

Airway microbiota and bronchial hyperresponsiveness in patients with suboptimally controlled asthma

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Background: Improvement in lung function after macrolide antibiotic therapy has been attributed to reduction in bronchial infection by specific bacteria. However, the airway might be populated by a more diverse microbiota, and clinical features of asthma might be associated with characteristics of the airway microbiota present.

Objective: We sought to determine whether relationships exist between the composition of the airway bacterial microbiota and clinical features of asthma using culture-independent tools capable of detecting the presence and relative abundance of most known bacteria.

Methods: In this pilot study bronchial epithelial brushings were collected from 65 adults with suboptimally controlled asthma participating in a multicenter study of the effects of clarithromycin on asthma control and 10 healthy control subjects. A combination of high-density 16S ribosomal RNA microarray and parallel clone library-sequencing analysis was used to profile the microbiota and examine relationships with clinical measurements.

Results: Compared with control subjects, 16S ribosomal RNA amplicon concentrations (a proxy for bacterial burden) and bacterial diversity were significantly higher among asthmatic patients. In multivariate analyses airway microbiota composition and diversity were significantly correlated with bronchial hyperresponsiveness. Specifically, the relative abundance of particular phylotypes, including members of the Comamonadaceae, Sphingomonadaceae, Oxalobacteraceae, and other bacterial families were highly correlated with the degree of bronchial hyperresponsiveness.

Conclusion: The composition of bronchial airway microbiota is associated with the degree of bronchial hyperresponsiveness

among patients with suboptimally controlled asthma. These findings support the need for further functional studies to examine the potential contribution of members of the airway microbiota in asthma pathogenesis. (*J Allergy Clin Immunol* 2010;■■■■:■■■■-■■■■.)

Key words: Microbiome, bacteria, asthma, 16S ribosomal RNA, PhyloChip

Interest in the potential role of bacterial colonization or infection of the bronchial mucosa in the pathogenesis of asthma has been raised by several recent reports: associations between bacterial colonization of neonatal airways and subsequent asthma development,¹ evidence of bronchial infection by specific intracellular bacteria among adult asthmatic patients,² and the efficacy of prolonged macrolide antibiotic treatment in subsets of asthmatic patients.³⁻⁵ Although the role of microbial infection in asthma pathogenesis remains unclear, studies to date have primarily applied culture-based or targeted molecular approaches to identify specific bacterial species of interest in the airways. However, recent developments in defining the human microbiome have demonstrated that the composition of bacterial communities colonizing mucosal surfaces, rather than simply the presence of individual species, can be important in defining states of health or disease.⁶⁻¹¹

Culture-independent microbiota profiling based on sequence polymorphisms in the 16S ribosomal RNA (16S rRNA) gene, which is present in all bacteria, has been widely applied in environmental ecologic studies¹²⁻¹⁴ and in studies of the human "superorganism."⁹⁻¹¹ 16S rRNA-based phylogenetic analysis through sequencing or phylogenetic arrays permits detection of

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Abbreviations used

ICS:	Inhaled corticosteroid
iNKT:	Invariant natural killer T
MIA:	Macrolides in Asthma
MRPP:	Multiresponse Permutation Procedure and Indicator Species Analysis
NMDS:	Nonmetric multidimensional scaling
Q-PCR:	Quantitative PCR
16S rRNA:	16S ribosomal RNA

uncultured or fastidious bacteria, providing information on community composition without *a priori* knowledge of those present.¹⁵⁻¹⁷ One such platform, the 16S rRNA PhyloChip, has been applied in a number of environmental^{12,14,15,18} and clinical^{6,19,20} studies. This high-density array contains approximately 500,000 probes that can differentiate approximately 8,500 bacterial taxa (defined as groups of organisms sharing $\geq 97\%$ 16S rRNA sequence homology)^{15,21} and demonstrates greater resolution of complex bacterial communities than traditional 16S rRNA clone library-sequencing approaches.^{6,18,21} It provides an ideal tool to examine relationships between microbiota composition, including the presence and relative abundance of members of the “rare biosphere,”²² and clinical characteristics of the disease.

Recognizing the frequency with which the tracheobronchial tree is exposed to the external environment and to secretions from the oropharynx or upper gastrointestinal tract, we hypothesized that complex bacterial communities might colonize asthmatic airway mucosa and exhibit relationships with clinical features of disease. Therefore in conjunction with a prospective study of the effects of extended clarithromycin therapy in adults with suboptimally controlled asthma,²³ we conducted a pilot study of the airway microbiota in 65 adult asthmatic patients and 10 healthy control subjects using the PhyloChip and parallel clone library sequencing. Bronchial airway samples from asthmatic patients possessed greater bacterial burden and diversity than those from healthy subjects. Furthermore, the degree of bronchial hyperresponsiveness exhibited by subjects was related to community composition and the relative abundance of specific bacterial families comprising the airway microbiota. Portions of these results have previously been presented in abstract form.^{24,25}

METHODS**Subjects**

Bronchial epithelial samples for microbial analysis were obtained from a subset of subjects enrolled in the Macrolides in Asthma (MIA) study²³ (NCT00318708, clinicaltrials.gov) conducted by the National Heart, Lung, and Blood Institute–sponsored Asthma Clinical Research Network. Briefly, adults with clinically stable but suboptimally controlled asthma, defined as persistent symptoms on the Asthma Control Questionnaire²⁶ after 4 weeks of standardized treatment with inhaled fluticasone, were studied. Relevant inclusion/exclusion criteria and study procedures are described in the Methods section in this article’s Online Repository at www.jacionline.org, including exclusion for symptoms of respiratory tract infection or asthma exacerbation within 6 weeks of the bronchoscopy visit. Bronchoscopy was performed before randomization to clarithromycin or placebo therapy. Three protected specimen bronchial brushings for microbiome analysis were obtained and sent to the University of California, San Francisco, where 10 healthy, non-smoking, nonatopic adults without asthma were also enrolled. All protocols were approved by the institutional review board at each center.

Sample processing

All samples first underwent screening by using PCR for the presence of the 16S rRNA gene with extracted total DNA (100 ng) and the universal 16S rRNA primers Bact-27F and Bact-1492R²⁷ in a 40-cycle reaction. Samples were deemed positive or negative for bacteria based on the presence or absence of a visible 16S rRNA PCR product. Samples with any evidence of a 16S rRNA PCR product were subsequently subjected to 8 PCR reactions (per sample) by using the same primer set across a temperature gradient (48°C to 58°C) to maximize bacterial diversity captured. Amplicons from each sample were then pooled, purified, and gel quantified with E-gels (Invitrogen, Carlsbad, Calif) before hybridization of a standardized quantity to the array for each sample, as previously described.^{6,15}

Quantitative PCR analysis

Quantitative PCR (Q-PCR) was performed for 21 samples to determine the total 16S rRNA copy number normalized to β -actin copy numbers. Further details are provided in the Methods section of this article’s Online Repository.

Data analysis

Relationships between microbiota structure and study variables were analyzed by using multivariate statistics in combination with the Multi-response Permutation Procedure and Indicator Species Analysis (MRPP) and nonmetric multidimensional scaling (NMDS) ordination.²⁸ Data were log

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TABLE I. Baseline characteristics of subjects

	Asthmatic patients (n = 65)	Healthy control subjects (n = 10)	P value
Age (y)	39.3 ± 11.2	35.5 ± 12.9	NS
Sex (% female/male)	52/48	60/40	NS
FEV ₁ (% predicted)	74.9 ± 15.6	94.1 ± 12.2	<.001
PC ₂₀ (mg · mL ⁻¹)	1.3 (2.9)*	>16	
Sputum eosinophils (%)	2.0 ± 5.2	NA	
Sputum neutrophils (%)	33.6 ± 23.7	NA	
Asthma Control Questionnaire score	1.8 ± 0.7	NA	
Total IgE (IU · mL ⁻¹)	128.4 (0.03)*	NA	

Asthmatic group			
	Analyzed by PhyloChip† (n = 42)	Unable to analyze by PhyloChip† (n = 23)	P value
Age (y)	40.4 ± 10.7	37.3 ± 12.1	.3
Sex (% female/male)	45/55	52/48	.4
FEV ₁ (% predicted)	75.5 ± 13.6	77 ± 14.8	.7
PC ₂₀ (mg · mL ⁻¹)*	1.2 (3.2)	1.8 (2.2)	.2
Sputum eosinophils (%)	2.2 ± 5.9	1.5 ± 3.3	.5
Sputum neutrophils (%)	30.0 ± 24.0	40.3 ± 22.3	.1
Asthma Control Questionnaire score	1.8 ± 0.8	1.8 ± 0.5	.6
Positive allergen skin test result (reaction to ≥1 allergen)	79% (33/42)	74% (17/23)	
Total IgE (IU · mL ⁻¹)*	114.6 (0.03)	158.3 (0.03)	.4
History of last oral corticosteroid use (no. of subjects)			
None since age 12 y	15	5	
Age 12 y to up to 2 years before study enrollment	13	7	.40‡
Within last 2 years before study enrollment	14	11	
Exacerbation events during study (no. of subjects)			
Within 1 wk of bronchoscopy	5	2	
>1 wk after bronchoscopy	3	2	.90‡
No exacerbations during study	34	19	

Values are presented as means ± SDs, except where noted.

NA, Not applicable; NS, not significant.

*Geometric mean (coefficient of variation) reported.

†Samples with a negative 16S rRNA PCR screen result or less than 100 ng of total 16S rRNA PCR product for hybridization were not analyzed by using PhyloChip.

‡Fisher exact P value.

transformed before analysis, where appropriate. Sorensen distance-based dissimilarity matrices were calculated and used for subsequent NMDS analysis to examine the relatedness of samples based on their microbiota composition. Three samples from asthmatic patients with mean relative Sorensen distances of greater than 2 deviations from the pooled mean were excluded for this analysis. Pearson correlations were performed to determine relationships between the relative abundance of all detected phylotypes and study variables with q value corrections for false discovery.²⁹ Significance was conservatively based on a false discovery rate of less than 3% and a probability of no more than 2 taxa being falsely identified as significant for each test. Community diversity was estimated by using Shannon indices³⁰ based on the number of taxa present (community “richness”) and their relative abundance (community “evenness”). Statistical analyses were conducted with PC-ORD version 5,³¹ JMP version 7 (SAS Institute, Inc, Chicago, Ill), and R software version 2.7.1 (<http://www.r-project.org>).

16S rRNA clone library sequencing

Clone libraries for a subset of patients were constructed (by using the same 16S rRNA amplicon pool hybridized to the array) and sequenced at the Department of Energy’s Joint Genome Institute (299–374 clones per library). Quality-filtered sequences were aligned and chimera checked with NAST³² and Bellerophon,³³ respectively, and then classified by means of G2-chip taxonomy (www.greengenes.lbl.gov).³⁴

Phylogenetic tree construction

Representative 16S rRNA sequences for taxa of interest were exported from the Greengenes database. A neighbor-joining tree with nearest-neighbor

interchange was produced with FastTree.³⁵ Trees were annotated by using the Interactive Tree of Life (<http://www.itol.embl.de/>).³⁶

RESULTS

Airway bacterial burden

Bronchial brushings were obtained from 75 subjects: 65 asthmatic patients and 10 healthy control subjects. Subjects’ characteristics are summarized in Table I. All asthmatic patients fulfilled entry criteria for the parent MIA trial,²³ and samples for this pilot study were processed as they were received with no additional selection criteria applied. On initial screening, 54 (83%) of 65 asthmatic patients and 8 (80%) of 10 control subjects exhibited a visible 16S rRNA PCR product. However, not all PCR-positive samples subsequently produced sufficient 16S rRNA amplicon for PhyloChip analysis. Although very small amplicon concentrations can be hybridized to the array, in our experience application of 250 ng provides good characterization of the respiratory microbiota.^{8,19} A greater proportion of asthmatic patients (37/65 [56.9%]) than healthy subjects (3/10 [30%]) produced 250 ng of amplicon, although this difference was not significant ($P = .17$). To increase the number of samples for comparative analyses, we analyzed the community composition detected by using the PhyloChip in 6 paired samples with both 100 and 250 ng of amplicon. Finding no significant difference in the community composition detected in paired samples (P_{MRPP}

> 0.1), 7 additional subjects (5 asthmatic patients and 2 healthy subjects) were assayed by using PhyloChip with 100 ng of amplicon. Therefore array data from a total of 47 subjects (42 asthmatic patients and 5 healthy control subjects) were obtained for the subsequent analyses (see Fig E1 in this article's Online Repository at www.jacionline.org).

To confirm that 16S rRNA amplicon concentrations (in nanograms per microliter) reported by means of gel quantification accurately reflected bacterial burden, we performed total 16S rRNA Q-PCR and regression analysis on these independent measurements, which demonstrated strong concordance ($r = 0.69$, $P < .001$). These data also confirmed that samples with sufficient amplicon for array analysis had significantly greater 16S rRNA copy numbers compared with those unable to be analyzed by using PhyloChip ($P = .002$). Therefore gel-quantified 16S rRNA amplicon concentrations were used as a proxy for bacterial burden to examine potential relationships between airway bacterial burden and clinical variables. Of the samples analyzed by using PhyloChip, bacterial burden was significantly higher in asthmatic samples compared with that seen in control samples ($P = .008$, Fig 1). Bacterial burden appeared to decrease with increasing methacholine PC₂₀ measurements, although this did not reach statistical significance ($r = -0.21$, $P = .09$), suggesting that community composition rather than actual bacterial burden might be more related to this clinical feature.

Airway microbiota structure and clinical features of asthma

Phylogenetic analysis identified 1941 bacterial taxa (detected in at least 1 subject) representing 161 bacterial families (see Table E1 in this article's Online Repository at www.jacionline.org). As a form of validation, we compared the phylogenetic distribution of airway microbiota detected by using the array with reference trees for airway bacteria reported in the Human Microbiome Project (http://www.hmpdacc.org/reference_genomes.php; accessed May 13, 2010)³⁷ and observed good agreement in the types of bacteria reported by both (data not shown). Community richness across samples from asthmatic patients was variable and ranged from 48 to 1240 taxa. Of the 5 healthy subjects, 3 exhibited low community richness (200-253 taxa), whereas 2 demonstrated greater richness (844 and 1121 taxa), suggesting that variability in airway microbiota composition was not exclusive to asthmatic patients.

We found no association between study center and variation in microbiota composition, indicating that sample collection by different operators in distinct geographic regions was not a major influence on community composition in this study. Multivariate analyses also showed no association between microbiota composition and spirometric measurements (FEV₁ and forced vital capacity), sputum eosinophil or neutrophil percentages, history of exacerbations, or systemic corticosteroid treatment within the previous 2 years. However, microbiota structure differed significantly based on asthmatic or healthy group assignment ($P_{MRPP} = .028$), and NMDS analysis demonstrated that variability in airway microbiota composition was correlated with both the degree of airway hyperresponsiveness (methacholine PC₂₀ concentrations; $r = 0.56$, $P < .001$; Fig 2, A) and bacterial burden ($r = -0.36$, $P = .015$; Fig 2, B). This suggests that the types and relative abundance of bacteria present in the airways are associated with these 2 variables.

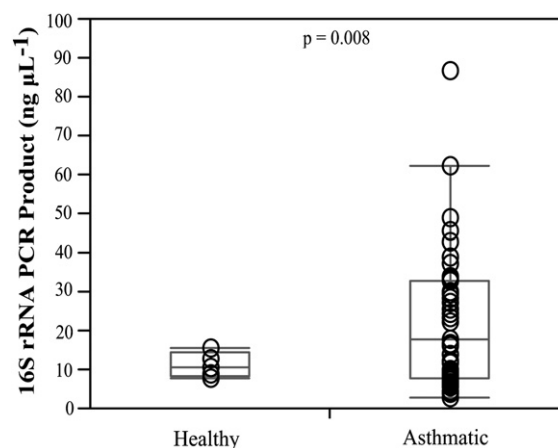


FIG 1. 16S rRNA bacterial burden in bronchial brushings from asthmatic patients and healthy subjects. Of subjects analyzed by using PhyloChip (total $n = 47$), asthmatic patients exhibited greater bacterial burden (measured concentration of 16S rRNA PCR product) than healthy subjects ($P = .008$, Welch t test with log-transformed data). Median and interquartile ranges are noted.

Airway bacterial diversity, community composition, and bronchial hyperresponsiveness

Asthmatic patients possessed greater airway microbiota diversity than control subjects ($P = .012$). Methacholine PC₂₀ concentrations were inversely correlated with diversity ($r = -0.46$, $P < .003$; Fig 2, C), suggesting a strong relationship between increased airway bacterial diversity and greater bronchial hyperresponsiveness.

Relationships between PC₂₀ and relative abundance of all taxa detected were analyzed to determine which of the airway microbiota were most associated with bronchial hyperresponsiveness. After false discovery correction, approximately 100 taxa demonstrated a significant ($P < .01$, $q \leq 0.015$) linear relationship between increasing relative abundance and greater bronchial hyperresponsiveness (Fig 3 and see Table E2 in this article's Online Repository at www.jacionline.org). These taxa, primarily belonging to the Proteobacteria, represented 31 bacterial families, such as the Comamonadaceae, Sphingomonadaceae, Nitrosomonadaceae, Oxalobacteraceae, and Pseudomonadaceae, and included a number of potentially interesting organisms. Although samples were collected in a manner to minimize oral secretion contamination (eg, use of triple-lumen protected specimen brushes and sample collection early in the procedure preferentially from upper lobes), we recognized the potential for organisms associated with the oropharynx to reside in the lower airways. Thus we investigated whether these approximately 100 phylotypes have previously been identified in the oral cavity by interrogating both the extensive human oral microbiome sequence database³⁸ and PubMed using species or genus names and the search terms "oral," "oropharynx," "mouth," or "tongue." The majority (87.5%) of these phylotypes were not found referenced to the oral cavity in either database.

Posttreatment bronchoscopy was not performed in the parent study, and therefore examination of relationships between clarithromycin-induced changes in airway microbiota composition and treatment outcomes was not possible. Instead, we explored whether relationships existed between pretreatment airway microbiota and posttreatment clinical outcomes. Airway bacterial

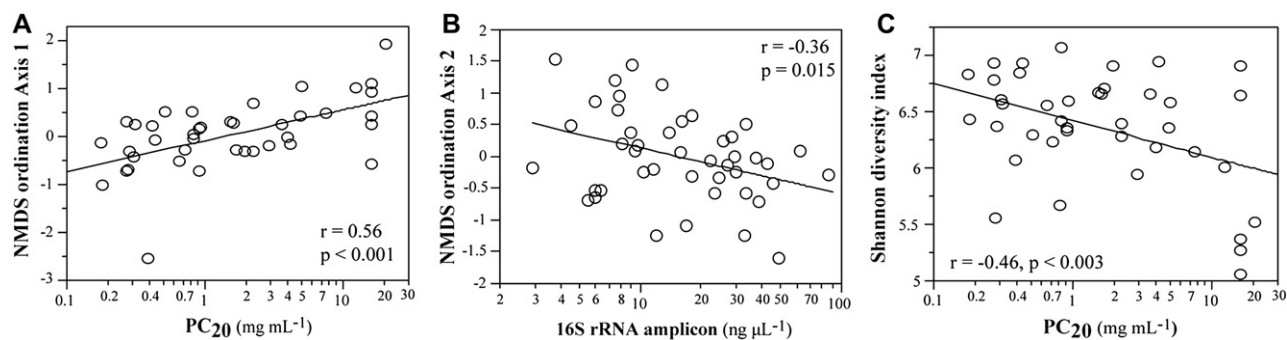


FIG 2. Relationships between variability in airway microbiota composition and community diversity with bronchial hyperresponsiveness. Each circle represents the microbiota present in a single sample ($n = 44$). **A** and **B**, NMDS ordination, based on Sorensen dissimilarity matrices, demonstrates that variability in community composition is most strongly related to bronchial hyperresponsiveness and bacterial burden. The NMDS axes have no inherent units and indicate spatial relationships of samples based on their phylogenetic (dis)similarity. Three samples from asthmatic patients were excluded due to extreme mean relative Sorensen distances from the pooled mean. **C**, Increased diversity (higher Shannon indices) is correlated with greater bronchial hyperresponsiveness (Pearson correlations with log-transformed data).

diversity was significantly greater in asthmatic subjects who demonstrated a significant reduction in bronchial reactivity in response to clarithromycin treatment (defined as at least a doubling in methacholine PC_{20} dose before and after treatment) than those with a smaller reduction ($P = .03$, Fig 4). This pattern was not evident in patients who received placebo intervention ($P = .64$).

16S rRNA clone library-sequencing validation

The PhyloChip, like other array technologies, is potentially susceptible to cross-hybridization, despite features of the array design intended to minimize this. 16S rRNA clone libraries were constructed with the same amplicon pool hybridized to the array for a subset of asthmatic patients ($n = 6$) to validate array-based findings. An average of 333 clones per sample were analyzed, yielding approximately 2000 nonchimeric sequences representing 197 taxa, the majority of which were present in more than 1 sample. The majority of bacterial subfamilies identified by means of sequencing were also present in the corresponding array dataset, validating large numbers of array-based positive hits (Table II). Two subfamilies (the Fusobacteriaceae subfamily 3 and Prevotellaceae subfamily 1) were detected by means of sequencing only in 2 samples (1 subfamily per sample). However, taxa within these subfamilies were very close (positive-fraction value = 0.84 and 0.75, respectively) to the conservative arbitrary cutoff (positive-fraction value ≥ 0.9) used to define array-based presence or absence.¹⁵ Clone library analysis also indicated that 2 samples (AB01 and AB04) were each dominated by a specific bacterial family. The majority of sequences for sample AB01 were classified as Pasteurellaceae subfamily 1 (this sample also exhibited the lowest array-reported community richness [48 taxa]), whereas for subject AB04, a majority of the sequences belonged to the Cellulomonadaceae.

DISCUSSION

To our knowledge, this is the first study to examine whether specific aspects of the airway microbiota are related to relevant clinical or physiologic features of asthma. Our findings suggest that bacterial diversity, variations in community composition, and the relative abundance of specific phylotypes are associated with the degree of bronchial hyperresponsiveness in asthmatic patients

administered inhaled corticosteroids (ICSs). This culture-independent study also expands the repertoire of organisms of potential relevance to asthma pathogenesis within this cohort beyond those previously implicated.^{1,2} These data, together with recent studies in other asthmatic patients,⁷ suggest that the microbiome of the airways, as with other discrete host niches, might be an important contributor to asthma pathophysiology and to the heterogeneity of disease.³⁹⁻⁴¹

Overall, these findings highlight 2 key aspects in defining airway health. The existence of a bronchial microbiota suggests that the bronchial tree is unlikely to be completely sterile and that the composition of its microbiome might directly or indirectly modulate airway function. The role of airway microbiota in airway disease is underinvestigated compared with other human niches, such as the intestinal microbiota, which has a demonstrated role in chronic inflammatory gastrointestinal diseases.^{10,42} That a bronchial epithelium-associated microbiota exists is not entirely unexpected, particularly in the setting of airway disease, ICS therapy, or both. Specific bacterial communities persist in the airways despite antimicrobial treatment in patients with chronic obstructive pulmonary disease and cystic fibrosis.^{8,19} Recently, Hilty et al⁷ also described airway microbiota in patients with mild-to-moderate asthma (all receiving ICS therapy), patients with chronic obstructive pulmonary disease, and healthy subjects. Those with airway disease had an increased prevalence of pathogenic Proteobacteria compared with control subjects, although relationships to clinical measurements were not examined in their study.

Complex microbial communities are now recognized to reside in various host mucosal sites⁴³ where perturbations of community structure are associated with disease.^{6,8,10,42} Moreover, the airway epithelium is increasingly recognized as important in immunologic responses to environmental and microbial exposures.⁴⁴ Thus the airway microbiome could potentially influence presentations of asthma. As such, our findings of specific community relationships with bronchial hyperresponsiveness in the context of a well-characterized asthmatic cohort receiving standardized baseline treatment implicate additional bacterial groups in asthma. These include a *Nitrosomonas* species possessing a functional nitric oxide reductase.⁴⁵ Their relative abundance might be a microbial indicator of airway concentrations of nitric oxide that,

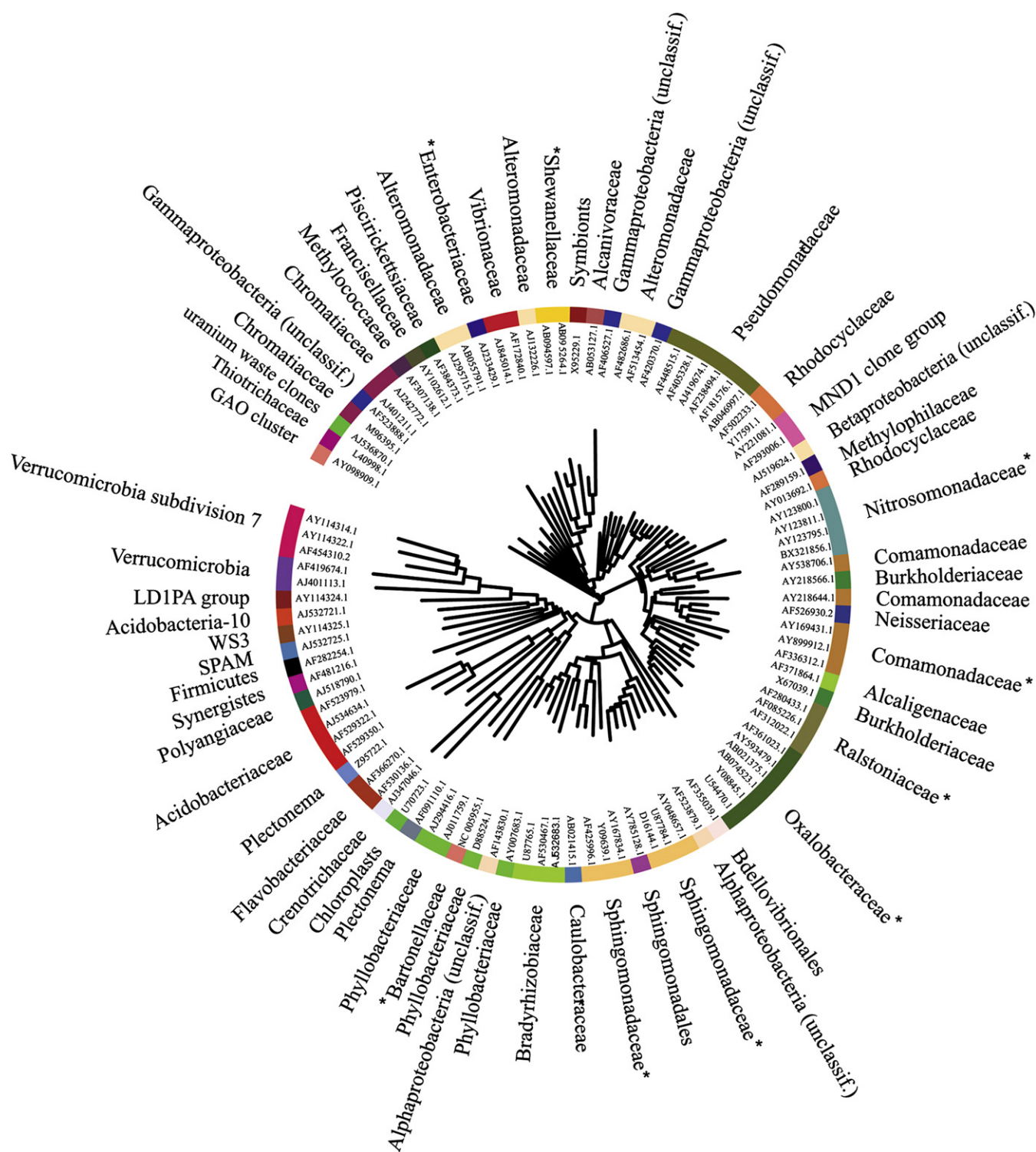


FIG 3. Phylogenetic tree based on 16S rRNA representative gene sequences (GenBank accession numbers) of the approximately 100 bacterial taxa highly correlated with greater bronchial hyperresponsiveness ($P < .01$, $q < 0.015$). Colors represent different bacterial families. Asterisks denote taxa with member species previously associated with clinical disease or possessing notable functional features (see also Table E2 in this article's Online Repository).

although not assessed in this study, reflect airway inflammation⁴⁶ and correlate with measures of airway hyperresponsiveness.⁴⁷ Also notable is *Oxalobacter formigenes* (Oxalobacteraceae), an

anaerobic bacterium known to be susceptible to macrolide antibiotics.⁴⁸ Other bacteria of interest include the Comamonadaceae and Sphingomonadaceae. Members of the Comamonadaceae,

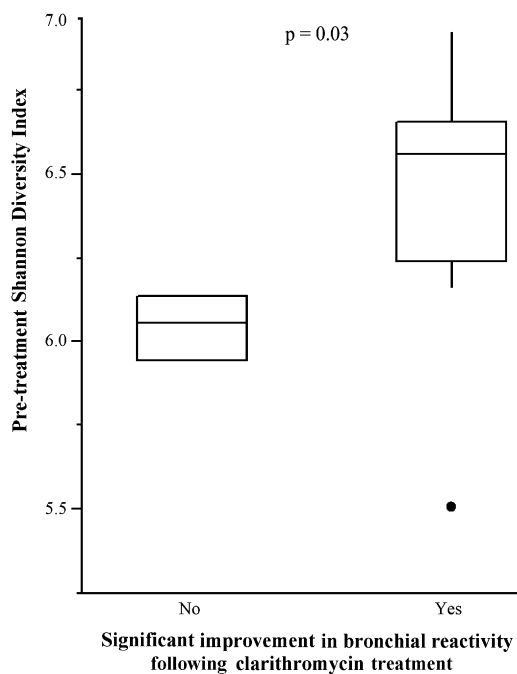


FIG 4. Baseline airway microbiota diversity and change in bronchial hyperresponsiveness with clarithromycin treatment. Sixteen asthmatic patients with pretreatment samples analyzed by means of microarray received clarithromycin therapy. Subjects with significant improvement in bronchial hyperresponsiveness after clarithromycin ($n = 9$) possessed higher pretreatment airway bacterial diversity than those with no significant response ($n = 3$). Four subjects with incomplete data because of study discontinuation were not included.

previously identified in patients with cystic fibrosis,⁴⁹ possess steroid-responsive degradation pathways,^{50,51} and their presence could plausibly be related to the selective pressure of ICS therapy. This raises the intriguing possibility that steroid nonresponsiveness, as observed in some asthmatic patients despite adherence to therapy,⁵² might be due in part to the presence of airway bacteria with steroid-degrading capacity.

Given the existence of airway microbiota, it is conceivable that the coincident presence of multiple potentially pathogenic bacteria contributes to persistent airway inflammation in asthma. This possibility is supported by the finding of neutrophilia in bronchial airway samples of some patients with severe asthma despite regular use of high-dose ICSs.⁵³ Such inflammation could represent an appropriate response by the host to inappropriate airway microbial colonization. For example, Sphingomonadaceae, members of which were significantly correlated with bronchial hyperresponsiveness, are characterized by the presence of cell-membrane glycosphingolipids, which are recognized by and can activate invariant natural killer T (iNKT) cells, resulting in induction of IL-4 and IL-13.^{54,55} Glycolipid activation of iNKT cells can also induce airway hyperreactivity independent of conventional CD4⁺ T cells.⁵⁶ Although the presence of iNKT cells in asthmatic airways remains controversial,^{57,58} our findings suggest a possible role for Sphingomonadaceae in airway pathophysiology and the possibility that the observed variability of iNKT cell populations in asthmatic patients might depend in part on the relative abundance of these species.

We recognize that this pilot study is limited by the relatively small number of subjects, especially healthy control subjects, and

by the absence of asthmatic patients not taking an ICS. Nonetheless, the data indicate that airway bacterial burden in subjects without airway disease is much lower than in asthmatic patients requiring ICS therapy. Because all asthmatic patients were required to be taking standardized ICSs for the parent study,²³ we are unable to infer whether the higher bacterial burden among asthmatic patients is a function of the disease itself or ICS treatment, although the relationships of bacterial burden and the composition and diversity of the microbiota to bronchial hyperresponsiveness are robust. Determining the effects of ICS use on the airway microbiome will require further investigation and is an important question given the wide use of ICS therapies in airway diseases, which, among patients with chronic obstructive pulmonary disease, has been associated with an increased risk of pneumonia.⁵⁹

The array-based analysis in this study identified a greater diversity of airway microbiota than has previously been described, although to our knowledge, there has been only one other study involving asthmatic patients that applied 16S rRNA phylogenetic analysis.⁷ In addition to clone library-sequencing validations, our results also agreed with those of Hilty et al⁷ in that we detected all bacterial phyla and genera identified in their study of the lower airways of 11 adult and 13 pediatric asthmatic patients on ICS therapy. The PhyloChip platform permits in-depth analysis of relatively large numbers of samples by using a standardized assay that applies several levels of stringent criteria for determining the microbiota profile in a given sample. It is impractical to perform sequence corroboration for every array-based positive hit. Moreover, the extent of microbial diversity detected is dependent on the community structure and the depth of sequencing performed.⁶⁰ Our study included the largest number of clones sequenced to date for asthmatic airway samples and confirmed the presence of many array-detected phylotypes, indicating that complex microbiota do exist in this niche.

Finally, we observed that asthmatic patients exhibiting a significant decrease in bronchial hyperresponsiveness after clarithromycin treatment in the parent study possessed greater pretreatment airway bacterial diversity than nonresponders. Despite the small number of subjects in this exploratory analysis, the trend is interesting given that prior studies have also observed decreased bronchial responsiveness after prolonged macrolide therapy.^{4,61} Furthermore, although the antimicrobial susceptibility of the entire airway microbiota is unknown, conceivably, a multitude of community members might be sensitive to macrolides, resulting in a reduction in bacterial diversity, burden, or both on treatment and manifesting clinically in a reduction in bronchial responsiveness. Thus although the efficacy of macrolides in airway disease is often attributed to their anti-inflammatory properties, their effectiveness could also reflect an extended spectrum of antibacterial activity against members of the airway microbiota, the composition of which, as in the setting of ICSs, might influence outcomes.

In summary, several features of the airway microbial community are significantly associated with the degree of bronchial hyperresponsiveness among patients with suboptimally controlled asthma. Despite limitations, these study findings are notable in providing the first evidence for the potential functional, physiologic, and clinical relevance of the airway microbiome in asthma. Our results suggest that variations in airway microbiome structure and function might exert distinct effects that contribute

TABLE II. Bacterial families identified by using both 16S rRNA clone library sequencing and 16S rRNA PhyloChip

AB01 (374)			AB02 (301)			AB03 (299)		
Phylum	Family	Subfamily	Phylum	Family	Subfamily	Phylum	Family	Subfamily
Firmicutes	Streptococcaceae	sf-1	Actinobacteria	Cellulomonadaceae	sf-1	Actinobacteria	Cellulomonadaceae	sf-1
Proteobacteria	Pasteurellaceae	sf-1	Bacteroidetes	Flavobacteriaceae	sf-1	Bacteroidetes	Prevotellaceae	sf-1
Bacteroidetes	Prevotellaceae	sf-1	Bacteroidetes	Porphyromonadaceae	sf-1	Firmicutes	Enterococcaceae	sf-1
			Bacteroidetes	Prevotellaceae	sf-1	Firmicutes	Peptococcaceae/ Acidaminococcaceae	sf-11
			Firmicutes	Lachnospiraceae	sf-5	Firmicutes	Peptostreptococcaceae	sf-5
			Firmicutes	Mycoplasmataceae	sf-1	Firmicutes	Staphylococcaceae	sf-1
			Firmicutes	Peptococcaceae/ Acidaminococcaceae	sf-11	Firmicutes	Streptococcaceae	sf-1
			Firmicutes	Peptostreptococcaceae	sf-5	Fusobacteria	Fusobacteriaceae	sf-1
			Firmicutes	Staphylococcaceae	sf-1	Fusobacteria	Fusobacteriaceae	sf-3
			Firmicutes	Streptococcaceae	sf-1	Proteobacteria	Campylobacteraceae	sf-3
			Fusobacteria	Fusobacteriaceae	sf-1	Proteobacteria	Pasteurellaceae	sf-1
			Fusobacteria	Fusobacteriaceae	sf-3	TM7	Unclassified	sf-1
			Proteobacteria	Campylobacteraceae	sf-3			
			Proteobacteria	Pasteurellaceae	sf-1			
			Spirochaetes	Spirochaetaceae	sf-1			
			TM7	Unclassified	sf-1			

AB04 (344)			AB05 (332)			AB32 (349)		
Phylum	Family	Subfamily	Phylum	Family	Subfamily	Phylum	Family	Subfamily
Actinobacteria	Cellulomonadaceae	sf-1	Actinobacteria	Micrococcaceae	sf-1	Actinobacteria	Corynebacteriaceae	sf-1
Bacteroidetes	Porphyromonadaceae	sf-1	Bacteroidetes	Flavobacteriaceae	sf-1	Bacteroidetes	Porphyromonadaceae	sf-1
Bacteroidetes	Prevotellaceae	sf-1	Bacteroidetes	Porphyromonadaceae	sf-1	Bacteroidetes	Prevotellaceae	sf-1
Firmicutes	Aerococcaceae	sf-1	Bacteroidetes	Prevotellaceae	sf-1	Firmicutes	Aerococcaceae	sf-1
Firmicutes	Lachnospiraceae	sf-5	Firmicutes	Aerococcaceae	sf-1	Firmicutes	Enterococcaceae	sf-1
Firmicutes	Peptococcaceae/ Acidaminococcaceae	sf-11	Firmicutes	Enterococcaceae	sf-1	Firmicutes	Lachnospiraceae	sf-5
Firmicutes	Peptostreptococcaceae	sf-5	Firmicutes	Erysipelotrichaceae	sf-3	Firmicutes	Mycoplasmataceae	sf-1
Firmicutes	Streptococcaceae	sf-1	Firmicutes	Lachnospiraceae	sf-5	Firmicutes	Peptococcaceae/ Acidaminococcaceae	sf-11
Fusobacteria	Fusobacteriaceae	sf-3	Firmicutes	Peptococcaceae/ Acidaminococcaceae	sf-11	Firmicutes	Peptostreptococcaceae	sf-5
Proteobacteria	Campylobacteraceae	sf-3	Firmicutes	Peptostreptococcaceae	sf-5	Firmicutes	Staphylococcaceae	sf-1
Proteobacteria	Pasteurellaceae	sf-1	Firmicutes	Staphylococcaceae	sf-1	Firmicutes	Streptococcaceae	sf-1
Proteobacteria	Pseudomonadaceae	sf-1	Firmicutes	Streptococcaceae	sf-1	Fusobacteria	Fusobacteriaceae	sf-1
			Fusobacteria	Fusobacteriaceae	sf-1	Fusobacteria	Fusobacteriaceae	sf-3
			Proteobacteria	Campylobacteraceae	sf-3	Proteobacteria	Campylobacteraceae	sf-3
			Proteobacteria	Pasteurellaceae	sf-1	Proteobacteria	Moraxellaceae	sf-3
			Proteobacteria	Pseudomonadaceae	sf-1	Proteobacteria	Pasteurellaceae	sf-1
			Spirochaetes	Spirochaetaceae	sf-1	Proteobacteria	Pseudomonadaceae	sf-1
			TM7	Unclassified	sf-1	TM7	Unclassified	sf-1

Phylotypes reported at the subfamily level classified by using Greengenes G2 chip taxonomy (number of clones sequenced per library indicated in parentheses). Subfamilies in boldface were undetected by means of array based on conservative criteria for determining taxon presence.

to asthma heterogeneity and provide novel targets and hypotheses for future studies on disease mechanisms.

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Clinical implications: Relationships between airway microbiota and clinical features of asthma were investigated by using culture-independent approaches. Among adults with suboptimally controlled asthma, bronchial hyperresponsiveness correlated strongly with airway microbiota composition and diversity.

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METHODS

Subject characterization and study procedures

For the MIA clinical trial, adult men and women 18 to 60 years of age meeting the diagnostic criteria for asthma were enrolled through 10 Asthma Clinical Research Network clinical research centers. Subjects had to have suboptimal asthma control, which was defined as persistent symptoms at least as severe as those of mild persistent asthma, as reflected by an Asthma Control Questionnaire score of greater than 1.25, after 4 weeks of standardized treatment with 88 μ g of fluticasone propionate administered twice daily through a metered-dose inhaler (GlaxoSmithKline, London, United Kingdom). Exclusion criteria included a smoking history of greater than 10 pack-years, unstable asthma, respiratory tract infection or exacerbation less than 6 weeks before enrollment, postbronchodilator FEV₁ of less than 60% of predicted value, and other pulmonary disease. The institutional review board at each center approved all study protocols. After the run-in treatment period with inhaled fluticasone, sputum induction was performed for differential cell counts, followed by flexible fiberoptic bronchoscopy 3 to 10 days later after achievement of local anesthesia, as previously described.^{E1} This was performed before randomization to treatment with clarithromycin or placebo in the parent trial. During bronchoscopy, 3 bronchial brushings with triple-lumen protected specimen brushes were obtained for microbiome analysis, primarily from the upper or middle lobes of the lung, and immediately placed into 2 mL of RNeasy Lysis Buffer. Samples were placed at 4°C for at least 24 hours before shipping on blue ice to the University of California, San Francisco. In addition, healthy nonsmoking adults were enrolled separately at the University of California, San Francisco, and ruled out for asthma and atopy based on the presence of normal spirometric results, normal bronchial reactivity to methacholine (PC₂₀ >16 mg/mL), and negative responses to skin testing with 10 mixes of allergens common to northern California.

Sample preparations and array processing

Sterilized forceps were used to transfer 3 protected specimen bronchial brushes to a single lysing matrix B tube containing 0.1-mm silica spheres (MP Biomedicals, Solon, Ohio). Original collection tubes were centrifuged at 12,000g, RNeasy Lysis Buffer was removed, and Buffer RLT (650 μ L, AllPrep kit; Qiagen, Valencia, Calif) was used to resuspend the pellet before transfer into the lysing matrix B tube containing the brushes. Bead beating at 5.5 m/s for 30 seconds was carried out with the FastPrep system (MP Biomedicals). Tubes were then centrifuged at 2,000g for 2 minutes, and the supernatant was transferred to a DNA spin column of the AllPrep Kit and further processed according to kit instructions.

Samples were screened by means of PCR for the presence of a 16S rRNA gene product with 100 ng of extracted DNA and 15 μ mol each of the universal 16S rRNA primers^{E2} Bact-27F (5'-AGAGTTTGATCCTGGCTCAG-3') and Bact-1492R (5'-GGTACCTTGTACGACTT-3') in 50- μ L volume reactions at an annealing temperature of 53°C for 40 cycles in an Eppendorf MasterCycler gradient PCR machine. In addition to negative controls, parallel poison control PCR reactions (with *Pseudomonas aeruginosa* DNA) were performed to rule out PCR inhibition for those samples with no evidence of 16S rRNA PCR product on a 1% ethidium bromide-stained agarose gel. Those with a PCR-positive screen for a 16S rRNA PCR product then proceeded to sample preparation for array hybridization and processing (Fig E1). For this, eight 25- μ L PCR reactions, each containing 100 ng of extracted sample DNA and 8 μ mol of each of Bact-27F and Bact-1492R primers, were performed in 30 cycles of amplification across a gradient of annealing temperatures (48°C to 58°C). 16S rRNA amplicons for each sample were then pooled, purified, and gel quantified before array hybridization (E-gel 2% and E-gel Low Range Quantitative Ladder, Invitrogen). A standard concentration of 250 ng (or 100 ng in 7 samples, as discussed in the Results section) of DNase-fragmented and biotin-labeled 16S rRNA amplicons from each sample spiked with known concentrations of synthetic 16S rRNA gene fragments and non-16S rRNA gene fragments as internal controls for interarray normalization was hybridized to each array, followed by washing, staining, and scanning of arrays (GeneArray scanner; Affymetrix, Santa Clara, Calif) as previously described.^{E3,E4}

Q-PCR

TriPLICATE 25- μ L reactions were performed in 21 samples by using the QuantiTect SYBR Green PCR master mix kit (Qiagen), 10 ng of extracted DNA,

and the 16S rRNA Q-PCR primers^{E5} 338-F (5'-ACTCTACGGGAGGCGAG-CAG-3') and 518-R (5'-ATTACCGCGGCTGCTGG-3') at a final concentration of 0.3 μ mol/L under the following conditions: 95°C for 10 minutes, followed by 40 cycles of denaturation at 95°C for 30 seconds, annealing at 53°C for 30 seconds, extension at 72°C for 30 seconds, and final extension at 72°C for 10 minutes. Standard curves at serial log concentrations of 1×10^2 to 1×10^8 were generated from a PCR product obtained by using the universal 16S rRNA primers Bact-27F and Bact-1492R to calculate total 16S rRNA gene copy numbers. Regression coefficients (r^2) for all standard curves were greater than 0.99. Total 16S rRNA copy numbers for each sample were normalized to mammalian β -actin copy numbers in each sample, which were determined by means of Q-PCR with β -actin primers, as previously described.^{E6}

Microarray data analysis

After scaling and normalization of the raw data, relatively conservative criteria were applied to determine the presence or absence of bacterial taxa by using previously described methods.^{E3,E4} Briefly, taxon presence was determined based on a positive-fraction value corresponding to 90% of the probe sets for an individual taxon. Each taxon probe set is comprised of a minimum of 11 probe pairs (a perfect match and a mismatch probe differing at a single central oligonucleotide) to distinguish taxa on the basis of at least 2 discriminatory loci on the 16S rRNA gene. Relative abundance estimates were based on averaged, log-transformed fluorescence intensities for each taxon. Sorensen distance measures were calculated by using the software package PC-ORD version 5. Three samples from asthmatic patients were identified as statistical outliers with a mean relative Sorensen distance of greater than 2 SDs from the pooled mean and were not included in the array-based analyses of community structure and diversity.

16S rRNA clone library-sequencing

Clone libraries were constructed by using the same 16S rRNA amplicon pool that was hybridized to the array. 16S rRNA PCR products were gel purified, and 3' adenine overhangs were reintroduced after amplification through Taq DNA polymerase for improved cloning efficiency. Purified amplicons were ligated to the pCR4-TOPO vector by using the TOPO TA Cloning Kit (Invitrogen). Ligation mixtures were electroporated into One Shot TOP10 Electrocomp *Escherichia coli* cells (Invitrogen) and plated on selective agar. Two hundred ninety-nine to 374 clones per library were sequenced on an ABI PRISM 3730 capillary DNA sequencer (Applied Biosystems, Foster City, Calif) at the Department of Energy's Joint Genome Institute (Walnut Creek, Calif), according to standard Joint Genome Institute protocols (www.jgi.doe.gov). Bidirectional sequence reads were end paired, trimmed for vector and PCR primer sequence, and filtered for quality. This yielded 1,997 sequences for 6 asthmatic libraries, which were aligned by using the NAST algorithm for multiple sequence alignment, checked for chimeras with Bellepheron, and classified by means of G2-chip taxonomy, all available as Greengenes Web-based tools (<http://greengenes.lbl.gov>). Taxa identified by means of clone library sequencing and by means of corresponding array data in these subjects were compared to determine the number of phylotypes detected by using the array, by sequencing alone, or by both methods.

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APPENDIX E1**Collaborators**

The following Asthma Clinical Research Network sites and investigators participated in the parent MIA trial, which obtained the clinical data analyzed in this study and additionally obtained the bronchial brushings analyzed in this study only:

Brigham & Women's Hospital, Boston, Mass: E. Israel, M. E. Wechsler

National Jewish Health, Denver, Colo: R. J. Martin, R. M. Cherniack, S. J. Szeffler, E. R. Sutherland

University of Wisconsin School of Medicine and Public Health, Madison, Wis: R. F. Lemanske, C. A. Sorkness, N. N. Jarjour, L. Denlinger.

University of California, San Francisco: H. A. Boushey, J. V. Fahy, S. C. Lazarus

Columbia University College of Physicians and Surgeons, New York, NY: E. DiMango

Duke University, Durham, NC: M. Kraft,

University of Texas Medical Branch, Galveston, Tex: W. J. Calhoun, B. T. Ameredes

Washington University, School of Medicine, St Louis, Mo: M. Castro, M. Walter

University of California, San Diego Medical Center, Calif: J. Ramsdell, S. I. Wasserman

Wake Forest University, School of Medicine, Winston-Salem, NC: E. Bleecker, D. Meyers, S. P. Peters, W. C. Moore, R. Pascual

Pennsylvania State College of Medicine, Hershey, Pa: V. M. Chinchilli, T. J. Craig, N. Icitovic, T. S. King

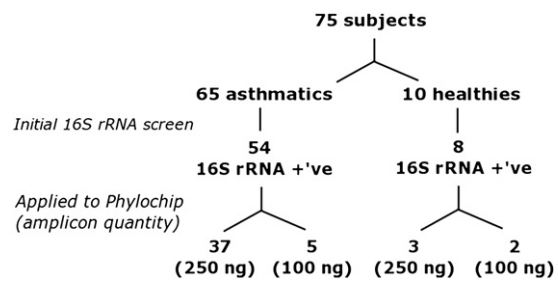
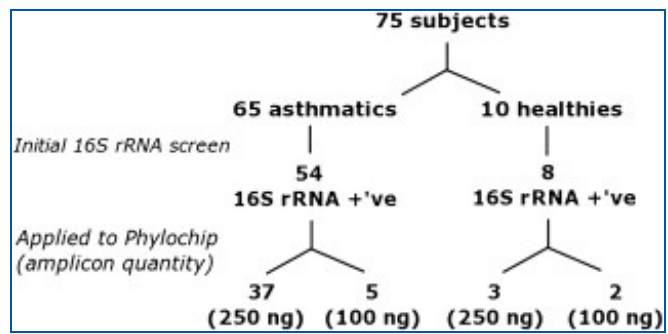


FIG E1. Diagram showing the sample evaluation process for PhyloChip analysis.



[High-quality image](#) (10 1K)Diagram showing the sample evaluation process for PhyloChip analysis.

Table E1. All bacterial taxa detected in protected bronchial epithelial brushings by 16S rRNA PhyloChip (present in at least one subject). Classification by ‘G2-Chip’ taxonomy (<http://greengenes.lbl.gov>) alphabetically by phylum.

<i>Phylum</i>	<i>Class</i>	<i>Family</i>	<i>Sub-family</i>	<i>PhyloChip taxon ID</i>	<i>Taxon representative species</i>
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_14	176	uranium mining waste clone JG37-AG-112
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_14	209	uranium mining waste clone JG37-AG-29
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_14	274	uranium mining waste clone JG37-AG-73
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_14	508	uranium mining waste clone JG37-AG-81
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_14	541	uranium mill soil sample clone GuBH2-AG-47
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_14	582	heavy metal-contaminated soil clone a13114
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_14	964	uranium mining waste clone JG37-AG-145
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_14	6335	forested wetland clone FW45
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_6	6345	soil sample clone JG36-TzT-77 bacterium
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_14	6350	soil isolate Ellin337
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_14	6356	forested wetland clone FW47
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_6	6359	PCE-contaminated site clone CLi114
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_6	6362	grassland soil clone DA052
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_14	6364	Solibacter usitatus Ellin6076
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_14	6366	PCB-polluted soil clone WD228
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_14	6368	soil clone UA2
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_14	6378	Acidobacterium capsulatum
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_14	6405	soil sample clone JG36-TzT-31 bacterium
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_14	6410	
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_14	6412	acid mine drainage clone TRB82
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_16	6414	PCE-contaminated site clone CLs73
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_14	6421	PCB-polluted soil clone WD217
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_6	6423	coal effluent wetland clone FW92
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_14	6424	sphagnum peat bog clone K-5b10
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_14	6425	Great Artesian Basin clone B27

Acidobacteria	Acidobacteria-6	Unclassified	sf_1	37	soil clone BAC-14A1
Acidobacteria	Acidobacteria-4	Unclassified	sf_1	87	activated sludge clone 2951
Acidobacteria	Acidobacteria-4	Unclassified	sf_1	435	anaerobic VC-degrading clone VC47 bacterium
Acidobacteria	Acidobacteria-6	Unclassified	sf_1	500	soil clone RB24
Acidobacteria	Acidobacteria-10	Unclassified	sf_1	516	uranium mining waste pile clone JG34-KF-153
Acidobacteria	Acidobacteria-5	Unclassified	sf_1	523	soil metagenomic library clone 17F9
Acidobacteria	Acidobacteria-6	Unclassified	sf_1	569	Holophaga/Acidobacterium phylum clone ii3-12
Acidobacteria	Unclassified	Unclassified	sf_1	572	forested wetland clone FW144
Acidobacteria	Acidobacteria-7	Unclassified	sf_1	588	TCB-transforming consortium clone SJA-36
Acidobacteria	Acidobacteria-4	Unclassified	sf_1	790	soil clone 11-25
Acidobacteria	Acidobacteria-6	Unclassified	sf_1	834	bioreactor clone mle1-25
Acidobacteria	Acidobacteria-6	Unclassified	sf_1	897	Mammoth cave clone CCM8b
Acidobacteria	Acidobacteria-6	Unclassified	sf_1	1049	soil clone C112
Acidobacteria	Unclassified	Unclassified	sf_1	4222	forested wetland clone FW105
Acidobacteria	Acidobacteria-4	Unclassified	sf_1	6348	soil clone RB41
Acidobacteria	Solibacteres	Unclassified	sf_1	6357	anaerobic benzene-degrading clone Cart-N4
Acidobacteria	Acidobacteria-4	Unclassified	sf_1	6363	soil clone 32-11
Acidobacteria	Solibacteres	Unclassified	sf_1	6367	TCE-contaminated site clone FTL227
Acidobacteria	Solibacteres	Unclassified	sf_1	6426	Great Artesian Basin clone B11
Actinobacteria	Actinobacteria	Acidimicrobiaceae	sf_1	1090	
Actinobacteria	Actinobacteria	Acidimicrobiaceae	sf_1	1360	forested wetland clone RCP2-103
Actinobacteria	Actinobacteria	Acidimicrobiaceae	sf_1	1749	forest soil clone DUNssu275 (-3A) (OTU#188)
Actinobacteria	Actinobacteria	Acidimicrobiaceae	sf_1	1856	forested wetland clone RCP2-105
Actinobacteria	Actinobacteria	Acidimicrobiaceae	sf_1	2014	marine sediment clone MB-A2-100
Actinobacteria	Actinobacteria	Acidimicrobiaceae	sf_1	2030	forested wetland clone RCP1-33
Actinobacteria	Actinobacteria	Acidothermaceae	sf_1	1399	uranium mill tailings clone Gitt-KF-183
Actinobacteria	Actinobacteria	Actinomycetaceae	sf_1	1193	Actinomyces canis
Actinobacteria	Actinobacteria	Actinomycetaceae	sf_1	1227	Actinomyces naeslundii
Actinobacteria	Actinobacteria	Actinomycetaceae	sf_1	1368	Actinomyces urogenitalis
Actinobacteria	Actinobacteria	Actinomycetaceae	sf_1	1649	Actinomyces graevenitzi str. CCUG 27294
Actinobacteria	Actinobacteria	Actinomycetaceae	sf_1	1672	Actinomyces odontolyticus str. CCUG 28084

Actinobacteria	Actinobacteria	Actinomycetaceae	sf_1	1684	Varibaculum cambriense str. CCUG 44998
Actinobacteria	Actinobacteria	Actinomycetaceae	sf_1	1883	Actinomyces funkei str. CCUG 42773
Actinobacteria	Actinobacteria	Actinomycetaceae	sf_1	2039	Actinomyces cardiffensis str. CCUG 44997
Actinobacteria	Actinobacteria	Actinomycetaceae	sf_1	2049	Arcanobacterium haemolyticum str. CIP 103370
Actinobacteria	Actinobacteria	Bifidobacteriaceae	sf_1	1109	Bifidobacterium thermacidophilum porcinum
Actinobacteria	Actinobacteria	Bifidobacteriaceae	sf_1	1351	Bifidobacterium psychraerophilum str. T16
Actinobacteria	Actinobacteria	Bifidobacteriaceae	sf_1	1444	Bifidobacteriaceae genomosp. C1
Actinobacteria	Actinobacteria	Bifidobacteriaceae	sf_1	1835	Bifidobacterium breve str. KB 92
Actinobacteria	Actinobacteria	Bifidobacteriaceae	sf_1	1875	
Actinobacteria	Actinobacteria	Bifidobacteriaceae	sf_1	1915	Bifidobacterium urinalis
Actinobacteria	Actinobacteria	Bifidobacteriaceae	sf_1	1967	Bifidobacterium pseudocatenulatum
Actinobacteria	Actinobacteria	Bifidobacteriaceae	sf_1	2040	Bifidobacterium adolescentis str. E-981074T
Actinobacteria	Actinobacteria	Brevibacteriaceae	sf_1	1745	Brevibacterium iodinum str. DSM 2062T
Actinobacteria	Actinobacteria	Cellulomonadaceae	sf_1	1431	Cellulomonadaceae str. W6
Actinobacteria	Actinobacteria	Cellulomonadaceae	sf_1	1449	Cellulomonadaceae str. WB13
Actinobacteria	Actinobacteria	Cellulomonadaceae	sf_1	1450	
Actinobacteria	Actinobacteria	Cellulomonadaceae	sf_1	1489	Tropheryma whippelii
Actinobacteria	Actinobacteria	Cellulomonadaceae	sf_1	1586	Cellulomonas gelida str. DSM 20111T
Actinobacteria	Actinobacteria	Cellulomonadaceae	sf_1	1589	Oerskovia turbata str. DSM 20577T
Actinobacteria	Actinobacteria	Cellulomonadaceae	sf_1	1748	Beutenbergia cavernosa str. DSM 12333
Actinobacteria	Actinobacteria	Cellulomonadaceae	sf_1	1780	Cellulomonas sp. IFO16240 str. IFO 16240
Actinobacteria	Actinobacteria	Cellulomonadaceae	sf_1	1923	Actinobacteria str. VeCb6
Actinobacteria	Actinobacteria	Coriobacteriaceae	sf_1	1226	Atopobium parvulum str. ATCC22793
Actinobacteria	Actinobacteria	Coriobacteriaceae	sf_1	1258	ground water deep-well Tomsk-7 clone
Actinobacteria	Actinobacteria	Coriobacteriaceae	sf_1	1294	
Actinobacteria	Actinobacteria	Coriobacteriaceae	sf_1	1459	termite gut homogenate clone Rs-J59 bacterium
Actinobacteria	Actinobacteria	Coriobacteriaceae	sf_1	1800	ground water deep-well Tomsk-7 clone
Actinobacteria	Actinobacteria	Coriobacteriaceae	sf_1	1924	Atopobium rimae str. ATCC49626
Actinobacteria	Actinobacteria	Coriobacteriaceae	sf_1	1926	Collinsella aerofaciens str. JCM7791
Actinobacteria	Actinobacteria	Coriobacteriaceae	sf_1	1956	Slackia heliotrinireducens str. ATCC 29202
Actinobacteria	Actinobacteria	Corynebacteriaceae	sf_1	1089	Corynebacterium mucifaciens

Actinobacteria	Actinobacteria	Corynebacteriaceae	sf_1	1192	Corynebacterium segmentosum str. CIP107068
Actinobacteria	Actinobacteria	Corynebacteriaceae	sf_1	1374	
Actinobacteria	Actinobacteria	Corynebacteriaceae	sf_1	1428	Corynebacterium simulans
Actinobacteria	Actinobacteria	Corynebacteriaceae	sf_1	1492	Corynebacterium tuscaniae str. ISS-5309
Actinobacteria	Actinobacteria	Corynebacteriaceae	sf_1	1517	Corynebacterium xerosis str. DSM 20743
Actinobacteria	Actinobacteria	Corynebacteriaceae	sf_1	1803	Corynebacterium spheniscorum
Actinobacteria	Actinobacteria	Corynebacteriaceae	sf_1	1820	Corynebacterium jeikeium str. ATCC 43734
Actinobacteria	Actinobacteria	Dermabacteraceae	sf_1	1504	Brachybacterium sacelli str. LMG 20338
Actinobacteria	Actinobacteria	Dermabacteraceae	sf_1	1677	Brachybacterium conglomeratum str. NCIB 9859
Actinobacteria	Actinobacteria	Dermabacteraceae	sf_1	2053	Brachybacterium nesterenkovi str. DSM 9573
Actinobacteria	Actinobacteria	Dermatophilaceae	sf_1	1852	Tonsillophilus suis str. HT1-19
Actinobacteria	Actinobacteria	Dermatophilaceae	sf_1	1990	EBPR sludge lab scale clone LPB21
Actinobacteria	Actinobacteria	Dietziaceae	sf_1	1872	Dietzia maris
Actinobacteria	Actinobacteria	Dietziaceae	sf_1	1970	Dietzia sp. str. E9_2
Actinobacteria	Actinobacteria	Frankiaceae	sf_1	1105	Frankia sp
Actinobacteria	Actinobacteria	Frankiaceae	sf_1	1161	Frankia sp. MRn2-2
Actinobacteria	Actinobacteria	Frankiaceae	sf_1	1286	Frankia sp. Sn5-8
Actinobacteria	Actinobacteria	Frankiaceae	sf_1	1644	Frankia sp. M16467
Actinobacteria	Actinobacteria	Gordoniaceae	sf_1	1116	Gordona terrae
Actinobacteria	Actinobacteria	Gordoniaceae	sf_1	1184	Gordonia alkanivorans
Actinobacteria	Actinobacteria	Gordoniaceae	sf_1	1191	Gordonia amarae str. DSM43392
Actinobacteria	Actinobacteria	Gordoniaceae	sf_1	1545	
Actinobacteria	Actinobacteria	Gordoniaceae	sf_1	1567	
Actinobacteria	Actinobacteria	Gordoniaceae	sf_1	1654	Gordonia polyisoprenivorans str. Y2K
Actinobacteria	Actinobacteria	Intrasporangiaceae	sf_1	1218	activated sludge foam clone 17
Actinobacteria	Actinobacteria	Intrasporangiaceae	sf_1	1935	
Actinobacteria	Actinobacteria	Kineosporiaceae	sf_1	1087	Kineosporia aurantiaca str. JCM3230
Actinobacteria	Actinobacteria	Kineosporiaceae	sf_1	1581	Cryptosporangium aurantiacum
Actinobacteria	Actinobacteria	Kineosporiaceae	sf_1	1598	lichen-dominated Antarctic community clone
Actinobacteria	Actinobacteria	Kineosporiaceae	sf_1	1893	Kineosporia aurantiaca str. NRLL B-16913
Actinobacteria	Actinobacteria	Kineosporiaceae	sf_1	1961	Kineococcus aurantiacus str. IFO 15268

Actinobacteria	Actinobacteria	Kribbella	sf_1	1839	Kribbella solani str. DSA1
Actinobacteria	Actinobacteria	Microbacteriaceae	sf_1	1106	
Actinobacteria	Actinobacteria	Microbacteriaceae	sf_1	1135	Rhodoglobus vestalii str. LV3
Actinobacteria	Actinobacteria	Microbacteriaceae	sf_1	1197	Arctic sea ice ARK10173
Actinobacteria	Actinobacteria	Microbacteriaceae	sf_1	1241	Microbacterium kitamiense CV88
Actinobacteria	Actinobacteria	Microbacteriaceae	sf_1	1404	freshwater isolate str. MWH-Ta3
Actinobacteria	Actinobacteria	Microbacteriaceae	sf_1	1437	freshwater clone SV1-16
Actinobacteria	Actinobacteria	Microbacteriaceae	sf_1	1507	Microbacterium sp. str. Pla-1
Actinobacteria	Actinobacteria	Microbacteriaceae	sf_1	1640	Microbacterium sp. str. IFO16060
Actinobacteria	Actinobacteria	Microbacteriaceae	sf_1	1667	Microbacterium lacticum
Actinobacteria	Actinobacteria	Microbacteriaceae	sf_1	1779	Microbacterium sp. str. VKM Ac-2048
Actinobacteria	Actinobacteria	Microbacteriaceae	sf_1	1804	Microbacterium resistens str. 2002-59119
Actinobacteria	Actinobacteria	Micrococcaceae	sf_1	1212	Rothia aerea str. GTC 867
Actinobacteria	Actinobacteria	Micrococcaceae	sf_1	1213	Kocuria roseus
Actinobacteria	Actinobacteria	Micrococcaceae	sf_1	1266	Arthrobacter psychrolactophilus
Actinobacteria	Actinobacteria	Micrococcaceae	sf_1	1324	glacial ice isolate str. CanDirty1
Actinobacteria	Actinobacteria	Micrococcaceae	sf_1	1494	Arthrobacter agilis str. DSM 20550
Actinobacteria	Actinobacteria	Micrococcaceae	sf_1	1557	Arthrobacter oxydans str. DSM 20119
Actinobacteria	Actinobacteria	Micrococcaceae	sf_1	1573	Arthrobacter nicotianae str. SB42
Actinobacteria	Actinobacteria	Micrococcaceae	sf_1	1582	gas hydrate clone AT425_EubD11
Actinobacteria	Actinobacteria	Micrococcaceae	sf_1	1593	Arthrobacter globiformis
Actinobacteria	Actinobacteria	Micrococcaceae	sf_1	1610	Arthrobacter sp str. AC-51
Actinobacteria	Actinobacteria	Micrococcaceae	sf_1	1686	Yania halotolerans str. YIM 70085
Actinobacteria	Actinobacteria	Micrococcaceae	sf_1	1724	Rothia mucilaginosa str. DSM
Actinobacteria	Actinobacteria	Micrococcaceae	sf_1	1889	Citricoccus sp. str. 2216.25.22
Actinobacteria	Actinobacteria	Micrococcaceae	sf_1	1966	TCE-contaminated site clone ccspost2208
Actinobacteria	Actinobacteria	Micrococcaceae	sf_1	2019	Micrococcus luteus str. HN2-11
Actinobacteria	Actinobacteria	Micrococcaceae	sf_1	2020	Rothia dentocariosa str. ChDC B200
Actinobacteria	Actinobacteria	Micrococcaceae	sf_1	2063	Rothia dentocariosa str. ATCC 17931
Actinobacteria	Actinobacteria	Micromonosporaceae	sf_1	1120	Actinoplanes violaceus str. IMSNU 22136
Actinobacteria	Actinobacteria	Micromonosporaceae	sf_1	1159	Actinoplanes durhamensis str. IMSNU 22124T

Actinobacteria	Actinobacteria	Micromonosporaceae	sf_1	1395	Catenuloplanes japonicus str. IFO14176
Actinobacteria	Actinobacteria	Micromonosporaceae	sf_1	1488	Actinoplanes utahensis str. IMSNU 20044T
Actinobacteria	Actinobacteria	Micromonosporaceae	sf_1	1542	Actinoplanes garbadinensis str. IMSNU 20040
Actinobacteria	Actinobacteria	Micromonosporaceae	sf_1	1615	Actinoplanes derwentensis str. IFO 14935T
Actinobacteria	Actinobacteria	Micromonosporaceae	sf_1	1633	Actinoplanes tuftoflagellus str. IMSNU 22135
Actinobacteria	Actinobacteria	Micromonosporaceae	sf_1	1641	Micromonospora marina str. JSM3-1
Actinobacteria	Actinobacteria	Micromonosporaceae	sf_1	1689	Actinoplanes yunnanensis str. IFO 14459T
Actinobacteria	Actinobacteria	Micromonosporaceae	sf_1	1760	Actinoplanes roseosporangius str. IMSNU 22133
Actinobacteria	Actinobacteria	Micromonosporaceae	sf_1	1876	Couchioplanes subsp. caeruleus str. IFO13939
Actinobacteria	Actinobacteria	Micromonosporaceae	sf_1	1910	Actinoplanes capillaceus str. K95-5561
Actinobacteria	Actinobacteria	Micromonosporaceae	sf_1	1931	Actinoplanes utahensis str. ATCC 31044
Actinobacteria	Actinobacteria	Micromonosporaceae	sf_1	1972	Actinoplanes regularis str. IFO 12514T
Actinobacteria	Actinobacteria	Micromonosporaceae	sf_1	2051	Couchioplanes subsp. caeruleus str. IFO13939
Actinobacteria	Actinobacteria	Microthrixineae	sf_1	1576	actinobacterium clone ML817J-10
Actinobacteria	Actinobacteria	Microthrixineae	sf_12	1721	heavy metal-contaminated soil clone a13156
Actinobacteria	Actinobacteria	Microthrixineae	sf_1	1964	bacterioplankton clone AEGEAN_247
Actinobacteria	Actinobacteria	Mycobacteriaceae	sf_1	1175	Mycobacterium cf. xenopi
Actinobacteria	Actinobacteria	Mycobacteriaceae	sf_1	1180	Mycobacterium palustre str. E846
Actinobacteria	Actinobacteria	Mycobacteriaceae	sf_1	1187	Mycobacterium aichiense str. JS618
Actinobacteria	Actinobacteria	Mycobacteriaceae	sf_1	1204	Mycobacterium sp. 3
Actinobacteria	Actinobacteria	Mycobacteriaceae	sf_1	1239	Mycobacterium ratisbonense str. SD4
Actinobacteria	Actinobacteria	Mycobacteriaceae	sf_1	1262	Mycobacterium holsaticum str. 1406
Actinobacteria	Actinobacteria	Mycobacteriaceae	sf_1	1308	Mycobacterium pyrenivorans str. DSM 44605
Actinobacteria	Actinobacteria	Mycobacteriaceae	sf_1	1312	
Actinobacteria	Actinobacteria	Mycobacteriaceae	sf_1	1317	Fort collins Horsetooth Reservoir clone HTDD3
Actinobacteria	Actinobacteria	Mycobacteriaceae	sf_1	1365	Mycobacterium chelonae str. CIP 104535T
Actinobacteria	Actinobacteria	Mycobacteriaceae	sf_1	1435	Mycobacterium cf. triplex 'isolate 23' 23
Actinobacteria	Actinobacteria	Mycobacteriaceae	sf_1	1637	Mycobacterium austroafricanum str. IFP2173
Actinobacteria	Actinobacteria	Mycobacteriaceae	sf_1	1650	Mycobacterium tuberculosis str. NCTC 7416
Actinobacteria	Actinobacteria	Mycobacteriaceae	sf_1	1681	Mycobacterium sp. str. 1B(CD)
Actinobacteria	Actinobacteria	Mycobacteriaceae	sf_1	1726	Mycobacterium terrae str. ATCC 15755

Actinobacteria	Actinobacteria	Mycobacteriaceae	sf_1	1781	Mycobacterium rhodesiae str. JS60
Actinobacteria	Actinobacteria	Mycobacteriaceae	sf_1	1860	Mycobacterium marinum
Actinobacteria	Actinobacteria	Mycobacteriaceae	sf_1	1885	Mycobacterium neoaurum str. ATCC 25795
Actinobacteria	Actinobacteria	Mycobacteriaceae	sf_1	1888	Mycobacterium brisbanense str. ATCC 49938
Actinobacteria	Actinobacteria	Mycobacteriaceae	sf_1	2034	Mycobacterium chlorophenolicum str. PCP-I
Actinobacteria	Actinobacteria	Nocardiaceae	sf_1	1142	
Actinobacteria	Actinobacteria	Nocardiaceae	sf_1	1146	Nocardia otitidiscaviarum str. S639
Actinobacteria	Actinobacteria	Nocardiaceae	sf_1	1261	Nocardia caishijiensis str. F829
Actinobacteria	Actinobacteria	Nocardiaceae	sf_1	1432	Nocardia veterana str. DSM 44445
Actinobacteria	Actinobacteria	Nocardiaceae	sf_1	1454	Nocardia yamanashiensis str. IFM 0265
Actinobacteria	Actinobacteria	Nocardiaceae	sf_1	1788	Rhodococcus species
Actinobacteria	Actinobacteria	Nocardiaceae	sf_1	1834	Nocardia transvalensis str. DSM 43405
Actinobacteria	Actinobacteria	Nocardiaceae	sf_1	1917	Nocardia otitidiscaviarum str. DSM43242
Actinobacteria	Actinobacteria	Nocardiaceae	sf_1	1940	Rhodococcus opacus str. B-4
Actinobacteria	Actinobacteria	Nocardiaceae	sf_1	2048	Nocardia uniformis str. DSM 43136
Actinobacteria	Actinobacteria	Nocardioidaceae	sf_1	1854	Aeromicrobium marinum str. T2
Actinobacteria	Actinobacteria	Nocardiopsaceae	sf_1	1385	Streptomonospora salina str. YIM90002
Actinobacteria	Actinobacteria	Promicromonosporaceae	sf_1	1671	Cellulosimicrobium cellulans str. NCIMB 11025
Actinobacteria	Actinobacteria	Promicromonosporaceae	sf_1	1711	Promicromonospora sukumoe str. DSM 44121
Actinobacteria	Actinobacteria	Propionibacteriaceae	sf_1	2002	Propionibacterium acnes #2929
Actinobacteria	Actinobacteria	Propionibacteriaceae	sf_1	2023	Propionibacterium propionicum
Actinobacteria	Actinobacteria	Pseudonocardiaceae	sf_1	1104	Amycolatopsis mediterranei str. NRRL B-3240
Actinobacteria	Actinobacteria	Pseudonocardiaceae	sf_1	1119	Amycolatopsis tolypomycina str. DSM 44544
Actinobacteria	Actinobacteria	Pseudonocardiaceae	sf_1	1343	Saccharomonospora azurea
Actinobacteria	Actinobacteria	Pseudonocardiaceae	sf_1	1402	
Actinobacteria	Actinobacteria	Pseudonocardiaceae	sf_1	1594	Amycolatopsis sp. str. GY307
Actinobacteria	Actinobacteria	Pseudonocardiaceae	sf_1	1824	Amycolatopsis sulphurea str. IMSNU 20060T
Actinobacteria	Actinobacteria	Pseudonocardiaceae	sf_1	1849	
Actinobacteria	Actinobacteria	Pseudonocardiaceae	sf_1	1863	
Actinobacteria	Actinobacteria	Rubrobacteraceae	sf_1	1384	
Actinobacteria	Actinobacteria	Rubrobacteraceae	sf_1	1551	soil isolate Ellin301

Actinobacteria	Actinobacteria	Rubrobacteraceae	sf_1	1612	lichen-dominated Antarctic clone FBP483
Actinobacteria	Actinobacteria	Rubrobacteraceae	sf_1	1739	
Actinobacteria	Actinobacteria	Rubrobacteraceae	sf_1	1843	uranium mining soil sample clone JG30-KF-A23
Actinobacteria	Actinobacteria	Rubrobacteraceae	sf_1	1901	earthworm burrow isolate B33D1
Actinobacteria	Actinobacteria	Sporichthyaceae	sf_1	1695	lichen-dominated Antarctic clone FBP417
Actinobacteria	Actinobacteria	Streptomycetaceae	sf_1	1111	Kitasatospora setae str. KM-6054
Actinobacteria	Actinobacteria	Streptomycetaceae	sf_1	1274	Trichotomospora caesia str. IFO14562
Actinobacteria	Actinobacteria	Streptomycetaceae	sf_1	1340	Streptomyces coelicolor
Actinobacteria	Actinobacteria	Streptomycetaceae	sf_1	1354	Streptomyces subrutilus str. DSM 40445
Actinobacteria	Actinobacteria	Streptomycetaceae	sf_1	1375	soil clone 228-1
Actinobacteria	Actinobacteria	Streptomycetaceae	sf_1	1544	Kitasatospora cystarginea str. IFO14836T
Actinobacteria	Actinobacteria	Streptomycetaceae	sf_1	1569	Streptomyces sampsonii str. ATCC25495
Actinobacteria	Actinobacteria	Streptomycetaceae	sf_1	1617	soil clone 41-1
Actinobacteria	Actinobacteria	Streptomycetaceae	sf_1	1639	Streptomyces coelicolor str. M145
Actinobacteria	Actinobacteria	Streptomycetaceae	sf_1	1690	Streptomyces galbus str. DSM40480
Actinobacteria	Actinobacteria	Streptomycetaceae	sf_3	1743	Streptomyces scabiei str. DNK-G01
Actinobacteria	Actinobacteria	Streptomycetaceae	sf_1	1771	Streptomyces setonii str. ATCC25497
Actinobacteria	Actinobacteria	Streptomycetaceae	sf_1	1786	Streptomyces bikiniensis str. DSM40581
Actinobacteria	Actinobacteria	Streptomycetaceae	sf_1	1983	Streptomyces cinnabarinus str. ISP 5467
Actinobacteria	Actinobacteria	Streptosporangiaceae	sf_1	1158	Streptosporangium roseum str. DSM43021T
Actinobacteria	Actinobacteria	Streptosporangiaceae	sf_1	1190	Nonomuraea polychroma str. IFO 14345
Actinobacteria	Actinobacteria	Streptosporangiaceae	sf_1	1224	Acrocarpospora corrugata str. DSM43316T
Actinobacteria	Actinobacteria	Streptosporangiaceae	sf_1	1587	Nonomuraea subsp. roseoviolacea str. SF 2303
Actinobacteria	Actinobacteria	Thermomonosporaceae	sf_1	1406	Actinomadura kijaniata str. DSM 43764T
Actinobacteria	Actinobacteria	Thermomonosporaceae	sf_1	1546	Actinomadura fulvescens str. DSM 43923T
Actinobacteria	Actinobacteria	Thermomonosporaceae	sf_1	1669	Pseudonocardiaceae str. PA123
Actinobacteria	Actinobacteria	Thermomonosporaceae	sf_1	1741	Actinomadura pelletieri str. IMSNU 22169T
Actinobacteria	Actinobacteria	Unclassified	sf_3	1130	Georgenia muralis str. 1A-C
Actinobacteria	Actinobacteria	Unclassified	sf_1	1217	DCP-dechlorinating consortium clone SHA-34
Actinobacteria	Actinobacteria	Unclassified	sf_2	1233	
Actinobacteria	Actinobacteria	Unclassified	sf_3	1243	termite gut homogenate clone Rs-M95 bacterium

Actinobacteria	Actinobacteria	Unclassified	sf_3	1296	termite gut homogenate clone Rs-M66 bacterium
Actinobacteria	Actinobacteria	Unclassified	sf_4	1337	Sturt arid-zone soil clone #0425-2M17
Actinobacteria	Actinobacteria	Unclassified	sf_3	1348	Antarctic community clone FBP406
Actinobacteria	Actinobacteria	Unclassified	sf_1	1367	
Actinobacteria	Actinobacteria	Unclassified	sf_1	1370	forested wetland clone RCP1-37
Actinobacteria	Actinobacteria	Unclassified	sf_3	1405	Arthrobacter ureafaciens str. DSM 20126
Actinobacteria	Actinobacteria	Unclassified	sf_3	1486	deep marine sediment clone MB-A2-108
Actinobacteria	Actinobacteria	Unclassified	sf_3	1577	termite gut homogenate clone Rs-N91 bacterium
Actinobacteria	BD2-10 group	Unclassified	sf_2	1652	marine sediment clone Bol7
Actinobacteria	Actinobacteria	Unclassified	sf_1	1666	
Actinobacteria	Actinobacteria	Unclassified	sf_1	1676	
Actinobacteria	Actinobacteria	Unclassified	sf_3	1687	Jonesia quinghaiensis str. DSM 15701
Actinobacteria	Actinobacteria	Unclassified	sf_1	1898	termite gut homogenate clone Rs-J10 bacterium
Actinobacteria	Actinobacteria	Unclassified	sf_3	1900	
Actinobacteria	Actinobacteria	Unclassified	sf_3	2045	hypersaline lake clone ML602J-44
AD3	Unclassified	Unclassified	sf_1	2338	uranium mining soil clone JG30-KF-C12
Aquificae	Aquificae	Hydrogenothermaceae	sf_1	737	Sulfurihydrogenibium azorense
Aquificae	Aquificae	Unclassified	sf_1	2364	Thermovibrio ammoniificans str. HB-1
Bacteroidetes	Bacteroidetes	Bacteroidaceae	sf_12	5256	termite gut homogenate clone Rs-D38 bacterium
Bacteroidetes	Bacteroidetes	Bacteroidaceae	sf_12	5320	Bacteroides distasonis
Bacteroidetes	Bacteroidetes	Bacteroidaceae	sf_12	5474	Bacteroides acidofaciens str.A24
Bacteroidetes	Bacteroidetes	Bacteroidaceae	sf_12	5621	TCE-dechlorinating microbial community clone
Bacteroidetes	Bacteroidetes	Bacteroidaceae	sf_6	5792	activated sludge foam clone 47
Bacteroidetes	Bacteroidetes	Bacteroidaceae	sf_12	5950	
Bacteroidetes	Bacteroidetes	Bacteroidaceae	sf_12	5837	
Bacteroidetes	Flavobacteria	Blattabacteriaceae	sf_1	5828	Blattabacterium species
Bacteroidetes	Sphingobacteria	Crenotrichaceae	sf_11	5334	autotrophic nitrifying biofilm clone NB-11
Bacteroidetes	Sphingobacteria	Crenotrichaceae	sf_11	5463	Flexibacter sancti str. IFO 16034
Bacteroidetes	Sphingobacteria	Crenotrichaceae	sf_11	5619	anaerobic VC-degrading clone VC10 bacterium
Bacteroidetes	Sphingobacteria	Crenotrichaceae	sf_11	5647	sponge clone TK44
Bacteroidetes	Sphingobacteria	Crenotrichaceae	sf_11	5654	Saprospira grandis str. ATCC23116

Bacteroidetes	Sphingobacteria	Crenotrichaceae	sf_11	5888	penguin droppings sediments clone KD9-169
Bacteroidetes	Sphingobacteria	Crenotrichaceae	sf_11	5987	
Bacteroidetes	Sphingobacteria	Crenotrichaceae	sf_11	6050	EBPR sludge lab scale clone LPB08
Bacteroidetes	Sphingobacteria	Crenotrichaceae	sf_11	6123	Flexibacter japonensis str. IFO 16041
Bacteroidetes	Sphingobacteria	Crenotrichaceae	sf_11	6143	Toolik Lake TLM09/TLMdgge12a
Bacteroidetes	Sphingobacteria	Crenotrichaceae	sf_11	6249	Haliscomenobacter hydrossis
Bacteroidetes	Sphingobacteria	Crenotrichaceae	sf_11	6267	Cilia- respiratory isolate str. 243-54
Bacteroidetes	Flavobacteria	Cryomorphaceae	sf_1	5400	Crocinitomix catalasitica str. IFO 15977
Bacteroidetes	Sphingobacteria	Flammeovirgaceae	sf_5	6084	Microscilla arenaria str. IFO 15982
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5267	bacterioplankton clone AEGEAN_179
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5317	Tenacibaculum maritimum str. IFO 15946
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5339	
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5352	Riemerella anatipestifer str. H-2565
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5367	bronchoalveolar lavage isolate str. MDA250
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5401	Capnocytophaga gingivalis str. ChDC OS45
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5423	Aequorivita antarctica str. QSSC9-14
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5434	Capnocytophaga sp. str. ChDC OS43
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5436	Arctic sea ice ARK10004
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5473	
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5490	
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5499	marine sediment clone Hyd24-2-2 bacterium
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5509	Cellulophaga sp. str. E14
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5521	Flavobacteriaceae str. SW269
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5588	
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5641	
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5645	supragingival plaque on tooth surfaces clone
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5695	marine sediment ridge clone bacterium
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5726	Bergeyella sp. oral AK152 clone
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5730	
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5758	Tenacibaculum sp. str. MGP-10
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5836	Capnocytophaga granulosa str. LMG 12119

Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5906	Capnocytophaga sputigena str. ATCC 33612
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5914	Psychroserpens burtonensis str. S2-64
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5915	ground water clone S15A-MN27 bacterium
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5942	
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5955	Flavobacterium sp. str. V4.MS.29 = MM_2747
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5969	Capnocytophaga ochracea str. ATCC 27872 T
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5971	Cytophaga uliginosa
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5991	Tenacibaculum ovoliticum str. IAM14318
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5997	Flavobacterium aquatile
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	6104	
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	6140	
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	6246	crevicular epithelial cells clone BU084
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	6248	Capnocytophaga sp. oral strain str. S3
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	6252	Riftia pachyptila's tube clone R103-B20
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	6269	acidic forest soil clone UC1
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	6274	
Bacteroidetes	Sphingobacteria	Flexibacteraceae	sf_19	5307	Microscilla sericea str. IFO 16561
Bacteroidetes	Sphingobacteria	Flexibacteraceae	sf_19	5357	Flexibacter ruber str. IFO 16677
Bacteroidetes	Sphingobacteria	Flexibacteraceae	sf_19	5364	Algoriphagus antarcticus str. LMG 21983
Bacteroidetes	Sphingobacteria	Flexibacteraceae	sf_19	5365	mesoeutrophic reservoir clone 30
Bacteroidetes	Sphingobacteria	Flexibacteraceae	sf_19	5366	Flexibacter roseolus str. IFO 16030
Bacteroidetes	Sphingobacteria	Flexibacteraceae	sf_19	5372	
Bacteroidetes	Sphingobacteria	Flexibacteraceae	sf_19	5542	Cytophaga sp. I-1787
Bacteroidetes	Sphingobacteria	Flexibacteraceae	sf_19	5563	Cytophaga sp. I-545
Bacteroidetes	Sphingobacteria	Flexibacteraceae	sf_19	5566	Hongiella mannitolivorans str. IMSNU
Bacteroidetes	Sphingobacteria	Flexibacteraceae	sf_19	5602	
Bacteroidetes	Sphingobacteria	Flexibacteraceae	sf_19	5667	penguin droppings sediments clone KD6-118
Bacteroidetes	Sphingobacteria	Flexibacteraceae	sf_19	5728	Cytophaga sp. str. MBIC04693
Bacteroidetes	Sphingobacteria	Flexibacteraceae	sf_19	5902	Taxeobacter sp. clone KL-2-4-3
Bacteroidetes	Sphingobacteria	Flexibacteraceae	sf_19	5994	Hymenobacter sp. str. NS/50
Bacteroidetes	Sphingobacteria	Flexibacteraceae	sf_19	6124	Flexibacter flexilis subsp. pelliculosus

Bacteroidetes	Sphingobacteria	Flexibacteraceae	sf_19	6261	Arctic sea ice cryoconite clone ARKCRY-50
Bacteroidetes	Sphingobacteria	Flexibacteraceae	sf_19	6297	EBPR sludge lab scale clone HP1A92
Bacteroidetes	Sphingobacteria	Flexibacteraceae	sf_20	10311	Cytophaga sp. str. BHI60-57B
Bacteroidetes	Bacteroidetes	Porphyromonadaceae	sf_1	5295	swine intestine clone p-987-s962-5
Bacteroidetes	Bacteroidetes	Porphyromonadaceae	sf_1	5429	
Bacteroidetes	Bacteroidetes	Porphyromonadaceae	sf_1	5454	Dysgonomonas wimpennyi str. ANFA2
Bacteroidetes	Bacteroidetes	Porphyromonadaceae	sf_1	5460	mouse feces clone F8
Bacteroidetes	Bacteroidetes	Porphyromonadaceae	sf_1	5510	sphagnum peat bog clone 26-4b2
Bacteroidetes	Bacteroidetes	Porphyromonadaceae	sf_1	5664	termite gut homogenate clone Rs-E83 bacterium
Bacteroidetes	Bacteroidetes	Porphyromonadaceae	sf_1	5680	termite gut clone Rs-106
Bacteroidetes	Bacteroidetes	Porphyromonadaceae	sf_1	5713	Porphyromonas catoniae str. ATCC 51270
Bacteroidetes	Bacteroidetes	Porphyromonadaceae	sf_1	5800	Porphyromonas endodontalis str. ATCC 35406
Bacteroidetes	Bacteroidetes	Porphyromonadaceae	sf_1	5817	termite gut homogenate clone Rs-N56 bacterium
Bacteroidetes	Bacteroidetes	Porphyromonadaceae	sf_1	5943	
Bacteroidetes	Bacteroidetes	Porphyromonadaceae	sf_1	5961	chlorobenzene-degrading clone IA-16
Bacteroidetes	Bacteroidetes	Porphyromonadaceae	sf_1	6012	mouse feces clone L11-6
Bacteroidetes	Bacteroidetes	Porphyromonadaceae	sf_1	6214	Tannerella forsythensis str. ATCC43037
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5249	Prevotella denticola str. ATCC 35308
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5331	tongue dorsa clone DO022
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5398	Prevotella ruminicola L16
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5403	Prevotella bryantii str. B14
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5408	Prevotella dentalis str. DSM 3688
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5426	tongue dorsa clone DO014
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5437	cow rumen clone BE1
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5453	subgingival dental plaque clone AU069
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5484	oral periodontitis clone FX046
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5706	oral cavity clone 3.3
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5718	Prevotella tannerae str. 29-1
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5720	Prevotella sp. str. E9_34
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5741	Prevotella veroralis
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5756	Prevotella intermedia str. ChDC KB53

Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5768	crevicular epithelial cells clone BU035
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5769	Bacteroidaceae str. A42
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5834	cow rumen clone BE6
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5893	tongue dorsa clone DO045
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5905	swine intestine clone p-2443-18B5
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5916	cow rumen clone BE14
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5926	cow rumen clone BF22
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5929	Prevotella albensis str. M384
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5940	Prevotella sp. str. E7_34
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	5946	tongue dorsa clone DO027
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	6011	rumen clone F24-B03
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	6045	Prevotella nigrescens str. ChDC B270
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	6047	deep marine sediment clone MB-A2-107
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	6066	human mouth isolate str. P4P_62
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	6072	subgingival dental plaque clone AA016
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	6091	cow rumen clone BE34
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	6109	
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	6118	
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	6152	rumen clone RF37
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	6169	subgingival dental plaque clone CY006
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	6179	subgingival dental plaque clone DA058
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	6207	cow rumen clone BF34
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	6239	tongue dorsa clone DO033
Bacteroidetes	Bacteroidetes	Prevotellaceae	sf_1	6259	
Bacteroidetes	Bacteroidetes	Rikenellaceae	sf_5	5356	uranium mining waste pile clone JG37-AG-150
Bacteroidetes	Bacteroidetes	Rikenellaceae	sf_5	5889	termite gut homogenate clone Rs-F73 bacterium
Bacteroidetes	Bacteroidetes	Rikenellaceae	sf_5	5892	anoxic bulk soil microcosm clone BSV73
Bacteroidetes	Bacteroidetes	Rikenellaceae	sf_5	5947	hydrothermal vent polychaete mucous clone
Bacteroidetes	Bacteroidetes	Rikenellaceae	sf_5	6173	subgingival dental plaque clone DA064
Bacteroidetes	Sphingobacteria	Sphingobacteriaceae	sf_1	5459	Pedobacter sp. An13
Bacteroidetes	Sphingobacteria	Sphingobacteriaceae	sf_1	5492	Sphingobacterium sp. str. HC-6155

Bacteroidetes	Sphingobacteria	Sphingobacteriaceae	sf_1	5513	crevicular epithelial cells clone AZ123
Bacteroidetes	Sphingobacteria	Sphingobacteriaceae	sf_1	5913	Sphingobacteriaceae str. Ellin160
Bacteroidetes	Sphingobacteria	Sphingobacteriaceae	sf_1	6158	municipal wastewater treatment isolate
Bacteroidetes	Sphingobacteria	Sphingobacteriaceae	sf_1	6272	Sphingobacterium heparinum
Bacteroidetes	Flavobacteria	Unclassified	sf_3	5248	Delaware River estuary clone 1G12
Bacteroidetes	Bacteroidetes	Unclassified	sf_15	5257	marine? clone KD3-67
Bacteroidetes	Bacteroidetes	Unclassified	sf_15	5353	trichloroethene-contaminated site clone
Bacteroidetes	Bacteroidetes	Unclassified	sf_15	5355	DCP-dechlorinating consortium clone SHA-5
Bacteroidetes	Sphingobacteria	Unclassified	sf_6	5439	Mono Lake clone ML635J-40 bacterium
Bacteroidetes	Bacteroidetes	Unclassified	sf_15	5475	SHA-25 clone
Bacteroidetes	Bacteroidetes	Unclassified	sf_15	5481	marine sediment above ridge clone bacterium
Bacteroidetes	Bacteroidetes	Unclassified	sf_15	5511	marine sediment above ridge clone bacterium
Bacteroidetes	Bacteroidetes	Unclassified	sf_15	5544	marine? clone KD3-17
Bacteroidetes	Bacteroidetes	Unclassified	sf_15	5573	termite gut clone Rs-D44 bacterium
Bacteroidetes	Bacteroidetes	Unclassified	sf_15	5578	ground water deep-well disposal site clone
Bacteroidetes	Unclassified	Unclassified	sf_4	5637	
Bacteroidetes	Unclassified	Unclassified	sf_6	5655	
Bacteroidetes	Unclassified	Unclassified	sf_4	5703	
Bacteroidetes	Unclassified	Unclassified	sf_1	5745	
Bacteroidetes	Bacteroidetes	Unclassified	sf_15	5783	Mono Lake clone ML635J-15 bacterium
Bacteroidetes	Bacteroidetes	Unclassified	sf_15	5784	fruiting body Pleurotus eryngii clone PE01
Bacteroidetes	Unclassified	Unclassified	sf_4	5785	Mono Lake clone ML635J-56
Bacteroidetes	Unclassified	Unclassified	sf_4	5787	Mono Lake clone ML635J-1 bacterium
Bacteroidetes	Bacteroidetes	Unclassified	sf_15	5802	DCP-dechlorinating consortium clone SHA-94
Bacteroidetes	Bacteroidetes	Unclassified	sf_15	5820	cow rumen clone BF24
Bacteroidetes	Bacteroidetes	Unclassified	sf_15	5874	hydrothermal vent polychaete mucous clone
Bacteroidetes	Bacteroidetes	Unclassified	sf_15	5890	penguin droppings sediments clone KD1-125
Bacteroidetes	Bacteroidetes	Unclassified	sf_15	5907	cow rumen clone BE36
Bacteroidetes	KSA1	Unclassified	sf_1	5951	CFB group clone ML615J-4
Bacteroidetes	Bacteroidetes	Unclassified	sf_15	5957	hydrothermal vent polychaete mucous clone
Bacteroidetes	Bacteroidetes	Unclassified	sf_15	5998	cow rumen clone BS9

Bacteroidetes	Bacteroidetes	Unclassified	sf_15	6046	chlorobenzene-degrading clone IIIB-1
Bacteroidetes	Bacteroidetes	Unclassified	sf_15	6069	corneal ulcer clone E1-K9
Bacteroidetes	Sphingobacteria	Unclassified	sf_3	6168	Toolik Lake clone TLM11/TLMdgge04
Bacteroidetes	Bacteroidetes	Unclassified	sf_15	6233	oral periodontitis clone FX069
Bacteroidetes	Sphingobacteria	Unclassified	sf_3	6298	travertine hot spring clone SM1C04
Bacteroidetes	Sphingobacteria	Unclassified	sf_3	6303	Toolik Lake clone TLM10/TLMdgge01
Bacteroidetes	Bacteroidetes	Unclassified	sf_15	6324	temperate estuarine mud clone KM02
BRC1	Unclassified	Unclassified	sf_2	118	penguin droppings sediments clone KD1-1
BRC1	Unclassified	Unclassified	sf_1	5051	soil clone PBS-III-24
BRC1	Unclassified	Unclassified	sf_1	5143	soil clone PBS-II-1
Caldithrix	Unclassified	Caldithraceae	sf_2	91	benzoate-degrading consortium clone BA059
Caldithrix	Unclassified	Caldithraceae	sf_1	2384	saltmarsh clone LCP-89
Chlamydiae	Chlamydiae	Chlamydiaceae	sf_1	4820	Chlamydophila pneumoniae str. AR39
Chlamydiae	Chlamydiae	Parachlamydiaceae	sf_1	4964	neutral pH mine biofilm clone 44a-B1-34
Chlamydiae	Chlamydiae	Simkaniaceae	sf_1	4702	Candidatus Rhabdochlamydia porcellionis clone
Chlorobi	Chlorobia	Chlorobiaceae	sf_1	262	Chlorobium ferrooxidans DSM 13031
Chlorobi	Chlorobia	Chlorobiaceae	sf_1	859	Chlorobium phaeovibrioides str. 2631
Chlorobi	Chlorobia	Chlorobiaceae	sf_1	995	Chlorobium limicola str. M1
Chlorobi	Unclassified	Unclassified	sf_8	549	benzene-degrading nitrate-reducing bacterium
Chlorobi	Unclassified	Unclassified	sf_8	636	benzene-degrading nitrate-reducing bacterium
Chlorobi	Unclassified	Unclassified	sf_6	5294	Mammoth cave clone CCM9b
Chlorobi	Unclassified	Unclassified	sf_8	5822	Saltmarsh mud clone K-790
Chlorobi	Unclassified	Unclassified	sf_1	5928	hydrothermal vent polychaete mucous clone
Chlorobi	Unclassified	Unclassified	sf_9	6146	sludge clone A12b
Chloroflexi	Anaerolineae	Unclassified	sf_9	72	sediments near Echo Riverclone CCD21
Chloroflexi	Anaerolineae	Unclassified	sf_1	76	DCP-dechlorinating consortium clone SHA-147
Chloroflexi	Anaerolineae	Unclassified	sf_9	94	DCP-dechlorinating consortium clone SHA-2
Chloroflexi	Anaerolineae	Unclassified	sf_1	106	DCP-dechlorinating consortium clone SHD-231
Chloroflexi	Chloroflexi-3	Unclassified	sf_5	119	Green non-sulfur isolate str. B1-5
Chloroflexi	Anaerolineae	Unclassified	sf_1	159	anaerobic bioreactor clone SHD-235
Chloroflexi	Anaerolineae	Unclassified	sf_9	205	uranium mining waste pile clone JG34-KF-221

Chloroflexi	Anaerolineae	Unclassified	sf_1	258	DCP-dechlorinating consortium clone SHD-14
Chloroflexi	Anaerolineae	Unclassified	sf_1	266	
Chloroflexi	Anaerolineae	Unclassified	sf_1	374	forest soil clone S041
Chloroflexi	Anaerolineae	Unclassified	sf_9	375	forest soil clone C043
Chloroflexi	Anaerolineae	Unclassified	sf_1	470	chlorobenzene-degrading clone SJA-35
Chloroflexi	Anaerolineae	Unclassified	sf_1	487	thermophilic granular sludge isolate bacterium
Chloroflexi	Anaerolineae	Unclassified	sf_9	576	DCP-dechlorinating consortium clone SHA-36
Chloroflexi	Anaerolineae	Unclassified	sf_1	583	anaerobic bioreactor clone SHD-238
Chloroflexi	Thermomicrobia	Unclassified	sf_2	652	uranium mining waste pile soil sample clone
Chloroflexi	Anaerolineae	Unclassified	sf_9	727	forest soil clone S0208
Chloroflexi	Unclassified	Unclassified	sf_7	757	DCP-dechlorinating consortium clone SHA-8
Chloroflexi	Anaerolineae	Unclassified	sf_1	765	anaerobic bioreactor clone SHD-71
Chloroflexi	Anaerolineae	Unclassified	sf_2	789	travertine hot spring clone SM1D10
Chloroflexi	Unclassified	Unclassified	sf_2	818	
Chloroflexi	Anaerolineae	Unclassified	sf_1	927	hydrothermal vent polychaete mucous clone
Chloroflexi	Anaerolineae	Unclassified	sf_9	946	temperate estuarine mud clone KM87
Chloroflexi	Thermomicrobia	Unclassified	sf_1	1041	Antarctic cryptoendolith clone FBP471
Chloroflexi	Unclassified	Unclassified	sf_5	1051	forest soil clone
Chloroflexi	Anaerolineae	Unclassified	sf_1	1071	denitrifying reactor clone 131
Chloroflexi	Dehalococcoidetes	Unclassified	sf_1	2339	uranium mill soil sample clone bacterium
Chloroflexi	Chloroflexi-4	Unclassified	sf_2	2344	forest soil clone C083
Chloroflexi	Dehalococcoidetes	Unclassified	sf_1	2367	deep marine sediment clone MB-B2-113
Chloroflexi	Dehalococcoidetes	Unclassified	sf_1	2397	deep marine sediment clone MB-C2-127
Chloroflexi	Dehalococcoidetes	Unclassified	sf_1	2438	deep marine sediment clone MB-A2-110
Chloroflexi	Dehalococcoidetes	Unclassified	sf_1	2445	deep marine sediment clone MB-A2-103
Chloroflexi	Dehalococcoidetes	Unclassified	sf_1	2485	
Chloroflexi	Dehalococcoidetes	Unclassified	sf_1	2497	forested wetland clone FW60
Chloroflexi	Unclassified	Unclassified	sf_12	2523	sponge clone TK10
Chloroflexi	Chloroflexi-4	Unclassified	sf_2	2532	trichloroethene-contaminated site clone b
Chloroflexi	Unclassified	Unclassified	sf_1	2534	forest soil clone S085
Chloroflexi	Anaerolineae	Unclassified	sf_9	2539	penguin droppings sediments clone KD4-96

Chloroflexi	Anaerolineae	Unclassified	sf_7	8542	sludge clone SBR2076
Coprothermobacteria	Unclassified	Unclassified	sf_1	751	Coprothermobacter sp. str. Dex80-3
Cyanobacteria	Cyanobacteria	Chloroplasts	sf_5	4966	Adiantum pedatum
Cyanobacteria	Cyanobacteria	Chloroplasts	sf_5	4967	Toolik Lake main station clone TLM14
Cyanobacteria	Cyanobacteria	Chloroplasts	sf_5	4976	Calypogeia muelleriana
Cyanobacteria	Cyanobacteria	Chloroplasts	sf_5	4984	Cape Hatteras picoplankton clone OM164
Cyanobacteria	Cyanobacteria	Chloroplasts	sf_13	5000	Mitracema yamamotoi
Cyanobacteria	Cyanobacteria	Chloroplasts	sf_5	5006	
Cyanobacteria	Cyanobacteria	Chloroplasts	sf_5	5039	Cape Hatteras picoplankton clone OM270
Cyanobacteria	Cyanobacteria	Chloroplasts	sf_5	5040	Solanum nigrum
Cyanobacteria	Cyanobacteria	Chloroplasts	sf_11	5098	Euglena tripteris str. UW OB
Cyanobacteria	Cyanobacteria	Chloroplasts	sf_5	5112	Cyanidium caldarium str. 14-1-1
Cyanobacteria	Cyanobacteria	Chloroplasts	sf_5	5120	cyanobacterium clone LD27
Cyanobacteria	Cyanobacteria	Chloroplasts	sf_11	5123	Lepocinclis fusiformis str. ACOI 1025
Cyanobacteria	Cyanobacteria	Chloroplasts	sf_5	5130	travertine hot spring clone SM2B11
Cyanobacteria	Cyanobacteria	Chloroplasts	sf_5	5147	Emiliania huxleyi str.
Cyanobacteria	Cyanobacteria	Chloroplasts	sf_5	5166	
Cyanobacteria	Cyanobacteria	Chloroplasts	sf_5	5182	Epifagus virginiana -- chloroplast
Cyanobacteria	Cyanobacteria	Chloroplasts	sf_5	5183	Pisum sativum -- chloroplast
Cyanobacteria	Cyanobacteria	Chloroplasts	sf_5	5192	Cycas revoluta
Cyanobacteria	Cyanobacteria	Chloroplasts	sf_5	5221	picoplankton clone OM20
Cyanobacteria	Unclassified	Unclassified	sf_5	270	drinking water system simulator clone HOCICi9
Cyanobacteria	Unclassified	Unclassified	sf_5	4993	Oscillatoria sp
Cyanobacteria	Unclassified	Unclassified	sf_5	4998	
Cyanobacteria	Cyanobacteria	Unclassified	sf_1	5001	sponge clone TK09
Cyanobacteria	Unclassified	Unclassified	sf_5	5002	Dactylococcopsis salina str. PCC 8305
Cyanobacteria	Cyanobacteria	Unclassified	sf_1	5004	Anabaena augstmalis
Cyanobacteria	Cyanobacteria	Unclassified	sf_1	5008	Synechococcus sp. str. PCC 7502
Cyanobacteria	Cyanobacteria	Unclassified	sf_1	5010	LPP-group cyanobacterium isolate str.
Cyanobacteria	Cyanobacteria	Unclassified	sf_1	5012	Synechococcus sp. str. PCC 6312
Cyanobacteria	Unclassified	Unclassified	sf_5	5015	Chlorogloeopsis fritschii str. PCC 6912

Cyanobacteria	Unclassified	Unclassified	sf_5	5027	
Cyanobacteria	Cyanobacteria	Unclassified	sf_1	5028	Cylindrospermopsis raciborskii str. 05E
Cyanobacteria	Unclassified	Unclassified	sf_5	5030	Hapalosiphon welwitschii
Cyanobacteria	Cyanobacteria	Unclassified	sf_1	5034	Spirulina subsalsa str. FACHB351
Cyanobacteria	Unclassified	Unclassified	sf_9	5038	Rumen isolate str. YS2
Cyanobacteria	Cyanobacteria	Unclassified	sf_1	5047	Anabaena circinalis str. AWQC150A
Cyanobacteria	Cyanobacteria	Unclassified	sf_1	5049	Oscillatoria spongelliae str. 520bg
Cyanobacteria	Cyanobacteria	Unclassified	sf_1	5057	Nodularia sphaerocarpa str. UTEX B 2093
Cyanobacteria	Unclassified	Unclassified	sf_5	5064	Oscillatoria neglecta str. M-82
Cyanobacteria	Cyanobacteria	Unclassified	sf_1	5072	Nodularia spumigena str. PCC73104
Cyanobacteria	Cyanobacteria	Unclassified	sf_1	5078	Planktothrix mougeotii str. TK4-5
Cyanobacteria	Unclassified	Unclassified	sf_9	5164	termite gut homogenate clone Rs-H34
Cyanobacteria	Cyanobacteria	Unclassified	sf_1	5174	Cylindrospermopsis raciborskii str. 23B
Cyanobacteria	Cyanobacteria	Unclassified	sf_1	5175	Cylindrospermopsis raciborskii str. 24C
Cyanobacteria	Cyanobacteria	Unclassified	sf_1	5184	Arthrospira platensis str. IAM M-135
Cyanobacteria	Unclassified	Unclassified	sf_6	5186	silica sinter depositing geothermal clone
Cyanobacteria	Unclassified	Unclassified	sf_5	5188	Acaryochloris marina str. MBIC11017
Cyanobacteria	Cyanobacteria	Unclassified	sf_1	5189	Oscillatoria sancta str. PCC 7515
Cyanobacteria	Cyanobacteria	Unclassified	sf_1	5190	Plectonema sp. str. F3
Cyanobacteria	Cyanobacteria	Unclassified	sf_1	5191	Cyanospira rippkae str. PCC 9501
Cyanobacteria	Cyanobacteria	Unclassified	sf_1	5199	Anabaena variabilis str. IAM M-204
Cyanobacteria	Unclassified	Unclassified	sf_8	5206	
Cyanobacteria	Cyanobacteria	Unclassified	sf_1	5210	lichen-dominated Antarctic community clone
Cyanobacteria	Cyanobacteria	Unclassified	sf_1	5219	Synechococcus sp. str. UH7
Deinococcus-Thermus	Unclassified	Unclassified	sf_1	178	Thermus sp. str. C4
Deinococcus-Thermus	Unclassified	Unclassified	sf_1	563	Vulcanithermus mediatlanticus str. TR
Deinococcus-Thermus	Unclassified	Unclassified	sf_2	637	hypersaline pond clone LA7-B27N
Deinococcus-Thermus	Unclassified	Unclassified	sf_1	886	
Deinococcus-Thermus	Unclassified	Unclassified	sf_3	920	
Dictyoglomi	Dictyoglomi	Dictyoglomaceae	sf_9	7579	marine clone Arctic96B-6
DSS1	Unclassified	Unclassified	sf_2	38	DCP-dechlorinating consortium clone SHA-109

DSS1	Unclassified	Unclassified	sf_1	4405	benzoate-degrading consortium clone BA143
Firmicutes	Mollicutes	Acholeplasmataceae	sf_1	3945	Ash witches'-broom phytoplasma str. AshWB
Firmicutes	Mollicutes	Acholeplasmataceae	sf_1	3955	Weeping tea tree phytoplasma tree
Firmicutes	Mollicutes	Acholeplasmataceae	sf_1	3961	Clover yellow edge mycoplasma-like organism
Firmicutes	Mollicutes	Acholeplasmataceae	sf_1	3975	Black raspberry witches'-broom phytoplasma str.
Firmicutes	Mollicutes	Acholeplasmataceae	sf_1	3976	
Firmicutes	Mollicutes	Acholeplasmataceae	sf_1	4044	
Firmicutes	Mollicutes	Acholeplasmataceae	sf_1	4045	Chinaberry yellows phytoplasma
Firmicutes	Mollicutes	Acholeplasmataceae	sf_1	4046	Pigeon pea mycoplasma-like organism
Firmicutes	Mollicutes	Acholeplasmataceae	sf_1	4064	Malus domestica isolate str. AT1/93
Firmicutes	Mollicutes	Acholeplasmataceae	sf_1	4092	Australia isolate str. BVGY
Firmicutes	Bacilli	Aerococcaceae	sf_1	3323	Trichococcus flocculiformis str. DSM 2094
Firmicutes	Bacilli	Aerococcaceae	sf_1	3326	Nostocoida limicola I str. Ben206
Firmicutes	Bacilli	Aerococcaceae	sf_1	3386	feedlot manure clone B87
Firmicutes	Bacilli	Aerococcaceae	sf_1	3435	cf. Alkalibacterium sp. isolate str. F1
Firmicutes	Bacilli	Aerococcaceae	sf_1	3504	Marinilactibacillus psychrotolerans str. O21
Firmicutes	Bacilli	Aerococcaceae	sf_1	3519	Granulicatella elegans str. DSM 11693
Firmicutes	Bacilli	Aerococcaceae	sf_1	3553	Desemzia incerta str. DSM 20581
Firmicutes	Bacilli	Aerococcaceae	sf_1	3615	Aerococcus urinaehominis str. CCUG 42038b
Firmicutes	Bacilli	Aerococcaceae	sf_1	3631	Abiotrophia defectiva str. (ATCC49176)
Firmicutes	Bacilli	Aerococcaceae	sf_1	3682	Dolosigranulum pigrum str. NCFB 2975
Firmicutes	Bacilli	Aerococcaceae	sf_1	3736	Desemzia incerta str. DSM 20581
Firmicutes	Bacilli	Aerococcaceae	sf_1	3782	
Firmicutes	Bacilli	Aerococcaceae	sf_1	3833	Carnobacterium alterfunditum
Firmicutes	Bacilli	Aerococcaceae	sf_1	3840	Trichococcus pasteurii str. KoTa2
Firmicutes	Bacilli	Aerococcaceae	sf_1	3866	Turicibacter sanguinis
Firmicutes	Bacilli	Aerococcaceae	sf_1	3870	Abiotrophia para-adiacens str. TKT1
Firmicutes	Bacilli	Alicyclobacillaceae	sf_1	3368	geothermal site isolate str. G1
Firmicutes	Bacilli	Alicyclobacillaceae	sf_1	3487	Alicyclobacillus acidocaldarius str. DSM 446
Firmicutes	Bacilli	Bacillaceae	sf_1	234	Bacillus vulcani str. 3S-1
Firmicutes	Bacilli	Bacillaceae	sf_1	283	Geobacillus thermocatenulatus str. DSM 730

Firmicutes	Bacilli	Bacillaceae	sf_1	305	Bacillus thermoleovorans
Firmicutes	Bacilli	Bacillaceae	sf_1	385	Geobacillus stearothermophilus str. T10
Firmicutes	Bacilli	Bacillaceae	sf_1	462	Geobacillus thermodenitrificans str. DSM 466
Firmicutes	Bacilli	Bacillaceae	sf_1	571	Bacillus caldotenax str. DSM 406
Firmicutes	Bacilli	Bacillaceae	sf_1	829	Geobacillus sp. str. YMTC1049
Firmicutes	Bacilli	Bacillaceae	sf_1	1050	Bacillus firmus CV93b
Firmicutes	Bacilli	Bacillaceae	sf_1	3283	Bacillus niacini str. IFO15566
Firmicutes	Bacilli	Bacillaceae	sf_1	3328	Pseudobacillus carolinae
Firmicutes	Bacilli	Bacillaceae	sf_1	3345	Bacillus pumilus str. S9
Firmicutes	Bacilli	Bacillaceae	sf_1	3370	Bacillus sp. str. TGS437
Firmicutes	Bacilli	Bacillaceae	sf_1	3383	
Firmicutes	Bacilli	Bacillaceae	sf_1	3385	Bacillus licheniformis str. SAFN-031
Firmicutes	Bacilli	Bacillaceae	sf_1	3419	Bacillus algalicola str. KMM 3737
Firmicutes	Bacilli	Bacillaceae	sf_1	3424	uranium mill tailings clone Gitt-KF-76
Firmicutes	Bacilli	Bacillaceae	sf_1	3439	Bacillus siralis str. 171544
Firmicutes	Bacilli	Bacillaceae	sf_1	3460	Geobacillus jurassicus str. DS1
Firmicutes	Bacilli	Bacillaceae	sf_1	3467	Bacillus luciferensis str. LMG 18422
Firmicutes	Bacilli	Bacillaceae	sf_1	3489	Bacillus silvestris str. SAFN-010
Firmicutes	Bacilli	Bacillaceae	sf_1	3492	Bacillus subtilis str. IAM 12118T
Firmicutes	Bacilli	Bacillaceae	sf_1	3509	Bacillus benzoovorans
Firmicutes	Bacilli	Bacillaceae	sf_1	3517	Planococcus maritimus str. TF-9
Firmicutes	Bacilli	Bacillaceae	sf_1	3540	Geobacillus thermoleovorans str. B23
Firmicutes	Bacilli	Bacillaceae	sf_1	3550	Bacillus megaterium str. QM B1551
Firmicutes	Bacilli	Bacillaceae	sf_1	3579	Bacillus sp. str. TGS750
Firmicutes	Bacilli	Bacillaceae	sf_1	3589	Bacillus senegalensis str. RS8; CIP 106 669
Firmicutes	Bacilli	Bacillaceae	sf_1	3612	Bacillus schlegelii str. ATCC 43741T
Firmicutes	Bacilli	Bacillaceae	sf_1	3650	
Firmicutes	Bacilli	Bacillaceae	sf_1	3661	Bacillus sp. str. 2216.25.2
Firmicutes	Bacilli	Bacillaceae	sf_1	3675	Bacillus mojaviensis str. M-1
Firmicutes	Bacilli	Bacillaceae	sf_1	3687	Filibacter limicola str. SAFN-012
Firmicutes	Bacilli	Bacillaceae	sf_1	3688	Bacillus sp. str. SAFN-006

Firmicutes	Bacilli	Bacillaceae	sf_1	3706	Bacillus sonorensis str. NRRL B-23155
Firmicutes	Bacilli	Bacillaceae	sf_1	3763	Geobacillus stearothermophilus
Firmicutes	Bacilli	Bacillaceae	sf_1	3820	Bacillus subtilis str. KL-120
Firmicutes	Bacilli	Bacillaceae	sf_1	3827	Bacillus acidogenesis str. 105-2
Firmicutes	Bacilli	Bacillaceae	sf_1	3831	Bacillus licheniformis str. KL-068
Firmicutes	Bacilli	Bacillaceae	sf_1	3836	Geobacillus stearothermophilus str. 46
Firmicutes	Bacilli	Bacillaceae	sf_1	3845	hot synthetic compost clone pPD15
Firmicutes	Bacilli	Bacillaceae	sf_1	3848	Bacillus sp. str. TUT1007
Firmicutes	Bacilli	Bacillaceae	sf_1	3894	Sporosarcina macmurdoensis str. CMS 21w
Firmicutes	Bacilli	Bacillaceae	sf_1	3898	compost clone 4-28
Firmicutes	Bacilli	Bacillaceae	sf_1	3900	Bacillus licheniformis str. DSM 13
Firmicutes	Bacilli	Bacillaceae	sf_1	3909	Bacillus subtilis subsp. Marburg str. 168
Firmicutes	Bacilli	Bacillaceae	sf_1	3918	Bacillus subtilis
Firmicutes	Bacilli	Bacillaceae	sf_1	3926	Lake Bogoria isolate 64B4
Firmicutes	Bacilli	Carnobacteriaceae	sf_1	3536	
Firmicutes	Bacilli	Carnobacteriaceae	sf_1	3792	Carnobacterium sp. str. D35
Firmicutes	Bacilli	Caryophanaceae	sf_1	3285	Caryophanon latum str. DSM 14151
Firmicutes	Clostridia	Clostridiaceae	sf_12	132	termite gut homogenate clone Rs-J36 bacterium
Firmicutes	Clostridia	Clostridiaceae	sf_12	206	termite gut homogenate clone Rs-P50 bacterium
Firmicutes	Clostridia	Clostridiaceae	sf_12	252	termite gut homogenate clone Rs-A28 bacterium
Firmicutes	Clostridia	Clostridiaceae	sf_12	2736	Alkaliphilus metalliredigenes str. QYMF
Firmicutes	Clostridia	Clostridiaceae	sf_12	2764	
Firmicutes	Clostridia	Clostridiaceae	sf_12	2786	Clostridium glycolicum str. CIN5
Firmicutes	Clostridia	Clostridiaceae	sf_12	2915	Tepidibacter thalassicus str. SC 562
Firmicutes	Clostridia	Clostridiaceae	sf_12	3004	Clostridium hylemonae str. TN-272
Firmicutes	Clostridia	Clostridiaceae	sf_12	3019	Tepidibacter formicigenes str. DV1184
Firmicutes	Clostridia	Clostridiaceae	sf_12	3021	Clostridium caminithemale str. DVird3
Firmicutes	Clostridia	Clostridiaceae	sf_12	3049	Clostridium paradoxum str. DSM 7308T
Firmicutes	Clostridia	Clostridiaceae	sf_12	3074	
Firmicutes	Clostridia	Clostridiaceae	sf_12	3077	Clostridium glycolicum str. DSM 1288
Firmicutes	Clostridia	Clostridiaceae	sf_12	3108	Clostridium paradoxum str. DSM 7308T

Firmicutes	Clostridia	Clostridiaceae	sf_12	3219	Great Artesian Basin clone R82
Firmicutes	Clostridia	Clostridiaceae	sf_12	4154	Clostridium tunisiense str. DSM 15206
Firmicutes	Clostridia	Clostridiaceae	sf_12	4156	MCB-contaminated groundwater-treating clone
Firmicutes	Clostridia	Clostridiaceae	sf_12	4157	termite gut homogenate clone Rs-A15 bacterium
Firmicutes	Clostridia	Clostridiaceae	sf_12	4169	
Firmicutes	Clostridia	Clostridiaceae	sf_12	4177	Clostridium subterminale DSM 2636
Firmicutes	Clostridia	Clostridiaceae	sf_12	4180	termite gut homogenate clone Rs-M23 bacterium
Firmicutes	Clostridia	Clostridiaceae	sf_12	4187	Clostridiales oral clone P4PB_122 P3
Firmicutes	Clostridia	Clostridiaceae	sf_12	4225	termite gut clone Rs-116
Firmicutes	Clostridia	Clostridiaceae	sf_12	4229	
Firmicutes	Clostridia	Clostridiaceae	sf_12	4244	termite gut homogenate clone Rs-K46 bacterium
Firmicutes	Clostridia	Clostridiaceae	sf_12	4265	termite gut homogenate clone Rs-N70 bacterium
Firmicutes	Clostridia	Clostridiaceae	sf_12	4266	termite gut homogenate clone Rs-M86 bacterium
Firmicutes	Clostridia	Clostridiaceae	sf_12	4267	termite gut clone Rs-114
Firmicutes	Clostridia	Clostridiaceae	sf_12	4271	chlorobenzene-degrading clone IIIA-3
Firmicutes	Clostridia	Clostridiaceae	sf_12	4272	termite gut homogenate clone Rs-M34 bacterium
Firmicutes	Clostridia	Clostridiaceae	sf_12	4275	Clostridium botulinum str. type G
Firmicutes	Clostridia	Clostridiaceae	sf_12	4278	granular sludge clone R1p16
Firmicutes	Clostridia	Clostridiaceae	sf_12	4296	Clostridiaceae str. A4d
Firmicutes	Clostridia	Clostridiaceae	sf_12	4297	
Firmicutes	Clostridia	Clostridiaceae	sf_12	4299	termite gut clone Rs-L02
Firmicutes	Clostridia	Clostridiaceae	sf_12	4300	termite gut clone Rs-060
Firmicutes	Clostridia	Clostridiaceae	sf_12	4306	UASB reactor granular sludge clone bacterium
Firmicutes	Clostridia	Clostridiaceae	sf_12	4310	termite gut clone Rs-056
Firmicutes	Clostridia	Clostridiaceae	sf_12	4321	termite gut homogenate clone Rs-C76 bacterium
Firmicutes	Clostridia	Clostridiaceae	sf_12	4339	Clostridium chauvoei str. ATCC 10092T
Firmicutes	Clostridia	Clostridiaceae	sf_12	4357	Lachnospiraceae bacterium 19gly4
Firmicutes	Clostridia	Clostridiaceae	sf_12	4359	termite gut homogenate clone Rs-C69 bacterium
Firmicutes	Clostridia	Clostridiaceae	sf_12	4364	oral endodontic infection clone MCE3_9
Firmicutes	Clostridia	Clostridiaceae	sf_12	4369	termite gut homogenate clone Rs-N73 bacterium
Firmicutes	Clostridia	Clostridiaceae	sf_12	4378	

Firmicutes	Clostridia	Clostridiaceae	sf_12	4406	termite gut homogenate clone Rs-J39 bacterium
Firmicutes	Clostridia	Clostridiaceae	sf_12	4415	termite gut homogenate clone Rs-K32 bacterium
Firmicutes	Clostridia	Clostridiaceae	sf_12	4418	termite gut homogenate clone Rs-H18 bacterium
Firmicutes	Clostridia	Clostridiaceae	sf_12	4424	termite gut homogenate clone Rs-M05 bacterium
Firmicutes	Clostridia	Clostridiaceae	sf_12	4427	Clostridium tyrobutyricum str. NIZO 51
Firmicutes	Clostridia	Clostridiaceae	sf_12	4459	termite gut clone Rs-109
Firmicutes	Clostridia	Clostridiaceae	sf_21	4471	termite gut clone Rs-058
Firmicutes	Clostridia	Clostridiaceae	sf_12	4475	termite gut homogenate clone Rs-N02 bacterium
Firmicutes	Clostridia	Clostridiaceae	sf_12	4477	termite gut homogenate clone Rs-N85 bacterium
Firmicutes	Clostridia	Clostridiaceae	sf_12	4502	
Firmicutes	Clostridia	Clostridiaceae	sf_12	4507	termite gut homogenate clone Rs-N21 bacterium
Firmicutes	Clostridia	Clostridiaceae	sf_12	4524	termite gut clone Rs-093
Firmicutes	Clostridia	Clostridiaceae	sf_12	4547	Clostridium paraputrificum str. DSM 2630
Firmicutes	Clostridia	Clostridiaceae	sf_12	4550	swine intestine clone p-320-a3
Firmicutes	Clostridia	Clostridiaceae	sf_12	4551	Clostridium acetobutylicum str. ATCC 824 (T)
Firmicutes	Clostridia	Clostridiaceae	sf_12	4554	termite gut clone Rs-068
Firmicutes	Clostridia	Clostridiaceae	sf_12	4555	Clostridium tyrobutyricum
Firmicutes	Clostridia	Clostridiaceae	sf_12	4560	Clostridium beijerinckii str. NCIMB9362
Firmicutes	Clostridia	Clostridiaceae	sf_12	4566	swine intestine clone p-2657-65A5
Firmicutes	Clostridia	Clostridiaceae	sf_12	4574	Clostridium acetobutylicum str. ATCC 824
Firmicutes	Clostridia	Clostridiaceae	sf_12	4575	Clostridium subterminale str. NCIMB 10746
Firmicutes	Clostridia	Clostridiaceae	sf_12	4582	swine intestine clone p-2600-9F5
Firmicutes	Clostridia	Clostridiaceae	sf_12	4584	Clostridium papyrosolvans str. DSM 2782
Firmicutes	Clostridia	Clostridiaceae	sf_12	4587	Clostridium botulinum str. 468; toxin type C
Firmicutes	Clostridia	Clostridiaceae	sf_12	4589	Clostridium butyricum str. ATCC43755
Firmicutes	Clostridia	Clostridiaceae	sf_12	4598	Clostridium sardiniense str. DSM 600
Firmicutes	Clostridia	Clostridiaceae	sf_12	4607	Clostridium novyi str. NCTC538
Firmicutes	Clostridia	Clostridiaceae	sf_12	4610	Clostridium putrefaciens str. DSM 1291
Firmicutes	Clostridia	Clostridiaceae	sf_12	4614	Clostridium sp. str. JC3
Firmicutes	Clostridia	Clostridiaceae	sf_12	4622	termite gut clone Rs-L36
Firmicutes	Clostridia	Clostridiaceae	sf_12	4627	termite gut homogenate clone Rs-A13 bacterium

Firmicutes	Clostridia	Clostridiaceae	sf_12	4637	termite gut clone Rs-088
Firmicutes	Clostridia	Clostridiaceae	sf_12	4638	
Firmicutes	Clostridia	Clostridiaceae	sf_12	10457	strain isolate str. Dex60-82
Firmicutes	Bacilli	Enterococcaceae	sf_1	3261	Enterococcus mundtii str. LMG 10748
Firmicutes	Bacilli	Enterococcaceae	sf_1	3288	hyper-ammonia producing swine storage clone
Firmicutes	Bacilli	Enterococcaceae	sf_1	3298	Enterococcus saccharolyticus str. LMG 11427
Firmicutes	Bacilli	Enterococcaceae	sf_1	3318	Enterococcus ratti str. ATCC 700914
Firmicutes	Bacilli	Enterococcaceae	sf_1	3382	
Firmicutes	Bacilli	Enterococcaceae	sf_1	3392	Vagococcus lutrae
Firmicutes	Bacilli	Enterococcaceae	sf_1	3433	Tetragenococcus muriaticus
Firmicutes	Bacilli	Enterococcaceae	sf_1	3598	Enterococcus solitarius str. DSM 5634
Firmicutes	Bacilli	Enterococcaceae	sf_1	3680	Melissococcus plutonius str. NCDO 2440
Firmicutes	Bacilli	Enterococcaceae	sf_1	3713	Enterococcus cecorum str. ATCC43198
Firmicutes	Bacilli	Enterococcaceae	sf_1	3881	Enterococcus dispar str. LMG 13521
Firmicutes	Mollicutes	Entomoplasmataceae	sf_1	4074	swine intestine clone p-2013-s959-5
Firmicutes	Mollicutes	Entomoplasmataceae	sf_2	4112	Entomoplasma somnilux str. ATCC 49194
Firmicutes	Mollicutes	Erysipelotrichaceae	sf_3	144	Eubacterium cylindroides
Firmicutes	Mollicutes	Erysipelotrichaceae	sf_3	768	
Firmicutes	Mollicutes	Erysipelotrichaceae	sf_3	3943	Coprobacillus cateniformis str. JCM 10603
Firmicutes	Mollicutes	Erysipelotrichaceae	sf_3	3952	Erysipelothrix rhusiopathiae str. Pecs 56
Firmicutes	Mollicutes	Erysipelotrichaceae	sf_3	3965	TCE-contaminated site clone ccslm238
Firmicutes	Mollicutes	Erysipelotrichaceae	sf_3	3981	phototrophic sludge clone PSB-M-3
Firmicutes	Mollicutes	Erysipelotrichaceae	sf_3	4038	Bulleidia moorei str. JCM 10647 RCA59-77
Firmicutes	Mollicutes	Erysipelotrichaceae	sf_3	4065	Clostridium ramosum M91
Firmicutes	Mollicutes	Erysipelotrichaceae	sf_3	4091	Bulleidia extructa str. DSM 13220
Firmicutes	Clostridia	Eubacteriaceae	sf_1	28	termite gut homogenate clone Rs-H81 bacterium
Firmicutes	Clostridia	Eubacteriaceae	sf_1	687	Acetobacterium wieringae str. DSM 1911
Firmicutes	Bacilli	Halobacillaceae	sf_1	3344	Halobacillus yeomjeoni str. MSS-402
Firmicutes	Bacilli	Halobacillaceae	sf_1	3488	Halobacillus salinus str. HSL-3
Firmicutes	Bacilli	Halobacillaceae	sf_1	3552	Paraliobacillus ryukyuensis
Firmicutes	Bacilli	Halobacillaceae	sf_1	3633	Bacillus clausii str. GMBAE 42

Firmicutes	Bacilli	Halobacillaceae	sf_1	3702	Amphibacillus xylanus str. DSM 6626
Firmicutes	Bacilli	Halobacillaceae	sf_1	3756	Salibacillus sp. str. YIM-kkny16
Firmicutes	Bacilli	Halobacillaceae	sf_1	3758	Amphibacillus sp. str. YIM-kkny10
Firmicutes	Bacilli	Halobacillaceae	sf_1	3769	Gracilibacillus sp. str. YIM-kkny13
Firmicutes	Bacilli	Halobacillaceae	sf_1	3849	Halobacillus litoralis str. SL-4
Firmicutes	Clostridia	Lachnospiraceae	sf_5	2668	termite gut homogenate clone Rs-G40 bacterium
Firmicutes	Clostridia	Lachnospiraceae	sf_5	2681	termite gut homogenate clone Rs-K41 bacterium
Firmicutes	Clostridia	Lachnospiraceae	sf_5	2693	ruminantium str. GA195
Firmicutes	Clostridia	Lachnospiraceae	sf_5	2698	termite gut homogenate clone Rs-B88 bacterium
Firmicutes	Clostridia	Lachnospiraceae	sf_5	2708	anaerobic digester clone AA02
Firmicutes	Clostridia	Lachnospiraceae	sf_5	2709	human stool clone B065
Firmicutes	Clostridia	Lachnospiraceae	sf_5	2756	Roseburia faecalis str. M6/1
Firmicutes	Clostridia	Lachnospiraceae	sf_5	2784	human colonic clone HuCB12
Firmicutes	Clostridia	Lachnospiraceae	sf_5	2801	Butyrivibrio fibrisolvens
Firmicutes	Clostridia	Lachnospiraceae	sf_5	2804	Clostridium amygdalinum str. BR-10
Firmicutes	Clostridia	Lachnospiraceae	sf_5	2825	Butyrivibrio fibrisolvens str. LP1265
Firmicutes	Clostridia	Lachnospiraceae	sf_5	2834	Butyrivibrio fibrisolvens str. OB156
Firmicutes	Clostridia	Lachnospiraceae	sf_5	2844	Pseudobutyrovibrio ruminis str. pC-XS2
Firmicutes	Clostridia	Lachnospiraceae	sf_5	2849	Butyrivibrio fibrisolvens str. NCDO 2435
Firmicutes	Clostridia	Lachnospiraceae	sf_5	2893	Ruminococcus obeum
Firmicutes	Clostridia	Lachnospiraceae	sf_5	2931	termite gut homogenate clone Rs-G77 bacterium
Firmicutes	Clostridia	Lachnospiraceae	sf_5	2937	swine intestine clone p-2482-18B5
Firmicutes	Clostridia	Lachnospiraceae	sf_5	2943	human thigh wound isolate str. MDA2477
Firmicutes	Clostridia	Lachnospiraceae	sf_5	2961	termite gut homogenate clone Rs-F92 bacterium
Firmicutes	Clostridia	Lachnospiraceae	sf_5	2965	oral endodontic infection clone MCE9_173
Firmicutes	Clostridia	Lachnospiraceae	sf_5	2975	faecal clone adhufec80.25
Firmicutes	Clostridia	Lachnospiraceae	sf_5	2991	rumen clone 3C3d-8
Firmicutes	Clostridia	Lachnospiraceae	sf_5	2994	termite gut clone Rs-L15
Firmicutes	Clostridia	Lachnospiraceae	sf_5	3001	human colonic clone HuCA20
Firmicutes	Clostridia	Lachnospiraceae	sf_5	3017	termite gut homogenate clone Rs-D48 bacterium
Firmicutes	Clostridia	Lachnospiraceae	sf_5	3033	human colonic clone HuCA15

Firmicutes	Clostridia	Lachnospiraceae	sf_5	3036	termite gut homogenate clone Rs-F27 bacterium
Firmicutes	Clostridia	Lachnospiraceae	sf_5	3038	swine intestine clone p-1594-c5
Firmicutes	Clostridia	Lachnospiraceae	sf_5	3042	swine intestine clone p-2876-6C5
Firmicutes	Clostridia	Lachnospiraceae	sf_5	3059	Butyrivibrio fibrisolvens str. NCDO 2249
Firmicutes	Clostridia	Lachnospiraceae	sf_5	3060	termite gut homogenate clone Rs-B14 bacterium
Firmicutes	Clostridia	Lachnospiraceae	sf_5	3066	Clostridium methoxybenzovorans
Firmicutes	Clostridia	Lachnospiraceae	sf_5	3075	Roseburia intestinalis str. L1-82
Firmicutes	Clostridia	Lachnospiraceae	sf_5	3076	Clostridium nexile
Firmicutes	Clostridia	Lachnospiraceae	sf_5	3087	Butyrivibrio hungatei str. Su6
Firmicutes	Clostridia	Lachnospiraceae	sf_5	3088	Clostridium sphenoides str. DSM 632
Firmicutes	Clostridia	Lachnospiraceae	sf_5	3089	Ruminococcus obeum
Firmicutes	Clostridia	Lachnospiraceae	sf_5	3107	oxidoreducens str. G2-2
Firmicutes	Clostridia	Lachnospiraceae	sf_5	3109	Catonella morbi str. ATCC 51271
Firmicutes	Clostridia	Lachnospiraceae	sf_5	3111	rumen clone 6C3d-11
Firmicutes	Clostridia	Lachnospiraceae	sf_5	3143	rumen clone 4C28d-24
Firmicutes	Clostridia	Lachnospiraceae	sf_5	3152	tongue dorsa clone DO016
Firmicutes	Clostridia	Lachnospiraceae	sf_5	3171	Lachnospira pectinoschiza
Firmicutes	Clostridia	Lachnospiraceae	sf_5	3174	
Firmicutes	Clostridia	Lachnospiraceae	sf_5	3218	termite gut homogenate clone Rs-N53
Firmicutes	Clostridia	Lachnospiraceae	sf_5	3236	Firmicutes sp. oral strain str. FTB41
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4155	termite gut homogenate clone Rs-K92 bacterium
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4164	ckncm322-B3-7 clone
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4167	termite gut homogenate clone Rs-D76 bacterium
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4212	termite gut clone Rs-061
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4273	termite gut homogenate clone Rs-M14 bacterium
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4281	granular sludge clone UASB_brew_B86
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4301	human subgingival plaque clone F058
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4315	termite gut homogenate clone Rs-N94 bacterium
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4330	cow rumen clone BE33
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4331	granular sludge clone UASB_brew_B84
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4335	termite gut homogenate clone Rs-N86 bacterium

Firmicutes	Clostridia	Lachnospiraceae	sf_5	4381	ckncm301-B3-28 clone
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4434	termite gut homogenate clone Rs-K11 bacterium
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4443	swine intestine clone p-3567-9F3
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4501	crevicular epithelial cells clone BU014
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4510	termite gut homogenate clone Rs-Q53 bacterium
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4511	ckncm314-B7-17 clone
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4512	granular sludge clone UASB_brew_B25
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4514	termite gut homogenate clone Rs-B34 bacterium
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4525	termite gut homogenate clone Rs-Q18 bacterium
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4533	termite gut homogenate clone Rs-N06 bacterium
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4535	ckncm297-B1-1 clone
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4539	termite gut homogenate clone Rs-C61 bacterium
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4540	termite gut homogenate clone Rs-M18 bacterium
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4567	human colonic clone HuCB5
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4571	Faecalibacterium prausnitzii str. ATCC 27766
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4613	rumen clone 3C0d-3
Firmicutes	Clostridia	Lachnospiraceae	sf_5	4623	human colonic clone HuCA1
Firmicutes	Bacilli	Lactobacillaceae	sf_1	3330	Lactobacillus kitasatonis str. KM9212
Firmicutes	Bacilli	Lactobacillaceae	sf_1	3342	Lactobacillus crispatus str. DSM 20584 T
Firmicutes	Bacilli	Lactobacillaceae	sf_1	3366	Lactobacillus saerimneri str.
Firmicutes	Bacilli	Lactobacillaceae	sf_1	3395	Lactobacillus reuteri str. DSM 20016 T
Firmicutes	Bacilli	Lactobacillaceae	sf_1	3418	Lactobacillus subsp. aviarius
Firmicutes	Bacilli	Lactobacillaceae	sf_1	3478	Lactobacillus crispatus str. ATCC33197
Firmicutes	Bacilli	Lactobacillaceae	sf_1	3490	Lactobacillus suntoryeus str. LH
Firmicutes	Bacilli	Lactobacillaceae	sf_1	3521	Pediococcus inopinatus str. DSM 20285
Firmicutes	Bacilli	Lactobacillaceae	sf_1	3526	Lactobacillus sakei
Firmicutes	Bacilli	Lactobacillaceae	sf_1	3547	Lactobacillus frumenti str. TMW 1.666
Firmicutes	Bacilli	Lactobacillaceae	sf_1	3566	Lactobacillus pontis str. LTH 2587
Firmicutes	Bacilli	Lactobacillaceae	sf_1	3600	Lactobacillus crispatus str. NCTC 4
Firmicutes	Bacilli	Lactobacillaceae	sf_1	3618	Lactobacillus jensenii str. KC36b
Firmicutes	Bacilli	Lactobacillaceae	sf_1	3634	Lactobacillus letivazi str. JCL3994

Firmicutes	Bacilli	Lactobacillaceae	sf_1	3678	Lactobacillus fornicalis str. TV1018
Firmicutes	Bacilli	Lactobacillaceae	sf_1	3696	Lactobacillus kalixensis str. Kx127A2
Firmicutes	Bacilli	Lactobacillaceae	sf_1	3703	Lactobacillus salivarius str. RA2115
Firmicutes	Bacilli	Lactobacillaceae	sf_1	3767	Lactobacillus suebicus str. CECT 5917T
Firmicutes	Bacilli	Lactobacillaceae	sf_1	3768	Lactobacillus perolens str. L532
Firmicutes	Bacilli	Lactobacillaceae	sf_1	3829	Lactobacillus paralimentarius str. DSM 13238
Firmicutes	Bacilli	Lactobacillaceae	sf_1	3842	Lactobacillus perolens str. L534
Firmicutes	Bacilli	Lactobacillaceae	sf_1	3885	Pediococcus pentosaceus
Firmicutes	Bacilli	Lactobacillaceae	sf_1	3914	Lactobacillus cypricasei str. LMK3
Firmicutes	Bacilli	Leuconostocaceae	sf_1	3497	Weissella koreensis S-5673
Firmicutes	Bacilli	Leuconostocaceae	sf_1	3573	Leuconostoc ficulneum str. FS-1
Firmicutes	Mollicutes	Mycoplasmataceae	sf_1	3929	Mycoplasma gypsbengalensis str. Gb-V33
Firmicutes	Mollicutes	Mycoplasmataceae	sf_1	3970	Mycoplasma canadense str. 275c
Firmicutes	Mollicutes	Mycoplasmataceae	sf_1	3991	Mycoplasma buccale str. CH20247(T)
Firmicutes	Mollicutes	Mycoplasmataceae	sf_1	3994	Mycoplasma faucium str. DC333(T)
Firmicutes	Mollicutes	Mycoplasmataceae	sf_1	3997	Mycoplasma salivarium str. PG20(T)
Firmicutes	Mollicutes	Mycoplasmataceae	sf_1	4014	Mycoplasma pulmonis str. UAB CTIP
Firmicutes	Mollicutes	Mycoplasmataceae	sf_1	4102	Mycoplasma zalophus str. 4296C
Firmicutes	Bacilli	Paenibacillaceae	sf_1	3299	Brevibacillus borstelensis str. LMG 15536
Firmicutes	Bacilli	Paenibacillaceae	sf_1	3415	Paenibacillus nematophilus str. NEM1b
Firmicutes	Bacilli	Paenibacillaceae	sf_1	3559	Paenibacillus turicensis str. MOL722
Firmicutes	Bacilli	Paenibacillaceae	sf_1	3567	Paenibacillus sp. str. T-168
Firmicutes	Bacilli	Paenibacillaceae	sf_1	3595	Paenibacillus sp. str. MB 2039
Firmicutes	Bacilli	Paenibacillaceae	sf_1	3630	
Firmicutes	Bacilli	Paenibacillaceae	sf_1	3641	Brevibacillus sp. MN 47.2a
Firmicutes	Bacilli	Paenibacillaceae	sf_1	3651	Paenibacillus borealis KK20
Firmicutes	Bacilli	Paenibacillaceae	sf_1	3891	Paenibacillus sp. str. DSM 1474
Firmicutes	Bacilli	Paenibacillaceae	sf_1	3922	Paenibacillus thiaminolyticus str. DSM 7262
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	39	forested wetland clone RCP2-71
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	59	swine intestine clone p-1941-s962-3
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	71	penguin droppings sediments clone KD2-97

Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	80	Selenomonas noxia str. ATCC 43541
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	126	oral periodontitis clone FY011
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	131	pig feces clone
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	150	
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	181	Allisonella histaminiformans str. MR2
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	242	Desulfosporosinus orientis str. DSMZ 7493
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	275	clone AKS21
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	300	benzene-contaminated groundwater clone
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	304	Selenomonas ruminantium str.JCM6582
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	392	oral endodontic infection clone MCE7_134
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	428	chlorobenzene-degrading clone IIIA-1
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	534	chlorobenzene-degrading clone IIA-26
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	562	oral endodontic infection clone MCE10_265
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	564	human subgingival plaque clone BS073
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	709	Selenomonas ruminantium str.S20
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	710	Centipeda periodontii str. HB-2
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	771	Dialister pneumosintes str. ATCC 33048
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	800	corneal ulcer clone E1-K16
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	862	Megasphaera micronuciformis
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	863	Dialister invisus str. E7_25
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	865	Selenomonas sputigena str. ATCC 35185
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	866	Veillonella ratti str. ATCC17746
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	940	Veillonella dispar str. DSM 20735
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	986	subgingival plaque clone EW076
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	992	anoxic bulk soil rice microcosm clone
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	999	human subgingival plaque clone CS015
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	1036	Great Artesian Basin clone G07
Firmicutes	Clostridia	Peptococc/Acidaminococc	sf_11	2473	
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	17	Peptostreptococcus sp. oral clone P4PA_156
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	58	Peptostreptococcus sp. str. E3_32
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	140	oral periodontitis clone EX153

Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	224	Finegoldia magna str. ATCC 29328
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	268	Sporanaerobacter acetigenes str. Lup33;
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	393	Anaerococcus vaginalis str. CCUG 31349
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	616	Peptoniphilus lacrimalis str. CCUG 31350
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	619	TCE-dechlorinating microbial community clone
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	668	Sedimentibacter sp. str. BRS2
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	919	Anaerococcus tetradius str. CCUG 46590
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	1037	Finegoldia magna
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	2679	termite gut homogenate clone BCf9-13
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	2694	oral periodontitis clone FX028
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	2710	DCP-dechlorinating consortium clone SHA-74
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	2714	termite gut homogenate clone Rs-N27 bacterium
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	2721	termite gut homogenate clone Rs-N71 bacterium
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	2722	termite gut homogenate clone Rs-E61 bacterium
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	2729	DCP-dechlorinating consortium clone SHA-58
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	2738	Mogibacterium neglectum str. ATCC 700924
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	2751	
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	2796	human subgingival plaque clone BB142
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	2797	hyper-ammonia producing swine storage clone
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	2800	Mogibacterium timidum str. ATCC 33093
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	2805	oral periodontitis clone FX033
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	2913	termite gut homogenate clone Rs-N82 bacterium
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	2988	termite gut clone Rs-050
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	2993	oral clone P2PB_46 P3
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	3080	termite gut homogenate clone Rs-F43 bacterium
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	3112	Evry municipal wastewater treatment plant clone
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	3153	infirmum str. W 1471
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	3182	termite gut homogenate clone Rs-Q64 bacterium
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	3193	nodatum str. ATCC 33099
Firmicutes	Clostridia	Peptostreptococcaceae	sf_5	3220	chlorobenzene-degrading clone IA-19
Firmicutes	Bacilli	Sporolactobacillaceae	sf_1	3365	Bacillus sp. clone ML615J-19

Firmicutes	Bacilli	Sporolactobacillaceae	sf_1	3747	Bacillus sp. str. C-59-2
Firmicutes	Bacilli	Sporolactobacillaceae	sf_1	3879	Lake Elmenteita isolate WE4
Firmicutes	Bacilli	Staphylococcaceae	sf_1	3258	Staphylococcus auricularis ATCC33753T
Firmicutes	Bacilli	Staphylococcaceae	sf_1	3284	
Firmicutes	Bacilli	Staphylococcaceae	sf_1	3432	deep-sea sediment isolate str. P_wp0225
Firmicutes	Bacilli	Staphylococcaceae	sf_1	3494	Micrococcus luteus B-P 26
Firmicutes	Bacilli	Staphylococcaceae	sf_1	3524	Gemella haemolysans
Firmicutes	Bacilli	Staphylococcaceae	sf_1	3545	
Firmicutes	Bacilli	Staphylococcaceae	sf_1	3569	Staphylococcus saprophyticus
Firmicutes	Bacilli	Staphylococcaceae	sf_1	3592	Staphylococcus caprae str. DSM 20608
Firmicutes	Bacilli	Staphylococcaceae	sf_1	3605	
Firmicutes	Bacilli	Staphylococcaceae	sf_1	3628	Staphylococcus haemolyticus str. CCM2737
Firmicutes	Bacilli	Staphylococcaceae	sf_1	3638	Staphylococcus sp str. AG-30
Firmicutes	Bacilli	Staphylococcaceae	sf_1	3654	Staphylococcus pettenkoferi str. B3117
Firmicutes	Bacilli	Staphylococcaceae	sf_1	3684	Staphylococcus sciuri
Firmicutes	Bacilli	Staphylococcaceae	sf_1	3724	Gemella bergeri str. 617-93
Firmicutes	Bacilli	Staphylococcaceae	sf_1	3794	
Firmicutes	Bacilli	Staphylococcaceae	sf_1	3822	Staphylococcus succinus str. SB72
Firmicutes	Bacilli	Streptococcaceae	sf_1	3250	Streptococcus bovis str. B315
Firmicutes	Bacilli	Streptococcaceae	sf_1	3251	Streptococcus cristatus str. ATCC 51100
Firmicutes	Bacilli	Streptococcaceae	sf_1	3253	derived cheese sample clone 32CR
Firmicutes	Bacilli	Streptococcaceae	sf_1	3287	tongue dorsum scrapings clone FP015
Firmicutes	Bacilli	Streptococcaceae	sf_1	3290	Streptococcus mitis str. Sm91
Firmicutes	Bacilli	Streptococcaceae	sf_1	3313	Streptococcus salivarius str. ATCC 7073
Firmicutes	Bacilli	Streptococcaceae	sf_1	3397	Streptococcus macedonicus str. ACA-DC 206
Firmicutes	Bacilli	Streptococcaceae	sf_1	3422	Streptococcus thermophilus str. DSM 20617
Firmicutes	Bacilli	Streptococcaceae	sf_1	3446	Streptococcus bovis str. HJ50
Firmicutes	Bacilli	Streptococcaceae	sf_1	3499	Streptococcus constellatus str. ATCC27823
Firmicutes	Bacilli	Streptococcaceae	sf_1	3543	
Firmicutes	Bacilli	Streptococcaceae	sf_1	3560	Streptococcus gallinaceus str. CCUG 42692
Firmicutes	Bacilli	Streptococcaceae	sf_1	3588	Streptococcus downei str. ATCC 33748

Firmicutes	Bacilli	Streptococcaceae	sf_1	3629	Streptococcus mutans str. UA96
Firmicutes	Bacilli	Streptococcaceae	sf_1	3637	str. 37236
Firmicutes	Bacilli	Streptococcaceae	sf_1	3685	Streptococcus gordonii str. ATCC 10558
Firmicutes	Bacilli	Streptococcaceae	sf_1	3699	Streptococcus agalactiae str. 2603V/R
Firmicutes	Bacilli	Streptococcaceae	sf_1	3722	Lactococcus Il1403 subsp. lactis str. IL1403
Firmicutes	Bacilli	Streptococcaceae	sf_1	3753	Streptococcus suis str. 8074
Firmicutes	Bacilli	Streptococcaceae	sf_1	3846	Streptococcus equi str. ATCC 43079
Firmicutes	Bacilli	Streptococcaceae	sf_1	3869	Streptococcus equi str. Tokyo1291
Firmicutes	Bacilli	Streptococcaceae	sf_1	3906	Streptococcus bovis str.ATCC 43143
Firmicutes	Bacilli	Streptococcaceae	sf_1	3907	aortic heart valve patient with endocarditis clone
Firmicutes	Clostridia	Syntrophomonadaceae	sf_5	2456	granular sludge clone R4b14
Firmicutes	Clostridia	Syntrophomonadaceae	sf_5	2483	trichloroethene-contaminated site clone
Firmicutes	Clostridia	Syntrophomonadaceae	sf_5	2543	
Firmicutes	Bacilli	Thermoactinomycetaceae	sf_1	3301	Thermoactinomyces sp. str. 700375
Firmicutes	Bacilli	Thermoactinomycetaceae	sf_1	3539	Laceyella sacchari str. KCTC 9789 ()
Firmicutes	Symbiobacteria	Unclassified	sf_1	77	thermal soil clone YNPFFP9
Firmicutes	Unclassified	Unclassified	sf_8	141	MCB-contaminated groundwater-treating clone
Firmicutes	Mollicutes	Unclassified	sf_6	149	Streptococcus pleomorphus
Firmicutes	Desulfotomaculum	Unclassified	sf_1	522	UASB granular sludge clone UT-1
Firmicutes	Unclassified	Unclassified	sf_8	546	Ferribacter thermoautotrophicus
Firmicutes	Clostridia	Unclassified	sf_17	926	
Firmicutes	Clostridia	Unclassified	sf_17	2324	
Firmicutes	Desulfotomaculum	Unclassified	sf_1	2351	Desulfotomaculum thermobenzoicum
Firmicutes	Desulfotomaculum	Unclassified	sf_1	2359	UASB granular sludge clone JP
Firmicutes	Clostridia	Unclassified	sf_3	2373	
Firmicutes	Symbiobacteria	Unclassified	sf_1	2388	G+C Gram-positive clone YNPRH70A
Firmicutes	Clostridia	Unclassified	sf_4	2398	deep marine sediment clone MB-C2-106
Firmicutes	Unclassified	Unclassified	sf_8	2433	Ferribacter thermoautotrophicus
Firmicutes	Desulfotomaculum	Unclassified	sf_1	2443	Desulfotomaculum thermoacetoxidans
Firmicutes	Desulfotomaculum	Unclassified	sf_1	2490	Desulfotomaculum solfataricum str. V21
Firmicutes	Desulfotomaculum	Unclassified	sf_1	2541	UASB granular sludge clone UT-2

Firmicutes	Clostridia	Unclassified	sf_17	2659	
Firmicutes	Clostridia	Unclassified	sf_17	2680	
Firmicutes	Clostridia	Unclassified	sf_17	2683	
Firmicutes	Catabacter	Unclassified	sf_4	2716	termite gut homogenate clone Rs-F76 bacterium
Firmicutes	Clostridia	Unclassified	sf_17	2730	
Firmicutes	Clostridia	Unclassified	sf_17	3139	
Firmicutes	Bacilli	Unclassified	sf_1	3289	Isobaculum melis CCUG 37660T
Firmicutes	Bacilli	Unclassified	sf_1	3434	termite gut homogenate clone Rs-C68 sp.
Firmicutes	Clostridia	Unclassified	sf_17	3476	
Firmicutes	Bacilli	Unclassified	sf_1	3481	
Firmicutes	Symbiobacteria	Unclassified	sf_3	3508	Symbiobacterium toebii str. SC-1
Firmicutes	Bacilli	Unclassified	sf_3	3743	
Firmicutes	Clostridia	Unclassified	sf_17	4168	
Firmicutes	Clostridia	Unclassified	sf_7	4216	
Firmicutes	Catabacter	Unclassified	sf_1	4261	termite gut homogenate clone Rs-G04 bacterium
Firmicutes	Catabacter	Unclassified	sf_1	4293	termite gut homogenate clone Rs-Q01 bacterium
Firmicutes	gut clone group	Unclassified	sf_1	4298	human mouth clone P4PA_66
Firmicutes	Anaerobranca	Unclassified	sf_1	4304	Mono Lake clone ML635J-34 G+C
Firmicutes	Clostridia	Unclassified	sf_17	4307	
Firmicutes	Catabacter	Unclassified	sf_4	4325	termite gut homogenate clone Rs-K21 bacterium
Firmicutes	Catabacter	Unclassified	sf_4	4503	termite gut homogenate clone Rs-H83 bacterium
Firmicutes	Catabacter	Unclassified	sf_4	4526	TCE-contaminated site clone ccs1m210
Firmicutes	Unclassified	Unclassified	sf_8	4536	Mono Lake clone ML635J-14 G+C
Firmicutes	gut clone group	Unclassified	sf_1	4616	rumen clone F23-C12
Fusobacteria	Fusobacteria	Fusobacteriaceae	sf_3	35	crevicular epithelial cells clone EI013
Fusobacteria	Fusobacteria	Fusobacteriaceae	sf_3	120	tongue dorsum scrapings clone FP036
Fusobacteria	Fusobacteria	Fusobacteriaceae	sf_3	367	Leptotrichia amnionii str. AMN-1
Fusobacteria	Fusobacteria	Fusobacteriaceae	sf_3	387	Leptotrichia wadeii str. LB16
Fusobacteria	Fusobacteria	Fusobacteriaceae	sf_3	455	crevicular epithelial cells clone EI022
Fusobacteria	Fusobacteria	Fusobacteriaceae	sf_1	488	Fusobacterium nucleatum str. ATCC 49256
Fusobacteria	Fusobacteria	Fusobacteriaceae	sf_3	558	Sneathia sanguinegens str. CCUG 41628T

Fusobacteria	Fusobacteria	Fusobacteriaceae	sf_3	644	Ilyobacter polytropus str. DSM 2926 T
Fusobacteria	Fusobacteria	Fusobacteriaceae	sf_3	694	tongue dorsa clone DR011
Fusobacteria	Fusobacteria	Fusobacteriaceae	sf_3	721	human mouth clone P2PB_51
Fusobacteria	Fusobacteria	Fusobacteriaceae	sf_3	739	Fusobacterium necrophorum str. B FnS-40
Fusobacteria	Fusobacteria	Fusobacteriaceae	sf_3	779	
Fusobacteria	Fusobacteria	Fusobacteriaceae	sf_3	1034	Ilyobacter tartaricus str. DSM 2382 T
Gemmatimonadetes	Unclassified	Unclassified	sf_5	227	uranium mining waste pile clone JG37-AG-36
Gemmatimonadetes	Unclassified	Unclassified	sf_5	317	penguin droppings sediments clone KD8-87
Gemmatimonadetes	Unclassified	Unclassified	sf_5	442	forest soil clone S0134
Gemmatimonadetes	Unclassified	Unclassified	sf_5	1127	uranium mining soil clone JG37-AG-21
Gemmatimonadetes	Unclassified	Unclassified	sf_5	1238	Gemmatimonas aurantiaca
Gemmatimonadetes	Unclassified	Unclassified	sf_5	1565	uranium mining waste pile clone JG34-KF-418
Gemmatimonadetes	Unclassified	Unclassified	sf_5	2047	soil clone #0319-7G21
Gemmatimonadetes	Unclassified	Unclassified	sf_5	9464	lodgepole pine rhizosphere soil
Gemmatimonadetes	Unclassified	Unclassified	sf_5	10112	forest soil clone NOS7.157WL
LD1PA group	Unclassified	Unclassified	sf_1	10118	anoxic marine sediment clone LD1-PA38
Lentisphaerae	Unclassified	Unclassified	sf_5	9704	Cytophaga sp. str. Dex80-64
Lentisphaerae	Unclassified	Unclassified	sf_5	10027	Cytophaga sp. str. Dex80-43
Lentisphaerae	Unclassified	Unclassified	sf_5	10330	Mono lake clone ML635J-58
marine group A	mgA-2	Unclassified	sf_1	6344	bacterioplankton clone ZA3648c
marine group A	mgA-1	Unclassified	sf_1	6408	Sargasso Sea
marine group A	mgA-1	Unclassified	sf_1	6454	marine clone SAR406
Natronoanaerobium	Unclassified	Unclassified	sf_1	769	fjord ikaite column clone un-c23
Natronoanaerobium	Unclassified	Unclassified	sf_1	2437	Mono Lake clone ML623J-19
Natronoanaerobium	Unclassified	Unclassified	sf_1	3570	Bacillus sp. clone ML1228J-1
Natronoanaerobium	Unclassified	Unclassified	sf_1	4377	Mono Lake clone ML635J-65 G+C
NC10	NC10-1	Unclassified	sf_1	452	vadose clone 5G01
NC10	NC10-1	Unclassified	sf_1	536	uranium mill tailings clone GuBH2-AD-8
NC10	Unclassified	Unclassified	sf_1	2516	TCE-contaminated site clone FTL22
NC10	NC10-2	Unclassified	sf_1	10254	uranium mill soil sample clone Sh765B-TzT-35
Nitrospira	Nitrospira	Nitrospiraceae	sf_1	179	Great Artesian Basin clone G19

Nitrospira	Nitrospira	Nitrospiraceae	sf_3	240	acid mine drainage clone AW4
Nitrospira	Nitrospira	Nitrospiraceae	sf_2	542	forested wetland clone FW19
Nitrospira	Nitrospira	Nitrospiraceae	sf_2	544	forested wetland clone FW5
Nitrospira	Nitrospira	Nitrospiraceae	sf_2	681	
Nitrospira	Nitrospira	Nitrospiraceae	sf_2	697	forested wetland clone FW118
Nitrospira	Nitrospira	Nitrospiraceae	sf_3	833	acid mine drainage clone BA29
Nitrospira	Nitrospira	Nitrospiraceae	sf_1	864	nitrifying sludge clone GC86
Nitrospira	Nitrospira	Nitrospiraceae	sf_1	984	uranium mining clone JG37-AG-131 sp.
OD1	OP11-5	Unclassified	sf_1	515	
OP10	CH21 cluster	Unclassified	sf_1	326	geothermal clone ST01-SN3H
OP10	Unclassified	Unclassified	sf_4	484	forested wetland clone FW68
OP10	CH21 cluster	Unclassified	sf_1	514	sludge clone SBRA136
OP10	Unclassified	Unclassified	sf_4	728	benzene-contaminated groundwater clone
OP10	Unclassified	Unclassified	sf_1	8413	DCP-dechlorinating consortium clone SHA-37
OP10	Unclassified	Unclassified	sf_5	9782	Rocky Mountain alpine soil clone S1a-1H
OP3	Unclassified	Unclassified	sf_2	349	soil clone PBS-25
OP3	Unclassified	Unclassified	sf_4	628	CB-contaminated groundwater clone GOUTB15
OP3	Unclassified	Unclassified	sf_3	1015	polluted aquifer clone BVC56
OP8	Unclassified	Unclassified	sf_3	598	Guaymas Basin sediment clone a2b010
OP9/JS1	OP9	Unclassified	sf_1	726	hot spring clone OPB72
OP9/JS1	OP9	Unclassified	sf_1	969	DCP-dechlorinating consortium clone SHA-1
OP9/JS1	JS1	Unclassified	sf_1	2380	Guaymas Basin vent clone B03R012
OP9/JS1	JS1	Unclassified	sf_1	2489	Guaymas Basin vent clone B01R005
OP9/JS1	JS1	Unclassified	sf_1	2491	deep marine sediment clone MB-B2-103
Planctomycetes	Planctomycetacia	Anammoxales	sf_2	4683	anoxic basin clone CY0ARA028B09
Planctomycetes	Planctomycetacia	Anammoxales	sf_4	4694	Colorado Horsetooth Reservoir clone HT2F11
Planctomycetes	Planctomycetacia	Anammoxales	sf_4	4695	Crater Lake clone CL500-15
Planctomycetes	Planctomycetacia	Anammoxales	sf_4	9662	Great Artesian Basin clone B83
Planctomycetes	Planctomycetacia	Pirellulae	sf_3	4670	
Planctomycetes	Planctomycetacia	Pirellulae	sf_3	4677	aerobic basin clone CY0ARA032A03
Planctomycetes	Planctomycetacia	Pirellulae	sf_3	4692	aerobic basin clone CY0ARA026G04

Planctomycetes	Planctomycetacia	Pirellulae	sf_3	4704	aerobic basin clone CY0ARA025E11
Planctomycetes	Planctomycetacia	Pirellulae	sf_3	4769	anoxic marine sediment clone LD1-PA40
Planctomycetes	Planctomycetacia	Pirellulae	sf_3	4803	Pirellula sp. str. ACM 3181
Planctomycetes	Planctomycetacia	Pirellulae	sf_3	4956	aerobic phosphorus-removal ecosystem clone
Planctomycetes	Planctomycetacia	Planctomycetaceae	sf_3	4652	anoxic basin clone CY0ARA028C04
Planctomycetes	Planctomycetacia	Planctomycetaceae	sf_3	4818	drinking water system simulator clone DSSD34
Planctomycetes	Planctomycetacia	Planctomycetaceae	sf_3	4831	Planctomyces brasiliensis
Planctomycetes	Planctomycetacia	Planctomycetaceae	sf_3	4855	aerobic basin clone CY0ARA026D10
Planctomycetes	Planctomycetacia	Planctomycetaceae	sf_3	4948	anoxic basin clone CY0ARA027D01
Planctomycetes	Planctomycetacia	Unclassified	sf_1	4895	deep marine sediment clone MB-C2-147
Planctomycetes	Planctomycetacia	Unclassified	sf_1	4897	deep marine sediment clone MB-C2-105
Planctomycetes	Planctomycetacia	Unclassified	sf_1	4930	DCP-dechlorinating consortium clone SHA-43
Proteobacteria	Alphaproteobacteria	Acetobacteraceae	sf_1	6637	Acetobacter aceti str. NCIB8621 DSM3508
Proteobacteria	Alphaproteobacteria	Acetobacteraceae	sf_1	7529	Gluconacetobacter europaeus str. ZIM B028 V3
Proteobacteria	Alphaproteobacteria	Acetobacteraceae	sf_1	7600	Acetobacter pomorum str. LTH2458
Proteobacteria	Gammaproteobacteria	Acidithiobacillaceae	sf_1	9224	Acidithiobacillus albertensis str. DSM 14366
Proteobacteria	Gammaproteobacteria	Aeromonadaceae	sf_1	8340	Aeromonas ichthiosmia
Proteobacteria	Gammaproteobacteria	Aeromonadaceae	sf_1	8364	Aeromonas allosaccharophila str. CECT 4199
Proteobacteria	Gammaproteobacteria	Aeromonadaceae	sf_1	8621	Aeromonas sp. PAR2A
Proteobacteria	Gammaproteobacteria	Aeromonadaceae	sf_1	9026	Haemophilus piscium str. NCIMB 1952
Proteobacteria	Gammaproteobacteria	Aeromonadaceae	sf_1	9245	cyanobacterial bloom and lake water clone -8
Proteobacteria	Gammaproteobacteria	Aeromonadaceae	sf_1	9294	sea isolate chemoorganotrophic O2-respiring
Proteobacteria	Gammaproteobacteria	Aeromonadaceae	sf_1	9440	Aeromonas sobria str. NCIMB 12065
Proteobacteria	Betaproteobacteria	Alcaligenaceae	sf_1	7737	atrazine-catabolizing methanol clone
Proteobacteria	Betaproteobacteria	Alcaligenaceae	sf_1	7768	swine intestine clone p-861-a5
Proteobacteria	Betaproteobacteria	Alcaligenaceae	sf_1	7788	atrazine-catabolizing methanol clone
Proteobacteria	Betaproteobacteria	Alcaligenaceae	sf_1	7838	Alcaligenes defragrans str. PD-19
Proteobacteria	Betaproteobacteria	Alcaligenaceae	sf_1	7902	Alcaligenes faecalis str. M3A
Proteobacteria	Betaproteobacteria	Alcaligenaceae	sf_1	7932	Achromobacter subsp. denitrificans
Proteobacteria	Betaproteobacteria	Alcaligenaceae	sf_1	7984	Waste-gas biofilter clone Bifciii38

Proteobacteria	Betaproteobacteria	Alcaligenaceae	sf_1	7992	Alcaligenes faecalis 5659-H
Proteobacteria	Betaproteobacteria	Alcaligenaceae	sf_1	8062	Brackiella oedipodis str. LMG 1945 R8846
Proteobacteria	Betaproteobacteria	Alcaligenaceae	sf_1	8094	Alcaligenes sp. str. VKM B-2263 dcm6
Proteobacteria	Gammaproteobacteria	Alcanivoraceae	sf_1	8335	Alcanivorax sp. str. K3-3 (MBIC 4323)
Proteobacteria	Gammaproteobacteria	Alcanivoraceae	sf_1	9658	Alcanivorax sp. str. Haw1
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8167	Alexandrium tamarense PCC 173a
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8172	Pseudoalteromonas sp. str. Bdeep-1
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8174	marine surface clone proteobacterium
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8196	
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8222	
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8318	Aestuariibacter salexigens str. JC2042
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8336	Alteromonas sp. str. MS23
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8368	Pseudoalteromonas mariniglutinosa
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8374	Agarivorans albus str. MKT 89
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8484	Alteromonadaceae isolate str. LA50
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8503	Arctic sea ice ARK10244
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8533	
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8578	Marinobacter lipolyticus str. SM-19
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8579	Psychromonas profunda str. 2825
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8580	Arctic seawater isolate str. R7076
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8594	Marinobacter sp. str. SBS
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8643	Pseudoalteromonas porphyrae str. S2-65
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8695	Arctic pack ice; northern Fram Strait
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8753	Idiomarina loihiensis str. GSP37
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8863	Alteromonas marina str. SW-47
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8916	Shewanella algae str. 43940
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8932	Pseudoalteromonas antarctica str. N-1
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8970	Arctic seawater isolate str. R9879
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8975	Alteromonas sp. str. NIBH P1M3
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8978	Arctic sea ice ARK10108
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9058	Pseudoalteromonas carrageenovora

Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9067	Shewanella algae str. ACM 4733
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9111	Pseudoalteromonas sp. str. E36
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9143	Pseudoalteromonas agarivorans str. KMM 255
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9148	Pseudoalteromonas ulvae str. UL13
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9149	Pseudoalteromonas piscicida str. Cura-d
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9205	marine clone Arctic96B-17
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9218	Pseudoalteromonas haloplanktis ATCC 14393
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9222	Shewanella hanedai str. CIP 103207T
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9230	Antarctic pack ice Southern Ocean clone
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9236	marine surface clone 18 proteobacterium
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9239	Arctic sea ice ARK10228
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9288	Alteromonas stellipolaris str. LMG 21861
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9292	
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9324	Pseudoalteromonas ruthenica str. KMM300
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9364	Pseudoalteromonas prydzensis str. MB8-11
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9369	Pseudoalteromonas luteoviolacea
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9384	Moritella viscosa str. NVI 88/478T
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9386	Alteromonas sp. str. NIBH P2M11
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9411	Shewanella waksmanii str. KMM 3823
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9416	marine isolate str. R8
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9486	Marine isolate str. GK-2001
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9501	sea water isolate str. BP-PH
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9562	Alteromonadaceae clone PH-B55N
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9640	exposed to diatom detritus isolate str. Tw-10
Proteobacteria	Alphaproteobacteria	Anaplasmataceae	sf_3	6628	Wolbachia pipientis
Proteobacteria	Alphaproteobacteria	Anaplasmataceae	sf_3	6648	Wolbachia sp
Proteobacteria	Alphaproteobacteria	Anaplasmataceae	sf_3	6803	Wolbachia sp. Dlem16SWol
Proteobacteria	Alphaproteobacteria	Anaplasmataceae	sf_3	6908	Rhinocyllus conicus endosymbiont
Proteobacteria	Alphaproteobacteria	Anaplasmataceae	sf_3	7481	Wolbachia pipientis
Proteobacteria	Alphaproteobacteria	Azospirillaceae	sf_1	6959	Rhodocista pekingensis str. 3-p
Proteobacteria	Alphaproteobacteria	Azospirillaceae	sf_1	7171	Azospirillum species

Proteobacteria	Alphaproteobacteria	Azospirillaceae	sf_1	7539	Rhodocista sp. AR2107
Proteobacteria	Alphaproteobacteria	Bartonellaceae	sf_1	7384	aortic heart valve with endocarditis clone v9
Proteobacteria	Alphaproteobacteria	Bartonellaceae	sf_1	7415	Bartonella quintana str. Toulouse
Proteobacteria	Alphaproteobacteria	Bartonellaceae	sf_1	7634	Bartonella henselae str. Houston-1
Proteobacteria	Alphaproteobacteria	Beijerinck/Rhodoplan/Methylocyst	sf_3	6651	Beijerinckia indica
Proteobacteria	Alphaproteobacteria	Beijerinck/Rhodoplan/Methylocyst	sf_3	7153	Methylocella tundrae str. Y1
Proteobacteria	Alphaproteobacteria	Beijerinck/Rhodoplan/Methylocyst	sf_3	7219	Methylosinus sporium
Proteobacteria	Alphaproteobacteria	Beijerinck/Rhodoplan/Methylocyst	sf_3	7275	Mammoth cave clone CCU18
Proteobacteria	Alphaproteobacteria	Beijerinck/Rhodoplan/Methylocyst	sf_3	7401	Scrippsiella trochoidea NEPCC 15
Proteobacteria	Alphaproteobacteria	Beijerinck/Rhodoplan/Methylocyst	sf_1	7591	
Proteobacteria	Alphaproteobacteria	Beijerinck/Rhodoplan/Methylocyst	sf_3	7640	Methylosinus trichosporium
Proteobacteria	Alphaproteobacteria	Bradyrhizobiaceae	sf_1	6636	Bradyrhizobium elkanii str. USDA 76
Proteobacteria	Alphaproteobacteria	Bradyrhizobiaceae	sf_1	6768	Rhodopseudomonas palustris str. GH
Proteobacteria	Alphaproteobacteria	Bradyrhizobiaceae	sf_1	6799	Rhodopseudomonas palustris str. ATCC 17001
Proteobacteria	Alphaproteobacteria	Bradyrhizobiaceae	sf_1	6867	heavy metal-contaminated soil clone a13131
Proteobacteria	Alphaproteobacteria	Bradyrhizobiaceae	sf_1	6878	Bradyrhizobium japonicum SD5
Proteobacteria	Alphaproteobacteria	Bradyrhizobiaceae	sf_1	6887	Bradyrhizobium str. YB2
Proteobacteria	Alphaproteobacteria	Bradyrhizobiaceae	sf_1	6941	Rhodopseudomonas rhenobacensis
Proteobacteria	Alphaproteobacteria	Bradyrhizobiaceae	sf_1	7029	
Proteobacteria	Alphaproteobacteria	Bradyrhizobiaceae	sf_1	7044	Afipia genosp. 2 str. G4438
Proteobacteria	Alphaproteobacteria	Bradyrhizobiaceae	sf_1	7126	ground water site radioactive proteobacterium
Proteobacteria	Alphaproteobacteria	Bradyrhizobiaceae	sf_1	7353	temperate estuarine mud clone HC65
Proteobacteria	Alphaproteobacteria	Bradyrhizobiaceae	sf_1	7390	Afipia genosp. 10 str. G8996
Proteobacteria	Alphaproteobacteria	Bradyrhizobiaceae	sf_1	7522	Bradyrhizobium sp. str. KKI14
Proteobacteria	Betaproteobacteria	Burkholderiaceae	sf_1	7720	penguin droppings sediments clone KD1-79
Proteobacteria	Betaproteobacteria	Burkholderiaceae	sf_1	7747	
Proteobacteria	Betaproteobacteria	Burkholderiaceae	sf_1	7771	Burkholderia glathei str. ATCC 29195T
Proteobacteria	Betaproteobacteria	Burkholderiaceae	sf_1	7914	Burkholderia andropogonis str. ATCC 19311T
Proteobacteria	Betaproteobacteria	Burkholderiaceae	sf_1	7957	Maconellicoccus hirsutus symbiont
Proteobacteria	Betaproteobacteria	Burkholderiaceae	sf_1	7969	Burkholderia sp.
Proteobacteria	Betaproteobacteria	Burkholderiaceae	sf_1	8011	Burkholderia graminis str. AUS35

Proteobacteria	Betaproteobacteria	Burkholderiaceae	sf_1	8068	Burkholderia caryophylli str. ATCC 25418
Proteobacteria	Betaproteobacteria	Burkholderiaceae	sf_1	8097	Burkholderia cepacia
Proteobacteria	Alphaproteobacteria	Caedibacteraceae	sf_5	6947	termite gut clone Rs-B60 proteobacterium
Proteobacteria	Alphaproteobacteria	Caedibacteraceae	sf_3	7010	periodontal pocket clone 10B6
Proteobacteria	Alphaproteobacteria	Caedibacteraceae	sf_4	7157	acid mine drainage clone ASL45
Proteobacteria	Epsilonproteobacteria	Campylobacteraceae	sf_3	10397	groundwater clone 1006
Proteobacteria	Epsilonproteobacteria	Campylobacteraceae	sf_3	10434	Campylobacter gracilis
Proteobacteria	Epsilonproteobacteria	Campylobacteraceae	sf_3	10446	
Proteobacteria	Epsilonproteobacteria	Campylobacteraceae	sf_3	10447	Sulfurospirillum deleyianum str. Spirillum 5175
Proteobacteria	Epsilonproteobacteria	Campylobacteraceae	sf_3	10456	Campylobacter showae
Proteobacteria	Epsilonproteobacteria	Campylobacteraceae	sf_3	10463	Campylobacter subsp. fetus
Proteobacteria	Epsilonproteobacteria	Campylobacteraceae	sf_3	10464	Campylobacter sp. str. NO2B
Proteobacteria	Epsilonproteobacteria	Campylobacteraceae	sf_3	10484	Campylobacter helveticus
Proteobacteria	Epsilonproteobacteria	Campylobacteraceae	sf_3	10523	Riftia pachyptila's tube clone R103-B70
Proteobacteria	Epsilonproteobacteria	Campylobacteraceae	sf_3	10538	Arcobacter cryaerophilus
Proteobacteria	Epsilonproteobacteria	Campylobacteraceae	sf_3	10540	Campylobacter showae str. LMG 12636
Proteobacteria	Gammaproteobacteria	Cardiobacteriaceae	sf_1	8536	Cardiobacterium hominis
Proteobacteria	Gammaproteobacteria	Cardiobacteriaceae	sf_1	9453	Cardiobacterium valvarum str. MDA3079
Proteobacteria	Alphaproteobacteria	Caulobacteraceae	sf_1	6781	Brevundimonas intermedia str. ATCC15262
Proteobacteria	Alphaproteobacteria	Caulobacteraceae	sf_1	6904	Brevundimonas vesicularis str. IAM 12105T
Proteobacteria	Alphaproteobacteria	Caulobacteraceae	sf_1	6909	Brevundimonas diminuta str. DSM 1635
Proteobacteria	Alphaproteobacteria	Caulobacteraceae	sf_1	6968	Brevundimonas diminuta str. IAM 12691T
Proteobacteria	Alphaproteobacteria	Caulobacteraceae	sf_1	7359	Brevundimonas bacterioides str. CB7
Proteobacteria	Alphaproteobacteria	Caulobacteraceae	sf_1	7366	Brevundimonas subvibrioides str. CB81
Proteobacteria	Alphaproteobacteria	Caulobacteraceae	sf_1	7436	Brevundimonas sp. str. FWC40
Proteobacteria	Gammaproteobacteria	Chromatiaceae	sf_1	8408	Thiorhodovibrio winogradskyi
Proteobacteria	Gammaproteobacteria	Chromatiaceae	sf_1	8546	Thiocapsa litoralis
Proteobacteria	Gammaproteobacteria	Chromatiaceae	sf_1	8697	Thiococcus sp. AT2204
Proteobacteria	Gammaproteobacteria	Chromatiaceae	sf_1	9048	Allochrochromatium sp. AT2202
Proteobacteria	Gammaproteobacteria	Chromatiaceae	sf_1	9052	
Proteobacteria	Gammaproteobacteria	Chromatiaceae	sf_1	9370	isolate str. HTB019

Proteobacteria	Gammaproteobacteria	Chromatiaceae	sf_1	9545	
Proteobacteria	Gammaproteobacteria	Chromatiaceae	sf_1	9571	Nitrosococcus oceanus
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7704	freshwater clone PRD01b009B
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7705	penguin droppings sediments clone KD4-7
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7718	Lampropedia hyalina str. DSM 15336
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7719	penguin droppings sediments clone KD2-46
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7735	soil clone
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7801	Toolik Lake clone proteobacterium
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7807	Aquaspirillum metamorphum str. DSM 1837
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7822	Polaromonas naphthalenivorans str. CJ2
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7827	
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7829	Xylophilus ampelinus str. ATCC 33914
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7847	penguin droppings sediments clone KD2-104
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7856	Variovorax paradoxus
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7888	Hydrogenophaga flava str. DSM 619T
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7919	strain isolate str. rM4
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7928	penguin droppings sediments clone KD5-43
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7941	groundwater-treating reactor clone RB9C10
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7943	Aquabacterium parvum str. B6
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7949	Variovorax paradoxus TG27
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7964	naphthalene-contaminated sediment clone 76
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7965	Anoxobacterium dechloraticum
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7982	marine? clone KD1-99
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7986	Arctic sea ice ARK10281
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7987	Acidovorax sp. str. OS-6
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7995	Ottowia thiooxydans str. K11
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	8003	hydrocarbon-degrading consortium clone AF1-8
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	8009	denitrifying reactor clone 81
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	8012	Acidovorax konjaci str. DSM 7481
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	8018	Acidovorax delafieldii str. ATCC 17505
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	8021	Acidovorax facilis str. CCUG 2113

Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	8022	Acidovorax avenae subsp. cattleyae
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	8031	strain isolate str. rJ10
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	8046	Acidovorax defluvii str. BSB411
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	8067	penguin droppings sediments clone KD3-141
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	8079	nephridia Eisenia foetida clone
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	8105	Hydrogenophaga taeniospiralis str. ATCC 49743
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	8112	Comamonas testosteroni str. SMCC B329
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	8138	Pseudomonas lanceolata str. ATCC 14669T
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	8139	Delftia tsuruhatensis str. AD9
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	8140	Schlegelella sp. str. KB1a
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	8152	nephridia Octolasion lacteum clone OI2-2
Proteobacteria	Gammaproteobacteria	Coxiellaceae	sf_3	7893	agricultural soil clone SC-I-71
Proteobacteria	Gammaproteobacteria	Coxiellaceae	sf_3	8457	5' clone CHAB-XI-27
Proteobacteria	Gammaproteobacteria	Coxiellaceae	sf_3	8969	uranium mining sample clone proteobacterium
Proteobacteria	Gammaproteobacteria	Coxiellaceae	sf_3	9198	uranium mining waste pile clone
Proteobacteria	Gammaproteobacteria	Coxiellaceae	sf_3	9444	forested wetland clone FW23
Proteobacteria	Deltaproteobacteria	Desulfoarculaceae	sf_2	10227	marine sediment clone Bol11
Proteobacteria	Deltaproteobacteria	Desulfobacteraceae	sf_5	9666	marine sediment clone Hyd89-13
Proteobacteria	Deltaproteobacteria	Desulfobacteraceae	sf_5	9712	Antarctic sediment clone SB4_98
Proteobacteria	Deltaproteobacteria	Desulfobacteraceae	sf_5	9777	Guaymas Basin vent clone B01R004
Proteobacteria	Deltaproteobacteria	Desulfobacteraceae	sf_5	9800	forested wetland clone FW57
Proteobacteria	Deltaproteobacteria	Desulfobacteraceae	sf_5	9818	temperate estuarine mud clone KM62
Proteobacteria	Deltaproteobacteria	Desulfobacteraceae	sf_5	9821	
Proteobacteria	Deltaproteobacteria	Desulfobacteraceae	sf_5	9875	hydrothermal sediment clone AF420354
Proteobacteria	Deltaproteobacteria	Desulfobacteraceae	sf_5	9939	marine methane seep clone 1427
Proteobacteria	Deltaproteobacteria	Desulfobacteraceae	sf_5	9940	Antarctic sediment clone SB2_56
Proteobacteria	Deltaproteobacteria	Desulfobacteraceae	sf_5	10031	Antarctic sediment clone SB1_49
Proteobacteria	Deltaproteobacteria	Desulfobacteraceae	sf_5	10046	Desulfobacterium cetonicum str. DSM 7267
Proteobacteria	Deltaproteobacteria	Desulfobacteraceae	sf_5	10083	Desulfobacter curvatus str. DSM 3379
Proteobacteria	Deltaproteobacteria	Desulfobacteraceae	sf_5	10136	Guaymas Basin vent clone B01R011
Proteobacteria	Deltaproteobacteria	Desulfobacteraceae	sf_5	10267	marine sediment clone Hyd89-61

Proteobacteria	Deltaproteobacteria	Desulfobacteraceae	sf_5	10268	
Proteobacteria	Deltaproteobacteria	Desulfobacteraceae	sf_5	10319	sulfate-reducing habitat clone SLM-CP-116
Proteobacteria	Deltaproteobacteria	Desulfobacteraceae	sf_5	10364	marine surface sediment clone SB2
Proteobacteria	Deltaproteobacteria	Desulfobulbaceae	sf_1	9734	Riftia pachyptila's tube clone R103-B13
Proteobacteria	Deltaproteobacteria	Desulfobulbaceae	sf_1	9739	gas hydrate clone Hyd89-51
Proteobacteria	Deltaproteobacteria	Desulfobulbaceae	sf_1	10047	epibiotic clone C11-D3
Proteobacteria	Deltaproteobacteria	Desulfobulbaceae	sf_1	10062	marine sediment clone Hyd24-11
Proteobacteria	Deltaproteobacteria	Desulfobulbaceae	sf_1	10107	marine sediment clone Hyd24-30
Proteobacteria	Deltaproteobacteria	Desulfobulbaceae	sf_1	10187	Mono Lake clone ML623J-57 proteobacterium
Proteobacteria	Deltaproteobacteria	Desulfohalobiaceae	sf_1	9894	Desulfonauticus submarinus str. 6N
Proteobacteria	Deltaproteobacteria	Desulfohalobiaceae	sf_1	10069	
Proteobacteria	Deltaproteobacteria	Desulfomicrobiaceae	sf_1	10079	Desulfomicrobium baculatum str. DSM 1742
Proteobacteria	Deltaproteobacteria	Desulfomicrobiaceae	sf_1	10370	Desulfomicrobium baculatum str. X
Proteobacteria	Deltaproteobacteria	Desulfovibrionaceae	sf_1	9709	termite gut clone Rs-N31 proteobacterium
Proteobacteria	Deltaproteobacteria	Desulfovibrionaceae	sf_1	9826	termite gut clone Rs-M72 proteobacterium
Proteobacteria	Deltaproteobacteria	Desulfovibrionaceae	sf_1	10016	termite gut clone Rs-N35 proteobacterium
Proteobacteria	Deltaproteobacteria	Desulfovibrionaceae	sf_1	10071	Desulfovibrio desulfuricans
Proteobacteria	Deltaproteobacteria	Desulfovibrionaceae	sf_1	10212	
Proteobacteria	Deltaproteobacteria	Desulfovibrionaceae	sf_1	10244	
Proteobacteria	Deltaproteobacteria	Desulfovibrionaceae	sf_1	10248	Desulfovibrio giganteus str. DSM 4370
Proteobacteria	Deltaproteobacteria	Desulfovibrionaceae	sf_1	10262	Desulfovibrio sp. str. Ac5.2
Proteobacteria	Deltaproteobacteria	Desulfuromonaceae	sf_1	10020	uranium mill soil sample proteobacterium
Proteobacteria	Gammaproteobacteria	Ectothiorhodospiraceae	sf_1	9450	Halorhodospira neutrophila str. SG 3304
Proteobacteria	Gammaproteobacteria	Ectothiorhodospiraceae	sf_1	9598	Mono Lake clone ML602J-47 proteobacterium
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_6	433	coal effluent wetland clone RCP2-6
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_6	646	Opitutus sp. str. SA-9
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	1206	Dermacentor variabilis symbiont
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8173	Photorhabdus asymbiotica str. ATCC 43949
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8182	Proteus vulgaris str. IFAM 1731
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8225	
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8236	Vryburgia amaryllidis symbiont

Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8251	Nitrogen-fixing isolate str. CANF3
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8282	Antonina pretiosa symbiont
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8283	Heterosylla texana symbiont
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8286	Cyphonococcus alpinus symbiont
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8362	Klebsiella pneumoniae str. ASR1
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8379	Erwinia amylovora EA G-5
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8467	Serratia marcescens subsp. sakuensis
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8473	Hafnia alvei
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8504	Dysmicoccus neobrevipes symbiont
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8505	Buttiauxella warmboldiae str. DSM 9404
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8510	Klebsiella pneumoniae str. DSM 30104
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8528	Enterobacter cloacae Nr. 3
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8529	Raoultella planticola 7
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8530	Enterobacteriaceae CF01Ent-1
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8554	Kluyvera ascorbata 69
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8564	Rahnella aquatilis str. ATCC 33989
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8603	Melanococcus albizziae symbiont
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8607	Amonostherium lichtensioides symbiont
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8627	Australicoccus grevilleae symbiont
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8631	
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8640	
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8642	Erwinia chrysanthemi str. 580
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8693	Pantoea agglomerans str. A40
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8700	Baumannia cicadellinicola
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8712	Serratia proteamaculans str. DSM 4543
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8739	Serratia entomophila str. DSM 12358
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8742	USA:New York isolate str. KN4
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8758	Pectobacterium cypripedii str. ATCC 29267
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8770	
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_6	8783	Alterococcus agarolyticus str. ADT3
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8801	Candidatus camponotii

Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8885	Morganella morganii str. AP28
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8886	Salmonella typhimurium LT2 str. SGSC1412
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8890	Raoultella planticola str. DR3
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8892	Aranicola proteolyticus
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8934	Pectobacterium subsp. carotovorum str. E155
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8936	Klebsiella oxytoca str. ChDC OS31
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	8974	Salmonella subsp. enterica serovar Agona str
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	9060	Enterobacter ludwigii str. EN-119
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	9135	intestine Zophobas mori clone
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	9142	Erwinia amylovora str. DSM 30165
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	9151	
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	9157	symbiont Acyrthosiphon pisum clone
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	9274	Enterobacter sp. CC1
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	9290	Baumannia cicadellinicola
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	9293	USA clone 14/7
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	9302	Pantoea subsp. stewartii str. GSPB 2626
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	9309	Buchnera sp
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	9337	Rahnella genosp. 3 str. DSM 30078
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	9345	Erwinia amylovora str. BC199(=Ea528)
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	9358	Salmonella subsp. enterica serovar Waycross
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	9361	Enterobacter intermedius str. JCM1238
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	9363	Citrobacter freundii str. CDC 621-64
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	9385	Australiococcus greville symbiont
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	9390	Enterobacter nimipressuralis str. LMG 10245-T
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	9417	Serratia fonticola str. DSM 4576
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	9420	
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	9496	
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	9594	Morganella morganii str. ATCC35200
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	9651	Pectobacterium subsp. atrosepticum str
Proteobacteria	Gammaproteobacteria	Francisellaceae	sf_1	8949	Caedibacter taeniospiralis
Proteobacteria	Gammaproteobacteria	Francisellaceae	sf_1	9554	Tilapia parasite TPT-541

Proteobacteria	Deltaproteobacteria	Geobacteraceae	sf_1	482	trichloroethene-contaminated proteobacterium
Proteobacteria	Deltaproteobacteria	Geobacteraceae	sf_1	9956	forested wetland clone FW140
Proteobacteria	Deltaproteobacteria	Geobacteraceae	sf_1	10171	
Proteobacteria	Gammaproteobacteria	Halomonadaceae	sf_1	8514	Chromohalobacter israelensis str. ATCC 43985
Proteobacteria	Gammaproteobacteria	Halomonadaceae	sf_1	8598	Halomonas desiderata str. FB2
Proteobacteria	Gammaproteobacteria	Halothiobacillaceae	sf_1	9181	Halothiobacillus neapolitanus str. DSM 581
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10385	
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10411	termite gut homogenate clone proteobacterium
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10417	temperate estuarine mud clone KM61
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10425	Sulfurimonas autotrophica str. OK5
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10428	Flexispira rappini FH 9702248
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10430	Helicobacter heilmannii str. MM2
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10432	Riftia pachyptila's tube clone R76-B51
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10436	Helicobacter aurati str. MIT 97-5075c
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10438	hydrocarbon seep clone GCA014
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10442	Helicobacter cetorum str. MIT 99-5656
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_23	10443	Helicobacter pylori str. 85D08
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10444	Helicobacter suncus str. Kaz-2
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10448	Helicobacter felis str. Dog-1
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10451	Helicobacter heilmannii str. C4S
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10454	Helicobacter pullorum str. NCTC 12826
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10462	Helicobacter rodentium str. MIT 96-1312
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10467	
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10482	hydrothermal vent polychaete mucous clone
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10507	gut homogenate clone Rs-M59 proteobacterium
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10518	Helicobacter pylori str. ATCC 49396T
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10520	Helicobacter sp. blood isolate 964
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10534	Helicobacter pylori
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10548	Helicobacter rappini W.Tee-Bat
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10552	Helicobacter winhamensis str. NLEP 97-1611
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10562	Helicobacter rappini W.Tee-Yu

Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10572	Helicobacter sp
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10576	Helicobacter sp. 'liver 3' str. liver 3
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10578	deep-sea hydrothermal vent sulfide clone
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10590	gut homogenate clone Rs-H40 proteobacterium
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10602	
Proteobacteria	Epsilonproteobacteria	Helicobacteraceae	sf_3	10614	strain isolate str. BHI80-49
Proteobacteria	Betaproteobacteria	Hydrogenophilaceae	sf_2	8756	Halothiobacillus sp.
Proteobacteria	Alphaproteobacteria	Hyphomicrobiaceae	sf_1	7392	
Proteobacteria	Alphaproteobacteria	Hyphomicrobiaceae	sf_1	7646	Hyphomicrobium aestuarii str. DSM 1564
Proteobacteria	Gammaproteobacteria	Legionellaceae	sf_1	8865	Arctic pack ice clone ARKCH2Br2-23
Proteobacteria	Gammaproteobacteria	Legionellaceae	sf_1	9617	Legionella feeleeii subsp. sgp 2 str. ATCC 35849
Proteobacteria	Alphaproteobacteria	Magnetospirillaceae	sf_1	6922	Dechlorospirillum sp. str. SN1
Proteobacteria	Alphaproteobacteria	Methylobacteriaceae	sf_1	7004	Methylobacterium fujisawaense
Proteobacteria	Alphaproteobacteria	Methylobacteriaceae	sf_1	7585	Methylobacterium thiocyanatum
Proteobacteria	Gammaproteobacteria	Methylococcaceae	sf_1	8243	isolate str. IR
Proteobacteria	Gammaproteobacteria	Methylococcaceae	sf_1	8645	Methylomicrobium buryatense str. 5B
Proteobacteria	Gammaproteobacteria	Methylococcaceae	sf_1	8821	Methylobacter psychrophilus str. Z-0021
Proteobacteria	Gammaproteobacteria	Methylococcaceae	sf_1	9438	marine sediment clone Hyd24-01
Proteobacteria	Betaproteobacteria	Methylophilaceae	sf_1	7892	Methylophilus leisingeri str. DSM 6813
Proteobacteria	Betaproteobacteria	Methylophilaceae	sf_1	8137	freshwater clone PRD01a011B
Proteobacteria	Gammaproteobacteria	Moraxellaceae	sf_3	8366	Psychrobacter frigidicola str. DSM 12411
Proteobacteria	Gammaproteobacteria	Moraxellaceae	sf_3	8574	
Proteobacteria	Gammaproteobacteria	Moraxellaceae	sf_3	8604	Moraxella oblonga str. IAM 14971
Proteobacteria	Gammaproteobacteria	Moraxellaceae	sf_3	8727	Alkanindiges hongkongensis str. HKU9
Proteobacteria	Gammaproteobacteria	Moraxellaceae	sf_3	8838	Psychrobacter psychrophilus CMS 28
Proteobacteria	Gammaproteobacteria	Moraxellaceae	sf_3	9359	Acinetobacter junii str. S33
Proteobacteria	Gammaproteobacteria	Moraxellaceae	sf_3	9428	hydrocarbon-degrading consortium clone
Proteobacteria	Gammaproteobacteria	Moraxellaceae	sf_3	9466	Acinetobacter tandoii str. 4N13
Proteobacteria	Gammaproteobacteria	Moraxellaceae	sf_3	9641	Acinetobacter haemolyticus
Proteobacteria	Deltaproteobacteria	Myxococcaceae	sf_1	10358	Myxococcus fulvus str. Mx f2
Proteobacteria	Epsilonproteobacteria	Nautiliaceae	sf_1	10416	hydrothermal vent clone VC2.1 Bac12

Proteobacteria	Betaproteobacteria	Neisseriaceae	sf_1	7662	Mars Odyssey Orbiter facility clone
Proteobacteria	Betaproteobacteria	Neisseriaceae	sf_1	7675	Neisseria sp. str. CCUG 46910
Proteobacteria	Betaproteobacteria	Neisseriaceae	sf_1	7701	Vitreoscilla stercoraria
Proteobacteria	Betaproteobacteria	Neisseriaceae	sf_1	7703	
Proteobacteria	Betaproteobacteria	Neisseriaceae	sf_1	7867	Neisseria canis
Proteobacteria	Betaproteobacteria	Neisseriaceae	sf_1	7885	Kingella kingae str. ATCC 23330
Proteobacteria	Betaproteobacteria	Neisseriaceae	sf_1	7945	Aquaspirillum serpens str. IAM 13944
Proteobacteria	Betaproteobacteria	Neisseriaceae	sf_1	8041	Aquaspirillum putridiconchylum
Proteobacteria	Betaproteobacteria	Neisseriaceae	sf_1	8092	Neisseria dentiae str. V33
Proteobacteria	Betaproteobacteria	Neisseriaceae	sf_1	8143	subgingival dental plaque clone AK105
Proteobacteria	Betaproteobacteria	Nitrosomonadaceae	sf_1	7682	Nitrosovibrio sp. str. RY6A
Proteobacteria	Betaproteobacteria	Nitrosomonadaceae	sf_1	7770	Nitrosomonas europaea str. ATCC 19718
Proteobacteria	Betaproteobacteria	Nitrosomonadaceae	sf_1	7789	
Proteobacteria	Betaproteobacteria	Nitrosomonadaceae	sf_1	7796	Nitrosospira sp. str. TYM9
Proteobacteria	Betaproteobacteria	Nitrosomonadaceae	sf_1	7805	Nitrosospira briensis str. Nsp10
Proteobacteria	Betaproteobacteria	Nitrosomonadaceae	sf_1	7858	
Proteobacteria	Betaproteobacteria	Nitrosomonadaceae	sf_1	7865	
Proteobacteria	Betaproteobacteria	Nitrosomonadaceae	sf_1	7931	Nitrosospira multiformis
Proteobacteria	Betaproteobacteria	Nitrosomonadaceae	sf_1	7976	Nitrosomonas sp. str. Nm86
Proteobacteria	Betaproteobacteria	Nitrosomonadaceae	sf_1	7989	Nitrosomonas sp. str. Nm59
Proteobacteria	Betaproteobacteria	Nitrosomonadaceae	sf_1	8145	Nitrosomonas eutropha str. Nm57
Proteobacteria	Deltaproteobacteria	Nitrospinaceae	sf_1	580	
Proteobacteria	Deltaproteobacteria	Nitrospinaceae	sf_2	594	uranium mining mill tailing clone
Proteobacteria	Gammaproteobacteria	Oceanospirillaceae	sf_1	9351	bacterioplankton clone ZA2333c
Proteobacteria	Betaproteobacteria	Oxalobacteraceae	sf_1	7743	Herbaspirillum sp. str. NAH4
Proteobacteria	Betaproteobacteria	Oxalobacteraceae	sf_1	7843	Massilia timonae timone
Proteobacteria	Betaproteobacteria	Oxalobacteraceae	sf_1	7845	Diaphorina citri symbiont
Proteobacteria	Betaproteobacteria	Oxalobacteraceae	sf_1	7866	Paucimonas lemoignei str. ATCC 17989T
Proteobacteria	Betaproteobacteria	Oxalobacteraceae	sf_1	7878	naphthalene-contaminated sediment clone 29
Proteobacteria	Betaproteobacteria	Oxalobacteraceae	sf_1	7921	Collimonas fungivorans str. Ter331
Proteobacteria	Betaproteobacteria	Oxalobacteraceae	sf_1	7968	Oxalobacter formigenes str. OXB ovinen rumen

Proteobacteria	Betaproteobacteria	Oxalobacteraceae	sf_1	8013	isolate str. A1020
Proteobacteria	Betaproteobacteria	Oxalobacteraceae	sf_1	8032	Aquaspirillum arcticum str. IAM 14963
Proteobacteria	Betaproteobacteria	Oxalobacteraceae	sf_1	8034	Janthinobacterium agaricidamnorum
Proteobacteria	Betaproteobacteria	Oxalobacteraceae	sf_1	8058	Herbaspirillum seropedicae str. ATCC 35892
Proteobacteria	Betaproteobacteria	Oxalobacteraceae	sf_1	8158	2-HNA producing isolate MC13289
Proteobacteria	Gammaproteobacteria	Pasteurellaceae	sf_1	8195	Haemophilus influenzae str. R2866
Proteobacteria	Gammaproteobacteria	Pasteurellaceae	sf_1	8228	Actinobacillus indolicus str. H1419
Proteobacteria	Gammaproteobacteria	Pasteurellaceae	sf_1	8308	Haemophilus actinomycetemcomitans
Proteobacteria	Gammaproteobacteria	Pasteurellaceae	sf_1	8409	human colonic mucosal biopsy clone ABL Cf1
Proteobacteria	Gammaproteobacteria	Pasteurellaceae	sf_1	8432	
Proteobacteria	Gammaproteobacteria	Pasteurellaceae	sf_1	8555	Haemophilus influenzae str. M9741
Proteobacteria	Gammaproteobacteria	Pasteurellaceae	sf_1	8614	Acidithiobacillus thiooxidans str. KCTC 8928P
Proteobacteria	Gammaproteobacteria	Pasteurellaceae	sf_1	8830	Actinobacillus sp. str. CCUG 24862
Proteobacteria	Gammaproteobacteria	Pasteurellaceae	sf_1	8848	str. 86355
Proteobacteria	Gammaproteobacteria	Pasteurellaceae	sf_1	8861	Haemophilus parasuis 427
Proteobacteria	Gammaproteobacteria	Pasteurellaceae	sf_1	8876	Mannheimia sp. R19.2 str. R19.2
Proteobacteria	Gammaproteobacteria	Pasteurellaceae	sf_1	8952	Actinobacillus lignieresii
Proteobacteria	Gammaproteobacteria	Pasteurellaceae	sf_1	9030	Volucrobacter amazonae str. B96/5
Proteobacteria	Gammaproteobacteria	Pasteurellaceae	sf_1	9213	Haemophilus quentini str. MCCM 02026
Proteobacteria	Gammaproteobacteria	Pasteurellaceae	sf_1	9237	
Proteobacteria	Gammaproteobacteria	Pasteurellaceae	sf_1	9263	Actinobacillus capsulatus
Proteobacteria	Gammaproteobacteria	Pasteurellaceae	sf_1	9349	Pasteurella sp. str. 91985
Proteobacteria	Gammaproteobacteria	Pasteurellaceae	sf_1	9360	Pasteurella multocida subsp. gallicida
Proteobacteria	Gammaproteobacteria	Pasteurellaceae	sf_1	9477	Haemophilus influenzae str. M11105
Proteobacteria	Gammaproteobacteria	Pasteurellaceae	sf_1	9533	Haemophilus segnis str. MCCM 00337
Proteobacteria	Gammaproteobacteria	Pasteurellaceae	sf_1	9587	Actinobacillus porcini str. H1498
Proteobacteria	Gammaproteobacteria	Pasteurellaceae	sf_1	9628	Histophilus somni str. CCUG 12839
Proteobacteria	Alphaproteobacteria	Phyllobacteriaceae	sf_1	6857	Mesorhizobium mediterraneum str. PECA20
Proteobacteria	Alphaproteobacteria	Phyllobacteriaceae	sf_1	7009	
Proteobacteria	Alphaproteobacteria	Phyllobacteriaceae	sf_1	7216	Ahrensia kielensis str. IAM12618
Proteobacteria	Alphaproteobacteria	Phyllobacteriaceae	sf_1	7300	marine isolate JP57

Proteobacteria	Alphaproteobacteria	Phyllobacteriaceae	sf_1	7381	Aminobacter aminovorans str. DSM7048T
Proteobacteria	Alphaproteobacteria	Phyllobacteriaceae	sf_1	7497	Pseudaminobacter salicylatoxidans str. KTC001
Proteobacteria	Gammaproteobacteria	Piscirickettsiaceae	sf_3	8664	Thiomicrospira sp. str. Milos-T2
Proteobacteria	Gammaproteobacteria	Piscirickettsiaceae	sf_3	9291	Methylophaga alcalica str. M39
Proteobacteria	Gammaproteobacteria	Piscirickettsiaceae	sf_3	9392	Methylophaga sp. str. V4.ME.29
Proteobacteria	Gammaproteobacteria	Piscirickettsiaceae	sf_3	9557	Riftia pachyptila's tube clone R76-B23
Proteobacteria	Deltaproteobacteria	Polyangiaceae	sf_3	9671	hydrothermal sediment clone AF420357
Proteobacteria	Deltaproteobacteria	Polyangiaceae	sf_4	9733	bacterioplankton clone ZA3735c
Proteobacteria	Deltaproteobacteria	Polyangiaceae	sf_3	9735	uranium mining clone JG37-AG-15
Proteobacteria	Deltaproteobacteria	Polyangiaceae	sf_3	9755	bacterioplankton clone ZA3704c
Proteobacteria	Deltaproteobacteria	Polyangiaceae	sf_3	9874	uranium mining waste pile proteobacterium
Proteobacteria	Deltaproteobacteria	Polyangiaceae	sf_3	9900	bioreactor clone mle1-27
Proteobacteria	Deltaproteobacteria	Polyangiaceae	sf_3	9912	uranium mining waste pile proteobacterium
Proteobacteria	Deltaproteobacteria	Polyangiaceae	sf_3	10082	uranium mining waste pile proteobacterium
Proteobacteria	Deltaproteobacteria	Polyangiaceae	sf_3	10249	soil sample uranium mining proteobacterium
Proteobacteria	Deltaproteobacteria	Polyangiaceae	sf_3	10298	marine tidal mat clone BTM36
Proteobacteria	Deltaproteobacteria	Polyangiaceae	sf_3	10309	Nannocystis exedens str. Na e571
Proteobacteria	Deltaproteobacteria	Polyangiaceae	sf_3	10353	sludge clone A9
Proteobacteria	Betaproteobacteria	Procabacteriaceae	sf_1	7709	Acanthamoeba sp. TUMSJ-226 symbiont
Proteobacteria	Betaproteobacteria	Procabacteriaceae	sf_1	8136	Acanthamoeba sp. UWC6 symbiont
Proteobacteria	Gammaproteobacteria	Pseudoalteromonadaceae	sf_1	9339	Pseudoalteromonas sp. str. 05
Proteobacteria	Gammaproteobacteria	Pseudoalteromonadaceae	sf_1	9627	Pseudoalteromonas sp
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	8209	uranium mining waste pile proteobacterium
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	8338	Pseudomonas synxantha str. DSM 13080 G
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	8344	Anabaena circinalis AWQC118C isolate
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	8433	Pseudomonas syringae
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	8474	ground water deep-well site proteobacterium
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	8508	Pseudomonas citronellolis str. TERIDB26
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	8513	Pseudomonas monteilii str. CIP 104883
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	8553	Pseudomonas fulva str. IAM 1587
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	8561	Pseudomonas sp. B65

Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	8601	<i>Pseudomonas marginalis</i> str. ATCC 10844T
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	8687	<i>Pseudomonas putida</i> str. ATCC 17472
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	8691	<i>Pseudomonas aeruginosa</i> str. PAO1
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	8708	
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	8725	<i>Pseudomonas</i> sp. str. 2N1-1
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	8755	<i>Pseudomonas</i> sp. SK-1-3-1
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	8777	<i>Pseudomonas</i> sp. str. KNA6-5
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	8813	<i>Lyrodus pedicellatus</i> symbiont
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	8852	<i>Pseudomonas stutzeri</i> str. KC
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	8853	<i>Pseudomonas cichorii</i> str. ATCC 10857T
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	9005	<i>Pseudomonas</i> sp. str. KY
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	9028	<i>Pseudomonas koreensis</i> str. Ps 9-14
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	9056	<i>Pseudomonas aeruginosa</i> str. #47
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	9068	<i>Pseudomonas stutzeri</i> str. A1501
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	9172	<i>Pseudomonas psychrophila</i> str. E-3
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	9175	<i>Pseudomonas extremorientalis</i> str. KMM3447
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	9219	<i>Pseudomonas</i> cf. <i>monteilii</i> 9
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	9221	<i>Pseudomonas fulgida</i> str. DSM 14938
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	9228	<i>Pseudomonas stutzeri</i> HY-105
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	9238	
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	9240	<i>Pseudomonas fluorescens</i> str. CHA0
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	9267	<i>Pseudomonas syringae</i> pv. <i>theae</i> str. PT1
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	9295	
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	9310	<i>Pseudomonas</i> sp. str. AC-167
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	9343	<i>Cellvibrio</i> subsp. <i>mixtus</i> str. ACM 2601
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	9366	Arctic seawater isolate str. R7366
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	9469	cf. <i>Pseudomonas</i> sp. clone Llangefni 52
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	9493	<i>Pseudomonas</i> sp. str. dcm7B
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	9613	<i>Pseudomonas flavescens</i> str. B62
Proteobacteria	Betaproteobacteria	Ralstoniaceae	sf_1	7761	<i>Ralstonia detusculanense</i> str. APF11
Proteobacteria	Betaproteobacteria	Ralstoniaceae	sf_1	7778	<i>Ralstonia insidiosa</i> str. CCUG 46388

Proteobacteria	Betaproteobacteria	Ralstoniaceae	sf_1	7823	Wautersia basilensis str. DSM 11853
Proteobacteria	Betaproteobacteria	Ralstoniaceae	sf_1	8110	Wautersia paucula str. LMG 3413
Proteobacteria	Betaproteobacteria	Ralstoniaceae	sf_1	8128	Cupriavidus necator
Proteobacteria	Alphaproteobacteria	Rhizobiaceae	sf_1	6683	Sinorhizobium fredii str. ATCC35423
Proteobacteria	Alphaproteobacteria	Rhizobiaceae	sf_1	6770	Rhizobium tropici str. LMG 9517
Proteobacteria	Alphaproteobacteria	Rhizobiaceae	sf_1	6964	Agrobacterium tumefaciens str. C58 Cereon
Proteobacteria	Alphaproteobacteria	Rhizobiaceae	sf_1	6972	Ensifer adhaerens str. LMG 20582
Proteobacteria	Alphaproteobacteria	Rhizobiaceae	sf_1	6974	Himalayas Kaza Spiti Valley Cold Desert isolate
Proteobacteria	Alphaproteobacteria	Rhizobiaceae	sf_1	7051	Mycoplana dimorpha str. IAM 13154
Proteobacteria	Alphaproteobacteria	Rhizobiaceae	sf_1	7457	
Proteobacteria	Alphaproteobacteria	Rhizobiaceae	sf_1	7568	Rhizobium etli str. USDA 2667 ATCC 14483
Proteobacteria	Alphaproteobacteria	Rhodobacteraceae	sf_1	312	Pseudorhodobacter ferrugineus str. IAM12616
Proteobacteria	Alphaproteobacteria	Rhodobacteraceae	sf_1	6652	marine clone Arctic96A-1
Proteobacteria	Alphaproteobacteria	Rhodobacteraceae	sf_1	6701	Roseobacter clone NAC11-3
Proteobacteria	Alphaproteobacteria	Rhodobacteraceae	sf_1	6980	Loktanella vestfoldensis str. LMG 22003
Proteobacteria	Alphaproteobacteria	Rhodobacteraceae	sf_1	6991	Rhodobacter sphaeroides str. 2.4.1
Proteobacteria	Alphaproteobacteria	Rhodobacteraceae	sf_1	7026	Leisingera methylohalidivorans str. MB2
Proteobacteria	Alphaproteobacteria	Rhodobacteraceae	sf_1	7040	Paracoccus alcaliphilus str. JCM 7364
Proteobacteria	Alphaproteobacteria	Rhodobacteraceae	sf_1	7084	Scrippsiella trochoidea NEPCC 15
Proteobacteria	Alphaproteobacteria	Rhodobacteraceae	sf_1	7130	Gram-negative MM 1
Proteobacteria	Alphaproteobacteria	Rhodobacteraceae	sf_1	7263	
Proteobacteria	Alphaproteobacteria	Rhodobacteraceae	sf_1	7433	Scrippsiella trochoidea NEPCC 15
Proteobacteria	Alphaproteobacteria	Rhodobacteraceae	sf_1	7453	Sulfitobacter sp. BIO-11
Proteobacteria	Betaproteobacteria	Rhodocyclaceae	sf_1	7762	Elbe River snow isolate Iso18 Iso18_1411
Proteobacteria	Betaproteobacteria	Rhodocyclaceae	sf_1	7800	upstream landfill clone BVC77
Proteobacteria	Betaproteobacteria	Rhodocyclaceae	sf_1	7817	TCE-contaminated site clone ccs265
Proteobacteria	Betaproteobacteria	Rhodocyclaceae	sf_1	7824	gut homogenate clone Rs-B77 proteobacterium
Proteobacteria	Betaproteobacteria	Rhodocyclaceae	sf_1	7907	Thauera aromatica str. LG356
Proteobacteria	Betaproteobacteria	Rhodocyclaceae	sf_1	7925	Thauera selenatis str. ATCC 55363T
Proteobacteria	Betaproteobacteria	Rhodocyclaceae	sf_1	7951	EBPR sludge lab scale clone HP1A03
Proteobacteria	Betaproteobacteria	Rhodocyclaceae	sf_1	7956	

Proteobacteria	Betaproteobacteria	Rhodocyclaceae	sf_1	8001	
Proteobacteria	Betaproteobacteria	Rhodocyclaceae	sf_1	8052	Dechloromonas aromatica str. RCB
Proteobacteria	Betaproteobacteria	Rhodocyclaceae	sf_1	8127	Zoogloea resiniphila str. PIV-3A2y
Proteobacteria	Betaproteobacteria	Rhodocyclaceae	sf_1	8131	
Proteobacteria	Betaproteobacteria	Rhodocyclaceae	sf_1	8156	phenol-degrading community clone MM1
Proteobacteria	Alphaproteobacteria	Rickettsiaceae	sf_1	6809	Rickettsia rickettsii str. Sawtooth
Proteobacteria	Alphaproteobacteria	Rickettsiaceae	sf_1	7556	Rickettsia bellii str. strains 369-C and G2D42
Proteobacteria	Alphaproteobacteria	Roseococcaceae	sf_1	7500	Great Artesian Basin clone B35
Proteobacteria	Gammaproteobacteria	Saccharospirillaceae	sf_1	8889	hypersaline Mono Lake clone ML110J-5
Proteobacteria	Alphaproteobacteria	SAR11	sf_2	7043	marine clone Arctic95D-8
Proteobacteria	Gammaproteobacteria	Shewanellaceae	sf_1	8201	Shewanella surugaensis str. c959
Proteobacteria	Gammaproteobacteria	Shewanellaceae	sf_1	8581	Shewanella benthica str. DB21MT-2
Proteobacteria	Gammaproteobacteria	Shewanellaceae	sf_1	8641	Moritella abyssi str. 2693
Proteobacteria	Gammaproteobacteria	Shewanellaceae	sf_1	8662	
Proteobacteria	Gammaproteobacteria	Shewanellaceae	sf_1	9081	Shewanella sp. str. MTW-1
Proteobacteria	Alphaproteobacteria	Sphingomonadaceae	sf_1	6650	Sphingomonas phyllosphaerae str. FA1
Proteobacteria	Alphaproteobacteria	Sphingomonadaceae	sf_1	6663	Sphingopyxis flavimaris str. SW-151
Proteobacteria	Alphaproteobacteria	Sphingomonadaceae	sf_1	6690	Porphyrobacter tepidarius str. OK5APO
Proteobacteria	Alphaproteobacteria	Sphingomonadaceae	sf_15	6700	Porphyrobacter tepidarius str. DSM 10594
Proteobacteria	Alphaproteobacteria	Sphingomonadaceae	sf_1	6749	Arctic sea ice ARK10031
Proteobacteria	Alphaproteobacteria	Sphingomonadaceae	sf_1	7016	Sphingomonas sp. str. SAFR-027
Proteobacteria	Alphaproteobacteria	Sphingomonadaceae	sf_15	7035	Sphingomonas asaccharolytica str. IFO 10564-T
Proteobacteria	Alphaproteobacteria	Sphingomonadaceae	sf_1	7036	Lutibacterium anuloederans str. LC8
Proteobacteria	Alphaproteobacteria	Sphingomonadaceae	sf_1	7075	Novosphingobium sp. str. K16
Proteobacteria	Alphaproteobacteria	Sphingomonadaceae	sf_1	7100	Novosphingobium capsulatum str. GIFU11526
Proteobacteria	Alphaproteobacteria	Sphingomonadaceae	sf_1	7215	travertine hot spring clone SM2B06
Proteobacteria	Alphaproteobacteria	Sphingomonadaceae	sf_1	7285	Sphingopyxis chilensis str. S37
Proteobacteria	Alphaproteobacteria	Sphingomonadaceae	sf_1	7319	Anabaena circinalis AWQC118C isolate
Proteobacteria	Alphaproteobacteria	Sphingomonadaceae	sf_1	7440	Sphingobium chungbukense str. DJ77
Proteobacteria	Alphaproteobacteria	Sphingomonadaceae	sf_1	7528	Sphingobium yanoikuyae str. GIFU9882
Proteobacteria	Alphaproteobacteria	Sphingomonadaceae	sf_1	7535	Sphingomonas paucimobilis str. GIFU2395

Proteobacteria	Alphaproteobacteria	Sphingomonadaceae	sf_1	7548	Afipia genosp. 13 str. G8991
Proteobacteria	Gammaproteobacteria	Succinivibrionaceae	sf_1	8822	Anaerobiospirillum sp. str. 3J102
Proteobacteria	Deltaproteobacteria	Syntrophaceae	sf_3	9665	Syntrophus gentianae str. HQgoe1
Proteobacteria	Deltaproteobacteria	Syntrophaceae	sf_3	9935	forested wetland clone FW117
Proteobacteria	Deltaproteobacteria	Syntrophaceae	sf_3	10067	benzoate-degrading consortium clone BA044
Proteobacteria	Deltaproteobacteria	Syntrophobacteraceae	sf_1	9661	DCP-dechlorinating consortium clone SHD-1
Proteobacteria	Deltaproteobacteria	Syntrophobacteraceae	sf_1	9731	clone JG37-AG-90 proteobacterium
Proteobacteria	Deltaproteobacteria	Syntrophobacteraceae	sf_1	9845	clone JG37-AG-128 proteobacterium
Proteobacteria	Deltaproteobacteria	Syntrophobacteraceae	sf_1	9864	clone JG37-AG-133 proteobacterium
Proteobacteria	Deltaproteobacteria	Syntrophobacteraceae	sf_1	10013	hydrothermal sediment clone AF420341
Proteobacteria	Deltaproteobacteria	Syntrophobacteraceae	sf_1	10021	uranium mill soil sample clone proteobacterium
Proteobacteria	Deltaproteobacteria	Syntrophobacteraceae	sf_1	10184	granular sludge clone R1p32
Proteobacteria	Deltaproteobacteria	Syntrophobacteraceae	sf_1	10221	granular sludge clone R3p4
Proteobacteria	Deltaproteobacteria	Syntrophobacteraceae	sf_1	10251	Syntrophobacter-like isolate
Proteobacteria	Gammaproteobacteria	Thiotrichaceae	sf_3	8321	Wadden Sea sediment clone Dangast A9
Proteobacteria	Gammaproteobacteria	Thiotrichaceae	sf_3	8477	marine sediment clone Limfjorden L8
Proteobacteria	Gammaproteobacteria	Thiotrichaceae	sf_3	8559	Thioploca ingrica
Proteobacteria	Gammaproteobacteria	Thiotrichaceae	sf_3	8703	Beggiatoa sp. str. AA5A
Proteobacteria	Gammaproteobacteria	Thiotrichaceae	sf_3	8741	marine sediment clone Limfjorden L10
Proteobacteria	Gammaproteobacteria	Thiotrichaceae	sf_3	8752	Beggiatoa sp. str. MS-81-1c
Proteobacteria	Gammaproteobacteria	Thiotrichaceae	sf_3	9015	Beggiatoa alba str. B18LD; ATCC 33555
Proteobacteria	Gammaproteobacteria	Thiotrichaceae	sf_3	9321	marine sediment clone Tokyo Bay D
Proteobacteria	Deltaproteobacteria	Unclassified	sf_9	244	deep marine sediment clone MB-C2-152
Proteobacteria	Deltaproteobacteria	Unclassified	sf_3	468	marine sediment clone Sva0515
Proteobacteria	Unclassified	Unclassified	sf_20	2520	
Proteobacteria	Deltaproteobacteria	Unclassified	sf_1	3084	coal effluent wetland clone RCP216
Proteobacteria	Alphaproteobacteria	Unclassified	sf_2	6639	
Proteobacteria	Alphaproteobacteria	Unclassified	sf_1	6653	Kaistobacter koreensis str. PB229
Proteobacteria	Alphaproteobacteria	Unclassified	sf_6	6665	hydrocarbon-degrading consortium clone
Proteobacteria	Alphaproteobacteria	Unclassified	sf_6	6694	forested wetland clone RCP2-92
Proteobacteria	Alphaproteobacteria	Unclassified	sf_2	6697	gut homogenate clone Rs-D84 proteobacterium

Proteobacteria	Alphaproteobacteria	Unclassified	sf_1	6711	Microvirga subterranea str. ATCC BAA-295
Proteobacteria	Alphaproteobacteria	Unclassified	sf_1	6732	Anabaena circinalis AWQC118C isolate str.
Proteobacteria	Alphaproteobacteria	Unclassified	sf_5	6735	Candidatus Pelagibacter ubique str. HTCC1002
Proteobacteria	Alphaproteobacteria	Unclassified	sf_1	6756	
Proteobacteria	Unclassified	Unclassified	sf_20	6763	
Proteobacteria	Alphaproteobacteria	Unclassified	sf_6	6776	Mammoth cave clone CCU22
Proteobacteria	Alphaproteobacteria	Unclassified	sf_1	6789	Shinella zoogloeoides str. ATCC 19623
Proteobacteria	Alphaproteobacteria	Unclassified	sf_4	6810	marine bacterioplankton clone MB13F01
Proteobacteria	Deltaproteobacteria	Unclassified	sf_1	6830	coal effluent wetland clone RCP124
Proteobacteria	Alphaproteobacteria	Unclassified	sf_6	6898	heavy metal-contaminated soil clone a13113
Proteobacteria	Alphaproteobacteria	Unclassified	sf_1	6899	
Proteobacteria	Alphaproteobacteria	Unclassified	sf_6	6918	soil near uranium mill tailings clone KCM-C-45
Proteobacteria	Alphaproteobacteria	Unclassified	sf_6	6920	Pseudovibrio denitrificans str. DN34
Proteobacteria	Alphaproteobacteria	Unclassified	sf_1	6945	Rhizobiales str. A48
Proteobacteria	Alphaproteobacteria	Unclassified	sf_6	6987	
Proteobacteria	Alphaproteobacteria	Unclassified	sf_5	7025	bacterioplankton clone ZA2526c
Proteobacteria	Alphaproteobacteria	Unclassified	sf_1	7028	
Proteobacteria	Alphaproteobacteria	Unclassified	sf_1	7060	
Proteobacteria	Alphaproteobacteria	Unclassified	sf_4	7105	Mariana trough hydrothermal vent clone
Proteobacteria	Alphaproteobacteria	Unclassified	sf_1	7123	uranium mining waste pile clone JG37-AG-102
Proteobacteria	Alphaproteobacteria	Unclassified	sf_6	7148	thermal soil clone YNPFFP3
Proteobacteria	Alphaproteobacteria	Unclassified	sf_1	7156	termite gut clone Rs-M62 proteobacterium
Proteobacteria	Alphaproteobacteria	Unclassified	sf_2	7188	termite gut clone Rs-B50 proteobacterium
Proteobacteria	Alphaproteobacteria	Unclassified	sf_1	7194	soil isolate Ellin362
Proteobacteria	Alphaproteobacteria	Unclassified	sf_1	7199	uranium mill tailings clone Gitt-KF-194
Proteobacteria	Alphaproteobacteria	Unclassified	sf_1	7222	Great Artesian Basin clone B79
Proteobacteria	Alphaproteobacteria	Unclassified	sf_1	7264	Bosea thiooxidans TJ1
Proteobacteria	Alphaproteobacteria	Unclassified	sf_6	7312	
Proteobacteria	Alphaproteobacteria	Unclassified	sf_6	7340	sample clone JG30-KF-AS50
Proteobacteria	Alphaproteobacteria	Unclassified	sf_6	7377	Rocky Mountain alpine soil clone W2b-8C
Proteobacteria	Deltaproteobacteria	Unclassified	sf_1	7382	marine clone Arctic95C-5

Proteobacteria	Alphaproteobacteria	Unclassified	sf_1	7400	sphagnum peat bog clone K-5b5
Proteobacteria	Alphaproteobacteria	Unclassified	sf_5	7471	sponge clone TK03
Proteobacteria	Alphaproteobacteria	Unclassified	sf_6	7572	
Proteobacteria	Alphaproteobacteria	Unclassified	sf_6	7575	
Proteobacteria	Alphaproteobacteria	Unclassified	sf_5	7592	marine bacterioplankton clone MB12A07
Proteobacteria	Alphaproteobacteria	Unclassified	sf_6	7647	
Proteobacteria	Betaproteobacteria	Unclassified	sf_1	7750	uranium mining waste pile clone JG37-AG-35
Proteobacteria	Betaproteobacteria	Unclassified	sf_3	7765	
Proteobacteria	Betaproteobacteria	Unclassified	sf_1	7766	
Proteobacteria	Betaproteobacteria	Unclassified	sf_1	7808	Mammoth cave clone CCU25
Proteobacteria	Betaproteobacteria	Unclassified	sf_1	7818	soil sample clone proteobacterium
Proteobacteria	Unclassified	Unclassified	sf_17	7819	
Proteobacteria	Betaproteobacteria	Unclassified	sf_1	7832	
Proteobacteria	Betaproteobacteria	Unclassified	sf_1	7879	
Proteobacteria	Betaproteobacteria	Unclassified	sf_3	7974	
Proteobacteria	Betaproteobacteria	Unclassified	sf_1	7993	soil clone 1326-2
Proteobacteria	Betaproteobacteria	Unclassified	sf_3	7997	
Proteobacteria	Betaproteobacteria	Unclassified	sf_1	8023	ferromanganous micronodule clone MND1
Proteobacteria	Betaproteobacteria	Unclassified	sf_1	8035	
Proteobacteria	Betaproteobacteria	Unclassified	sf_3	8036	soil sample clone Sh765B-TzT-132 proteobacterium
Proteobacteria	Betaproteobacteria	Unclassified	sf_1	8037	Chitinimonas taiwanensis str. cf
Proteobacteria	Betaproteobacteria	Unclassified	sf_3	8045	
Proteobacteria	Betaproteobacteria	Unclassified	sf_3	8114	
Proteobacteria	Betaproteobacteria	Unclassified	sf_1	8148	agricultural soil clone SC-I-84
Proteobacteria	Deltaproteobacteria	Unclassified	sf_4	8169	forested wetland clone RCP2-54
Proteobacteria	Gammaproteobacteria	Unclassified	sf_1	8231	uranium waste soil clone JG30a-KF-21
Proteobacteria	Gammaproteobacteria	Unclassified	sf_3	8245	
Proteobacteria	Unclassified	Unclassified	sf_8	8247	
Proteobacteria	Gammaproteobacteria	Unclassified	sf_3	8327	Arctic sea ice ARK10148
Proteobacteria	Gammaproteobacteria	Unclassified	sf_3	8339	water 5 m downstream manure clone 35ds5

Proteobacteria	Gammaproteobacteria	Unclassified	sf_1	8403	Selenate-reducing isolate str. KE4OH1
Proteobacteria	Gammaproteobacteria	Unclassified	sf_1	8430	Salmonella bongori str. JEO 4162
Proteobacteria	Unclassified	Unclassified	sf_21	8509	
Proteobacteria	Gammaproteobacteria	Unclassified	sf_1	8532	
Proteobacteria	Gammaproteobacteria	Unclassified	sf_3	8587	Mars Odyssey Orbiter encapsulation clone T5-3
Proteobacteria	Gammaproteobacteria	Unclassified	sf_1	8605	bacterioplankton clone ZA2525c
Proteobacteria	Gammaproteobacteria	Unclassified	sf_3	8606	
Proteobacteria	Gammaproteobacteria	Unclassified	sf_3	8646	
Proteobacteria	Gammaproteobacteria	Unclassified	sf_1	8654	inactive hydrothermal vent clone IheB2-31
Proteobacteria	Gammaproteobacteria	Unclassified	sf_3	8676	
Proteobacteria	Gammaproteobacteria	Unclassified	sf_3	8714	Marinobacter hydrocarbonoclasticus
Proteobacteria	Gammaproteobacteria	Unclassified	sf_1	8747	uranium waste soil clone JG30-KF-CM35
Proteobacteria	Alphaproteobacteria	Unclassified	sf_6	8780	clone GR-296.II.89 GR-296.II.89
Proteobacteria	Gammaproteobacteria	Unclassified	sf_4	8855	
Proteobacteria	Gammaproteobacteria	Unclassified	sf_3	8926	inactive hydrothermal vent clone IheB2-13
Proteobacteria	Gammaproteobacteria	Unclassified	sf_1	8957	marine clone Arctic97C-5
Proteobacteria	Gammaproteobacteria	Unclassified	sf_3	8959	bacterioplankton clone AEGEAN_133
Proteobacteria	Gammaproteobacteria	Unclassified	sf_3	8961	Calymmatobacter magna symbiont
Proteobacteria	Gammaproteobacteria	Unclassified	sf_1	8962	bacterioplankton clone AEGEAN_234
Proteobacteria	Gammaproteobacteria	Unclassified	sf_1	8980	activated sludge clone SBRL2_19
Proteobacteria	Gammaproteobacteria	Unclassified	sf_1	9008	activated sludge clone SBRQ157
Proteobacteria	Gammaproteobacteria	Unclassified	sf_3	9044	hydrothermal sediment clone AF420370
Proteobacteria	Gammaproteobacteria	Unclassified	sf_1	9059	activated sludge clone SBRH10
Proteobacteria	Gammaproteobacteria	Unclassified	sf_3	9105	
Proteobacteria	Gammaproteobacteria	Unclassified	sf_3	9124	Weser estuary clone DC8-80-1 proteobacterium
Proteobacteria	Gammaproteobacteria	Unclassified	sf_1	9128	Lucina nassula gill symbiont
Proteobacteria	Gammaproteobacteria	Unclassified	sf_1	9246	Mammoth Cave sediment clone CCD24
Proteobacteria	Gammaproteobacteria	Unclassified	sf_3	9279	
Proteobacteria	Gammaproteobacteria	Unclassified	sf_1	9282	
Proteobacteria	Gammaproteobacteria	Unclassified	sf_1	9344	Shewanella algae str. ATCC 51192
Proteobacteria	Gammaproteobacteria	Unclassified	sf_3	9367	Naha Vents Hawaii isolate str. PV-4

Proteobacteria	Gammaproteobacteria	Unclassified	sf_1	9418	uranium mining clone JG37-AG-14
Proteobacteria	Gammaproteobacteria	Unclassified	sf_1	9458	uranium mining clone JG37-AG-94
Proteobacteria	Gammaproteobacteria	Unclassified	sf_3	9473	northern Fram Strait clone ARKDMS-58
Proteobacteria	Gammaproteobacteria	Unclassified	sf_3	9498	
Proteobacteria	Gammaproteobacteria	Unclassified	sf_1	9556	Seepiophila jonesi symbiont
Proteobacteria	Unclassified	Unclassified	sf_8	9558	
Proteobacteria	Gammaproteobacteria	Unclassified	sf_3	9568	forested wetland clone RCP2-96
Proteobacteria	Unclassified	Unclassified	sf_20	9618	
Proteobacteria	Deltaproteobacteria	Unclassified	sf_1	9678	coal effluent wetland clone RCP185
Proteobacteria	Deltaproteobacteria	Unclassified	sf_9	9738	marine methane seep clone 1513
Proteobacteria	Deltaproteobacteria	Unclassified	sf_4	9741	uranium mining clone JG37-AG-30
Proteobacteria	Deltaproteobacteria	Unclassified	sf_9	9760	deep marine sediment clone MB-A2-137
Proteobacteria	Deltaproteobacteria	Unclassified	sf_9	9763	
Proteobacteria	Deltaproteobacteria	Unclassified	sf_9	9784	Antarctic sediment clone LH5_30
Proteobacteria	Deltaproteobacteria	Unclassified	sf_9	9798	uranium mill clone GuBH2-AD/TzT-67 p
Proteobacteria	Deltaproteobacteria	Unclassified	sf_3	9813	hydrothermal sediment clone AF420340
Proteobacteria	Deltaproteobacteria	Unclassified	sf_1	9828	termite gut homogenate clone proteobacterium
Proteobacteria	Deltaproteobacteria	Unclassified	sf_9	9876	deep marine sediment clone MB-B2-106
Proteobacteria	Deltaproteobacteria	Unclassified	sf_4	9884	forested wetland clone RCP2-62
Proteobacteria	Deltaproteobacteria	Unclassified	sf_9	9890	termite gut homogenate clone proteobacterium
Proteobacteria	Deltaproteobacteria	Unclassified	sf_9	9911	
Proteobacteria	Deltaproteobacteria	Unclassified	sf_1	9945	acid mine drainage clone BA18
Proteobacteria	Deltaproteobacteria	Unclassified	sf_4	9951	forested wetland clone FW13
Proteobacteria	Deltaproteobacteria	Unclassified	sf_1	9959	forested wetland clone FW110
Proteobacteria	Deltaproteobacteria	Unclassified	sf_9	9975	TCE-contaminated site clone ccs1m247
Proteobacteria	Deltaproteobacteria	Unclassified	sf_4	10024	hydrothermal sediment clone AF420338
Proteobacteria	Deltaproteobacteria	Unclassified	sf_7	10048	
Proteobacteria	Deltaproteobacteria	Unclassified	sf_9	10049	DCP-dechlorinating consortium clone SHA-72
Proteobacteria	Deltaproteobacteria	Unclassified	sf_1	10076	Great Artesian Basin clone G13
Proteobacteria	Deltaproteobacteria	Unclassified	sf_1	10084	acid mine drainage clone AS6
Proteobacteria	Unclassified	Unclassified	sf_28	10091	

Proteobacteria	Deltaproteobacteria	Unclassified	sf_1	10092	heavy metal-contaminated soil clone a13134
Proteobacteria	Deltaproteobacteria	Unclassified	sf_1	10259	
Proteobacteria	Epsilonproteobacteria	Unclassified	sf_1	10384	deep-sea hydrothermal vent clone VC1.2-cl06
Proteobacteria	Epsilonproteobacteria	Unclassified	sf_1	10405	hydrothermal sediment clone AF420346
Proteobacteria	Epsilonproteobacteria	Unclassified	sf_1	10407	hydrothermal sediment clone AF420342
Proteobacteria	Epsilonproteobacteria	Unclassified	sf_1	10414	penguin droppings sediments clone KD2-34
Proteobacteria	Epsilonproteobacteria	Unclassified	sf_1	10427	hydrothermal vent Pacific Ocean clone
Proteobacteria	Epsilonproteobacteria	Unclassified	sf_1	10475	hydrothermal sediment clone AF420359
Proteobacteria	Epsilonproteobacteria	Unclassified	sf_1	10480	hydrothermal vent polychaete mucous clone
Proteobacteria	Epsilonproteobacteria	Unclassified	sf_1	10489	S17sBac16 complete clone
Proteobacteria	Epsilonproteobacteria	Unclassified	sf_1	10497	reactor granular sludge clone proteobacterium
Proteobacteria	Epsilonproteobacteria	Unclassified	sf_1	10530	hydrothermal vent Pacific Ocean clone
Proteobacteria	Epsilonproteobacteria	Unclassified	sf_1	10543	hydrothermal vent clone PVB_10
Proteobacteria	Gammaproteobacteria	Vibrionaceae	sf_1	8723	Vibrio calviensis str. RE35F/12
Proteobacteria	Gammaproteobacteria	Vibrionaceae	sf_1	8798	Vibrio aestuarianus str. KT0901
Proteobacteria	Gammaproteobacteria	Vibrionaceae	sf_1	8888	Vibrio aestuarianus str. 01/151
Proteobacteria	Gammaproteobacteria	Vibrionaceae	sf_1	8999	Photobacterium leiognathi str. LN101
Proteobacteria	Alphaproteobacteria	Xanthobacteraceae	sf_1	6660	Azorhizobium caulinodans str. ORS 571
Proteobacteria	Gammaproteobacteria	Xanthomonadaceae	sf_3	8538	
Proteobacteria	Gammaproteobacteria	Xanthomonadaceae	sf_3	8577	Xanthomonas axonopodis pv. citri str. MA
Proteobacteria	Gammaproteobacteria	Xanthomonadaceae	sf_3	8689	Dyemonas todaii str. XD10
Proteobacteria	Gammaproteobacteria	Xanthomonadaceae	sf_3	8983	Iron oxidising strain ES-1
Proteobacteria	Gammaproteobacteria	Xanthomonadaceae	sf_3	9167	pea aphid symbiont clone APe4_38
Proteobacteria	Gammaproteobacteria	Xanthomonadaceae	sf_3	9270	Stenotrophomonas rhizophila str. e-p10
Proteobacteria	Gammaproteobacteria	Xanthomonadaceae	sf_3	9286	Stenotrophomonas maltophilia str. LMG 11104
Proteobacteria	Gammaproteobacteria	Xanthomonadaceae	sf_3	9320	Waste-gas biofilter clone BIyi3
Proteobacteria	Gammaproteobacteria	Xanthomonadaceae	sf_3	9332	wetland ecosystem isolate str. WJ2 WJ2
SPAM	Unclassified	Unclassified	sf_1	705	uranium tailings soil clone Sh765B-AG-45
SPAM	Unclassified	Unclassified	sf_1	738	uranium mining waste clone JG34-KF-252
Spirochaetes	Spirochaetes	Leptospiraceae	sf_3	6470	neutral pH mine biofilm clone 44a-B1-48
Spirochaetes	Spirochaetes	Leptospiraceae	sf_3	6496	Leptospira interrogans serovar Copenhageni

Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6458	termite gut clone NkS34
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6459	Spirochaeta sp. str. BHI80-158
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6460	termite gut homogenate clone Rs-B69 sp.
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6473	termite gut homogenate clone Rs-B29 sp.
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6476	termite gut clone NkS50
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6477	Mastotermes darwiniensis clone mp3 of
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6479	Treponema sp
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6484	Treponema amylovorum HA2P
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6487	termite gut homogenate clone Rs-D52 sp.
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6488	Treponema primitia str. ZAS-1
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6489	Mastotermes darwiniensis clone mp1 of
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6490	termite gut homogenate clone BCf4-14
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6491	termite gut homogenate clone BCf8-03
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_2	6493	Borrelia anserina str. ES-1
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6494	termite gut homogenate clone Rs-C47 sp.
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6502	Treponema denticola str. ATCC35405
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6505	Treponema sp. str. G179
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6506	termite gut homogenate clone Rs-J58 sp.
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6507	termite gut clone NkS-Ste2
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6508	termite hindgut clone mpsp2
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_3	6514	termite gut homogenate clone Rs-B68 sp.
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6523	termite gut homogenate clone Rs-J64 sp.
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6526	Treponema sp. str. 7CPL208
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6529	termite gut homogenate clone BCf10-21
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6531	Treponema sp. str. V:19:D36
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6532	termite gut clone NkS39
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6547	Mono Lake clone ML623J-23 bacterium
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6549	forested wetland clone RCP1-64
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6552	termite gut homogenate clone Rs-E91 sp.
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6554	termite gut homogenate clone Rs-A43 sp.
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6557	spirochete clone ML320J-13

Spirochaetes	Spirochaetes	Spirochaetaceae	sf_3	6558	Spirochaeta culicis str. BR91
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6562	forested wetland clone RCP1-96
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6565	termite gut clone NkS-Oxy25
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6568	Spirochaeta sp
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6570	Treponema maltophilum periodontitis patient BR
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6571	Mastotermes darwiniensis clone mp4 of
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6573	termite gut clone NkS7
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6575	TCE-contaminated site clone ccs1m226
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6579	termite gut clone NkS83
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6580	Treponema sp. str. III:C:BA213
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6583	termite gut homogenate clone Rs-J42 sp.
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6604	Treponema socranskii subsp. buccale
Spirochaetes	Spirochaetes	Spirochaetaceae	sf_1	6623	termite gut homogenate clone Rs-D46 sp.
SR1	Unclassified	Unclassified	sf_1	2900	
SR1	Unclassified	Unclassified	sf_1	2983	
Synergistes	Unclassified	Unclassified	sf_3	60	Flexistipes sp. str. E3_33
Synergistes	Unclassified	Unclassified	sf_3	117	termite gut homogenate clone Rs-D89
Synergistes	Unclassified	Unclassified	sf_3	353	UASB reactor granular sludge clone
Synergistes	Unclassified	Unclassified	sf_3	601	terephthalate-degrading consortium clone TA19
Synergistes	Unclassified	Unclassified	sf_3	719	Synergistes sp. P1 str. P4G_18
Synergistes	Unclassified	Unclassified	sf_3	740	swine intestine clone p-4292-4Wa3
Synergistes	Unclassified	Unclassified	sf_3	808	oral cavity clone BH017
Termite group 1	Unclassified	Unclassified	sf_2	437	termite gut homogenate clone Rs-D43 group
Termite group 1	Unclassified	Unclassified	sf_2	722	termite gut homogenate clone Rs-H93 group
Thermodesulfobacteria	Thermodesulfobacteria	Thermodesulfobacteriaceae	sf_1	667	Geothermobacterium ferrireducens
Thermotogae	Thermotogae	Thermotogaceae	sf_4	51	Thermosipho sp. str. MV1063
TM6	Unclassified	Unclassified	sf_1	9803	forest soil clone S1204
TM6	Unclassified	Unclassified	sf_1	10203	forest soil clone NOS7.2WL
TM7	TM7-3	Unclassified	sf_1	2697	midgut Pachnoda ephippiata larva clone
TM7	TM7-3	Unclassified	sf_1	2917	arid soil clone C026
TM7	Unclassified	Unclassified	sf_1	3025	

TM7	TM7-3	Unclassified	sf_1	3145	tongue dorsa clone DR034
TM7	TM7-3	Unclassified	sf_1	3151	activated sludge foam clone 71
TM7	Unclassified	Unclassified	sf_1	3679	
TM7	Unclassified	Unclassified	sf_1	5061	
TM7	Unclassified	Unclassified	sf_1	5177	
TM7	TM7-3	Unclassified	sf_1	8040	oral cavity clone BE109
TM7	TM7-3	Unclassified	sf_1	8155	oral periodontitis clone EW086
Unclassified	Unclassified	Unclassified	sf_160	226	
Unclassified	Unclassified	Unclassified	sf_106	243	hot spring clone OPB25
Unclassified	Unclassified	Unclassified	sf_160	267	
Unclassified	Unclassified	Unclassified	sf_160	333	
Unclassified	Unclassified	Unclassified	sf_160	485	thermal spring mat clone O1aA90
Unclassified	Unclassified	Unclassified	sf_160	651	
Unclassified	Unclassified	Unclassified	sf_160	895	
Unclassified	Unclassified	Unclassified	sf_93	925	4MB-degrading consortium clone UASB_TL26
Unclassified	Unclassified	Unclassified	sf_160	1914	
Unclassified	Unclassified	Unclassified	sf_160	2396	
Unclassified	Unclassified	Unclassified	sf_160	2488	
Unclassified	Unclassified	Unclassified	sf_95	2545	anaerobic sludge isolate str. JE
Unclassified	Unclassified	Unclassified	sf_88	3098	
Unclassified	Unclassified	Unclassified	sf_156	4291	Mono Lake clone ML635J-21 G+C
Unclassified	Unclassified	Unclassified	sf_160	4410	
Unclassified	Unclassified	Unclassified	sf_34	4668	
Unclassified	Unclassified	Unclassified	sf_160	6337	
Unclassified	Unclassified	Unclassified	sf_140	6355	
Unclassified	Unclassified	Unclassified	sf_160	6360	
Unclassified	Unclassified	Unclassified	sf_160	6401	
Unclassified	Unclassified	Unclassified	sf_160	6430	
Unclassified	Unclassified	Unclassified	sf_160	6456	
Unclassified	Unclassified	Unclassified	sf_160	7767	
Unclassified	Unclassified	Unclassified	sf_132	9820	

Unclassified	Unclassified	Unclassified	sf_92	9999	termite gut homogenate clone Rs-J96
Unclassified	Unclassified	Unclassified	sf_160	10012	
Verrucomicrobia	Verrucomicrobiae	Unclassified	sf_3	11	sludge clone H2
Verrucomicrobia	Unclassified	Unclassified	sf_3	40	Elbe river clone DEV055
Verrucomicrobia	Verrucomicrobiae	Unclassified	sf_4	169	anoxic marine sediment clone LD1-PA26
Verrucomicrobia	Unclassified	Unclassified	sf_4	288	Prostheco bacter de j ongeii
Verrucomicrobia	Unclassified	Unclassified	sf_3	486	Elbe river clone DEV045
Verrucomicrobia	Unclassified	Unclassified	sf_5	686	Guaymas Basin hydrothermal sediment clone
Verrucomicrobia	Verrucomicrobiae	Unclassified	sf_3	792	termite gut clone Rs-P07 bacterium
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobia subdivision 5	sf_1	111	Mono Lake clone ML635J-35
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobia subdivision 5	sf_1	530	anoxic marine sediment clone LD1-PB20
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobia subdivision 5	sf_1	533	anoxic marine sediment clone LD1-PB12
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobia subdivision 5	sf_1	547	anoxic marine sediment clone LD1-PB1
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobia subdivision 5	sf_1	629	anoxic marine sediment clone LD1-PA50
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobia subdivision 5	sf_1	885	soil clone PBS-III-26
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobia subdivision 7	sf_1	446	anoxic marine sediment clone LD1-PA34
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobia subdivision 7	sf_1	559	anoxic marine sediment clone LD1-PA20
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobia subdivision 7	sf_1	760	Mono lake clone ML316M-1
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiaceae	sf_7	29	Fucophilus fucoidanolyticus str. SI-1234
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiaceae	sf_6	203	Akkermansia muciniphila
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiaceae	sf_6	613	hydrothermal vent mucous clone
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiaceae	sf_6	871	
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiaceae	sf_1	1024	rumen clone BS5
Verrucomicrobia	Verrucomicrobiae	Xiphinematobacteraceae	sf_3	888	Candidatus Xiphinematobacter brevicolli
WS3	Unclassified	Unclassified	sf_3	95	marine sediment ridge clone Hyd24-32
WS3	Unclassified	Unclassified	sf_1	2537	anoxic marine sediment clone LD1-PA39
WS5	Unclassified	Unclassified	sf_2	8119	Guaymas Basin sediment clone a2b013

Table E2. Bacterial Taxa Significantly Associated with Greater Bronchial Hyperresponsiveness.Classification by 'G2-Chip' taxonomy (<http://greengenes.lbl.gov>) alphabetically by family. See footnotes.

Phylum	Class	Family	Sub-family	PhyloChip taxon ID	Taxon representative species	Correlation coefficient [#]	p-value	q-value	Notes*
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_6	6345	uranium mining soil clone	0.53	<0.001	0.007	
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_6	6423	coal effluent clone	0.52	<0.001	0.009	
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_16	6414	PCE-contaminated site clone	0.50	<0.001	0.009	
Acidobacteria	Acidobacteria	Acidobacteriaceae	sf_6	6359	PCE-contaminated site clone	0.48	<0.005	0.012	
Acidobacteria	Betaproteobacteria	Alcaligenaceae	sf_1	7768	swine intestine clone	0.52	<0.001	0.007	
Proteobacteria	Gammaproteobacteria	Alcanivoraceae	sf_1	9658	Alcanivorax sp.	0.47	<0.005	0.015	
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8594	Marinobacter sp.	0.55	<0.001	0.007	
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9288	Alteromonas stellipolaris	0.54	<0.001	0.007	
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8484	Alteromonadaceae isolate	0.52	<0.001	0.009	
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	8172	Pseudoalteromonas sp.	0.46	<0.005	0.012	
Proteobacteria	Gammaproteobacteria	Alteromonadaceae	sf_1	9384	Moritella viscosa	0.45	<0.005	0.015	
Proteobacteria	Alphaproteobacteria	Bartonellaceae	sf_1	7415	Bartonella quintana	0.54	<0.001	0.006	*
Proteobacteria	Alphaproteobacteria	Bradyrhizobiaceae	sf_1	7044	Afipia genosp.	0.52	<0.001	0.007	
Proteobacteria	Alphaproteobacteria	Bradyrhizobiaceae	sf_1	6878	Bradyrhizobium japonicum	0.51	<0.005	0.015	
Proteobacteria	Betaproteobacteria	Burkholderiaceae	sf_1	7720	droppings sediments clone	0.49	<0.005	0.010	
Proteobacteria	Betaproteobacteria	Burkholderiaceae	sf_1	8068	Burkholderia caryophylli	0.45	<0.005	0.015	
Proteobacteria	Alphaproteobacteria	Caulobacteraceae	sf_1	6968	Brevundimonas diminuta	0.52	<0.005	0.012	*
Cyanobacteria	Cyanobacteria	Chloroplasts	sf_5	5039	plankton clone	0.54	<0.001	0.009	
Proteobacteria	Gammaproteobacteria	Chromatiaceae	sf_1	9571	Nitrosococcus oceanus	0.63	<0.001	0.002	
Proteobacteria	Gammaproteobacteria	Chromatiaceae	sf_1	8546	Thiocapsa litoralis	0.58	<0.001	0.003	
Proteobacteria	Gammaproteobacteria	Chromatiaceae	sf_1	8697	Thiococcus sp.	0.48	<0.005	0.010	
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	8140	Schlegelella sp.	0.48	<0.001	0.010	
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7856	Variovorax paradoxus	0.56	<0.005	0.011	

Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	8139	Delftia tsuruhatensis	0.51	<0.005	0.013	
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	7705	droppings sediments clone	0.48	<0.005	0.013	
Proteobacteria	Betaproteobacteria	Comamonadaceae	sf_1	8112	Comamonas testosteroni	0.51	<0.005	0.014	*
Bacteroidetes	Sphingobacteria	Crenotrichaceae	sf_11	5647	sponge clone TK44	0.48	<0.005	0.015	
Proteobacteria	Gammaproteobacteria	Enterobacteriaceae	sf_1	9417	Serratia fonticola	0.48	<0.005	0.013	*
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5645	supragingival plaque clone	0.47	<0.001	0.009	
Bacteroidetes	Flavobacteria	Flavobacteriaceae	sf_1	5758	Tenacibaculum sp.	0.46	<0.005	0.013	
Proteobacteria	Gammaproteobacteria	Francisellaceae	sf_1	8949	Caedibacter taeniospiralis	0.54	<0.001	0.010	
Proteobacteria	Gammaproteobacteria	Methylococcaceae	sf_1	8645	Methylomicrobium buryatense	0.52	<0.001	0.007	
Proteobacteria	Betaproteobacteria	Methylophilaceae	sf_1	8137	freshwater clone	0.50	<0.001	0.010	
Proteobacteria	Betaproteobacteria	Neisseriaceae	sf_1	7662	encapsulation clone	0.51	<0.001	0.009	
Proteobacteria	Betaproteobacteria	Nitrosomonadaceae	sf_1	7805	Nitrospira briensis	0.62	<0.001	0.002	
Proteobacteria	Betaproteobacteria	Nitrosomonadaceae	sf_1	8145	Nitrosomonas eutropha	0.59	<0.001	0.004	*
Proteobacteria	Betaproteobacteria	Nitrosomonadaceae	sf_1	7770	Nitrosomonas europaea	0.53	<0.001	0.007	*
Proteobacteria	Betaproteobacteria	Nitrosomonadaceae	sf_1	7989	Nitrosomonas sp.	0.52	<0.001	0.010	
Acidobacteria	Betaproteobacteria	Oxalobacteraceae	sf_1	8034	Janthinobacterium agaricidamnorum	0.55	<0.001	0.006	
Acidobacteria	Betaproteobacteria	Oxalobacteraceae	sf_1	8032	Aquaspirillum arcticum	0.55	<0.001	0.007	
Proteobacteria	Betaproteobacteria	Oxalobacteraceae	sf_1	7843	Massilia timonae timone	0.50	<0.001	0.010	
Proteobacteria	Betaproteobacteria	Oxalobacteraceae	sf_1	7921	Collimonas fungivorans	0.48	<0.005	0.012	macrolide-susceptible <i>Oxalobacter formigenes</i> in this taxon
Proteobacteria	Betaproteobacteria	Oxalobacteraceae	sf_1	7866	Paucimonas lemoignei	0.51	<0.005	0.012	
Proteobacteria	Betaproteobacteria	Oxalobacteraceae	sf_1	7743	Herbaspirillum sp.	0.46	<0.005	0.012	
Proteobacteria	Alphaproteobacteria	Phyllobacteriaceae	sf_1	7497	Pseudaminobacter salicylatoxidans	0.60	<0.001	0.003	
Proteobacteria	Alphaproteobacteria	Phyllobacteriaceae	sf_1	7381	Aminobacter aminovorans	0.57	<0.001	0.004	
Proteobacteria	Alphaproteobacteria	Phyllobacteriaceae	sf_1	7300	marine isolate JP57	0.53	<0.001	0.007	
Proteobacteria	Alphaproteobacteria	Phyllobacteriaceae	sf_1	7216	Ahrensia kielensis	0.53	<0.001	0.009	
Proteobacteria	Gammaproteobacteria	Piscirickettsiaceae	sf_3	9291	Methylophaga alcalica	0.49	<0.005	0.012	
Proteobacteria	Deltaproteobacteria	Polyangiaceae	sf_3	9735	clone JG37-AG-15	0.52	<0.005	0.012	

Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	9343	Cellvibrio subsp. mixtus	0.54	<0.001	0.006	
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	9175	Pseudomonas extremorientalis	0.52	<0.001	0.009	
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	9238	Pseudomonas pseudoalcaligenes	0.48	<0.001	0.009	
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	9219	Pseudomonas cf. monteilii	0.51	<0.005	0.010	
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	8344	Anabaena circinalis isolate	0.47	<0.005	0.011	
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	8725	Pseudomonas sp.	0.48	<0.005	0.012	
Proteobacteria	Gammaproteobacteria	Pseudomonadaceae	sf_1	8553	Pseudomonas fulva	0.47	<0.005	0.014	
Proteobacteria	Betaproteobacteria	Ralstoniaceae	sf_1	8110	Wautersia paucula	0.64	<0.001	0.002	*
Proteobacteria	Betaproteobacteria	Ralstoniaceae	sf_1	7823	Wautersia basileensis	0.47	<0.005	0.013	
Proteobacteria	Betaproteobacteria	Ralstoniaceae	sf_1	7761	Ralstonia detusculanense	0.45	<0.005	0.014	
Proteobacteria	Betaproteobacteria	Rhodocyclaceae	sf_1	7800	upstream clone	0.46	<0.005	0.012	
Proteobacteria	Betaproteobacteria	Rhodocyclaceae	sf_1	7925	Thauera selenatis	0.46	<0.005	0.014	
Proteobacteria	Betaproteobacteria	Rhodocyclaceae	sf_1	7951	sludge lab clone	0.47	<0.005	0.014	
Proteobacteria	Gammaproteobacteria	Shewanellaceae	sf_1	8201	Shewanella surugaensis	0.59	<0.001	0.002	
Proteobacteria	Gammaproteobacteria	Shewanellaceae	sf_1	9081	Shewanella sp.	0.45	<0.005	0.014	*
Proteobacteria	Alphaproteobacteria	Sphingomonadaceae	sf_1	6690	Porphyrobacter tepidarius	0.69	<0.001	0.001	
Proteobacteria	Alphaproteobacteria	Sphingomonadaceae	sf_1	7548	Afipia genosp.	0.61	<0.001	0.004	
Proteobacteria	Alphaproteobacteria	Sphingomonadaceae	sf_1	7535	Sphingomonas paucimobilis	0.55	<0.001	0.009	*
Proteobacteria	Alphaproteobacteria	Sphingomonadaceae	sf_15	7035	Sphingomonas asaccharolytica	0.54	<0.001	0.009	
Proteobacteria	Alphaproteobacteria	Sphingomonadaceae	sf_1	7016	Sphingomonas sp.	0.51	<0.005	0.012	
Proteobacteria	Alphaproteobacteria	Sphingomonadaceae	sf_1	7319		0.54	<0.005	0.012	
Proteobacteria	Gammaproteobacteria	Thiotrichaceae	sf_3	8559	Thioploca ingrica	0.53	<0.001	0.009	
Acidobacteria	Acidobacteria-10	Unclassified	sf_1	516	uranium mining clone	0.50	<0.001	0.007	
Acidobacteria	Acidobacteria-4	Unclassified	sf_1	6348	soil clone RB41	0.55	<0.001	0.007	
Proteobacteria	Alphaproteobacteria	Unclassified	sf_6	6665	hydrocarbon-degrading clone	0.50	<0.001	0.010	
Proteobacteria	Alphaproteobacteria	Unclassified	sf_6	6694	forested wetland clone	0.51	<0.005	0.014	
Proteobacteria	Deltaproteobacteria	Unclassified	sf_1	7382	Arctic marine clone	0.45	<0.005	0.015	
Proteobacteria	Betaproteobacteria	Unclassified	sf_3	8036	uranium millsoil clone	0.53	<0.001	0.007	
Proteobacteria	Alphaproteobacteria	Unclassified	sf_1	7199	uranium mill tailings	0.54	<0.001	0.007	

					clone			
Firmicutes	Unclassified	Unclassified	sf_8	546	Ferribacter thermoautotrophicus	0.50	<0.005	0.013
Proteobacteria	Gammaproteobacteria	Unclassified	sf_3	8959	bacterioplankton clone	0.54	<0.001	0.007
Proteobacteria	Gammaproteobacteria	Unclassified	sf_3	9568	forested wetland clone	0.54	<0.001	0.009
Proteobacteria	Gammaproteobacteria	Unclassified	sf_3	9044	hydrothermal clone	0.48	<0.005	0.012
Proteobacteria	Gammaproteobacteria	Unclassified	sf_1	8980	activated sludge clone	0.64	<0.001	0.002
LD1PA group	Unclassified	Unclassified	sf_1	10118	anoxic sediment clone	0.52	<0.001	0.008
Proteobacteria	Betaproteobacteria	Unclassified	sf_1	8023	ferromanganous clone	0.49	<0.001	0.010
Proteobacteria	Betaproteobacteria	Unclassified	sf_1	7808	cave clone CCU25	0.48	<0.005	0.015
Cyanobacteria	Cyanobacteria	Unclassified	sf_1	5190	Plectonema sp. str. F3	0.45	<0.005	0.014
SPAM	Unclassified	Unclassified	sf_1	738	uranium waste clone	0.52	<0.005	0.014
Proteobacteria	Alphaproteobacteria	Unclassified	sf_1	6653	Kaistobacter koreensis	0.53	<0.005	0.010
Proteobacteria	Gammaproteobacteria	Unclassified	sf_1	9128	Lucina nassula symbiont	0.60	<0.001	0.003
Synergistes	Unclassified	Unclassified	sf_3	60	Flexistipes sp.	0.57	<0.001	0.005
Proteobacteria	Gammaproteobacteria	Unclassified	sf_1	8231	uranium soil clone	0.51	<0.001	0.010
Verrucomicrobia	Unclassified	Unclassified	sf_3	486	river clone DEV045	0.51	<0.001	0.009
Verrucomicrobia	Unclassified	Unclassified	sf_5	686	sediment clone	0.51	<0.001	0.010
WS3	Unclassified	Unclassified	sf_1	2537	anoxic sediment clone	0.54	<0.005	0.005
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobia subdivision 7	sf_1	446	anoxic sediment clone	0.58	<0.001	0.007
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobia subdivision 7	sf_1	559	anoxic sediment clone	0.57	<0.001	0.007
Proteobacteria	Verrucomicrobiae	Verrucomicrobia subdivision 7	sf_1	760	lake clone ML316M-1	0.52	<0.005	0.013
Proteobacteria	Gammaproteobacteria	Vibrionaceae	sf_1	8888	Vibrio aestuarianus	0.56	<0.001	0.003
Proteobacteria	Gammaproteobacteria	Vibrionaceae	sf_1	8798	Vibrio aestuarianus	0.48	<0.001	0.009

Pearson's correlation with q -value correction for false discovery. Significance level defined at $p < 0.01$, $q \leq 0.015$.

* taxa with member species previously reported either to be potentially pathogenic, or that possess notable, known functional features.