28	True		d__Bacteria;p__Firmicutes;c__Bacilli; o__Staphylococcales;f__Staphylococ caceae;g__Staphylococcus	2	0.00
5c09851da6fa2dc e3f470ae14beeb4 d1	58ae911 973b74ff c_1	99.766	16666	17092	V3V4	Streptococ cus_agalac tiae_ATC C_BAA_6 11	True	d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Streptococcace ae;g__Streptococcus;s__Streptococcu s_agalactiae	d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Streptococcace ae;g__Streptococcus	210	0.21
7aa282961d474a 9fe44dea17c37b2 cf5	58ae911 973b74ff c_1	99.766	16666	17092	V3V4	Streptococ cus_agalac tiae_ATC C_BAA_6 11	True	d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Streptococcace ae;g__Streptococcus;s__Streptococcu s_agalactiae	d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Streptococcace ae;g__Streptococcus	1	0.00
ae724118f1bdef6 e863be0561de2a aff	1eb3021 faaec49c 2_1	99.766	45532 5	45575 1	V3V4	Escherichi a_coli_AT CC_70092 6	True		d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Enterobacter ales;f__Enterobacteriaceae;g__Escher ichia-Shigella	33	0.03
9a645346307544 8b4ef5e1b93fe2e 362	5964adb 8d0df4f de_1	99.766	47782 9	47825 5	V3V4	Lactobacill us_gasseri _ATCC_33 323	True	d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Lactobacillacea e;g__Lactobacillus;s__Lactobacillus_ gasseri	d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Lactobacillacea e;g__Lactobacillus	2070	2.08
88de790328dd10 b3ebad7cb963d1 7770	adb6d5 13b7374 f84_1	98.444	17219	17474	V3V4	Streptococ cus_muta ns_ATCC_ 700610	True		d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Streptococcace ae;g__Streptococcus	2	0.00
cb9c3959a2d40c bc54a6fb9714c88 1ca	5964adb 8d0df4f de_1	99.766	47782 9	47825 5	V3V4	Lactobacill us_gasseri _ATCC_33 323	True	d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Lactobacillacea e;g__Lactobacillus;s__Lactobacillus_ gasseri	d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Lactobacillacea e;g__Lactobacillus	5	0.01
51732e34618ee0 de8cb1b1d79c58 5fc3	5964adb 8d0df4f de_1	98.829	47782 9	47825 5	V3V4	Lactobacill us_gasseri _ATCC_33 323	True		d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Lactobacillacea e;g__Lactobacillus	2.00E +00	0.00
24af7433c4486d1 fd3fd32423ad69 9b5	045df7c 7cb0f42 b5_1	99.203	12229 84	12227 34	V3V4	Neisseria_ meningiti dis_ATCC _BAA_335	True		d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Burkholderia les;f__Neisseriaceae;g__Neisseria	2	0.00

b6635d67cb594473ddba9f8cfba5d13d	d889f9d d971b473d_1	100	34787 3	34745 2	V3V4	Phocaeicola_vulgatus_ATCC_8482	True	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_vulgatus	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	4744	4.76
e4c0868fdefcdf2037ab5f7a071e4cc7	2b7fa0e1de5f42de_1	100	18285 9	18327 2	V3V4	Deinococcus_radiodurans_ATCC_BAA_816	True	d__Bacteria;p__Deinococcota;c__Deinococci;o__Deinococcales;f__Deinococcaceae;g__Deinococcus;s__Deinococcus_radiodurans	d__Bacteria;p__Deinococcota;c__Deinococci;o__Deinococcales;f__Deinococcaceae;g__Deinococcus	2036	2.04
318669d5d926e9b81ca6911da00a14ea	3042186b85304e8d_1	100	9691	10092	V3V4	Clostridium_beijerinckii_ATCC_C_35702	True		d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	12195	12.25
64a7212b599e1f720f712f4a72f567a2	adb6d513b7374f84_1	97.613	17048	17465	V3V4	Streptococcus_mutans_ATCC_700610	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_mutans	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	1	0.00
b4d126d7b5117251ec9a72501c1093c8	5964adb8d0df4fde_1	97.658	47782 9	47825 5	V3V4	Lactobacillus_gasseri_ATCC_33323	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	2	0.00
63fcdf02bc7b34ab33308d40414e7307	d889f9d d971b473d_1	99.526	34787 3	34745 2	V3V4	Phocaeicola_vulgatus_ATCC_8482	True	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_vulgatus	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	822	0.83
908e9b387f6b9ce7d3f794e658fba37e	f5bcb58692924cb7_1	99.766	15976 43	15972 17	V3V4	Staphylococcus_epidermidis_ATCC_12228	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	897	0.90
056129de3ff9eab079fac9ec56181a4a	2504aeb524e74d25_1	100	22967 3	23009 4	V3V4	Porphyromonas_gingivalis_ATCC_33277	True	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Porphyromonas;s__Porphyromonas_gingivalis	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Porphyromonas	6361	6.39
afa4f6bdca4c647eb4492953ac855721	c45a1c57adf4460e_2	99.757	23449	23859	V3V4	Bifidobacterium_adolescentis_ATCC_15703	True		d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	147	0.15
3f3a0eaeaa9c0690b6ede1b17b4fd8ce	c45a1c57adf4460e_2	100	23449	23859	V3V4	Bifidobacterium_adolescentis_	True	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	3815	3.83

						ATCC_15703		ium;s__Bifidobacterium_adolescentis			
521820dea22098c03e64451bdeca66be	c45a1c57adff4460e_2	98.718	23626	23859	V3V4	Bifidobacterium_adolescentis_ATCC_15703	True		d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	12	0.01
e31c7e269125382d9bd6ee8fcc1fde21	d889f9dd971b473d_1	99.527	347873	347452	V3V4	Phocaeicola_vulgatus_ATCC_8482	True	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_vulgatus	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	965	0.97
332b70897316f7f62b81dfc53f41ca52	266a835027f7464b_2	100	38225	37824	V3V4	Rhodobacter_sphaeroides_ATCC_17029	True	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Rhodobacter;s__Rhodobacter_sphaeroides	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Rhodobacter	762	0.77
ffc36e27c82042664a16bcd4d380b286	1eb3021faaec49c2_1	100	455325	455751	V3V4	Escherichia_coli_ATCC_700926	True		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	6772	6.80
f71e5aacd4c976a1833958c2870b1d8b	045df7c7cb0f42b5_1	100	1223181	1222755	V3V4	Neisseria_meningitidis_ATCC_BAA_335	True	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Neisseriaceae;g__Neisseria;s__Neisseria_meningitidis	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Neisseriaceae;g__Neisseria	3480	3.50
88a3a8e95e3605bd051054f937cd e102	3042186b85304e8d_1	99.751	9691	10092	V3V4	Clostridium_beijerinckii_ATCC_35702	True		d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	904	0.91
e8de9432f2ada1078a2fda56ba92675a	4762fdd895094939_1	100	96706	97108	V3V4	Helicobacter_pylori_ATCC_700392	True	d__Bacteria;p__Campilobacterota;c__Campylobacteria;o__Campylobacterales;f__Helicobacteraceae;g__Helicobacter;s__Helicobacter_pylori	d__Bacteria;p__Campilobacterota;c__Campylobacteria;o__Campylobacterales;f__Helicobacteraceae;g__Helicobacter	3097	3.11
052ba7abaeaa968c4f79e3f97d1f0a2f	285a115d88c043f1_1	100	678693	679119	V3V4	Pseudomonas_aeruginosa_ATCC_9027	True		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	2581	2.59
c42488aff4cc842bf285a401dba39cc4	89e35fec14744942_1	100	528661	529080	V3V4	Schaalia_odontolytica_ATCC_17982	True	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Actinomyces;s__Schaalia_odontolytica	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Actinomyces	2260	2.27
b05f5459e068b529b2c41e659efdef34	9dc637a985b042c4_1	100	605572	605971	V3V4	Cutibacterium_acnes_ATCC_11828	True		d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Propionibacteriales;f__Propionibacteriaceae;g__Cutibacterium	411	0.41

892a20bbdc3ce599dc0c5d9f0866c352	27b35dd1651e48dd_1	100	213739	214165	V3V4	Enterococcus_faecalis_ATCC_47077	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	2860	2.87
5c035b54ac1cea1c1da765208a66520	5964adb8d0df4fde_1	99.766	477829	478255	V3V4	Lactobacillus_gasseri_ATCC_33323	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus_gasseri	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1747	1.75
c3a3a503752209bc052b3995236b079f	58ae911973b74ffc_1	100	16666	17092	V3V4	Streptococcus_agalactiae_ATC_C_BAA_611	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_agalactiae	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	6597	6.63
04be702b895fe5ed0568344daf564276	38ad2dab3e5e43b7_1	100	628061	628487	V3V4	Staphylococcus_aureus_subsp_aureus_ATCC_BAA_1556	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	4304	4.32
ef5af48ec2b6c023c5de28c59cb08a40	adb6d513b7374f84_1	100	17048	17474	V3V4	Streptococcus_mutans_ATCC_700610	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_mutans	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	6030	6.06
99f8f7fb3dc2bb4e0990397d1c9e5dc4	38ad2dab3e5e43b7_1	99.766	628061	628487	V3V4	Staphylococcus_aureus_subsp_aureus_ATCC_BAA_1556	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	804	0.81
194692a65aff7f21d0d0029503feed5	adb6d513b7374f84_1	99.766	17048	17474	V3V4	Streptococcus_mutans_ATCC_700610	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_mutans	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	227	0.23
4e7848491cf85b1d56d3c920629ba5de	285a115d88c043f1_1	97.418	678695	679119	V3V4	Pseudomonas_aeruginosa_ATC_C_9027	True		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	2.30E+01	0.02
b8f980ec6ad0c86efb83bd1f64c3a252	d889f9dd971b473d_1	99.763	347873	347452	V3V4	Phocaeicola_vulgatus_ATCC_8482	True	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_vulgatus	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	1030	1.03
3f298e5dbea50d14bc52110ff80df5c0	5964adb8d0df4fde_1	97.19	477829	478255	V3V4	Lactobacillus_gasseri	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1	0.00

						_ATCC_33 323					
c49cc7c2c45bd7a87913453e515ea14f	071a82bb90b94c6f_1	100	495134	495561	V3V4	Acinetobacter_baumannii_ATCC_17978	True	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter_baumannii	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter	6724	6.75
170cb61a735e0bfe7a859f4613210635	27b35dd1651e48dd_1	98.084	213906	214165	V3V4	Enterococcus_faecalis_ATCC_47077	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	1	0.00
8cb24777cb48dde0aac60dfeca125d10	5371a9904eb64361_1	100	9266	9693	V3V4	Bacillus_pacificus_ATCC_10987	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus	7565	7.60
f85cf38f782a314e3ab5965a58f2e46e	285a115d88c043f1_1	99.766	678693	679119	V3V4	Pseudomonas_aeruginosa_ATCC_9027	True		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	1	0.00
c4252de734fefdf07ede127685ee56	f5bcb58692924cb7_1	98.834	1597643	1597217	V3V4	Staphylococcus_epidermidis_ATCC_12228	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	1	0.00
9b23053de8f4269fe6b5ce286dfbef3c	5964adb8d0df4fde_1	100	477829	478255	V3V4	Lactobacillus_gasseri_ATCC_33323	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus_gasseri	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1153	1.16
c1f46ee956e06530a83aa00914e4c7cb	adb6d513b7374f84_1	99.766	17048	17474	V3V4	Streptococcus_mutans_ATCC_700610	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_mutans	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	1	0.00
3f460e58e5d5db0dbaf1a71ceef1525d	5964adb8d0df4fde_1	97.424	477829	478255	V3V4	Lactobacillus_gasseri_ATCC_33323	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	5	0.01
f8cad6522103a22e0788a989a039a794	266a835027f7464b_2	97.79	37792	37612	V5V6	Rhodobacter_sphaeroides_ATCC_17029	True	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Paracoccus;s__uncultured_Paracoccus	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Paracoccus	24	0.03
c640b138c428758d0ee70015ffffebd	58ae911973b74ffc_1	97.382	17124	17314	V5V6	Streptococcus_agalactiae_ATCC_BAA_611	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_gordonii	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	137	0.20

75e81af1ea94c080a5e24422bf0f8270	5371a9904eb64361_1	97.283	9725	9908	V5V6	Bacillus_pacificus_ATCC_10987	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus	199	0.28
41ad2a26bdea29ce20ce5c2f716b71e5	5964adb8d0df4fde_1	97.283	478287	478470	V5V6	Lactobacillus_gasseri_ATCC_33323	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus_mundtii	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	137	0.20
b9a27f523947e6b31eaff94f591a55de	5371a9904eb64361_1	100	9725	9924	V5V6	Bacillus_pacificus_ATCC_10987	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus	312	0.44
1d9d72ff20c4f8425b3aa55e1d742dc0	285a115d88c043f1_1	97.802	679151	679332	V5V6	Pseudomonas_aeruginosa_ATCC_9027	True	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__Pseudomonas_aeruginosa	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	72	0.10
4ba5a36a442f7295337341bae584d319	3042186b85304e8d_1	99.5	10124	10323	V5V6	Clostridium_beijerinckii_ATCC_35702	True	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__uncultured_Clostridium	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	1536	2.19
42ae093ca8e3d07f4f5318f40d0a20da	3042186b85304e8d_1	100	10124	10340	V5V6	Clostridium_beijerinckii_ATCC_35702	True	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__uncultured_Clostridium	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	99	0.14
b7f8ec8c56ea6c5a877b899bfa65f6cf	27b35dd1651e48dd_1	97.283	214197	214380	V5V6	Enterococcus_faecalis_ATCC_47077	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	90	0.13
d00984415738187f2bd75ba771f699d4	3042186b85304e8d_1	99.5	10124	10323	V5V6	Clostridium_beijerinckii_ATCC_35702	True	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__uncultured_Clostridium	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	3582	5.11
e0604154e9581bc0b7e1f13c57121882	f5bcb58692924cb7_1	99.502	1597185	1596986	V5V6	Staphylococcus_epidermidis_ATCC_12228	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus;s__Staphylococcus_epidermidis	d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	15	0.02
79dbaba672642ebd014b1e7b9b328112	071a82bb90b94c6f_1	100	19023	19242	V5V6	Acinetobacter_baumannii_ATCC_17978	True		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter	8033	11.45

6a2f7caa6b9c38ac8d74597de800bc87	2504aeb524e74d25_1	100	230126	230325	V5V6	Porphyromonas_gingivalis_ATCC_33277	True			8152	11.62
012b9a89e0c38429987cfa5126ca9e98	58ae911973b74ffc_1	100	17124	17323	V5V6	Streptococcus_agalactiae_ATCC_BAA_611	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_gordonii	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	202	0.29
e0a2bef6846fbd1aa22828c8a8086c86	89e35fec14744942_1	100	529112	529324	V5V6	Schaalia_odontolytica_ATCC_17982	True		d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Actinomyces	141	0.20
21d6f50624ff01e5bee69a84112530a0	f5bcb58692924cb7_1	100	1597185	1596986	V5V6	Staphylococcus_epidermidis_ATCC_12228	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus;s__Staphylococcus_sp.	d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	9126	13.01
3704c6a53ad64ba61b11b9bb6e7e06f7	3042186b85304e8d_1	100	10124	10323	V5V6	Clostridium_beijerinckii_ATCC_35702	True	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__uncultured_Clostridium	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	21062	30.03
56c7c15ecc0af90185a9c2e39af9a4a4	1eb3021faaec49c2_1	100	455783	455994	V5V6	Escherichia_coli_ATCC_700926	True	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella;s__Escherichia_coli	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	387	0.55
9a38446a8cba2f1f974a622d8092fb1	3042186b85304e8d_1	98.913	10124	10306	V5V6	Clostridium_beijerinckii_ATCC_35702	True	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__uncultured_Clostridium	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	10	0.01
91c2afa196dfa8a99f1dda3f89470f7d	2504aeb524e74d25_1	100	230126	230349	V5V6	Porphyromonas_gingivalis_ATCC_33277	True			61	0.09
28b80793effa80e95f17ba78f86ba3a1	5964adb8d0df4fde_1	100	478287	478487	V5V6	Lactobacillus_gasseri_ATCC_33323	True			105	0.15
8eead67fce32a188c8e0264c8c648a2d	4762fdd895094939_1	100	97140	97366	V5V6	Helicobacter_pylori_ATCC_700392	True	d__Bacteria;p__Campilobacterota;c__Campylobacteria;o__Campylobacterales;f__Helicobacteraceae;g__uncultured	d__Bacteria;p__Campilobacterota;c__Campylobacteria;o__Campylobacterales;f__Helicobacteraceae;g__uncultured	116	0.17

								ured;s__uncultured_Epsilonproteobacteria			
fce4db9d80643391cfd2508ac33fa8d	2b7fa0e1de5f42de_1	97.207	183304	183482	V5V6	Deinococcus_radiourans_ATCC_BAA_816	True	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_13;s__rumen_bacterium	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_13	33	0.05
0fa7e151a8f8896c85778ba8addc5103	4762fdd895094939_1	98.37	97140	97322	V5V6	Helicobacter_pylori_ATCC_700392	True			15	0.02
f2497fa105c39ed688f04e4a8bb515a	adb6d513b7374f84_1	100	17506	17718	V5V6	Streptococcus_mutans_ATCC_700610	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_gordonii	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	423	0.60
e6b816d934aea16c3b7dd7e8b25a37d0	5371a9904eb64361_1	98.953	9725	9915	V5V6	Bacillus_pacificus_ATCC_10987	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus	157	0.22
5ea873145571ae5cc0af20f573bae47f	5964adb8d0df4fde_1	98.37	478287	478470	V5V6	Lactobacillus_gasseri_ATCC_33323	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus_mundtii	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	104	0.15
ddf00153358dd52bbc1a5646ff83ff19	c45a1c57adff4460e_2	100	23891	24087	V5V6	Bifidobacterium_adolescentis_ATCC_15703	True	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium_sp.	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	1212	1.73
ab2cd68e1a2959f94c31e0a25fcf6b10	285a115d88c043f1_1	100	679151	679370	V5V6	Pseudomonas_aeruginosa_ATCC_9027	True	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__Pseudomonas_aeruginosa	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	136	0.19
f32884e8124f8ed14a6a973f9e59b65f	d889f9dd971b473d_1	100	347420	347221	V5V6	Phocaeicola_vulgatus_ATCC_8482	True	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__Paludibacter;s__uncultured_bacterium	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__Paludibacter	7810	11.14
e9de1e3fc5a26f227056f0678cdec4df	d889f9dd971b473d_1	99.5	347420	347221	V5V6	Phocaeicola_vulgatus_ATCC_8482	True	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__Paludibacter;s__uncultured_bacterium	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__Paludibacter	5106	7.28
f9050ac7af24954bcf69dd15c8a47e64	27b35dd1651e48dd_1	98.37	214197	214380	V5V6	Enterococcus_faecalis	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	73	0.10



						_ATCC_47077					
0dfd270b9832257283af9b9f78acc52b	1eb3021faaec49c2_1	98.585	455783	455994	V5V6	Escherichia_coli_ATCC_700926	True	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella;s__Escherichia_coli	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	45	0.06
2de4f95c844ab13c180b39c7568462a0					V5V6			d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_13;s__rumen_bacterium	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_13	83	0.12
928d3dc22f242a87f28f9219c099c075					V5V6			d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Paracoccus;s__uncultured_Paracoccus	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Paracoccus	19	0.03
8046b007682c31562cd6f016415cb45f					V5V6					12	0.02
c42e0b7c52736f3bd883bf490b386e9e					V5V6				d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	13	0.02
634f27f65e3b8ec24f659647f103077					V5V6			d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter_sp.	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter	6	0.01
81feba462792be505fe7ad9288c6616c					V5V6					15	0.02
c79e84621eddb90c282e75399d80fe76					V5V6			d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_gordonii	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	7	0.01
fbfec8c1653111db7b8f9a5acf06e0e4					V5V6				d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Oxalobacteraceae;g__Herbaspirillum	2	0.00
3f52d098be6c09dc2688c232e0522e6e					V5V6					74	0.11
e3007d82e148295473b573cb0cfd1802					V5V6					22	0.03

ea6cfd2f886a465e1f22845677ca43e					V5V6				6	0.01
678715dd463dd71ad724f2490dfd7364					V5V6				16	0.02
a7468bfe80697ea6b0e8655125ffbec9					V5V6	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus_mundtii		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	90	0.13
4bf0aeed2b0e74b2bc4e2447e45fa6cf					V5V6			d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococaceae;g__Staphylococcus	12	0.02
105b900b8b271fc1279a9f00f63fd8da					V5V6	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_gordonii		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	128	0.18
6beaac5c0c09537786551f0740e1f8e6	38ad2da b3e5e43 b7_1	100	62851 9	62871 8	V5V6	Staphylococcus_aureus_subsp_aureus_A TCC_BAA_1556	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococaceae;g__Staphylococcus	373	0.53
2d171c4fcb88172f9022e70d09b64578					V5V6			d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__uncultured_Clostridium	25	0.04
9356c352f9e2de6d1675a9a73c9608b6					V5V6			d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__uncultured_Clostridium	60	0.09
3b08e2713ab41b7a404cfaa9ad2e833a					V5V6			d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_gordonii	1	0.00
792bf390207b1d9bc70595633c70b17f					V5V6			d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Paracoccus;s__uncultured_Paracoccus	18	0.03
e25ebbf67c652da38afef831ff1bda3f					V5V6			d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Paracoccus;s__uncultured_Paracoccus	35	0.05

56f1751149e7f17b825efca9b0ec1569					V5V6			d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Mesorhizobium;s__Mesorhizobium_sp.	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Mesorhizobium	6	0.01
5903cb99ef12f590c6c3de7e367df82d					V5V6					1	0.00
c6c3ab4e828fb40d6e05967b7aac9338					V5V6					93	0.13
c81def64b8f2523ef3c7fefc8711edf6					V5V6			d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_gordonii	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	11	0.02
ef3199891723da4b0a64b80682bad a68					V5V6					2	0.00
d77aa435264c499b17b7e0eeb121a585	27b35dd1651e48dd_1	100	214197	214396	V5V6	Enterococcus_faecalis_ATCC_47077	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus_faecalis	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	123	0.18
20392706f8152cfe29c2fe551e5c408d	2b7fa0e1de5f42de_1	98.324	183304	183482	V5V6	Deinococcus_radiourans_ATCC_BAA_816	True			20	0.03
5a6c87d6a4eb5e114959f6192f29b641	c45a1c57adf4460e_2	100	23609	23861	V5V6	Bifidobacterium_adolescentis_ATCC_15703	True			30	0.04
d087f1ce2b06f0b0deb360e308d878c1	045df7c7cb0f42b5_1	100	1222723	1222504	V5V6	Neisseria_meningitidis_ATCC_BAA_335	True	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Chromobacteriaceae;g__Vogesella;s__uncultured_bacterium	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Chromobacteriaceae;g__Vogesella	114	0.16
421770193803d8f3fe9cf981628b1cde	1eb3021faaec49c2_1	100	455528	455753	V4	Escherichia_coli_ATCC_700926	True		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	3	0.00
ab6b7b90747341ce39f82d0a22a1d37d					V4				d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;g__Methylobacterium-Methylobacterium	4	0.00

a0a0b67a4c65c67 78fe8e1e04e7e3d 49	V4	d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcaceae;g__Clostridioides;s__Clostridioides_difficile	d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcaceae;g__Clostridioides	9	0.00
efe485bddd633d 28fa7694f38d036 08f	V4			2	0.00
8375d98f3453435 40e7a4d73b2eb1 f82	V4		d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	6	0.00
3481fa43fe5fba6 aecdc7f9aae6ed9 c0	V4			160	0.07
4cbfff144d4e7a4 e0f4619ed505be0 70	V4			55	0.02
f5f5e0da8973046 2abaf6301a95571 93	V4		d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Faecalibacterium	20	0.01
fb428d07d03e32 be0b85eacbed10 df0a	V4	d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Coprococcus;s__Coprococcus_eutactus	d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Coprococcus	19	0.01
ec6732c2e0d4cf6 4b3d0350e7fe3d efb	V4		d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Roseburia	41	0.02
247dd7bf282099 0e45df15e2ca76d bd1	V4			1	0.00
c939ee112ba9826 65e012437dae05 c1e	V4			186	0.08
2c982937754e632 1f861027032db8 0f7	V4		d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	13	0.01
35cbb315e019e0 a8768d4b73862d f415	V4		d__Bacteria;p__Actinobacteriota;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;g__Collinsella	11	0.00
9c754ee09188996 02c8196cfc5a756 92	V4			6	0.00

685a1812a6e46f7 2d7cf1f4a060b8e 96					V4				d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Corynebacteriales;f__Corynebacteriaceae;g__Corynebacterium	3	0.00
99bccd58aaeb00f 98e22add40be6e 36b					V4			d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcae;g__Clostridioides;s__Clostridioides_difficile	d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcae;g__Clostridioides	408	0.17
fa531a9e5007f7d 080e555401270d 85a					V4				d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium	105	0.04
cd3526e9ddf608 ed31c4f3d648ca8 034					V4				d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Sutterellaceae;g__Parasutterella	6	0.00
a19be9fe0ba2ea2 84bd53cb94f622 471					V4				d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	2	0.00
5a6c87d6a4eb5e 114959f6192f29b 641	c45a1c5 7adf446 0e_2	100	23609	23861	V4	Bifidobacterium_adolescentis_ATCC_15703	True		d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	9848	4.17
8df399e29acb5a5 83f449a82db4e17 c9					V4				d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	46	0.02
da5bc53279a680 c25d503cb1bdc0 e57a	9dc637a 985b042 c4_1	100	60573 0	60597 7	V4	Cutibacterium_acnes_ATCC_11828	True		d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Propionibacteriales;f__Propionibacteriaceae;g__Cutibacterium	3097	1.31
463d246ab2d6bc 2481d5aab8de07 5a8b	9dc637a 985b042 c4_1	100	60575 4	60597 7	V4	Cutibacterium_acnes_ATCC_11828	True		d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Propionibacteriales;f__Propionibacteriaceae;g__Cutibacterium	3	0.00
e7cfd084265c4df 4856ca07b1c9b2 4ee	adb6d5 13b7374 f84_1	100	17225	17476	V4	Streptococcus_mutans_ATCC_700610	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_mutans	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	10661	4.52
65d43491988bfe5 57da4d86a5ba25 dae	f5bcb58 692924c b7_1	100	15974 67	15972 15	V4	Staphylococcus_epidermidis_ATCC_12228	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	27015	11.45

e3055f1b3a2ef5ff e239567f02e0e75 8	58ae911 973b74ffc_1	100	16843	17094	V4	Streptococ cus_agalac tie_ATC C_BAA_6 11	True	d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Streptococcace ae;g__Streptococcus;s__Streptococcu s_agalactiae	d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Streptococcace ae;g__Streptococcus	13110	5.55
e832be098a5318 684958d1430526 7752	4762fdd 8950949 39_1	100	96857	97110	V4	Helicobact er_pylori_ ATCC_700 392	True	d__Bacteria;p__Campilobacterota;c__ _Campylobacteria;o__Campylobacte rales;f__Helicobacteraceae;g__Helico bacter;s__Helicobacter_pylori	d__Bacteria;p__Campilobacterota;c__ _Campylobacteria;o__Campylobacte rales;f__Helicobacteraceae;g__Helico bacter	5943	2.52
9fd9ac1df429568 b5d1ca6aa0b9f0 b34	071a82b b90b94c 6f_1	99.213	18741	18993	V4	Acinetoba cter_baum annii_ATC C_17978	True		d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Pseudomona dales;f__Moraxellaceae;g__Acinetob acter	16	0.01
df8456a1abfb4c 8a2c450b44378d 4cb	89e35fec 1474494 2_1	100	52883 0	52908 2	V4	Schaalia_o dontolytic a_ATCC_1 7982	True	d__Bacteria;p__Actinobacteriota;c__ Actinobacteria;o__Actinomycetales;f__ Actinomycetaceae;g__Actinomyce s;s__Schaalia_odontolytica	d__Bacteria;p__Actinobacteriota;c__ Actinobacteria;o__Actinomycetales;f__ Actinomycetaceae;g__Actinomyce s	4128	1.75
cb97fb83d4c8cc6 eccded352a4ca3f 8f	3042186 b85304e 8d_1	99.605	9842	10094	V4	Clostridiu m_beijerin ckii_ATC C_35702	True	d__Bacteria;p__Firmicutes;c__Clostr idia;o__Clostridiales;f__Clostridiace ae;g__Clostridium_sensu_stricto_1;s__ Clostridium_beijerinckii	d__Bacteria;p__Firmicutes;c__Clostr idia;o__Clostridiales;f__Clostridiace ae;g__Clostridium_sensu_stricto_1	1954	0.83
ff9d93d7b7e4678 7568f2d241caeaf 3b	285a115 d88c043 f1_1	100	67886 9	67912 1	V4	Pseudomo nas_aerugi nosa_ATC C_9027	True		d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Pseudomona dales;f__Pseudomonadaceae;g__Pse udomonas	5608	2.38
2385fe1c2dd5a3f 83237272a66440 88b	2b7fa0e 1de5f42 de_1	100	18302 2	18327 4	V4	Deinococc us_radiod urans_AT CC_BAA_ 816	True	d__Bacteria;p__Deinococcota;c__Dei nococci;o__Deinococcales;f__Deinoc occaceae;g__Deinococcus;s__Deinoc occus_radiodurans	d__Bacteria;p__Deinococcota;c__Dei nococci;o__Deinococcales;f__Deinoc occaceae;g__Deinococcus	9108	3.86
bdf8a260946246 22d68509a87fa75 ba7	5371a99 04eb643 61_1	100	9443	9695	V4	Bacillus_p acificus_A TCC_1098 7	True		d__Bacteria;p__Firmicutes;c__Bacilli; o__Bacillales;f__Bacillaceae;g__Bacill us	23458	9.94
e21e804c8cb49a5 e0492b8fc545422 0f	2504aeb 524e74d 25_1	100	22984 4	23009 6	V4	Porphyro monas_gi ngivalis_A TCC_3327 7	True	d__Bacteria;p__Bacteroidota;c__Bact eroidia;o__Bacteroidales;f__Porphyr omonadaceae;g__Porphyromonas;s__ _Porphyromonas_gingivalis	d__Bacteria;p__Bacteroidota;c__Bact eroidia;o__Bacteroidales;f__Porphyr omonadaceae;g__Porphyromonas	8004	3.39
dfc86cefa76e3e3 d93e7eea450e68 07	266a835 027f746 4b_2	100	38074	37822	V4	Rhodobact er_sphaer oides_AT CC_17029	True		d__Bacteria;p__Proteobacteria;c__Al phaproteobacteria;o__Rhodobacteral es;f__Rhodobacteraceae;g__Rhodoba cter	3076	1.30

b2062ae94fb00a931014b67b499295a8	d889f9d d971b47 3d_1	99.605	34770 2	34745 0	V4	Phocaeicola_vulgaris_ATCC_8482	True	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_vulgatus	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	2269	0.96
1d19b18db48daa1837d18d3171334ded	f5bcb58 692924c b7_1	99.605	15974 67	15972 15	V4	Staphylococcus_epidermidis_ATCC_12228	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	2051	0.87
096e60ea01b8425c20593919d66c37d2	5371a99 04eb643 61_1	98.819	9443	9695	V4	Bacillus_pacificus_ATCC_10987	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus	3	0.00
99deb3c5ecb022ec05609ebd1112a557	d889f9d d971b47 3d_1	100	34770 2	34745 0	V4	Phocaeicola_vulgaris_ATCC_8482	True	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_vulgatus	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	11308	4.79
ea403646ed22d679fa4586263d8fc32f	071a82b b90b94c 6f_1	100	18741	18993	V4	Acinetobacter_baumannii_ATCC_17978	True		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter	16954	7.18
4e8d7a4662640b90817f015280cf5713	3042186 b85304e 8d_1	100	9842	10094	V4	Clostridium_beijerinckii_ATCC_35702	True		d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	30566	12.95
8001826dafd338cf078dd28c2eae05ed	d889f9d d971b47 3d_1	99.605	34770 2	34745 0	V4	Phocaeicola_vulgaris_ATCC_8482	True	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_vulgatus	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	2140	0.91
9908fffab7ed4f3bec44cda2f5084d49	27b35d d1651e4 8dd_1	100	21391 5	21416 7	V4	Enterococcus_faecalis_ATCC_47077	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	8450	3.58
8224351b2abd16dd4d58c3015ff5e795	045df7c 7cb0f42 b5_1	100	12230 05	12227 53	V4	Neisseria_meningitidis_ATCC_BAA_335	True	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Neisseriaceae;g__Neisseria;s__Neisseria_meningitidis	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Neisseriaceae;g__Neisseria	9076	3.85
d46e2205f0c6ecf67b51f83d111c509c	1eb3021 faaec49c 2_1	100	45550 1	45575 3	V4	Escherichia_coli_ATCC_700926	True		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	13582	5.75
0df6c802966e8670279671824da4f10a	5964adb 8d0df4f de_1	100	47800 5	47825 7	V4	Lactobacillus_gasseri	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	13490	5.72

		_ATCC_33 323				
EU776082.1.1401	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella;s__uncultured_bacterium	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	3	0.00	
MF629745.1.1219	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter_cloacae	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Enterobacter	6	0.01	
AF349929.1.1503	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus_sp.	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	18	0.02	
CP020424.2046841.204	Multiplex			4	0.00	
EU511507.1.1388_005	Multiplex			1	0.00	
DQ809036.1.1400_002	Multiplex			10.02	0.01	
JX426120.1.1502	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus_plantarum	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	6	0.01	
CP019858.4077753.407	Multiplex			3	0.00	
CP012650.1579871.158	Multiplex			6	0.01	
KC584759.1.1459	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella_sp.	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Klebsiella	2	0.00	
JN013122.1.1460_053	Multiplex			1	0.00	
JF772072.1.1504	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella_oxytoca	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Klebsiella	2	0.00	
MF369967.1.1401	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus_faecium	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	2	0.00	



EU776683.1.1429	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	19	0.02
KY228992.1.1320	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus_sp.	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1	0.00
LFDY01000027.1 24228.	Multiplex			11	0.01
DQ057465.1.147 1_001	Multiplex			3.19	0.00
DQ823798.1.141 5	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Muribaculaceae;s__uncultured_bacterium	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Muribaculaceae	3	0.00
EU776602.1.1302	Multiplex	d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcaceae;g__Terrisporobacter;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcaceae;g__Terrisporobacter	25	0.03
CP019858.10931 94.109	Multiplex			7	0.01
AAML04000003. 230439.	Multiplex			4	0.00
KM819125.1.152 7	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__uncultured_Bacillus	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1	0.00
EU772368.1.1408	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Leuconostocaceae;g__Leuconostoc;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Leuconostocaceae;g__Leuconostoc	4	0.00
DQ002385.1.148 6_001	Multiplex			12.29	0.01
EF096405.1.1378 _011	Multiplex			2.35	0.00
EF406388.1.1504 _077	Multiplex			1.99	0.00
EF097505.1.1302	Multiplex	d__Bacteria;p__Actinobacteriota;c__Coriobacteriia;o__Coriobacteriales;f__Atopobiaceae;g__Coriobacteriaceae_UCG-002;s__uncultured_bacterium	d__Bacteria;p__Actinobacteriota;c__Coriobacteriia;o__Coriobacteriales;f__Atopobiaceae;g__Coriobacteriaceae_UCG-002	1	0.00

EU467051.1.1321	Multiplex	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	2	0.00
GQ416526.1.1465_001	Multiplex			0.41	0.00
AM286415.17506.18994_001	Multiplex			7235.31	8.45
GQ448270.1.1398	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella;s__uncultured_bacterium	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella	7	0.01
CP015126.1170520.117	Multiplex			7	0.01
FN668375.4306350.430	Multiplex			130	0.15
KP641129.1.1470	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella;s__uncultured_bacterium	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	4	0.00
EU136678.1.2011_001	Multiplex			4984.34	5.82
JQ471932.1.1385	Multiplex	d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium;s__uncultured_bacterium	d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium	2	0.00
HQ745021.1.1418	Multiplex	d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium;s__uncultured_organism	d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium	46	0.05
CP018044.567281.5688	Multiplex			1	0.00
EU778419.1.1388	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella;s__uncultured_bacterium	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	52	0.06
CP011118.356520.358068_001	Multiplex			183.07	0.21
CP026598.16203.17711	Multiplex	d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcace	d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-	14	0.02

		ae;g__Clostridioides;s__Clostridioides_difficile	Tissierellales;f__Peptostreptococcaceae;g__Clostridioides		
EU451868.1.1386_001	Multiplex			1	0.00
AJ289177.1.1394	Multiplex	d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium;s__uncultured_eubacterium	d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium	23	0.03
KF625184.1.1787	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Yersiniaceae;g__Serratia;s__Serratia_proteamaculans	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Yersiniaceae;g__Serratia	5	0.01
HQ798408.1.1428	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_organism	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	1	0.00
HQ818413.1.1435	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_organism	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	4	0.00
JQ477578.1.1386	Multiplex	d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium;s__uncultured_bacterium	d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium	4	0.00
KR027010.1.1568	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__bacterium_NXKED9	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus	5	0.01
JX003602.1.1336	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus_plantarum	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	15	0.02
CP015966.2805828.280	Multiplex			9	0.01
DQ801774.1.1401	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_bacterium	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	6	0.01
MH899355.1.1236	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus_casei	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	4	0.00
MUJV01000001.176.164	Multiplex			5	0.01

EU453007.1.1441	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1	0.00
CP012323.1102504.110	Multiplex			41	0.05
JN559663.1.1511	Multiplex	d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Lachnospiraceae_UCG-004;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Lachnospiraceae_UCG-004	19	0.02
DQ818682.1.1490	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	45	0.05
CP028529.16107.17614	Multiplex	d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcaceae;g__Clostridioides;s__Clostridioides_difficile	d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcaceae;g__Clostridioides	112	0.13
EU511242.1.1396_005	Multiplex			1	0.00
DQ808680.1.1386	Multiplex	d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Faecalibacterium;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Faecalibacterium	17	0.02
DQ818104.1.1460	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	4	0.00
GQ156444.1.1349	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella;s__uncultured_bacterium	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	1	0.00
FAGH01000127.1.1295	Multiplex	d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcaceae;g__Clostridioides;s__Clostridioides_difficile	d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcaceae;g__Clostridioides	16	0.02
EU772591.1.1407	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	42	0.05

CP012266.24417 1.2457	Multiplex			2	0.00
CQBO01000060. 27.1557	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Yersiniaceae;g__Yersinia;s__Yersinia_frederiksenii	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Yersiniaceae;g__Yersinia	6	0.01
GU808376.1.149 6	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Erwiniaceae;g__Pantoea;s__uncultured_bacterium	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Erwiniaceae;g__Pantoea	10	0.01
GQ897892.1.148 1	Multiplex	d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcaceae;g__Romboutsia;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcaceae;g__Romboutsia	15	0.02
CP009846.39631 35.396	Multiplex			28	0.03
AM277978.1.152 5	Multiplex	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__uncultured_bacterium	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	9	0.01
EU460412.1.1431 _001	Multiplex			91.7	0.11
CP020424.20413 90.204	Multiplex			8	0.01
EU772683.1.1391	Multiplex	d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Blautia;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Blautia	23	0.03
EU774926.1.1421	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1	0.00
GQ155746.1.135 9	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	3	0.00
LF649083.20.148 0	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus_paraplanarum	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	14	0.02
FN665654.13832 7.139831_006	Multiplex			19224	22.46

MK045817.1.1425	Multiplex	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium_longum	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	6	0.01
EU776680.1.1401_001	Multiplex			16.99	0.02
DQ814052.1.1485	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Yersiniaceae;g__Serratia;s__uncultured_bacterium	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Yersiniaceae;g__Serratia	14	0.02
DQ089673.1.1505	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter_cloacae	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Enterobacter	2	0.00
FJ976017.1.1357	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__uncultured_Lactobacillaceae	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1	0.00
HQ804113.1.1452	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_d__organism	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	12	0.01
HQ767681.1.1432	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_d__organism	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	27	0.03
JF043143.1.1362	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Klebsiella;s__uncultured_bacterium	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Klebsiella	24	0.03
DQ795160.1.1400	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella;s__uncultured_bacterium	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella	2	0.00
EU767611.1.1349	Multiplex	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__uncultured_bacterium	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	5	0.01
EU467709.1.1380	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_d__bacterium	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	9	0.01
JQ002525.1.1373	Multiplex	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__uncultured_bacterium	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	4	0.00

		_Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium_choerinum	_Bifidobacteriaceae;g__Bifidobacterium		
DQ799377.1.1384	Multiplex	d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Ruminococcus;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Ruminococcus	1	0.00
JQ475464.1.1374	Multiplex	d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium;s__uncultured_bacterium	d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium	29	0.03
CP017954.2756793.275	Multiplex			1	0.00
GQ477833.1.1442	Multiplex	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Acetobacterales;f__Acetobacteraceae;g__Acetobacter;s__uncultured_bacterium	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Acetobacterales;f__Acetobacteraceae;g__Acetobacter	14	0.02
FPLN01008504.13.1528	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__metagenome	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	1	0.00
JQ468014.1.1391	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__Capnocytophaga;s__uncultured_bacterium	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__Capnocytophaga	3	0.00
HQ800683.1.1439	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_organism	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	14	0.02
FJ975799.1.1361	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__uncultured_Lactobacillales	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	28	0.03
EF097527.1.1405_001	Multiplex			0.99	0.00
GQ448246.1.1389	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_bacterium	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	11	0.01
D86186.1.1530	Multiplex	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium_choerinum	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	8	0.01

AB969632.1.1565	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1	0.00
DQ798156.1.1398	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_bacterium	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	2	0.00
EU458418.1.1398	Multiplex	d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__[Ruminococcus]_torques_group;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__[Ruminococcus]_torques_group	38	0.04
FN667917.1.1426	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus_sp.	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	2	0.00
JQ477027.1.1419	Multiplex	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Actinomycetes;s__uncultured_bacterium	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Actinomycetes	11	0.01
KF842135.1.1408	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_bacterium	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	34	0.04
EU778419.1.1388_001	Multiplex			92.61	0.11
EU456966.1.1435_002	Multiplex			1.16	0.00
EU762218.1.1357	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_bacterium	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	34	0.04
HQ762784.1.1447_001	Multiplex			463.2	0.54
EU560876.1.1492_014	Multiplex			11.9	0.01
AM286415.3550757.355	Multiplex			1	0.00
EF097373.1.1429	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	7	0.01



CP010888.64864 8.6501	Multiplex			28	0.03
EU511760.1.1389 _004	Multiplex			1.99	0.00
DQ794217.1.139 7	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_bacterium	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	7	0.01
EU777738.1.1370	Multiplex	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Sarcina;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Sarcina	3	0.00
EU287343.1.1529	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	12	0.01
EU775617.1.1401	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella;s__uncultured_bacterium	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	37	0.04
KF817757.1.1414	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Yersiniaceae;g__Rahnella1;s__Rahnella_aquatilis	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Yersiniaceae;g__Rahnella1	5	0.01
EU457166.1.1396	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_bacterium	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	2	0.00
EU458418.1.1398 _015	Multiplex			119	0.14
KT424977.1.1468	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__Shewanellaceae;g__Shewanella;s__Shewanella_sp.	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__Shewanellaceae;g__Shewanella	46	0.05
CP002246.11893 58.119	Multiplex			2	0.00
BAAX01003885. 346.185	Multiplex			24	0.03
EU778512.1.1403 _001	Multiplex			42.13	0.05
CP019858.12424 3.1257	Multiplex			16	0.02

EU510219.1.1285_014	Multiplex			1.16	0.00
DQ824048.1.1400_001	Multiplex			0.18	0.00
AL935263.2944928.294	Multiplex			2	0.00
KM819108.1.1529	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__uncultured_Bacillus	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1	0.00
EU775617.1.1401_001	Multiplex			1896.28	2.22
HQ818432.1.1426	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_d__organism	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	11	0.01
HQ774712.1.1452_001	Multiplex			0.3	0.00
CP019857.10819.12310	Multiplex	d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcaceae;g__Clostridioides;s__Clostridioides_difficile	d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcaceae;g__Clostridioides	13	0.02
CQBX01000005.209397.	Multiplex			11	0.01
EU451957.1.1393_001	Multiplex			3	0.00
KM819135.1.1519	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__uncultured_Bacillus	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	2	0.00
CP022544.1495640.149	Multiplex			1	0.00
CP027190.484364.4859	Multiplex			16	0.02
FPLN01003709.10.1525	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__metagenome	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	9	0.01
DQ800097.1.1403	Multiplex	d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Lachnospiraceae_UCG-004;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Lachnospiraceae_UCG-004	11	0.01

MH548358.1.1508					Multiplex			d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus_plantarum	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1	0.00
JQ809309.1.1538					Multiplex			d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__uncultured_Lactobacillaceae	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1	0.00
EF406803.1.1509_078					Multiplex					0.02	0.00
DQ800202.1.1374					Multiplex			d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Ruminococcus;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Ruminococcus	2	0.00
JQ861287.1.1510_001	1eb3021faaec49c2_1	97.543	4584412	4582910	Multiplex	Escherichia_coli_ATCC_700926	True			0.42	0.00
JN208201.1.1488	1eb3021faaec49c2_1	97.383	3660897	3659410	Multiplex	Escherichia_coli_ATCC_700926	True	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter_sp.	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Enterobacter	29	0.03
CP031558.1500822.1502336_001	4762fdd895094939_1	98.328	96370	97853	Multiplex	Helicobacter_pylori_ATCC_700392	True			1234	1.44
DQ325862.1.1349	c45a1c57adf4460e_2	98.298	23119	24468	Multiplex	Bifidobacterium_adolescentis_ATCC_15703	True	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__uncultured_bacterium	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	3	0.00
EU451160.1.1434_001	5964adb8d0df4fde_1	97.629	477450	478879	Multiplex	Lactobacillus_gasseri_ATCC_33323	True			2.15	0.00
HQ807338.1.1448	1eb3021faaec49c2_1	98.758	3660866	3659419	Multiplex	Escherichia_coli_ATCC_700926	True	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella;s__uncultured_organism	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	4	0.00
MH105767.1.1436	27b35dd1651e48dd_1	98.468	213417	214852	Multiplex	Enterococcus_faecalis_ATCC_47077	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus_faecalis	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	25	0.03

CP029907.37143 63.371	1eb3021 faaec49c 2_1	97.508	11525 80	11541 02	Multiplex	Escherichi a_coli_AT CC_70092 6	True			8	0.01
CP024019.97500. 99009	4762fdd 8950949 39_1	99.73	96370	97853	Multiplex	Helicobact er_pylori_ ATCC_700 392	True	d__Bacteria;p__Campilobacterota;c__ _Campylobacteria;o__Campylobacte rales;f__Helicobacteraceae;g__Helico bacter;s__Helicobacter_pylori	d__Bacteria;p__Campilobacterota;c__ _Campylobacteria;o__Campylobacte rales;f__Helicobacteraceae;g__Helico bacter	4	0.00
GQ155927.1.137 1	27b35d d1651e4 8dd_1	98.939	21347 1	21478 9	Multiplex	Enterococc us_faecalis _ATCC_47 077	True	d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Enterococcacea e;g__Enterococcus;s__uncultured_ba cterium	d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Enterococcacea e;g__Enterococcus	5	0.01
HQ762728.1.143 7	d889f9d d971b47 3d_1	97.985	25877 52	25891 84	Multiplex	Phocaeicol a_vulgatu s_ATCC_8 482	True	d__Bacteria;p__Bacteroidota;c__Bact eroidia;o__Bacteroidales;f__Bacteroi daceae;g__Bacteroides;s__unculture d__organism	d__Bacteria;p__Bacteroidota;c__Bact eroidia;o__Bacteroidales;f__Bacteroi daceae;g__Bacteroides	4	0.00
DQ905255.1.145 4	d889f9d d971b47 3d_1	98.418	20954 69	20969 22	Multiplex	Phocaeicol a_vulgatu s_ATCC_8 482	True	d__Bacteria;p__Bacteroidota;c__Bact eroidia;o__Bacteroidales;f__Bacteroi daceae;g__Bacteroides;s__unculture d__bacterium	d__Bacteria;p__Bacteroidota;c__Bact eroidia;o__Bacteroidales;f__Bacteroi daceae;g__Bacteroides	6	0.01
HQ793115.1.145 3	d889f9d d971b47 3d_1	98.486	34820 8	34682 2	Multiplex	Phocaeicol a_vulgatu s_ATCC_8 482	True	d__Bacteria;p__Bacteroidota;c__Bact eroidia;o__Bacteroidales;f__Bacteroi daceae;g__Bacteroides;s__unculture d__organism	d__Bacteria;p__Bacteroidota;c__Bact eroidia;o__Bacteroidales;f__Bacteroi daceae;g__Bacteroides	4	0.00
MXOH01000001. 553880.555401_0 01	1eb3021 faaec49c 2_1	97.639	11525 80	11541 01	Multiplex	Escherichi a_coli_AT CC_70092 6	True			0.47	0.00
AP011943.11492 68.115	4762fdd 8950949 39_1	99.461	96370	97853	Multiplex	Helicobact er_pylori_ ATCC_700 392	True			15	0.02
AP009256.19883 80.198	c45a1c5 7adf446 0e_2	100	23099	24608	Multiplex	Bifidobact erium_ado lescentis_ ATCC_157 03	True			19	0.02
CP002246.41582 44.4159734_001	1eb3021 faaec49c 2_1	97.455	36608 89	36594 02	Multiplex	Escherichi a_coli_AT CC_70092 6	True			0.3	0.00
HQ774224.1.141 7	d889f9d d971b47 3d_1	99.012	20954 76	20968 90	Multiplex	Phocaeicol a_vulgatu	True	d__Bacteria;p__Bacteroidota;c__Bact eroidia;o__Bacteroidales;f__Bacteroi	d__Bacteria;p__Bacteroidota;c__Bact eroidia;o__Bacteroidales;f__Bacteroi daceae;g__Bacteroides	3	0.00

						s_ATCC_8482		daceae;g__Bacteroides;s__uncultured_organism			
CP009561.1275010.127	1eb3021faaec49c2_1	97.507	1152580	1154101	Multiplex	Escherichia_coli_ATCC_700926	True			2	0.00
CP030233.4191849.419	1eb3021faaec49c2_1	97.244	1152580	1154101	Multiplex	Escherichia_coli_ATCC_700926	True			3	0.00
JQ446508.1.1373	27b35dd1651e48dd_1	98.621	213452	214827	Multiplex	Enterococcus_faecalis_ATCC_47077	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus_faecalis	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	2	0.00
CP029992.3310618.331	1eb3021faaec49c2_1	97.636	1152580	1154101	Multiplex	Escherichia_coli_ATCC_700926	True			1	0.00
CP011975.2004273.200					Multiplex					2	0.00
KM506787.1.1448					Multiplex			d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus_plantarum	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	2	0.00
CP009712.4129838.413					Multiplex					7	0.01
EU777753.1.1312					Multiplex			d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia-Shigella;s__uncultured_bacterium	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia-Shigella	5	0.01
EU767274.1.1360					Multiplex			d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__uncultured_bacterium	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	6	0.01
AJKY01000083.3720.52					Multiplex					21	0.02
FN665654.138327.1398					Multiplex					12	0.01
HQ761701.1.1434					Multiplex			d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_organism	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	3	0.00

EU454583.1.1411_019					Multiplex					2.99	0.00
CP028526.334281.3357					Multiplex					35	0.04
CQEC01000020.91536.9					Multiplex					28	0.03
AY634580.1.1308					Multiplex			d__Bacteria;p__Campilobacterota;c__Campylobacteria;o__Campylobacterales;f__Helicobacteraceae;g__Helicobacter;s__uncultured_Helicobacter	d__Bacteria;p__Campilobacterota;c__Campylobacteria;o__Campylobacterales;f__Helicobacteraceae;g__Helicobacter	28	0.03
CP009364.3139876.314					Multiplex					17	0.02
DQ797217.1.1403					Multiplex			d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_bacterium	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	9	0.01
CP012323.10819.12309					Multiplex			d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococaceae;g__Clostridioides;s__Clostridioides_difficile	d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococaceae;g__Clostridioides	7	0.01
HQ810958.1.1447_001	d889f9d d971b47 3d_1	98.135	34819 7	34675 9	Multiplex	Phocaeicola_vulgatus_ATCC_8482	True			0.32	0.00
HQ793333.1.1443	1eb3021 faaec49c 2_1	99.422	36608 81	36594 98	Multiplex	Escherichia_coli_ATCC_700926	True	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia-Shigella;s__uncultured_organism	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia-Shigella	9	0.01
JQ187021.1.1359	c45a1c5 7adf446 0e_1	97.277	18501 47	18488 01	Multiplex	Bifidobacterium_adolescentis_ATCC_15703	True	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__uncultured_bacterium	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	47	0.05
AF506794.1.1466	4762fdd 8950949 39_1	97.614	96370	97835	Multiplex	Helicobacter_pylori_ATCC_700392	True	d__Bacteria;p__Campilobacterota;c__Campylobacteria;o__Campylobacterales;f__Helicobacteraceae;g__Helicobacter;s__Helicobacter_heilmannii	d__Bacteria;p__Campilobacterota;c__Campylobacteria;o__Campylobacterales;f__Helicobacteraceae;g__Helicobacter	1	0.00
EU655795.1.1320_001					Multiplex					1	0.00
HQ741049.1.1434_001	d889f9d d971b47 3d_1	98.953	47445 93	47431 63	Multiplex	Phocaeicola_vulgatus	True			6718.65	7.85

						s_ATCC_8482					
HQ802459.1.1485_001	27b35dd1651e48dd_1	98.991	213399	214884	Multiplex	Enterococcus_faecalis_ATCC_47077	True			0.18	0.00
KF843118.1.1413_009	1eb3021faaec49c2_1	97.013	3660907	3659509	Multiplex	Escherichia_coli_ATCC_700926	True			2.79	0.00
EU136687.1.1985	d889f9dd971b473d_1	100	2095444	2096948	Multiplex	Phocaeicola_vulgaris_ATCC_8482	True	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_vulgatus	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	2	0.00
HQ771701.1.1438_001	d889f9dd971b473d_1	98.956	348191	346759	Multiplex	Phocaeicola_vulgaris_ATCC_8482	True			0.3	0.00
FPLO01005702.1.1404	c45a1c57adf4460e_2	99.004	23204	24608	Multiplex	Bifidobacterium_adolescentis_ATCC_15703	True	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__metagenome	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	24	0.03
CP029595.3631004.363	1eb3021faaec49c2_1	97.244	1152580	1154101	Multiplex	Escherichia_coli_ATCC_700926	True			5	0.01
CP022712.1786281.1787846_001	27b35dd1651e48dd_1	99.351	213371	214911	Multiplex	Enterococcus_faecalis_ATCC_47077	True			2978.78	3.48
CP030236.2819838.2821391_004	1eb3021faaec49c2_1	97.967	1152580	1154101	Multiplex	Escherichia_coli_ATCC_700926	True			0.39	0.00
HQ810947.1.1443	d889f9dd971b473d_1	98.406	348195	346760	Multiplex	Phocaeicola_vulgaris_ATCC_8482	True	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_organism	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	27	0.03
CP030838.463295.464833_001	1eb3021faaec49c2_1	97.246	454975	456496	Multiplex	Escherichia_coli_ATCC_700926	True			107.97	0.13

CP012268.31240 33.3125588_001	1eb3021 faaec49c 2_1	97.375	36609 09	36593 88	Multiplex	Escherichi a_coli_AT CC_70092 6	True			2929. 26	3.42
EU723852.1.1527 _001	27b35d d1651e4 8dd_1	99.147	21337 4	21488 9	Multiplex	Enterococc us_faecalis _ATCC_47 077	True			0.18	0.00
ABAK02000001. 2157381	1eb3021 faaec49c 2_1	97.705	36609 09	36593 88	Multiplex	Escherichi a_coli_AT CC_70092 6	True			2	0.00
JN981928.1.1516 _004	1eb3021 faaec49c 2_1	98.809	36609 09	36594 04	Multiplex	Escherichi a_coli_AT CC_70092 6	True			0.2	0.00
D86197.1.1437_0 01	c45a1c5 7adf446 0e_2	99.087	23185	24608	Multiplex	Bifidobact erium_ado lescentis_ ATCC_157 03	True			6048. 81	7.07
CP026197.41704 8.4185	1eb3021 faaec49c 2_1	97.113	11525 80	11541 01	Multiplex	Escherichi a_coli_AT CC_70092 6	True			2	0.00
AJ301831.1.1554	27b35d d1651e4 8dd_1	99.676	21337 1	21491 1	Multiplex	Enterococc us_faecalis _ATCC_47 077	True	d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Enterococcacea e;g__Enterococcus;s__Enterococcus_ faecalis	d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Enterococcacea e;g__Enterococcus	14	0.02
CP023005.20081 38.200	c45a1c5 7adf446 0e_1	99.934	18501 67	18486 61	Multiplex	Bifidobact erium_ado lescentis_ ATCC_157 03	True			44	0.05
AP011945.11762 63.117	4762fdd 8950949 39_1	99.663	96370	97853	Multiplex	Helicobact er_pylori_ ATCC_700 392	True			4	0.00
CXRJ01000078.4 200.57	27b35d d1651e4 8dd_1	97.542	21337 1	21491 1	Multiplex	Enterococc us_faecalis _ATCC_47 077	True			7	0.01



HQ778631.1.143 3	d889f9d d971b47 3d_1	97.491	25877 64	25891 93	Multiplex	Phocaeicol a_vulgatu s_ATCC_8 482	True	d__Bacteria;p__Bacteroidota;c__Bact eroidia;o__Bacteroidales;f__Bacteroi daceae;g__Bacteroides;s__unculture d_organism	d__Bacteria;p__Bacteroidota;c__Bact eroidia;o__Bacteroidales;f__Bacteroi daceae;g__Bacteroides	6	0.01
HQ814803.1.145 3	d889f9d d971b47 3d_1	98.986	44319 36	44305 57	Multiplex	Phocaeicol a_vulgatu s_ATCC_8 482	True	d__Bacteria;p__Bacteroidota;c__Bact eroidia;o__Bacteroidales;f__Bacteroi daceae;g__Bacteroides;s__unculture d_organism	d__Bacteria;p__Bacteroidota;c__Bact eroidia;o__Bacteroidales;f__Bacteroi daceae;g__Bacteroides	2	0.00
CP026807.33419 63.334	1eb3021 faaec49c 2_1	99.671	11525 80	11541 01	Multiplex	Escherichi a_coli_AT CC_70092 6	True			2	0.00
AP012600.14327 22.143	4762fdd 8950949 39_1	99.73	96370	97853	Multiplex	Helicobact er_pylori_ ATCC_700 392	True			4	0.00
HQ739773.1.144 2	1eb3021 faaec49c 2_1	99.141	11525 96	11539 91	Multiplex	Escherichi a_coli_AT CC_70092 6	True	d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Enterobacter ales;f__Enterobacteriaceae;g__Escher ichia-Shigella;s__uncultured_bacterium	d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Enterobacter ales;f__Enterobacteriaceae;g__Escher ichia-Shigella	2	0.00
LT558811.1.1486	c45a1c5 7adf446 0e_1	99.048	18501 54	18486 85	Multiplex	Bifidobact erium_ado lescentis_ ATCC_157 03	True	d__Bacteria;p__Actinobacteriota;c__ Actinobacteria;o__Bifidobacteriales;f__ Bifidobacteriaceae;g__Bifidobacter ium;s__Bifidobacterium_adolescenti s	d__Bacteria;p__Actinobacteriota;c__ Actinobacteria;o__Bifidobacteriales;f__ Bifidobacteriaceae;g__Bifidobacter ium	9	0.01
CP015574.38546 79.385	1eb3021 faaec49c 2_1	97.31	11525 80	11541 01	Multiplex	Escherichi a_coli_AT CC_70092 6	True			3	0.00
CP022712.17862 81.178	27b35d d1651e4 8dd_1	99.351	21337 1	21491 1	Multiplex	Enterococc us_faecalis _ATCC_47 077	True			33	0.04
AY634599.1.1307	4762fdd 8950949 39_1	99.375	96471	97750	Multiplex	Helicobact er_pylori_ ATCC_700 392	True	d__Bacteria;p__Campilobacterota;c__ _Campylobacteria;o__Campylobacte rales;f__Helicobacteraceae;g__Helico bacter;s__uncultured_Helicobacter	d__Bacteria;p__Campilobacterota;c__ _Campylobacteria;o__Campylobacte rales;f__Helicobacteraceae;g__Helico bacter	1	0.00
CP030235.20500 34.205	1eb3021 faaec49c 2_1	97.31	11525 80	11541 01	Multiplex	Escherichi a_coli_AT CC_70092 6	True			3	0.00

HQ815539.1.1438	d889f9d d971b47 3d_1	98.329	25877 42	25891 69	Multiplex	Phocaeicola_vulgatus_ATCC_8482	True	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_organism	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	5	0.01
CP022139.4711002.471	1eb3021 faaec49c 2_1	97.244	11525 80	11541 01	Multiplex	Escherichia_coli_ATCC_700926	True			7	0.01
CP010437.2145122.214	c45a1c5 7adf446 0e_2	98.844	23099	24566	Multiplex	Bifidobacterium_adolescentis_ATCC_15703	True			3	0.00
EU456992.1.1435_002	5964adb 8d0df4f de_1	98.259	47745 0	47887 9	Multiplex	Lactobacillus_gasseri_ATCC_33323	True			0.02	0.00
CP026325.1211466.121	4762fdd 8950949 39_1	100	96370	97853	Multiplex	Helicobacter_pylori_ATCC_700392	True			3	0.00
EU764185.1.1352	c45a1c5 7adf446 0e_1	98.816	18501 47	18488 02	Multiplex	Bifidobacterium_adolescentis_ATCC_15703	True	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__uncultured_bacterium	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	37	0.04
FJ611793.1.1416	c45a1c5 7adf446 0e_1	98.804	18501 47	18487 29	Multiplex	Bifidobacterium_adolescentis_ATCC_15703	True	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium_adolescentis	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	9	0.01
GQ155993.1.1370	27b35d d1651e4 8dd_1	97.801	21347 1	21478 9	Multiplex	Enterococcus_faecalis_ATCC_47077	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	5	0.01
AY850534.1.1248					Multiplex			d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__uncultured_bacterium	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	3	0.00
HQ765079.1.1455					Multiplex			d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_organism	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	4	0.00

FPLN01001016.2 .1422	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__metagenome	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	9	0.01
AJ133496.1.1479	Multiplex	d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium;s__Fusobacterium_nucleatum	d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium	67	0.08
KC011147.1.1494 _005	Multiplex			85.34	0.10
EU775002.1.1308	Multiplex	d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__UCG-011;g__UCG-011;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__UCG-011;g__UCG-011	4	0.00
EU463378.1.1375	Multiplex	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	4	0.00
DQ345464.1.152 3	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Tetragenococcus;s__uncultured_compost	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Tetragenococcus	6	0.01
AJ621551.1.1466	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus_graminis	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	5	0.01
EU776535.1.1401	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella;s__uncultured_bacterium	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	15	0.02
MH392797.1.148 8	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus_plantarum	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	22	0.03
MG028631.1.145 4	Multiplex	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium_sp.	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	1	0.00
HQ778752.1.142 9	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_organism	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	3	0.00

FN538970.13462 9.1361	Multiplex			6	0.01
DQ015435.1.134 1_001	Multiplex			1	0.00
CP002246.16659 3.1680	Multiplex			8	0.01
HQ806906.1.143 7	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_organism	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	7	0.01
JF766405.1.1514_001	Multiplex			15596 .18	18.22
EF179833.1.1502	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Klebsiella;s__uncultured_bacterium	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Klebsiella	5	0.01
JX426119.1.1502	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus_plantarum	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	2	0.00
EU511872.1.1384_002	Multiplex			3	0.00
HQ728217.1.150 0	Multiplex	d__Bacteria;p__Spirochaetota;c__Spirochaetia;o__Spirochaetales;f__Spirochaetaceae;g__Sphaerochaeta;s__uncultured_bacterium	d__Bacteria;p__Spirochaetota;c__Spirochaetia;o__Spirochaetales;f__Spirochaetaceae;g__Sphaerochaeta	1	0.00
AXLF01000003.4 612176.4613708_001	Multiplex			135.9 8	0.16
AB573068.1.1481	Multiplex	d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium;s__Fusobacterium_nucleatum	d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium	6	0.01
KM819119.1.153 6	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__uncultured_Bacillus	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	1	0.00
CP019469.23204. 24685	Multiplex	d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcaceae;g__Clostridioides;s__Clostridioides_difficile	d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcaceae;g__Clostridioides	3	0.00

KX960105.1.1558	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus_faecalis	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	14	0.02
FJ975785.1.1361_001	Multiplex			63.96	0.07
EF097149.1.1403_018	Multiplex			1.16	0.00
AM180355.4007692.400	Multiplex			1	0.00
HQ777715.1.1440	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_organism	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	6	0.01
AB222700.1.1488	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_finegoldii	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	3	0.00
AB006658.1.1520	Multiplex	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium_breve	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	6	0.01
EU468339.1.1395	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	8	0.01
AM286415.1019206.102	Multiplex			3	0.00
AB616133.1.1466	Multiplex	d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium;s__Fusobacterium_simiae	d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium	5	0.01
X73450.1.1470	Multiplex	d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcaceae;g__Clostridioides;s__Clostridioides_difficile	d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcaceae;g__Clostridioides	12	0.01
CP025044.39590.41097	Multiplex	d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcaceae;g__Clostridioides;s__Clostridioides_difficile	d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcaceae;g__Clostridioides	43	0.05

EU773007.1.1247	Multiplex	d__Bacteria;p__Actinobacteriota;c__Coriobacteriia;o__Coriobacteriales;f__Eggerthellaceae;g__Enterorhabdus;s__uncultured_bacterium	d__Bacteria;p__Actinobacteriota;c__Coriobacteriia;o__Coriobacteriales;f__Eggerthellaceae;g__Enterorhabdus	8	0.01
KF066950.1.1341	Multiplex	d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium;s__uncultured_bacterium	d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium	18	0.02
EU776680.1.1401	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia-Shigella;s__uncultured_bacterium	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia-Shigella	4	0.00
KF842515.1.1412	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia-Shigella;s__uncultured_bacterium	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia-Shigella	21	0.02
KX057696.1.1515_002	Multiplex			3479.3	4.06
HL282422.2.1545	Multiplex	d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium;s__unidentified	d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium	10	0.01
AGRM01000003.578375.	Multiplex			5	0.01
KJ722780.1.1464	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus_plantarum	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	3	0.00
EU775673.1.1399	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia-Shigella;s__uncultured_bacterium	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia-Shigella	76	0.09
KJ123815.1.1513_001	Multiplex			0.33	0.00
AY959011.1.1496_001	Multiplex			0.08	0.00
CP009787.3194722.319	Multiplex			2	0.00
EU828415.1.1454	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderia	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderia	7	0.01

		les;f__Oxalobacteraceae;g__Janthino bacterium;s__uncultured_bacterium	les;f__Oxalobacteraceae;g__Janthino bacterium		
HM557383.1.137 1	Multiplex	d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Enterobacter ales;f__Enterobacteriaceae;g__Entero bacter;s__uncultured_bacterium	d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Enterobacter ales;f__Enterobacteriaceae;g__Entero bacter	3	0.00
EU778456.1.1401	Multiplex	d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Enterobacter ales;f__Enterobacteriaceae;g__Escher ichia- Shigella;s__uncultured_bacterium	d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Enterobacter ales;f__Enterobacteriaceae;g__Escher ichia-Shigella	32	0.04
EU560820.1.1485	Multiplex	d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Enterobacter ales;f__Enterobacteriaceae;g__Escher ichia- Shigella;s__uncultured_bacterium	d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Enterobacter ales;f__Enterobacteriaceae;g__Escher ichia-Shigella	69	0.08
CP019858.39376 14.393	Multiplex			101	0.12
KP256081.1.1512	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Lactobacillacea e;g__Lactobacillus;s__Lactobacillus_ pentosus	d__Bacteria;p__Firmicutes;c__Bacilli; o__Lactobacillales;f__Lactobacillacea e;g__Lactobacillus	30	0.04
AY081984.1.1503	Multiplex	d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Pseudomona dales;f__Pseudomonadaceae;g__Pse udomonas;s__uncultured_bacterium	d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Pseudomona dales;f__Pseudomonadaceae;g__Pse udomonas	3	0.00
AY850535.1.1224	Multiplex	d__Bacteria;p__Actinobacteriota;c__ Actinobacteria;o__Bifidobacteriales;f__ Bifidobacteriaceae;g__Bifidobacter ium;s__uncultured_bacterium	d__Bacteria;p__Actinobacteriota;c__ Actinobacteria;o__Bifidobacteriales;f__ Bifidobacteriaceae;g__Bifidobacter ium	2	0.00
HQ745182.1.143 4	Multiplex	d__Bacteria;p__Bacteroidota;c__Bact eroidia;o__Bacteroidales;f__Bacteroi daceae;g__Bacteroides;s__unculture d_organism	d__Bacteria;p__Bacteroidota;c__Bact eroidia;o__Bacteroidales;f__Bacteroi daceae;g__Bacteroides	5	0.01
JQ467938.1.1393	Multiplex	d__Bacteria;p__Fusobacteriota;c__Fu sobacteriia;o__Fusobacteriales;f__Le ptotrichiaceae;g__Leptotrichia;s__un cultured_bacterium	d__Bacteria;p__Fusobacteriota;c__Fu sobacteriia;o__Fusobacteriales;f__Le ptotrichiaceae;g__Leptotrichia	90	0.11
KX957774.1.1421	Multiplex	d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Enterobacter ales;f__Enterobacteriaceae;g__Entero bacter;s__Enterobacter_cloacae	d__Bacteria;p__Proteobacteria;c__Ga mmaproteobacteria;o__Enterobacter ales;f__Enterobacteriaceae;g__Entero bacter	5	0.01

HQ790343.1.143 2	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_organism	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	6	0.01
DQ014744.1.133 8	Multiplex	d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Lachnoclostridium;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Lachnoclostridium	1	0.00
EF097675.1.1407	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Muribaculaceae;s__uncultured_bacterium	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Muribaculaceae	1	0.00
HQ819022.1.143 9_001	Multiplex			8616. 22	10.07
DQ441256.1.131 3	Multiplex	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;g__Alistipes;s__uncultured_bacterium	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;g__Alistipes	7	0.01
EU451156.1.1374 _009	Multiplex			1	0.00
HQ819061.1.143 8	Multiplex	d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium;s__uncultured_organism	d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium	4	0.00
EU622695.1.1497 _058	Multiplex			1	0.00
JF121027.1.1363	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Yersiniaceae;g__Serratia;s__uncultured_bacterium	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Yersiniaceae;g__Serratia	2	0.00
EF603126.1.1475 _079	Multiplex			3.99	0.00
CP009367.41955 09.419	Multiplex			3	0.00
EF179121.1.1461	Multiplex	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Yersiniaceae;g__Yersinia;s__Yersinia_bercovieri	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Yersiniaceae;g__Yersinia	7	0.01
KM819129.1.152 8	Multiplex	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__uncultured_Bacillus	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	6	0.01



DQ002385.1.1486						Multiplex			d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Yersiniaceae;g__Serratia_serratia_marcescens	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Yersiniaceae;g__Serratia	2	0.00
EU778438.1.1420						Multiplex			d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	7	0.01
CP010888.654100.6556						Multiplex					66	0.08
HQ819061.1.1438_001						Multiplex					10.78	0.01
EF406402.1.1499_010						Multiplex					0.02	0.00
HQ810939.1.1381						Multiplex			d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_organism	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	8	0.01
EU560876.1.1492						Multiplex			d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__uncultured_bacterium	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	9	0.01
CDQP01001253.198.170						Multiplex					5	0.01
KC936918.1.1479						Multiplex			d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium;s__uncultured_bacterium	d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium	3	0.00
EU778438.1.1420_005						Multiplex					103.82	0.12
HQ800646.1.1455						Multiplex			d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_organism	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	1	0.00
09a8fa70427aa68f16934c729b826071	1eb3021faaec49c2_1	99.454	3660889	3659426	Full-length	Escherichia_coli_ATCC_700926	True			d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	308	0.99
4bec1cb362f10c0518dae936b3032c6f	38ad2dab3e5e43b7_1	99.932	627724	629197	Full-length	Staphylococcus_aureus_subsp_aureus_ATCC_BAA_1556	True			d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	224	0.72

51d51e872348c3c5e3b70be7f91c4a32	071a82bb90b94c6f_1	100	494810	496268	Full-length	Acinetobacter_baumannii_ATC_C_17978	True	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter_baumannii	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter	2360	7.60
cd1af128eb857acddeb168e57245021ec	38ad2dab3e5e43b7_1	99.796	627724	629197	Full-length	Staphylococcus_aureus_subsp__aureus_ATCC_BAA_1556	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	212	0.68
d5ebbbf0f104adc463156fca557bb6fc					Full-length			d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Akkermansiaceae;g__Akkermansia;s__Akkermansia_muciniphila	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Akkermansiaceae;g__Akkermansia	12	0.04
7983269916ac14fd4655f0a0c60f8694	9dc637a985b042c4_1	100	605244	606690	Full-length	Cutibacterium_acnes_ATCC_11828	True		d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Propionibacteriales;f__Propionibacteriaceae;g__Cutibacterium	958	3.08
d8a3399acd76da73c1b2b8a3683a7540					Full-length				d__Bacteria;p__Cyanobacteria;c__Cyanobacteriia;o__Chloroplast;f__Chloroplast;g__Chloroplast	24	0.08
c0089458dae2c0559162e58eb2661873	1eb3021faaec49c2_1	100	454995	456458	Full-length	Escherichia_coli_ATCC_700926	True		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	281	0.90
a0530711bdec8d611872863731f96dde	adb6d513b7374f84_1	100	16704	18182	Full-length	Streptococcus_mutans_ATCC_700610	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_mutans	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	1293	4.16
994cb47a2b400e6185743e1765244faf	38ad2dab3e5e43b7_1	99.932	627724	629197	Full-length	Staphylococcus_aureus_subsp__aureus_ATCC_BAA_1556	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	214	0.69
13bc41e35faa4f40a01de5a972c0c4ac	1eb3021faaec49c2_1	100	3660889	3659426	Full-length	Escherichia_coli_ATCC_700926	True		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	611	1.97
9fc4609d84db9e441de7db46d7172ae4	1eb3021faaec49c2_1	100	1152600	1154063	Full-length	Escherichia_coli_ATCC_700926	True		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	256	0.82

0bf3e0641c88ec588bc66b567c3fa63d	1eb3021faaec49c2_1	99.932	3660889	3659426	Full-length	Escherichia_coli_ATCC_700926	True		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	285	0.92
9eda36e35469eb0ba4b8045fa7acabd0	d889f9dd971b473d_1	99.862	2587739	2589188	Full-length	Phocaeicola_vulgatus_ATCC_8482	True	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_vulgatus	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	274	0.88
339aac7377a0d948a52bc0b2bf3dfda8	d889f9dd971b473d_1	100	2095461	2096910	Full-length	Phocaeicola_vulgatus_ATCC_8482	True	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_vulgatus	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	350	1.13
e7b11bfbee47d834b64203b6c1294201	3042186b85304e8d_1	99.93	2256227	2257660	Full-length	Clostridium_beijerinckii_ATCC_35702	True	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__Clostridium_beijerinckii	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	153	0.49
2f66c5bd318dfac1e9738ffd54ca88b8	3042186b85304e8d_1	100	5769886	5768453	Full-length	Clostridium_beijerinckii_ATCC_35702	True	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__Clostridium_beijerinckii	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	304	0.98
a0ec2668157ffb2374ece8cad58ecc5f	285a115d88c043f1_1	100	678369	679826	Full-length	Pseudomonas_aeruginosa_ATCC_9027	True	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__Pseudomonas_aeruginosa	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	630	2.03
0ed2d53fd823b2ef922b6f349cade1cd	045df7c7cb0f42b5_1	100	1223511	1222049	Full-length	Neisseria_meningitidis_ATCC_BAA_335	True	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Neisseriaceae;g__Neisseria;s__Neisseria_meningitidis	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Neisseriaceae;g__Neisseria	2291	7.37
7dcace79bc8188077e07b0085aa57b7f	5371a9904eb64361_1	100	8928	10400	Full-length	Bacillus_pacificus_ATCC_10987	True		d__Bacteria;p__Firmicutes;c__Bacillio__Bacillales;f__Bacillaceae;g__Bacillus	496	1.60
aab4d379026eb5e6a7e2b32ec4c715e7	f5bcb58692924cb7_1	99.796	1722262	1720790	Full-length	Staphylococcus_epidermidis_ATCC_12228	True		d__Bacteria;p__Firmicutes;c__Bacillio__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	307	0.99
efe5e4e4ba300f45c88da09e3e9cd3e4	285a115d88c043f1_1	100	5383111	5381654	Full-length	Pseudomonas_aeruginosa_ATCC_9027	True	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__Pseudomonas_aeruginosa	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	216	0.70

ad20976e0e8c7e5adcb7f11b5fcf7830	d889f9d d971b47 3d_1	99.862	44319 43	44304 94	Full-length	Phocaeicola_vulgatus_ATCC_8482	True	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_vulgatus	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	271	0.87
d5cb708aa8b5ddc54ca7e0528124fe20	2b7fa0e 1de5f42 de_1	100	25624 88	25610 65	Full-length	Deinococcus_radiodurans_ATCC_BAA_816	True	d__Bacteria;p__Deinococcota;c__Deinococci;o__Deinococcales;f__Deinococcaceae;g__Deinococcus;s__Deinococcus_radiodurans	d__Bacteria;p__Deinococcota;c__Deinococci;o__Deinococcales;f__Deinococcaceae;g__Deinococcus	374	1.20
34b695df3f78278d604299f2c4adc80c	2b7fa0e 1de5f42 de_1	100	18254 8	18397 1	Full-length	Deinococcus_radiodurans_ATCC_BAA_816	True	d__Bacteria;p__Deinococcota;c__Deinococci;o__Deinococcales;f__Deinococcaceae;g__Deinococcus;s__Deinococcus_radiodurans	d__Bacteria;p__Deinococcota;c__Deinococci;o__Deinococcales;f__Deinococcaceae;g__Deinococcus	1031	3.32
3feab8f97f15836d17829bc4ea074162	3042186 b85304e 8d_1	99.93	44587 4	44730 7	Full-length	Clostridium_beijerinckii_ATCC_35702	True	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__Clostridium_beijerinckii	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	175	0.56
b2ef16dee036f7ce8b9b74a7234111c1	3042186 b85304e 8d_1	99.861	34048 22	34033 89	Full-length	Clostridium_beijerinckii_ATCC_35702	True	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__Clostridium_beijerinckii	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	144	0.46
9f3938b0148e6fa857077444480b6fd3	d889f9d d971b47 3d_1	99.724	47446 05	47431 56	Full-length	Phocaeicola_vulgatus_ATCC_8482	True	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_vulgatus	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	257	0.83
aaf82c612373bafcef3509b72ee24809	3042186 b85304e 8d_1	99.93	57698 86	57684 53	Full-length	Clostridium_beijerinckii_ATCC_35702	True	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__Clostridium_beijerinckii	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	194	0.62
61de72098cbf9f693f09c863d1c5a586	2504aeb 524e74d 25_1	100	22933 8	23079 1	Full-length	Porphyromonas_gingivalis_ATCC_33277	True	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Porphyromonas;s__Porphyromonas_gingivalis	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Porphyromonas	2925	9.41
a8f0a9703e902a87d6be02364e684c50	3042186 b85304e 8d_1	100	57758 23	57743 90	Full-length	Clostridium_beijerinckii_ATCC_35702	True	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__Clostridium_beijerinckii	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	215	0.69
913abfe7ecfd10c4eb54ea1dea67f07c	4762fdd 8950949 39_1	100	96390	97815	Full-length	Helicobacter_pylori_ATCC_700392	True	d__Bacteria;p__Campilobacterota;c__Campylobacteria;o__Campylobacteriales;f__Helicobacteraceae;g__Helicobacter;s__Helicobacter_pylori	d__Bacteria;p__Campilobacterota;c__Campylobacteria;o__Campylobacteriales;f__Helicobacteraceae;g__Helicobacter	1125	3.62

b56b7466c84c7ca53aa71e4ce25f61b0	c45a1c57adf4460e_2	100	23119	24570	Full-length	Bifidobacterium_adolescentis_ATCC_15703	True	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium_adolescentis	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	447	1.44
0ccaf57fc10e3ca943b9911e91c05de1	3042186b85304e8d_1	100	2267882	2269315	Full-length	Clostridium_beijerinckii_ATCC_35702	True	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__Clostridium_beijerinckii	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	170	0.55
d669559001b98da82874fac6581afc1c	3042186b85304e8d_1	100	4548532	4547099	Full-length	Clostridium_beijerinckii_ATCC_35702	True	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__Clostridium_beijerinckii	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	171	0.55
21b49156bf40185385c31d7db91a5ad5	5371a9904eb64361_1	100	325854	327326	Full-length	Bacillus_pacificus_ATCC_10987	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus	62	0.20
56fa3c3172361f91fadde5f221e6f5b4	c45a1c57adf4460e_2	99.243	23119	24570	Full-length	Bifidobacterium_adolescentis_ATCC_15703	True	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium_adolescentis	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	119	0.38
26cfdb2bcbd3a64a84e9b237d94a97eb	27b35dd1651e48dd_1	100	213391	214873	Full-length	Enterococcus_faecalis_ATCC_47077	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus_faecalis	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	738	2.38
07b2978940b50886f3866b04b7f982cf	58ae911973b74ffc_1	100	16330	17800	Full-length	Streptococcus_agalactiae_ATCC_BAA_611	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_agalactiae	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	2250	7.24
7932226c8cd025d2ea117b03d48f63e8	3042186b85304e8d_1	99.93	9364	10797	Full-length	Clostridium_beijerinckii_ATCC_35702	True	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__Clostridium_beijerinckii	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	190	0.61
34babcf1732962962d2fbbbadf3af637	f5bcb58692924cb7_1	100	1597980	1596508	Full-length	Staphylococcus_epidermidis_ATCC_12228	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	190	0.61
a7e2262894c30111bfd4daee5736414f	f5bcb58692924cb7_1	99.932	1597980	1596508	Full-length	Staphylococcus_epidermidis_	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	37	0.12

ATCC_12228											
3cc006600b219858ac3c647f2613a32a	d889f9d d971b473d_1	99.931	34820 8	34675 9	Full-length	Phocaeicola_vulgatus_ATCC_8482	True	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_vulgatus	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	568	1.83
f3cfb383dcfb753cad226072f6665784	f5bcb58 692924cb7_1	100	23359 12	23344 40	Full-length	Staphylococcus_epidermidis_ATCC_12228	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	648	2.09
dd586a1ae04ed2d129d944286ae71f61	f5bcb58 692924cb7_1	100	17222 62	17207 90	Full-length	Staphylococcus_epidermidis_ATCC_12228	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus	410	1.32
a5ebdb1225c13ba7cfd2467533fc6da6	c45a1c5 7adf4460e_1	100	18501 47	18486 99	Full-length	Bifidobacterium_adolescentis_ATCC_15703	True	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium_adolescentis	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	110	0.35
8348a732f75c6a0439af2ebffbacc5ff1	3042186 b85304e8d_1	99.861	20309 91	20324 24	Full-length	Clostridium_beijerinckii_ATCC_35702	True	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__Clostridium_beijerinckii	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	140	0.45
4c67b666ce2da2054aec0ba50dd1e494	d889f9d d971b473d_1	99.931	20954 61	20969 10	Full-length	Phocaeicola_vulgatus_ATCC_8482	True	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_vulgatus	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	78	0.25
fce86ef2355971d83413788cbb660531	5964adb 8d0df4fde_1	100	47747 0	47896 4	Full-length	Lactobacillus_gasseri_ATCC_33323	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus_gasseri	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	2102	6.77
04d3de55f475a0888205c9507901a096	89e35fec 14744942_1	100	52833 2	52979 4	Full-length	Schaalia_odontolytica_ATCC_17982	True	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Actinomycetes;s__Schaalia_odontolytica	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Actinomycetes	112	0.36
021408f68ac3d943f7e16261373b2a61	3042186 b85304e8d_1	99.93	92466 0	92609 3	Full-length	Clostridium_beijerinckii_ATCC_35702	True	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__Clostridium_beijerinckii	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	164	0.53
bc7d5e82dae59e2e5e8321bb5c5eae4b	adb6d5 13b7374f84_1	100	16601 54	16586 76	Full-length	Streptococcus_muta	True	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	903	2.91

						ns_ATCC_700610		ae;g__Streptococcus;s__Streptococcus_mutans			
1f1158dbb4126e5a7f04094b61700493	3042186b85304e8d_1	100	142194	143627	Full-length	Clostridium_beijerinckii_ATCC_35702	True	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__Clostridium_beijerinckii	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	292	0.94
985d4a0d4d7e7d255af6a92044ae5901	38ad2dab3e5e43b7_1	99.932	627724	629197	Full-length	Staphylococcus_aureus_subsp__aureus_ATCC_BAA_1556	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococaceae;g__Staphylococcus	233	0.75
92bcc461c3dbfbeb88759ada02f95a6b	5371a9904eb64361_1	100	616926	618398	Full-length	Bacillus_pacificus_ATCC_10987	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus	54	0.17
27be187284317979c93fd2218ee3722e	38ad2dab3e5e43b7_1	100	627724	629197	Full-length	Staphylococcus_aureus_subsp__aureus_ATCC_BAA_1556	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococaceae;g__Staphylococcus	467	1.50
b80a1bd6b19379171cafb03a4ddb26a3	266a835027f7464b_2	100	38523	37135	Full-length	Rhodobacter_sphaeroides_ATCC_17029	True	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Rhodobacter;s__Rhodobacter_sphaeroides	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Rhodobacter	488	1.57
3b44c0cd22f7eeac2386b9f2d475930a	1eb3021faaec49c2_1	100	4584392	4582929	Full-length	Escherichia_coli_ATCC_700926	True		d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	311	1.00
d3eab112b21cbea371f808f940fa4b0c	f5bcb58692924cb7_1	99.796	1722262	1720790	Full-length	Staphylococcus_epidermidis_ATCC_12228	True		d__Bacteria;p__Firmicutes;c__Bacilli;o__Staphylococcales;f__Staphylococaceae;g__Staphylococcus	231	0.74
37d8a0129a66dba216a600739d34631	3042186b85304e8d_1	100	5743540	5742107	Full-length	Clostridium_beijerinckii_ATCC_35702	True	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__Clostridium_beijerinckii	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	1.83E+02	0.59
7809550a0f7794b926ffcebad7542089	3042186b85304e8d_1	99.861	3404822	3403389	Full-length	Clostridium_beijerinckii_ATCC_35702	True	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__Clostridium_beijerinckii	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	222	0.71

070e52443d30c5 d9e99c8cb06412 db1a	3042186 b85304e 8d_1	99.93	59394 87	59380 54	Full-length	Clostridium_beijerinckii_ATC C_35702	True	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1;s__Clostridium_beijerinckii	d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	2.11E+02	0.68
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