Supplemental Online Content

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eAppendix. Supplemental Methods

Study design, participants, and protocol

We conducted a nested matched case-control study to investigate the association between nasal microbiota and postoperative infectious complications using participants selected from a prospective cohort study of elective high risk clean surgical procedures. The protocol for subjects enrolled in the prospective surgical cohort study, which served as the parent to the current microbiome study, was previously published[1]. Of the 802 subjects enrolled into the cohort at the Johns Hopkins Hospital or the University of Maryland Medical Center (from 2/1/2007 to 9/30/2014), we identified 53 participants who developed the composite infectious outcome (deep SSI, bacteremia, or pneumonia) within 6 months of the index surgical procedure. We selected non-infected controls to match cases (~3:1) by age (+/- 5 years), sex, and surgical procedure; for some cases, only 2 matches were identified (yielding a total of 144 controls). We targeted a sample size of ~200 cases plus controls given the financial resources available to us to conduct the microbiome analyses. Cases and controls were selected from a prospective surgical cohort because of the high incidence of bacterial disease expression in the weeks immediately following surgery, allowing temporal inference to be drawn regarding characteristics of microbiota in an infection-free state (before surgery) and subsequent development of clinical infection after a high risk exposure (i.e. surgery).

Patients were eligible for inclusion in the original cohort if they were ≥40 years old and underwent any of the following elective clean surgical procedures: cardiac surgery (coronary artery bypass or valve), vascular surgery (aortic or lower extremity revascularization or open aneurysm repair), spinal fusion, or craniotomy. These surgical procedures were selected because of the relatively high risk for postoperative SSI and pneumonia and because they share a common pathologic basis for SSI, including the type of infecting pathogen, that is, predominantly skin and mucosal flora. Patients were excluded for any of the following: history of immunodeficiency syndrome, autoimmune disease, immunosuppressive medications in the past 6 months (oral corticosteroids <5 days was allowed if not current at the time of surgery), central venous catheter was inserted before surgery, any infection/antibiotic therapy at the time of surgery (excluding antibiotics for perioperative prophylaxis), or inability to obtain written informed consent. (None of the participants was intubated at baseline.)

Baseline information from all subjects was obtained from in-person interviews and medical chart review. The following data elements, which could potentially confound the relation between the main exposure (i.e. nasal microbiome cluster class) and primary outcome (i.e. composite of postoperative SSI, bacteremia, or pneumonia), were recorded: demographics (age, sex, race), baseline comorbidities, infection or hospitalization in the year prior to surgery, American Society of Anesthesiologists Class, Charlson Comorbidity score, inpatient/outpatient status at time of surgery, and study site (Johns Hopkins Hospital, University of Maryland Medical Center). A previous report in twins indicated that genetic factors contribute to composition of nasal microbiota[2]. Because genetic architecture is known to differ by race, we included race as a demographic variable to adjust for potential confounding between the main exposure (nasal microbiome cluster class) and infectious outcome. Race was self-reported by each participant. The following comorbidities were recorded: obesity (BMI >/=30 by weight and height recorded at time of surgery), diabetes, hypertension, myocardial infarction, congestive heart failure, peripheral vascular disease, cerebrovascular disease (previous stroke or TIA), chronic obstructive pulmonary disease (COPD), smoking history (past or present), gastric ulcer disease, chronic liver disease, renal failure requiring dialysis, history of cancer (past or in the context of the scheduled surgical procedure). Each comorbidity was dichotomized and recorded as present if endorsed by the patient during the baseline interview or if the comorbidity was recorded as present in the hospital record admission history and physical. For the diagnoses of diabetes, hypertension, and COPD, the subject also required concurrent treatment with a therapeutic agent for that disease for the comorbidity to be recorded as present; i.e., oral hypoglycemic agent or insulin for diabetes, anti-hypertensive agent for hypertension, inhaled bronchodilator or inhaled steroid for COPD.

Identification of *S aureus* from nasal swabs by clinical culture

Both anterior nares were swabbed with culturettes at the baseline visit before surgery. Swabs were transported to the clinical laboratory and plated to Chromagar S. aureus (BD Diagnostics, Sparks, MD) then stored at -80C for subsequent extraction of bacterial DNA for 16S rRNA gene sequencing (see below). Plates were incubated in the dark at 37°C for a minimum of 20 hours and then reincubated for another 24 hours, if negative. All mauve colonies were confirmed as *S aureus* positive using latex agglutination (Staphaurex Plus; Remel, Lenexa, KS).

Main exposure

We classified each of the 197 participants in this case-control study based solely on features derived from 16S rRNA gene sequencing of the material extracted from each subject's preoperative nasal swab. Nasal microbiome cluster class served as the main exposure. Two critical steps- 16S rRNA gene sequencing followed by unsupervised clustering analysis- were taken to classify nasal microbiota samples independently and agnostic of the baseline covariates and infection case/control status of each participant. A detailed description of these two steps follows below:

Microbiota profiling using 16S rRNA gene sequencing

Total metagenomic DNA was extracted and isolated from nasal swabs as previously described[3,4]. Briefly, samples were thawed and spun down, the resulting cell pellet was resuspended in 1 ml ice-cold PBS and transferred into Lysing Matrix B tubes (MP Biomedicals, Solon, OH). Bacterial lysis was then performed using two rounds of enzymatic lysis, first with a cocktail composed of lysozyme, mutanolysin, proteinase K, and then with lysostaphin, followed by mechanical lysis using bead beating. The mgDNA was then further purified using the Zymo fecal DNA kit (Zymogen). Negative extraction controls (PBS) were processed in parallel with each extraction to ensure no contaminating DNA was introduced during the DNA extraction process and PCRs. All samples included in our analyses had negative controls.

Microbiota profiling was performed by PCR amplification of the V3V4 hypervariable region of the 16S rRNA gene, followed by sequencing on the Illumina MiSeq 300-bp paired-reads platform (Illumina, San Diego, CA) using procedures previously published[5,6]. Sample barcoding was performed using the dual-indexing strategy for multiplexed sequencing developed at the Institute for Genome Sciences[5,6]. PCRs were set-up in 96-well microtiter plates using the 319F and 806R 16S universal primers, each of which also included a linker sequence required for Illumina sequencing, and also a 12-bp heterogeneity spacer index sequence aimed at minimizing biases associated with low-diversity amplicon sequencing[5,6]. No-template negative controls were processed for each primer pair. The presence of PCR amplicons was confirmed using gel electrophoresis, after which the SequalPrep normalization plate kit (Life Technologies, Inc.) was used for cleanup and normalization before sequencing.

Following sequencing, initial processing of the raw 16S sequences (read pair merging, read trimming and chimera filtering) was performed as previously described[4]. We then used QIIME 1.9.1[7] to generate an open-reference operational taxonomic unit (OTU) matrix and to perform all downstream analyses. In the process, sequence reads were clustered using a 97% similarity cutoff with UCLUST version 1.2.22 and aligned using PyNAST v1.2.2 against a core

Greengenes database vgg_13_8[8]. OTUs were assigned a taxonomic annotation using the RDP Classifier v2.0.2[9] and labeled to the most specific known taxonomic level. When taxonomic classification was not possible for a given taxa level, OTUs were labeled as "unclassified".

Clustering analysis of nasal microbial profiles

CountClust[10] (R package) was used to assign each sample to a clustering group based on the counts for each taxonomic unit in each sample. CountClust fits a topic mixed membership model to visualize and annotate clusters, extracting the top features driving cluster membership. Grades of membership modeling (GoM) was used to determine the number of clusters that provided best fit to the data. GoM allows each sample to have some proportion of its membership – partial membership – in each cluster. For microbiome data, the partial membership assumption corresponds to each sample having some proportion of its reads from each cluster, and each cluster is characterized by a probability vector of relative taxa expression levels. In our analysis, we used these partial membership weights to assign each sample to a cluster. To determine the optimal number of clusters, we computed log Bayes factor (provided in CountClust) and compared model fit under k=2 to 5 versus a null single cluster model. The log Bayes factor was corrected for the number of parameters fitted in each model. We evaluated the data with k = 2 to 5 and found that k=2 produced the largest Bayes factor. Because sample cluster assignment may differ between different random seeds, despite similar cluster characteristics in feature abundance, we ran CountClust under 100 different random seeds. We chose the random seed that produced the largest Bayes Factors across different random seeds and sample cluster membership.

Primary and secondary outcomes

The primary outcome was a composite of deep SSI, pneumonia, or bacteremia, as defined by CDC surveillance criteria[11], occurring within 6 months postoperatively. Bacteremia was defined as the occurrence of one or more positive blood cultures for a pathogenic organism or 2 or more positive cultures at different times for a skin commensal. Secondary outcomes were SSI, pneumonia, and bacteremia separately, the composite outcome at 30 days, and death at 6 months.

Outcomes were ascertained during the 6 month follow-up period after surgery for all participants involved in the original cohort. Follow-up data were obtained from each participant by study team personnel using in-person or phone interview and by review of medical records. Follow-up occurred daily during the inpatient phase of care immediately following the index surgical procedure and then at 30 days and 6 months after the date of surgery. Outpatient follow-up consisted of scripted mail and/or phone surveys. In addition, medical records were obtained from any primary or specialty care visits and for emergency department encounters and hospitalizations that occurred after discharge from the index surgical procedure. All outcomes reported by patients were confirmed from the obtained medical records, and in cases of death, from death certificates and/or autopsy reports. The social security death index was queried for loses to follow-up.

The outcomes for participants in this nested matched case-control study, like all outcomes in the original cohort, were adjudicated by trained research nurses.

Statistical analyses

Aggregated counts of rRNA sequences to the species level annotation were batch corrected and used for differential abundance analysis. To account for the variability in sequencing depth we performed cumulative sum scaling (CSS)[12]. To identify taxa significantly different between clusters and accounting for the sparsity inherent to 16S rRNA gene sequencing, we performed differential abundance analysis using a zero-inflated log-normal model as implemented within metagenomeSeq version 1.21.1 9 (software publically available at 10.18129/B9.bioc.metagenomeSeq)[13]. To characterize the within-sample (alpha) diversity, we calculated Shannon's Diversity Index (H). To characterize the between-sample (beta) diversity, we performed Principal Component Analysis on CSS $\log_2$ normalized species abundances.

Generalized linear model (GLM) analyses were performed to determine the factors associated with primary and secondary outcomes, unadjusted and adjusted for potentially cofounding covariates. Weighted probability of assignment to microbiome cluster class served as the main exposure. Models were defined using a binomial probability distribution and a logit link function. In a first step, demographic and comorbidities risk factors were tested individually between clusters. In a second step, a propensity score (PS) for cluster assignment was estimated. To estimate the PS, we used multivariable logistic regression analysis that included all of the baseline variables. Inverse probability of treatment weights (IPTW) used the PS to form a weight. The IPTW approach used weights based on the propensity score to create a sample in which the distribution of measured baseline covariates was independent of cluster assignment. The weights were incorporated in the multivariable weighted logistic regression model to predict infectious outcome.

We bootstrapped propensity score analyses by selecting ~70% of the 197 subjects in 500 subsamples, maintaining a fixed ratio of cases to controls in the subsamples (1:2.8). In each subsample, we first selected the case subjects with matched control subjects. We randomly sampled 38 cases in each subsample with replacement and then iteratively sampled matched control subjects for each case subject until the ratio of case vs control subject satisfied our requirement. The number of subjects in each of the 500 subsamples ranged between 122 to144.

We examined the association of infection with alpha diversity and abundance of individual microbial taxa using logistic regression. Due to skewness in the abundance (count) of microbial taxa, we log transformed counts to approximate normality. Analyses were performed using the R version 3.2.2 (R foundation for Statistical Computing, Vienna, Austria). Statistical significance was set at $p\text{-value} < 0.05$ and all tests were two-sided. Benjamini-Hochberg false discovery procedure was used to correct for multiple comparisons.

Data access

Github site which contains all scripts to reproduce our analysis.
https://jhsiao999.github.io/nasalmicrobiome/

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eTable 1. Association of Taxa Abundance With Microbiome Cluster Class

Taxa	samples clust1	samples clust2	counts clust1	counts clust2	logFC	se	p-value	q-value
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Mycobacteriaceae;g__Mycobacterium;s__	28	11	76	7171	3.631E+00	0.6016	1.580E-09	5.310E-07
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__;g__;s__	154	30	1808	13825	1.609E+00	0.2868	2.020E-08	3.390E-06
k__Bacteria;p__Chloroflexi;c__Thermomicrobia;o__JG30-KF-CM45;f__;g__;s__	11	9	22	3152	4.098E+00	0.7514	4.950E-08	4.140E-06
k__Bacteria;p__TM7;c__TM7-1;o__;f__;g__;s__	19	10	46	6605	3.603E+00	0.6587	4.510E-08	4.140E-06
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__;g__;s__	27	15	84	12099	3.057E+00	0.5651	6.330E-08	4.240E-06
k__Bacteria;p__Actinobacteria;c__Thermoleophilia;o__Solirubrobacterales;f__;g__;s__	11	12	19	2749	3.806E+00	0.7125	9.220E-08	4.550E-06
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Oxalobacteraceae;g__;s__	139	29	2924	102400	1.756E+00	0.3292	9.520E-08	4.550E-06
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__;s__	128	29	2737	60889	1.508E+00	0.3139	1.570E-06	6.550E-05
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Microbacteriaceae;g__;s__	44	12	214	8241	2.668E+00	0.5643	2.270E-06	8.440E-05
k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Acidimicrobiales;f__;g__;s__	12	10	17	1134	3.266E+00	0.7003	3.100E-06	1.037E-04
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__SMB53;s__	19	11	87	5762	2.969E+00	0.6553	5.890E-06	1.793E-04
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__;s__	16	9	47	2918	3.099E+00	0.6901	7.090E-06	1.979E-04
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__;s__	23	16	285	1648	2.332E+00	0.5398	1.560E-05	4.021E-04
k__Bacteria;p__TM7;c__TM7-3;o__;f__;g__;s__	49	20	951	2999	1.832E+00	0.4285	1.920E-05	4.584E-04
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__[Exiguobacteraceae];g__Exiguobacterium;s__	41	14	137	2999	2.024E+00	0.4865	3.180E-05	7.104E-04
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__Parvimonas;s__	28	8	211	751	2.589E+00	0.6532	7.410	1.551

							E-05	E-03
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Legionellales;f__Legionellaceae;g__;s__	7	8	8	1892	3.509E+00	0.9033	1.027E-04	1.911E-03
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Propionibacteriaceae;g__Propionibacterium;s__	153	21	14734	662	-1.646E+00	0.4236	1.022E-04	1.911E-03
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Moraxella;s__	46	12	17486	121207	3.354E+00	0.8735	1.235E-04	2.177E-03
k__Bacteria;p__Bacteroidetes;c__Sphingobacteriia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Sphingobacterium;s__	6	8	11	110	3.258E+00	0.8664	1.697E-04	2.843E-03
k__Bacteria;p__Cyanobacteria;c__Synechococcophycideae;o__Synechococcales;f__Synechococcaceae;g__Synechococcus;s__	12	2	26	1593	4.373E+00	1.1851	2.248E-04	3.274E-03
k__Bacteria;p__[Thermi];c__Deinococci;o__Deinococcales;f__Deinococcaceae;g__Deinococcus;s__	27	13	401	37448	2.549E+00	0.6880	2.112E-04	3.274E-03
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Microbacteriaceae;g__Microbacterium;s__	55	18	343	25345	1.697E+00	0.4596	2.221E-04	3.274E-03
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Methylophilales;f__Methylophilaceae;g__;s__	4	5	4	606	3.794E+00	1.0598	3.434E-04	4.793E-03
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__;s__	59	20	630	1329	1.512E+00	0.4244	3.659E-04	4.903E-03
k__Bacteria;p__Acidobacteria;c__[Chloracidobacteria];o__RB41;f__Ellin6075;g__;s__	17	9	151	1918	2.437E+00	0.6860	3.818E-04	4.919E-03
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Granulicatella;s__	86	16	2677	14065	1.759E+00	0.5001	4.363E-04	5.413E-03
k__Bacteria;p__TM7;c__SC3;o__;f__;g__;s__	10	7	21	3266	3.192E+00	0.9148	4.852E-04	5.459E-03
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rickettsiales;f__;g__;s__	9	6	30	1105	3.100E+00	0.8844	4.574E-04	5.459E-03
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Actinomyces;s__	111	24	3395	5006	1.310E+00	0.3756	4.889E-04	5.459E-03
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Peptostreptococcus;s__	15	6	107	492	2.758E+00	0.7981	5.492E-04	5.575E-03
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__;g__;s__	12	9	34	872	2.489E+00	0.7201	5.463E-04	5.575E-03
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Novosphingobium;s__	13	11	41	260	2.214E+00	0.6386	5.265	5.575

							E-04	E-03
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__	161	30	36652	62811	1.137E+00	0.3298	5.681E-04	5.597E-03
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__;s__	34	13	157	2040	1.749E+00	0.5109	6.178E-04	5.914E-03
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__longum	13	11	65	836	2.443E+00	0.7192	6.822E-04	6.349E-03
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__Hyphomicrobium;s__	7	10	25	1637	2.930E+00	0.8723	7.825E-04	7.085E-03
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Paracoccus;s__marcusii	32	13	85	1483	1.575E+00	0.4708	8.227E-04	7.253E-03
k__Bacteria;p__Bacteroidetes;c__Cytophagia;o__Cytophagales;f__Cytophagaceae;g__Hymenobacter;s__	23	11	122	15245	2.284E+00	0.6942	1.001E-03	8.385E-03
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;g__Atopobium;s__	37	9	204	401	1.813E+00	0.5505	9.914E-04	8.385E-03
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Methylocystaceae;g__Methylosinus;s__	5	8	5	252	2.928E+00	0.8954	1.077E-03	8.803E-03
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;g__;s__	17	10	68	3389	2.319E+00	0.7123	1.131E-03	9.024E-03
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Alcaligenaceae;g__;s__	25	10	166	1177	2.153E+00	0.6630	1.164E-03	9.070E-03
k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Acidimicrobiales;f__EB1017;g__;s__	3	9	3	172	3.320E+00	1.0418	1.439E-03	1.095E-02
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__Rhodoplanes;s__	12	10	21	259	2.004E+00	0.6317	1.515E-03	1.103E-02
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Nocardioidaceae;g__;s__	35	13	288	683	1.606E+00	0.5061	1.506E-03	1.103E-02
k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Acidimicrobiales;f__C111;g__;s__	9	8	35	749	2.669E+00	0.8510	1.712E-03	1.220E-02
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Veillonella;s__dispar	114	19	7907	9307	1.299E+00	0.4178	1.878E-03	1.258E-02
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Bradyrhizobiaceae;g__;s__	111	27	1318	969	8.217E-01	0.2637	1.836E-03	1.258E-02
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Micrococcus;s__	145	27	466	37	-6.42	0.2064	1.873	1.258

					0E-01		E-03	E-02
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Propionibacteriaceae;g__Propionibacterium;s__granulosum	154	27	922	73	-6.364E-01	0.2057	1.972E-03	1.296E-02
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__;s__	67	17	629	16591	1.438E+00	0.4698	2.203E-03	1.420E-02
k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Acidimicrobiales;f__Microthrixaceae;g__;s__	3	8	3	219	3.354E+00	1.1142	2.607E-03	1.648E-02
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Anoxybacillus;s__kestanbolensis	147	27	2201	108	-9.320E-01	0.3104	2.677E-03	1.661E-02
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Stenotrophomonas;s__	145	26	588	47	-6.092E-01	0.2122	4.088E-03	2.490E-02
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__Anaerococcus;s__	159	27	128879	9195	-1.169E+00	0.4086	4.222E-03	2.495E-02
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingomonas;s__	72	19	1131	9483	1.159E+00	0.4052	4.246E-03	2.495E-02
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__;g__;s__	66	4	1648	29	-2.695E+00	0.9457	4.368E-03	2.514E-02
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Acetobacteraceae;g__;s__	26	10	94	393	1.679E+00	0.5899	4.429E-03	2.514E-02
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Paenisporosarcina;s__	25	8	79	2314	1.983E+00	0.6992	4.575E-03	2.554E-02
k__Bacteria;p__Cyanobacteria;c__Chloroplast;o__Chlorophyta;f__Trebouxiophyceae;g__;s__	8	6	28	16300	3.440E+00	1.2225	4.897E-03	2.689E-02
k__Bacteria;p__Synergistetes;c__Synergistia;o__Synergistales;f__Dethiosulfovibrionaceae;g__TG5;s__	4	3	26	176	3.627E+00	1.3003	5.285E-03	2.856E-02
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__Rhodocyclaceae;g__;s__	17	9	32	388	1.872E+00	0.6781	5.776E-03	3.043E-02
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Rhodospirillaceae;g__;s__	31	14	199	777	1.358E+00	0.4924	5.814E-03	3.043E-02
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Microbacteriaceae;g__CandidatusAquiluna;s__rubra	4	4	9	2574	3.823E+00	1.3900	5.959E-03	3.071E-02
k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium;s__	74	15	2241	1500	1.257E+00	0.4723	7.790E-03	3.954E-02
k__Bacteria;p__Chlamydiae;c__Chlamydiia;o__Chlamydiales;f__;g__;s__	3	6	3	648	3.414E+00	1.3084	9.062	4.531

							E-03	E-02
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Intrasporangiaceae;g__;s__	38	8	387	5313	1.801E+00	0.7041	1.054E-02	5.191E-02
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Flavobacteriaceae;g__Flavobacterium;s__	46	14	482	2096	1.331E+00	0.5282	1.174E-02	5.701E-02
k__Bacteria;p__Proteobacteria;c__TA18;o__PHOS-HD29;f__;g__;s__	2	7	2	112	3.215E+00	1.2860	1.243E-02	5.866E-02
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingopyxis;s__	4	9	8	470	2.681E+00	1.0713	1.231E-02	5.866E-02
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Aeromonadales;f__Aeromonadaceae;g__;s__	33	8	191	1067	1.647E+00	0.6655	1.333E-02	6.203E-02
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Moryella;s__	24	7	283	2262	1.974E+00	0.8009	1.370E-02	6.287E-02
k__Bacteria;p__TM6;c__SJA-4;o__;f__;g__;s__	2	6	2	1458	3.891E+00	1.5907	1.444E-02	6.521E-02
k__Bacteria;p__TM7;c__;o__;f__;g__;s__	6	7	16	2793	2.609E+00	1.0727	1.499E-02	6.521E-02
k__Bacteria;p__Firmicutes;c__Erysipelotrichi;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Bulleidia;s__	8	7	53	755	2.463E+00	1.0118	1.494E-02	6.521E-02
k__Bacteria;p__Cyanobacteria;c__Chloroplast;o__Stramenopiles;f__;g__;s__	8	7	54	1063	2.393E+00	0.9823	1.485E-02	6.521E-02
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__;s__	112	26	1968	1393	8.153E-01	0.3371	1.559E-02	6.696E-02
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Oribacterium;s__	21	9	134	1226	1.787E+00	0.7405	1.582E-02	6.707E-02
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminococcus;s__	28	8	453	27	-1.629E+00	0.6947	1.904E-02	7.974E-02
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Agrobacterium;s__	42	12	325	856	1.243E+00	0.5335	1.979E-02	7.988E-02
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella;s__melaninogenica	80	16	2634	9623	1.133E+00	0.4858	1.975E-02	7.988E-02
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__;s__	144	25	334	41	-4.812E-01	0.2062	1.963E-02	7.988E-02
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Pseudoxanthomonas;s__mexicana	3	3	4	164	3.242E+00	1.4001	2.058	8.151

							E-02	E-02
k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales;f__Leptotrichiaceae;g__Leptotrichia;s__	73	20	2445	4266	1.107E+00	0.4786	2.068E-02	8.151E-02
k__Bacteria;p__Cyanobacteria;c__Chloroplast;o__Chlorophyta;f__;g__;s__	3	4	7	1523	3.435E+00	1.4974	2.180E-02	8.490E-02
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Phyllobacteriaceae;g__;s__	16	9	68	137	1.473E+00	0.6459	2.256E-02	8.590E-02
k__Bacteria;p__Firmicutes;c__Bacilli;o__Gemellales;f__Gemellaceae;g__;s__	64	14	1204	2580	1.128E+00	0.4946	2.256E-02	8.590E-02
k__Bacteria;p__Bacteroidetes;c__Sphingobacteriia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Pedobacter;s__	60	16	668	9667	1.061E+00	0.4674	2.327E-02	8.757E-02
k__Bacteria;p__Bacteroidetes;c__Sphingobacteriia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__;s__	5	7	77	913	2.334E+00	1.0395	2.476E-02	9.215E-02
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Oxalobacteraceae;g__Janthinobacterium;s__	23	8	70	754	1.551E+00	0.6946	2.557E-02	9.415E-02
k__Bacteria;p__[Thermi];c__Deinococci;o__Deinococcales;f__Trueperaceae;g__Truepera;s__	7	5	46	466	2.367E+00	1.0641	2.615E-02	9.521E-02
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__;s__	38	14	428	328	1.165E+00	0.5261	2.682E-02	9.659E-02
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Nocardioidaceae;g__Aeromicrobium;s__	2	5	4	136	3.118E+00	1.4196	2.805E-02	9.811E-02
k__Bacteria;p__Firmicutes;c__Bacilli;o__Turicibacterales;f__Turicibacteraceae;g__Turicibacter;s__	7	9	65	497	1.827E+00	0.8321	2.811E-02	9.811E-02
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;g__;s__	32	12	233	458	1.249E+00	0.5682	2.791E-02	9.811E-02
k__Bacteria;p__TM6;c__F38;o__;f__;g__;s__	3	6	3	540	2.789E+00	1.2838	2.982E-02	1.030E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Paracoccus;s__aminovorans	144	28	272	49	-4.016E-01	0.1856	3.044E-02	1.041E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Acetobacteraceae;g__Roseomonas;s__mucosa	14	2	201	8	-2.809E+00	1.3054	3.139E-02	1.062E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Geodermatophilaceae;g__;s__	28	8	159	187	1.385E+00	0.6458	3.197E-02	1.071E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__;g__;s__	2	5	3	184	3.030E+00	1.4191	3.277	1.076

							E-02	E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Nocardiaceae;g__Rhodococcus;s__	31	6	131	22359	1.804E+00	0.8445	3.263E-02	1.076E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Enhydrobacter;s__	155	29	3146	2308	6.912E-01	0.3270	3.454E-02	1.123E-01
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__0319-6G20;g__;s__	9	3	132	3	-2.445E+00	1.1612	3.525E-02	1.136E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Rothia;s__dentocariosa	70	16	1208	2122	1.029E+00	0.4897	3.567E-02	1.138E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Hyphomonadaceae;g__;s__	3	6	11	203	2.524E+00	1.2129	3.743E-02	1.183E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Faecalibacterium;s__prausnitzii	17	9	124	230	1.464E+00	0.7069	3.839E-02	1.202E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Microbacteriaceae;g__Salinibacterium;s__	29	9	131	3773	1.432E+00	0.6965	3.975E-02	1.233E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Methylobacteriaceae;g__;s__	27	9	207	219	1.162E+00	0.5716	4.198E-02	1.290E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Rothia;s__mucilaginosa	117	23	7641	20362	9.409E-01	0.4654	4.321E-02	1.316E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__	11	5	36	36	1.722E+00	0.8702	4.784E-02	1.444E-01
k__Bacteria;p__[Thermi];c__Deinococci;o__Deinococcales;f__Deinococcaceae;g__Deinococcus;s__aquatilis	2	4	2	710	3.205E+00	1.6233	4.833E-02	1.446E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Kaistobacter;s__	29	12	252	751	1.129E+00	0.5752	4.967E-02	1.472E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__anginosus	30	11	276	854	1.273E+00	0.6514	5.058E-02	1.486E-01
k__Bacteria;p__Firmicutes;c__Erysipelotrichi;o__Erysipelotrichales;f__Erysipelotrichaceae;g__;s__	4	5	5	55	2.172E+00	1.1206	5.259E-02	1.532E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Gemellales;f__Gemellaceae;g__Gemella;s__	145	27	384	99	-3.866E-01	0.2000	5.330E-02	1.539E-01
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Flavobacteriaceae;g__Capnocytophaga;s__	48	9	737	461	1.252E+00	0.6507	5.443E-02	1.549E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__;s__	89	15	729	3050	8.533E-01	0.4439	5.457	1.549

							E-02	E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Haemophilus;s__	52	10	1560	143861	1.354E+00	0.7125	5.742E-02	1.616E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Rubellimicrobium;s__	20	8	176	1244	1.486E+00	0.7847	5.829E-02	1.627E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Coprococcus;s__	6	3	66	3	-2.246E+00	1.1930	5.971E-02	1.653E-01
k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria;o__Campylobacterales;f__Campylobacteraceae;g__Arcobacter;s__	8	6	17	744	1.809E+00	0.9689	6.191E-02	1.700E-01
k__Bacteria;p__Actinobacteria;c__Thermoleophilia;o__Solirubrobacterales;f__Conexibacteraceae;g__;s__	2	6	3	180	2.620E+00	1.4087	6.285E-02	1.701E-01
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Bdellovibrionales;f__Bdellovibrionaceae;g__Bdellovibrio;s__	14	6	66	188	1.401E+00	0.7533	6.296E-02	1.701E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Carnobacterium;s__	38	5	287	13	-1.568E+00	0.8501	6.517E-02	1.733E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus;s__	43	15	1827	588	9.205E-01	0.4986	6.487E-02	1.733E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Nocardioidaceae;g__Nocardioides;s__plantarum	2	5	2	94	2.598E+00	1.4177	6.692E-02	1.765E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__Rhodocyclaceae;g__Zoogloea;s__	2	6	2	245	2.749E+00	1.5039	6.751E-02	1.767E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingomonas;s__echinoides	38	10	328	1379	1.021E+00	0.5608	6.857E-02	1.781E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__;s__	28	8	530	32	-1.208E+00	0.6777	7.466E-02	1.924E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptococcaceae;g__Peptococcus;s__	7	4	33	30	1.732E+00	0.9784	7.666E-02	1.960E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__Finegoldia;s__	141	23	50194	3616	-8.165E-01	0.4633	7.798E-02	1.979E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Phyllobacteriaceae;g__Mesorhizobium;s__	4	6	26	344	1.870E+00	1.0638	7.883E-02	1.985E-01
k__Bacteria;p__TM7;c__TM7-3;o__EW055;f__;g__;s__	2	8	9	284	2.431E+00	1.3912	8.051E-02	2.013E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Limnohabitans;s__	3	8	9	212	1.945E+00	1.1271	8.433	2.093

							E-02	E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Oxalobacteraceae;g__Ralstonia;s__	128	27	1312	709	6.225E-01	0.3644	8.753E-02	2.156E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Megamonas;s__	2	3	29	223	2.665E+00	1.5836	9.239E-02	2.259E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Neisseriales;f__Neisseriaceae;g__Neisseria;s__	84	16	4172	4899	8.963E-01	0.5338	9.313E-02	2.261E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Catonella;s__	2	3	32	186	2.673E+00	1.6009	9.499E-02	2.289E-01
k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales;f__Leptotrichiaceae;g__;s__	2	4	2	81	2.519E+00	1.5619	1.068E-01	2.556E-01
k__Bacteria;p__Bacteroidetes;c__[Saprospirae];o__[Saprospirales];f__Chitinophagaceae;g__;s__	2	7	25	245	2.030E+00	1.2655	1.087E-01	2.558E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Jeotgalicoccus;s__	21	4	543	206	1.522E+00	0.9503	1.092E-01	2.558E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__minor	7	7	19	87	1.388E+00	0.8658	1.089E-01	2.558E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Nocardioidaceae;g__Friedmanniella;s__	8	3	46	5	-1.721E+00	1.0793	1.108E-01	2.578E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Scardovia;s__	10	6	147	124	1.584E+00	0.9975	1.124E-01	2.597E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Sporichthyaceae;g__;s__	6	5	21	70	1.527E+00	0.9722	1.163E-01	2.668E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Hydrogenophaga;s__	4	5	16	1782	2.010E+00	1.2917	1.197E-01	2.694E-01
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__[Weeksellaceae];g__;s__	16	5	107	130	1.327E+00	0.8531	1.198E-01	2.694E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Lautropia;s__	21	6	231	136	1.176E+00	0.7540	1.188E-01	2.694E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__iners	55	9	406	35	-7.910E-01	0.5135	1.235E-01	2.757E-01
k__Bacteria;p__Verrucomicrobia;c__[Spartobacteria];o__[Chthoniobacterales];f__[Chthoniobacteraceae];g__CandidatusXiphinematobacter;s__	2	3	44	195	2.444E+00	1.5927	1.249E-01	2.771E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__adolescentis	17	8	74	149	9.095E-01	0.6082	1.348	2.951

							E-01	E-01
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__[Paraprevotellaceae];g__[Prevotella];s__	42	10	576	433	9.018E-01	0.6018	1.340E-01	2.951E-01
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__[Weeksellaceae];g__Elizabethkingia;s__meningoseptica	12	4	16	104	1.365E+00	0.9270	1.409E-01	3.065E-01
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Porphyromonas;s__	74	16	1959	769	7.321E-01	0.4998	1.430E-01	3.090E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Dialister;s__	62	13	2830	272	-8.118E-01	0.5635	1.497E-01	3.215E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__fragi	114	23	2237	835	4.980E-01	0.3523	1.575E-01	3.360E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__zeae	3	3	33	32	2.042E+00	1.4619	1.624E-01	3.444E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Tepidimonas;s__	47	2	281	4	-1.712E+00	1.2421	1.680E-01	3.540E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Paracoccus;s__	49	12	275	209	6.901E-01	0.5062	1.728E-01	3.617E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__SBla14;f__;g__;s__	2	3	5	5	2.086E+00	1.5513	1.787E-01	3.706E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Aurantimonadaceae;g__;s__	17	6	41	72	1.002E+00	0.7482	1.803E-01	3.706E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Arthrobacter;s__	19	10	142	179	8.532E-01	0.6365	1.801E-01	3.706E-01
k__Bacteria;p__Bacteroidetes;c__[Saprospirae];o__[Saprospirales];f__Chitinophagaceae;g__Flavisolibacter;s__	6	3	585	345	1.904E+00	1.4473	1.884E-01	3.758E-01
k__Bacteria;p__Synergistetes;c__Synergistia;o__Synergistales;f__Synergistaceae;g__vadinCA02;s__	4	3	4	49	1.614E+00	1.2300	1.895E-01	3.758E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Dermacoccaceae;g__Dermacoccus;s__	22	3	880	10	-1.522E+00	1.1527	1.868E-01	3.758E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Acidovorax;s__delafieldii	4	6	36	533	1.519E+00	1.1535	1.878E-01	3.758E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Vibrionales;f__Pseudoalteromonadaceae;g__Pseudoalteromonas;s__	12	4	125	217	1.389E+00	1.0619	1.907E-01	3.758E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Micrococcus;s__luteus	21	5	66	11	-1.01	0.7670	1.869	3.758

					2E+00		E-01	E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Delftia;s__	135	28	6776	3663	4.377E-01	0.3339	1.900E-01	3.758E-01
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella;s__intermedia	5	2	49	83	1.869E+00	1.4520	1.980E-01	3.875E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Selenomonas;s__	37	12	802	320	7.577E-01	0.5898	1.989E-01	3.875E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Bradyrhizobiaceae;g__Bradyrhizobium;s__	146	27	405	64	-2.533E-01	0.1979	2.006E-01	3.884E-01
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella;s__nanceiensis	20	5	120	32	1.000E+00	0.7897	2.054E-01	3.954E-01
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Syntrophobacterales;f__Syntrophobacteraceae;g__;s__	2	4	2	96	1.930E+00	1.5439	2.112E-01	3.957E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Microbacteriaceae;g__Leucobacter;s__	7	8	54	164	1.201E+00	0.9569	2.096E-01	3.957E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Aggregatibacter;s__segnis	12	5	123	122	1.137E+00	0.9097	2.114E-01	3.957E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Planomicrobium;s__	23	9	114	453	8.874E-01	0.7076	2.099E-01	3.957E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Facklamia;s__	36	6	325	57	-8.844E-01	0.7026	2.082E-01	3.957E-01
k__Bacteria;p__Actinobacteria;c__Thermoleophilia;o__Solirubrobacterales;f__Solirubrobacteraceae;g__;s__	6	5	12	40	1.239E+00	0.9971	2.138E-01	3.980E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__Gallicola;s__	8	3	83	342	1.636E+00	1.3325	2.195E-01	4.042E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__	36	11	242	175	6.609E-01	0.5384	2.196E-01	4.042E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Corynebacteriaceae;g__Corynebacterium;s__durum	37	6	458	622	9.402E-01	0.7754	2.253E-01	4.124E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__;s__	7	4	22	15	1.202E+00	1.0087	2.333E-01	4.247E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Veillonella;s__parvula	15	5	80	75	9.425E-01	0.8043	2.413E-01	4.369E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__Peptoniphilus;s__	137	24	61085	10405	-5.60	0.4828	2.457	4.425

					5E-01		E-01	E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__Rhodocyclaceae;g__Dechloromonas;s__	2	8	17	343	1.720E+00	1.4954	2.499E-01	4.453E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Haemophilus;s__parainfluenzae	66	10	1794	3352	7.477E-01	0.6511	2.508E-01	4.453E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Propionibacteriaceae;g__;s__	19	9	86	97	7.272E-01	0.6338	2.512E-01	4.453E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__[Ruminococcus];s__	14	9	51	48	7.382E-01	0.6482	2.548E-01	4.492E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Geobacillus;s__	50	9	1066	118	-7.666E-01	0.6845	2.627E-01	4.608E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Microbacteriaceae;g__Rathayibacter;s__caricis	6	2	367	116	1.703E+00	1.5927	2.849E-01	4.917E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__	11	4	72	14	-1.103E+00	1.0327	2.855E-01	4.917E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Morganella;s__	71	3	698	31	-1.062E+00	0.9944	2.857E-01	4.917E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Abiotrophia;s__	33	6	570	506	8.137E-01	0.7639	2.868E-01	4.917E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Aggregatibacter;s__	17	9	320	96	8.028E-01	0.7550	2.877E-01	4.917E-01
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Flavobacteriaceae;g__Capnocytophaga;s__ochracea	3	3	5	7	1.412E+00	1.3371	2.909E-01	4.922E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Burkholderia;s__	145	30	768	2251	2.530E-01	0.2389	2.896E-01	4.922E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Acidovorax;s__	2	3	7	102	1.796E+00	1.7097	2.934E-01	4.940E-01
k__Bacteria;p__Spirochaetes;c__Spirochaetes;o__Spirochaetales;f__Spirochaetaceae;g__Treponema;s__	3	2	31	29	1.666E+00	1.5967	2.966E-01	4.964E-01
k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales;f__Leptotrichiaceae;g__Sneathia;s__	13	3	230	4	-1.141E+00	1.0959	2.978E-01	4.964E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Staphylococcus;s__	167	30	131054	4931	-1.554E+00	1.5058	3.022E-01	4.986E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnospira;s__	4	2	9	34	1.526E+00	1.4757	3.011	4.986

							E-01	E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Serratia;s__marcescens	11	2	1161	3	-1.575E+00	1.5516	3.101E-01	5.093E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Mogibacteriaceae];g__;s__	14	4	58	62	9.428E-01	0.9419	3.168E-01	5.177E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Polaromonas;s__	17	7	32	58	6.283E-01	0.6407	3.268E-01	5.314E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__1-68;s__	17	4	334	387	9.977E-01	1.0300	3.327E-01	5.359E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__	162	29	8909	2257	3.163E-01	0.3258	3.317E-01	5.359E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Pseudonocardiaceae;g__Pseudonocardia;s__	9	2	51	10	-1.277E+00	1.3381	3.400E-01	5.400E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Pseudonocardiaceae;g__Actinomycetospora;s__	5	4	14	10	1.041E+00	1.0915	3.404E-01	5.400E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Brevundimonas;s__diminuta	19	6	163	189	7.982E-01	0.8332	3.381E-01	5.400E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Megasphaera;s__	30	8	279	126	5.968E-01	0.6277	3.417E-01	5.400E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Thermoanaerobacterales;f__Caldicellulosiruptoraceae;g__Caldicellulosiruptor;s__saccharolyticus	13	4	138	38	-9.405E-01	0.9929	3.435E-01	5.403E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Staphylococcus;s__epidermidis	167	30	15399	702	-1.269E+00	1.3450	3.455E-01	5.409E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Yaniellaceae;g__Yaniella;s__	4	2	14	9	1.324E+00	1.4135	3.489E-01	5.437E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Comamonas;s__	29	5	339	74	-7.505E-01	0.8118	3.552E-01	5.509E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__[Ruminococcus];s__gnavus	3	4	64	190	1.370E+00	1.4989	3.609E-01	5.545E-01
k__Bacteria;p__Cyanobacteria;c__4C0d-2;o__MLE1-12;f__;g__;s__	116	19	2903	5222	3.830E-01	0.4186	3.602E-01	5.545E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Brucellaceae;g__;s__	22	9	74	34	5.361E-01	0.5971	3.693E-01	5.623E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__viridiflava	47	14	673	741	4.714E-01	0.5242	3.685	5.623

							E-01	E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__;s__	167	30	228426	13928	-1.484E+00	1.6665	3.731E-01	5.637E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Proteus;s__	21	5	4981	852	1.025E+00	1.1523	3.735E-01	5.637E-01
k__Bacteria;p__Bacteroidetes;c__[Saprospirae];o__[Saprospirales];f__Chitinophagaceae;g__Sediminibacterium;s__	109	19	3014	438	-3.557E-01	0.4073	3.824E-01	5.744E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Sanguibacteraceae;g__Sanguibacter;s__	3	4	5	30	1.176E+00	1.3550	3.852E-01	5.761E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Neisseriales;f__Neisseriaceae;g__Eikenella;s__	6	4	28	20	9.324E-01	1.0910	3.927E-01	5.796E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Neisseriales;f__Neisseriaceae;g__Kingella;s__	14	4	137	66	8.656E-01	1.0109	3.919E-01	5.796E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Methylobacteriaceae;g__Methylobacterium;s__adhaesivum	22	6	115	107	6.179E-01	0.7207	3.913E-01	5.796E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Neisseriales;f__Neisseriaceae;g__Neisseria;s__subflava	10	2	87	10	-1.140E+00	1.3583	4.013E-01	5.812E-01
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Paludibacter;s__	8	5	47	62	8.571E-01	1.0210	4.012E-01	5.812E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Mycoplana;s__	21	8	131	184	5.588E-01	0.6675	4.025E-01	5.812E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__;s__	107	23	1698	798	2.949E-01	0.3497	3.991E-01	5.812E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__johnsonii	151	26	825	281	-2.245E-01	0.2644	3.959E-01	5.812E-01
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__;g__;s__	29	5	286	200	7.084E-01	0.8509	4.052E-01	5.825E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Hylemonella;s__	3	4	24	7	-1.064E+00	1.2936	4.107E-01	5.865E-01
k__Bacteria;p__Bacteroidetes;c__[Saprospirae];o__[Saprospirales];f__Saprospiraceae;g__;s__	4	6	70	143	9.640E-01	1.1737	4.115E-01	5.865E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__;s__	2	5	10	84	1.152E+00	1.4116	4.146E-01	5.885E-01
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__[Weeksellaceae];g__Chryseobacterium;s__	153	29	2726	9296	2.616E-01	0.3238	4.191	5.925

							E-01	E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Corynebacteriaceae;g__Corynebacterium;s__	166	29	1822190	120246	-1.448E+00	1.8067	4.227E-01	5.950E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Staphylococcus;s__aureus	166	28	21401	433	-1.326E+00	1.6644	4.258E-01	5.968E-01
k__Bacteria;p__WPS-2;c__;o__;f__;g__;s__	5	5	115	308	8.729E-01	1.1174	4.347E-01	6.068E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Cardiobacteriales;f__Cardiobacteriaceae;g__Cardiobacterium;s__	6	2	18	9	1.044E+00	1.3441	4.375E-01	6.082E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__	9	2	310	36	-1.196E+00	1.5713	4.467E-01	6.184E-01
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella;s__copri	9	5	140	103	-7.606E-01	1.0096	4.512E-01	6.221E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Dermabacteraceae;g__Dermabacter;s__	39	7	301	56	-4.893E-01	0.6576	4.568E-01	6.272E-01
k__Bacteria;p__Bacteroidetes;c__Cytophagia;o__Cytophagales;f__Cytophagaceae;g__Spirosoma;s__	3	2	64	747	1.213E+00	1.6503	4.625E-01	6.323E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Oceanospirillales;f__Halomonadaceae;g__Halomonas;s__	162	29	3507	1138	1.912E-01	0.2624	4.661E-01	6.348E-01
k__Bacteria;p__SR1;c__;o__;f__;g__;s__	4	4	24	57	8.874E-01	1.2262	4.693E-01	6.364E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Nakamurellaceae;g__;s__	6	7	21	51	7.288E-01	1.0132	4.719E-01	6.375E-01
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Parabacteroides;s__	5	2	10	13	1.018E+00	1.4339	4.776E-01	6.396E-01
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uniformis	17	8	166	102	5.183E-01	0.7324	4.792E-01	6.396E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__Shewanellaceae;g__Shewanella;s__algae	157	29	2115	714	1.848E-01	0.2590	4.756E-01	6.396E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micromonosporaceae;g__;s__	5	4	65	10	-8.298E-01	1.1918	4.863E-01	6.464E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Propionibacteriaceae;g__Propionibacterium;s__acnes	166	30	320674	21902	-1.216E+00	1.8046	5.006E-01	6.571E-01
k__Bacteria;p__Tenericutes;c__Mollicutes;o__Mycoplasmatales;f__Mycoplasmataceae;g__Mycoplasma;s__	3	4	71	42	-9.04	1.3429	5.008	6.571

					1E-01		E-01	E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Corynebacteriaceae;g__Corynebacterium;s__lubricantis	8	4	48	122	6.601E-01	0.9835	5.021E-01	6.571E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingobium;s__	37	9	249	189	3.983E-01	0.5875	4.978E-01	6.571E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Phascolarctobacterium;s__	6	4	52	50	-7.265E-01	1.1022	5.098E-01	6.645E-01
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;g__Eggerthella;s__lenta	2	4	10	20	9.825E-01	1.5119	5.158E-01	6.685E-01
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__[Paraprevotellaceae];g__[Prevotella];s__tannerae	13	2	98	51	-8.819E-01	1.3660	5.185E-01	6.685E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__Shewanellaceae;g__Shewanella;s__	17	8	101	13	4.095E-01	0.6357	5.195E-01	6.685E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Methylobacteriaceae;g__Methylobacterium;s__	47	11	496	130	3.582E-01	0.5578	5.208E-01	6.685E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Propionibacteriaceae;g__Microlunatus;s__	3	3	9	24	8.724E-01	1.3797	5.272E-01	6.691E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Geodermatophilaceae;g__Modestobacter;s__	10	3	113	7	-7.207E-01	1.1453	5.292E-01	6.691E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__reuteri	13	4	126	525	7.115E-01	1.1347	5.306E-01	6.691E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Dermabacteraceae;g__Brachybacterium;s__conglomeratum	35	7	191	50	4.018E-01	0.6418	5.313E-01	6.691E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Neisseriales;f__Neisseriaceae;g__;s__	124	22	44053	4758	-3.474E-01	0.5483	5.263E-01	6.691E-01
k__Bacteria;p__Acidobacteria;c__Acidobacteria-6;o__iii1-15;f__;g__;s__	6	4	145	73	-7.406E-01	1.1914	5.342E-01	6.693E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Sinobacteraceae;g__;s__	80	20	1013	280	2.239E-01	0.3613	5.354E-01	6.693E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__;f__;g__;s__	63	12	609	657	3.024E-01	0.4989	5.444E-01	6.779E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__;g__;s__	20	9	142	121	3.865E-01	0.6421	5.472E-01	6.790E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Mogibacteriaceae];g__Mogibacterium;s__	5	3	11	6	7.148E-01	1.2035	5.525	6.830

							E-01	E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__WAL_1855D;s__	21	3	707	1400	7.314E-01	1.2565	5.605E-01	6.903E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Phyllobacteriaceae;g__Aminobacter;s__	8	6	41	116	5.060E-01	0.9040	5.756E-01	7.064E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Phyllobacteriaceae;g__Phyllobacterium;s__	144	30	490	535	1.304E-01	0.2346	5.784E-01	7.072E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Nocardiaceae;g__Rhodococcus;s__fascians	4	2	13	4	-7.966E-01	1.4688	5.876E-01	7.157E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Actinobacillus;s__parahaemolyticus	11	3	79	157	6.137E-01	1.1435	5.915E-01	7.180E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Veillonella;s__	20	4	360	49	-4.887E-01	0.9295	5.991E-01	7.245E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Varibaculum;s__	16	3	152	14	-5.358E-01	1.0326	6.038E-01	7.250E-01
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella;s__	96	23	11849	1386	2.256E-01	0.4324	6.018E-01	7.250E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Gordoniaceae;g__Gordonia;s__	5	3	108	46	6.405E-01	1.3193	6.274E-01	7.479E-01
k__Bacteria;p__TM7;c__TM7-3;o__CW040;f__F16;g__;s__	8	4	61	113	5.612E-01	1.1520	6.261E-01	7.479E-01
k__Bacteria;p__Chloroflexi;c__Ellin6529;o__;f__;g__;s__	7	6	27	48	4.028E-01	0.8726	6.444E-01	7.655E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__;s__	19	10	84	103	2.647E-01	0.5963	6.571E-01	7.778E-01
k__Bacteria;p__Cyanobacteria;c__Nostocophycideae;o__Stigonematales;f__Rivulariaceae;g__Calothrix;s__	5	2	229	139	-7.036E-01	1.6023	6.606E-01	7.792E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Bradyrhizobiaceae;g__Bosea;s__genosp.	14	6	56	38	3.520E-01	0.8166	6.664E-01	7.833E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__Devosia;s__	35	11	242	220	2.380E-01	0.5613	6.715E-01	7.866E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Alcaligenaceae;g__Achromobacter;s__	89	20	948	304	-1.641E-01	0.4017	6.830E-01	7.972E-01
k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Acidimicrobiales;f__Microthrixaceae;g__CandidatusMicrothrix;s__parvicella	4	2	17	10	5.742E-01	1.4673	6.955	7.994

							E-01	E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Amaricoccus;s__	3	4	8	39	5.541E-01	1.3874	6.896E-01	7.994E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Alkanindiges;s__	4	3	12	42	5.130E-01	1.3327	7.003E-01	7.994E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Rhizobium;s__	6	3	50	19	-4.721E-01	1.2366	7.027E-01	7.994E-01
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__[Weeksellaceae];g__Wautersiella;s__	5	3	9	12	4.702E-01	1.2444	7.055E-01	7.994E-01
k__Bacteria;p__Cyanobacteria;c__Oscillatoriophycideae;o__Chroococcales;f__Xenococcaceae;g__;s__	20	5	794	795	-3.685E-01	0.9644	7.024E-01	7.994E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Oxalobacteraceae;g__Cupriavidus;s__	30	3	218	13	-3.607E-01	0.9573	7.063E-01	7.994E-01
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella;s__nigrescens	20	5	103	72	2.958E-01	0.7808	7.048E-01	7.994E-01
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;g__Collinsella;s__aerofaciens	21	7	187	203	2.798E-01	0.7304	7.016E-01	7.994E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__;s__	165	30	28143	171053	6.425E-01	1.8241	7.247E-01	8.146E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Cellulomonadaceae;g__Cellulomonas;s__	23	4	158	47	-3.230E-01	0.9103	7.228E-01	8.146E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Vibrionales;f__Vibrionaceae;g__Vibrio;s__	13	2	44	9	-4.313E-01	1.2654	7.332E-01	8.215E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Alloiococcus;s__	87	16	245413	35744	2.721E-01	0.8266	7.420E-01	8.286E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Blautia;s__	38	11	349	289	1.766E-01	0.5588	7.520E-01	8.369E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__	89	15	2425	1389	1.463E-01	0.4858	7.633E-01	8.467E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Variovorax;s__paradoxus	151	30	624	374	-6.074E-02	0.2055	7.676E-01	8.487E-01
k__Bacteria;p__Cyanobacteria;c__Oscillatoriophycideae;o__Chroococcales;f__Xenococcaceae;g__Chroococcidiopsis;s__	8	3	70	43	-3.276E-01	1.2000	7.849E-01	8.649E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Dietziaceae;g__;s__	5	3	26	14	3.368E-01	1.2699	7.908	8.684

							E-01	E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__	144	27	12292	1218	-8.047E-02	0.3069	7.932E-01	8.684E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__;s__	13	6	39	56	2.002E-01	0.7751	7.962E-01	8.688E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Psychrobacter;s__sanguinis	14	2	36	15	-3.079E-01	1.2241	8.014E-01	8.712E-01
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Dorea;s__	6	4	47	21	2.742E-01	1.1027	8.036E-01	8.712E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Phenylobacterium;s__	6	5	50	14	-2.354E-01	0.9935	8.127E-01	8.782E-01
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Oxalobacteraceae;g__Janthinobacterium;s__lividum	156	30	3010	1456	-6.666E-02	0.2853	8.153E-01	8.782E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__;s__	40	6	256	281	1.537E-01	0.6982	8.257E-01	8.841E-01
k__Bacteria;p__[Thermi];c__Deinococci;o__Thermales;f__Thermaceae;g__Thermus;s__	67	11	1197	302	-1.229E-01	0.5593	8.260E-01	8.841E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Brevibacteriaceae;g__Brevibacterium;s__	40	9	1058	119	-1.380E-01	0.6615	8.347E-01	8.905E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Aerococcus;s__	15	3	151	14	-2.247E-01	1.1190	8.409E-01	8.941E-01
k__Bacteria;p__Cyanobacteria;c__Chloroplast;o__Streptophyta;f__;g__;s__	110	21	5634	1447	-7.896E-02	0.3996	8.434E-01	8.941E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__Psychromonadaceae;g__Psychromonas;s__	3	2	33	12	2.444E-01	1.5984	8.785E-01	9.172E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Dietziaceae;g__Dietzia;s__	10	2	287	5	-2.128E-01	1.4051	8.796E-01	9.172E-01
k__Bacteria;p__Firmicutes;c__Erysipelotrichi;o__Erysipelotrichales;f__Erysipelotrichaceae;g__[Eubacterium];s__biforme	4	3	8	12	-1.964E-01	1.3203	8.818E-01	9.172E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__	47	7	527	174	1.066E-01	0.7117	8.810E-01	9.172E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Erwinia;s__	27	7	146	26	-1.065E-01	0.6633	8.725E-01	9.172E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Kocuria;s__rhizophila	77	15	21509	2495	8.936E-02	0.5764	8.768	9.172

							E-01	E-01
k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria;o__Campylobacterales;f__Campylobacteraceae;g__Campylobacter;s__	69	14	4611	374	-8.045E-02	0.5530	8.843E-01	9.172E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Actinobaculum;s__	10	2	42	33	1.640E-01	1.2892	8.987E-01	9.293E-01
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingopyxis;s__alaskensis	2	3	4	12	1.686E-01	1.6492	9.186E-01	9.398E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__[Chromatiaceae];g__Rheinheimera;s__	2	4	19	18	1.586E-01	1.4780	9.146E-01	9.398E-01
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Psychrobacter;s__	14	4	27	9	9.196E-02	0.9173	9.201E-01	9.398E-01
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__	30	9	471	314	6.942E-02	0.6382	9.134E-01	9.398E-01
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__caccae	5	2	23	32	1.235E-01	1.4600	9.326E-01	9.494E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus;s__flexus	5	3	30	13	1.062E-01	1.3136	9.356E-01	9.494E-01
k__Bacteria;p__Bacteroidetes;c__Cytophagia;o__Cytophagales;f__Cytophagaceae;g__Dyadobacter;s__	3	4	38	43	-1.031E-01	1.3281	9.381E-01	9.494E-01
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__[Weeksellaceae];g__Cloacibacterium;s__	44	9	349	236	3.330E-02	0.6085	9.564E-01	9.650E-01
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__;s__	18	5	72	33	3.569E-02	0.7851	9.637E-01	9.695E-01
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Nocardioidaceae;g__Propionicimonas;s__	7	7	423	69	-3.987E-02	0.9883	9.678E-01	9.707E-01
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__ovatus	7	4	219	65	5.892E-03	1.2341	9.962E-01	9.962E-01
k__Bacteria;p__[Thermi];c__Deinococci;o__Deinococcales;f__Deinococcaceae;g__CM44;s__	1	2	1	115	NA	NA	NA	NA
k__Bacteria;p__Acidobacteria;c__[Chloracidobacteria];o__DS-100;f__;g__;s__	1	6	1	434	NA	NA	NA	NA
k__Bacteria;p__Acidobacteria;c__[Chloracidobacteria];o__RB41;f__;g__;s__	0	3	0	74	NA	NA	NA	NA
k__Bacteria;p__Acidobacteria;c__Acidobacteria-6;o__CCU21;f__;g__;s__	1	3	6	30	NA	NA	NA	NA
k__Bacteria;p__Acidobacteria;c__Acidobacteria-6;o__iii1-15;f__mb2424;g__;s__	1	5	10	111	NA	NA	NA	NA
k__Bacteria;p__Acidobacteria;c__DA052;o__Ellin6513;f__;g__;s__	2	0	65	0	NA	NA	NA	NA

k__Bacteria;p__Acidobacteria;c__Holophagae;o__Holophagales;f__Holophagaceae;g__Geothrix;s__	0	2	0	40	NA	NA	NA	NA
k__Bacteria;p__Acidobacteria;c__Sva0725;o__Sva0725;f__;g__;s__	0	6	0	60	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__ACK-M1;g__;s__	0	3	0	144	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Mobiluncus;s__	7	1	133	1	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Geodermatophilaceae;g__Geodermatophilus;s__	5	0	11	0	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Intrasporangiaceae;g__Arsenicicoccus;s__	2	0	21	0	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Kineosporiaceae;g__Kineococcus;s__	3	0	73	0	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Kocuria;s__	4	1	8	2	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Nesterenkonia;s__	0	2	0	40	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Nocardiopsaceae;g__;s__	5	0	15	0	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Propionibacteriaceae;g__Luteococcus;s__	2	1	22	1	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Pseudonocardiaceae;g__Saccharopolyspora;s__	5	0	75	0	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Streptomycetaceae;g__Streptomyces;s__	6	0	40	0	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Williamsiaceae;g__Williamsia;s__	5	1	61	3	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;g__Slackia;s__	0	2	0	37	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__KIST-JJY010;o__;f__;g__;s__	1	2	2	80	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Rubrobacteria;o__Rubrobacterales;f__Rubrobacteraceae;g__Rubrobacter;s__	1	3	1	108	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Thermoleophilia;o__Gaiellales;f__;g__;s__	1	5	1	243	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Thermoleophilia;o__Gaiellales;f__AK1AB1_02E;g__;s__	1	4	8	79	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Thermoleophilia;o__Gaiellales;f__Gaiellaceae;g__;s__	4	1	37	26	NA	NA	NA	NA
k__Bacteria;p__Aquificae;c__Aquificae;o__Aquificales;f__Aquificaceae;g__;s__	4	1	45	2	NA	NA	NA	NA
k__Bacteria;p__Armatimonadetes;c__[Fimbriimonadia];o__[Fimbriimonadales];f__[Fimbriimonadaceae];g__Fimbriimonas;s__	5	0	21	0	NA	NA	NA	NA
k__Bacteria;p__Bacteroidetes;c__[Rhodothermi];o__[Rhodothermales];f__Rhodothermaceae;g__Rubricoccus;s__	0	2	0	724	NA	NA	NA	NA
k__Bacteria;p__Bacteroidetes;c__[Saprospirae];o__[Saprospirales];f__Chitinophagaceae;g__Segetibacter;s__	1	2	29	39	NA	NA	NA	NA
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__BA008;g__;s__	0	1	0	57	NA	NA	NA	NA
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__;s__	0	2	0	53	NA	NA	NA	NA
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Dysgonomonas;s__	5	1	93	1	NA	NA	NA	NA
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Tannerella;s__	3	0	43	0	NA	NA	NA	NA
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__S24-7;g__;s__	1	0	21	0	NA	NA	NA	NA
k__Bacteria;p__Bacteroidetes;c__Cytophagia;o__Cytophagales;f__Cytophagaceae;g__;s__	1	3	69	48	NA	NA	NA	NA
k__Bacteria;p__Bacteroidetes;c__Cytophagia;o__Cytophagales;f__Cytophagaceae;g__Rhodocytophaga;s__	1	0	78	0	NA	NA	NA	NA

k__Bacteria;p__Bacteroidetes;c__Cytophagia;o__Cytophagales;f__Cytophagaceae;g__Rudanella;s__	1	2	1	474	NA	NA	NA	NA
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Cryomorphaceae;g__Fluviicola;s__	1	0	22	0	NA	NA	NA	NA
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Flavobacteriaceae;g__;s__	1	3	22	101	NA	NA	NA	NA
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Flavobacteriaceae;g__Myroides;s__	2	0	27	0	NA	NA	NA	NA
k__Bacteria;p__Bacteroidetes;c__Sphingobacteriia;o__Sphingobacteriales;f__;g__;s__	1	1	44	137	NA	NA	NA	NA
k__Bacteria;p__Chlamydiae;c__Chlamydiia;o__Chlamydiales;f__Parachlamydiaceae;g__;s__	1	6	1	181	NA	NA	NA	NA
k__Bacteria;p__Chlamydiae;c__Chlamydiia;o__Chlamydiales;f__Parachlamydiaceae;g__CandidatusProtochlamydia;s__	1	1	3	644	NA	NA	NA	NA
k__Bacteria;p__Chlamydiae;c__Chlamydiia;o__Chlamydiales;f__Parachlamydiaceae;g__Parachlamydia;s__	0	1	0	22	NA	NA	NA	NA
k__Bacteria;p__Chlamydiae;c__Chlamydiia;o__Chlamydiales;f__Rhabdochlamydiaceae;g__CandidatusRhabdochlamydia;s__	0	1	0	97	NA	NA	NA	NA
k__Bacteria;p__Chlorobi;c__Ignavibacteria;o__Ignavibacteriales;f__Ignavibacteriaceae;g__;s__	0	1	0	71	NA	NA	NA	NA
k__Bacteria;p__Chloroflexi;c__;o__;f__;g__;s__	0	6	0	34	NA	NA	NA	NA
k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__A31;f__S47;g__;s__	0	4	0	49	NA	NA	NA	NA
k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__Anaerolineales;f__Anaerolinaceae;g__Anaerolinea;s__	1	0	26	0	NA	NA	NA	NA
k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__Caldilineales;f__Caldilineaceae;g__;s__	1	6	1	58	NA	NA	NA	NA
k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__Caldilineales;f__Caldilineaceae;g__Caldilinea;s__	1	7	1	346	NA	NA	NA	NA
k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__H39;f__;g__;s__	0	2	0	55	NA	NA	NA	NA
k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__SHA-20;f__;g__;s__	0	2	0	93	NA	NA	NA	NA
k__Bacteria;p__Chloroflexi;c__Chloroflexi;o__[Roseiflexales];f__[Kouleothrixaceae];g__Kouleothrix;s__	0	1	0	52	NA	NA	NA	NA
k__Bacteria;p__Chloroflexi;c__Chloroflexi;o__AKIW781;f__;g__;s__	2	0	40	0	NA	NA	NA	NA
k__Bacteria;p__Chloroflexi;c__TK10;o__AKYG885;f__Dolo_23;g__;s__	0	5	0	63	NA	NA	NA	NA
k__Bacteria;p__Chloroflexi;c__TK17;o__mle1-48;f__;g__;s__	0	4	0	88	NA	NA	NA	NA
k__Bacteria;p__Cyanobacteria;c__4C0d-2;o__SM1D11;f__;g__;s__	0	1	0	71	NA	NA	NA	NA
k__Bacteria;p__Cyanobacteria;c__4C0d-2;o__YS2;f__;g__;s__	1	5	1	117	NA	NA	NA	NA
k__Bacteria;p__Cyanobacteria;c__Chloroplast;o__Chlorophyta;f__Chlamydomonadaceae;g__;s__	0	2	0	74	NA	NA	NA	NA
k__Bacteria;p__Cyanobacteria;c__Oscillatoriophycideae;o__Chroococcales;f__;g__;s__	0	2	0	93	NA	NA	NA	NA
k__Bacteria;p__Cyanobacteria;c__Oscillatoriophycideae;o__Chroococcales;f__Cyanobacteriaceae;g__Cyanobacterium;s__	0	1	0	24	NA	NA	NA	NA
k__Bacteria;p__Cyanobacteria;c__Oscillatoriophycideae;o__Oscillatoriales;f__Phormidiaceae;g__Phormidium;s__	2	0	326	0	NA	NA	NA	NA
k__Bacteria;p__Cyanobacteria;c__Synechococcophycideae;o__Pseudanabaenales;f__;g__;s__	1	0	29	0	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__;o__;f__;g__;s__	2	0	26	0	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__;s__	11	1	75	77	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Listeriaceae;g__Brochothrix;s__	9	0	64	0	NA	NA	NA	NA

k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Paenibacillaceae;g__Aneurinibacillus;s__	1	1	1	31	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Sporosarcina;s__	4	1	5	4	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Salinicoccus;s__	2	0	27	0	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Gemellales;f__;g__;s__	16	0	32	0	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__;g__;s__	13	1	46	1	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Alkalibacterium;s__	7	0	294	0	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Trichococcus;s__	1	0	37	0	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Vagococcus;s__	5	0	6	0	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__;s__	6	0	390	0	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Pediococcus;s__	1	0	238	0	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Leuconostocaceae;g__Leuconostoc;s__	13	1	80	1	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Leuconostocaceae;g__Weissella;s__	4	1	9	3	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__;s__	1	2	1	46	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__;s__	3	0	35	0	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__Helcococcus;s__	5	1	54	2	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__ph2;s__	13	0	103	0	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Christensenellaceae;g__;s__	1	0	24	0	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Eubacteriaceae;g__Acetobacterium;s__	0	6	0	33	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Eubacteriaceae;g__Pseudoramibacter_Eubacterium;s__	0	4	0	88	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Shuttleworthia;s__	9	0	37	0	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__;s__	0	3	0	114	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Anaeromusa;s__	0	3	0	41	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Schwartzia;s__	1	1	5	69	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__vadinHB04;s__	0	1	0	34	NA	NA	NA	NA
k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales;f__;g__;s__	1	1	1	87	NA	NA	NA	NA
k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__u114;s__	0	5	0	17	NA	NA	NA	NA
k__Bacteria;p__Gemmatimonadetes;c__Gemm-1;o__;f__;g__;s__	0	1	0	43	NA	NA	NA	NA
k__Bacteria;p__Gemmatimonadetes;c__Gemm-3;o__;f__;g__;s__	2	0	48	0	NA	NA	NA	NA
k__Bacteria;p__Gemmatimonadetes;c__Gemmatimonadetes;o__;f__;g__;s__	1	0	18	0	NA	NA	NA	NA
k__Bacteria;p__Gemmatimonadetes;c__Gemmatimonadetes;o__Gemmatimonadales;f__;g__;s__	0	2	0	153	NA	NA	NA	NA
k__Bacteria;p__GN02;c__BD1-5;o__;f__;g__;s__	1	1	1	69	NA	NA	NA	NA

k__Bacteria;p__GN02;c__GKS2-174;o__;f__;g__;s__	0	1	0	26	NA	NA	NA	NA
k__Bacteria;p__Kazan-3B-28;c__;o__;f__;g__;s__	0	2	0	36	NA	NA	NA	NA
k__Bacteria;p__Nitrospirae;c__Nitrospira;o__Nitrospirales;f__Nitrospiraceae;g__Nitrospira;s__	1	3	1	447	NA	NA	NA	NA
k__Bacteria;p__OD1;c__;o__;f__;g__;s__	0	5	0	95	NA	NA	NA	NA
k__Bacteria;p__OD1;c__ABY1;o__;f__;g__;s__	0	1	0	41	NA	NA	NA	NA
k__Bacteria;p__OD1;c__SM2F11;o__;f__;g__;s__	0	1	0	176	NA	NA	NA	NA
k__Bacteria;p__OP11;c__WCHB1-64;o__d153;f__;g__;s__	1	1	19	30	NA	NA	NA	NA
k__Bacteria;p__Planctomycetes;c__C6;o__d113;f__;g__;s__	0	1	0	34	NA	NA	NA	NA
k__Bacteria;p__Planctomycetes;c__Phycisphaerae;o__Phycisphaerales;f__;g__;s__	1	0	25	0	NA	NA	NA	NA
k__Bacteria;p__Planctomycetes;c__Phycisphaerae;o__WD2101;f__;g__;s__	2	0	22	0	NA	NA	NA	NA
k__Bacteria;p__Planctomycetes;c__Planctomycetia;o__B97;f__;g__;s__	1	5	1	73	NA	NA	NA	NA
k__Bacteria;p__Planctomycetes;c__Planctomycetia;o__Gemmatales;f__Gemmataceae;g__;s__	0	3	0	299	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__BD7-3;f__;g__;s__	0	2	0	145	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Arthrospira;s__	4	1	5	4	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Bradyrhizobiaceae;g__Balneimonas;s__	7	0	23	0	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Brucellaceae;g__Ochrobactrum;s__	15	1	68	2	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__Parvibaculum;s__	1	0	71	0	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__Pedomicrobium;s__	0	3	0	49	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Methylocystaceae;g__;s__	5	0	36	0	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Jannaschia;s__	0	2	0	32	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Rhodobacter;s__	1	6	1	57	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Acetobacteraceae;g__Roseococcus;s__	1	3	1	110	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Rhodospirillaceae;g__Azospirillum;s__	1	3	2	71	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rickettsiales;f__mitochondria;g__;s__	17	0	555	0	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rickettsiales;f__Rickettsiaceae;g__;s__	1	5	1	131	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Zymomonas;s__	0	3	0	40	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__;f__;g__;s__	0	1	0	40	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__ASSO-13;f__;g__;s__	1	4	1	103	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__;g__;s__	0	3	0	64	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__;s__	0	2	0	33	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Variovorax;s__	5	0	9	0	NA	NA	NA	NA

k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Ellin6067;f__;g__;s__	0	3	0	23	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Hydrogenophilales;f__Hydrogenophilaceae;g__Thiobacillus;s__	9	1	43	7	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Neisseriales;f__Neisseriaceae;g__Microvirgula;s__	0	2	0	42	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Nitrosomonadales;f__Nitrosomonadaceae;g__;s__	1	4	1	145	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Procabacteriales;f__Procabacteriaceae;g__;s__	1	4	1	377	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__Rhodocyclaceae;g__C39;s__	0	3	0	51	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__Rhodocyclaceae;g__Hydrogenophilus;s__	9	0	61	0	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__SC-I-84;f__;g__;s__	0	6	0	232	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__;f__;g__;s__	0	2	0	143	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Bdellovibrionales;f__Bacteriovoracaceae;g__;s__	4	1	64	73	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfobacterales;f__Desulfobulbaceae;g__Desulfobulbus;s__	1	2	11	65	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__FAC87;f__;g__;s__	0	1	0	38	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__MIZ46;f__;g__;s__	0	1	0	30	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__OM27;g__;s__	3	0	20	0	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__Polyangiaceae;g__;s__	0	2	0	137	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__NB1-j;f__JTB38;g__;s__	0	1	0	37	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__NKB15;f__;g__;s__	0	3	0	28	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Spirobacillales;f__;g__;s__	0	3	0	1918	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Syntrophobacterales;f__Syntrophaceae;g__Desulfomonile;s__	0	3	0	39	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Syntrophobacterales;f__Syntrophorhabdaceae;g__;s__	0	1	0	23	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria;o__Campylobacterales;f__Campylobacteraceae;g__Sulfurospirillum;s__	0	3	0	42	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria;o__Campylobacterales;f__Helicobacteraceae;g__;s__	1	2	1	24	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__;f__;g__;s__	4	0	27	0	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Aeromonadales;f__Aeromonadaceae;g__Tolumonas;s__	1	2	7	194	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__[Chromatiaceae];g__;s__	6	0	9	0	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__OM60;g__;s__	0	1	0	21	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Chromatiales;f__Chromatiaceae;g__Allochromatium;s__	0	1	0	116	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Chromatiales;f__Halothiobacillaceae;g__Thiovirga;s__	0	1	0	123	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Buchnera;s__	1	0	29	0	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__	10	0	26	0	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Yersinia;s__	6	0	9	0	NA	NA	NA	NA

k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__HOC36;f__;g__;s__	0	2	0	888	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Legionellales;f__;g__;s__	1	7	5	1471	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Legionellales;f__Coxiellaceae;g__;s__	0	5	0	326	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Legionellales;f__Coxiellaceae;g__Aquicella;s__	1	7	6	1922	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Legionellales;f__Francisellaceae;g__;s__	0	1	0	23	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Legionellales;f__Legionellaceae;g__Legionella;s__	1	5	1	479	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Legionellales;f__Legionellaceae;g__Tatlockia;s__	0	1	0	32	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Methylococcales;f__Methylococcaceae;g__Methylocaldum;s__	0	2	0	197	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Oceanospirillales;f__Halomonadaceae;g__;s__	1	0	62	0	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Thiotrichales;f__Thiotrichaceae;g__Thiothrix;s__	0	3	0	37	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Vibrionales;f__Vibrionaceae;g__Photobacterium;s__	5	0	73	0	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Luteimonas;s__	3	0	35	0	NA	NA	NA	NA
k__Bacteria;p__Spirochaetes;c__Spirochaetes;o__Sphaerochaetales;f__Sphaerochaetaceae;g__Sphaerochaeta;s__	0	2	0	140	NA	NA	NA	NA
k__Bacteria;p__TM6;c__SJA-4;o__S1198;f__;g__;s__	0	4	0	112	NA	NA	NA	NA
k__Bacteria;p__TM7;c__TM7-3;o__CW040;f__;g__;s__	6	1	99	2	NA	NA	NA	NA
k__Bacteria;p__TM7;c__TM7-3;o__I025;f__;g__;s__	1	1	1	185	NA	NA	NA	NA
k__Bacteria;p__Verrucomicrobia;c__[Spartobacteria];o__[Chthoniobacterales];f__[Chthoniobacteraceae];g__DA101;s__	1	0	47	0	NA	NA	NA	NA
k__Bacteria;p__WS3;c__PRR-12;o__Sediment-1;f__PRR-10;g__;s__	0	1	0	23	NA	NA	NA	NA
k__Bacteria;p__WS6;c__SC72;o__WCHB1-15;f__;g__;s__	0	3	0	29	NA	NA	NA	NA
k__Bacteria;p__Chlamydiae;c__Chlamydiia;o__Chlamydiales;f__Parachlamydiaceae;g__Parachlamydia;s__acanthamoebae	0	2	0	133	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Peptostreptococcus;s__anaerobius	5	0	17	0	NA	NA	NA	NA
k__Bacteria;p__Synergistetes;c__Synergistia;o__Synergistales;f__Dethiosulfovibrionaceae;g__Jonquetella;s__anthropi	1	0	65	0	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Mycobacteriaceae;g__Mycobacterium;s__arupense	1	3	1	25	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Bdellovibrionales;f__Bdellovibrionaceae;g__Bdellovibrio;s__bacteriovorus	0	1	0	78	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Corynebacteriaceae;g__Corynebacterium;s__bovis	2	0	22	0	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Lysobacter;s__brunescens	0	2	0	104	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Neisseriales;f__Neisseriaceae;g__Neisseria;s__cinerea	1	2	10	39	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Oxalobacteraceae;g__Polynucleobacter;s__cosmopolitanus	0	2	0	139	NA	NA	NA	NA
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Parabacteroides;s__distasonis	5	1	15	7	NA	NA	NA	NA
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Porphyromonas;s__endodontalis	10	1	42	2	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Actinomyces;s__europaeus	4	1	74	15	NA	NA	NA	NA

k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Flavobacteriaceae;g__Flavobacterium;s__frigidarium	6	0	7	0	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Haemophilus;s__influenzae	6	0	748	0	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Microbacteriaceae;g__Agrococcus;s__jenensis	9	1	19	14	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Rhizobium;s__leguminosarum	13	0	333	0	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Leuconostocaceae;g__Leuconostoc;s__mesenteroides	7	1	18	68	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Methylophilales;f__Methylophilaceae;g__Methylotenera;s__mobilis	1	6	3	535	NA	NA	NA	NA
k__Bacteria;p__Verrucomicrobia;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Verrucomicrobiaceae;g__Akkermansia;s__muciniphila	1	4	1	9	NA	NA	NA	NA
k__Bacteria;p__Bacteroidetes;c__Sphingobacteriia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Sphingobacterium;s__multivorum	15	1	130	4	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Alloiococcus;s__otitis	6	0	46	0	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Kocuria;s__palustris	5	1	8	2	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Staphylococcus;s__pettenkoferi	6	0	15	0	NA	NA	NA	NA
k__Bacteria;p__Synergistetes;c__Synergistia;o__Synergistales;f__Dethiosulfovibrionaceae;g__Pyramidobacter;s__piscolens	0	1	0	70	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Arthrobacter;s__psychrolactophilus	5	1	22	2	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Jeotgalicoccus;s__psychrophilus	8	0	33	0	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Marinilactibacillus;s__psychrotolerans	2	0	44	0	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__rhizosphaerae	29	1	184	2	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Microbispora;s__rosea	10	1	76	91	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__schindleri	5	0	193	0	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Staphylococcus;s__sciuri	11	1	43	79	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus;s__selenatarsenatis	8	0	85	0	NA	NA	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__sobrinus	2	1	72	1	NA	NA	NA	NA
k__Bacteria;p__Spirochaetes;c__Spirochaetes;o__Spirochaetales;f__Spirochaetaceae;g__Treponema;s__socranskii	1	2	1	33	NA	NA	NA	NA
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Flavobacteriaceae;g__Flavobacterium;s__succinicans	10	1	17	2	NA	NA	NA	NA
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Corynebacteriaceae;g__Corynebacterium;s__variabile	15	1	102	1	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingomonas;s__wittichii	5	0	111	0	NA	NA	NA	NA
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingomonas;s__yabuuchiae	3	1	22	30	NA	NA	NA	NA

eTable 2. Association of Taxa Abundance With Composite Infectious Outcome

taxa	rank cluster	rank infection	infection q-value	infection OR	infection lower 95	infection upper 95
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Aggregatibacter;s__segnis	177	1	1.148E-03	1.610	1.336	1.986
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Moraxella;s__	19	2	1.302E-03	1.162	1.091	1.240
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__;f__;g__;s__	269	3	4.397E-03	0.741	0.641	0.848
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Salmonella;s__	111	4	5.636E-03	1.626	1.305	2.086
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Jeotgalicoccus;s__	142	5	1.055E-02	1.320	1.151	1.530
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Propionibacteriaceae;g__;s__	189	6	1.055E-02	1.417	1.190	1.702
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__[Paraprevotellaceae];g__[Prevotella];s__	153	7	1.055E-02	1.269	1.124	1.437
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__;s__	307	8	1.284E-02	0.454	0.284	0.659
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Variovorax;s__paradoxus	303	9	1.284E-02	1.410	1.182	1.703
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptococcaceae;g__Peptococcus;s__	131	10	1.302E-02	1.594	1.255	2.081
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Propionibacteriaceae;g__Propionibacterium;s__acnes	253	11	1.302E-02	0.818	0.732	0.910
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Oxalobacteraceae;g__Janthinobacterium;s__lividum	311	12	1.302E-02	1.277	1.121	1.461
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Haemophilus;s__	119	13	1.328E-02	1.158	1.072	1.258
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Propionibacteriaceae;g__Propionibacterium;s__granulosum	51	14	1.557E-02	0.706	0.580	0.854
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__;s__	93	15	1.629E-02	0.774	0.666	0.888
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Flavobacteriaceae;g__Capnocytophaga;s__ochracea	197	16	1.629E-02	2.563	1.603	4.809
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__Finegoldia;s__	132	17	1.629E-02	0.866	0.798	0.939
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Morganella;s__	194	18	1.629E-02	0.743	0.622	0.871
k__Bacteria;p__Cyanobacteria;c__Chloroplast;o__Streptophyta;f__;g__;s__	316	19	1.931E-02	1.160	1.066	1.265
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Novosphingobium;s__	33	20	2.017E-02	0.719	0.586	0.863
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__Anaerococcus;s__	56	21	2.017E-02	0.864	0.792	0.940
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Bradyrhizobiaceae;g__Bosea;s__genosp.	285	22	2.067E-02	0.607	0.440	0.794
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__;s__	231	23	2.091E-02	0.839	0.755	0.929
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Brevibacteriaceae;g__Brevibacterium;s__	314	24	2.298E-02	1.236	1.090	1.405
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Propionibacteriaceae;g__Propionibacterium;s__	18	25	2.298E-02	0.862	0.788	0.941
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfobacterales;f__Desulfobulbaceae;g__Desulfobulbus;s__	476	26	2.395E-02	2.068	1.466	3.868
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Geodermatophilaceae;g__Modestobacter;s__	263	27	2.484E-02	0.484	0.290	0.714
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Phyllobacteriaceae;g__Phyllobacterium;s__	274	28	2.484E-02	1.285	1.105	1.502
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__;s__	184	29	2.484E-02	0.449	0.252	0.686

k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Facklamia;s__	179	30	2.861 E-02	1.252	1.090	1.440
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Aerococcus;s__	315	31	2.960 E-02	0.565	0.376	0.777
k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__u114;s__	429	32	2.960 E-02	0.266	0.098	0.541
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Actinobacillus;s__parahaemolyticus	276	33	3.403 E-02	1.435	1.156	1.839
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Scardovia;s__	145	34	3.784 E-02	1.361	1.126	1.684
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;g__Atopobium;s__	40	35	3.794 E-02	1.190	1.064	1.332
k__Bacteria;p__Synergistetes;c__Synergistia;o__Synergistales;f__Synergistaceae;g__vadinCA02;s__	165	36	3.866 E-02	0.341	0.131	0.596
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Catonella;s__	139	37	3.866 E-02	1.415	1.148	1.822
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Paracoccus;s__	160	38	4.210 E-02	1.211	1.068	1.375
k__Bacteria;p__Firmicutes;c__Erysipelotrichi;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Bulleidia;s__	76	39	4.210 E-02	1.261	1.086	1.479
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Staphylococcus;s__aureus	239	40	4.244 E-02	0.834	0.738	0.939
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__Parvimonas;s__	16	41	4.453 E-02	1.168	1.053	1.296
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__Shewanellaceae;g__Shewanella;s__	260	42	4.794 E-02	0.618	0.432	0.834
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__;g__;s__	408	43	4.833 E-02	0.281	0.099	0.577
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Sporosarcina;s__	405	44	5.180 E-02	2.036	1.337	3.718
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Staphylococcus;s__sciuri	546	45	5.379 E-02	1.501	1.170	2.089
k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__A31;f__S47;g__;s__	384	46	5.837 E-02	1.761	1.216	2.730
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Kocuria;s__	349	47	5.837 E-02	2.655	1.450	6.058
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__;s__	402	48	5.837 E-02	1.459	1.148	1.981
k__Bacteria;p__SR1;c__;o__;f__;g__;s__	247	49	6.181 E-02	1.430	1.116	1.862
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Mycobacteriaceae;g__Mycobacterium;s__arupense	519	50	6.181 E-02	2.526	1.406	5.334
k__Bacteria;p__Spirochaetes;c__Spirochaetes;o__Spirochaetales;f__Spirochaetaceae;g__Treponema;s__socranskii	549	51	6.181 E-02	1.622	1.195	2.451
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Hydrogenophaga;s__	147	52	6.340 E-02	0.678	0.495	0.868
k__Bacteria;p__Bacteroidetes;c__Sphingobacteriia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Sphingobacterium;s__	20	53	6.436 E-02	0.630	0.420	0.837
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__;s__	35	54	6.436 E-02	0.845	0.745	0.950
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__Gallicola;s__	181	55	6.436 E-02	1.280	1.078	1.548
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Propionibacteriaceae;g__Microlunatus;s__	262	56	6.436 E-02	0.589	0.384	0.835
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__;g__;s__	101	57	6.788 E-02	1.351	1.089	1.695
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Phascolarctobacterium;s__	257	58	7.066 E-02	0.379	0.159	0.679
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Kocuria;s__palustris	537	59	7.110 E-02	2.285	1.304	4.584
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Microbispora;s__rosea	544	60	7.110 E-02	1.394	1.112	1.842

k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;g__Slackia;s__	356	61	7.137E-02	1.885	1.298	3.609
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella;s__copri	243	62	7.287E-02	0.665	0.473	0.875
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__	208	63	8.260E-02	0.841	0.737	0.958
k__Bacteria;p__Planctomycetes;c__Planctomycetia;o__Gemmatales;f__Gemmataceae;g__;s__	446	64	8.548E-02	1.469	1.117	2.027
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Limnohabitans;s__	135	65	1.003E-01	0.759	0.602	0.929
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Corynebacteriaceae;g__Corynebacterium;s__durum	183	66	1.015E-01	1.170	1.035	1.325
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella;s__nanceiensis	174	67	1.029E-01	1.256	1.050	1.505
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella;s__intermedia	171	68	1.029E-01	1.310	1.068	1.650
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Eubacteriaceae;g__Pseudoramibacter_Eubacterium;s__	422	69	1.034E-01	1.366	1.084	1.803
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Nocardioidaceae;g__Propionicimonas;s__	334	70	1.140E-01	0.615	0.398	0.872
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Burkholderia;s__	198	71	1.143E-01	1.164	1.031	1.318
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__;s__	297	72	1.172E-01	1.135	1.026	1.260
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__ASSO-13;f__;g__;s__	462	73	1.197E-01	0.542	0.303	0.837
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__Helcococcus;s__	418	74	1.197E-01	1.732	1.150	2.873
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Nocardiaceae;g__Rhodococcus;s__fascians	275	75	1.201E-01	0.476	0.238	0.820
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__[Ruminococcus];s__	190	76	1.201E-01	0.720	0.539	0.928
k__Bacteria;p__Actinobacteria;c__Thermoleophilia;o__Solirubrobacterales;f__Solirubrobacteraceae;g__;s__	180	77	1.213E-01	0.456	0.191	0.763
k__Bacteria;p__Acidobacteria;c__[Chloracidobacteria];o__DS-100;f__;g__;s__	337	78	1.216E-01	1.249	1.042	1.508
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Agrobacterium;s__	81	79	1.216E-01	0.875	0.780	0.974
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingomonas;s__echinoides	129	80	1.216E-01	0.878	0.786	0.975
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__longum	36	81	1.216E-01	0.804	0.661	0.952
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rickettsiales;f__Rickettsiaceae;g__;s__	459	82	1.216E-01	0.632	0.410	0.891
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Psychrobacter;s__	327	83	1.216E-01	0.629	0.403	0.887
k__Bacteria;p__[Thermi];c__Deinococci;o__Thermales;f__Thermaceae;g__Thermus;s__	313	84	1.278E-01	0.870	0.772	0.976
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Carnobacterium;s__	125	85	1.356E-01	0.761	0.592	0.945
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingopyxis;s__	71	86	1.356E-01	1.253	1.037	1.529
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__anginosus	114	87	1.396E-01	1.143	1.019	1.283
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Yaniellaceae;g__Yaniella;s__	215	88	1.485E-01	1.529	1.071	2.278
k__Bacteria;p__Cyanobacteria;c__Oscillatoriophycideae;o__Chroococcales;f__Xenococcaceae;g__;s__	293	89	1.508E-01	1.159	1.019	1.320
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Megamonas;s__	137	90	1.515E-01	0.581	0.284	0.831
k__Bacteria;p__Actinobacteria;c__Rubrobacteria;o__Rubrobacterales;f__Rubrobacteraceae;g__Rubrobacter;s__	358	91	1.515E-01	1.325	1.038	1.710

k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Delftia;s__	170	92	1.515E-01	1.121	1.016	1.242
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__;g__;s__	2	93	1.558E-01	1.113	1.013	1.224
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__[Ruminococcus];s__gnavus	217	94	1.580E-01	1.427	1.078	2.069
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Nitrosomonadales;f__Nitrosomonadaceae;g__;s__	469	95	1.598E-01	1.501	1.074	2.268
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__viridiflava	220	96	1.617E-01	0.889	0.798	0.985
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__	302	97	1.617E-01	1.125	1.013	1.251
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Leuconostocaceae;g__Leuconostoc;s__mesenteroides	532	98	1.686E-01	1.491	1.087	2.336
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Kaistobacter;s__	113	99	1.722E-01	0.864	0.754	0.983
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__;g__;s__	58	100	1.796E-01	0.845	0.718	0.980
k__Bacteria;p__Kazan-3B-28;c__;o__;f__;g__;s__	436	101	1.796E-01	0.744	0.545	0.951
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Neisseriales;f__Neisseriaceae;g__Neisseria;s__subflava	228	102	1.894E-01	1.367	1.026	1.857
k__Bacteria;p__TM7;c__TM7-3;o__EW055;f__;g__;s__	134	103	1.894E-01	0.844	0.712	0.980
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Dorea;s__	309	104	1.911E-01	1.338	1.022	1.775
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Veillonella;s__	277	105	1.981E-01	1.194	1.010	1.415
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Actinomyces;s__europaeus	527	106	1.981E-01	1.330	1.025	1.784
k__Bacteria;p__Actinobacteria;c__Thermoleophilia;o__Gaiellales;f__Gaiellaceae;g__;s__	361	107	2.070E-01	1.550	1.065	2.613
k__Bacteria;p__Actinobacteria;c__Thermoleophilia;o__Gaiellales;f__AK1AB1_02E;g__;s__	360	108	2.070E-01	1.417	1.021	2.017
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Staphylococcus;s__	202	109	2.105E-01	0.884	0.784	0.995
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Aggregatibacter;s__	196	110	2.110E-01	1.186	1.005	1.399
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Nesterenkonia;s__	350	111	2.145E-01	1.244	1.010	1.557
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__Rhodocyclaceae;g__Zoogloea;s__	128	112	2.158E-01	1.288	1.009	1.664
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Ellin6067;f__;g__;s__	466	113	2.158E-01	3.223	1.340	12.749
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Micrococcus;s__luteus	169	114	2.220E-01	1.277	1.004	1.630
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Erwinia;s__	321	115	2.244E-01	0.779	0.599	0.984
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Phenylobacterium;s__	310	116	2.251E-01	0.556	0.270	0.905
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__zeae	158	117	2.258E-01	1.390	1.022	2.018
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__;s__	221	118	2.258E-01	0.893	0.798	0.999
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Dermabacteraceae;g__Brachybacterium;s__conglomeratum	265	119	2.293E-01	0.833	0.687	0.993
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Mogibacteriaceae];g__;s__	205	120	2.293E-01	1.222	1.001	1.502
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Dysgonomonas;s__	368	121	2.322E-01	1.912	1.076	4.045
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Microbacteriaceae;g__Microbacterium;s__	23	122	2.322E-01	0.910	0.825	0.999

k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Dietziaceae;g__;s__	305	123	2.322E-01	0.595	0.295	0.903
k__Bacteria;p__Chloroflexi;c__;o__;f__;g__;s__	383	124	2.322E-01	1.402	0.997	1.988
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Leuconostocaceae;g__Leuconostoc;s__	414	125	2.334E-01	0.286	0.047	0.715
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Zymomonas;s__	460	126	2.350E-01	1.427	0.997	2.090
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Comamonas;s__	216	127	2.350E-01	0.808	0.638	0.991
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Dermabacteraceae;g__Dermabacter;s__	244	128	2.350E-01	0.828	0.676	0.996
k__Bacteria;p__Firmicutes;c__Erysipelotrichi;o__Erysipelotrichales;f__Erysipelotrichaceae;g__[Eubacterium];s__biforme	319	129	2.390E-01	0.437	0.146	0.886
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingomonas;s__	57	130	2.390E-01	0.920	0.844	1.001
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Acidovorax;s__	199	131	2.459E-01	1.308	0.997	1.766
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Staphylococcus;s__epidermidis	214	132	2.532E-01	0.870	0.751	1.005
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Microbacteriaceae;g__Rathayibacter;s__caricis	192	133	2.633E-01	0.841	0.688	0.997
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Stenotrophomonas;s__	55	134	2.663E-01	0.825	0.670	1.010
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Psychrobacter;s__sanguinis	308	135	2.663E-01	0.604	0.313	0.958
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Actinobaculum;s__	324	136	2.668E-01	1.285	0.987	1.703
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__[Weeksellaceae];g__Elizabethkingia;s__meningoseptica	154	137	2.703E-01	0.833	0.675	1.002
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Mogibacteriaceae];g__Mogibacterium;s__	271	138	2.703E-01	1.427	0.975	2.120
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Porphyromonas;s__endodontalis	526	139	2.726E-01	1.508	0.979	2.430
k__Bacteria;p__Firmicutes;c__Bacilli;o__Gemellales;f__;g__;s__	407	140	2.732E-01	0.468	0.167	0.923
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__[Weeksellaceae];g__;s__	148	141	2.745E-01	1.183	0.986	1.425
k__Bacteria;p__Acidobacteria;c__Acidobacteria-6;o__CCU21;f__;g__;s__	339	142	2.755E-01	1.549	0.989	2.671
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Cardiobacteriales;f__Cardiobacteriaceae;g__Cardiobacterium;s__	241	143	2.780E-01	0.426	0.106	0.852
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Microbacteriaceae;g__;s__	9	144	2.904E-01	0.925	0.846	1.005
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__[Paraprevotellaceae];g__[Prevotella];s__tannerae	259	145	2.909E-01	1.193	0.981	1.458
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__;s__	83	146	2.981E-01	0.832	0.676	1.020
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Syntrophobacterales;f__Syntrophobacteraceae;g__;s__	175	147	2.986E-01	1.332	0.969	1.863
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella;s__nigrescens	295	148	3.009E-01	1.194	0.977	1.461
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Alcaligenaceae;g__Achromobacter;s__	287	149	3.070E-01	0.910	0.817	1.012
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__fragi	157	150	3.070E-01	1.093	0.989	1.209
k__Bacteria;p__Chloroflexi;c__Thermomicrobia;o__JG30-KF-CM45;f__;g__;s__	3	151	3.141E-01	1.081	0.988	1.182
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__;s__	236	152	3.168E-01	1.261	0.964	1.652
k__Bacteria;p__Verrucomicrobia;c__[Spartobacteria];o__[Chthoniobacterales];f__[Chthoniobacteraceae];g__CandidatusXiphinematobacter;s__	151	153	3.168E-01	0.868	0.726	1.011

k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;s__	242	154	3.186E-01	0.665	0.352	0.970
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;g__Collinsella;s__aerofaciens	296	155	3.198E-01	0.843	0.683	1.018
k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria;o__Campylobacterales;f__Campylobacteraceae;g__Campylobacter;s__	323	156	3.296E-01	0.916	0.826	1.013
k__Bacteria;p__[Thermi];c__Deinococci;o__Deinococcales;f__Deinococcaceae;g__Deinococcus;s__	22	157	3.296E-01	1.073	0.988	1.165
k__Bacteria;p__WPS-2;c__;o__;f__;g__;s__	240	158	3.296E-01	0.799	0.594	1.017
k__Bacteria;p__Bacteroidetes;c__Cytophagia;o__Cytophagales;f__Cytophagaceae;g__;s__	371	159	3.296E-01	1.264	0.959	1.680
k__Bacteria;p__Verrucomicrobia;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Verrucomicrobiaceae;g__Akkermansia;s__muciniphila	534	160	3.296E-01	0.572	0.279	1.060
k__Bacteria;p__Synergistetes;c__Synergistia;o__Synergistales;f__Dethiosulfovibrionaceae;g__TG5;s__	62	161	3.296E-01	1.182	0.971	1.452
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Thiotrichales;f__Thiotrichaceae;g__Thiothrix;s__	506	162	3.394E-01	0.815	0.625	1.024
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella;s__melaninogenica	82	163	3.425E-01	1.073	0.986	1.167
k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__Caldilineales;f__Caldilineaceae;g__;s__	386	164	3.436E-01	1.254	0.954	1.645
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__;s__	52	165	3.441E-01	1.072	0.986	1.166
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Sanguibacteraceae;g__Sanguibacter;s__	224	166	3.454E-01	0.810	0.616	1.030
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rickettsiales;f__mitochondria;g__;s__	458	167	3.454E-01	0.658	0.354	1.007
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Microbacteriaceae;g__Agrococcus;s__jenensis	530	168	3.486E-01	0.335	0.045	0.851
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Oxalobacteraceae;g__;s__	7	169	3.489E-01	1.071	0.986	1.165
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__rhizosphaerae	543	170	3.517E-01	0.785	0.564	1.031
k__Bacteria;p__TM6;c__SJA-4;o__S1198;f__;g__;s__	510	171	3.517E-01	1.380	0.946	2.142
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Rhizobium;s__leguminosarum	531	172	3.582E-01	0.606	0.253	0.963
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Serratia;s__marcescens	204	173	3.694E-01	0.676	0.366	1.000
k__Bacteria;p__Bacteroidetes;c__Sphingobacteriia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__;s__	90	174	3.704E-01	0.894	0.771	1.023
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Kocuria;s__rhizophila	322	175	3.752E-01	1.077	0.981	1.182
k__Bacteria;p__Acidobacteria;c__Acidobacteria-6;o__iii1-15;f__mb2424;g__;s__	340	176	3.752E-01	1.241	0.944	1.638
k__Bacteria;p__Chloroflexi;c__TK10;o__AKYG885;f__Dolo_23;g__;s__	392	177	3.752E-01	1.287	0.933	1.778
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__;s__	464	178	3.855E-01	0.826	0.633	1.038
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Methylobacteriaceae;g__Methylobacterium;s__	261	179	3.855E-01	0.904	0.792	1.026
k__Bacteria;p__Cyanobacteria;c__Oscillatoriophycideae;o__Chroococcales;f__;g__;s__	397	180	3.858E-01	1.245	0.938	1.664
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Legionellales;f__;g__;s__	498	181	3.858E-01	0.895	0.771	1.026
k__Bacteria;p__Cyanobacteria;c__Chloroplast;o__Chlorophyta;f__Trebouxiophyceae;g__;s__	61	182	3.858E-01	0.934	0.849	1.015
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Haemophilus;s__parainfluenzae	188	183	3.858E-01	0.919	0.820	1.021
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__[Exiguobacteraceae];g__Exiguobacterium;s__	15	184	3.858E-01	1.085	0.976	1.205

k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__reuteri	264	185	3.858E-01	1.149	0.959	1.381
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__Devosia;s__	286	186	3.858E-01	0.904	0.790	1.027
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Microbacteriaceae;g__Salinibacterium;s__	108	187	3.858E-01	0.926	0.834	1.019
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Tepidimonas;s__	159	188	3.858E-01	0.860	0.699	1.037
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Oxalobacteraceae;g__Cupriavidus;s__	294	189	3.879E-01	0.852	0.682	1.040
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;g__;s__	96	190	4.046E-01	1.097	0.969	1.239
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;g__;s__	42	191	4.226E-01	0.912	0.800	1.028
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Neisseriales;f__Neisseriaceae;g__Neisseria;s__	138	192	4.235E-01	1.066	0.977	1.163
k__Bacteria;p__Cyanobacteria;c__4C0d-2;o__MLE1-12;f__;g__;s__	218	193	4.421E-01	1.067	0.976	1.166
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Spirobacillales;f__;g__;s__	483	194	4.421E-01	0.921	0.816	1.025
k__Bacteria;p__TM7;c__TM7-3;o__CW040;f__F16;g__;s__	281	195	4.421E-01	1.185	0.935	1.511
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella;s__	279	196	4.421E-01	1.067	0.975	1.168
k__Bacteria;p__TM7;c__TM7-3;o__CW040;f__;g__;s__	511	197	4.421E-01	0.597	0.214	1.038
k__Bacteria;p__OD1;c__;o__;f__;g__;s__	438	198	4.421E-01	0.866	0.701	1.048
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__;g__;s__	463	199	4.435E-01	1.353	0.893	2.163
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Faecalibacterium;s__prausnitzii	107	200	4.451E-01	1.112	0.956	1.291
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Coprococcus;s__	121	201	4.451E-01	1.319	0.896	2.000
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Dialister;s__	156	202	4.457E-01	0.927	0.830	1.029
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__Rhodocyclaceae;g__;s__	63	203	4.457E-01	0.869	0.705	1.051
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Corynebacteriaceae;g__Corynebacterium;s__	238	204	4.595E-01	0.940	0.860	1.027
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__SMB53;s__	11	205	4.595E-01	1.072	0.969	1.185
k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria;o__Campylobacterales;f__Helicobacteraceae;g__;s__	487	206	4.595E-01	1.240	0.907	1.699
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Methylophilales;f__Methylophilaceae;g__Methylotenera;s__mobilis	533	207	4.595E-01	1.134	0.944	1.360
k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__SHA-20;f__;g__;s__	389	208	4.662E-01	1.211	0.913	1.611
k__Bacteria;p__Bacteroidetes;c__[Saprospirae];o__[Saprospirales];f__Saprospiraceae;g__;s__	235	209	4.662E-01	1.186	0.923	1.524
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Geobacillus;s__	191	210	4.668E-01	1.086	0.962	1.225
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Eubacteriaceae;g__Acetobacterium;s__	421	211	4.676E-01	1.282	0.887	1.847
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Rhodospirillaceae;g__;s__	64	212	4.714E-01	1.080	0.964	1.208
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Nocardioidaceae;g__Friedmanniella;s__	144	213	4.714E-01	0.789	0.540	1.095
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Brucellaceae;g__Ochrobactrum;s__	450	214	4.714E-01	0.677	0.342	1.122
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Geodermatophilaceae;g__;s__	100	215	4.714E-01	0.912	0.793	1.042

k__Bacteria;p__Chlamydiae;c__Chlamydiia;o__Chlamydiales;f__Parachlamydiaceae;g__;s__	378	216	4.714E-01	1.162	0.927	1.454
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Rothia;s__mucilaginosa	110	217	4.714E-01	1.055	0.974	1.143
k__Bacteria;p__Bacteroidetes;c__[Saprospirae];o__[Saprospirales];f__Chitinophagaceae;g__Sediminibacterium;s__	223	218	4.734E-01	0.936	0.848	1.032
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Neisseriales;f__Neisseriaceae;g__Neisseria;s__cinerea	523	219	4.791E-01	1.210	0.907	1.631
k__Bacteria;p__Acidobacteria;c__Sva0725;o__Sva0725;f__;g__;s__	343	220	4.849E-01	1.225	0.898	1.667
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Parabacteroides;s__distasonis	525	221	4.853E-01	0.607	0.210	1.097
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus;s__flexus	330	222	4.880E-01	0.800	0.534	1.079
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Legionellales;f__Legionellaceae;g__Legionella;s__	502	223	5.019E-01	1.140	0.929	1.397
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Vibrionales;f__Pseudoalteromonadaceae;g__Pseudoalteromonas;s__	168	224	5.132E-01	1.108	0.942	1.303
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Anoxybacillus;s__kestanbolensis	54	225	5.138E-01	0.912	0.788	1.051
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Microbacteriaceae;g__Leucobacter;s__	176	226	5.138E-01	0.905	0.768	1.051
k__Bacteria;p__Chloroflexi;c__Ellin6529;o__;f__;g__;s__	282	227	5.138E-01	1.185	0.904	1.547
k__Bacteria;p__Chlamydiae;c__Chlamydiia;o__Chlamydiales;f__Parachlamydiaceae;g__Parachlamydia;s__acanthamoebae	516	228	5.138E-01	1.176	0.907	1.523
k__Bacteria;p__Cyanobacteria;c__4C0d-2;o__YS2;f__;g__;s__	395	229	5.250E-01	1.196	0.895	1.597
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Citrobacter;s__	495	230	5.350E-01	0.607	0.221	1.211
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rickettsiales;f__;g__;s__	29	231	5.376E-01	0.908	0.769	1.055
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Dermacoccaceae;g__Dermacoccus;s__	166	232	5.376E-01	1.122	0.928	1.355
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Parabacteroides;s__	249	233	5.388E-01	0.710	0.344	1.130
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__1-68;s__	207	234	5.391E-01	1.081	0.950	1.227
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Phyllobacteriaceae;g__Mesorhizobium;s__	133	235	5.391E-01	1.116	0.930	1.333
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Variovorax;s__	465	236	5.391E-01	1.944	0.673	7.018
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Flavobacteriaceae;g__Flavobacterium;s__succinicans	550	237	5.391E-01	1.360	0.813	2.274
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Phyllobacteriaceae;g__;s__	87	238	5.394E-01	1.108	0.935	1.309
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__	306	239	5.411E-01	0.937	0.840	1.044
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__	320	240	5.411E-01	0.907	0.767	1.059
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__;s__	78	241	5.440E-01	0.941	0.851	1.041
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__;f__;g__;s__	474	242	5.440E-01	1.242	0.864	1.854
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__ovatus	335	243	5.440E-01	1.164	0.899	1.507
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Pseudonocardiaceae;g__Pseudonocardia;s__	209	244	5.449E-01	1.215	0.872	1.700
k__Bacteria;p__Actinobacteria;c__Thermoleophilia;o__Solirubrobacterales;f__;g__;s__	6	245	5.449E-01	1.052	0.965	1.146
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Hydrogenophilales;f__Hydrogenophilaceae;g__Thiobacillus;s__	467	246	5.541E-01	0.762	0.436	1.144

k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Microbacteriaceae;g__CandidatusAquiluna;s__rubra	65	247	5.645E-01	0.940	0.840	1.040
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Listeriaceae;g__Brochothrix;s__	403	248	5.645E-01	0.742	0.382	1.147
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Bradyrhizobiaceae;g__Balneimonas;s__	449	249	5.658E-01	0.556	0.126	1.224
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__;s__	25	250	5.706E-01	1.061	0.956	1.177
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Nocardiaceae;g__Rhodococcus;s__	102	251	5.706E-01	1.083	0.940	1.248
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Rothia;s__dentocariosa	105	252	5.706E-01	1.055	0.960	1.158
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__;g__;s__	5	253	5.706E-01	1.044	0.968	1.124
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Haemophilus;s__influenzae	529	254	5.706E-01	0.531	0.072	1.067
k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria;o__Campylobacterales;f__Campylobacteraceae;g__Arcobacter;s__	122	255	5.742E-01	0.866	0.652	1.094
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Bdellovibrionales;f__Bacteriovoracaceae;g__;s__	475	256	5.742E-01	0.683	0.243	1.141
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Brevundimonas;s__diminuta	211	257	5.742E-01	1.095	0.930	1.287
k__Bacteria;p__Acidobacteria;c__Acidobacteria-6;o__iii1-15;f__;g__;s__	267	258	5.742E-01	1.145	0.896	1.460
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__;s__	283	259	5.755E-01	1.103	0.924	1.313
k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales;f__Leptotrichiaceae;g__;s__	140	260	5.815E-01	0.751	0.394	1.168
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Methylobacteriaceae;g__;s__	109	261	5.858E-01	1.074	0.943	1.221
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Oxalobacteraceae;g__Polynucleobacter;s__cosmopolitanus	524	262	5.873E-01	0.910	0.759	1.070
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnospira;s__	203	263	5.873E-01	0.753	0.390	1.168
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__Rhodoplanes;s__	45	264	5.970E-01	1.101	0.920	1.312
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Lautropia;s__	149	265	6.031E-01	0.919	0.781	1.069
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Acetobacteraceae;g__Roseomonas;s__mucosa	99	266	6.122E-01	1.140	0.886	1.464
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Flavobacteriaceae;g__Flavobacterium;s__	69	267	6.122E-01	1.058	0.951	1.175
k__Bacteria;p__TM7;c__TM7-3;o__I025;f__;g__;s__	512	268	6.166E-01	0.735	0.294	1.155
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__Peptoniphilus;s__	186	269	6.263E-01	0.962	0.894	1.036
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__	34	270	6.272E-01	1.057	0.951	1.179
k__Bacteria;p__Bacteroidetes;c__[Rhodothermi];o__[Rhodothermales];f__Rhodothermaceae;g__Rubricoccus;s__	364	271	6.297E-01	1.099	0.911	1.320
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__[Chromatiaceae];g__;s__	490	272	6.311E-01	0.442	0.044	1.474
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Alloiococcus;s__otitis	536	273	6.325E-01	0.629	0.164	1.286
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__	328	274	6.325E-01	0.929	0.801	1.069
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Methylococcales;f__Methylococcaceae;g__Methylocaldum;s__	504	275	6.325E-01	0.922	0.778	1.073
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Rhodospirillaceae;g__Azospirillum;s__	457	276	6.325E-01	0.811	0.510	1.179
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Aeromonadales;f__Aeromonadaceae;g__;s__	72	277	6.325E-01	0.924	0.786	1.073

k__Bacteria;p__Tenericutes;c__Mollicutes;o__Mycoplasmatales;f__Mycoplasmataceae;g__Mycoplasma;s__	254	278	6.366E-01	1.131	0.880	1.451
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__ACK-M1;g__;s__	344	279	6.366E-01	0.917	0.763	1.080
k__Bacteria;p__Cyanobacteria;c__Synechococcophycideae;o__Synechococcales;f__Synechococcaceae;g__Synechococcus;s__	21	280	6.383E-01	0.946	0.842	1.051
k__Bacteria;p__Bacteroidetes;c__Cytophagia;o__Cytophagales;f__Cytophagaceae;g__Hymenobacter;s__	39	281	6.385E-01	1.049	0.953	1.152
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__WAL_1855D;s__	272	282	6.482E-01	0.934	0.807	1.065
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Flavobacteriaceae;g__;s__	375	283	6.482E-01	0.917	0.762	1.084
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__;s__	13	284	6.539E-01	0.947	0.847	1.056
k__Bacteria;p__Bacteroidetes;c__Cytophagia;o__Cytophagales;f__Cytophagaceae;g__Rudanella;s__	373	285	6.539E-01	1.099	0.900	1.335
k__Bacteria;p__TM6;c__F38;o__;f__;g__;s__	97	286	6.618E-01	0.917	0.759	1.089
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Nocardioidaceae;g__Nocardioides;s__plantarum	127	287	6.623E-01	0.915	0.754	1.094
k__Bacteria;p__Chlamydiae;c__Chlamydiia;o__Chlamydiales;f__Parachlamydiaceae;g__CandidatusProtochlamydia;s__	379	288	6.623E-01	0.821	0.454	1.149
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__minor	143	289	6.646E-01	0.878	0.654	1.137
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Alloiococcus;s__	300	290	6.651E-01	1.026	0.972	1.083
k__Bacteria;p__TM7;c__;o__;f__;g__;s__	75	291	6.651E-01	0.924	0.772	1.083
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Staphylococcus;s__pettenkoferi	538	292	6.651E-01	0.506	0.064	1.578
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Sporichthyaceae;g__;s__	146	293	6.651E-01	1.122	0.874	1.429
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Neisseriales;f__Neisseriaceae;g__Kingella;s__	226	294	6.651E-01	0.895	0.690	1.116
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Corynebacteriaceae;g__Corynebacterium;s__bovis	521	295	6.651E-01	1.832	0.669	22.122
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Salinicoccus;s__	406	296	6.651E-01	1.799	0.684	21.010
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Nocardioidaceae;g__;s__	46	297	6.651E-01	0.947	0.841	1.063
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__SC-I-84;f__;g__;s__	473	298	6.651E-01	1.100	0.892	1.346
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Vibrionales;f__Vibrionaceae;g__Vibrio;s__	299	299	6.651E-01	1.170	0.827	1.642
k__Bacteria;p__[Thermi];c__Deinococci;o__Deinococcales;f__Deinococcaceae;g__Deinococcus;s__aquatilis	112	300	6.651E-01	0.927	0.779	1.084
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Flavobacteriaceae;g__Capnocytophaga;s__	117	301	6.694E-01	0.944	0.830	1.066
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Geodermatophilaceae;g__Geodermatophilus;s__	346	302	6.802E-01	0.590	0.113	1.515
k__Bacteria;p__Gemmatimonadetes;c__Gemm-3;o__;f__;g__;s__	431	303	6.802E-01	1.465	0.662	5.137
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micromonosporaceae;g__;s__	252	304	6.816E-01	0.871	0.627	1.164
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Alkanindiges;s__	290	305	6.816E-01	1.151	0.834	1.574
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Aurantimonadaceae;g__;s__	162	306	6.816E-01	1.072	0.916	1.250
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Paracoccus;s__marcusii	38	307	6.876E-01	0.946	0.833	1.069
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingobium;s__	256	308	6.977E-01	0.934	0.795	1.087

k__Bacteria;p__Bacteroidetes;c__[Saprospirae];o__[Saprospirales];f__Chitinophagaceae;g__Segetibacter;s__	365	309	6.977E-01	0.793	0.385	1.244
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Phyllobacteriaceae;g__Aminobacter;s__	273	310	6.977E-01	0.924	0.766	1.102
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Arthrobacter;s__	163	311	6.996E-01	1.069	0.914	1.246
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Rhodobacter;s__	455	312	6.996E-01	0.915	0.738	1.115
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Vibrionales;f__Vibrionaceae;g__Photobacterium;s__	507	313	6.996E-01	0.805	0.398	1.228
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__	193	314	7.030E-01	0.847	0.553	1.213
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__;s__	424	315	7.152E-01	0.837	0.503	1.223
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Methylocystaceae;g__Methylosinus;s__	41	316	7.188E-01	0.941	0.809	1.084
k__Bacteria;p__Actinobacteria;c__KIST-JJY010;o__;f__;g__;s__	357	317	7.291E-01	0.926	0.759	1.107
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Paenibacillaceae;g__Aneurinibacillus;s__	404	318	7.370E-01	0.756	0.299	1.365
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__;s__	130	319	7.473E-01	0.924	0.749	1.117
k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Acidimicrobiales;f__Microthrixaceae;g__CandidatusMicrothrix;s__parvicella	288	320	7.479E-01	0.845	0.513	1.242
k__Bacteria;p__Actinobacteria;c__Thermoleophilia;o__Solirubrobacterales;f__Conexibacteraceae;g__;s__	123	321	7.479E-01	1.092	0.871	1.357
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Rubellimicrobium;s__	120	322	7.491E-01	0.949	0.827	1.079
k__Bacteria;p__Cyanobacteria;c__Chloroplast;o__Chlorophyta;f__Chlamydomonadaceae;g__;s__	396	323	7.501E-01	0.925	0.751	1.117
k__Bacteria;p__Acidobacteria;c__[Chloracidobacteria];o__RB41;f__Ellin6075;g__;s__	26	324	7.501E-01	1.048	0.927	1.181
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Propionibacteriaceae;g__Luteococcus;s__	352	325	7.501E-01	1.293	0.664	3.152
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__;s__	12	326	7.501E-01	0.954	0.841	1.074
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Methylocystaceae;g__;s__	453	327	7.501E-01	0.754	0.275	1.389
k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Acidimicrobiales;f__EB1017;g__;s__	44	328	7.501E-01	0.936	0.787	1.105
k__Bacteria;p__Cyanobacteria;c__Chloroplast;o__Chlorophyta;f__;g__;s__	86	329	7.501E-01	0.958	0.853	1.065
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Peptostreptococcus;s__anaerobius	517	330	7.502E-01	0.684	0.163	1.517
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Lysobacter;s__brunescens	522	331	7.520E-01	0.781	0.280	1.305
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Corynebacteriaceae;g__Corynebacterium;s__lubricantis	255	332	7.528E-01	0.924	0.744	1.128
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Flavobacteriaceae;g__Flavobacterium;s__frigidarium	528	333	7.528E-01	0.617	0.120	1.875
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminococcus;s__	80	334	7.528E-01	0.935	0.778	1.110
k__Bacteria;p__Firmicutes;c__Bacilli;o__Turicibacterales;f__Turicibacteraceae;g__Turicibacter;s__	95	335	7.559E-01	1.061	0.905	1.238
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Hyphomonadaceae;g__;s__	106	336	7.638E-01	1.093	0.855	1.384
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__[Weeksellaceae];g__Cloacibacterium;s__	332	337	7.638E-01	1.057	0.909	1.224
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__Hyphomicrobium;s__	37	338	7.642E-01	0.954	0.835	1.080
k__Bacteria;p__Spirochaetes;c__Spirochaetes;o__Spirochaetales;f__Spirochaetaceae;g__Treponema;s__	200	339	7.752E-01	1.118	0.810	1.526

k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Rhizobium;s__	291	340	7.752E-01	1.120	0.808	1.532
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Streptomycetaceae;g__Streptomyces;s__	354	341	7.752E-01	1.243	0.656	2.371
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Procabacteriales;f__Procabacteriaceae;g__;s__	470	342	7.926E-01	0.899	0.630	1.188
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus;s__selenatarsenatis	547	343	7.969E-01	0.786	0.316	1.417
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Oxalobacteraceae;g__Ralstonia;s__	136	344	7.978E-01	0.962	0.860	1.075
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Bdellovibrionales;f__Bdellovibrionaceae;g__Bdellovibrio;s__	124	345	8.194E-01	1.068	0.873	1.296
k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__Caldilineales;f__Caldilineaceae;g__Caldilinea;s__	387	346	8.194E-01	1.066	0.874	1.289
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Moryella;s__	73	347	8.194E-01	0.954	0.822	1.093
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Blautia;s__	301	348	8.194E-01	0.956	0.833	1.092
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__[Chromatiaceae];g__Rheinheimera;s__	326	349	8.263E-01	0.865	0.527	1.312
k__Bacteria;p__Bacteroidetes;c__Cytophagia;o__Cytophagales;f__Cytophagaceae;g__Spirosoma;s__	245	350	8.291E-01	1.058	0.882	1.258
k__Bacteria;p__Chloroflexi;c__TK17;o__mle1-48;f__;g__;s__	393	351	8.427E-01	1.134	0.742	1.716
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Vagococcus;s__	411	352	8.457E-01	0.613	0.075	2.406
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__johnsonii	232	353	8.473E-01	1.048	0.902	1.216
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Legionellales;f__Legionellaceae;g__;s__	17	354	8.473E-01	1.039	0.916	1.175
k__Bacteria;p__Chlamydiae;c__Chlamydiia;o__Chlamydiales;f__;g__;s__	67	355	8.532E-01	0.964	0.850	1.083
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__Rhodocyclaceae;g__Hydrogenophilus;s__	472	356	8.532E-01	0.872	0.507	1.312
k__Bacteria;p__[Thermi];c__Deinococci;o__Deinococcales;f__Deinococcaceae;g__CM44;s__	336	357	8.720E-01	1.081	0.818	1.408
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus;s__	126	358	8.720E-01	1.040	0.908	1.189
k__Bacteria;p__Planctomycetes;c__Planctomycetia;o__B97;f__;g__;s__	445	359	8.720E-01	1.095	0.794	1.485
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Mobiluncus;s__	345	360	8.737E-01	1.090	0.797	1.468
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Pseudonocardiaceae;g__Saccharopolyspora;s__	353	361	8.761E-01	0.855	0.415	1.386
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__	182	362	8.761E-01	1.045	0.893	1.219
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Nocardiopsaceae;g__;s__	351	363	8.761E-01	0.797	0.293	1.628
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Peptostreptococcus;s__	31	364	8.770E-01	1.037	0.909	1.177
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__;g__;s__	233	365	8.954E-01	1.044	0.888	1.220
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__;s__	333	366	8.954E-01	1.049	0.875	1.250
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingopyxis;s__alaskensis	325	367	8.954E-01	0.834	0.391	1.574
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Paracoccus;s__aminovorans	98	368	8.954E-01	1.059	0.855	1.314
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Cellulomonadaceae;g__Cellulomonas;s__	298	369	8.954E-01	0.949	0.774	1.146
k__Bacteria;p__Cyanobacteria;c__Chloroplast;o__Stramenopiles;f__;g__;s__	77	370	8.954E-01	1.028	0.925	1.137

k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uniformis	250	371	8.954E-01	1.049	0.873	1.251
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Legionellales;f__Coxiellaceae;g__Aquicella;s__	500	372	9.003E-01	0.954	0.786	1.134
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Arthrobacter;s__psychrolactophilus	540	373	9.003E-01	1.115	0.714	1.694
k__Bacteria;p__Bacteroidetes;c__Cytophagia;o__Cytophagales;f__Cytophagaceae;g__Dyadobacter;s__	331	374	9.003E-01	0.949	0.769	1.153
k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Acidimicrobiales;f__C111;g__;s__	47	375	9.053E-01	0.971	0.864	1.084
k__Bacteria;p__Bacteroidetes;c__[Saprospirae];o__[Saprospirales];f__Chitinophagaceae;g__Flavisolibacter;s__	164	376	9.056E-01	0.937	0.700	1.189
k__Bacteria;p__Bacteroidetes;c__[Saprospirae];o__[Saprospirales];f__Chitinophagaceae;g__;s__	141	377	9.066E-01	0.962	0.821	1.117
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__;g__;s__	270	378	9.072E-01	0.953	0.781	1.149
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Williamsiaceae;g__Williamsia;s__	355	379	9.072E-01	1.104	0.721	1.648
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Jannaschia;s__	454	380	9.072E-01	1.105	0.725	1.639
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__Psychromonadaceae;g__Psychromonas;s__	317	381	9.072E-01	0.901	0.554	1.327
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__SBla14;f__;g__;s__	161	382	9.118E-01	1.103	0.723	1.640
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Oceanospirillales;f__Halomonadaceae;g__Halomonas;s__	246	383	9.275E-01	0.963	0.822	1.130
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Gordoniaceae;g__Gordonia;s__	280	384	9.305E-01	1.074	0.774	1.462
k__Bacteria;p__Bacteroidetes;c__Sphingobacteriia;o__Sphingobacteriales;f__;g__;s__	377	385	9.315E-01	0.902	0.497	1.346
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Nakamurellaceae;g__;s__	248	386	9.391E-01	0.948	0.739	1.190
k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Acidimicrobiales;f__;g__;s__	10	387	9.448E-01	1.023	0.922	1.132
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Acetobacteraceae;g__Roseococcus;s__	456	388	9.503E-01	1.062	0.797	1.389
k__Bacteria;p__Nitrospirae;c__Nitrospira;o__Nitrospirales;f__Nitrospiraceae;g__Nitrospira;s__	437	389	9.618E-01	1.059	0.791	1.389
k__Bacteria;p__TM7;c__SC3;o__;f__;g__;s__	28	390	9.618E-01	0.977	0.872	1.088
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Veillonella;s__parvula	185	391	9.621E-01	1.046	0.837	1.293
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__BD7-3;f__;g__;s__	447	392	9.703E-01	1.084	0.701	1.628
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Paludibacter;s__	229	393	9.841E-01	0.947	0.700	1.233
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Oxalobacteraceae;g__Janthinobacterium;s__	91	394	9.905E-01	0.971	0.827	1.128
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__caccae	329	395	9.905E-01	0.923	0.566	1.375
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Pseudoxanthomonas;s__mexicana	84	396	9.905E-01	1.059	0.763	1.435
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Mycobacteriaceae;g__Mycobacterium;s__	1	397	9.905E-01	0.985	0.904	1.068
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Intrasporangiaceae;g__;s__	68	398	9.905E-01	0.978	0.864	1.100
k__Bacteria;p__Firmicutes;c__Clostridia;o__Thermoanaerobacterales;f__Caldicellulosiruptoraceae;g__Caldicellulosiruptor;s__saccharolyticus	213	399	9.905E-01	1.042	0.818	1.311
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Veillonella;s__dispar	48	400	9.905E-01	1.013	0.939	1.094

k__Bacteria;p__Gemmatimonadetes;c__Gemmatimonadetes;o__Gemmatimonadales;f__;g__;s__	433	401	9.905E-01	1.047	0.788	1.361
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__[Weeksellaceae];g__Chryseobacterium;s__	237	402	9.905E-01	0.981	0.875	1.097
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Megasphaera;s__	212	403	9.905E-01	1.023	0.889	1.171
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Oribacterium;s__	79	404	9.905E-01	1.022	0.893	1.162
k__Bacteria;p__Firmicutes;c__Erysipelotrichi;o__Erysipelotrichales;f__Erysipelotrichaceae;g__;s__	115	405	9.905E-01	0.959	0.734	1.230
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Porphyromonas;s__	155	406	9.905E-01	0.985	0.897	1.081
k__Bacteria;p__Bacteroidetes;c__Sphingobacteriia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Sphingobacterium;s__multivorum	535	407	9.905E-01	1.054	0.745	1.453
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Legionellales;f__Coxiellaceae;g__;s__	499	408	9.905E-01	1.034	0.827	1.276
k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Acidimicrobiales;f__Microthrixaceae;g__;s__	53	409	9.905E-01	0.976	0.829	1.138
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Luteimonas;s__	508	410	9.905E-01	0.861	0.197	2.106
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Granulicatella;s__	27	411	9.905E-01	0.988	0.909	1.071
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Planomicrobium;s__	178	412	9.905E-01	1.017	0.909	1.133
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Alcaligenaceae;g__;s__	43	413	9.905E-01	0.986	0.893	1.083
k__Bacteria;p__Firmicutes;c__Bacilli;o__Gemellales;f__Gemellaceae;g__Gemella;s__	116	414	9.905E-01	1.030	0.844	1.256
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Proteus;s__	222	415	9.905E-01	1.020	0.886	1.165
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__Shewanellaceae;g__Shewanella;s__algae	251	416	9.905E-01	0.978	0.840	1.141
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__;g__;s__	32	417	9.905E-01	0.979	0.844	1.128
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__;s__	416	418	9.905E-01	1.059	0.675	1.592
k__Bacteria;p__TM7;c__TM7-3;o__;f__;g__;s__	14	419	9.905E-01	1.013	0.924	1.109
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Hylemonella;s__	234	420	9.905E-01	1.097	0.536	2.124
k__Bacteria;p__Bacteroidetes;c__Sphingobacteriia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Pedobacter;s__	89	421	9.905E-01	1.013	0.922	1.111
k__Bacteria;p__Cyanobacteria;c__Nostocophycideae;o__Stigonematales;f__Rivulariaceae;g__Calothrix;s__	284	422	9.905E-01	0.967	0.743	1.221
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__Rhodocyclaceae;g__Dechloromonas;s__	187	423	9.905E-01	1.026	0.840	1.241
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingomonas;s__yabuuchiae	553	424	9.905E-01	0.941	0.529	1.467
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Actinomyces;s__	30	425	9.905E-01	0.989	0.909	1.076
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__;s__	8	426	9.905E-01	0.988	0.898	1.087
k__Bacteria;p__TM6;c__SJA-4;o__;f__;g__;s__	74	427	9.905E-01	1.019	0.873	1.179
k__Bacteria;p__Firmicutes;c__Bacilli;o__Gemellales;f__Gemellaceae;g__;s__	88	428	9.905E-01	0.988	0.897	1.086
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Neisseriales;f__Neisseriaceae;g__;s__	266	429	9.905E-01	1.009	0.939	1.083
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;s__adolescentis	152	430	9.905E-01	0.978	0.807	1.172

k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__;s__	118	431	9.905E-01	1.011	0.922	1.108
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Polaromonas;s__	206	432	9.905E-01	0.974	0.772	1.218
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Methylophilales;f__Methylophilaceae;g__;s__	24	433	9.905E-01	1.016	0.885	1.159
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Sinobacteraceae;g__;s__	268	434	9.905E-01	0.987	0.882	1.104
k__Bacteria;p__Acidobacteria;c__[Chloracidobacteria];o__RB41;f__;g__;s__	338	435	9.905E-01	1.036	0.747	1.402
k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales;f__Leptotrichiaceae;g__Sneathia;s__	201	436	9.905E-01	0.971	0.733	1.248
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Corynebacteriaceae;g__Corynebacterium;s__variabile	551	437	9.905E-01	0.965	0.680	1.317
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__Rhodocyclaceae;g__C39;s__	471	438	9.905E-01	1.045	0.672	1.565
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Varibaculum;s__	278	439	9.905E-01	0.974	0.740	1.248
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Paenisporosarcina;s__	60	440	9.905E-01	0.991	0.901	1.084
k__Bacteria;p__TM7;c__TM7-1;o__;f__;g__;s__	4	441	9.905E-01	0.990	0.899	1.087
k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium;s__	66	442	9.905E-01	1.009	0.923	1.102
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Bradyrhizobiaceae;g__;s__	49	443	9.905E-01	1.011	0.903	1.134
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__0319-6G20;g__;s__	104	444	9.905E-01	0.969	0.668	1.326
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;g__Eggerthella;s__lenta	258	445	9.905E-01	1.038	0.660	1.573
k__Bacteria;p__[Thermi];c__Deinococci;o__Deinococcales;f__Trueperaceae;g__Truepera;s__	92	446	9.905E-01	1.015	0.842	1.210
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Abiotrophia;s__	195	447	9.905E-01	0.989	0.864	1.124
k__Bacteria;p__Cyanobacteria;c__Oscillatoriophycideae;o__Chroococcales;f__Xenococcaceae;g__Chroococcidiopsis;s__	304	448	9.905E-01	1.023	0.765	1.340
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__ph2;s__	419	449	9.905E-01	0.971	0.650	1.372
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Enhydrobacter;s__	103	450	9.905E-01	1.010	0.896	1.137
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Brucellaceae;g__;s__	219	451	9.905E-01	1.015	0.837	1.222
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Intrasporangiaceae;g__Arsenicicoccus;s__	347	452	9.905E-01	0.938	0.265	2.121
k__Bacteria;p__Actinobacteria;c__Thermoleophilia;o__Gaiellales;f__;g__;s__	359	453	9.905E-01	1.009	0.876	1.155
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__Pedomicrobium;s__	452	454	9.905E-01	1.025	0.693	1.469
k__Bacteria;p__Proteobacteria;c__TA18;o__PHOS-HD29;f__;g__;s__	70	455	9.905E-01	0.988	0.822	1.178
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Acetobacteraceae;g__;s__	59	456	9.905E-01	1.008	0.883	1.147
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__;s__	312	457	9.905E-01	1.010	0.860	1.177
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Neisseriales;f__Neisseriaceae;g__Eikenella;s__	225	458	9.905E-01	0.982	0.715	1.308
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Tannerella;s__	369	459	9.905E-01	0.956	0.338	1.986
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__NKB15;f__;g__;s__	482	460	9.905E-01	0.984	0.737	1.287
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Micrococcus;s__	50	461	9.905E-01	1.012	0.827	1.239

k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Shuttleworthia;s__	423	462	9.905E-01	0.978	0.626	1.434
k__Bacteria;p__Acidobacteria;c__DA052;o__Ellin6513;f__;g__;s__	341	463	9.905E-01	1.028	0.531	1.747
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Methylobacteriaceae;g__Methylobacterium;s__adhaesivum	227	464	9.905E-01	0.993	0.860	1.139
k__Bacteria;p__WS6;c__SC72;o__WCHB1-15;f__;g__;s__	515	465	9.905E-01	0.986	0.731	1.303
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Nocardioidaceae;g__Aeromicrobium;s__	94	466	9.905E-01	1.008	0.855	1.177
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__;s__	412	467	9.905E-01	1.021	0.582	1.627
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Mycoplana;s__	230	468	9.905E-01	1.007	0.853	1.181
k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales;f__Leptotrichiaceae;g__Leptotrichia;s__	85	469	9.905E-01	0.997	0.911	1.089
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Bradyrhizobiaceae;g__Bradyrhizobium;s__	173	470	9.905E-01	0.994	0.806	1.226
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Selenomonas;s__	172	471	9.905E-01	0.997	0.891	1.111
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__[Weeksellaceae];g__Wautersiella;s__	292	472	9.905E-01	0.993	0.616	1.512
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__sobrinus	548	473	9.905E-01	0.000	NA	220880.319
k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__H39;f__;g__;s__	388	474	9.905E-01	2719.537	0.000	NA
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Christensenellaceae;g__;s__	420	475	9.905E-01	18.386	0.000	NA
k__Bacteria;p__Synergistetes;c__Synergistia;o__Synergistales;f__Dethiosulfovibrionaceae;g__Pyramidobacter;s__piscolens	539	476	9.905E-01	18.766	0.003	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Pediococcus;s__	413	477	9.905E-01	9.553	0.000	NA
k__Bacteria;p__GN02;c__GKS2-174;o__;f__;g__;s__	435	478	9.905E-01	69.417	0.000	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Jeotgalicoccus;s__psychrophilus	541	479	9.905E-01	0.000	NA	NA
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Dietziaceae;g__Dietzia;s__	318	480	9.905E-01	0.000	NA	120603.867
k__Bacteria;p__Spirochaetes;c__Spirochaetes;o__Sphaerochaetales;f__Sphaerochaetaceae;g__Sphaerochaeta;s__	509	481	9.905E-01	27.369	0.005	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Aeromonadales;f__Aeromonadaceae;g__Tolumonas;s__	489	482	9.905E-01	0.021	NA	5711.099
k__Bacteria;p__GN02;c__BD1-5;o__;f__;g__;s__	434	483	9.905E-01	0.001	NA	NA
k__Bacteria;p__Gemmatimonadetes;c__Gemmatimonadetes;o__;f__;g__;s__	432	484	9.905E-01	0.033	NA	NA
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__S24-7;g__;s__	370	485	9.905E-01	0.043	NA	NA
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__Parvibaculum;s__	451	486	9.905E-01	0.088	NA	27507934.820
k__Bacteria;p__Synergistetes;c__Synergistia;o__Synergistales;f__Dethiosulfovibrionaceae;g__Jonquetella;s__anthropi	518	487	9.905E-01	0.084	NA	36656530.930
k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__Anaerolineales;f__Anaerolinaceae;g__Anaerolinea;s__	385	488	9.905E-01	0.046	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Oceanospirillales;f__Halomonadaceae;g__;s__	505	489	9.905E-01	0.075	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Leuconostocaceae;g__Weissella;s__	415	490	9.905E-01	0.000	NA	NA
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Syntrophobacterales;f__Syntrophaceae;g__Desulfomonile;s__	484	491	9.905E-01	0.001	0.000	2851.329

k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Schwartzia;s__	426	492	9.905E-01	78.634	0.000	NA
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingomonas;s__wittichii	552	493	9.905E-01	0.000	NA	NA
k__Bacteria;p__Aquificae;c__Aquificae;o__Aquificales;f__Aquificaceae;g__;s__	362	494	9.905E-01	0.000	NA	NA
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Pseudonocardiaceae;g__Actinomycetospora;s__	210	495	9.905E-01	0.000	0.000	199982.076
k__Bacteria;p__Chloroflexi;c__Chloroflexi;o__[Roseiflexales];f__[Kouleothrixaceae];g__Kouleothrix;s__	390	496	9.905E-01	35.324	0.000	NA
k__Bacteria;p__WS3;c__PRR-12;o__Sediment-1;f__PRR-10;g__;s__	514	497	9.905E-01	77.372	0.000	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__OM60;g__;s__	491	498	9.905E-01	86.221	0.000	NA
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__NB1-j;f__JTB38;g__;s__	481	499	9.905E-01	47.267	0.000	NA
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__FAC87;f__;g__;s__	477	500	9.905E-01	46.124	0.000	NA
k__Bacteria;p__Gemmatimonadetes;c__Gemm-1;o__;f__;g__;s__	430	501	9.905E-01	41.335	0.000	NA
k__Bacteria;p__Planctomycetes;c__C6;o__d113;f__;g__;s__	442	502	9.905E-01	51.185	0.000	NA
k__Bacteria;p__Chloroflexi;c__Chloroflexi;o__AKIW781;f__;g__;s__	391	503	9.905E-01	0.038	NA	58531943.310
k__Bacteria;p__Chlamydiae;c__Chlamydiia;o__Chlamydiales;f__Parachlamydiaceae;g__Parachlamydia;s__	380	504	9.905E-01	0.007	NA	NA
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Syntrophobacterales;f__Syntrophorhabdaceae;g__;s__	485	505	9.905E-01	0.007	NA	NA
k__Bacteria;p__Cyanobacteria;c__Oscillatoriophycideae;o__Chroococcales;f__Cyanobacteriaceae;g__Cyanobacterium;s__	398	506	9.905E-01	0.008	NA	96840309.240
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Legionellales;f__Legionellaceae;g__Tatlockia;s__	503	507	9.905E-01	0.011	NA	21006759.360
k__Bacteria;p__Chlamydiae;c__Chlamydiia;o__Chlamydiales;f__Rhabdochlamydiaceae;g__CandidatusRhabdochlamydia;s__	381	508	9.905E-01	0.034	NA	329869.646
k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales;f__;g__;s__	428	509	9.905E-01	0.004	NA	NA
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Kineosporiaceae;g__Kineococcus;s__	348	510	9.905E-01	0.000	NA	NA
k__Bacteria;p__Armatimonadetes;c__[Fimbriimonadia];o__[Fimbriimonadales];f__[Fimbriimonadaceae];g__Fimbriimonas;s__	363	511	9.905E-01	0.000	NA	NA
k__Bacteria;p__OD1;c__SM2F11;o__;f__;g__;s__	440	512	9.905E-01	0.070	NA	662524.372
k__Bacteria;p__OD1;c__ABY1;o__;f__;g__;s__	439	513	9.905E-01	0.027	NA	80027541.210
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__BA008;g__;s__	366	514	9.905E-01	0.036	NA	20653084.220
k__Bacteria;p__Chlorobi;c__Ignavibacteria;o__Ignavibacteriales;f__Ignavibacteriaceae;g__;s__	382	515	9.905E-01	0.042	NA	9289530.494
k__Bacteria;p__Cyanobacteria;c__4C0d-2;o__SM1D11;f__;g__;s__	394	516	9.905E-01	0.042	NA	9289530.494
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Chromatiales;f__Chromatiaceae;g__Allochromatium;s__	492	517	9.905E-01	0.057	NA	1985986.742
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__vadinHB04;s__	427	518	9.905E-01	0.023	NA	NA
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__MIZ46;f__;g__;s__	478	519	9.905E-01	0.020	NA	NA

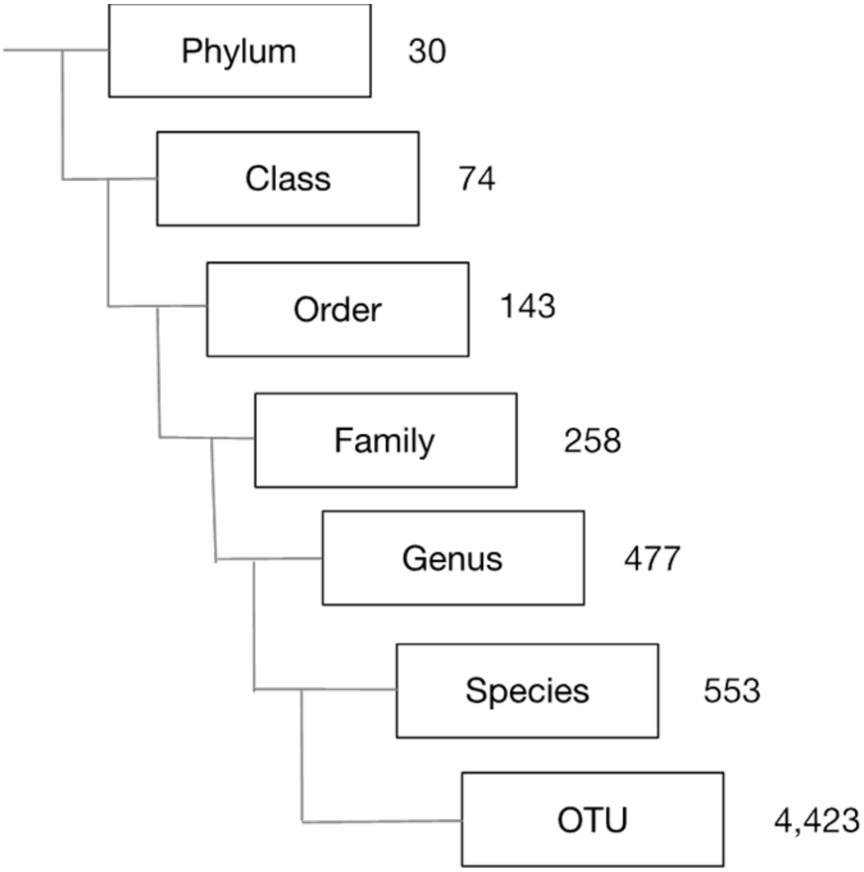
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Legionellales;f__Francisellaceae;g__;s__	501	520	9.905E-01	0.015	NA	NA
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Bdellovibrionales;f__Bdellovibrionaceae;g__Bdellovibrio;s__bacteriovorus	520	521	9.905E-01	0.044	NA	6746394.794
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__;f__;g__;s__	461	522	9.905E-01	0.027	NA	89335300.220
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Chromatiales;f__Halothiobacillaceae;g__Thiovirga;s__	493	523	9.905E-01	0.058	NA	1684114.103
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__Polyangiaceae;g__;s__	480	524	9.905E-01	NA	0.000	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Marinilactibacillus;s__psychrotolerans	542	525	9.905E-01	0.004	NA	NA
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Arthrospira;s__	448	526	9.905E-01	0.000	NA	NA
k__Bacteria;p__Acidobacteria;c__Holophagae;o__Holophagales;f__Holophagaceae;g__Geothrix;s__	342	527	9.905E-01	0.003	NA	48283753.330
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__;s__	367	528	9.905E-01	0.000	NA	NA
k__Bacteria;p__Firmicutes;c__;o__;f__;g__;s__	401	529	9.905E-01	0.000	NA	NA
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Neisseriales;f__Neisseriaceae;g__Microvirgula;s__	468	530	9.905E-01	0.000	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__;f__;g__;s__	488	531	9.905E-01	0.000	NA	NA
k__Bacteria;p__OP11;c__WCHB1-64;o__d153;f__;g__;s__	441	532	9.905E-01	0.009	NA	NA
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__;s__	417	533	9.905E-01	0.015	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__schindleri	545	534	9.905E-01	0.000	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Yersinia;s__	496	535	9.905E-01	0.000	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__HOC36;f__;g__;s__	497	536	9.905E-01	0.009	NA	18524743.660
k__Bacteria;p__Cyanobacteria;c__Oscillatoriophycideae;o__Oscillatoriales;f__Phormidiaceae;g__Phormidium;s__	399	537	9.905E-01	0.001	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Trichococcus;s__	410	538	9.905E-01	14.193	0.000	NA
k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria;o__Campylobacterales;f__Campylobacteraceae;g__Sulfurospirillum;s__	486	539	9.905E-01	0.000	NA	NA
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Anaeromusa;s__	425	540	9.905E-01	0.000	NA	NA
k__Bacteria;p__Planctomycetes;c__Phycisphaerae;o__Phycisphaerales;f__;g__;s__	443	541	9.905E-01	0.102	NA	NA
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__OM27;g__;s__	479	542	9.905E-01	0.000	NA	NA
k__Bacteria;p__Planctomycetes;c__Phycisphaerae;o__WD2101;f__;g__;s__	444	543	9.905E-01	0.000	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Alkalibacterium;s__	409	544	9.905E-01	0.000	NA	NA
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Flavobacteriaceae;g__Myroides;s__	376	545	9.905E-01	0.000	NA	NA
k__Bacteria;p__Bacteroidetes;c__Cytophagia;o__Cytophagales;f__Cytophagaceae;g__Rhodocytophaga;s__	372	546	9.905E-01	0.092	NA	NA
k__Bacteria;p__Cyanobacteria;c__Synechococcophycideae;o__Pseudanabaenales;f__;g__;s__	400	547	9.905E-01	0.057	NA	NA
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__iners	150	548	9.905E-01	0.999	0.861	1.154

k__Bacteria;p__Verrucomicrobia;c__[Spartobacteria];o__[Chthoniobacterales];f__[Chthoniobacteraceae];g__DA101;s__	513	549	9.905 E-01	0.071	NA	NA
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Buchnera;s__	494	550	9.905 E-01	0.040	NA	NA
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Cryomorphaceae;g__Fluviicola;s__	374	551	9.905 E-01	0.052	NA	NA
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Amaricoccus;s__	289	552	9.916 E-01	1.003	0.633	1.503
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Acidovorax;s__delafieldii	167	553	9.984 E-01	1.000	0.784	1.249

eTable 3. Association of Individual Taxa and Cluster Class With Composite Infectious Outcome

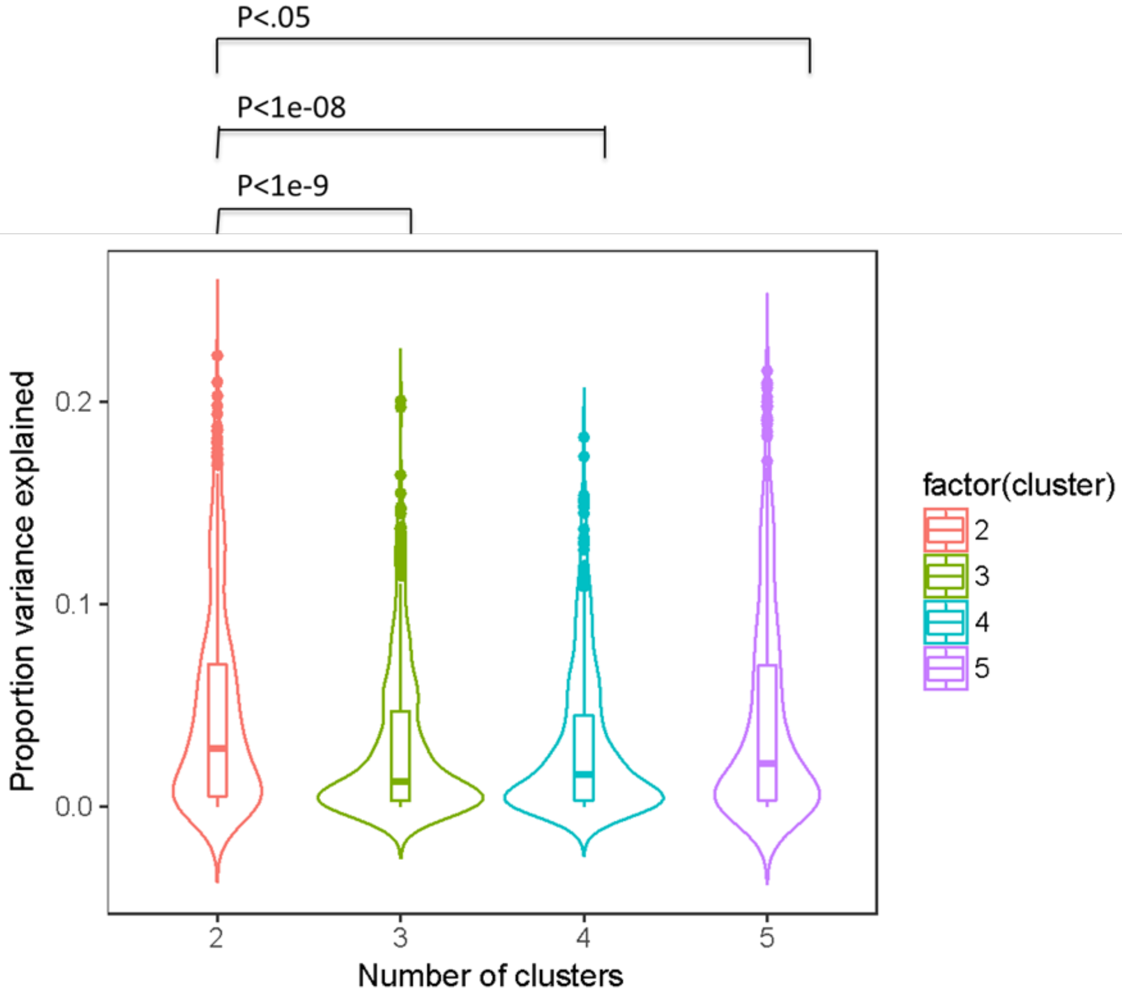
Variables	**Unadjusted Odds Ratio**	**P value**	**Adjusted Odds Ratio**	**P value**
Moraxella spp.	1.17 (1.05,1.29)	0.003	1.16 (1.00,1.34)	0.04
Propionibacterium granulosum	0.86 (0.79,0.94)	0.001	0.91 (0.79,1.06)	0.25
Novosphingobium spp.	1.16 (1.10,1.24)	<0.001	1.13 (1.05,1.23)	0.001
Anaerococcus spp.	0.71 (0.59,0.86)	<0.001	0.43 (0.31,0.57)	<0.001
Propionibacterium spp.	1.19 (1.06,1.33)	0.002	0.98 (0.83,1.15)	0.87
Atopobium spp.	0.70 (0.58,0.85)	<0.001	0.69 (0.53,0.89)	0.005
Parvimonas spp.	0.86 (0.79,0.94)	<0.001	0.94 (0.82,1.07)	0.36
Cluster 2 probability	6.18 (3.30,11.7)	<0.001	6.71 (2.91,15.84)	<0.001

eFigure 1. Taxonomic Classification of 16S rRNA Gene Sequences Identified From Preoperative Nasal Swabs



Numbers of uniquely annotated taxa against the Greengenes database within each clade identified from 4,423 operational taxonomic units (OTUs).

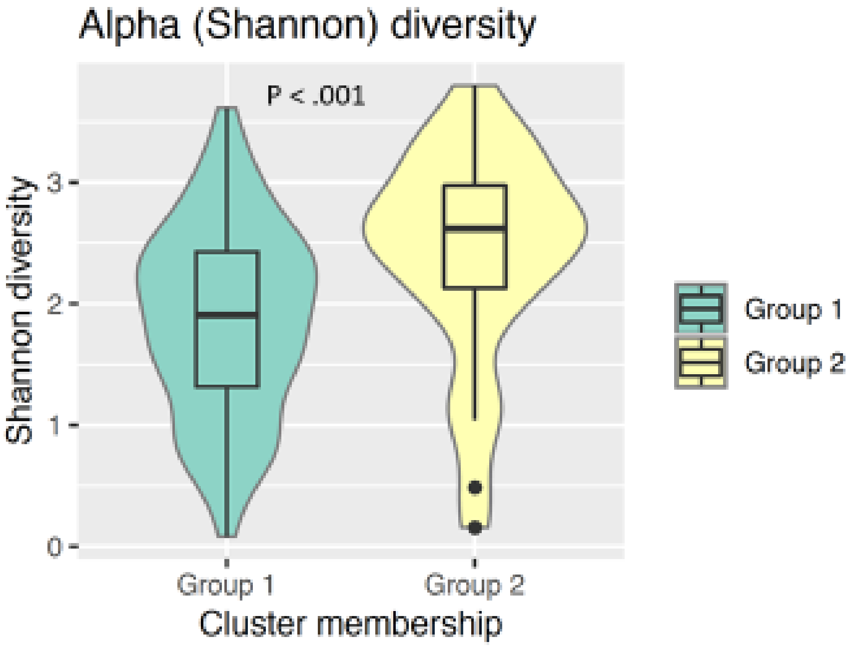
eFigure 2. Violin Plots of Variance Associated With Microbiome Cluster



Along the abscissa are the number of clusters defined from K = 2 to K = 5. The ordinate represents the variance explained by cluster (within to between sum of squares). Cluster of K = 2 has the greatest (median) variability explained in comparison to other cluster representations and is the most parsimonious.

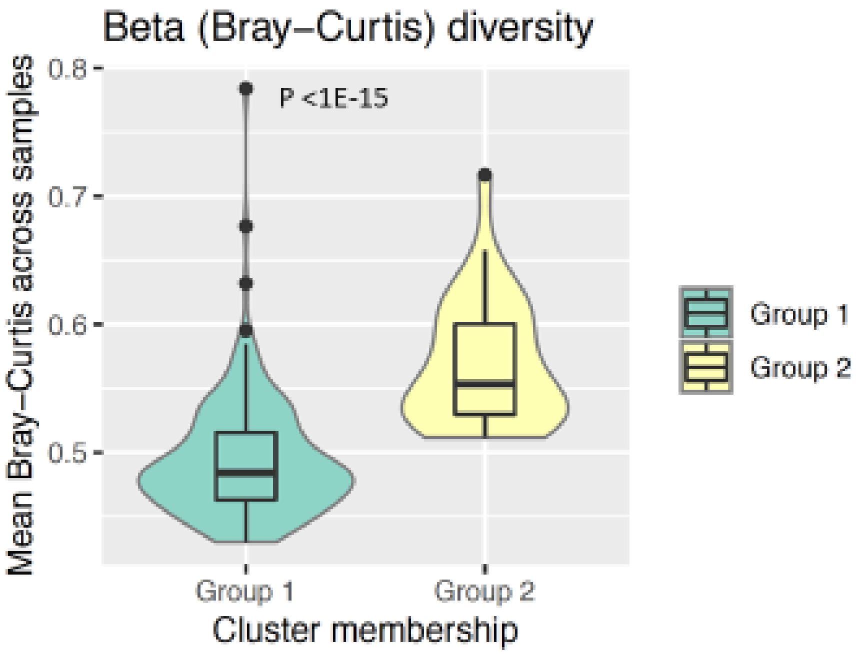
eFigure 3. Diversity Characterization of Nasal Microbiota by Cluster Class

eFigure 3A. Microbiome diversity metrics by cluster class: Alpha (Shannon) diversity



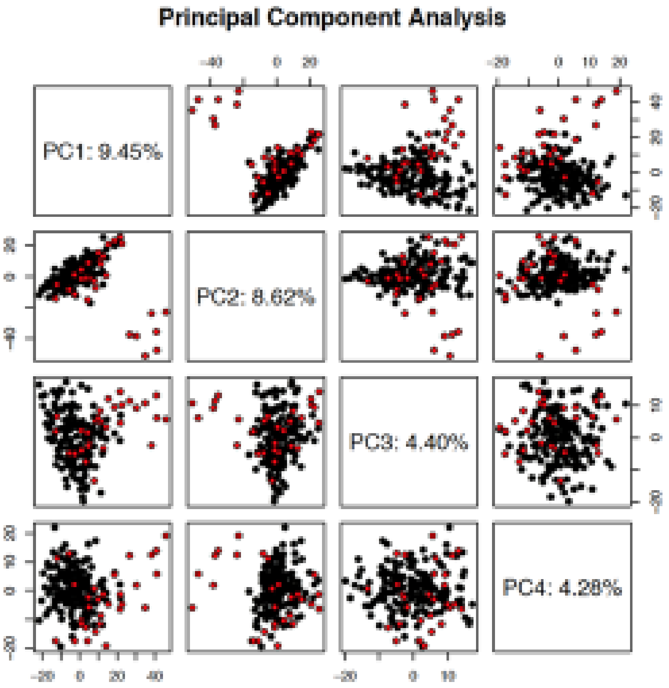
eFigure 3A shows violin plots describing sample Shannon diversity in each of the microbiome clusters. There is significantly less diversity within cluster1 (Group 1) compared to cluster2 (Group 2).

eFigure 3B. Microbiome diversity metrics by cluster class: Beta diversity



eFigure 3B shows violin plots describing the average Bray-Curtis distance (beta diversity) for each sample within by microbiome cluster. Cluster1 (Group 1) is a significantly more homogeneous (less diverse) than cluster2.

eFigure 3C. Microbiome diversity metrics by cluster class: Principal Components Analysis



eFigure 3C is a pairwise scatterplot of the first through fourth principal components. Each point represents an individual patient sample, black= cluster1 (Group 1) and red= cluster2 (Group 2); proportion of variance explained by each principal component (PC) shown (%).