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A Persistent and Diverse Airway Microbiota Present during Chronic Obstructive Pulmonary Disease Exacerbations

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Abstract

Acute exacerbations of chronic obstructive pulmonary disease (COPD) are a major source of morbidity and contribute significantly to healthcare costs. Although bacterial infections are implicated in nearly 50% of exacerbations, only a handful of pathogens have been consistently identified in COPD airways, primarily by culture-based methods, and the bacterial microbiota in acute exacerbations remains largely uncharacterized. The aim of this study was to comprehensively profile airway bacterial communities using a culture-independent microarray, the 16S rRNA PhyloChip, of a cohort of COPD patients requiring ventilatory support and antibiotic therapy for exacerbation-related respiratory failure. PhyloChip analysis revealed the presence of over 1,200 bacterial taxa representing 140 distinct families, many previously undetected in airway diseases; bacterial community composition was strongly influenced by the duration of intubation. A core community of 75 taxa was detected in all patients, many of which are known pathogens. Bacterial community diversity in COPD airways is substantially greater than previously recognized and includes a number of potential pathogens detected in the setting of antibiotic exposure. Comprehensive assessment of the COPD airway microbiota using high-throughput, culture-independent methods may prove key to understanding the relationships between airway bacterial colonization, acute exacerbation, and clinical outcomes in this and other chronic inflammatory airway diseases.

Introduction

Chronic obstructive pulmonary disease (COPD) affects more than 12 million individuals in the United States and is the fourth leading cause of chronic morbidity and mortality (Rabe et al., 2007). A significant proportion of COPD-related healthcare costs are attributable to hospitalization for respiratory exacerbations (Mannino and Braman, 2007), with severe exacerbations having been associated with high mortality rates (Connors et al., 1996; Nseir et al., 2006). Bacterial infections are implicated in approximately 50% of COPD exacerbations (Sethi and Murphy, 2008). However, in most studies to date, bacterial identification has primarily relied on culture-based methods (Papi et al., 2006; Rosell et al., 2005; Soler et al., 2007) or species-specific, targeted PCR approaches (Murphy et al., 2004). Therefore, the true depth of bacterial diversity present in COPD airways is unknown, and the potential role for mixed-species bacterial communities in the pathogenesis of chronic airway colonization and acute exacerbations have been largely overlooked.

It is increasingly recognized that the human host is colonized by diverse, site-specific microbial communities that constitute the human microbiome (Dethlefsen et al., 2007; Eckburg et al., 2005). Growing interest in characterizing these consortia and their interactions with the host, is exemplified by the formation in 2008 of the International Human Microbiome Consortium (IHMC), a collaborative effort to merge data generated through the U.S. NIH Human Microbiome Project (HMP; http://nihroadmap.nih.gov/hmp) and the E.U. Metagenomics of the Human Intestinal Tract (MetaHIT; www.metahit.eu) initiatives. Constant exposure of the respiratory tract with the external environment could conceivably lead to important microbe–microbe and microbe–host interactions, yet the human airway microbiota, particularly that present in the context of pulmonary disease, remains largely uncharacterized. Given the limitations of culture-based

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methods, culture-independent approaches that identify species, or groups of closely related species, based on sequence polymorphisms in conserved genes, such as the 16S ribosomal RNA (16S rRNA) gene, enable a more comprehensive assessment of microbial members present in a mixed-species population. Such methods have increasingly been applied to identify bacterial consortia in a variety of human niches with demonstration that community composition is related to disease states such as obesity, ventilator-associated pneumonia and cystic fibrosis airway disease (Flanagan et al., 2007; Harris et al., 2007; Rogers et al., 2004; Turnbaugh et al., 2006).

An alternative approach to traditional culture-independent methods of microbial community analysis is the 16S rRNA PhyloChip, a high-density microarray containing 500,000 probes that can detect approximately 8,500 bacterial taxa [taxa are defined as a group of bacteria sharing at least 97% sequence homology within the 16S rRNA gene sequence; (Brodie et al., 2006)] The PhyloChip has previously been shown to detect substantially greater bacterial diversity compared in parallel with traditional clone library sequencing approaches (Brodie et al., 2006; DeSantis et al., 2007; Flanagan et al., 2007). Using this microarray, we analyzed airway specimens from eight COPD patients who were being managed for severe respiratory exacerbations to determine if a more diverse bacterial community is present during pulmonary exacerbation in the setting of antibiotic administration.

Materials and Methods

Subject selection and sample collection

Potential subjects for this study were screened from a database of airway specimens collected between August 2004 and April 2006 from mechanically ventilated patients admitted to the intensive care units at Moffitt-Long Hospital (University of California, San Francisco), who were enrolled in a parent study of *Pseudomonas aeruginosa* in intubated patients (Flanagan et al., 2007). Subjects admitted to the ICU with a primary diagnosis of "COPD exacerbation" were identified for inclusion in our study. Available endotracheal aspirates (ETAs) from eight patients were processed for 16S rRNA PhyloChip analysis, as detailed below. To compare results from PhyloChip analysis with conventional clinical cultures, we obtained results of quantitative clinical laboratory bacterial cultures (blood agar, chocolate agar, and EMB media) performed on minibronchoalveolar lavage (m-BAL) airway samples, collected within 1–5 days of the ETA specimen analyzed by PhyloChip, as previously described (Flanagan et al., 2007). We have previously found m-BALs to possess a similar bacterial community composition to that of ETAs obtained concurrently from the same patient (Flanagan et al., 2007). Clinical data (Table 1) were recorded in a secure database, including whether a diagnosis of pneumonia by conventional clinical and radiologic criteria (Zhuo et al., 2008) was made during the patient's hospitalization and the time frame between diagnosis and collection of airway samples. The Committee on Human Research at UCSF approved all study protocols, and all patients or their surrogates provided written, informed consent.

DNA extraction, 16S rRNA gene amplification, PhyloChip processing

Total DNA was extracted from ETAs (200 μL) using a bead-beating step (5.5 m s^{-1} for 30 s, FastPrep system) (MP Biomedicals, Cleveland, OH) prior to nucleic acid extraction using the Wizard Genomic DNA Purification kit (Promega, Madison, WI). Twelve, 25-cycle PCR reactions, containing 100 ng of DNA, 2.5 mM each of dNTPs, 1.5 μM each primer (Bact-27F and Bact-1492R) (Lane, 1991) and 0.02 U/μL of *ExTaq* (Takara Bio, Japan), were performed for each sample across a gradient of annealing temperatures (48–58°C), to maximize the diversity recovered. The resulting PCR products were pooled and gel-purified using the MinElute Gel Extraction kit (Qiagen, Chatsworth, CA). Known concentrations of synthetic 16S rRNA gene fragments and non-16S rRNA gene fragments were spiked into the pooled, purified PCR product, which served as internal standards for normalization. A total of 250 ng of purified PCR product per sample was fragmented, biotin-labeled, and hybridized to the microarray as previously described (Brodie et al., 2006). Washing, staining, and scanning of arrays were conducted according to standard Affymetrix protocols. Background subtraction, noise calculations and scaling were carried out as described previously (Brodie et al., 2006; DeSantis et al., 2007).

Analysis of PhyloChip data

Relatively conservative detection and quantification criteria for each taxon were applied, as previously described (DeSantis et al., 2007). Briefly, probe-pairs consisting of a perfectly matched and mismatched cross hybridization control probe (containing a mismatch at the 13th nucleotide) were scored as positive if they met two criteria: (1) the fluorescence intensity of the perfectly matched probe was $\geq$1.3 times greater than that of the mismatched probe, and (2) the difference in intensity in each probe pair was 130 times greater than the squared noise value for that array. The positive fraction (pf) of probe sets (minimum of 11, median of 24 probe-pairs per taxon) was calculated, and a taxon was considered "present" if the calculated pf was $\geq$90%. Statistical analyses were performed in the R environment (www.R-project.org), using the ecological community analysis package *vegan* (version 1.16-1). Log-transformed fluorescence intensities were used to calculate Bray-Curtis dissimilarity measures of ecological distance. Nonmetric multidimensional scaling (NMDS), a nonparametric ordination method that maps community relatedness, in this case using the Bray-Curtis distance metric, was used to assess variability in bacterial community structure. The function *adonis* (Anderson, 2001), which conducts a matrix-based nonparametric analysis of variance, was applied to explore relationships between community composition and clinical variables, including age, gender, number of intubation days, presence of pneumonia, time frame between pneumonia diagnosis and sample collection, antibiotic and corticosteroid treatments, and survival to ICU discharge. Between-group differences in taxon abundance were assessed by two-tailed *t*-testing with significance adjusted for false discovery using *q*-values, as previously described (Storey and Tibshirani, 2003). Taxa exhibiting q values $<$0.05, a p-value $\leq$0.02 and a change of $>$1,000 fluorescence units (log-fold change in 16S rRNA copy number) were considered statistically and biologically significant. Phylogenetic trees were constructed using representative 16S rRNA sequences from the Greengenes database (DeSantis et al., 2006). A neighbor-joining tree with nearest-neighbor interchange was produced using FastTree (Price et al., 2009)

Table 1. Clinical Characteristics of Subjects and Samples

Patient	Age	Gender	Intubation days at sample collection	Antimicrobial therapy received within the past month	Days of active antimicrobial therapy at time of sample collection	Culture results[a]
1	63	M	16	ceftazidime	16	*PA*[b*]
2	69	F	6	vancomycin, tobramycin, levofloxacin	5	*PA*[b*]
3	78	M	1	vancomycin, piperacillin/tazobactam, levofloxacin	1	*PA*[b*], *KP*[b*], *AF*
4	78	M	21	piperacillin/tazobactam	31	*PA*[b*], *SM*[b*]
5	86	F	17	levofloxacin	17	*PA*[b*]
6	85	F	16	doxycycline, moxifloxacin, vancomycin	1	*PA*[b*]
7	61	M	5	vancomycin, piperacillin/tazobactam	7	*PA*[b*], *SA*[b]
8	73	M	3	piperacillin/tazobactam	3	*PA*[b], *EA*[b*]

[a] mini-BAL, minibronchoalveolar lavage clinical culture. The most recent, available culture data were obtained from within 1–5 days prior to the endotracheal aspirate sample analyzed by PhyloChip.

[b] Detected by PhyloChip; *≥10,000 colony-forming units on quantitative mini-BAL culture.

PA, *Pseudomonas aeruginosa;* KP, *Klebsiella pneumoniae;* SA, *Staphylococcus aureus;* EA, *Enterobacter aerogenes;* SM, *Stenotrophomonas maltophilia;* AF, *Aspergillus fumigatus.*

and uploaded to the Interactive Tree of Life project (http://itol.embl.de/) for annotation (Letunic and Bork, 2007).

Quantitative polymerase chain reaction (Q-PCR)

To confirm that changes in array fluorescence intensities were reflective of changes in target organism abundance, triplicate, Q-PCR reactions were performed for selected taxa containing species of interest, using a Stratagene MxP3000 real-time system and the QuantiTect SYBR Green PCR kit (Qiagen). Primers for taxa containing selected species of interest were designed based on PhyloChip probes for the target taxon (Table 2). Reaction conditions were similar to those previously described (Brodie et al., 2007) with the exception that 10 ng of DNA extract were used in 40 cycles of reaction using the annealing temperatures listed in Table 2 for each primer set. Regression analyses of inverse cycle threshold values plotted against PhyloChip fluorescence intensities were determined for each targeted taxon.

Results

16S rRNA PhyloChip analysis identified a total of 1,213 bacterial taxa present in airway samples from COPD patients obtained during the course of acute exacerbations (complete list is provided in Table 3; see at end of article). Despite recent or ongoing exposure to antibiotics across the group, the mean number of taxa detected in each sample was 411 ± 246 taxa (SD). Identified taxa represented a diverse group of species belonging to 38 bacterial phyla and 140 distinct families (Fig. 1A). Bacterial families detected included members of the Pseudomonadaceae, Pasteurellaceae, Helicobacteraceae, Enterobacteriaceae, Comamonadaceae, Burkholderiaceae, and Alteromonadaceae, among many others. In addition, recently described phyla such as the TM7 subgroup of Gram-positive uncultivable bacteria were also detected in the airways of these patients (Table 3).

Interpersonal variation in bacterial richness (number of taxa detected) was noted across the patient samples (Fig. 1B). Four subjects (patients 1, 4, 5, and 6) exhibited communities with significantly fewer taxa ($p < 0.002$) compared with the other four subjects. Patients in which fewer bacterial taxa were detected tended to possess more members of the Pseudomonadaceae. In contrast, members of the Clostridiaceae, Lachnospiraceae, Bacillaceae, and Peptostreptococcaceae were detected more commonly in those patients with richer communities (patients 2, 3, 7). Patient 8 was observed to possess a large proportion of taxa belonging to the Enterobacteriaceae family, which have been associated with more advanced COPD lung disease (Sethi and Murphy, 2008). Interestingly, this patient had radiographic evidence of coexisting bronchiectasis, which was not present in the other patients.

Given the variation in bacterial richness among samples, which suggested differences in bacterial community composition, NMDS was used to assess variation in bacterial community structure (based on Bray-Curtis dissimilarity measures) across the sample cohort. This revealed two

Table 2. Primers Used for Q-PCR Validation of Targeted Species

Species	Primers	Annealing temperature
P. aeruginosa	5′-CAGTAAGTTAATACCTTGCTGTGCTG-3′ 5′- TGCTGAACCACCTACGCGC-3′	55°C
S. maltophilia	5′-GCCGGCTAATACCTGGTTGGGA-3′ 5′- CTACCCTCTACCACACTCTAGTCGC-3′	55°C
H. cetorum	5′-GCGTTACTCGGAATCACTGGGCGTA-3′ 5′- ATGAGTATTCCTCTTGATCTCTACG-3′	48°C
C. mucosalis	5′-ATGTGGTTTAATTCGAAGATACGCG-3′ 5′- CACGAGCTGACGACAGCCGTGCAGC-3′	52°C

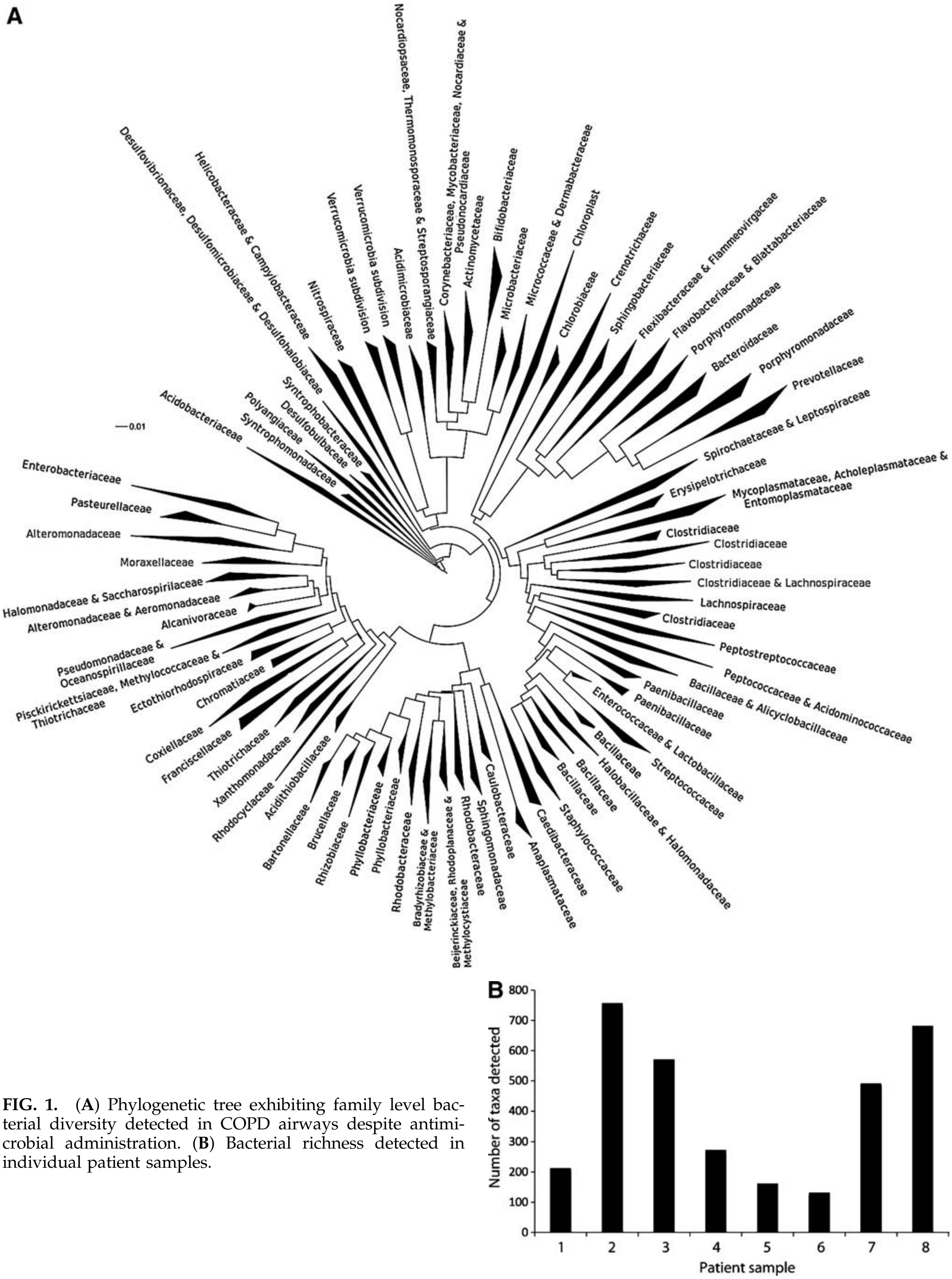

FIG. 1. (**A**) Phylogenetic tree exhibiting family level bacterial diversity detected in COPD airways despite antimicrobial administration. (**B**) Bacterial richness detected in individual patient samples.

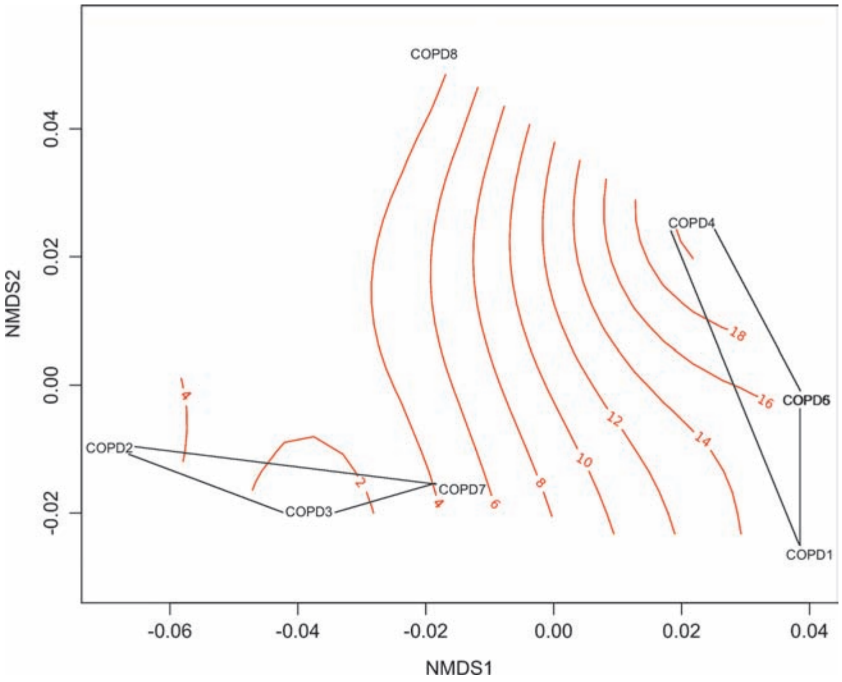

FIG. 2. NMDS analysis demonstrates that bacterial community composition is highly influenced by the duration of intubation (red isotherms). Subjects COPD 5 and COPD 6 are superimposed on the right side of the figure, indicative of highly similar bacterial community composition.

distinct groups of patient samples and confirmed that patient 8 represented a structurally distinct airway community (Fig. 2). Although the cohort was small, given this separation of subjects based on differing bacterial community structures, the influence of available clinical parameters on community composition was explored. Matrix-based, nonparametric multivariate analysis of variance (Anderson, 2001) revealed that across the cohort, the number of elapsed intubation days was significantly associated with bacterial community composition and structure, accounting for the greatest percentage of the observed variability (44%, $p < 0.03$; Fig. 2). Group 1 patient samples (patients 2, 3, and 7) were characterized by a shorter intubation duration prior to ETA sample collection ($\leq$6 days), while those in Group 2 were intubated for significantly longer periods of time ($p < 0.0007$; patients 1, 4, 5, and 6; $\geq$16 days) and exhibited a significantly less rich community composition compared to that of Group 1 ($p < 0.025$). Given the community variation between Group 1 and Group 2, differences in the relative abundance of all detected taxa were assessed between the groups, which identified 153 taxa with significantly different relative abundances (Table 4; see at end of article). All of these significant taxa were present in higher abundance in Group 1, the majority of which (77%) belonged to the phylum Firmicutes. These included species such as *Lactobacillus kitasatonis*, *L. perolens, L. sakei,* and *Bacillus clausii*, as well as known pathogenic species such as *Streptococcus constellatus*, which is a member of the *Streptoccocus milleri* group (SMG; Table 4). No other clinical variable [including diagnosis of pneumonia ($n = 6$; $p < 0.4$) or the number of days between pneumonia diagnosis and sample collection (range: 3–52 days; $p < 0.6$)] demonstrated a significant association with bacterial community composition in this cohort.

A common "core" of 75 bacterial taxa representing 27 classified bacterial families was identified in all patients analyzed (Fig. 3). This core group included members of the Pseudomonadaceae, Enterobacteriaceae, Campylobacteraceae, and Helicobacteraceae, amongst others. In addition, taxa containing species of pathogenic potential, such as *Arcobacter cryaerophilus*, *Brevundimonas diminuta, Leptospira interrogans,* as well as *P. aeruginosa*, were detected in all patients (a complete list of the core taxa is provided in Table 5; see at end of article). We also analyzed the array data for organisms that have previously been associated with COPD airways (Sethi and Murphy, 2008). *Haemophilus influenzae* was detected by the array in two subjects (patients 2 and 8), although corresponding m-BAL cultures were negative for this organism. *Moraxella catarrhalis* was not detected by PhyloChip or culture in any patient sample. However, other phylogenetically related members in the *Moraxellaceae* family, including *Moraxella oblonga*, *Acinetobacter haemolyticus*, and *Psychrobacter psychrophilus* were identified by the array in 80–100% of subjects (Table 3). *Streptococcus pneumoniae* was detected in four subjects (patients 2, 3, 7 and 8) despite all m-BALs being culture-negative for this species. Finally, we also examined PhyloChip data for the presence of the atypical bacteria, *Mycoplasma pneumoniae* and *Chlamydophila pneumoniae*, which are associated with 3–5% percent of exacerbations (Sethi and Murphy, 2008). Neither was detected by the PhyloChip, although a related species, *Mycoplasma pulmonis*, was identified in a single individual (patient 3).

Quantitative PCR was performed to validate that changes in reported array fluorescence intensities for targeted taxa correlated with changes in target species copy number for a selection of known airway pathogens (*P. aeruginosa* and *Stenotrophomonas maltophilia*) and two characteristic gastrointestinal organisms (*Campylobacter mucosalis* and *Helicobacter cetorum*). Regression analysis of species abundance determined by Q-PCR and array fluorescence intensity

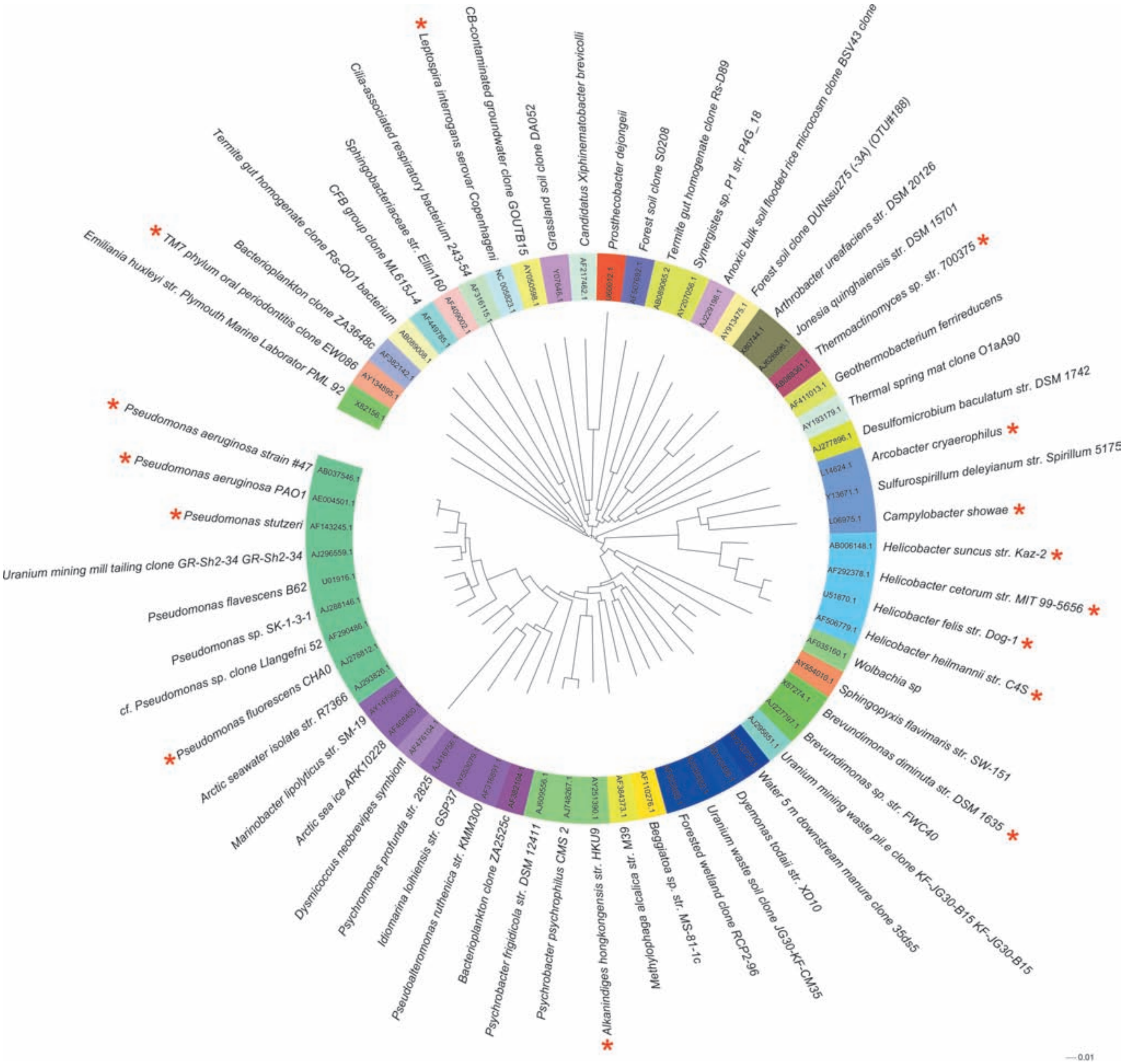

FIG. 3. Phylogenetic tree illustrating core bacterial taxa detected in COPD airways samples in this study. Known pathogens are denoted with an asterix; distinct bacterial families are indicated by different colors.

demonstrated strong concordance between the two independent methods for each target organism (Table 6), confirming their presence in these COPD airway samples and the ability of the array to accurately reflect changes in organism relative abundance.

Discussion

Although nearly half of acute COPD exacerbations are associated with bacterial infection, our knowledge of the microbial species associated with these events is limited to a handful of organisms detected primarily by culture-based methods (Papi et al., 2006; Rosell et al., 2005; Soler et al., 2007). The overall aim of this study was to begin to address the overarching question whether previously undetected bacterial species exist in the airways of COPD patients during acute exacerbations. High-resolution, culture-independent analysis using the 16S rRNA PhyloChip revealed a much greater diversity of bacteria than has previously been appreciated in the airways of COPD patients being managed for severe exacerbations, including members of the Pseudomonadaceae, Enterobacteriaceae, and Helicobacteraceae, among others. The potential for a diverse airway bacterial community to play a role in chronic airway colonization and inflammation, a feature of COPD, has not been previously considered.

The identification of a diversity of bacterial communities in respiratory samples from COPD patients experiencing severe exacerbations suggests that the pathogenesis of these events could involve a polymicrobial process. Future studies in a larger cohort of patients, including nonintubated COPD

Table 6. Correlation Results for Species Abundance by Q-PCR and 16S rRNA PhyloChip

Target species	R *value*	p *Value*
P. aeruginosa	0.77	<0.05
S. maltophilia	0.80	<0.05
Campylobacter mucosalis	0.68	<0.10
Helicobacter cetorum	0.79	<0.05

patients with a greater range of exacerbation severity, will be necessary to determine relationships between community composition, structure, and pulmonary health. Only a handful of bacterial species, such as *H. influenzae* and *P. aeruginosa*, have previously been associated with COPD exacerbations. The possible role of other bacterial community members with pathogenic potential identified in this study, e.g. *A. cryaerophilus*, *B. diminuta*, and *L. interrogans*, may merit further investigation. Many of these species have been implicated in other pathogenic processes such as endocarditis (Han and Andrade, 2005; Marques da Silva et al., 2006; Paster et al., 2002) and bacteremia (Hsueh et al., 1997; Woo et al., 2001). *L. interrogans*, the causative agent of human leptospirosis (Gaudie et al., 2008), has recently been shown to induce pulmonary lesions in an experimental animal model of airway infection (Marinho et al., 2009) and pulmonary hemorrhage in severe cases (Dall'Antonia et al., 2008). Their potential for pathogenesis suggests the possibility of a role for these organisms in COPD chronic airway disease. Future studies involving functional and mechanistic analyses will be necessary to further assess this.

Multiple oropharyngeal and gut-associated bacterial species were also identified by PhyloChip analysis, suggesting a potential role in COPD exacerbations. Although contamination by oropharyngeal secretions is always a possibility, samples were collected through an endotracheal tube, diminishing the degree of direct contamination. Ongoing microaspiration during intubation, however, cannot be completely prevented, and it has been suggested that the oral cavity and gastrointestinal tract act as a microbial reservoir for seeding the airways in vulnerable patient populations (Garrouste-Orgeas et al., 1997; Heyland and Mandell, 1992; Orozco-Levi et al., 2003). In our study the relative abundance of targeted gastrointestinal-associated species, *H. cetorum* and *C. mucosalis* (Figura et al., 1993; Garcia-Amado et al., 2007), were confirmed by independent Q-PCR in airway samples from these patients. The presence of oropharyngeal or gut-associated bacteria in the lower airways may have significant implications for a disease population with greater risks from pulmonary infections. For example, Duan et al. (2003) demonstrated in a rat model that coinfection of *P. aeruginosa* with oropharyngeal bacterial species (isolated from cystic fibrosis patient sputa) resulted in enhanced lung damage and upregulation of *P. aeruginosa* virulence gene expression. In our study, *P. aeruginosa* and oropharyngeal and gut-associated species were present in the airways of all patients studied, suggesting the potential for enhanced pathogenesis in this patient population.

We recognize that our study numbers are small and represent a severely ill group of COPD patients. Therefore, caution must be exercised in extrapolating these findings to a broader group of COPD patients, especially nonintubated individuals experiencing less severe exacerbations. Although facilitating access to lower respiratory specimens that are otherwise challenging to obtain during severe exacerbations, the intubation status of these patients is an important consideration in weighing these findings. Although protracted intubation was associated with decreased bacterial community richness, the possibility for a more diverse bacterial community to play a role at least at the onset of exacerbation-associated respiratory failure remains. Control samples from nonintubated COPD and non-COPD patients were not available for this study, nor were longitudinal samples from these patients. In a previous study, however, we have found that endotracheal samples obtained from patients briefly intubated for elective surgery produced no detectable 16S rRNA PCR product (Flanagan et al., 2007). The lack of an association between duration of active antimicrobial therapy and bacterial community structure is most likely due to both the small study numbers as well as the administration of previous antibiotic courses up to one month prior to sample collection in the study (e.g., patient 6).

Results of this study highlight the advantages of complementing culture-based methods with higher resolution approaches for bacterial detection to provide a more comprehensive assessment of the airway microbiota present in COPD patients. Culture-independent methods are particularly relevant to identify viable but nonculturable species that produce and exist in biofilms (Rayner et al., 1998), which are characteristic of chronic airway infections (Costerton et al., 1999; Singh et al., 2000) and have recently been implicated in COPD (Martinez-Solano et al., 2008). Because our PhyloChip analysis was based on DNA extracted from airway samples, it does not provide information on the viability of the species detected. However, we have previously noted that within 24 h of antimicrobial administration to cystic fibrosis patients, bacterial richness decreased approximately 10-fold as detected by the PhyloChip (Lynch, unpublished data). This suggests that DNA turnover is relatively rapid in the airways of chronic pulmonary disease patients, and that the taxa detected during antimicrobial administration in our COPD patients largely represent the viable portion of the community. This is supported by the finding that the PhyloChip detected all species that were isolated by concurrent clinical laboratory culture. Independent Q-PCR analysis of selected taxa also demonstrated strong concordance between calculated 16S rRNA copy number and PhyloChip-based fluorescence intensities, validating the abundance of individual species detected by the array. Although both cultures and the microarray demonstrated low detection rates for *H. influenzae and M. catarrhalis,* two species commonly associated with COPD exacerbation (potentially due to antibiotic-mediated clearance), only the PhyloChip identified other *Haemophilus* species across the majority of patients in this study, as well as other members of the Moraxellaceae family. Although these molecular methods may identify potentially relevant species undetected by culture, they provide no information on the viability or activity of these species. Hence, the significance of detecting species phylogenetically related to known pathogens in COPD airways is unclear, but may merit further study.

Conclusions

Application of the 16S rRNA PhyloChip to airway secretions from COPD patients during severe respiratory exacerbations requiring ventilatory support and antibiotic administration, demonstrated the presence of diverse bacterial communities, whose structural variation in this cohort was related to the duration of intubation. A core community of bacterial taxa comprised of many known pathogens, some not previously associated with COPD, was common to all patients studied. Given that the disease model of COPD is generally characterized by chronic airway colonization, recurrent infection-related exacerbations, and a persistent state of chronic airway inflammation, these results highlight the need to consider the polymicrobial community present in COPD airways and the potential functional effects of these consortia on immune response and pulmonary health. Identification of relationships that exist between bacterial communities, their collective gene expression, concomitant host response, and clinical outcomes may ultimately lead to improved understanding of the pathogenesis of COPD.

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Author Disclosure Statement

The authors declare that no competing financial interests exist.

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Table 3. All Bacterial Taxa Detected by 16S rRNA Phylochip in Airway Samples of COPD Patients Being Treated for Severe Exacerbations

Phylum	*Class*	*Order*	*Family*	*S-F*[a]	*Taxon ID*[b]	*Representative species*[c]
Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	sf_14	508	uranium mining waste pile clone JG37-AG-81 sp.
Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	sf_14	541	uranium mill tailings soil sample clone GuBH2-AG-47 sp.
Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	sf_14	209	uranium mining waste pile clone JG37-AG-29 sp.
Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	sf_14	6425	Great Artesian Basin clone B27
Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	sf_14	6335	forested wetland clone FW45
Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	sf_6	6345	soil sample uranium mining waste pile near town Johanngeorgenstadt clone JG36-TzT-77 bacterium
Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	sf_14	6350	soil isolate Ellin337
Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	sf_14	6356	forested wetland clone FW47
Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	sf_6	6359	PCE-contaminated site clone CLi114
Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	sf_6	6362	grassland soil clone DA052
Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	sf_14	6366	PCB-polluted soil clone WD228
Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	sf_14	6368	soil clone UA2
Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	sf_14	6378	*Acidobacterium capsulatum*
Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	sf_14	6410	
Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	sf_14	6412	acid mine drainage clone TRB82
Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	sf_16	6414	PCE-contaminated site clone CLs73
Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	sf_14	6421	PCB-polluted soil clone WD217
Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	sf_6	6423	coal effluent wetland clone FW92
Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	sf_14	6424	sphagnum peat bog clone K-5b10
Acidobacteria	Unclassified	Unclassified	Unclassified	sf_1	572	forested wetland clone FW144
Acidobacteria	Acidobacteria-4	Ellin6075/11-25	Unclassified	sf_1	435	anaerobic VC-degrading enrichment clone VC47 bacterium
Acidobacteria	Acidobacteria-5	Unclassified	Unclassified	sf_1	523	soil metagenomic library clone 17F9
Acidobacteria	Acidobacteria-4	Ellin6075/11-25	Unclassified	sf_1	790	soil clone 11-25
Acidobacteria	Acidobacteria-4	Ellin6075/11-25	Unclassified	sf_1	87	activated sludge clone 2951
Acidobacteria	Acidobacteria-6	Unclassified	Unclassified	sf_1	350	Mammoth cave clone CCM15a
Acidobacteria	Acidobacteria-6	Unclassified	Unclassified	sf_1	897	Mammoth cave clone CCM8b
Acidobacteria	Acidobacteria-6	Unclassified	Unclassified	sf_1	1049	soil clone C112
Acidobacteria	Solibacteres	Unclassified	Unclassified	sf_1	6426	Great Artesian Basin clone B11
Acidobacteria	Acidobacteria-4	Unclassified	Unclassified	sf_1	6363	soil clone 32-11
Acidobacteria	Unclassified	Unclassified	Unclassified	sf_1	4222	forested wetland clone FW105
Actinobacteria	Actinobacteria	Acidimicrobiales	Acidimicrobiaceae	sf_1	1090	
Actinobacteria	Actinobacteria	Acidimicrobiales	Acidimicrobiaceae	sf_1	1749	forest soil clone DUNssu275 (-3A) (OTU#188)
Actinobacteria	Actinobacteria	Acidimicrobiales	Acidimicrobiaceae	sf_1	1856	forested wetland clone RCP2-105
Actinobacteria	Actinobacteria	Acidimicrobiales	Acidimicrobiaceae	sf_1	1360	forested wetland clone RCP2-103
Actinobacteria	Actinobacteria	Actinomycetales	Acidothermaceae	sf_1	1399	uranium mill tailings clone Gitt-KF-183
Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	sf_1	1684	*Varibaculum cambriense* str. CCUG 44998
Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	sf_1	1227	*Actinomyces naeslundii*
Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	sf_1	1672	*Actinomyces odontolyticus* str. CCUG 28084
Actinobacteria	Actinobacteria	Actinomycetales	Actinosynnemataceae	sf_1	1463	*Saccharothrix texasensis* str. NRRL B-16107T
Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	sf_1	1351	*Bifidobacterium psychraerophilum* str. T16
Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	sf_1	1967	*Bifidobacterium pseudocatenulatum* str. JCM1200

Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	sf_1	2040	*Bifidobacterium adolescentis* str. E-981074T
Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	sf_1	1109	*Bifidobacterium thermacidophilum* porcinum subsp. suis str. P3-14 subsp.
Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	sf_1	1987	human subgingival plaque clone CX010
Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	sf_1	1444	Bifidobacteriaceae genomosp. C1
Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	sf_1	1835	*Bifidobacterium breve* str. KB 92
Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	sf_1	1875	
Actinobacteria	Actinobacteria	Actinomycetales	Cellulomonadaceae	sf_1	1586	*Cellulomonas gelida* str. DSM 20111T
Actinobacteria	Actinobacteria	Actinomycetales	Cellulomonadaceae	sf_1	1748	*Beutenbergia cavernosa* str. DSM 12333
Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	sf_1	1258	ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A-MN25
Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	sf_1	1800	ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A-MN100
Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	sf_1	1958	Atopobium vaginae VA14183_00
Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	sf_1	1517	*Corynebacterium xerosis* str. DSM 20743
Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	sf_1	1492	*Corynebacterium tuscaniae* str. ISS-5309
Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	sf_1	1820	*Corynebacterium jeikeium* str. ATCC 43734
Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	sf_1	1089	*Corynebacterium mucifaciens* National Microbiology Laboratory Special identifier 01-0118
Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	sf_1	1374	
Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	sf_1	1428	*Corynebacterium simulans* National Microbiology Laboratory Special identifier 00-0186
Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	sf_1	1493	*Corynebacterium tuberculostearicum* str. CIP102346
Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	sf_1	1803	*Corynebacterium spheniscorum* str. CCUG 45512
Actinobacteria	Actinobacteria	Actinomycetales	Dermabacteraceae	sf_1	2053	*Brachybacterium nesterenkovii* str. DSM 9573
Actinobacteria	Actinobacteria	Actinomycetales	Kineosporiaceae	sf_1	1598	lichen-dominated Antarctic cryptoendolithic community clone FBP402
Actinobacteria	Actinobacteria	Actinomycetales	Kineosporiaceae	sf_1	1961	*Kineococcus aurantiacus* str. IFO 15268
Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	sf_1	1667	*Microbacterium lacticum*
Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	sf_1	1197	Arctic sea ice ARK10173
Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	sf_1	1437	freshwater clone SV1-16
Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	sf_1	1266	*Arthrobacter psychrolactophilus*
Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	sf_1	1557	*Arthrobacter oxydans* str. DSM 20119
Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	sf_1	1593	*Arthrobacter globiformis*
Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	sf_1	1610	*Arthrobacter* sp str. AC-51
Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	sf_1	1966	TCE-contaminated site clone ccspost2208
Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	sf_1	1324	glacial ice isolate str. CanDirty1
Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	sf_1	1494	*Arthrobacter agilis* str. DSM 20550
Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	sf_1	1573	*Arthrobacter nicotianae* str. SB42
Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	sf_1	1889	*Citricoccus* sp. str. 2216.25.22
Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	sf_1	2019	*Micrococcus luteus* str. HN2-11
Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	sf_1	1724	*Rothia mucilaginosa* str. DSM
Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	sf_1	2020	*Rothia dentocariosa* str. ChDC B200
Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	sf_1	2063	*Rothia dentocariosa* str. ATCC 17931
Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	sf_1	1213	*Kocuria roseus*
Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	sf_1	1876	*Couchioplanes* subsp. caeruleus str. IFO13939

(*continued*)

Table 3. (Continued)

Phylum	*Class*	*Order*	*Family*	*S-F*[a]	*Taxon ID*[b]	*Representative species*[c]
Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	sf_1	1175	*Mycobacterium* cf. xenopi 'Hymi_Wue Tb_939/99' str. Hymi_Wue Tb_939/99
Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	sf_1	1262	*Mycobacterium holsaticum* str. 1406
Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	sf_1	1308	*Mycobacterium pyrenivorans* str. DSM 44605
Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	sf_1	1365	*Mycobacterium chelonae* str. CIP 104535T
Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	sf_1	1650	*Mycobacterium tuberculosis* str. NCTC 7416 H37Rv
Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	sf_1	1726	*Mycobacterium terrae* str. ATCC 15755
Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	sf_1	1834	*Nocardia transvalensis* str. DSM 43405
Actinobacteria	Actinobacteria	Actinomycetales	Nocardiopsaceae	sf_1	1385	*Streptomonospora salina* str. YIM90002
Actinobacteria	Actinobacteria	Actinomycetales	Promicromonosporaceae	sf_1	1671	*Cellulosimicrobium cellulans* str. NCIMB 11025
Actinobacteria	Actinobacteria	Actinomycetales	Promicromonosporaceae	sf_1	1711	*Promicromonospora sukumoe* str. DSM 44121
Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	sf_1	1863	
Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	sf_1	1343	*Saccharomonospora azurea* str. M.Goodfel K161 = NA128 (type st
Actinobacteria	Actinobacteria	Rubrobacterales	Rubrobacteraceae	sf_1	1551	soil isolate Ellin301
Actinobacteria	Actinobacteria	Rubrobacterales	Rubrobacteraceae	sf_1	1739	
Actinobacteria	Actinobacteria	Rubrobacterales	Rubrobacteraceae	sf_1	1843	uranium mining waste pile soil sample clone JG30-KF-A23
Actinobacteria	Actinobacteria	Actinomycetales	Sporichthyaceae	sf_1	1695	lichen-dominated Antarctic cryptoendolithic community clone FBP417
Actinobacteria	Actinobacteria	Actinomycetales	Streptosporangiaceae	sf_1	1190	*Nonomuraea polychroma* str. IFO 14345
Actinobacteria	Actinobacteria	Actinomycetales	Thermomonosporaceae	sf_1	1741	*Actinomadura pelletieri* str. IMSNU 22169T
Actinobacteria	Actinobacteria	Actinomycetales	Thermomonosporaceae	sf_1	1546	*Actinomadura fulvescens* str. DSM 43923T
Actinobacteria	Actinobacteria	Unclassified	Unclassified	sf_2	1233	
Actinobacteria	Actinobacteria	Unclassified	Unclassified	sf_1	1898	termite gut homogenate clone Rs-J10 bacterium
Actinobacteria	Actinobacteria	Unclassified	Unclassified	sf_1	1367	
Actinobacteria	Actinobacteria	Unclassified	Unclassified	sf_1	1370	forested wetland clone RCP1-37
Actinobacteria	Actinobacteria	Acidimicrobiales	Unclassified	sf_1	1666	
Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	sf_4	1337	Sturt arid-zone soil clone #0425-2M17
Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	sf_3	1486	deep marine sediment clone MB-A2-108
Actinobacteria	Actinobacteria	Unclassified	Unclassified	sf_1	1676	
Actinobacteria	Actinobacteria	Acidimicrobiales	Unclassified	sf_1	1217	DCP-dechlorinating consortium clone SHA-34
Actinobacteria	BD2-10 group	Unclassified	Unclassified	sf_2	1652	marine sediment clone Bol7
Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	sf_3	2045	hypersaline lake clone ML602J-44
Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	sf_3	1130	*Georgenia muralis* str. 1A-C
Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	sf_3	1687	*Jonesia quinghaiensis* str. DSM 15701
Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	sf_3	1243	termite gut homogenate clone Rs-M95 bacterium
Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	sf_3	1577	termite gut homogenate clone Rs-N91 bacterium
Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	sf_3	1405	*Arthrobacter ureafaciens* str. DSM 20126
AD3	Unclassified	Unclassified	Unclassified	sf_1	2338	uranium mining waste pile soil clone JG30-KF-C12
Bacteroidetes	Bacteroidetes	Bacteroidales	Bacteroidaceae	sf_12	5256	termite gut homogenate clone Rs-D38 bacterium
Bacteroidetes	Bacteroidetes	Bacteroidales	Bacteroidaceae	sf_12	5320	*Bacteroides distasonis*
Bacteroidetes	Bacteroidetes	Bacteroidales	Bacteroidaceae	sf_12	5474	*Bacteroides acidofaciens* str.A24

Bacteroidetes	Bacteroidetes	Bacteroidales	Bacteroidaceae	sf_12	5551	*Bacteroides uniformis*
Bacteroidetes	Bacteroidetes	Bacteroidales	Bacteroidaceae	sf_12	5979	*Bacteroides fragilis* str. YCH46
Bacteroidetes	Flavobacteria	Flavobacteriales	Blattabacteriaceae	sf_1	5828	*Blattabacterium* species
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Crenotrichaceae	sf_11	5334	autotrophic nitrifying biofilm clone NB-11
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Crenotrichaceae	sf_11	5619	anaerobic VC-degrading enrichment clone VC10 bacterium
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Crenotrichaceae	sf_11	5888	penguin droppings sediments clone KD9-169
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Crenotrichaceae	sf_11	6123	*Flexibacter japonensis* str. IFO 16041
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Crenotrichaceae	sf_11	6267	Cilia-respiratory isolate str. 243-54
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Crenotrichaceae	sf_11	6249	*Haliscomenobacter hydrossis*
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flammeovirgaceae	sf_5	6084	*Microscilla arenaria* str. IFO 15982
Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	sf_1	6079	synonym: CFB group clone APe4_42
Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	sf_1	5367	patient's bronchoalveolar lavage isolate str. MDA2507 sp.
Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	sf_1	5915	groundwater deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A-MN27 bacterium
Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	sf_1	5997	*Flavobacterium aquatile*
Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	sf_1	6274	
Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	sf_1	5317	*Tenacibaculum maritimum* str. IFO 15946
Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	sf_1	5991	*Tenacibaculum ovolyticum* str. IAM14318
Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	sf_1	6252	Riftia pachyptila's tube clone R103-B20
Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	sf_1	5263	subgingival plaque clone DZ074
Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	sf_1	5401	*Capnocytophaga gingivalis* str. ChDC OS45
Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	sf_1	5836	*Capnocytophaga granulosa* str. LMG 12119; FDC SD4
Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	sf_1	5423	*Aequorivita antarctica* str. QSSC9-14
Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	sf_1	5942	
Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	sf_1	5955	*Flavobacterium* sp. str. V4.MS.29 = MM_2747
Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	sf_1	5971	*Cytophaga uliginosa*
Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	sf_1	5436	Arctic sea ice ARK10004
Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	sf_1	5473	
Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	sf_1	5267	bacterioplankton clone AEGEAN_179
Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	sf_1	5914	*Psychroserpens burtonensis* str. S2-64
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	sf_19	5563	*Cytophaga* sp. I-545
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	sf_19	5542	*Cytophaga* sp. I-1787
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	sf_19	5307	*Microscilla sericea* str. IFO 16561
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	sf_19	5357	*Flexibacter ruber* str. IFO 16677
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	sf_19	5372	
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	sf_19	5566	*Hongiella mannitolivorans* str. IMSNU 14012 JC2050
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	sf_19	5667	penguin droppings sediments clone KD6-118
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	sf_19	5994	*Hymenobacter* sp. str. NS/50
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	sf_19	6124	*Flexibacter flexilis* subsp. pelliculosus str. IFO 16028 subsp.
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	sf_19	6297	EBPR sludge lab scale clone HP1A92
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	sf_20	10311	*Cytophaga* sp. str. BHI60-57B
Bacteroidetes	Bacteroidetes	Bacteroidales	Porphyromonadaceae	sf_1	5295	swine intestine clone p-987-s962-5
Bacteroidetes	Bacteroidetes	Bacteroidales	Porphyromonadaceae	sf_1	5680	termite gut clone Rs-106

(*continued*)

Table 3. (Continued)

Phylum	*Class*	*Order*	*Family*	*S-F*[a]	*Taxon ID*[b]	*Representative species*[c]
Bacteroidetes	Bacteroidetes	Bacteroidales	Porphyromonadaceae	sf_1	5800	*Porphyromonas endodontalis* str. ATCC 35406
Bacteroidetes	Bacteroidetes	Bacteroidales	Porphyromonadaceae	sf_1	5817	termite gut homogenate clone Rs-N56 bacterium
Bacteroidetes	Bacteroidetes	Bacteroidales	Porphyromonadaceae	sf_1	5961	chlorobenzene-degrading consortium clone IA-16
Bacteroidetes	Bacteroidetes	Bacteroidales	Porphyromonadaceae	sf_1	5454	*Dysgonomonas wimpennyi* str. ANFA2
Bacteroidetes	Bacteroidetes	Bacteroidales	Porphyromonadaceae	sf_1	5510	sphagnum peat bog clone 26-4b2
Bacteroidetes	Bacteroidetes	Bacteroidales	Porphyromonadaceae	sf_1	6012	mouse feces clone L11-6
Bacteroidetes	Bacteroidetes	Bacteroidales	Porphyromonadaceae	sf_1	5460	mouse feces clone F8
Bacteroidetes	Bacteroidetes	Bacteroidales	Prevotellaceae	sf_1	5718	*Prevotella tannerae* str. 29-1
Bacteroidetes	Bacteroidetes	Bacteroidales	Prevotellaceae	sf_1	5437	cow rumen clone BE1
Bacteroidetes	Bacteroidetes	Bacteroidales	Prevotellaceae	sf_1	5916	cow rumen clone BE14
Bacteroidetes	Bacteroidetes	Bacteroidales	Prevotellaceae	sf_1	6011	rumen clone F24-B03
Bacteroidetes	Bacteroidetes	Bacteroidales	Prevotellaceae	sf_1	6152	rumen clone RF37
Bacteroidetes	Bacteroidetes	Bacteroidales	Prevotellaceae	sf_1	6259	
Bacteroidetes	Bacteroidetes	Bacteroidales	Prevotellaceae	sf_1	5249	*Prevotella denticola* str. ATCC 35308
Bacteroidetes	Bacteroidetes	Bacteroidales	Prevotellaceae	sf_1	5484	oral periodontitis clone FX046
Bacteroidetes	Bacteroidetes	Bacteroidales	Prevotellaceae	sf_1	5706	oral cavity clone 3.3
Bacteroidetes	Bacteroidetes	Bacteroidales	Prevotellaceae	sf_1	5769	*Bacteroidaceae* str. A42
Bacteroidetes	Bacteroidetes	Bacteroidales	Prevotellaceae	sf_1	5905	swine intestine clone p-2443-18B5
Bacteroidetes	Bacteroidetes	Bacteroidales	Prevotellaceae	sf_1	5940	*Prevotella* sp. str. E7_34
Bacteroidetes	Bacteroidetes	Bacteroidales	Prevotellaceae	sf_1	5946	tongue dorsa clone DO027
Bacteroidetes	Bacteroidetes	Bacteroidales	Prevotellaceae	sf_1	6047	deep marine sediment clone MB-A2-107
Bacteroidetes	Bacteroidetes	Bacteroidales	Prevotellaceae	sf_1	6239	tongue dorsa clone DO033
Bacteroidetes	Bacteroidetes	Bacteroidales	Rikenellaceae	sf_5	5892	anoxic bulk soil flooded rice microcosm clone BSV73
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	sf_1	5513	crevicular epithelial cells clone AZ123
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	sf_1	5913	*Sphingobacteriaceae* str. Ellin160
Bacteroidetes	Bacteroidetes	Bacteroidales	Unclassified	sf_15	5573	termite gut homogenate clone Rs-D44 bacterium
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Unclassified	sf_6	5439	Mono Lake at depth 35 m station 6 July 2000 clone ML635J-40 bacterium
Bacteroidetes	Bacteroidetes	Bacteroidales	Unclassified	sf_15	5475	SHA-25 clone
Bacteroidetes	Bacteroidetes	Bacteroidales	Unclassified	sf_15	5544	marine? clone KD3-17
Bacteroidetes	Bacteroidetes	Bacteroidales	Unclassified	sf_15	5783	Mono Lake at depth 35 m station 6 July 2000 clone ML635J-15 bacterium
Bacteroidetes	Bacteroidetes	Bacteroidales	Unclassified	sf_15	5874	*Paralvinella palmiformis* mucus secretions clone P. palm 53 bacterium
Bacteroidetes	Bacteroidetes	Bacteroidales	Unclassified	sf_15	5890	penguin droppings sediments clone KD1-125
Bacteroidetes	Bacteroidetes	Bacteroidales	Unclassified	sf_15	6046	chlorobenzene-degrading consortium clone IIIB-1
Bacteroidetes	Bacteroidetes	Bacteroidales	Unclassified	sf_15	5820	cow rumen clone BF24
Bacteroidetes	Unclassified	Unclassified	Unclassified	sf_1	5745	
Bacteroidetes	Flavobacteria	Flavobacteriales	Unclassified	sf_3	5248	Delaware River estuary clone 1G12
Bacteroidetes	Bacteroidetes	Bacteroidales	Unclassified	sf_15	5355	DCP-dechlorinating consortium clone SHA-5
Bacteroidetes	Bacteroidetes	Bacteroidales	Unclassified	sf_15	5481	marine sediment above hydrate ridge clone Hyd89-72 bacterium

Bacteroidetes	Unclassified	Unclassified	Unclassified	sf_4	5703	
Bacteroidetes	Unclassified	Unclassified	Unclassified	sf_4	5785	Mono Lake at depth 35 m station 6 July 2000 clone ML635J-56
Bacteroidetes	Unclassified	Unclassified	Unclassified	sf_4	5787	Mono Lake at depth 35 m station 6 July 2000 clone ML635J-1 bacterium
Bacteroidetes	Bacteroidetes	Bacteroidales	Unclassified	sf_15	5957	*Paralvinella palmiformis* mucus secretions clone P. palm C/20 bacterium
Bacteroidetes	Bacteroidetes	Bacteroidales	Unclassified	sf_15	6324	temperate estuarine mud clone KM02
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Unclassified	sf_3	6168	Toolik Lake main station at 3 m depth clone TLM11/TLMdgge04
Bacteroidetes	KSA1	Unclassified	Unclassified	sf_1	5951	CFB group clone ML615J-4
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Unclassified	sf_3	6298	travertine hot spring clone SM1C04
BRC1	Unclassified	Unclassified	Unclassified	sf_2	118	penguin droppings sediments clone KD1-1
BRC1	Unclassified	Unclassified	Unclassified	sf_1	5051	soil clone PBS-III-24
BRC1	Unclassified	Unclassified	Unclassified	sf_1	5143	soil clone PBS-II-1
Caldithrix	Unclassified	Caldithrales	Caldithraceae	sf_2	91	benzoate-degrading consortium clone BA059
Caldithrix	Unclassified	Caldithrales	Caldithraceae	sf_1	2384	saltmarsh clone LCP-89
Chlamydiae	Chlamydiae	Chlamydiales	Chlamydiaceae	sf_1	4820	*Chlamydophila pneumoniae* str. AR39
Chlamydiae	Chlamydiae	Chlamydiales	Parachlamydiaceae	sf_1	4964	neutral pH mine biofilm clone 44a-B1-34
Chlorobi	Chlorobia	Chlorobiales	Chlorobiaceae	sf_1	262	*Chlorobium ferrooxidans* DSM 13031 str. KofoX
Chlorobi	Chlorobia	Chlorobiales	Chlorobiaceae	sf_1	859	*Chlorobium phaeovibrioides* str. 2631
Chlorobi	Chlorobia	Chlorobiales	Chlorobiaceae	sf_1	995	*Chlorobium limicola* str. M1
Chlorobi	Unclassified	Unclassified	Unclassified	sf_8	5822	Saltmarsh mud clone K-790
Chlorobi	Unclassified	Unclassified	Unclassified	sf_6	5294	Mammoth cave clone CCM9b
Chlorobi	Unclassified	Unclassified	Unclassified	sf_9	6146	sludge clone A12b
Chlorobi	Unclassified	Unclassified	Unclassified	sf_8	549	benzene-degrading nitrate-reducing consortium clone Cart-N2 bacterium
Chlorobi	Unclassified	Unclassified	Unclassified	sf_8	636	benzene-degrading nitrate-reducing consortium clone Cart-N3 bacterium
Chloroflexi	Thermomicrobia	Unclassified	Unclassified	sf_1	1041	Antarctic cryptoendolith clone FBP471
Chloroflexi	Unclassified	Unclassified	Unclassified	sf_2	818	
Chloroflexi	Unclassified	Unclassified	Unclassified	sf_5	1051	forest soil clone DUNssu055 (-2B) (OTU#087)
Chloroflexi	Anaerolineae	Chloroflexi-1a	Unclassified	sf_1	927	Paralvinella palmiformis mucus secretions clone P. palm C 37 bacterium
Chloroflexi	Thermomicrobia	Unclassified	Unclassified	sf_2	652	uranium mining waste pile soil sample clone JG30-KF-CM45
Chloroflexi	Anaerolineae	Chloroflexi-1a	Unclassified	sf_1	106	DCP-dechlorinating consortium clone SHD-231
Chloroflexi	Anaerolineae	Unclassified	Unclassified	sf_9	375	forest soil clone C043
Chloroflexi	Anaerolineae	Chloroflexi-1a	Unclassified	sf_1	487	thermophilic UASB granular sludge isolate str. IMO-1 bacterium
Chloroflexi	Anaerolineae	Unclassified	Unclassified	sf_9	576	DCP-dechlorinating consortium clone SHA-36
Chloroflexi	Anaerolineae	Chloroflexi-1a	Unclassified	sf_1	583	anaerobic bioreactor clone SHD-238
Chloroflexi	Anaerolineae	Unclassified	Unclassified	sf_9	72	sediments collected at Charon's Cascade near Echo River October 2000 clone CCD21
Chloroflexi	Anaerolineae	Unclassified	Unclassified	sf_9	727	forest soil clone S0208
Chloroflexi	Unclassified	Unclassified	Unclassified	sf_7	757	DCP-dechlorinating consortium clone SHA-8
Chloroflexi	Anaerolineae	Chloroflexi-1a	Unclassified	sf_1	76	DCP-dechlorinating consortium clone SHA-147
Chloroflexi	Anaerolineae	Chloroflexi-1b	Unclassified	sf_2	789	travertine hot spring clone SM1D10
Chloroflexi	Anaerolineae	Unclassified	Unclassified	sf_9	946	temperate estuarine mud clone KM87

(*continued*)

TABLE 3. (CONTINUED)

Phylum	*Class*	*Order*	*Family*	*S-F*[a]	*Taxon ID*[b]	*Representative species*[c]
Chloroflexi	Dehalococcoidetes	Unclassified	Unclassified	sf_1	2339	uranium mill tailings soil sample clone Sh765B-TzT-20 bacterium
Chloroflexi	Dehalococcoidetes	Unclassified	Unclassified	sf_1	2367	deep marine sediment clone MB-B2-113
Chloroflexi	Dehalococcoidetes	Unclassified	Unclassified	sf_1	2438	deep marine sediment clone MB-A2-110
Chloroflexi	Dehalococcoidetes	Unclassified	Unclassified	sf_1	2445	deep marine sediment clone MB-A2-103
Chloroflexi	Dehalococcoidetes	Unclassified	Unclassified	sf_1	2485	
Chloroflexi	Dehalococcoidetes	Unclassified	Unclassified	sf_1	2497	forested wetland clone FW60
Chloroflexi	Unclassified	Unclassified	Unclassified	sf_12	2523	sponge clone TK10
Chloroflexi	Chloroflexi-4	Unclassified	Unclassified	sf_2	2344	forest soil clone C083
Chloroflexi	Unclassified	Unclassified	Unclassified	sf_1	2534	forest soil clone S085
Coprothermobacteria	Unclassified	Unclassified	Unclassified	sf_1	751	Coprothermobacter sp. str. Dex80-3
Cyanobacteria	Cyanobacteria	Chloroplasts	Chloroplasts	sf_5	4967	Toolik Lake main station at 3 m depth clone TLM14
Cyanobacteria	Cyanobacteria	Chloroplasts	Chloroplasts	sf_5	5147	*Emiliania huxleyi* str. Plymouth Marine Laborator PML 92
Cyanobacteria	Cyanobacteria	Chloroplasts	Chloroplasts	sf_5	5112	*Cyanidium caldarium* str. 14-1-1
Cyanobacteria	Cyanobacteria	Chloroplasts	Chloroplasts	sf_5	5006	
Cyanobacteria	Cyanobacteria	Chloroplasts	Chloroplasts	sf_11	5098	*Euglena tripteris* str. UW OB
Cyanobacteria	Cyanobacteria	Chloroplasts	Chloroplasts	sf_11	5123	*Lepocinclis fusiformis* str. ACOI 1025
Cyanobacteria	Cyanobacteria	Chloroplasts	Chloroplasts	sf_5	4966	*Adiantum pedatum*
Cyanobacteria	Cyanobacteria	Chloroplasts	Chloroplasts	sf_5	4976	*Calypogeia muelleriana*
Cyanobacteria	Cyanobacteria	Chloroplasts	Chloroplasts	sf_13	5000	*Mitrastema yamamotoi*
Cyanobacteria	Cyanobacteria	Chloroplasts	Chloroplasts	sf_5	5040	*Solanum nigrum*
Cyanobacteria	Cyanobacteria	Chloroplasts	Chloroplasts	sf_5	5182	*Epifagus virginiana*—chloroplast
Cyanobacteria	Cyanobacteria	Chloroplasts	Chloroplasts	sf_5	5183	*Pisum sativum*—chloroplast
Cyanobacteria	Cyanobacteria	Chloroplasts	Chloroplasts	sf_5	5192	*Cycas revoluta*
Cyanobacteria	Unclassified	Unclassified	Unclassified	sf_5	4998	
Cyanobacteria	Cyanobacteria	Thermosynechococcus	Unclassified	sf_1	5012	*Synechococcus* sp. str. PCC 6312
Cyanobacteria	Unclassified	Unclassified	Unclassified	sf_9	5038	Rumen isolate str. YS2
Cyanobacteria	Unclassified	Unclassified	Unclassified	sf_9	5164	termite gut homogenate clone Rs-H34
Cyanobacteria	Cyanobacteria	Oscillatoriales	Unclassified	sf_1	5189	*Oscillatoria sancta* str. PCC 7515
Cyanobacteria	Unclassified	Unclassified	Unclassified	sf_5	5015	*Chlorogloeopsis fritschii* str. PCC 6912
Cyanobacteria	Unclassified	Unclassified	Unclassified	sf_5	5030	*Hapalosiphon welwitschii*
Cyanobacteria	Cyanobacteria	Nostocales	Unclassified	sf_1	5057	*Nodularia sphaerocarpa* str. UTEX B 2093
Cyanobacteria	Cyanobacteria	Oscillatoriales	Unclassified	sf_1	5049	*Oscillatoria spongeliae* str. 520 bg
Cyanobacteria	Cyanobacteria	Plectonema	Unclassified	sf_1	5190	*Plectonema* sp. str. F3
Cyanobacteria	Unclassified	Unclassified	Unclassified	sf_8	5206	
Deinococcus-Thermus	Unclassified	Unclassified	Unclassified	sf_1	178	*Thermus* sp. str. C4
Deinococcus-Thermus	Unclassified	Unclassified	Unclassified	sf_1	563	*Vulcanithermus mediatlanticus* str. TR
Deinococcus-Thermus	Unclassified	Unclassified	Unclassified	sf_2	637	hypersaline pond clone LA7-B27N
Deinococcus-Thermus	Unclassified	Unclassified	Unclassified	sf_3	920	
DSS1	Unclassified	Unclassified	Unclassified	sf_2	38	DCP-dechlorinating consortium clone SHA-109
DSS1	Unclassified	Unclassified	Unclassified	sf_1	4405	benzoate-degrading consortium clone BA143
Firmicutes	Mollicutes	Acholeplasmatales	Acholeplasmataceae	sf_1	3955	Weeping tea tree witches’ broom phytoplasma tree

Firmicutes	Mollicutes	Acholeplasmatales	Acholeplasmataceae	sf_1	3961	Clover yellow edge mycoplasma-like organism
Firmicutes	Mollicutes	Acholeplasmatales	Acholeplasmataceae	sf_1	3975	Black raspberry witches' broom phytoplasma str. BRWB witches' broom room
Firmicutes	Mollicutes	Acholeplasmatales	Acholeplasmataceae	sf_1	3976	
Firmicutes	Mollicutes	Acholeplasmatales	Acholeplasmataceae	sf_1	4044	
Firmicutes	Mollicutes	Acholeplasmatales	Acholeplasmataceae	sf_1	4045	Chinaberry yellows phytoplasma
Firmicutes	Mollicutes	Acholeplasmatales	Acholeplasmataceae	sf_1	4046	Pigeon pea witches' broom mycoplasma-like organism
Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	sf_1	3386	feedlot manure clone B87
Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	sf_1	3522	*Aerococcus viridans*
Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	sf_1	3631	*Abiotrophia defectiva* str. GIFU12707 (ATCC49176)
Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	sf_1	3870	*Abiotrophia para-adiacens* str. TKT1
Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	sf_1	3323	*Trichococcus flocculiformis* str. DSM 2094
Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	sf_1	3326	Nostocoida limicola I str. Ben206
Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	sf_1	3504	*Marinilactibacillus psychrotolerans* str. O21
Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	sf_1	3553	*Desemzia incerta* str. DSM 20581
Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	sf_1	3833	*Carnobacterium alterfunditum*
Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	sf_1	3840	*Trichococcus pasteurii* str. KoTa2
Firmicutes	Bacilli	Bacillales	Alicyclobacillaceae	sf_1	3368	geothermal site isolate str. G1
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3612	*Bacillus schlegelii* str. ATCC 43741T
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3419	*Bacillus algicola* str. KMM 3737
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3424	uranium mill tailings clone Gitt-KF-76
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3661	*Bacillus* sp. str. 2216.25.2
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3688	*Bacillus* sp. str. SAFN-006
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3926	Lake Bogoria isolate 64B4
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	234	*Bacillus vulcani* str. 3S-1
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	283	*Geobacillus thermocatenulatus* str. DSM 730
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	305	*Bacillus thermoleovorans*
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3460	*Geobacillus jurassicus* str. DS1
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3540	*Geobacillus thermoleovorans* str. B23
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3763	*Geobacillus stearothermophilus*
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3836	*Geobacillus stearothermophilus* str. 46
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	385	*Geobacillus stearothermophilus* str. T10
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	462	*Geobacillus thermodenitrificans* str. DSM 466
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	571	*Bacillus caldotenax* str. DSM 406
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	829	*Geobacillus* sp. str. YMTC1049
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3635	*Bacillus aeolius* str. 4-1
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3827	*Bacillus acidogenesis* str. 105-2
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3845	hot synthetic compost clone pPD15
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3895	*Bacillus sporothermodurans* str. M215
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3283	*Bacillus niacini* str. IFO15566
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3439	*Bacillus siralis* str. 171544
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3589	*Bacillus senegalensis* str. RS8; CIP 106 669
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3650	
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	1050	*Bacillus firmus* CV93b
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	246	*Bacillus* sp. 6160m-C1
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3550	*Bacillus megaterium* str. QM B1551

(*continued*)

TABLE 3. (CONTINUED)

Phylum	*Class*	*Order*	*Family*	*S-F*[a]	*Taxon ID*[b]	*Representative species*[c]
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3345	*Bacillus pumilus* str. S9
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3328	*Pseudobacillus carolinae*
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3370	*Bacillus* sp. str. TGS437
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3492	*Bacillus subtilis* str. IAM 12118T
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3579	*Bacillus* sp. str. TGS750
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3675	*Bacillus mojavensis* str. M-1
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3706	*Bacillus sonorensis* str. NRRL B-23155
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3831	*Bacillus licheniformis* str. KL-068
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3900	*Bacillus licheniformis* str. DSM 13
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3909	*Bacillus subtilis* subsp. Marburg str. 168
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3918	*Bacillus subtilis*
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3467	*Bacillus luciferensis* str. LMG 18422
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3489	*Bacillus silvestris* str. SAFN-010
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3482	garbage compost isolate str. M32
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3383	
Firmicutes	Bacilli	Bacillales	Bacillaceae	sf_1	3517	*Planococcus maritimus* str. TF-9
Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	sf_1	3536	
Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	sf_1	3792	*Carnobacterium* sp. str. D35
Firmicutes	Bacilli	Bacillales	Caryophanaceae	sf_1	3285	*Caryophanon latum* str. DSM 14151
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	2764	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	3021	*Clostridium caminithermale* str. DVird3
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	2915	*Tepidibacter thalassicus* str. SC 562
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	3049	*Clostridium paradoxum* str. DSM 7308T
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	3077	*Clostridium glycolicum* str. DSM 1288
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4156	MCB-contaminated groundwater-treating reactor clone RA9C1
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4173	termite gut homogenate clone Rs-D81 bacterium
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4187	*Clostridiales* oral clone P4PB_122 P3
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4278	granular sludge clone R1p16
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4297	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4300	termite gut clone Rs-060
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4310	termite gut clone Rs-056
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4364	oral endodontic infection clone MCE3_9
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4406	termite gut homogenate clone Rs-J39 bacterium
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4477	termite gut homogenate clone Rs-N85 bacterium
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4502	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4584	*Clostridium papyrosolvens* str. DSM 2782
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4614	*Clostridium* sp. str. JC3
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4622	termite gut clone Rs-L36
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4638	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4554	termite gut clone Rs-068
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4180	termite gut homogenate clone Rs-M23 bacterium
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4225	termite gut clone Rs-116
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4265	termite gut homogenate clone Rs-N70 bacterium
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4266	termite gut homogenate clone Rs-M86 bacterium

Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4272	termite gut homogenate clone Rs-M34 bacterium
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4321	termite gut homogenate clone Rs-C76 bacterium
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4357	Lachnospiraceae bacterium 19gly4
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4359	termite gut homogenate clone Rs-C69 bacterium
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4369	termite gut homogenate clone Rs-N73 bacterium
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4415	termite gut homogenate clone Rs-K32 bacterium
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4418	termite gut homogenate clone Rs-H18 bacterium
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4475	termite gut homogenate clone Rs-N02 bacterium
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4507	termite gut homogenate clone Rs-N21 bacterium
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4524	termite gut clone Rs-093
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4550	swine intestine clone p-320-a3
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4559	cow rumen clone BF30
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4566	swine intestine clone p-2657-65A5
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4582	swine intestine clone p-2600-9F5
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4627	termite gut homogenate clone Rs-A13 bacterium
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4306	UASB reactor granular sludge clone PD-UASB-4 bacterium
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4607	*Clostridium novyi* str. NCTC538
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4229	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4551	*Clostridium acetobutylicum* str. ATCC 824 (T)
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4339	*Clostridium chauvoei* str. ATCC 10092T
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4598	*Clostridium sardiniense* str. DSM 600
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	sf_12	4169	
Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	sf_1	3261	*Enterococcus mundtii* str. LMG 10748
Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	sf_1	3288	Isolation and identification hyper-ammonia producing swine storage pits manure
Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	sf_1	3298	*Enterococcus saccharolyticus* str. LMG 11427
Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	sf_1	3318	*Enterococcus ratti* str. ATCC 700914
Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	sf_1	3382	
Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	sf_1	3392	*Vagococcus lutrae* str. m1134/97/1; CCUG 39187
Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	sf_1	3433	*Tetragenococcus muriaticus*
Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	sf_1	3598	*Enterococcus solitarius* str. DSM 5634
Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	sf_1	3680	*Melissococcus plutonius* str. NCDO 2440
Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	sf_1	3713	*Enterococcus cecorum* str. ATCC43198
Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	sf_1	3881	Enterococcus dispar str. LMG 13521
Firmicutes	Mollicutes	Entomoplasmatales	Entomoplasmataceae	sf_1	4074	swine intestine clone p-2013-s959-5
Firmicutes	Mollicutes	Anaeroplasmatales	Erysipelotrichaceae	sf_3	3952	*Erysipelothrix rhusiopathiae* str. Pecs 56
Firmicutes	Mollicutes	Anaeroplasmatales	Erysipelotrichaceae	sf_3	3965	TCE-contaminated site clone ccslm238
Firmicutes	Mollicutes	Anaeroplasmatales	Erysipelotrichaceae	sf_3	3981	phototrophic sludge clone PSB-M-3
Firmicutes	Mollicutes	Anaeroplasmatales	Erysipelotrichaceae	sf_3	768	
Firmicutes	Clostridia	Clostridiales	Eubacteriaceae	sf_1	28	termite gut homogenate clone Rs-H81 bacterium
Firmicutes	Bacilli	Bacillales	Halobacillaceae	sf_1	3633	*Bacillus clausii* str. GMBAE 42
Firmicutes	Bacilli	Bacillales	Halobacillaceae	sf_1	3344	*Halobacillus yeomjeoni* str. MSS-402
Firmicutes	Bacilli	Bacillales	Halobacillaceae	sf_1	3488	*Halobacillus salinus* str. HSL-3
Firmicutes	Bacilli	Bacillales	Halobacillaceae	sf_1	3702	*Amphibacillus xylanus* str. DSM 6626
Firmicutes	Bacilli	Bacillales	Halobacillaceae	sf_1	3756	*Salibacillus* sp. str. YIM-kkny16
Firmicutes	Bacilli	Bacillales	Halobacillaceae	sf_1	3769	*Gracilibacillus* sp. str. YIM-kkny13
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	2698	termite gut homogenate clone Rs-B88 bacterium
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	2804	*Clostridium amygdalinum* str. BR-10

(*continued*)

TABLE 3. (CONTINUED)

Phylum	*Class*	*Order*	*Family*	*S-F*[a]	*Taxon ID*[b]	*Representative species*[c]
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	2961	termite gut homogenate clone Rs-F92 bacterium
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	3042	swine intestine clone p-2876-6C5
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	3036	termite gut homogenate clone Rs-F27 bacterium
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	2668	termite gut homogenate clone Rs-G40 bacterium
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	3017	termite gut homogenate clone Rs-D48 bacterium
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	3076	*Clostridium nexile*
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	2825	*Butyrivibrio fibrisolvens* str. LP1265
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	2834	*Butyrivibrio fibrisolvens* str. OB156
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	2844	*Pseudobutyrivibrio ruminis* str. pC-XS2
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	3059	*Butyrivibrio fibrisolvens* str. NCDO 2249
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	2994	termite gut clone Rs-L15
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	3038	swine intestine clone p-1594-c5
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	3171	*Lachnospira pectinoschiza*
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	2931	termite gut homogenate clone Rs-G77 bacterium
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	3060	termite gut homogenate clone Rs-B14 bacterium
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	3218	termite gut homogenate clone Rs-N53
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	2681	termite gut homogenate clone Rs-K41 bacterium
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	4212	termite gut clone Rs-061
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	4273	termite gut homogenate clone Rs-M14 bacterium
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	4281	granular sludge clone UASB_brew_B86
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	4315	termite gut homogenate clone Rs-N94 bacterium
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	4331	granular sludge clone UASB_brew_B84
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	4335	termite gut homogenate clone Rs-N86 bacterium
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	4434	termite gut homogenate clone Rs-K11 bacterium
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	4510	termite gut homogenate clone Rs-Q53 bacterium
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	4511	ckncm314-B7-17 clone
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	4512	granular sludge clone UASB_brew_B25
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	4514	termite gut homogenate clone Rs-B34 bacterium
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	4533	termite gut homogenate clone Rs-N06 bacterium
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	4535	ckncm297-B1-1 clone
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	4539	termite gut homogenate clone Rs-C61 bacterium
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	4540	termite gut homogenate clone Rs-M18 bacterium
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	4567	human colonic clone HuCB5
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	4571	*Faecalibacterium prausnitzii* str. ATCC 27766
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	4613	rumen clone 3C0d-3
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	4623	human colonic clone HuCA1
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	sf_5	4525	termite gut homogenate clone Rs-Q18 bacterium
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	sf_1	3330	*Lactobacillus kitasatonis* str. KM9212
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	sf_1	3342	*Lactobacillus crispatus* str. DSM 20584 T
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	sf_1	3478	*Lactobacillus crispatus* str. ATCC33197
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	sf_1	3490	*Lactobacillus suntoryeus* str. LH
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	sf_1	3618	*Lactobacillus jensenii* str. KC36b
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	sf_1	3696	*Lactobacillus kalixensis* str. Kx127A2; LMG 22115T; DSM 16043T; CCUG 48459T
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	sf_1	3395	*Lactobacillus reuteri* str. DSM 20016 T

Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	sf_1	3547	*Lactobacillus frumenti* str. TMW 1.666
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	sf_1	3566	*Lactobacillus pontis* str. LTH 2587
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	sf_1	3798	*Lactobacillus fermentum* str. MD-9
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	sf_1	3521	*Pediococcus inopinatus* str. DSM 20285
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	sf_1	3885	*Pediococcus pentosaceus*
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	sf_1	3634	*Lactobacillus letivazi* str. JCL3994
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	sf_1	3767	*Lactobacillus suebicus* str. CECT 5917T
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	sf_1	3810	*Lactobacillus brevis*
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	sf_1	3829	*Lactobacillus paralimentarius* str. DSM 13238
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	sf_1	3366	*Lactobacillus saerimneri* str. GDA154 LMG 22087 DSM 16049 (T); CCUG 48462 (T)
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	sf_1	3418	*Lactobacillus* subsp. aviarius
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	sf_1	3703	*Lactobacillus salivarius* str. RA2115
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	sf_1	3914	*Lactobacillus cypricasei* str. LMK3
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	sf_1	3821	*Lactobacillus casei*
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	sf_1	3768	*Lactobacillus perolens* str. L532
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	sf_1	3526	*Lactobacillus sakei*
Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae	sf_1	3497	*Weissella koreensis* S-5673
Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae	sf_1	3573	*Leuconostoc ficulneum* str. FS-1
Firmicutes	Mollicutes	Mycoplasmatales	Mycoplasmataceae	sf_1	3929	*Mycoplasma gypsbengalensis* str. Gb-V33
Firmicutes	Mollicutes	Mycoplasmatales	Mycoplasmataceae	sf_1	3997	*Mycoplasma salivarium* str. PG20(T)
Firmicutes	Mollicutes	Mycoplasmatales	Mycoplasmataceae	sf_1	4014	*Mycoplasma pulmonis* str. UAB CTIP
Firmicutes	Bacilli	Bacillales	Paenibacillaceae	sf_1	3415	*Paenibacillus nematophilus* str. NEM1b
Firmicutes	Bacilli	Bacillales	Paenibacillaceae	sf_1	3630	
Firmicutes	Bacilli	Bacillales	Paenibacillaceae	sf_1	3595	*Paenibacillus* sp. str. MB 2039
Firmicutes	Bacilli	Bacillales	Paenibacillaceae	sf_1	3299	*Brevibacillus borstelensis* str. LMG 15536
Firmicutes	Bacilli	Bacillales	Paenibacillaceae	sf_1	3641	*Brevibacillus* sp. MN 47.2a
Firmicutes	Bacilli	Bacillales	Paenibacillaceae	sf_1	319	*Ammoniphilus oxalaticus* str. RAOx-FF
Firmicutes	Bacilli	Bacillales	Paenibacillaceae	sf_1	625	*Ammoniphilus oxalivorans* str. RAOx-FS
Firmicutes	Clostridia	Clostridiales	Peptococc/ Acidaminococc	sf_11	304	*Selenomonas ruminantium* str.JCM6582
Firmicutes	Clostridia	Clostridiales	Peptococc/ Acidaminococc	sf_11	709	*Selenomonas ruminantium* str.S20
Firmicutes	Clostridia	Clostridiales	Peptococc/ Acidaminococc	sf_11	710	*Centipeda periodontii* str. HB-2
Firmicutes	Clostridia	Clostridiales	Peptococc/ Acidaminococc	sf_11	131	pig feces clone
Firmicutes	Clostridia	Clostridiales	Peptococc/ Acidaminococc	sf_11	181	*Allisonella histaminiformans* str. MR2
Firmicutes	Clostridia	Clostridiales	Peptococc/ Acidaminococc	sf_11	59	swine intestine clone p-1941-s962-3
Firmicutes	Clostridia	Clostridiales	Peptococc/ Acidaminococc	sf_11	940	*Veillonella dispar* str. DSM 20735
Firmicutes	Clostridia	Clostridiales	Peptococc/ Acidaminococc	sf_11	1036	Great Artesian Basin clone G07
Firmicutes	Clostridia	Clostridiales	Peptococc/ Acidaminococc	sf_11	428	chlorobenzene-degrading consortium clone IIIA-1
Firmicutes	Clostridia	Clostridiales	Peptococc/ Acidaminococc	sf_11	534	chlorobenzene-degrading consortium clone IIA-26

(continued)

TABLE 3. (CONTINUED)

Phylum	*Class*	*Order*	*Family*	*S-F*[a]	*Taxon ID*[b]	*Representative species*[c]
Firmicutes	Clostridia	Clostridiales	Peptococc/ Acidaminococc	sf_11	992	anoxic bulk soil flooded rice microcosm clone BSV43 clone
Firmicutes	Clostridia	Clostridiales	Peptococc/ Acidaminococc	sf_11	242	*Desulfosporosinus orientis* str. DSMZ 7493
Firmicutes	Clostridia	Clostridiales	Peptococc/ Acidaminococc	sf_11	300	benzene-contaminated groundwater clone ZZ12C8
Firmicutes	Clostridia	Clostridiales	Peptococc/ Acidaminococc	sf_11	39	forested wetland clone RCP2-71
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	sf_5	2721	termite gut homogenate clone Rs-N71 bacterium
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	sf_5	2729	DCP-dechlorinating consortium clone SHA-58
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	sf_5	2679	termite gut homogenate clone BCf9-13
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	sf_5	2694	oral periodontitis clone FX028
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	sf_5	2714	termite gut homogenate clone Rs-N27 bacterium
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	sf_5	2913	termite gut homogenate clone Rs-N82 bacterium
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	sf_5	3080	termite gut homogenate clone Rs-F43 bacterium
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	sf_5	3112	Evry municipal wastewater treatment plant clone 012C11_B_SD_P15
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	sf_5	3182	termite gut homogenate clone Rs-Q64 bacterium
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	sf_5	2993	oral clone P2PB_46 P3
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	sf_5	2738	*Mogibacterium neglectum* str. ATCC 700924 (= P9a-h)
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	sf_5	2805	oral periodontitis clone FX033
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	sf_5	2797	Isolation and identification hyper-ammonia producing swine storage pits manure
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	sf_5	619	TCE-dechlorinating microbial community clone 1G
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	sf_5	224	*Finegoldia magna* str. ATCC 29328
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	sf_5	58	*Peptostreptococcus* sp. str. E3_32
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	sf_5	1037	*Finegoldia magna*
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	sf_5	616	*Peptoniphilus lacrimalis* str. CCUG 31350
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	sf_5	393	*Anaerococcus vaginalis* str. CCUG 31349
Firmicutes	Bacilli	Bacillales	Sporolactobacillaceae	sf_1	3365	*Bacillus* sp. clone ML615J-19
Firmicutes	Bacilli	Bacillales	Sporolactobacillaceae	sf_1	3747	*Bacillus* sp. str. C-59-2
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	sf_1	3258	*Staphylococcus auricularis* str. MAFF911484 ATCC33753T
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	sf_1	3284	
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	sf_1	3545	
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	sf_1	3569	*Staphylococcus saprophyticus*
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	sf_1	3585	
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	sf_1	3592	*Staphylococcus caprae* str. DSM 20608
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	sf_1	3605	
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	sf_1	3628	*Staphylococcus haemolyticus* str. CCM2737
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	sf_1	3638	*Staphylococcus* sp str. AG-30
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	sf_1	3654	*Staphylococcus pettenkoferi* str. B3117
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	sf_1	3684	*Staphylococcus sciuri*

Firmicutes	Bacilli	Bacillales	Staphylococcaceae	sf_1	3794	
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	sf_1	3822	*Staphylococcus succinus* str. SB72
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	sf_1	3494	*Micrococcus luteus* B-P 26
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	sf_1	3865	*Macrococcus lamae* str. CCM 4815
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	sf_1	3432	deep-sea sediment isolate str. P_wp0225
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	sf_1	3722	Lactococcus Il1403 subsp. lactis str. IL1403
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	sf_1	3869	*Streptococcus equi* subsp. zooepidemicus str. Tokyo1291 subsp.
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	sf_1	3699	*Streptococcus agalactiae* str. 2603V/R
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	sf_1	3907	aortic heart valve patient with endocarditis clone v6
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	sf_1	3250	*Streptococcus bovis* str. B315
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	sf_1	3253	derived cheese sample clone 32CR
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	sf_1	3313	*Streptococcus salivarius* str. ATCC 7073
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	sf_1	3397	*Streptococcus macedonicus* str. ACA-DC 206 LAB617
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	sf_1	3422	*Streptococcus thermophilus* str. DSM 20617
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	sf_1	3543	
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	sf_1	3588	*Streptococcus downei* str. ATCC 33748
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	sf_1	3906	*Streptococcus bovis* str.ATCC 43143
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	sf_1	3499	*Streptococcus constellatus* str. ATCC27823
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	sf_1	3446	*Streptococcus bovis* str. HJ50
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	sf_1	3560	*Streptococcus gallinaceus* str. CCUG 42692
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	sf_1	3753	*Streptococcus suis* str. 8074
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	sf_1	3251	*Streptococcus cristatus* str. ATCC 51100
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	sf_1	3287	tongue dorsum scrapings clone FP015
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	sf_1	3290	*Streptococcus mitis* str. Sm91
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	sf_1	3629	*Streptococcus mutans* str. UA96
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	sf_1	3685	*Streptococcus gordonii* str. ATCC 10558
Firmicutes	Clostridia	Clostridiales	Syntrophomonadaceae	sf_5	2456	granular sludge clone R4b14
Firmicutes	Bacilli	Bacillales	Thermoactinomycetaceae	sf_1	3301	*Thermoactinomyces* sp. str. 700375
Firmicutes	Unclassified	Unclassified	Unclassified	sf_8	546	*Ferribacter thermoautotrophicus*
Firmicutes	Clostridia	Clostridiales	Unclassified	sf_17	2324	
Firmicutes	Desulfotomaculum	Unclassified	Unclassified	sf_1	2351	*Desulfotomaculum thermobenzoicum* str. DSM 6193
Firmicutes	Desulfotomaculum	Unclassified	Unclassified	sf_1	2359	UASB granular sludge clone JP
Firmicutes	Clostridia	Unclassified	Unclassified	sf_3	2373	
Firmicutes	Symbiobacteria	Symbiobacterales	Unclassified	sf_1	2388	G+C Gram-positive clone YNPRH70A
Firmicutes	Unclassified	Unclassified	Unclassified	sf_8	2433	Ferribacter thermoautotrophicus str. JW/JH-Fiji-2
Firmicutes	Desulfotomaculum	Unclassified	Unclassified	sf_1	2443	*Desulfotomaculum thermoacetoxidans* str. DSM 5813
Firmicutes	Desulfotomaculum	Unclassified	Unclassified	sf_1	2490	*Desulfotomaculum solfataricum* str. V21
Firmicutes	Clostridia	Unclassified	Unclassified	sf_4	2398	deep marine sediment clone MB-C2-106
Firmicutes	Symbiobacteria	Symbiobacterales	Unclassified	sf_1	77	thermal soil clone YNPFFP9
Firmicutes	Clostridia	Clostridiales	Unclassified	sf_17	926	
Firmicutes	Desulfotomaculum	Unclassified	Unclassified	sf_1	198	*Pelotomaculum* sp. str. JT
Firmicutes	Catabacter	Unclassified	Unclassified	sf_4	2716	termite gut homogenate clone Rs-F76 bacterium
Firmicutes	Clostridia	Clostridiales	Unclassified	sf_17	3476	
Firmicutes	Bacilli	Lactobacillales	Unclassified	sf_1	3289	Isobaculum melis CCUG 37660T

(continued)

Table 3. (Continued)

Phylum	*Class*	*Order*	*Family*	*S-F*[a]	*Taxon ID*[b]	*Representative species*[c]
Firmicutes	Bacilli	Lactobacillales	Unclassified	sf_1	3481	
Firmicutes	Clostridia	Clostridiales	Unclassified	sf_17	4168	
Firmicutes	Catabacter	Unclassified	Unclassified	sf_4	4503	termite gut homogenate clone Rs-H83 bacterium
Firmicutes	Unclassified	Unclassified	Unclassified	sf_8	4536	Mono Lake at depth 35m station 6 July 2000 clone ML635J-14 G+C
Firmicutes	Clostridia	Unclassified	Unclassified	sf_7	4216	
Firmicutes	Catabacter	Unclassified	Unclassified	sf_1	4261	termite gut homogenate clone Rs-G04 bacterium
Firmicutes	Catabacter	Unclassified	Unclassified	sf_1	4293	termite gut homogenate clone Rs-Q01 bacterium
Firmicutes	gut clone group	Unclassified	Unclassified	sf_1	4298	human mouth clone P4PA_66
Firmicutes	Clostridia	Clostridiales	Unclassified	sf_17	4307	
Firmicutes	Catabacter	Unclassified	Unclassified	sf_4	4526	TCE-contaminated site clone ccslm210
Firmicutes	gut clone group	Unclassified	Unclassified	sf_1	4616	rumen clone F23-C12
Fusobacteria	Fusobacteria	Fusobacterales	Fusobacteriaceae	sf_3	367	*Leptotrichia amnionii* str. AMN-1
Fusobacteria	Fusobacteria	Fusobacterales	Fusobacteriaceae	sf_3	558	*Sneathia sanguinegens* str. CCUG 41628T
Fusobacteria	Fusobacteria	Fusobacterales	Fusobacteriaceae	sf_1	488	*Fusobacterium nucleatum* subsp. vincentii str. ATCC 49256
Gemmatimonadetes	Unclassified	Unclassified	Unclassified	sf_5	442	forest soil clone S0134
Gemmatimonadetes	Unclassified	Unclassified	Unclassified	sf_5	227	uranium mining waste pile clone JG37-AG-36
Gemmatimonadetes	Unclassified	Unclassified	Unclassified	sf_5	9464	lodgepole pine rhizosphere soil British Columbia Ministry Forests Long-Term Soil Productivity
Gemmatimonadetes	Unclassified	Unclassified	Unclassified	sf_5	10112	forest soil clone NOS7.157WL
Gemmatimonadetes	Unclassified	Unclassified	Unclassified	sf_5	317	penguin droppings sediments clone KD8-87
Gemmatimonadetes	Unclassified	Unclassified	Unclassified	sf_5	1127	uranium mining waste pile near Johanngeorgenstadt soil clone JG37-AG-21
Gemmatimonadetes	Unclassified	Unclassified	Unclassified	sf_5	1565	uranium mining waste pile clone JG34-KF-418
Gemmatimonadetes	Unclassified	Unclassified	Unclassified	sf_5	2047	soil clone #0319-7G21
LD1PA group	Unclassified	Unclassified	Unclassified	sf_1	10118	anoxic marine sediment clone LD1-PA38
Lentisphaerae	Unclassified	Unclassified	Unclassified	sf_5	10027	*Cytophaga* sp. str. Dex80-43
Lentisphaerae	Unclassified	Unclassified	Unclassified	sf_5	10330	Mono lake clone ML635J-58
Lentisphaerae	Unclassified	Unclassified	Unclassified	sf_5	9704	*Cytophaga* sp. str. Dex80-64
marine group A	mgA-2	Unclassified	Unclassified	sf_1	6344	bacterioplankton clone ZA3648c
marine group A	mgA-1	Unclassified	Unclassified	sf_1	6408	Sargasso Sea
marine group A	mgA-1	Unclassified	Unclassified	sf_1	6454	marine clone SAR406
Natronoanaerobium	Unclassified	Unclassified	Unclassified	sf_1	769	fjord ikaite column clone un-c23
Natronoanaerobium	Unclassified	Unclassified	Unclassified	sf_1	2437	Mono Lake at depth 23m station 6 July 2000 clone ML623J-19
Natronoanaerobium	Unclassified	Unclassified	Unclassified	sf_1	3570	*Bacillus* sp. clone ML1228J-1
Natronoanaerobium	Unclassified	Unclassified	Unclassified	sf_1	3745	Mono Lake at depth 35m station 6 July 2000 clone ML635J-45
Natronoanaerobium	Unclassified	Unclassified	Unclassified	sf_1	4377	Mono Lake at depth 35m station 6 July 2000 clone ML635J-65 G+C
NC10	NC10-1	Unclassified	Unclassified	sf_1	452	vadose clone 5G01
NC10	NC10-1	Unclassified	Unclassified	sf_1	536	uranium mill tailings clone GuBH2-AD-8
NC10	NC10-2	Unclassified	Unclassified	sf_1	10254	uranium mill tailings soil sample clone Sh765B-TzT-35

Nitrospira	Nitrospira	Nitrospirales	Nitrospiraceae	sf_1	984	uranium mining waste pile clone JG37-AG-131 sp.
Nitrospira	Nitrospira	Nitrospirales	Nitrospiraceae	sf_2	542	forested wetland clone FW19
Nitrospira	Nitrospira	Nitrospirales	Nitrospiraceae	sf_2	544	forested wetland clone FW5
Nitrospira	Nitrospira	Nitrospirales	Nitrospiraceae	sf_2	697	forested wetland clone FW118
OP10	CH21 cluster	Unclassified	Unclassified	sf_1	326	geothermal clone ST01-SN3H
OP10	Unclassified	Unclassified	Unclassified	sf_4	484	forested wetland clone FW68
OP10	CH21 cluster	Unclassified	Unclassified	sf_1	514	sludge clone SBRA136
OP10	Unclassified	Unclassified	Unclassified	sf_5	9782	Rocky Mountain alpine soil clone S1a-1H
OP3	Unclassified	Unclassified	Unclassified	sf_4	628	CB-contaminated groundwater clone GOUTB15
OP3	Unclassified	Unclassified	Unclassified	sf_2	349	soil clone PBS-25
OP9/JS1	OP9	Unclassified	Unclassified	sf_1	726	hot spring clone OPB72
OP9/JS1	OP9	Unclassified	Unclassified	sf_1	969	DCP-dechlorinating consortium clone SHA-1
phylum_tax	class_tax	order_tax	family_tax	subfamily	otu_id	rep_prokMSAname
Planctomycetes	Planctomycetacia	Planctomycetales	Anammoxales	sf_2	4683	anoxic basin clone CY0ARA028B09
Planctomycetes	Planctomycetacia	Planctomycetales	Anammoxales	sf_4	4694	USA: Colorado Fort collins Horsetooth Reservoir clone HT2F11
Planctomycetes	Planctomycetacia	Planctomycetales	Anammoxales	sf_4	9662	Great Artesian Basin clone B83
Planctomycetes	Planctomycetacia	Planctomycetales	Pirellulae	sf_3	4670	
Planctomycetes	Planctomycetacia	Planctomycetales	Pirellulae	sf_3	4677	aerobic basin clone CY0ARA032A03
Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	sf_3	4652	anoxic basin clone CY0ARA028C04
Planctomycetes	Planctomycetacia	Planctomycetales	Planctomycetaceae	sf_3	4948	anoxic basin clone CY0ARA027D01
Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	sf_1	7529	*Gluconacetobacter europaeus* str. ZIM B028 V3
Proteobacteria	Gammaproteobacteria	Acidithiobacillales	Acidithiobacillaceae	sf_1	8320	acid mine drainage clone BA11
Proteobacteria	Gammaproteobacteria	Acidithiobacillales	Acidithiobacillaceae	sf_1	8552	*Acidithiobacillus ferrooxidans* str. D2
Proteobacteria	Gammaproteobacteria	Acidithiobacillales	Acidithiobacillaceae	sf_1	9224	*Acidithiobacillus albertensis* str. DSM 14366
Proteobacteria	Gammaproteobacteria	Acidithiobacillales	Acidithiobacillaceae	sf_1	9497	*Acidithiobacillus ferrooxidans* str. ATCC 19859
Proteobacteria	Gammaproteobacteria	Aeromonadales	Aeromonadaceae	sf_1	9294	Arctic deep sea Isolation common chemoorganotrophic oxygen-respiring polar current d 1210
Proteobacteria	Gammaproteobacteria	Aeromonadales	Aeromonadaceae	sf_1	8340	*Aeromonas ichthiosmia*
Proteobacteria	Gammaproteobacteria	Aeromonadales	Aeromonadaceae	sf_1	8364	*Aeromonas allosaccharophila* str. CECT 4199
Proteobacteria	Gammaproteobacteria	Aeromonadales	Aeromonadaceae	sf_1	8621	*Aeromonas* sp. PAR2A
Proteobacteria	Gammaproteobacteria	Aeromonadales	Aeromonadaceae	sf_1	9000	*Aeromonas culicicola* str. MTCC 3249
Proteobacteria	Gammaproteobacteria	Aeromonadales	Aeromonadaceae	sf_1	9026	*Haemophilus piscium* str. NCIMB 1952
Proteobacteria	Gammaproteobacteria	Aeromonadales	Aeromonadaceae	sf_1	9440	*Aeromonas sobria* str. NCIMB 12065
Proteobacteria	Gammaproteobacteria	Aeromonadales	Aeromonadaceae	sf_1	9494	*Aeromonas molluscorum* str. 849T
Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	sf_1	7737	atrazine-catabolizing microbial presence methanol clone KRA30+06A
Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	sf_1	7768	swine intestine clone p-861-a5
Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	sf_1	7788	atrazine-catabolizing microbial absence methanol clone KRA30-58
Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	sf_1	7838	*Alcaligenes defragrans* str. PD-19
Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	sf_1	7902	*Alcaligenes faecalis* str. M3A
Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	sf_1	7932	Achromobacter subsp. denitrificans str. DSM 30026 (T)
Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	sf_1	7984	Waste-gas biofilter clone BIfciii38
Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	sf_1	7992	*Alcaligenes faecalis* 5659-H
Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	sf_1	8062	*Brackiella oedipodis* str. LMG 1945 R8846

(*continued*)

Table 3. (Continued)

Phylum	*Class*	*Order*	*Family*	*S-F*[a]	*Taxon ID*[b]	*Representative species*[c]
Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	sf_1	8094	*Alcaligenes* sp. str. VKM B-2263 dcm6
Proteobacteria	Gammaproteobacteria	Oceanospirillales	Alcanivoraceae	sf_1	8335	*Alcanivorax* sp. str. K3-3 (MBIC 4323)
Proteobacteria	Gammaproteobacteria	Oceanospirillales	Alcanivoraceae	sf_1	9658	*Alcanivorax* sp. str. Haw1
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9035	*Microbulbifer* sp. str. JAMB-A94
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8348	Arctic sea ice ARK10038
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8484	Alteromonadaceae isolate str. LA50
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8503	Arctic sea ice ARK10244
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8578	*Marinobacter lipolyticus* str. SM-19
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8594	*Marinobacter* sp. str. SBS
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9239	Arctic sea ice ARK10228
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8196	
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8222	
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8600	*Colwellia piezophila* str. Y223G
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8753	*Idiomarina loihiensis* str. GSP37
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8174	attached marine recovered surface clone 17 proteobacterium
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8318	*Aestuariibacter salexigens* str. JC2042
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8374	*Agarivorans albus* str. MKT 89
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8533	
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8695	Arctic pack ice; northern Fram Strait; 80 31.1 N; 01 deg 59.7 min E clone ARKIA-34
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8863	*Alteromonas marina* str. SW-47
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8970	Arctic seawater isolate str. R9879
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8978	Arctic sea ice ARK10108
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9230	Antarctic pack ice Lasarev Sea Southern Ocean clone ANTXI/4_14-62 sea
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9236	attached marine recovered surface clone 18 proteobacterium
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9288	*Alteromonas stellipolaris* str. LMG 21861
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9292	
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9501	sea water isolate str. BP-PH
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9562	Alteromonadaceae clone PH-B55N
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8172	*Pseudoalteromonas* sp. str. Bdeep-1
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8336	*Alteromonas* sp. str. MS23
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8580	Arctic seawater isolate str. R7076
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8932	*Pseudoalteromonas antarctica* str. N-1
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8975	*Alteromonas* sp. str. NIBH P1M3
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9058	*Pseudoalteromonas carrageenovora* str. ATCC 12662T
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9111	*Pseudoalteromonas* sp. str. E36
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9143	*Pseudoalteromonas agarivorans* str. KMM 255
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9205	marine clone Arctic96B-17
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9218	*Pseudoalteromonas haloplanktis* str. ATCC 14393
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9324	*Pseudoalteromonas ruthenica* str. KMM300
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9386	*Alteromonas* sp. str. NIBH P2M11

Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9640	exposed to diatom detritus isolate str. Tw-10 Tw-10
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8643	*Pseudoalteromonas porphyrae* str. S2-65
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9369	*Pseudoalteromonas luteoviolacea* str. NCIMB 1893T
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9222	*Shewanella hanedai* str. CIP 103207T
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9384	*Moritella viscosa* str. NVI 88/478T
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8916	*Shewanella algae* str. 43940
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9067	*Shewanella algae* str. ACM 4733
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9416	marine isolate str. R8
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9586	*Shewanella gaetbuli* str. TF-27
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8579	*Psychromonas profunda* str. 2825
Proteobacteria	Alphaproteobacteria	Rickettsiales	Anaplasmataceae	sf_3	6628	*Wolbachia pipientis*
Proteobacteria	Alphaproteobacteria	Rickettsiales	Anaplasmataceae	sf_3	6648	*Wolbachia* sp
Proteobacteria	Alphaproteobacteria	Rickettsiales	Anaplasmataceae	sf_3	6803	*Wolbachia* sp. Dlem16SWol
Proteobacteria	Alphaproteobacteria	Rickettsiales	Anaplasmataceae	sf_3	6908	*Rhinocyllus conicus* endosymbiont
Proteobacteria	Alphaproteobacteria	Rickettsiales	Anaplasmataceae	sf_3	7481	*Wolbachia pipientis*
Proteobacteria	Alphaproteobacteria	Rhizobiales	Bartonellaceae	sf_1	7056	*Bartonella schoenbuchensis* str. R1
Proteobacteria	Alphaproteobacteria	Rhizobiales	Bartonellaceae	sf_1	7384	aortic heart valve patient with endocarditis clone v9
Proteobacteria	Alphaproteobacteria	Rhizobiales	Bartonellaceae	sf_1	7415	*Bartonella quintana* str. Toulouse
Proteobacteria	Alphaproteobacteria	Rhizobiales	Bartonellaceae	sf_1	7634	*Bartonella henselae* str. Houston-1
Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bdellovibrionaceae	sf_1	10010	uranium mining waste pile clone JG37-AG-139 proteobacterium
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Beijerinck/Rhodoplan/ Methylocyst	sf_3	7401	*Scrippsiella trochoidea* NEPCC 15
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Beijerinck/Rhodoplan/ Methylocyst	sf_3	6651	*Beijerinckia indica*
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Beijerinck/Rhodoplan/ Methylocyst	sf_3	7275	Mammoth cave clone CCU18
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Beijerinck/Rhodoplan/ Methylocyst	sf_3	7219	*Methylosinus sporium*
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Beijerinck/Rhodoplan/ Methylocyst	sf_3	7640	*Methylosinus trichosporium*
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Beijerinck/Rhodoplan/ Methylocyst	sf_3	6762	acidic forest soil clone UP8
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Beijerinck/Rhodoplan/ Methylocyst	sf_3	7153	*Methylocella tundrae* str. Y1
Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	sf_1	7029	
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Bradyrhizobiaceae	sf_1	7403	*Oligotropha carboxidovorans* str. S23
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Bradyrhizobiaceae	sf_1	6927	*Nitrobacter hamburgensis* str. X14
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Bradyrhizobiaceae	sf_1	6768	*Rhodopseudomonas palustris* str. GH
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Bradyrhizobiaceae	sf_1	6799	*Rhodopseudomonas palustris* str. ATCC 17001
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Bradyrhizobiaceae	sf_1	7316	
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Bradyrhizobiaceae	sf_1	7333	*Afipia genosp.* 4 str. G3644
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Bradyrhizobiaceae	sf_1	6941	*Rhodopseudomonas rhenobacensis* str. Klemme Rb
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Bradyrhizobiaceae	sf_1	7087	*Bradyrhizobium japonicum* HA1
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Bradyrhizobiaceae	sf_1	7398	*Bradyrhizobium japonicum* str. USDA 38
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Bradyrhizobiaceae	sf_1	6636	*Bradyrhizobium elkanii* str. USDA 76
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Bradyrhizobiaceae	sf_1	6867	heavy metal-contaminated soil clone a13131

(*continued*)

TABLE 3. (CONTINUED)

Phylum	*Class*	*Order*	*Family*	*S-F*[a]	*Taxon ID*[b]	*Representative species*[c]
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Bradyrhizobiaceae	sf_1	6887	*Bradyrhizobium* str. YB2
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Bradyrhizobiaceae	sf_1	7044	*Afipia genosp.* 2 str. G4438
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Bradyrhizobiaceae	sf_1	7126	ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A-MN96 proteobacterium
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Bradyrhizobiaceae	sf_1	7390	*Afipia genosp.* 10 str. G8996
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Bradyrhizobiaceae	sf_1	7477	*Bradyrhizobium elkanii* str. SEMIA 6028
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Bradyrhizobiaceae	sf_1	7522	*Bradyrhizobium* sp. str. KKI14
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Bradyrhizobiaceae	sf_1	6878	*Bradyrhizobium japonicum* SD5
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Bradyrhizobiaceae	sf_1	6917	*Bradyrhizobium japonicum* str. IAM 12608
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Bradyrhizobiaceae	sf_1	7353	temperate estuarine mud clone HC65
Proteobacteria	Alphaproteobacteria	Rhizobiales	Brucellaceae	sf_1	6757	*Ochrobactrum anthropi* str. ESC1
Proteobacteria	Alphaproteobacteria	Rhizobiales	Brucellaceae	sf_1	6981	*Ochrobactrum gallinifaecis* str. Iso 196
Proteobacteria	Alphaproteobacteria	Rhizobiales	Brucellaceae	sf_1	6995	
Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	sf_1	7720	penguin droppings sediments clone KD1-79
Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	sf_1	7771	*Burkholderia glathei* str. ATCC 29195T
Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	sf_1	7782	*Burkholderia hospita* str. LMG 20598T
Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	sf_1	7969	*Burkholderia* sp.
Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	sf_1	8059	*Burkholderia caribensis* str. MWAP71
Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	sf_1	8068	*Burkholderia caryophylli* str. ATCC 25418
Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	sf_1	7747	
Proteobacteria	Alphaproteobacteria	Consistiales	Caedibacteraceae	sf_4	7157	acid mine drainage clone ASL45
Proteobacteria	Alphaproteobacteria	Consistiales	Caedibacteraceae	sf_5	6947	termite gut homogenate clone Rs-B60 proteobacterium
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	sf_3	10446	
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	sf_3	10461	deepest cold-seep area Japan Trench clone JTB360 proteobacterium
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	sf_3	10523	Riftia pachyptila's tube clone R103-B70
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	sf_3	10538	*Arcobacter cryaerophilus*
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	sf_3	10447	*Sulfurospirillum deleyianum* str. Spirillum 5175
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	sf_3	10464	*Campylobacter* sp. str. NO2B
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	sf_3	10434	*Campylobacter gracilis*
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	sf_3	10456	*Campylobacter showae*
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	sf_3	10463	*Campylobacter subsp. fetus*
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	sf_3	10484	*Campylobacter helveticus*
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	sf_3	10540	*Campylobacter showae* str. LMG 12636
Proteobacteria	Gammaproteobacteria	Cardiobacteriales	Cardiobacteriaceae	sf_1	8536	*Cardiobacterium hominis*
Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	sf_1	7486	*Asticcacaulis excentricus* str. ATCC15261
Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	sf_1	6781	*Brevundimonas intermedia* str. MBIC2712 ATCC15262
Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	sf_1	6904	*Brevundimonas vesicularis* str. IAM 12105T
Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	sf_1	6909	*Brevundimonas diminuta* str. DSM 1635
Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	sf_1	6968	*Brevundimonas diminuta* str. IAM 12691T
Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	sf_1	7359	*Brevundimonas bacteroides* str. CB7
Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	sf_1	7366	*Brevundimonas subvibrioides* str. CB81

Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	sf_1	7436	*Brevundimonas* sp. str. FWC40
Proteobacteria	Gammaproteobacteria	Chromatiales	Chromatiaceae	sf_1	9048	*Allochromatium* sp. AT2202
Proteobacteria	Gammaproteobacteria	Chromatiales	Chromatiaceae	sf_1	8546	*Thiocapsa litoralis*
Proteobacteria	Gammaproteobacteria	Chromatiales	Chromatiaceae	sf_1	8527	
Proteobacteria	Gammaproteobacteria	Chromatiales	Chromatiaceae	sf_1	8697	*Thiococcus* sp. AT2204
Proteobacteria	Gammaproteobacteria	Chromatiales	Chromatiaceae	sf_1	9054	
Proteobacteria	Gammaproteobacteria	Chromatiales	Chromatiaceae	sf_1	9052	
Proteobacteria	Gammaproteobacteria	Chromatiales	Chromatiaceae	sf_1	9356	
Proteobacteria	Gammaproteobacteria	Chromatiales	Chromatiaceae	sf_1	9370	isolate str. HTB019
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	8112	*Comamonas testosteroni* str. SMCC B329
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	7704	freshwater clone PRD01b009B
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	7705	penguin droppings sediments clone KD4-7
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	7801	Toolik Lake main station at 3 m depth clone TLM05/TLMdgge10 proteobacterium
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	7829	*Xylophilus ampelinus* str. ATCC 33914
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	7928	penguin droppings sediments clone KD5-43
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	7941	MCB-contaminated groundwater-treating reactor clone RB9C10
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	7986	Arctic sea ice ARK10281
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	8138	*Pseudomonas lanceolata* str. ATCC 14669T
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	8139	*Delftia tsuruhatensis* str. AD9
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	7856	*Variovorax paradoxus*
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	7964	napthalene-contaminated sediment clone 76
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	7888	*Hydrogenophaga flava* str. DSM 619T
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	7919	strain isolate str. rM4
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	7987	*Acidovorax* sp. str. OS-6
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	8012	*Acidovorax konjaci* str. DSM 7481
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	8018	*Acidovorax delafieldii* str. ATCC 17505
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	8021	*Acidovorax facilis* str. CCUG 2113
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	8022	*Acidovorax avenae* subsp. cattleyae str. NCPPB 961 subsp.
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	8031	strain isolate str. rJ10
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	8046	*Acidovorax defluvii* str. BSB411
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	8152	nephridia *Octolasion lacteum* clone Ol2-2
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	7807	*Aquaspirillum metamorphum* str. DSM 1837
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	7884	Germany:Elbe River clone Elb37
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	sf_1	7965	*Anoxobacterium dechloraticum*
Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae	sf_3	7893	agricultural soil clone SC-I-71
Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae	sf_3	8457	5′ clone CHAB-XI-27
Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae	sf_3	9198	uranium mining waste pile clone KF-JG30-B15 KF-JG30-B15
Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae	sf_3	8969	uranium mining waste pile soil sample clone JG30-KF-C15 proteobacterium
Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae	sf_3	9444	forested wetland clone FW23
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfoarculaceae	sf_2	10227	marine sediment clone Bol11
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	sf_5	9666	marine sediment above hydrate ridge clone Hyd89-13 proteobacterium
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	sf_5	9875	hydrothermal sediment clone AF420354

(*continued*)

Table 3. (Continued)

Phylum	*Class*	*Order*	*Family*	*S-F*[a]	*Taxon ID*[b]	*Representative species*[c]
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	sf_5	9800	forested wetland clone FW57
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	sf_5	10268	
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	sf_5	10046	*Desulfobacterium cetonicum* str. DSM 7267 oil recovery water
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	sf_5	10239	
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	sf_5	10319	sulfate-reducing habitat clone SLM-CP-116
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	sf_5	10031	Antarctic sediment clone SB1_49
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	sf_5	10083	*Desulfobacter curvatus* str. DSM 3379
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	sf_5	9940	Antarctic sediment clone SB2_56
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae	sf_1	10047	epibiontic clone C11-D3
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae	sf_1	10187	Mono Lake at depth 23 m station 6 July 2000 clone ML623J-57 proteobacterium
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae	sf_1	9734	*Riftia pachyptila*'s tube clone R103-B13
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae	sf_1	9739	gas hydrate clone Hyd89-51
Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfohalobiaceae	sf_1	9894	*Desulfonauticus submarinus* str. 6N
Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfomicrobiaceae	sf_1	10079	*Desulfomicrobium baculatum* str. DSM 1742
Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	sf_1	10262	*Desulfovibrio* sp. str. Ac5.2
Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	sf_1	10248	*Desulfovibrio giganteus* str. DSM 4370
Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	sf_1	10016	termite gut homogenate clone Rs-N35 proteobacterium
Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	sf_1	9826	termite gut homogenate clone Rs-M72 proteobacterium
Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	sf_1	10071	*Desulfovibrio desulfuricans*
Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	sf_1	10212	
Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	sf_1	9709	termite gut homogenate clone Rs-N31 proteobacterium
Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Desulfuromonaceae	sf_1	10020	uranium mill tailings soil sample clone GuBH2-AG-114 proteobacterium
Proteobacteria	Gammaproteobacteria	Chromatiales	Ectothiorhodospiraceae	sf_1	9450	*Halorhodospira neutrophila* str. SG 3304
Proteobacteria	Gammaproteobacteria	Chromatiales	Ectothiorhodospiraceae	sf_1	9598	Mono Lake at depth 2 m station 6 July 2000 clone ML602J-47 proteobacterium
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_6	433	coal effluent wetland clone RCP2-6
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_6	646	*Opitutus* sp. str. SA-9
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9309	*Buchnera* sp
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8742	USA:New York isolate str. KN4
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_6	8783	*Alterococcus agarolyticus* str. ADT3; CCRC17102
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9135	intestine *Zophobas mori* clone
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9358	*Salmonella* subsp. enterica serovar Waycross str. Swy1 subsp.
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9496	
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8886	*Salmonella typhimurium* LT2 str. SGSC1412
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8740	*Erwinia chrysanthemi* str. 573
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9651	*Pectobacterium* subsp. atrosepticum str. GSPB 1710
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8379	*Erwinia amylovora* EA G-5

Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9142	*Erwinia amylovora* str. DSM 30165
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9252	*Pantoea cedenensis* str. A34
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9345	*Erwinia amylovora* str. BC199(=Ea528)
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8554	*Kluyvera ascorbata* 69
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8885	*Morganella morganii* str. AP28
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9363	*Citrobacter freundii* str. CDC 621-64
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9594	*Morganella morganii* str. ATCC35200
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8758	*Pectobacterium cypripedii* str. ATCC 29267
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8282	*Antonina pretiosa* symbiont
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8693	*Pantoea agglomerans* str. A40
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8700	*Baumannia cicadellinicola*
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9302	*Pantoea* subsp. stewartii str. GSPB 2626
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8236	*Vryburgia amaryllidis* symbiont
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8504	*Dysmicoccus neobrevipes* symbiont
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8603	*Melanococcus albizziae* symbiont
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8607	*Amonostherium lichtensioides* symbiont
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8624	*Erium globosum* symbiont
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9290	*Baumannia cicadellinicola*
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9293	USA clone 14/7
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9420	
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8934	*Pectobacterium* subsp. carotovorum str. E155 subsp.
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9266	Parasite BEV of E.variegatus
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8467	*Serratia marcescens* subsp. sakuensis str. KRED subsp.
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9348	
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8505	*Buttiauxella warmboldiae* str. DSM 9404
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8528	*Enterobacter cloacae* Nr. 3
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8530	*Enterobacteriaceae* CF01Ent-1
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8640	
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8936	*Klebsiella oxytoca* str. ChDC OS31
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9060	*Enterobacter ludwigii* str. EN-119 = DSMZ 16688
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9274	*Enterobacter* sp. CC1
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9361	*Enterobacter intermedius* str. JCM1238
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9390	*Enterobacter nimipressuralis* str. LMG 10245-T
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8251	Nitrogen-fixing isolate str. CANF3
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8529	*Raoultella planticola* 7
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8627	*Australicoccus grevilleae* symbiont
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8770	
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8890	*Raoultella planticola* str. DR3
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8362	*Klebsiella pneumoniae* str. ASR1
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8510	*Klebsiella pneumoniae* str. DSM 30104
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8773	
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8286	*Cyphonococcus alpinus* symbiont
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8711	*Serratia odorifera* str. DSM 4582
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8712	*Serratia proteamaculans* str. DSM 4543
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8739	*Serratia entomophila* str. DSM 12358
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8892	*Aranicola proteolyticus*
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9151	

(*continued*)

TABLE 3. (CONTINUED)

Phylum	*Class*	*Order*	*Family*	*S-F*[a]	*Taxon ID*[b]	*Representative species*[c]
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9417	*Serratia fonticola* str. DSM 4576
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8631	*Planococcus ficus* symbiont
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8283	*Heteropsylla texana* symbiont
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8173	*Photorhabdus asymbiotica* str. ATCC 43949
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8225	
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8642	*Erwinia chrysanthemi* str. 580
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9029	*Photorhabdus asymbiotica* subsp. australis str. MB
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8473	*Hafnia alvei*
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9265	*Rahnella aquatilis* k 8
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9337	*Rahnella genosp.* 3 str. DSM 30078
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8564	*Rahnella aquatilis* str. ATCC 33989
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9157	Secondary symbiont type-U Acyrthosiphon pisum (rrs) clone 5B type-U
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	9262	*Yersinia aldovae* str. A125
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	1206	*Dermacentor variabilis* symbiont
Proteobacteria	Gammaproteobacteria	Thiotrichales	Francisellaceae	sf_1	9554	*Tilapia parasite* TPT-541
Proteobacteria	Gammaproteobacteria	Thiotrichales	Francisellaceae	sf_1	8949	*Caedibacter taeniospiralis*
Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	sf_1	482	trichloroethene-contaminated site clone FTLM205 proteobacterium
Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	sf_1	10171	
Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	sf_1	8514	*Chromohalobacter israelensis* str. ATCC 43985 T
Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	sf_1	8562	*Halomonas* sp. str. TNB I20
Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	sf_1	8576	*Halomonas* sp. Ko502
Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	sf_1	8598	*Halomonas desiderata* str. FB2
Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	sf_1	8854	*Halomonas variabilis* str. ANT9112
Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	sf_1	9471	Boston Harbor surface water isolate str. UMB18C UMB18C
Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	sf_1	9141	*Halomonas* sp. SK1
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10385	
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10428	*Flexispira rappini* FH 9702248
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10430	*Helicobacter heilmannii* str. MM2
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10436	*Helicobacter aurati* str. MIT 97-5075c
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10442	*Helicobacter cetorum* str. MIT 99-5656
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10444	*Helicobacter suncus* str. Kaz-2
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10448	*Helicobacter felis* str. Dog-1
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10451	*Helicobacter heilmannii* str. C4S
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10454	*Helicobacter pullorum* str. NCTC 12826
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10462	*Helicobacter rodentium* str. MIT 96-1312
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10518	*Helicobacter pylori* str. ATCC 49396T
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10520	*Helicobacter* sp. blood isolate 964
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10548	*Helicobacter rappini* W.Tee-Bat
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10552	*Helicobacter winghamensis* str. NLEP 97-1611
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10562	*Helicobacter rappini* W.Tee-Yu
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10425	*Sulfurimonas autotrophica* str. OK5

Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10411	termite gut homogenate clone Rs-P71 proteobacterium
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10432	*Riftia pachyptila*'s tube clone R76-B51
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10438	hydrocarbon seep clone GCA014
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10590	termite gut homogenate clone Rs-H40 proteobacterium
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10614	strain isolate str. BHI80-49
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10417	temperate estuarine mud clone KM61
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10467	
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10507	termite gut homogenate clone Rs-M59 proteobacterium
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Hyphomicrobiaceae	sf_1	7646	*Hyphomicrobium aestuarii* str. DSM 1564
Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	sf_1	7392	
Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	sf_1	8865	Arctic pack ice; northern Fram Strait; 80 31.1 N; 01 deg 59.7 min E clone ARKCH2Br2-23
Proteobacteria	Alphaproteobacteria	Azospirillales	Magnetospirillaceae	sf_1	6922	*Dechlorospirillum* sp. str. SN1
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Methylobacteriaceae	sf_1	7585	*Methylobacterium thiocyanatum* str. ALL/SCN-P
Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	sf_1	8243	isolate str. IR
Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	sf_1	8821	*Methylobacter psychrophilus* str. Z-0021
Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	sf_1	9438	marine sediment above hydrate ridge clone Hyd24-01 proteobacterium
Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	sf_1	8137	freshwater clone PRD01a011B
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	sf_3	8366	*Psychrobacter frigidicola* str. DSM 12411
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	sf_3	8604	*Moraxella oblonga* str. IAM 14971
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	sf_3	8838	*Psychrobacter psychrophilus* CMS 28
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	sf_3	8727	*Alkanindiges hongkongensis* str. HKU9
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	sf_3	9359	*Acinetobacter junii* str. S33
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	sf_3	9428	hydrocarbon-degrading consortium clone AF2-1D
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	sf_3	9466	*Acinetobacter tandoii* str. 4N13
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	sf_3	9641	*Acinetobacter haemolyticus*
Proteobacteria	Deltaproteobacteria	Myxococcales	Myxococcaceae	sf_1	10358	*Myxococcus fulvus* str. Mx f2
Proteobacteria	Epsilonproteobacteria	Nautiliales	Nautiliaceae	sf_1	10477	S17sBac5 complete clone
Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	sf_1	7945	*Aquaspirillum serpens* str. IAM 13944
Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	sf_1	7675	*Neisseria* sp. str. CCUG 46910
Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	sf_1	7662	Mars Odyssey Orbiter and encapsulation facility clone T5-1 sp.
Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae	sf_1	7789	
Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae	sf_1	7976	*Nitrosomonas* sp. str. Nm86
Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae	sf_1	7770	*Nitrosomonas europaea* str. ATCC 19718
Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae	sf_1	8145	*Nitrosomonas eutropha* str. Nm57
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Nitrospinaceae	sf_2	594	uranium mining mill tailing clone GR-296.II.52 GR-296.I.52
Proteobacteria	Gammaproteobacteria	Oceanospirillales	Oceanospirillaceae	sf_1	9351	bacterioplankton clone ZA2333c
Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	sf_1	7743	*Herbaspirillum* sp. str. NAH4
Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	sf_1	7843	*Massilia timonae timone*
Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	sf_1	7845	*Diaphorina citri symbiont*
Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	sf_1	7866	*Paucimonas lemoignei* str. ATCC 17989T
Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	sf_1	7878	napthalene-contaminated sediment clone 29

(*continued*)

Table 3. (Continued)

Phylum	*Class*	*Order*	*Family*	*S-F*[a]	*Taxon ID*[b]	*Representative species*[c]
Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	sf_1	7921	*Collimonas fungivorans* str. Ter331
Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	sf_1	7968	*Oxalobacter formigenes* str. OXB ovinen rumen
Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	sf_1	8013	isolate str. A1020
Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	sf_1	8032	*Aquaspirillum arcticum* str. IAM 14963
Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	sf_1	8034	*Janthinobacterium agaricidamnosum* str. W1r3T
Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	sf_1	8058	*Herbaspirillum seropedicae* str. DSM 6445 ATCC 35892
Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	sf_1	9360	*Pasteurella multocida* subsp. gallicida str. MCCM 00021 subsp.
Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	sf_1	9349	*Pasteurella* sp. str. 91985
Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	sf_1	8195	*Haemophilus influenzae* str. R2866
Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	sf_1	8555	*Haemophilus influenzae* str. M9741
Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	sf_1	9213	*Haemophilus quentini* str. MCCM 02026
Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	sf_1	9477	*Haemophilus influenzae* str. M11105
Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	sf_1	8228	*Actinobacillus indolicus* str. H1419
Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	sf_1	8861	*Haemophilus parasuis* 427
Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	sf_1	8614	*Acidithiobacillus thiooxidans* str. KCTC 8928P
Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	sf_1	8952	*Actinobacillus lignieresii*
Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	sf_1	9263	*Actinobacillus capsulatus*
Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	sf_1	8876	*Mannheimia* sp. R19.2 str. R19.2; CCUG 38463 R19.2
Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	sf_1	9237	
Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	sf_1	8409	human colonic mucosal biopsy clone ABLCf1
Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	sf_1	8432	
Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	sf_1	8848	str. 86355
Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	sf_1	9533	*Haemophilus segnis* str. MCCM 00337
Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	sf_1	9628	*Histophilus somni* str. CCUG 12839
Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	sf_1	6857	*Mesorhizobium mediterraneum* str. PECA20
Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	sf_1	6692	*Phyllobacterium trifolii* str. PETP02
Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	sf_1	6916	lake microbial mat isolate str. R-9219
Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	sf_1	6966	*Mesorhizobium tianshanense* str. -1BS; USDA 3592
Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	sf_1	7009	
Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	sf_1	7216	*Ahrensia kielensis* str. IAM12618
Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	sf_1	7379	*Phyllobacterium myrsinacearum* HM35
Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	sf_1	7381	*Aminobacter aminovorans* str. DSM7048T
Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	sf_1	7497	*Pseudaminobacter salicylatoxidans* str. KTC001
Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	sf_1	7300	marine isolate JP57
Proteobacteria	Gammaproteobacteria	Thiotrichales	Piscirickettsiaceae	sf_3	8664	*Thiomicrospira* sp. str. Milos-T2
Proteobacteria	Gammaproteobacteria	Thiotrichales	Piscirickettsiaceae	sf_3	9027	*Thiomicrospira crunogena* str. XCL-2
Proteobacteria	Gammaproteobacteria	Thiotrichales	Piscirickettsiaceae	sf_3	9557	*Riftia pachyptila*'s tube clone R76-B23
Proteobacteria	Gammaproteobacteria	Thiotrichales	Piscirickettsiaceae	sf_3	9291	*Methylophaga alcalica* str. M39
Proteobacteria	Gammaproteobacteria	Thiotrichales	Piscirickettsiaceae	sf_3	9392	*Methylophaga* sp. str. V4.ME.29 = MM_2343
Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	sf_3	10249	soil sample uranium mining waste pile near town Johanngeorgenstadt clone JG36-TzT-168 proteobacterium

Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	sf_3	10298	marine tidal mat clone BTM36
Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	sf_3	10353	sludge clone A9
Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	sf_3	9671	hydrothermal sediment clone AF420357
Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	sf_3	9735	uranium mining waste pile clone JG37-AG-15 proteobacterium
Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	sf_3	9755	bacterioplankton clone ZA3704c
Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	sf_3	9874	uranium mining waste pile clone JG34-KF-243 proteobacterium
Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	sf_3	9900	bioreactor clone mle1-27
Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	sf_3	10082	uranium mining waste pile clone JG37-AG-33 proteobacterium
Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	sf_4	9733	bacterioplankton clone ZA3735c
Proteobacteria	Betaproteobacteria	Procabacteriales	Procabacteriaceae	sf_1	8136	*Acanthamoeba* sp. UWC6 symbiont
Proteobacteria	Gammaproteobacteria	Alteromonadales	Pseudoalteromonadaceae	sf_1	9627	*Pseudoalteromonas* sp
Proteobacteria	Gammaproteobacteria	Alteromonadales	Pseudoalteromonadaceae	sf_1	9339	*Pseudoalteromonas* sp. str. 05
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8813	*Lyrodus pedicellatus* symbiont
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9300	*Lyrodus pedicellatus* symbiont
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8487	
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8508	*Pseudomonas citronellolis* str. TERIDB26
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8691	*Pseudomonas aeruginosa* str. PAO1
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8754	*Pseudomonas* sp. str. P400Y-1
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9002	*Paederus fuscipes* endosymbiont
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9056	*Pseudomonas aeruginosa* str. #47
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9588	*Pseudomonas citronellolis* str. TERIDB18
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8288	
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8777	*Pseudomonas* sp. str. KNA6-5
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8852	*Pseudomonas stutzeri* str. KC
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9068	*Pseudomonas stutzeri* str. A1501
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9228	*Pseudomonas stutzeri* HY-105
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9295	
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8344	*Anabaena circinalis* AWQC118C isolate str. UNSW3
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8553	*Pseudomonas fulva* str. IAM 1587
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8725	*Pseudomonas* sp. str. 2N1-1
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8850	*Agrobacterium agile* str. IAM12615
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9238	
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9005	*Pseudomonas* sp. str. KY
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9613	*Pseudomonas flavescens* str. B62
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8474	ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A-MN7 proteobacterium
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8513	*Pseudomonas monteilii* str. CIP 104883
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9049	uranium mining mill tailing clone GR-Sh2-34 GR-Sh2-34
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9219	*Pseudomonas cf. monteilii* 9
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9343	*Cellvibrio* subsp. mixtus str. ACM 2601
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9469	cf. *Pseudomonas* sp. clone Llangefni 52
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9493	*Pseudomonas* sp. str. dcm7B

(*continued*)

TABLE 3. (CONTINUED)

Phylum	*Class*	*Order*	*Family*	*S-F*[a]	*Taxon ID*[b]	*Representative species*[c]
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8209	uranium mining waste pile clone JG37-AG-122 proteobacterium
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8433	*Pseudomonas syringae* pv. broussonetiae str. KOZ 8101 pv.
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8635	
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8853	*Pseudomonas cichorii* str. ATCC 10857T
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9028	*Pseudomonas koreensis* str. Ps 9-14
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9240	*Pseudomonas fluorescens* str. CHA0
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9267	*Pseudomonas syringae* pv. theae str. PT1
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9310	*Pseudomonas* sp. str. AC-167
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8338	*Pseudomonas synxantha* str. DSM 13080 G
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8561	*Pseudomonas* sp. B65
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8601	*Pseudomonas marginalis* str. ATCC 10844T
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8687	*Pseudomonas putida* str. ATCC 17472
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8708	
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9175	*Pseudomonas extremorientalis* str. KMM3447
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9221	*Pseudomonas fulgida* str. DSM 14938 = LMG 2146 P 515/12
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9243	*Pseudomonas tolaasii* str. LMG 2342T ()
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9366	Arctic seawater isolate str. R7366
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8755	*Pseudomonas* sp. SK-1-3-1
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9172	*Pseudomonas psychrophila* str. E-3
Proteobacteria	Betaproteobacteria	Burkholderiales	Ralstoniaceae	sf_1	7823	*Wautersia basilensis* str. DSM 11853
Proteobacteria	Betaproteobacteria	Burkholderiales	Ralstoniaceae	sf_1	8110	*Wautersia paucula* str. LMG 3413
Proteobacteria	Betaproteobacteria	Burkholderiales	Ralstoniaceae	sf_1	8128	*Cupriavidus necator*
Proteobacteria	Betaproteobacteria	Burkholderiales	Ralstoniaceae	sf_1	7761	*Ralstonia detusculanense* str. APF11
Proteobacteria	Betaproteobacteria	Burkholderiales	Ralstoniaceae	sf_1	7778	*Ralstonia insidiosa* str. CCUG 46388
Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	sf_1	7051	*Mycoplana dimorpha* str. IAM 13154
Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	sf_1	6683	*Sinorhizobium fredii* str. ATCC35423
Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	sf_1	6725	*Sinorhizobium meliloti* str. 1021
Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	sf_1	6972	*Ensifer adhaerens* str. LMG 20582
Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	sf_1	6974	India: Himalayas Kaza Spiti Valley Cold Desert isolate str. Kaza-35 Kaza-35
Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	sf_1	6770	*Rhizobium tropici* str. LMG 9517
Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	sf_1	6871	*Rhizobium mongolense* str. USDA 1832
Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	sf_1	7135	*Rhizobium gallicum* str. FL27
Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	sf_1	7568	*Rhizobium etli* str. USDA 2667 ATCC 14483 SEMIA 043
Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	sf_1	6798	*Agrobacterium tumefaciens* TG14
Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	sf_1	6804	*Rhizobium* sp. str. SH19312
Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	sf_1	6964	*Agrobacterium tumefaciens* str. C58 Cereon
Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	sf_1	7334	*Agrobacterium tumefaciens* C4
Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	sf_1	7041	*Rhizobium huautlense* str. SO2 ()
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	sf_1	6701	*Roseobacter* clone NAC11-3
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	sf_1	6980	*Loktanella vestfoldensis* str. LMG 22003

Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	sf_1	7433	*Scrippsiella trochoidea* NEPCC 15
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	sf_1	7453	*Sulfitobacter* sp. BIO-11
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	sf_1	6888	hydrothermal vent strain str. TB66
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	sf_1	7026	*Leisingera methylohalidivorans* str. MB2
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	sf_1	7263	
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	sf_1	7040	*Paracoccus alcaliphilus* str. JCM 7364
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	sf_1	7508	lichen-dominated Antarctic cryptoendolithic community clone FBP492 proteobacterium
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	sf_1	6991	*Rhodobacter sphaeroides* str. 2.4.1
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	sf_1	7084	*Scrippsiella trochoidea* NEPCC 15
Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	sf_1	7800	sample taken upstream landfill clone BVC77 landfill
Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	sf_1	7817	TCE-contaminated site clone ccs265
Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	sf_1	7956	
Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	sf_1	8127	*Zoogloea resiniphila* str. PIV-3A2y
Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	sf_1	8131	
Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	sf_1	7907	*Thauera aromatica* str. LG356
Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	sf_1	7925	*Thauera selenatis* str. ATCC 55363T
Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	sf_1	8156	industrial-phenol-degrading community clone MM1 sp.
Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	sf_1	7824	termite gut homogenate clone Rs-B77 proteobacterium
Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	sf_1	7762	Elbe River snow isolate Iso18 Iso18_1411
Proteobacteria	Alphaproteobacteria	Rickettsiales	Rickettsiaceae	sf_1	7556	*Rickettsia bellii* str. strains 369-C and G2D42
Proteobacteria	Gammaproteobacteria	Oceanospirillales	Saccharospirillaceae	sf_1	8889	hypersaline Mono Lake clone ML110J-5
Proteobacteria	Alphaproteobacteria	Consistiales	SAR11	sf_2	7043	marine clone Arctic95D-8
Proteobacteria	Gammaproteobacteria	Alteromonadales	Shewanellaceae	sf_1	8581	*Shewanella benthica* str. DB21MT-2
Proteobacteria	Gammaproteobacteria	Alteromonadales	Shewanellaceae	sf_1	8641	*Moritella abyssi* str. 2693
Proteobacteria	Gammaproteobacteria	Alteromonadales	Shewanellaceae	sf_1	9081	*Shewanella* sp. str. MTW-1
Proteobacteria	Gammaproteobacteria	Alteromonadales	Shewanellaceae	sf_1	8662	
Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	sf_1	7440	*Sphingobium chungbukense* str. DJ77
Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	sf_1	7528	*Sphingobium yanoikuyae* str. GIFU9882
Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	sf_1	7548	Afipia genosp. 13 str. G8991
Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	sf_1	6650	*Sphingomonas phyllosphaerae* str. FA1
Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	sf_1	7016	*Sphingomonas* sp. str. SAFR-027
Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	sf_1	7535	*Sphingomonas paucimobilis* str. GIFU2395
Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	sf_15	7035	*Sphingomonas asaccharolytica* str. IFO 10564-T
Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	sf_1	7215	travertine hot spring clone SM2B06
Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	sf_1	6663	*Sphingopyxis flavimaris* str. SW-151
Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	sf_1	7100	*Novosphingobium capsulatum* str. GIFU11526
Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	sf_1	7036	*Lutibacterium anuloederans* str. LC8
Proteobacteria	Gammaproteobacteria	Aeromonadales	Succinivibrionaceae	sf_1	8822	*Anaerobiospirillum* sp. str. 3J102
Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	sf_3	10067	benzoate-degrading consortium clone BA044
Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae	sf_1	9864	uranium mining waste pile clone JG37-AG-133 proteobacterium
Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae	sf_1	10013	hydrothermal sediment clone AF420341
Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae	sf_1	10021	uranium mill tailings soil sample clone Sh765B-TzT-29 proteobacterium

(*continued*)

Table 3. (Continued)

Phylum	*Class*	*Order*	*Family*	*S-F*[a]	*Taxon ID*[b]	*Representative species*[c]
Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae	sf_1	9731	uranium mining waste pile clone JG37-AG-90 proteobacterium
Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae	sf_1	9845	uranium mining waste pile clone JG37-AG-128 proteobacterium
Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae	sf_1	10184	granular sludge clone R1p32
Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae	sf_1	10221	granular sludge clone R3p4
Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae	sf_1	10294	*Desulfacinum hydrothermale* str. MT-96
Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacteraceae	sf_1	9661	DCP-dechlorinating consortium clone SHD-1
Proteobacteria	Gammaproteobacteria	Thiotrichales	Thiotrichaceae	sf_3	8321	Wadden Sea sediment clone Dangast A9
Proteobacteria	Gammaproteobacteria	Thiotrichales	Thiotrichaceae	sf_3	8741	marine sediment clone Limfjorden L10
Proteobacteria	Gammaproteobacteria	Thiotrichales	Thiotrichaceae	sf_3	8752	*Beggiatoa* sp. str. MS-81-1c
Proteobacteria	Gammaproteobacteria	Thiotrichales	Thiotrichaceae	sf_3	9015	*Beggiatoa alba* str. B18LD; ATCC 33555
Proteobacteria	Gammaproteobacteria	Thiotrichales	Thiotrichaceae	sf_3	9321	marine sediment clone Tokyo Bay D
Proteobacteria	Gammaproteobacteria	Thiotrichales	Thiotrichaceae	sf_3	8703	*Beggiatoa* sp. str. AA5A
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Unclassified	sf_3	468	marine sediment clone Sva0515
Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	sf_6	7377	Rocky Mountain alpine soil clone W2b-8C
Proteobacteria	Alphaproteobacteria	Verorhodospirilla	Unclassified	sf_1	7109	diesel-polluted Bohai Gulf isolate str. M-5 M-5
Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	sf_6	7340	uranium mining waste pile soil sample clone JG30-KF-AS50
Proteobacteria	Alphaproteobacteria	Azospirillales	Unclassified	sf_1	7400	sphagnum peat bog clone K-5b5
Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	sf_6	6694	forested wetland clone RCP2-92
Proteobacteria	Alphaproteobacteria	Azospirillales	Unclassified	sf_1	6732	*Anabaena circinalis* AWQC118C isolate str. UNSW7
Proteobacteria	Alphaproteobacteria	Acetobacterales	Unclassified	sf_1	7028	
Proteobacteria	Alphaproteobacteria	Ellin314/wr0007	Unclassified	sf_1	7123	uranium mining waste pile near Johanngeorgenstadt soil clone JG37-AG-102
Proteobacteria	Alphaproteobacteria	Ellin314/wr0007	Unclassified	sf_1	7222	Great Artesian Basin clone B79
Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	sf_6	7575	
Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	sf_1	6726	
Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	sf_6	6920	Pseudovibrio denitrificans str. DN34
Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	sf_6	6954	
Proteobacteria	Alphaproteobacteria	Ellin329/Riz1046	Unclassified	sf_1	6945	*Rhizobiales* str. A48
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Unclassified	sf_1	7067	*Blastochloris sulfoviridis* str. GN1
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Unclassified	sf_1	7264	Bosea thiooxidans TJ1
Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	sf_1	7339	
Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	sf_6	6898	heavy metal-contaminated soil clone a13113
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Unclassified	sf_1	7199	uranium mill tailings clone Gitt-KF-194
Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	sf_1	6899	
Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	sf_6	6665	hydrocarbon-degrading consortium clone 4-Org2-22
Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	sf_6	7312	
Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	sf_1	6789	*Shinella zoogloeoides* str. ATCC 19623
Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	sf_2	6697	termite gut homogenate clone Rs-D84 proteobacterium

Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	sf_2	7188	termite gut homogenate clone Rs-B50 proteobacterium
Proteobacteria	Alphaproteobacteria	Consistiales	Unclassified	sf_4	7105	Mariana trough hydrothermal vent water 0.2micro-m filterable fraction clone MT-NB25
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Unclassified	sf_5	7471	sponge clone TK03
Proteobacteria	Alphaproteobacteria	Consistiales	Unclassified	sf_5	6735	*Candidatus Pelagibacter* ubique str. HTCC1002
Proteobacteria	Unclassified	Unclassified	Unclassified	sf_20	6763	
Proteobacteria	Alphaproteobacteria	Rickettsiales	Unclassified	sf_2	6639	
Proteobacteria	Alphaproteobacteria	Rickettsiales	Unclassified	sf_1	7156	termite gut homogenate clone Rs-M62 proteobacterium
Proteobacteria	Deltaproteobacteria	AMD clone group	Unclassified	sf_1	6830	coal effluent wetland clone RCP124
Proteobacteria	Alphaproteobacteria	Sphingomonadales	Unclassified	sf_1	6653	*Kaistobacter koreensis* str. PB229
Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Unclassified	sf_1	7382	marine clone Arctic95C-5
Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	sf_6	6987	
Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	sf_6	7572	
Proteobacteria	Betaproteobacteria	Burkholderiales	Unclassified	sf_1	8035	
Proteobacteria	Betaproteobacteria	MND1 clone group	Unclassified	sf_1	7808	Mammoth cave clone CCU25
Proteobacteria	Betaproteobacteria	Unclassified	Unclassified	sf_3	8007	
Proteobacteria	Betaproteobacteria	Unclassified	Unclassified	sf_3	8036	Uranium mill tailings soil sample clone Sh765B-TzT-132 proteobacterium
Proteobacteria	Betaproteobacteria	Unclassified	Unclassified	sf_3	7974	
Proteobacteria	Betaproteobacteria	Unclassified	Unclassified	sf_3	8114	
Proteobacteria	Betaproteobacteria	MND1 clone group	Unclassified	sf_1	8023	ferromanganous micronodule clone MND1
Proteobacteria	Betaproteobacteria	Unclassified	Unclassified	sf_3	8045	
Proteobacteria	Betaproteobacteria	MND1 clone group	Unclassified	sf_1	7818	soil sample uranium mining waste pile near town Johanngeorgenstadt clone JG36-TzT-215 proteobacterium
Proteobacteria	Betaproteobacteria	Neisseriales	Unclassified	sf_1	8037	*Chitinimonas taiwanensis* str. cf
Proteobacteria	Betaproteobacteria	Unclassified	Unclassified	sf_3	7997	
Proteobacteria	Gammaproteobacteria	uranium waste clones	Unclassified	sf_1	8747	uranium waste soil clone JG30-KF-CM35
Proteobacteria	Gammaproteobacteria	GAO cluster	Unclassified	sf_1	9059	activated sludge clone SBRH10
Proteobacteria	Gammaproteobacteria	aquatic clone group	Unclassified	sf_1	9246	Mammoth Cave sediment clone CCD24
Proteobacteria	Gammaproteobacteria	Unclassified	Unclassified	sf_3	9498	
Proteobacteria	Gammaproteobacteria	Unclassified	Unclassified	sf_3	9568	forested wetland clone RCP2-96
Proteobacteria	Gammaproteobacteria	Chromatiales	Unclassified	sf_1	9282	
Proteobacteria	Gammaproteobacteria	Legionellales	Unclassified	sf_1	9418	uranium mining waste pile clone JG37-AG-14 proteobacterium
Proteobacteria	Deltaproteobacteria	EB1021 group	Unclassified	sf_4	8169	forested wetland clone RCP2-54
Proteobacteria	Gammaproteobacteria	Symbionts	Unclassified	sf_1	8403	Selenate-reducing isolate str. KE4OH1
Proteobacteria	Gammaproteobacteria	Unclassified	Unclassified	sf_3	8488	
Proteobacteria	Gammaproteobacteria	Unclassified	Unclassified	sf_3	8646	
Proteobacteria	Gammaproteobacteria	Unclassified	Unclassified	sf_3	8676	
Proteobacteria	Gammaproteobacteria	Unclassified	Unclassified	sf_3	8926	inactive deep-sea hydrothermal vent chimneys clone IheB2-13
Proteobacteria	Gammaproteobacteria	aquatic clone group	Unclassified	sf_1	8957	marine clone Arctic97C-5
Proteobacteria	Gammaproteobacteria	Unclassified	Unclassified	sf_3	9105	
Proteobacteria	Gammaproteobacteria	Unclassified	Unclassified	sf_3	9124	10e-6 dilution marine samples Weser estuary clone DC8-80-1 proteobacterium

(*continued*)

Table 3. (Continued)

Phylum	*Class*	*Order*	*Family*	*S-F*[a]	*Taxon ID*[b]	*Representative species*[c]
Proteobacteria	Gammaproteobacteria	Symbionts	Unclassified	sf_1	9128	Lucina nassula gill symbiont
Proteobacteria	Gammaproteobacteria	Unclassified	Unclassified	sf_3	9394	
Proteobacteria	Gammaproteobacteria	Symbionts	Unclassified	sf_1	9556	*Seepiophila jonesi* symbiont
Proteobacteria	Gammaproteobacteria	SUP05	Unclassified	sf_1	8605	bacterioplankton clone ZA2525c
Proteobacteria	Gammaproteobacteria	SUP05	Unclassified	sf_1	8654	inactive deep-sea hydrothermal vent chimneys clone IheB2-31
Proteobacteria	Gammaproteobacteria	SUP05	Unclassified	sf_1	8965	*Bathymodiolus thermophilus* gill symbiont
Proteobacteria	Gammaproteobacteria	uranium waste clones	Unclassified	sf_1	8231	uranium waste soil clone JG30a-KF-21
Proteobacteria	Gammaproteobacteria	Unclassified	Unclassified	sf_3	8339	water 5 m downstream manure clone 35ds5
Proteobacteria	Gammaproteobacteria	Ellin307/WD2124	Unclassified	sf_1	8532	
Proteobacteria	Gammaproteobacteria	Ellin307/WD2124	Unclassified	sf_1	9458	uranium mining waste pile clone JG37-AG-94 proteobacterium
Proteobacteria	Gammaproteobacteria	SAR86	Unclassified	sf_1	8962	bacterioplankton clone AEGEAN_234
Proteobacteria	Gammaproteobacteria	Legionellales	Unclassified	sf_3	8587	Mars Odyssey Orbiter and encapsulation facility clone T5-3
Proteobacteria	Gammaproteobacteria	GAO cluster	Unclassified	sf_1	9468	activated sludge clone SBRL2_40
Proteobacteria	Gammaproteobacteria	Unclassified	Unclassified	sf_4	8855	
Proteobacteria	Unclassified	Unclassified	Unclassified	sf_8	9558	
Proteobacteria	Gammaproteobacteria	Oceanospirillales	Unclassified	sf_3	8230	
Proteobacteria	Gammaproteobacteria	Unclassified	Unclassified	sf_3	8245	
Proteobacteria	Gammaproteobacteria	Unclassified	Unclassified	sf_3	8883	
Proteobacteria	Gammaproteobacteria	Unclassified	Unclassified	sf_3	9044	hydrothermal sediment clone AF420370
Proteobacteria	Gammaproteobacteria	Thiotrichales	Unclassified	sf_1	8323	hydrothermal sediment clone AF420363
Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	sf_6	8780	uranium mining mill tailing clone GR-296.II.89 GR-296.II.89
Proteobacteria	Gammaproteobacteria	Oceanospirillales	Unclassified	sf_3	8327	Arctic sea ice ARK10148
Proteobacteria	Gammaproteobacteria	Unclassified	Unclassified	sf_3	8606	
Proteobacteria	Gammaproteobacteria	Unclassified	Unclassified	sf_3	8714	*Marinobacter hydrocarbonoclasticus* str. ATCC 27132T
Proteobacteria	Gammaproteobacteria	Unclassified	Unclassified	sf_3	8959	bacterioplankton clone AEGEAN_133
Proteobacteria	Gammaproteobacteria	Alteromonadales	Unclassified	sf_1	8483	*Rheinheimera baltica* str. OS140 Baltic # 166
Proteobacteria	Gammaproteobacteria	Shewanella	Unclassified	sf_1	9344	*Shewanella algae* str. ATCC 51192
Proteobacteria	Gammaproteobacteria	Unclassified	Unclassified	sf_3	9367	USA: Pacific Ocean seawater Naha Vents Hawaii isolate str. PV-4
Proteobacteria	Gammaproteobacteria	Unclassified	Unclassified	sf_3	9473	Arctic pack ice; northern Fram Strait; 80 31.1 N; 01 deg 59.7 min E clone ARKDMS-58
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Unclassified	sf_1	8430	*Salmonella bongori* str. JEO 4162
Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Unclassified	sf_1	9828	termite gut homogenate clone Rs-M89 proteobacterium
Proteobacteria	Deltaproteobacteria	Myxococcales	Unclassified	sf_1	10092	heavy metal-contaminated soil clone a13134
Proteobacteria	Deltaproteobacteria	Myxococcales	Unclassified	sf_1	10259	
Proteobacteria	Deltaproteobacteria	Unclassified	Unclassified	sf_7	10048	
Proteobacteria	Deltaproteobacteria	Unclassified	Unclassified	sf_9	10049	DCP-dechlorinating consortium clone SHA-72
Proteobacteria	Deltaproteobacteria	Unclassified	Unclassified	sf_9	9760	deep marine sediment clone MB-A2-137
Proteobacteria	Deltaproteobacteria	Unclassified	Unclassified	sf_9	9784	Antarctic sediment clone LH5_30

Proteobacteria	Deltaproteobacteria	Unclassified	Unclassified	sf_9	9798	uranium mill tailings soil sample clone GuBH2-AD/TzT-67 proteobacterium
Proteobacteria	Deltaproteobacteria	Unclassified	Unclassified	sf_9	9876	deep marine sediment clone MB-B2-106
Proteobacteria	Deltaproteobacteria	EB1021 group	Unclassified	sf_4	9884	forested wetland clone RCP2-62
Proteobacteria	Deltaproteobacteria	AMD clone group	Unclassified	sf_1	10084	acid mine drainage clone AS6
Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Unclassified	sf_1	10076	Great Artesian Basin clone G13
Proteobacteria	Deltaproteobacteria	dechlorinating clone group	Unclassified	sf_1	9959	forested wetland clone FW110
Proteobacteria	Deltaproteobacteria	EB1021 group	Unclassified	sf_4	10024	hydrothermal sediment clone AF420338
Proteobacteria	Deltaproteobacteria	AMD clone group	Unclassified	sf_1	9678	coal effluent wetland clone RCP185
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Unclassified	sf_4	9951	forested wetland clone FW13
Proteobacteria	Deltaproteobacteria	Unclassified	Unclassified	sf_9	9738	marine methane seep clone 1513
Proteobacteria	Deltaproteobacteria	AMD clone group	Unclassified	sf_1	9945	acid mine drainage clone BA18
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Unclassified	sf_3	9813	hydrothermal sediment clone AF420340
Proteobacteria	Deltaproteobacteria	Unclassified	Unclassified	sf_9	9890	termite gut homogenate clone Rs-K70 proteobacterium
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Unclassified	sf_1	10543	hydrothermal vent clone PVB_10
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Unclassified	sf_1	10427	hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH3_17_BAC_16SrRNA_9N_EPR
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Unclassified	sf_1	10475	hydrothermal sediment clone AF420359
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Unclassified	sf_1	10480	*Paralvinella palmiformis* mucus secretions clone P. palm C 84 proteobacterium
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Unclassified	sf_1	10489	S17sBac16 complete clone
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Unclassified	sf_1	10497	UASB reactor granular sludge clone PD-UASB-2 proteobacterium
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Unclassified	sf_1	10530	hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH5_6_BAC_16SrRNA_9N_EPR
Proteobacteria	Unclassified	Unclassified	Unclassified	sf_20	2520	
Proteobacteria	Deltaproteobacteria	Unclassified	Unclassified	sf_9	244	deep marine sediment clone MB-C2-152
Proteobacteria	Deltaproteobacteria	AMD clone group	Unclassified	sf_1	3084	coal effluent wetland clone RCP216
Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	sf_1	8999	*Photobacterium leiognathi* str. LN101
Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	sf_1	8665	*Vibrio gallicus* str. CIP 107867; HT 3-3
Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	sf_1	8267	*Vibrio pomeroyi* str. LMG 20537
Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	sf_1	8798	*Vibrio aestuarianus* str. KT0901
Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	sf_1	8888	*Vibrio aestuarianus* str. 01/151
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Xanthobacteraceae	sf_1	6660	*Azorhizobium caulinodans* str. ORS 571
Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	sf_3	9167	pea aphid symbiont clone APe4_38
Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	sf_3	8689	*Dyemonas todaii* str. XD10
Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	sf_3	9332	wetland ecosystem constructed to remediate mine drainage isolate str. WJ2 WJ2
Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	sf_3	8392	penguin droppings sediments clone KD2-14
Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	sf_3	8983	Iron oxidizing strain ES-1
Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	sf_3	9031	municipal wastewater treatment bioreactor clone LB-P bacterium
Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	sf_3	9320	Waste-gas biofilter clone BIyi3
Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	sf_3	8577	*Xanthomonas axonopodis* pv. citri str. MA
Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	sf_3	9569	

(*continued*)

Table 3. (Continued)

Phylum	*Class*	*Order*	*Family*	*S-F*[a]	*Taxon ID*[b]	*Representative species*[c]
Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	sf_3	8538	
Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	sf_3	8563	*Pseudoxanthomonas mexicana* str. AMX 26B
Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	sf_3	9270	*Stenotrophomonas rhizophila* str. e-p10
Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	sf_3	9286	*Stenotrophomonas maltophilia* str. LMG 11104
SPAM	Unclassified	Unclassified	Unclassified	sf_1	705	uranium tailings soil clone Sh765B-AG-45
SPAM	Unclassified	Unclassified	Unclassified	sf_1	738	uranium mining waste clone JG34-KF-252
Spirochaetes	Spirochaetes	Spirochaetales	Leptospiraceae	sf_3	6496	*Leptospira interrogans* serovar Copenhageni str. Fiocruz L1-130
Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	sf_1	6459	*Spirochaeta* sp. str. BHI80-158
Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	sf_3	6558	*Spironema culicis* str. BR91
Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	sf_1	6526	*Treponema* sp. str. 7CPL208
Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	sf_1	6479	*Treponema* sp
Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	sf_1	6580	*Treponema* sp. str. III:C:BA213
Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	sf_1	6458	termite gut clone NkS34
Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	sf_1	6494	termite gut homogenate clone Rs-C47 sp.
Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	sf_1	6562	forested wetland clone RCP1-96
Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	sf_1	6507	termite gut clone NkS-Ste2
Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	sf_1	6476	termite gut clone NkS50
Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	sf_1	6488	*Treponema primitia* str. ZAS-1
Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	sf_1	6490	termite gut homogenate clone BCf4-14
Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	sf_1	6491	termite gut homogenate clone BCf8-03
Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	sf_1	6506	termite gut homogenate clone Rs-J58 sp.
Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	sf_1	6508	termite hindgut clone mpsp2
Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	sf_1	6523	termite gut homogenate clone Rs-J64 sp.
Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	sf_1	6565	termite gut clone NkS-Oxy25
Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	sf_1	6571	*Mixotricha paradoxa* is flagellate hindgut Mastotermes darwiniensis clone mp4 of
Synergistes	Unclassified	Unclassified	Unclassified	sf_3	117	termite gut homogenate clone Rs-D89
Synergistes	Unclassified	Unclassified	Unclassified	sf_3	353	UASB reactor granular sludge clone PD-UASB-13 G+C
Synergistes	Unclassified	Unclassified	Unclassified	sf_3	60	*Flexistipes* sp. str. E3_33
Synergistes	Unclassified	Unclassified	Unclassified	sf_3	601	terephthalate-degrading consortium clone TA19
Synergistes	Unclassified	Unclassified	Unclassified	sf_3	719	*Synergistes* sp. P1 str. P4G_18
Synergistes	Unclassified	Unclassified	Unclassified	sf_3	740	swine intestine clone p-4292-4Wa3
Synergistes	Unclassified	Unclassified	Unclassified	sf_3	808	oral cavity clone BH017
Termite group 1	Unclassified	Unclassified	Unclassified	sf_2	437	termite gut homogenate clone Rs-D43 group
Thermodesulfobacteria	Thermodesulfobacteria	Thermodesulfobacteriales	Thermodesulfobacteriaceae	sf_1	667	*Geothermobacterium ferrireducens*
Thermotogae	Thermotogae	Thermotogales	Thermotogaceae	sf_4	51	*Thermosipho* sp. str. MV1063
TM6	Unclassified	Unclassified	Unclassified	sf_1	9803	forest soil clone S1204
TM7	Unclassified	Unclassified	Unclassified	sf_1	5177	
TM7	TM7-3	Unclassified	Unclassified	sf_1	8155	oral periodontitis clone EW086
TM7	TM7-3	Unclassified	Unclassified	sf_1	2697	midgut homogenate Pachnoda ephippiata larva clone PeM47
TM7	Unclassified	Unclassified	Unclassified	sf_1	3025	
Unclassified	Unclassified	Unclassified	Unclassified	sf_93	925	4MB-degrading consortium clone UASB_TL26

Unclassified	Unclassified	Unclassified	Unclassified	sf_106	243	hot spring clone OPB25
Unclassified	Unclassified	Unclassified	Unclassified	sf_160	485	thermal spring mat clone O1aA90
Unclassified	Unclassified	Unclassified	Unclassified	sf_160	226	
Unclassified	Unclassified	Unclassified	Unclassified	sf_160	333	
Unclassified	Unclassified	Unclassified	Unclassified	sf_160	651	
Unclassified	Unclassified	Unclassified	Unclassified	sf_160	6430	
Unclassified	Unclassified	Unclassified	Unclassified	sf_160	6456	
Unclassified	Unclassified	Unclassified	Unclassified	sf_160	6360	
Unclassified	Unclassified	Unclassified	Unclassified	sf_140	6355	
Unclassified	Unclassified	Unclassified	Unclassified	sf_160	7444	
Unclassified	Unclassified	Unclassified	Unclassified	sf_160	7767	
Unclassified	Unclassified	Unclassified	Unclassified	sf_160	10012	
Unclassified	Unclassified	Unclassified	Unclassified	sf_95	2545	anaerobic sludge isolate str. JE
Unclassified	Unclassified	Unclassified	Unclassified	sf_160	2488	
Unclassified	Unclassified	Unclassified	Unclassified	sf_156	4291	Mono Lake at depth 35m station 6 July 2000 clone ML635J-21 G+C
Unclassified	Unclassified	Unclassified	Unclassified	sf_160	4410	
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Unclassified	sf_4	169	anoxic marine sediment clone LD1-PA26
Verrucomicrobia	Unclassified	Unclassified	Unclassified	sf_3	40	Elbe river clone DEV055
Verrucomicrobia	Unclassified	Unclassified	Unclassified	sf_3	486	Elbe river clone DEV045
Verrucomicrobia	Unclassified	Unclassified	Unclassified	sf_5	686	hydrothermal vent sediment clone a2b018
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Unclassified	sf_3	11	sludge clone H2
Verrucomicrobia	Unclassified	Unclassified	Unclassified	sf_4	288	*Prosthecobacter dejongeii*
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Unclassified	sf_3	792	termite gut homogenate clone Rs-P07 bacterium
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobia SD 5	sf_1	530	anoxic marine sediment clone LD1-PB20
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobia SD 5	sf_1	533	anoxic marine sediment clone LD1-PB12
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobia SD 5	sf_1	547	anoxic marine sediment clone LD1-PB1
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobia SD 5	sf_1	629	anoxic marine sediment clone LD1-PA50
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobia SD 7	sf_1	446	anoxic marine sediment clone LD1-PA34
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobia SD 7	sf_1	559	anoxic marine sediment clone LD1-PA20
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobia SD 7	sf_1	760	Mono lake clone ML316M-1
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	sf_7	29	*Fucophilus fucoidanolyticus* str. SI-1234
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	sf_6	871	
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Xiphinematobacteraceae	sf_3	888	Candidatus *Xiphinematobacter brevicolli*
WS3	Unclassified	Unclassified	Unclassified	sf_3	95	marine sediment above hydrate ridge clone Hyd24-32
WS3	Unclassified	Unclassified	Unclassified	sf_1	2537	anoxic marine sediment clone LD1-PA39
WS5	Unclassified	Unclassified	Unclassified	sf_2	8119	hydrothermal vent sediment clone a2b013

[a] S-F, Subfamily identification; [b] Taxon ID, PhyloChip Taxon identification number; [c] Representative species, Taxon bacterial species identifier.

Table 4. Bacterial Taxa with Significant Differences in Relative Abundance between COPD Patient Group 1 (≤6 Intubation Days) and Group 2 (≥16 Intubation Days)

Phylum	*Class*	*Order*	*Family*	*S-F*[a]	*Taxon ID*[b]	*Representative species*[c]	p-*value*	q-*value*	*Fluorescence difference (Group 1 – Group 2)*
Firmicutes	Symbiobacteria	Symbiobacterales	Unclassified	1	77	thermal soil clone YNPFFP9	<0.001	<0.01	1264
Proteobacteria	Deltaproteobacteria	Unclassified	Unclassified	9	244	deep marine sediment clone MB-C2-152	<0.02	<0.05	1048
Chloroflexi	Anaerolineae	Unclassified	Unclassified	9	375	forest soil clone C043	<0.02	<0.05	1873
Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	1	482	trichloroethene-contaminated site clone FTLM205 proteobacterium	≤0.01	<0.05	1092
OP10	CH21 cluster	Unclassified	Unclassified	1	514	sludge clone SBRA136	<0.01	<0.05	1081
Chlorobi	Unclassified	Unclassified	Unclassified	8	636	benzene-degrading nitrate-reducing consortium clone Cart-N3 bacterium	<0.01	<0.05	1475
Unclassified	Unclassified	Unclassified	Unclassified	160	651		<0.01	<0.05	1750
Chloroflexi	Unclassified	Unclassified	Unclassified	7	757	DCP-dechlorinating consortium clone SHA-8	<0.001	<0.01	1619
Natronoanaerobium	Unclassified	Unclassified	Unclassified	1	769	fjord ikaite column clone un-c23	<0.001	<0.01	1305
Firmicutes	Clostridia	Clostridiales	Peptococc/ Acidaminococc	11	940	*Veillonella dispar* str. DSM 20735	<0.01	<0.05	1150
OP9/JS1	OP9	Unclassified	Unclassified	1	969	DCP-dechlorinating consortium clone SHA-1	<0.02	<0.05	1190
Firmicutes	Bacilli	Bacillales	Bacillaceae	1	1050	*Bacillus firmus* CV93b	≤0.001	<0.05	1746
Actinobacteria	Actinobacteria	Unclassified	Unclassified	1	1898	termite gut homogenate clone Rs-J10 bacterium	<0.01	<0.05	1906
AD3	Unclassified	Unclassified	Unclassified	1	2338	uranium mining waste pile soil clone JG30-KF-C12	<0.001	<0.01	1148
Chloroflexi	Dehalococcoidetes	Unclassified	Unclassified	1	2339	uranium mill tailings soil sample clone Sh765B-TzT-20 bacterium	<0.02	<0.05	1532
Chloroflexi	Unclassified	Unclassified	Unclassified	1	2534	forest soil clone S085	<0.001	<0.01	1193
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	5	2668	termite gut homogenate clone Rs-G40 bacterium	<0.01	<0.05	2395
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	5	2694	oral periodontitis clone FX028	<0.02	<0.05	1338
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	5	2714	termite gut homogenate clone Rs-N27 bacterium	<0.01	<0.05	2061
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	5	2729	DCP-dechlorinating consortium clone SHA-58	<0.01	<0.05	1402
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	5	2797	Isolation and identification hyper-ammonia producing swine storage pits manure	<0.01	<0.05	1611
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	5	2805	oral periodontitis clone FX033	<0.02	<0.05	1625
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	5	2834	*Butyrivibrio fibrisolvens* str. OB156	<0.01	<0.05	1005
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	5	2994	termite gut clone Rs-L15	<0.001	<0.01	3929

Firmicutes	Clostridia	Clostridiales	Clostridiaceae	12	3021	*Clostridium caminithermale* str. DVird3	<0.01	<0.05	1944
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	5	3038	swine intestine clone p-1594-c5	<0.01	<0.05	1363
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	5	3059	*Butyrivibrio fibrisolvens* str. NCDO 2249	<0.01	<0.05	1069
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	5	3060	termite gut homogenate clone Rs-B14 bacterium	<0.001	<0.01	3703
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	5	3076	*Clostridium nexile*	<0.001	<0.01	1395
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	12	3077	*Clostridium glycolicum* str. DSM 1288	<0.01	<0.05	1953
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	5	3171	*Lachnospira pectinoschiza*	<0.01	<0.05	1398
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	5	3182	termite gut homogenate clone Rs-Q64 bacterium	≤ 0.01	<0.05	1107
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	1	3250	*Streptococcus bovis* str. B315	<0.001	<0.01	4284
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	1	3251	*Streptococcus cristatus* str. ATCC 51100	<0.01	<0.05	3986
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	1	3253	derived cheese sample clone 32CR	<0.02	<0.05	2680
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	1	3258	*Staphylococcus auricularis* str. MAFF911484 ATCC33753T	<0.01	<0.05	1525
Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	1	3261	*Enterococcus mundtii* str. LMG 10748	<0.02	<0.05	2560
Firmicutes	Bacilli	Bacillales	Bacillaceae	1	3283	*Bacillus niacini* str. IFO15566	<0.01	<0.05	1201
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	1	3284		<0.01	<0.05	1347
Firmicutes	Bacilli	Bacillales	Caryophanaceae	1	3285	*Caryophanon latum* str. DSM 14151	<0.01	<0.05	1499
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	1	3287	tongue dorsum scrapings clone FP015	<0.01	<0.05	3582
Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	1	3288	Isolation and identification hyper-ammonia producing swine storage pits manure	<0.01	<0.05	2528
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	1	3290	*Streptococcus mitis* str. Sm91	≤ 0.01	<0.05	3971
Firmicutes	Bacilli	Bacillales	Paenibacillaceae	1	3299	*Brevibacillus borstelensis* str. LMG 15536	<0.02	<0.05	1035
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	1	3313	*Streptococcus salivarius* str. ATCC 7073	<0.001	<0.01	3189
Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	1	3318	*Enterococcus ratti* str. ATCC 700914	<0.02	<0.05	2272
Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	1	3323	*Trichococcus flocculiformis* str. DSM 2094	<0.01	<0.05	1431
Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	1	3326	*Nostocoida limicola* I str. Ben206	<0.01	<0.05	2363
Firmicutes	Bacilli	Bacillales	Bacillaceae	1	3328	*Pseudobacillus carolinae*	<0.001	<0.01	2370
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	1	3330	*Lactobacillus kitasatonis* str. KM9212	<0.02	<0.05	1389
Firmicutes	Bacilli	Bacillales	Sporolactobacillaceae	1	3365	*Bacillus* sp. clone ML615J-19	<0.001	<0.01	1757
Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	1	3386	feedlot manure clone B87	<0.01	<0.05	2321
Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	1	3392	*Vagococcus lutrae* str. m1134/97/1; CCUG 39187	<0.001	≤ 0.01	1976

(*continued*)

Table 4. (Continued)

Phylum	*Class*	*Order*	*Family*	*S-F*[a]	*Taxon ID*[b]	*Representative species*[c]	p-*value*	q-*value*	*Fluorescence difference (Group 1 – Group 2)*
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	1	3397	*Streptococcus macedonicus* str. ACA-DC 206 LAB617	<0.01	<0.05	4011
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	1	3418	*Lactobacillus* subsp. aviarius	<0.01	<0.05	3036
Firmicutes	Bacilli	Bacillales	Bacillaceae	1	3419	*Bacillus algicola* str. KMM 3737	<0.01	<0.05	1590
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	1	3422	*Streptococcus thermophilus* str. DSM 20617	<0.01	<0.05	3243
Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	1	3433	*Tetragenococcus muriaticus*	<0.01	<0.05	2715
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	1	3446	*Streptococcus bovis* str. HJ50	<0.01	<0.05	3846
Firmicutes	Bacilli	Lactobacillales	Unclassified	1	3481		<0.01	<0.05	2102
Firmicutes	Bacilli	Bacillales	Bacillaceae	1	3489	*Bacillus silvestris* str. SAFN-010	<0.001	<0.01	1206
Firmicutes	Bacilli	Bacillales	Bacillaceae	1	3492	*Bacillus subtilis* str. IAM 12118T	<0.01	<0.05	1320
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	1	3494	*Micrococcus luteus* B-P 26	≤ 0.01	<0.05	1334
Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae	1	3497	*Weissella koreensis* S-5673	<0.02	<0.05	1457
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	1	3499	Streptococcus constellatus str. ATCC27823	<0.01	<0.05	4476
Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	1	3504	*Marinilactibacillus psychrotolerans* str. O21	<0.01	<0.05	1505
Firmicutes	Bacilli	Bacillales	Bacillaceae	1	3517	*Planococcus maritimus* str. TF-9	<0.01	<0.05	1358
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	1	3521	*Pediococcus inopinatus* str. DSM 20285	<0.001	<0.05	1122
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	1	3526	*Lactobacillus sakei*	<0.02	<0.05	1609
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	1	3545		<0.01	<0.05	1372
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	1	3547	*Lactobacillus frumenti* str. TMW 1.666	<0.01	<0.05	1491
Firmicutes	Bacilli	Bacillales	Bacillaceae	1	3550	*Bacillus megaterium* str. QM B1551	≤ 0.001	<0.05	1620
Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	1	3553	*Desemzia incerta* str. DSM 20581	<0.001	<0.01	1553
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	1	3560	*Streptococcus gallinaceus* str. CCUG 42692	<0.001	<0.01	2835
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	1	3566	*Lactobacillus pontis* str. LTH 2587	<0.01	<0.05	2320
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	1	3569	*Staphylococcus saprophyticus*	<0.01	<0.05	1391
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	1	3588	*Streptococcus downei* str. ATCC 33748	<0.01	<0.05	2440
Firmicutes	Bacilli	Bacillales	Bacillaceae	1	3589	*Bacillus senegalensis* str. RS8; CIP 106 669	≤ 0.02	<0.05	1198
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	1	3592	*Staphylococcus caprae* str. DSM 20608	≤ 0.01	<0.05	1322
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	1	3605		<0.01	<0.05	1472
Firmicutes	Bacilli	Bacillales	Bacillaceae	1	3612	*Bacillus schlegelii* str. ATCC 43741T	<0.01	<0.05	1224
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	1	3628	*Staphylococcus haemolyticus* str. CCM2737	<0.01	<0.05	1572
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	1	3629	*Streptococcus mutans* str. UA96	<0.01	<0.05	1466

Firmicutes	Bacilli	Bacillales	Halobacillaceae	1	3633	*Bacillus clausii* str. GMBAE 42	<0.001	<0.01	2363
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	1	3634	*Lactobacillus letivazi* str. JCL3994	<0.01	<0.05	1586
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	1	3638	*Staphylococcus* sp str. AG-30	<0.01	<0.05	1359
Firmicutes	Bacilli	Bacillales	Paenibacillaceae	1	3641	*Brevibacillus* sp. MN 47.2a	<0.02	<0.05	1735
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	1	3654	*Staphylococcus pettenkoferi* str. B3117	<0.01	<0.05	1310
Firmicutes	Bacilli	Bacillales	Bacillaceae	1	3661	*Bacillus* sp. str. 2216.25.2	<0.01	<0.05	1593
Firmicutes	Bacilli	Bacillales	Bacillaceae	1	3675	*Bacillus mojavensis* str. M-1	<0.01	<0.05	1535
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	1	3684	*Staphylococcus sciuri*	<0.02	<0.05	1324
Firmicutes	Bacilli	Bacillales	Halobacillaceae	1	3702	*Amphibacillus xylanus* str. DSM 6626	≤0.01	<0.05	1523
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	1	3703	*Lactobacillus salivarius* str. RA2115	<0.01	<0.05	1636
Firmicutes	Bacilli	Bacillales	Bacillaceae	1	3706	*Bacillus sonorensis* str. NRRL B-23155	<0.02	<0.05	1324
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	1	3722	*Lactococcus* Il1403 subsp. lactis str. IL1403	≤0.001	<0.05	2673
Firmicutes	Bacilli	Bacillales	Sporolactobacillaceae	1	3747	*Bacillus* sp. str. C-59-2	<0.001	<0.01	1959
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	1	3753	*Streptococcus suis* str. 8074	<0.02	<0.05	3463
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	1	3767	*Lactobacillus suebicus* str. CECT 5917T	<0.01	<0.05	2031
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	1	3768	*Lactobacillus perolens* str. L532	<0.001	<0.001	1593
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	1	3794		<0.01	<0.05	1324
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	1	3822	*Staphylococcus succinus* str. SB72	<0.01	<0.05	1358
Firmicutes	Bacilli	Bacillales	Bacillaceae	1	3827	*Bacillus acidogenesis* str. 105-2	<0.01	<0.05	1996
Firmicutes	Bacilli	Bacillales	Bacillaceae	1	3831	*Bacillus licheniformis* str. KL-068	<0.01	<0.05	2057
Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	1	3833	*Carnobacterium alterfunditum*	<0.001	<0.01	2781
Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	1	3840	*Trichococcus pasteurii* str. KoTa2	<0.001	<0.01	2656
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	1	3869	*Streptococcus equi* subsp. zooepidemicus str. Tokyo1291 subsp.	≤0.01	<0.05	1766
Firmicutes	Bacilli	Bacillales	Bacillaceae	1	3900	*Bacillus licheniformis* str. DSM 13	<0.01	<0.05	1261
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	1	3906	*Streptococcus bovis* str.ATCC 43143	<0.001	<0.01	4284
Firmicutes	Bacilli	Bacillales	Bacillaceae	1	3909	*Bacillus subtilis* subsp. Marburg str. 168	<0.01	<0.05	1367
Firmicutes	Bacilli	Bacillales	Bacillaceae	1	3918	*Bacillus subtilis*	<0.001	<0.01	1486
Firmicutes	Mollicutes	Anaeroplasmatales	Erysipelotrichaceae	3	3965	TCE-contaminated site clone ccslm238	≤0.01	<0.05	1844
Firmicutes	Mollicutes	Anaeroplasmatales	Erysipelotrichaceae	3	3981	phototrophic sludge clone PSB-M-3	<0.01	<0.05	1361
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	12	4180	termite gut homogenate clone Rs-M23 bacterium	<0.01	<0.05	1383
Firmicutes	Clostridia	Unclassified	Unclassified	7	4216		<0.001	<0.01	2447
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	12	4266	termite gut homogenate clone Rs-M86 bacterium	<0.01	<0.05	1302
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	5	4281	granular sludge clone UASB_brew_B86	≤0.001	<0.05	1333
Firmicutes	gut clone group	Unclassified	Unclassified	1	4298	human mouth clone P4PA_66	<0.01	<0.05	1991

(continued)

Table 4. (Continued)

Phylum	*Class*	*Order*	*Family*	*S-F*[a]	*Taxon ID*[b]	*Representative species*[c]	p-*value*	q-*value*	*Fluorescence difference (Group 1 – Group 2)*
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	12	4306	UASB reactor granular sludge clone PD-UASB-4 bacterium	<0.01	<0.05	1483
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	12	4321	termite gut homogenate clone Rs-C76 bacterium	≤0.01	<0.05	1362
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	5	4331	granular sludge clone UASB_brew_B84	<0.01	<0.05	1091
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	12	4339	*Clostridium chauvoei* str. ATCC 10092T	<0.02	<0.05	1542
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	12	4369	termite gut homogenate clone Rs-N73 bacterium	<0.01	<0.05	1579
Natronoanaerobium	Unclassified	Unclassified	Unclassified	1	4377	Mono Lake at depth 35 m station 6 July 2000 clone ML635J-65 G+C	<0.01	<0.05	1585
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	12	4418	termite gut homogenate clone Rs-H18 bacterium	<0.02	<0.05	1173
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	5	4434	termite gut homogenate clone Rs-K11 bacterium	<0.01	<0.05	1298
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	12	4475	termite gut homogenate clone Rs-N02 bacterium	<0.001	<0.01	1853
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	12	4477	termite gut homogenate clone Rs-N85 bacterium	0.01	<0.05	1505
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	12	4507	termite gut homogenate clone Rs-N21 bacterium	≤0.01	<0.05	1169
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	5	4510	termite gut homogenate clone Rs-Q53 bacterium	<0.02	<0.05	1896
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	5	4512	granular sludge clone UASB_brew_B25	<0.01	<0.05	1006
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	5	4514	termite gut homogenate clone Rs-B34 bacterium	≤0.001	<0.05	1800
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	12	4524	termite gut clone Rs-093	<0.02	<0.05	1269
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	5	4533	termite gut homogenate clone Rs-N06 bacterium	<0.01	<0.05	1671
Firmicutes	Unclassified	Unclassified	Unclassified	8	4536	Mono Lake at depth 35 m station 6 July 2000 clone ML635J-14 G+C	<0.01	<0.05	1005
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	5	4540	termite gut homogenate clone Rs-M18 bacterium	<0.01	<0.05	1962
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	12	4598	*Clostridium sardiniense* str. DSM 600	<0.02	<0.05	1253
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	12	4607	*Clostridium novyi* str. NCTC538	<0.01	<0.05	1082
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	5	4613	rumen clone 3C0d-3	<0.02	<0.05	1321
Firmicutes	gut clone group	Unclassified	Unclassified	1	4616	rumen clone F23-C12	<0.01	<0.05	2628

Firmicutes	Clostridia	Clostridiales	Clostridiaceae	12	4622	termite gut clone Rs-L36	≤ 0.01	<0.05	1112
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	12	4638		<0.01	<0.05	2515
Cyanobacteria	Unclassified	Unclassified	Unclassified	9	5038	Rumen isolate str. YS2	<0.001	<0.01	1724
Bacteroidetes	Bacteroidetes	Unclassified	Unclassified	15	5481	marine sediment above hydrate ridge clone Hyd89-72 bacterium	<0.02	<0.05	2056
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	19	5542	*Cytophaga* sp. I-1787	<0.01	<0.05	2304
Bacteroidetes	Bacteroidetes	Bacteroidales	Unclassified	15	5783	Mono Lake at depth 35 m station 6 July 2000 clone ML635J-15 bacterium	<0.01	<0.05	1032
Bacteroidetes	Bacteroidetes	Bacteroidales	Unclassified	15	5874	*Paralvinella palmiformis* mucus secretions clone P. palm 53 bacterium	<0.02	<0.05	1805
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	19	6124	*Flexibacter flexilis* subsp. pelliculosus str. IFO 16028 subsp.	<0.001	<0.01	1387
Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	1	6459	*Spirochaeta* sp. str. BHI80-158	<0.001	≤ 0.01	2558
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Unclassified	3	9813	hydrothermal sediment clone AF420340	<0.01	<0.05	1453
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	5	9875	hydrothermal sediment clone AF420354	<0.01	<0.05	1147
Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	1	10171		<0.01	<0.05	1375
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfoarculaceae	2	10227	marine sediment clone Bol11	<0.01	<0.05	1549
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	5	10319	sulfate-reducing habitat clone SLM-CP-116	<0.01	<0.05	1235

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[a]S-F, Subfamily identification; [b]Taxon ID, PhyloChip Taxon identification number; [c]Representative species, Taxon bacterial species identifier.

Table 5. Core Community of Bacterial Taxa Detected in all COPD Patients during Treatment for Severe Exacerbations (Representative Species with a Proven Role in Mammalian Pathogenesis are Highlighted)

Phylum	*Class*	*Order*	*Family*	*S-F*[a]	*Taxon ID*[b]	*Representative species*[c]
Actinobacteria	Actinobacteria	Acidimicrobiales	Acidimicrobiaceae	sf_1	1749	forest soil clone DUNssu275 (-3A) (OTU#188)
Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	sf_6	6362	grassland soil clone DA052
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8578	*Marinobacter lipolyticus* str. SM-19
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9239	Arctic sea ice ARK10228
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8222	
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8753	*Idiomarina loihiensis* str. GSP37
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	9324	*Pseudoalteromonas ruthenica* str. KMM300
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	sf_1	8579	*Psychromonas profunda* str. 2825
Proteobacteria	Alphaproteobacteria	Rickettsiales	Anaplasmataceae	sf_3	6648	*Wolbachia* sp
Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	sf_1	7747	
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	sf_3	10538	*Arcobacter cryaerophilus*
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	sf_3	10447	*Sulfurospirillum deleyianum* str. Spirillum 5175
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	sf_3	10456	*Campylobacter showae*
Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	sf_1	6909	*Brevundimonas diminuta* str. DSM 1635
Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	sf_1	7436	*Brevundimonas* sp. str. FWC40
Cyanobacteria	Cyanobacteria	Chloroplasts	Chloroplasts	sf_5	5147	*Emiliania huxleyi* str. Plymouth Marine Laborator PML 92
Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae	sf_3	9198	uranium mining waste pile clone KF-JG30-B15 KF-JG30-B15
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Crenotrichaceae	sf_11	6267	Cilia-respiratory isolate str. 243-54
Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfomicrobiaceae	sf_1	10079	*Desulfomicrobium baculatum* str. DSM 1742
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	sf_1	8504	*Dysmicoccus neobrevipes* symbiont
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10385	
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10442	*Helicobacter cetorum* str. MIT 99-5656
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10444	*Helicobacter suncus* str. Kaz-2
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10448	*Helicobacter felis* str. Dog-1
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Helicobacteraceae	sf_3	10451	*Helicobacter heilmannii* str. C4S
Spirochaetes	Spirochaetes	Spirochaetales	Leptospiraceae	sf_3	6496	*Leptospira interrogans* serovar Copenhageni str. Fiocruz L1-130
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	sf_3	8366	*Psychrobacter frigidicola* str. DSM 12411
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	sf_3	8838	*Psychrobacter psychrophilus* CMS 28
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	sf_3	8727	*Alkanindiges hongkongensis* str. HKU9
Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae	sf_1	7789	
Firmicutes	Clostridia	Clostridiales	Peptococc/Acidaminococc	sf_11	992	anoxic bulk soil flooded rice microcosm clone BSV43 clone
Planctomycetes	Planctomycetacia	Planctomycetales	Pirellulae	sf_3	4670	
Proteobacteria	Gammaproteobacteria	Thiotrichales	Piscirickettsiaceae	sf_3	9291	*Methylophaga alcalica* str. M39
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8691	*Pseudomonas aeruginosa* str. PAO1
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9056	*Pseudomonas aeruginosa* str. #47
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9068	*Pseudomonas stutzeri* str. A1501
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9295	
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9613	*Pseudomonas flavescens* str. B62
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9049	uranium mining mill tailing clone GR-Sh2-34 GR-Sh2-34
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9469	cf. *Pseudomonas* sp. clone Llangefni 52
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9240	*Pseudomonas fluorescens* str. CHA0
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	9366	Arctic seawater isolate str. R7366
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	sf_1	8755	*Pseudomonas* sp. SK-1-3-1
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	sf_1	5913	*Sphingobacteriaceae* str. Ellin160

Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	sf_1	6663	Sphingopyxis flavimaris str. SW-151
Firmicutes	Bacilli	Bacillales	Thermoactinomycetaceae	sf_1	3301	*Thermoactinomyces* sp. str. 700375
Thermodesulfobacteria	Thermodesulfobacteria	Thermodesulfobacteriales	Thermodesulfobacteriaceae	sf_1	667	*Fjonesia*
Proteobacteria	Gammaproteobacteria	Thiotrichales	Thiotrichaceae	sf_3	8752	*Beggiatoa* sp. str. MS-81-1c
Chloroflexi	Unclassified	Unclassified	Unclassified	sf_2	818	
Verrucomicrobia	Unclassified	Unclassified	Unclassified	sf_4	288	*Prosthecobacter dejongeii*
Synergistes	Unclassified	Unclassified	Unclassified	sf_3	117	termite gut homogenate clone Rs-D89
Synergistes	Unclassified	Unclassified	Unclassified	sf_3	719	*Synergistes* sp. P1 str. P4G_18
OP3	Unclassified	Unclassified	Unclassified	sf_4	628	CB-contaminated groundwater clone GOUTB15
Unclassified	Unclassified	Unclassified	Unclassified	sf_160	485	thermal spring mat clone O1aA90
Unclassified	Unclassified	Unclassified	Unclassified	sf_160	226	
Bacteroidetes	KSA1	Unclassified	Unclassified	sf_1	5951	CFB group clone ML615J-4
Chloroflexi	Anaerolineae	Unclassified	Unclassified	sf_9	727	forest soil clone S0208
Cyanobacteria	Unclassified	Unclassified	Unclassified	sf_8	5206	
marine group A	mgA-2	Unclassified	Unclassified	sf_1	6344	bacterioplankton clone ZA3648c
Unclassified	Unclassified	Unclassified	Unclassified	sf_160	6430	
Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	sf_6	7575	
TM7	TM7-3	Unclassified	Unclassified	sf_1	8155	oral periodontitis clone EW086
Proteobacteria	Gammaproteobacteria	uranium waste clones	Unclassified	sf_1	8747	uranium waste soil clone JG30-KF-CM35
Proteobacteria	Gammaproteobacteria	Unclassified	Unclassified	sf_3	9568	forested wetland clone RCP2-96
Proteobacteria	Gammaproteobacteria	SUP05	Unclassified	sf_1	8605	bacterioplankton clone ZA2525c
Proteobacteria	Gammaproteobacteria	Unclassified	Unclassified	sf_3	8339	water 5 m downstream manure clone 35ds5
Proteobacteria	Gammaproteobacteria	Unclassified	Unclassified	sf_4	8855	
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Unclassified	sf_1	10480	*Paralvinella palmiformis* mucus secretions cloneP. palm C 84 proteobacterium
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Unclassified	sf_1	10530	hydrothermal vent 9 degrees North East Rise PacificOcean clone CH5_6_BAC_16SrRNA_9N_EPR
Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	sf_3	1687	*Jonesia quinghaiensis* str. DSM 15701
Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	sf_3	1405	*Arthrobacter ureafaciens* str. DSM 20126
Firmicutes	Clostridia	Unclassified	Unclassified	sf_3	2373	
Firmicutes	Catabacter	Unclassified	Unclassified	sf_1	4293	termite gut homogenate clone Rs-Q01 bacterium
Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	sf_3	8689	*Dyemonas todaii* str. XD10
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Xiphinematobacteraceae	sf_3	888	*Candidatus Xiphinematobacter brevicolli*

[a]S-F, Subfamily identification; [b]Taxon ID, PhyloChip Taxon identification number; [c]Representative species, Taxon bacterial species identifier.