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Supplementary Materials for

Sinus Microbiome Diversity Depletion and *Corynebacterium tuberculostearicum* Enrichment Mediates Rhinosinusitis

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The PDF file includes:

Fig. S1. *Muc5A* mRNA expression (normalized to β-actin) is significantly increased in CRS patient samples compared to healthy subjects.
Fig. S2. Linear regression of qPCR-derived *C. tuberculostearicum* abundance with array-reported florescence intensity and SNOT-20 score indicates strong concordance between qPCR and array-generated findings and confirms a strong positive relationship between *C. tuberculostearicum* abundance and symptom severity.
Fig. S3. Murine experimental design.
Fig. S4. qPCR quantification of *C. tuberculostearicum* and *L. sakei* load in murine sinus tissue.
Table S1. Bacterial taxa detected in study samples.
Table S2. Bacterial taxa detected in significantly altered abundance in CRS patient versus healthy subject sinuses.
Table S3. Bacterial taxa significantly correlated with sinus symptom severity.
Table S4. Significance values for comparative goblet cell number per micrometer of epithelial cell surface across mouse treatment groups.
Table S5. Significance values for comparative goblet cell number per micrometer of epithelial cell surface across mouse treatment groups that include animals instilled with *L. sakei*.
Table S6. Kolmogorov-Smirnov assessment of data distribution.

Supplementary Material.

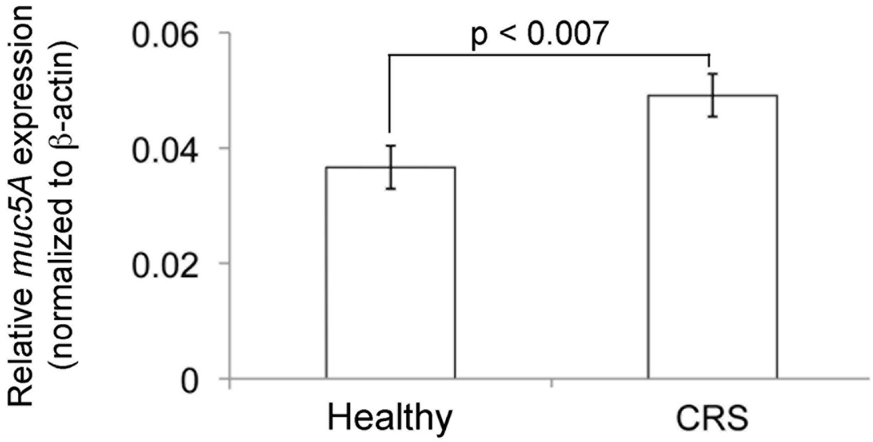

Figure S1. *Muc5A* mRNA expression (normalized to β-actin) is significantly increased in CRS patient samples compared to healthy subjects.

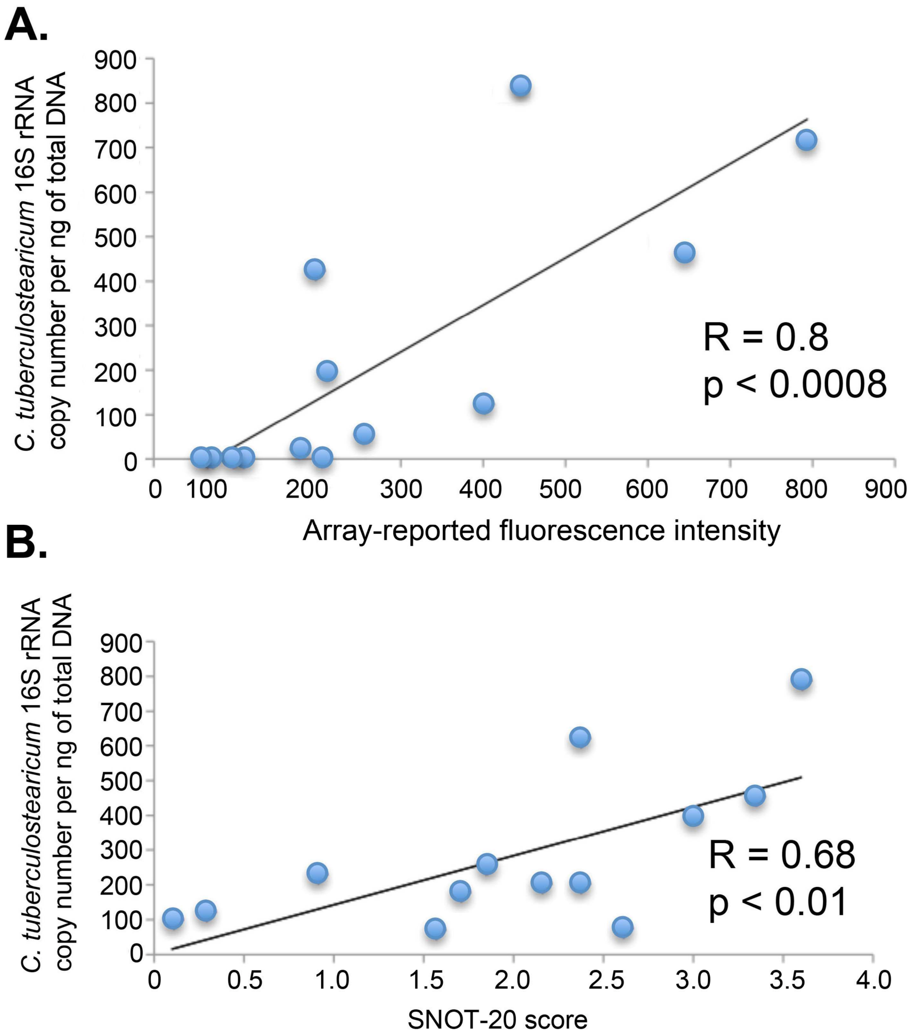

Figure S2. Linear regression of qPCR-derived *C. tuberculostearicum* abundance with array-reported florescence intensity and SNOT-20 score indicates strong concordance between qPCR and array-generated findings and confirms a strong positive relationship between *C. tuberculostearicum* abundance and symptom severity.

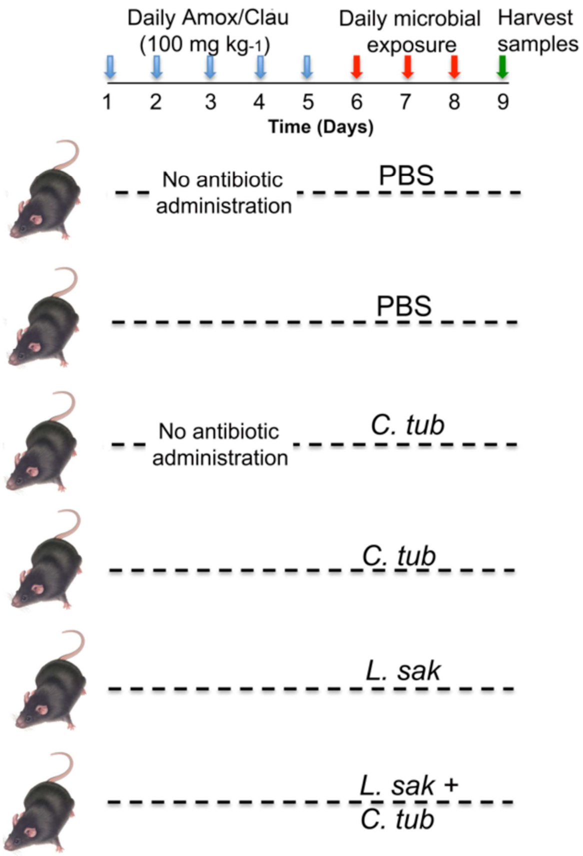

Figure S3. Murine experimental design. Amox, Amoxicillun; Clau, Clavulanate.

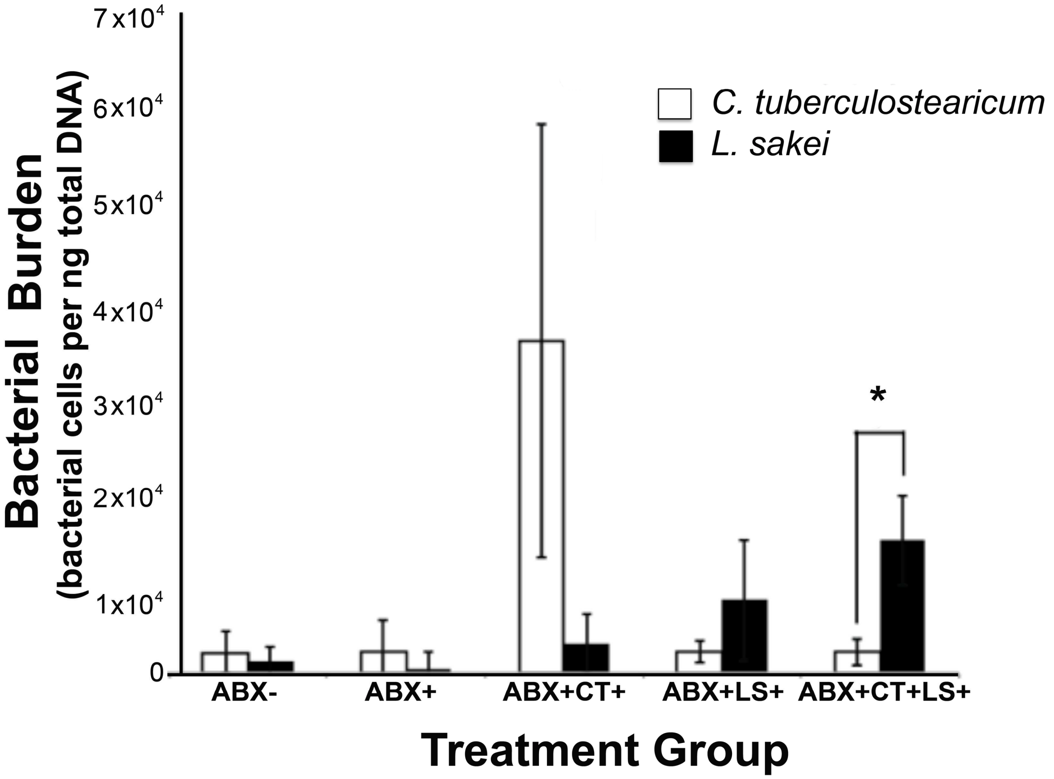

Figure S4. qPCR quantification of *C. tuberculostearium* and *L. sakei* load in murine sinus tissue. Asterisk (*) denotes statistical significance ($p < 0.05$; students t-test). Total 16S rRNA copy number per species was normalized to known number of 16S rRNA copies per genome for each species.

Because of their size, tables S1, S2 and S3 are appended as independent files.

Table S1. Bacterial taxa detected in study samples.

Table S2. Bacterial taxa detected in significantly altered abundance in CRS patient versus healthy subject sinuses.

Table S3. Bacterial taxa significantly correlated with sinus symptom severity.

Table S4. Significance values for comparative goblet cell number per micrometer of epithelial cell surface across mouse treatment groups (Fig. 3).

	AB- CT-	AB+ CT-	AB- CT+	AB+ CT+
AB- CT-	-	0.36	0.011	0.0034
AB+ CT-	-	-	0.0012	0.0001
AB- CT+	-	-	-	0.0076
AB+ CT+	-	-	-	-

Table S5. Significance values for comparative goblet cell number per micrometer of epithelial cell surface across mouse treatment groups that include animals instilled with *L. sakei* (Fig. 4).

	AB- CT-	AB+ CT-	AB+ LS+	AB+ CT+	AB+ CT+ LS+
AB- CT-	-	1	0.2002	0.0099	0.2082
AB+ CT-	-	-	0.2002	0.0099	0.2082
AB+ LS+	-	-	-	0.0118	0.5717
AB+ CT+	-	-	-	-	0.0141
AB+ CT+ LS+	-	-	-	-	-

Table S1. Bacterial taxa detected in study samples

Phylum	Family	SF	Taxon ID	Accession	prokMSA Name
Acidobacteria	Unclassified	sf_1	523	AF245036.1	soil metagenomic library clone 17F9
Acidobacteria	Acidobacteriaceae	sf_14	541	AJ519667.1	uranium mill tailings soil sample clone GuBH2-AG-47 sp.
Acidobacteria	Acidobacteriaceae	sf_6	6362	Y07646.1	grassland soil clone DA052
Acidobacteria	Acidobacteriaceae	sf_14	6421	AJ292576.1	PCB-polluted soil clone WD217
Acidobacteria	Acidobacteriaceae	sf_14	6335	AF523984.1	forested wetland clone FW45
Acidobacteria	Acidobacteriaceae	sf_6	6345	AJ534634.1	soil sample uranium mining waste pile near town Johanngeorgenstadt clone JG36-TzT-77 bacterium
Acidobacteria	Acidobacteriaceae	sf_14	6350	AF498719.1	soil isolate Ellin337
Acidobacteria	Acidobacteriaceae	sf_6	6359	AF529322.1	PCE-contaminated site clone CLi114
Acidobacteria	Acidobacteriaceae	sf_16	6414	AF529350.1	PCE-contaminated site clone CLs73
Acidobacteria	Acidobacteriaceae	sf_6	6423	AF523979.1	coal effluent wetland clone FW92
Acidobacteria	Acidobacteriaceae	sf_14	6364	AY234728.1	Solibacter usitatus Ellin6076
Acidobacteria	Acidobacteriaceae	sf_14	6424	AF524859.1	sphagnum peat bog clone K-5b10
Acidobacteria	Acidobacteriaceae	sf_14	508	AJ519382.1	uranium mining waste pile clone JG37-AG-81 sp.
Acidobacteria	Unclassified	sf_1	572	AF523986.1	forested wetland clone FW144
Acidobacteria	Unclassified	sf_1	6426	AF407714.1	Great Artesian Basin clone B11
Acidobacteria	Acidobacteriaceae	sf_14	6425	AF407719.1	Great Artesian Basin clone B27
Acidobacteria	Acidobacteriaceae	sf_14	6410		
Acidobacteria	Unclassified	sf_1	87	AF097766.1	activated sludge clone 2951
Acidobacteria	Unclassified	sf_1	6367	AF529104.1	TCE-contaminated site clone FTL227
Acidobacteria	Unclassified	sf_1	1049	AF013534.2	soil clone C112
Acidobacteria	Unclassified	sf_1	790	Z95709.1	soil clone 11-25
Acidobacteria	Unclassified	sf_1	6357	AY118153.1	anaerobic benzene-degrading clone Cart-N4
Acidobacteria	Unclassified	sf_1	435	AY211077.1	anaerobic VC-degrading enrichment clone VC47 bacterium
Acidobacteria	Acidobacteriaceae	sf_14	6378	D26171.1	Acidobacterium capsulatum
Acidobacteria	Acidobacteriaceae	sf_14	6412	AF047646.1	acid mine drainage clone TRB82
Acidobacteria	Unclassified	sf_1	588	AJ009461.1	TCB-transforming consortium clone SJA-36
Acidobacteria	Unclassified	sf_1	4222	AF523991.1	forested wetland clone FW105
Acidobacteria	Unclassified	sf_1	897	AY221071.1	Mammoth cave clone CCM8b
Acidobacteria	Unclassified	sf_1	516	AJ532721.1	uranium mining waste pile clone JG34-KF-153
Acidobacteria	Acidobacteriaceae	sf_14	964	AJ519392.1	uranium mining waste pile clone JG37-AG-145 sp.
Acidobacteria	Acidobacteriaceae	sf_14	6368	AF200698.1	soil clone UA2
Acidobacteria	Acidobacteriaceae	sf_14	6366	AJ292578.1	PCB-polluted soil clone WD228
Acidobacteria	Acidobacteriaceae	sf_14	208	AJ519665.1	uranium mill tailings soil sample clone GuBH2-AD-9 sp.
Acidobacteria	Acidobacteriaceae	sf_14	105	AJ535239.1	marine sediment above hydrate ridge clone Hyd24-44 sp.
Acidobacteria	Unclassified	sf_1	100	AJ534631.1	soil sample uranium mining waste pile near town Johanngeorgenstadt clone JG36-TzT-10
Acidobacteria	Unclassified	sf_1	37	AY214904.2	soil clone BAC-14A1
Acidobacteria	Unclassified	sf_1	500	Z95717.1	soil clone RB24
Actinobacteria	Unclassified	sf_3	1687	AJ626896.1	Jonesia quinghaiensis str. DSM 15701
Actinobacteria	Unclassified	sf_3	1243	AB089076.1	termite gut homogenate clone Rs-M95 bacterium
Actinobacteria	Unclassified	sf_3	1405	X80744.1	Arthrobacter ureafaciens str. DSM 20126
Actinobacteria	Micrococcaceae	sf_1	2019	AF057289.1	Micrococcus luteus str. HN2-11
Actinobacteria	Microbacteriaceae	sf_1	1437	AJ575522.1	freshwater clone SV1-16
Actinobacteria	Corynebacteriaceae	sf_1	1517	X84446.1	Corynebacterium xerosis str. DSM 20743

Actinobacteria	Corynebacteriaceae	sf_1	1492	AY677186.1	Corynebacterium tuscaniae str. ISS-5309
Actinobacteria	Corynebacteriaceae	sf_1	1820	U87823.1	Corynebacterium jeikeium str. ATCC 43734
Actinobacteria	Corynebacteriaceae	sf_1	1374		
Actinobacteria	Corynebacteriaceae	sf_1	1428	AF537604.1	Corynebacterium simulans National Microbiology Laboratory Special identifier 00-0186
Actinobacteria	Bifidobacteriaceae	sf_1	1444	AY278612.1	Bifidobacteriaceae genomosp. C1
Actinobacteria	Acidimicrobiaceae	sf_1	1749	AY913475.1	forest soil clone DUNssu275 (-3A) (OTU#188)
Actinobacteria	Acidimicrobiaceae	sf_1	1856	AF523913.1	forested wetland clone RCP2-105
Actinobacteria	Rubrobacteraceae	sf_1	1551	AF498683.1	soil isolate Ellin301
Actinobacteria	Actinomycetaceae	sf_1	1684	AJ428402.1	Varibaculum cambriense str. CCUG 44998
Actinobacteria	Bifidobacteriaceae	sf_1	1351	AY174108.1	Bifidobacterium psychraerophilum str. T16
Actinobacteria	Bifidobacteriaceae	sf_1	1967	D86187.1	Bifidobacterium pseudocatenulatum str. JCM1200
Actinobacteria	Bifidobacteriaceae	sf_1	2040	AF275881.1	Bifidobacterium adolescentis str. E-981074T
Actinobacteria	Bifidobacteriaceae	sf_1	1109	AY148470.1	Bifidobacterium thermacidophilum porcinum subsp. suis str. P3-14 subsp.
Actinobacteria	Bifidobacteriaceae	sf_1	1835	AY513712.1	Bifidobacterium breve str. KB 92
Actinobacteria	Bifidobacteriaceae	sf_1	1875		
Actinobacteria	Corynebacteriaceae	sf_1	1803	AJ429234.1	Corynebacterium spheniscorum str. CCUG 45512
Actinobacteria	Unclassified	sf_1	1898	AB089074.1	termite gut homogenate clone Rs-J10 bacterium
Actinobacteria	Cellulomonadaceae	sf_1	1748	Y18378.1	Beutenbergia cavernosa str. DSM 12333
Actinobacteria	Micrococcaceae	sf_1	1266	AF134179.1	Arthrobacter psychrolactophilus
Actinobacteria	Unclassified	sf_3	1577	AB089072.1	termite gut homogenate clone Rs-N91 bacterium
Actinobacteria	Micrococcaceae	sf_1	1213	X87756.1	Kocuria roseus
Actinobacteria	Kineosporiaceae	sf_1	1961	X77958.1	Kineococcus aurantiacus str. IFO 15268
Actinobacteria	Acidimicrobiaceae	sf_1	1360	AF523917.1	forested wetland clone RCP2-103
Actinobacteria	Mycobacteriaceae	sf_1	1262	AJ310467.1	Mycobacterium holsaticum str. 1406
Actinobacteria	Mycobacteriaceae	sf_1	1650	X58890.1	Mycobacterium tuberculosis str. NCTC 7416 H37Rv
Actinobacteria	Cellulomonadaceae	sf_1	1586	X83800.1	Cellulomonas gelida str. DSM 20111T
Actinobacteria	Promicromonosporaceae	sf_1	1671	X79453.1	Cellulosimicrobium cellulans str. NCIMB 11025
Actinobacteria	Rubrobacteraceae	sf_1	1843	AJ536866.1	uranium mining waste pile soil sample clone JG30-KF-A23
Actinobacteria	Micrococcaceae	sf_1	1557	X83408.1	Arthrobacter oxydans str. DSM 20119
Actinobacteria	Micrococcaceae	sf_1	1593	M23411.1	Arthrobacter globiformis
Actinobacteria	Micrococcaceae	sf_1	1610	X86595.1	Arthrobacter sp str. AC-51
Actinobacteria	Micrococcaceae	sf_1	1966	AY133106.1	TCE-contaminated site clone ccspost2208
Actinobacteria	Micrococcaceae	sf_1	1324	AF479325.1	glacial ice isolate str. CanDirty1
Actinobacteria	Micrococcaceae	sf_1	1494	X80748.1	Arthrobacter agilis str. DSM 20550
Actinobacteria	Micrococcaceae	sf_1	1573	AJ315492.1	Arthrobacter nicotianae str. SB42
Actinobacteria	Unclassified	sf_1	1676		
Actinobacteria	Mycobacteriaceae	sf_1	1187	AF498656.1	Mycobacterium aichiense str. JS618
Actinobacteria	Mycobacteriaceae	sf_1	1308	AJ431371.1	Mycobacterium pyrenivorans str. DSM 44605
Actinobacteria	Mycobacteriaceae	sf_1	1726	X52925.1	Mycobacterium terrae str. ATCC 15755
Actinobacteria	Corynebacteriaceae	sf_1	1089	AF537600.1	Corynebacterium mucifaciens National Microbiology Laboratory Special identifier 01-0118
Actinobacteria	Unclassified	sf_2	1652	AY193208.1	marine sediment clone Bol7
Actinobacteria	Nocardiopsaceae	sf_1	1385	AF178988.1	Streptomonospora salina str. YIM90002
Actinobacteria	Acidimicrobiaceae	sf_1	1090		
Actinobacteria	Unclassified	sf_1	1217	AJ306762.2	DCP-dechlorinating consortium clone SHA-34
Actinobacteria	Micrococcaceae	sf_1	1686	AY228479.1	Yania halotolerans str. YIM 70085
Actinobacteria	Unclassified	sf_3	2045	AF507852.1	hypersaline lake clone ML602J-44
Actinobacteria	Micrococcaceae	sf_1	1724	X95483.1	Rothia mucilaginosa str. DSM
Actinobacteria	Propionibacteriaceae	sf_1	2002	AB108484.1	Propionibacterium acnes #2929

Actinobacteria	Mycobacteriaceae	sf_1	2034	X79094.1	Mycobacterium chlorophenolicum str. PCP-I
Actinobacteria	Mycobacteriaceae	sf_1	1175	AJ243481.1	Mycobacterium cf. xenopi 'Hymi_Wue Tb_939/99' str. Hymi_Wue Tb_939/99
Actinobacteria	Streptomycetaceae	sf_1	1354	X80825.1	Streptomyces subrutilus str. DSM 40445
Actinobacteria	Thermomonosporaceae	sf_1	1546	AJ420137.1	Actinomadura fulvescens str. DSM 43923T
Actinobacteria	Actinomycetaceae	sf_1	1227	AB062278.1	Actinomyces naeslundii
Actinobacteria	Pseudonocardiaceae	sf_1	1863		
Actinobacteria	Unclassified	sf_4	1337	AF234118.1	Sturt arid-zone soil clone #0425-2M17
Actinobacteria	Micromonosporaceae	sf_1	1641	AB196714.1	Micromonospora marina str. JSM3-1
Actinobacteria	Frankiaceae	sf_1	1286	AJ408875.1	Frankia sp. Sn5-8
Actinobacteria	Sporichthyaceae	sf_1	1695	AY250883.1	lichen-dominated Antarctic cryptoendolithic community clone FBP417
Actinobacteria	Unclassified	sf_1	1370	AF523912.1	forested wetland clone RCP1-37
Actinobacteria	Promicromonosporaceae	sf_1	1711	AJ272024.1	Promicromonospora sukumoe str. DSM 44121
Actinobacteria	Micrococcaceae	sf_1	1889	AB094464.1	Citricoccus sp. str. 2216.25.22
Actinobacteria	Dermabacteraceae	sf_1	2053	X91033.1	Brachybacterium nesterenkovii str. DSM 9573
Actinobacteria	Dietziaceae	sf_1	1970	AF481211.1	Dietzia sp. str. E9_2
Actinobacteria	Cellulomonadaceae	sf_1	1450		
Actinobacteria	Unclassified	sf_3	1296	AB089080.1	termite gut homogenate clone Rs-M66 bacterium
Actinobacteria	Micromonosporaceae	sf_1	1910	AB013495.2	Actinoplanes capillaceus str. K95-5561
Actinobacteria	Nocardiaceae	sf_1	1142		
Actinobacteria	Propionibacteriaceae	sf_1	2023	AJ315953.1	Propionibacterium propionicum str. DSM 43307T
Actinobacteria	Micromonosporaceae	sf_1	1633	AJ277585.1	Actinoplanes tuftoflagellus str. IMSNU 22135
Actinobacteria	Mycobacteriaceae	sf_1	1239	AJ271863.1	Mycobacterium ratisbonense str. SD4
Actinobacteria	Mycobacteriaceae	sf_1	1681	AY227356.1	Mycobacterium sp. str. 1B(CD)
Actinobacteria	Microbacteriaceae	sf_1	1404	AJ507468.1	freshwater isolate str. MWH-Ta3
Actinobacteria	Nocardioidaceae	sf_1	1854	AY166703.1	Aeromicrobium marinum str. T2
Actinobacteria	Micromonosporaceae	sf_1	1615	AB036999.1	Actinoplanes derwentensis str. IFO 14935T
Actinobacteria	Dietziaceae	sf_1	1872	X79290.1	Dietzia maris
Actinobacteria	Acidimicrobiaceae	sf_1	2014	AY093455.1	marine sediment clone MB-A2-100
Actinobacteria	Pseudonocardiaceae	sf_1	1343	Z38017.1	Saccharomonospora azurea str. M.Goodfel K161=NA128 (type st
Actinobacteria	Nocardiaceae	sf_1	1940	AB178563.1	Rhodococcus opacus str. B-4
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Actinobacteria	Cellulomonadaceae	sf_1	1923	AJ229245.1	Actinobacteria str. VeCb6
Actinobacteria	Micrococcaceae	sf_1	2020	AF543278.1	Rothia dentocariosa str. ChDC B200
Actinobacteria	Kineosporiaceae	sf_1	1598	AY250880.1	lichen-dominated Antarctic cryptoendolithic community clone FBP402
Actinobacteria	Micromonosporaceae	sf_1	1159	AJ277568.1	Actinoplanes durhamensis str. IMSNU 22124T
Actinobacteria	Mycobacteriaceae	sf_1	1888	AY012577.2	Mycobacterium brisbanense str. W6743; ATCC 49938
Actinobacteria	Dermatophilaceae	sf_1	1852	AB096085.1	Tonsillophilus suis str. HT1-19
Actinobacteria	Micromonosporaceae	sf_1	2051	D85479.1	Couchioplanes subsp. caeruleus str. IFO13939
Actinobacteria	Mycobacteriaceae	sf_1	1204	M95488.1	Mycobacterium sp. 3
Actinobacteria	Mycobacteriaceae	sf_1	1365	AY457072.1	Mycobacterium chelonae str. CIP 104535T
Actinobacteria	Nocardiaceae	sf_1	1432	AF430055.1	Nocardia veterana str. DSM 44445
Actinobacteria	Coriobacteriaceae	sf_1	1459	AB089077.1	termite gut homogenate clone Rs-J59 bacterium
Actinobacteria	Unclassified	sf_1	1666		
Actinobacteria	Unclassified	sf_3	1348	AY250882.1	lichen-dominated Antarctic cryptoendolithic community clone FBP406

Actinobacteria	Streptomycetaceae	sf_1	1375	AF423240.1	soil clone 228-1
Actinobacteria	Streptosporangiaceae	sf_1	1158	X89947.1	Streptosporangium roseum str. DSM43021T
Actinobacteria	Streptosporangiaceae	sf_1	1190	U48977.1	Nonomuraea polychroma str. IFO 14345
Actinobacteria	Unclassified	sf_3	1130	X94155.2	Georgenia muralis str. 1A-C
Actinobacteria	Micromonosporaceae	sf_1	1972	AB037011.1	Actinoplanes regularis str. IFO 12514T
Actinobacteria	Mycobacteriaceae	sf_1	1435	AJ276890.1	Mycobacterium cf. triplex 'isolate 23' 23
Actinobacteria	Nocardioidaceae	sf_1	1208	AF005021.1	Aeromicrobium erythreum str. NRRL B-3381
Actinobacteria	Mycobacteriaceae	sf_1	1860	AF251565.1	Mycobacterium marinum
Actinobacteria	Thermomonosporaceae	sf_1	1406	X97890.1	Actinomadura kijaniata str. DSM 43764T
Actinobacteria	Gordoniaceae	sf_1	1184	AB065369.1	Gordonia alkanivorans
Actinobacteria	Streptomycetaceae	sf_3	1743	AB026214.1	Streptomyces scabiei str. DNK-G01
Actinobacteria	Streptomycetaceae	sf_1	1544	AB022872.1	Kitasatospora cystarginea str. IFO14836T
Actinobacteria	Streptomycetaceae	sf_1	1771	D63872.1	Streptomyces setonii str. ATCC25497
Actinobacteria	Streptosporangiaceae	sf_1	1224	X89941.1	Acrocarpospora corrugata str. DSM43316T
Actinobacteria	Microbacteriaceae	sf_1	1197	AF468440.1	Arctic sea ice ARK10173
Actinobacteria	Cellulomonadaceae	sf_1	1431	AB078838.1	Cellulomonadaceae str. W6
Actinobacteria	Actinomycetaceae	sf_1	2039	AJ421779.1	Actinomyces cardiffensis str. CCUG 44997
Actinobacteria	Micromonosporaceae	sf_1	1488	AJ277574.1	Actinoplanes utahensis str. IMSNU 20044T
Actinobacteria	Micromonosporaceae	sf_1	1760	AJ277583.1	Actinoplanes roseosporangius str. IMSNU 22133
Actinobacteria	Propionibacteriaceae	sf_1	1371	AJ003057.1	Propionibacterium granulosum str. DSM 20700
Actinobacteria	Mycobacteriaceae	sf_1	1781	AF498650.1	Mycobacterium rhodesiae str. JS60
Actinobacteria	Mycobacteriaceae	sf_1	1885	AF480593.1	Mycobacterium neoaurum str. ATCC 25795
Actinobacteria	Unclassified	sf_2	1233		
Actinobacteria	Coriobacteriaceae	sf_1	1800	AJ534681.1	ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A-MN100
Actinobacteria	Kineosporiaceae	sf_1	1581	AJ293746.1	Cryptosporangium aurantiacum str. IMSNU 22120
Actinobacteria	Brevibacteriaceae	sf_1	1745	X83813.1	Brevibacterium iodinum str. DSM 2062T
Actinobacteria	Actinomycetaceae	sf_1	2049	AJ234059.1	Arcanobacterium haemolyticum str. CIP 103370
Actinobacteria	Micromonosporaceae	sf_1	1931	X80823.1	Actinoplanes utahensis str. ATCC 31044
Actinobacteria	Gordoniaceae	sf_1	1545		
Actinobacteria	Gordoniaceae	sf_1	1654	AF416719.1	Gordonia polyisoprenivorans str. Y2K
Actinobacteria	Rubrobacteraceae	sf_1	1901	AY039806.1	earthworm burrow isolate B33D1
Actinobacteria	Streptosporangiaceae	sf_1	1587	AB039960.1	Nonomuraea subsp. roseoviolacea str. SF 2303
Actinobacteria	Microbacteriaceae	sf_1	1804	AY244784.1	Microbacterium resistens str. 2002-59119
Actinobacteria	Microbacteriaceae	sf_1	1106		
Actinobacteria	Micrococcaceae	sf_1	2063	M59055.1	Rothia dentocariosa str. ATCC 17931
Actinobacteria	Micromonosporaceae	sf_1	1689	AB047516.1	Actinoplanes yunnanensis str. IFO 14459T
Actinobacteria	Frankiaceae	sf_1	1161	AJ408876.1	Frankia sp. MRn2-2
Actinobacteria	Rubrobacteraceae	sf_1	1739		
Actinobacteria	Corynebacteriaceae	sf_1	1192	AJ439344.1	Corynebacterium segmentosum str. CIP107068 (CCUG37878)
Actinobacteria	Corynebacteriaceae	sf_1	1493	AJ438045.1	Corynebacterium tuberculostearicum str. CIP102346
Actinobacteria	Streptomycetaceae	sf_1	1436	AF117304.1	Streptomyces malaysiensis str. ATB-11
Actinobacteria	Micromonosporaceae	sf_1	1542	AJ277575.1	Actinoplanes garbadinensis str. IMSNU 20040
Actinobacteria	Micromonosporaceae	sf_1	1766	X93195.1	Dactylosporangium salmoneum str. DSM 43910
Actinobacteria	Gordoniaceae	sf_1	1567		
Actinobacteria	Nocardiaceae	sf_1	1769	AF430064.1	Nocardia sp. str. DSM 46067
Actinobacteria	Coriobacteriaceae	sf_1	1258	AJ534678.1	ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A-MN25
Actinobacteria	Microthrixineae	sf_1	1964	AF406548.1	bacterioplankton clone AEGEAN_247
Actinobacteria	Streptosporangiaceae	sf_1	1189	AF191734.1	Streptosporangium subroseum str. 7113
Actinobacteria	Streptosporangiaceae	sf_1	1595		

Actinobacteria	Microbacteriaceae	sf_1	1667	AB007415.1	Microbacterium lacticum
Actinobacteria	Mycobacteriaceae	sf_1	1312		
Actinobacteria	Gordoniaceae	sf_1	1191	X80635.1	Gordonia amarae str. DSM43392
Actinobacteria	Frankiaceae	sf_1	1644	AJ408870.1	Frankia sp. M16467
Actinobacteria	Kineosporiaceae	sf_1	1087	AB003931.1	Kineosporia aurantiaca str. JCM3230
Actinobacteria	Kineosporiaceae	sf_1	1893	AF095336.1	Kineosporia aurantiaca str. NRLL B-16913
Actinobacteria	Unclassified	sf_3	1900		
Actinobacteria	Nocardiaceae	sf_1	1787	AF430046.1	Nocardia pseudovaccinii str. DSM 43406
Actinobacteria	Nocardiaceae	sf_1	1917	X80611.1	Nocardia otitidiscaviarum str. DSM43242
Actinobacteria	Coriobacteriaceae	sf_1	1926	AB011815.1	Collinsella aerofaciens str. JCM7791
Actinobacteria	Streptomycetaceae	sf_1	1274	AB006154.1	Trichotomospora caesia str. IFO14562
Actinobacteria	Streptomycetaceae	sf_1	1639	X60514.1	Streptomyces coelicolor str. M145 ssp. A3(2)
Actinobacteria	Thermomonosporaceae	sf_1	1669	AF223348.1	Pseudonocardiaceae str. PA123
Actinobacteria	Microbacteriaceae	sf_1	1135	AJ459101.1	Rhodoglobus vestalii str. LV3
Actinobacteria	Microbacteriaceae	sf_1	1921	AJ292036.1	Firmicutes isolate str. d8
Actinobacteria	Microbacteriaceae	sf_1	1241	AJ717353.1	Microbacterium kitamiense CV88
Actinobacteria	Microbacteriaceae	sf_1	1779	AB042083.1	Microbacterium sp. str. VKM Ac-2048
Actinobacteria	Microbacteriaceae	sf_1	1186	AF505514.1	Cryocola antiquus str. VKM 103PF
Actinobacteria	Cellulomonadaceae	sf_1	1240	AB078847.1	Cellulomonadaceae str. WB9
Actinobacteria	Cellulomonadaceae	sf_1	1449	AB078851.1	Cellulomonadaceae str. WB13
Actinobacteria	Cellulomonadaceae	sf_1	1589	X83806.1	Oerskovia turbata str. DSM 20577T
Actinobacteria	Dermabacteraceae	sf_1	1504	AJ415380.1	Brachybacterium sacelli str. LMG 20338
Actinobacteria	Actinomycetaceae	sf_1	1672	AJ234041.1	Actinomyces odontolyticus str. CCUG 28084
Actinobacteria	Mycobacteriaceae	sf_1	1180	AJ308603.1	Mycobacterium palustre str. E846
Actinobacteria	Nocardiaceae	sf_1	1146	AF430068.1	Nocardia otitidiscaviarum str. S639
Actinobacteria	Nocardiaceae	sf_1	2048	AF430044.1	Nocardia uniformis str. DSM 43136
Actinobacteria	Unclassified	sf_3	1201	AJ347031.1	sponge clone TK39
Actinobacteria	Microthrixineae	sf_1	1576	AF454307.1	actinobacterium clone ML817J-10
Actinobacteria	Acidimicrobiaceae	sf_1	2030	AF523914.1	forested wetland clone RCP1-33
Actinobacteria	Unclassified	sf_3	1486	AY093463.1	deep marine sediment clone MB-A2-108
Actinobacteria	Streptomycetaceae	sf_1	1690	X79325.1	Streptomyces galbus str. DSM40480
Actinobacteria	Microbacteriaceae	sf_1	1705		
Actinobacteria	Microbacteriaceae	sf_1	1098		
Actinobacteria	Dermabacteraceae	sf_1	1677	X91030.1	Brachybacterium conglomeratum str. NCIB 9859
Actinobacteria	Dermabacteraceae	sf_1	1736	AJ415376.1	Brachybacterium rhamnosum str. LMG 19848
Actinobacteria	Pseudonocardiaceae	sf_1	1824	AJ293756.1	Amycolatopsis sulphurea str. IMSNU 20060T
Actinobacteria	Mycobacteriaceae	sf_1	1317	AF418956.1	USA: Colorado Fort collins Horsetooth Reservoir clone HTDD3
Actinobacteria	Mycobacteriaceae	sf_1	1637	AF190800.1	Mycobacterium austroafricanum str. IFP2173
Actinobacteria	Gordoniaceae	sf_1	1116	X79286.1	Gordona terrae
Actinobacteria	Corynebacteriaceae	sf_1	1826	AF537598.1	Corynebacterium kroppenstedtii National Microbiology Laboratory Special identifier 00-0244
Actinobacteria	Coriobacteriaceae	sf_1	1924	AF292371.1	Atopobium rimae str. ATCC49626
Actinobacteria	Coriobacteriaceae	sf_1	2021	AB089070.1	termite gut homogenate clone Rs-D41 bacterium
Actinobacteria	Acidothermaceae	sf_1	1399	AJ532700.1	uranium mill tailings clone Gitt-KF-183
Actinobacteria	Streptomycetaceae	sf_1	1983	AJ399487.1	Streptomyces cinnabarinus str. ISP 5467
Actinobacteria	Streptomycetaceae	sf_1	1229	AF074412.1	Streptacidiphilus carbonis str. JL 415; DSM 41754
Actinobacteria	Intrasporangiaceae	sf_1	1225	AB030911.1	Tetrasphaera elongata str. Lp2
Actinobacteria	Intrasporangiaceae	sf_1	1674	AJ310085.1	Janibacter terrae str. DSM 13953T
Actinobacteria	Propionibacteriaceae	sf_1	1152	AF287756.1	Propionibacterium sp. oral strain str. FMA5 oral
Actinobacteria	Pseudonocardiaceae	sf_1	1402		
Actinobacteria	Nocardiaceae	sf_1	1261	AF459443.1	Nocardia caishijiensis str. F829
Actinobacteria	Nocardiaceae	sf_1	1304	AF421564.1	Nocardia sp. str. 99-08-244A

Actinobacteria	Nocardiaceae	sf_1	1805	AJ303008.1	Nocardia ignorata str. IMMIB R-1434 DSM 44496 = NRRL B-24141
AD3	Unclassified	sf_1	2338	AJ536867.1	uranium mining waste pile soil clone JG30-KF-C12
Aquificae	Unclassified	sf_1	2364	AY263403.1	Thermovibrio ammoniificans str. HB-1
Bacteroidetes	Unclassified	sf_15	5573	AB088930.1	termite gut homogenate clone Rs-D44 bacterium
Bacteroidetes	Unclassified	sf_6	5439	AF507859.1	Mono Lake at depth 35 m station 6 July 2000 clone ML635J-40 bacterium
Bacteroidetes	Unclassified	sf_15	5783	AF507869.2	Mono Lake at depth 35 m station 6 July 2000 clone ML635J-15 bacterium
Bacteroidetes	Unclassified	sf_15	5874	AJ441239.1	hydrothermal vent polychaete mucous clone P. palm A 53
Bacteroidetes	Unclassified	sf_4	5785	AF507862.1	Mono Lake at depth 35 m station 6 July 2000 clone ML635J-56
Bacteroidetes	Unclassified	sf_1	5951	AF449785.1	CFB group clone ML615J-4
Bacteroidetes	Unclassified	sf_3	6298	AF445661.1	travertine hot spring clone SM1C04
Bacteroidetes	Sphingobacteriaceae	sf_1	5913	AF409002.1	Sphingobacteriaceae str. Ellin160
Bacteroidetes	Rikenellaceae	sf_5	5892	AJ229217.1	anoxic bulk soil flooded rice microcosm clone BSV73
Bacteroidetes	Flavobacteriaceae	sf_1	5352	AY871820.2	Riemerella anatipestifer str. H-2565
Bacteroidetes	Flammeovirgaceae	sf_5	6084	AB078078.1	Microscilla arenaria str. IFO 15982
Bacteroidetes	Crenotrichaceae	sf_11	6249	M58790.2	Haliscomenobacter hydrossis
Bacteroidetes	Blattabacteriaceae	sf_1	5828	Z35664.1	Blattabacterium species
Bacteroidetes	Unclassified	sf_15	5475	AJ249101.1	SHA-25 clone
Bacteroidetes	Unclassified	sf_15	5890	AY218551.1	penguin droppings sediments clone KD1-125
Bacteroidetes	Porphyromonadaceae	sf_1	5295	AF371910.1	swine intestine clone p-987-s962-5
Bacteroidetes	Porphyromonadaceae	sf_1	5454	AY643492.1	Dysgonomonas wimpennyi str. ANFA2
Bacteroidetes	Unclassified	sf_15	5820	AY244902.1	cow rumen clone BF24
Bacteroidetes	Unclassified	sf_3	5248	AY274839.1	Delaware River estuary clone 1G12
Bacteroidetes	Flavobacteriaceae	sf_1	6252	AF449259.1	Riftia pachyptila's tube clone R103-B20
Bacteroidetes	Unclassified	sf_15	5481	AJ535258.1	marine sediment above hydrate ridge clone Hyd89-72 bacterium
Bacteroidetes	Unclassified	sf_4	5787	AF507860.1	Mono Lake at depth 35 m station 6 July 2000 clone ML635J-1 bacterium
Bacteroidetes	Unclassified	sf_3	6168	AF534435.1	Toolik Lake main station at 3 m depth clone TLM11/TLMdgge04
Bacteroidetes	Flexibacteraceae	sf_19	5667	AY218749.1	penguin droppings sediments clone KD6-118
Bacteroidetes	Sphingobacteriaceae	sf_1	5513	AF385549.1	crevicular epithelial cells clone AZ123
Bacteroidetes	Bacteroidaceae	sf_12	5256	AB088925.1	termite gut homogenate clone Rs-D38 bacterium
Bacteroidetes	Unclassified	sf_15	6069	AJ289174.1	corneal ulcer clone E1-K9
Bacteroidetes	Porphyromonadaceae	sf_1	5817	AB088927.2	termite gut homogenate clone Rs-N56 bacterium
Bacteroidetes	Porphyromonadaceae	sf_1	5961	AJ488070.1	chlorobenzene-degrading consortium clone IA-16
Bacteroidetes	Porphyromonadaceae	sf_1	5510	AF524856.1	sphagnum peat bog clone 26-4b2
Bacteroidetes	Porphyromonadaceae	sf_1	6012	AJ400264.1	mouse feces clone L11-6
Bacteroidetes	Prevotellaceae	sf_1	6011	AB185583.1	rumen clone F24-B03
Bacteroidetes	Prevotellaceae	sf_1	6152	AF001768.1	rumen clone RF37
Bacteroidetes	Porphyromonadaceae	sf_1	5460	AJ400267.2	mouse feces clone F8
Bacteroidetes	Prevotellaceae	sf_1	5484	AY134905.1	oral periodontitis clone FX046
Bacteroidetes	Prevotellaceae	sf_1	5769	AB081578.1	Bacteroidaceae str. A42
Bacteroidetes	Prevotellaceae	sf_1	5905	AF371893.1	swine intestine clone p-2443-18B5
Bacteroidetes	Prevotellaceae	sf_1	5946	AF385511.1	tongue dorsa clone DO027
Bacteroidetes	Prevotellaceae	sf_1	6047	AY093462.1	deep marine sediment clone MB-A2-107
Bacteroidetes	Flavobacteriaceae	sf_1	5997	M62797.1	Flavobacterium aquatile
Bacteroidetes	Flavobacteriaceae	sf_1	5991	AB032506.1	Tenacibaculum ovolyticum str. IAM14318

Bacteroidetes	Flavobacteriaceae	sf_1	5971	M62799.1	Cytophaga uliginosa
Bacteroidetes	Sphingobacteriaceae	sf_1	6158	AF538748.1	municipal wastewater treatment bioreactor isolate str. CAGY10
Bacteroidetes	Crenotrichaceae	sf_11	6267	AF316115.1	Cilia- respiratory isolate str. 243-54
Bacteroidetes	Flexibacteraceae	sf_19	5372		
Bacteroidetes	Flexibacteraceae	sf_19	5566	AY264838.1	Hongiella mannitolivorans str. IMSNU 14012 JC2050
Bacteroidetes	Flexibacteraceae	sf_19	6124	AB078054.1	Flexibacter flexilis subsp. pelliculosus str. IFO 16028 subsp.
Bacteroidetes	Prevotellaceae	sf_1	5398	AY699286.1	Prevotella ruminicola L16
Bacteroidetes	Prevotellaceae	sf_1	5916	AY244931.1	cow rumen clone BE14
Bacteroidetes	Prevotellaceae	sf_1	5940	AF481226.1	Prevotella sp. str. E7_34
Bacteroidetes	Unclassified	sf_15	5957	AJ441217.1	hydrothermal vent polychaete mucous clone P. palm C/A 20
Bacteroidetes	Unclassified	sf_15	5544	AY188304.1	marine? clone KD3-17
Bacteroidetes	Bacteroidaceae	sf_12	5320	M86695.1	Bacteroides distasonis
Bacteroidetes	Prevotellaceae	sf_1	5403	AJ006457.1	Prevotella bryantii str. B14 (DSM 11371 species)
Bacteroidetes	Prevotellaceae	sf_1	5249	AY323524.1	Prevotella denticola str. ATCC 35308
Bacteroidetes	Prevotellaceae	sf_1	5331	AF385519.1	tongue dorsa clone DO022
Bacteroidetes	Prevotellaceae	sf_1	6239	AF385512.1	tongue dorsa clone DO033
Bacteroidetes	Flavobacteriaceae	sf_1	5915	AJ534682.1	ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A-MN27 bacterium
Bacteroidetes	Flavobacteriaceae	sf_1	6274		
Bacteroidetes	Flavobacteriaceae	sf_1	5317	AB078057.1	Tenacibaculum maritimum str. IFO 15946
Bacteroidetes	Flavobacteriaceae	sf_1	5942		
Bacteroidetes	Flavobacteriaceae	sf_1	5473		
Bacteroidetes	Flavobacteriaceae	sf_1	5914	AY771714.1	Psychroserpens burtonensis str. S2-64
Bacteroidetes	Unclassified	sf_15	6324	AY216445.1	temperate estuarine mud clone KM02
Bacteroidetes	Crenotrichaceae	sf_11	5619	AY211072.1	anaerobic VC-degrading enrichment clone VC10 bacterium
Bacteroidetes	Crenotrichaceae	sf_11	6123	AB078055.1	Flexibacter japonensis str. IFO 16041
Bacteroidetes	Unclassified	sf_15	6233	AY134906.1	oral periodontitis clone FX069
Bacteroidetes	Porphyromonadaceae	sf_1	5713	X82823.1	Porphyromonas catoniae str. ATCC 51270
Bacteroidetes	Prevotellaceae	sf_1	6259		
Bacteroidetes	Flavobacteriaceae	sf_1	5401	AF543295.1	Capnocytophaga gingivalis str. ChDC OS45
Bacteroidetes	Flavobacteriaceae	sf_1	6248	AY005073.1	Capnocytophaga sp. oral strain str. S3
Bacteroidetes	Flavobacteriaceae	sf_1	5267	AF406541.1	bacterioplankton clone AEGEAN_179
Bacteroidetes	Flavobacteriaceae	sf_1	6269	AY080916.1	acidic forest soil clone UC1
Bacteroidetes	Unclassified	sf_4	5703		
Bacteroidetes	Sphingobacteriaceae	sf_1	5492	AF492000.1	Sphingobacterium sp. str. HC-6155
Bacteroidetes	Flavobacteriaceae	sf_1	6104		
Bacteroidetes	Bacteroidaceae	sf_12	5950		
Bacteroidetes	Flavobacteriaceae	sf_1	5730		
Bacteroidetes	Flexibacteraceae	sf_19	5563	AB073573.2	Cytophaga sp. I-545
Bacteroidetes	Flavobacteriaceae	sf_1	5436	AF468406.1	Arctic sea ice ARK10004
Bacteroidetes	Flexibacteraceae	sf_19	5602		
Bacteroidetes	Flexibacteraceae	sf_19	5994	AJ549285.1	Hymenobacter sp. str. NS/50
Bacteroidetes	Flexibacteraceae	sf_20	10311	AJ431236.1	Cytophaga sp. str. BHI60-57B
Bacteroidetes	Flexibacteraceae	sf_19	6297	AF502211.1	EBPR sludge lab scale clone HP1A92
Bacteroidetes	Flavobacteriaceae	sf_1	5726	AY008691.1	Bergeyella sp. oral AK152 clone
Bacteroidetes	Flavobacteriaceae	sf_1	5906	X67609.1	Capnocytophaga sputigena str. ATCC 33612
Bacteroidetes	Unclassified	sf_15	5784	AY838556.1	fruiting body Pleurotus eryngii clone PE01

Bacteroidetes	Porphyromonadaceae	sf_1	5800	AY253728.1	Porphyromonas endodontalis str. ATCC 35406
Bacteroidetes	Prevotellaceae	sf_1	5718	AF183403.1	Prevotella tannerae str. 29-1
Bacteroidetes	Prevotellaceae	sf_1	5706	U43698.1	oral cavity clone 3.3
Bacteroidetes	Unclassified	sf_1	5745		
Bacteroidetes	Crenotrichaceae	sf_11	6143	AF534433.1	Toolik Lake main station at 3 m depth clone TLM09/TLMdgge12a
Bacteroidetes	Flexibacteraceae	sf_19	6261	AF468338.1	Arctic sea ice cryoconite clone ARKCRY-50
Bacteroidetes	Flexibacteraceae	sf_19	5542	AB073595.2	Cytophaga sp. I-1787
Bacteroidetes	Flavobacteriaceae	sf_1	5836	U41348.1	Capnocytophaga granulosa str. LMG 12119; FDC SD4
Bacteroidetes	Flavobacteriaceae	sf_1	5969	U41350.1	Capnocytophaga ochracea str. ATCC 27872 T
Bacteroidetes	Flavobacteriaceae	sf_1	5955	AJ244701.1	Flavobacterium sp. str. V4.MS.29 = MM_2747
Bacteroidetes	Unclassified	sf_15	5355	AJ306736.1	DCP-dechlorinating consortium clone SHA-5
Bacteroidetes	Crenotrichaceae	sf_11	5463	AB078068.1	Flexibacter sancti str. IFO 16034
Bacteroidetes	Rikenellaceae	sf_5	5889	AB088945.1	termite gut homogenate clone Rs-F73 bacterium
Bacteroidetes	Prevotellaceae	sf_1	5437	AY244919.1	cow rumen clone BE1
Bacteroidetes	Prevotellaceae	sf_1	5426	AF385509.1	tongue dorsa clone DO014
Bacteroidetes	Crenotrichaceae	sf_11	5334	AB117715.1	autotrophic nitrifying biofilm clone NB-11
Bacteroidetes	Flexibacteraceae	sf_19	5366	AB078061.1	Flexibacter roseolus str. IFO 16030
Bacteroidetes	Unclassified	sf_15	5353	AF529128.1	trichloroethene-contaminated site clone FTLpost3 bacterium
Bacteroidetes	Prevotellaceae	sf_1	6066	AY207061.1	human mouth isolate str. P4P_62
Bacteroidetes	Prevotellaceae	sf_1	5893	AF385515.1	tongue dorsa clone DO045
Bacteroidetes	Flavobacteriaceae	sf_1	5423	AF170754.1	Aequorivita antarctica str. QSSC9-14
Bacteroidetes	Flavobacteriaceae	sf_1	5521	AF493689.1	Flavobacteriaceae str. SW269
Bacteroidetes	Prevotellaceae	sf_1	5926	AY244900.1	cow rumen clone BF22
Bacteroidetes	Flavobacteriaceae	sf_1	5367	AY238333.1	patient's bronchoalveolar lavage isolate str. MDA2507 sp.
Bacteroidetes	Unclassified	sf_15	5511	AJ535256.1	marine sediment above hydrate ridge clone Hyd-B2-1 bacterium
Bacteroidetes	Unclassified	sf_15	5578	AJ534685.1	ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A-MN91
Bacteroidetes	Rikenellaceae	sf_5	5947	AJ441218.1	hydrothermal vent polychaete mucous clone P. palm C/A 221
Bacteroidetes	Porphyromonadaceae	sf_1	5429		
Bacteroidetes	Flavobacteriaceae	sf_1	6246	AF385569.1	crevicular epithelial cells clone BU084
Bacteroidetes	Crenotrichaceae	sf_11	5888	AY218661.1	penguin droppings sediments clone KD9-169
Bacteroidetes	Prevotellaceae	sf_1	5720	AF481227.1	Prevotella sp. str. E9_34
Bacteroidetes	Flavobacteriaceae	sf_1	5301		
Bacteroidetes	Flavobacteriaceae	sf_1	5933	AB015481.1	Flavobacterium columnare str. PH-97028 (IAM 14821)
Bacteroidetes	Flavobacteriaceae	sf_1	5589		
Bacteroidetes	Unclassified	sf_15	5257	AY188307.1	marine? clone KD3-67
Bacteroidetes	Bacteroidaceae	sf_6	5792	AF513095.1	activated sludge foam clone 47
Bacteroidetes	Flexibacteraceae	sf_19	5307	AB078082.1	Microscilla sericea str. IFO 16561
BRC1	Unclassified	sf_2	118	AY218548.1	penguin droppings sediments clone KD1-1
BRC1	Unclassified	sf_1	5051	AJ390454.1	soil clone PBS-III-24
BRC1	Unclassified	sf_1	5143	AJ390438.1	soil clone PBS-II-1
Caldithrix	Caldithraceae	sf_2	91	AF323775.1	benzoate-degrading consortium clone BA059
Caldithrix	Caldithraceae	sf_1	2384	AF286032.1	saltmarsh clone LCP-89
Chlamydiae	Parachlamydiaceae	sf_1	4964	AY082465.1	neutral pH mine biofilm clone 44a-B1-34
Chlamydiae	Chlamydiaceae	sf_1	4820	NC_002179.2	Chlamydophila pneumoniae str. AR39
Chlorobi	Chlorobiaceae	sf_1	262	Y18253.1	Chlorobium ferrooxidans DSM 13031 str. KofoX

Chlorobi	Unclassified	sf_9	6146	AF234699.1	sludge clone A12b
Chlorobi	Unclassified	sf_8	636	AY118152.1	benzene-degrading nitrate-reducing consortium clone Cart-N3 bacterium
Chlorobi	Chlorobiaceae	sf_1	859	Y08105.1	Chlorobium phaeovibrioides str. 2631
Chlorobi	Unclassified	sf_6	5294	AY221073.1	Mammoth cave clone CCM9b
Chlorobi	Chlorobiaceae	sf_1	995	AB054671.1	Chlorobium limicola str. M1
Chlorobi	Unclassified	sf_8	5822	AJ428454.1	Saltmarsh mud clone K-790
Chlorobi	Unclassified	sf_8	549	AY118151.1	benzene-degrading nitrate-reducing consortium clone Cart-N2 bacterium
Chloroflexi	Unclassified	sf_5	1051	AY913277.1	forest soil clone DUNssu055 (-2B) (OTU#087)
Chloroflexi	Unclassified	sf_9	205	AJ532729.1	uranium mining waste pile clone JG34-KF-221
Chloroflexi	Unclassified	sf_9	375	AF507690.1	forest soil clone C043
Chloroflexi	Unclassified	sf_9	946	AY216458.1	temperate estuarine mud clone KM87
Chloroflexi	Unclassified	sf_1	2367	AY093473.1	deep marine sediment clone MB-B2-113
Chloroflexi	Unclassified	sf_1	2438	AY093464.1	deep marine sediment clone MB-A2-110
Chloroflexi	Unclassified	sf_1	2485		
Chloroflexi	Unclassified	sf_1	2497	AF524015.1	forested wetland clone FW60
Chloroflexi	Unclassified	sf_2	818		
Chloroflexi	Unclassified	sf_9	727	AF507692.1	forest soil clone S0208
Chloroflexi	Unclassified	sf_2	2344	AF507700.1	forest soil clone C083
Chloroflexi	Unclassified	sf_1	258	AJ306793.1	DCP-dechlorinating consortium clone SHD-14
Chloroflexi	Unclassified	sf_1	2534	AF507693.1	forest soil clone S085
Chloroflexi	Unclassified	sf_1	2339	AJ519643.1	uranium mill tailings soil sample clone Sh765B-TzT-20 bacterium
Chloroflexi	Unclassified	sf_1	106	AJ306798.1	DCP-dechlorinating consortium clone SHD-231
Chloroflexi	Unclassified	sf_9	576	AJ306746.2	DCP-dechlorinating consortium clone SHA-36
Chloroflexi	Unclassified	sf_7	757	AJ306741.2	DCP-dechlorinating consortium clone SHA-8
Chloroflexi	Unclassified	sf_1	1041	AY250886.1	Antarctic cryptoendolith clone FBP471
Chloroflexi	Unclassified	sf_9	72	AY221035.1	sediments collected at Charon's Cascade near Echo River October 2000 clone CCD21
Chloroflexi	Unclassified	sf_1	583	AJ278171.2	anaerobic bioreactor clone SHD-238
Chloroflexi	Unclassified	sf_12	2523	AJ347055.1	sponge clone TK10
Chloroflexi	Unclassified	sf_2	789	AF445676.1	travertine hot spring clone SM1D10
Chloroflexi	Unclassified	sf_1	927	AJ441227.1	hydrothermal vent polychaete mucous clone P. palm C 37
Chloroflexi	Unclassified	sf_1	765	AJ278167.1	anaerobic bioreactor clone SHD-71
Chloroflexi	Unclassified	sf_1	76	AJ306749.1	DCP-dechlorinating consortium clone SHA-147
Chloroflexi	Unclassified	sf_1	2397	AY093480.1	deep marine sediment clone MB-C2-127
Chloroflexi	Unclassified	sf_9	2539	AY218649.1	penguin droppings sediments clone KD4-96
Chloroflexi	Unclassified	sf_2	2532	AF529110.1	trichloroethene-contaminated site clone FTL276 bacterium
Chloroflexi	Unclassified	sf_1	266		
Chloroflexi	Unclassified	sf_1	1071	AJ412677.1	denitrifying reactor clone 131
Chloroflexi	Unclassified	sf_1	159	AJ278169.1	anaerobic bioreactor clone SHD-235
Chloroflexi	Unclassified	sf_1	374	AF507691.1	forest soil clone S041
Chloroflexi	Unclassified	sf_5	635	AF418964.1	USA: Colorado Fort collins Horsetooth Reservoir clone HTH4
Chloroflexi	Unclassified	sf_1	905	AF154100.1	hydrocarbon seep clone GCA112
Chloroflexi	Unclassified	sf_1	2370	AF004928.2	Dehalococcoides ethenogenes str. strain 195
Coprothermobacteria	Unclassified	sf_1	751	AJ431258.1	Coprothermobacter sp. str. Dex80-3
Crenarchaeota	Unclassified	sf_1	2587	AB019729.1	hydrothermal vent clone pIVWA11
Cyanobacteria	Unclassified	sf_1	5190	AF091110.1	Plectonema sp. str. F3
Cyanobacteria	Chloroplasts	sf_5	5147	X82156.1	Emiliania huxleyi str. Plymouth Marine Laborator

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Cyanobacteria	Unclassified	sf_5	4998		
Cyanobacteria	Chloroplasts	sf_5	4967	AF534438.1	Toolik Lake main station at 3 m depth clone TLM14
Cyanobacteria	Unclassified	sf_8	5206		
Cyanobacteria	Unclassified	sf_5	5030	AY034793.1	Hapalosiphon welwitschii
Cyanobacteria	Chloroplasts	sf_13	5000	U67742.1	Mitrastema yamamotoi
Cyanobacteria	Unclassified	sf_1	5189	AB039015.1	Oscillatoria sancta str. PCC 7515
Cyanobacteria	Unclassified	sf_1	5001	AJ347056.1	sponge clone TK09
Cyanobacteria	Chloroplasts	sf_5	5130	AF445714.1	travertine hot spring clone SM2B11
Cyanobacteria	Chloroplasts	sf_5	5006		
Cyanobacteria	Chloroplasts	sf_11	5098	AF289245.1	Euglena tripteris str. UW OB
Cyanobacteria	Chloroplasts	sf_11	5123	AF289249.1	Lepocinclis fusiformis str. ACOI 1025
Cyanobacteria	Chloroplasts	sf_5	4966	AF244549.1	Adiantum pedatum
Cyanobacteria	Chloroplasts	sf_5	4976	AF244550.1	Calypogeia muelleriana
Cyanobacteria	Chloroplasts	sf_5	5040	Y18934.1	Solanum nigrum
Cyanobacteria	Chloroplasts	sf_5	5182	M81884.1	Epifagus virginiana -- chloroplast
Cyanobacteria	Chloroplasts	sf_5	5183	M37430.1	Pisum sativum -- chloroplast
Cyanobacteria	Chloroplasts	sf_5	5192	AF244551.1	Cycas revoluta
Cyanobacteria	Unclassified	sf_1	5057	AJ781148.1	Nodularia sphaerocarpa str. UTEX B 2093
Cyanobacteria	Unclassified	sf_9	5038	AF544207.1	Rumen isolate str. YS2
Cyanobacteria	Unclassified	sf_1	5034	AF329394.1	Spirulina subsalsa str. FACHB351
Cyanobacteria	Unclassified	sf_1	5049	AF420444.1	Oscillatoria spongeliae str. 520bg
Cyanobacteria	Unclassified	sf_9	5164	AB089123.1	termite gut homogenate clone Rs-H34
Cyanobacteria	Unclassified	sf_5	5015	AB093489.1	Chlorogloeopsis fritschii str. PCC 6912
Cyanobacteria	Unclassified	sf_5	5027		
Cyanobacteria	Unclassified	sf_6	5186	AY222299.1	silica sinter depositing geothermal power station discharge drain clone ST01-SN2C
Cyanobacteria	Unclassified	sf_1	5219	AF448074.1	Synechococcus sp. str. UH7
Cyanobacteria	Unclassified	sf_1	5010	AF170757.1	LPP-group cyanobacterium isolate str. QSSC5cya QSSC5cya
Cyanobacteria	Unclassified	sf_1	5210	AY250881.1	lichen-dominated Antarctic cryptoendolithic community clone FBP403
Cyanobacteria	Chloroplasts	sf_5	5112	X52985.1	Cyanidium caldarium str. 14-1-1
Cyanobacteria	Unclassified	sf_5	5064	AB003168.1	Oscillatoria neglecta str. M-82
Cyanobacteria	Chloroplasts	sf_5	5166		
Cyanobacteria	Unclassified	sf_5	5188	AY163573.1	Acaryochloris marina str. MBIC11017
Cyanobacteria	Chloroplasts	sf_5	5060	X82155.1	Skeletonema pseudocostatum str. CSIRO CS-76
Cyanobacteria	Unclassified	sf_1	4978	AB058225.1	LPP-group isolate str. MBIC10087
Cyanobacteria	Chloroplasts	sf_5	5039	U70723.1	Cape Hatteras picoplankton clone OM270
Cyanobacteria	Unclassified	sf_5	270	AY328558.1	drinking water system simulator clone HOClCi9
Deinococcus-Thermus	Unclassified	sf_3	920		
Deinococcus-Thermus	Unclassified	sf_1	563	AJ507298.1	Vulcanithermus mediatlanticus str. TR
Deinococcus-Thermus	Unclassified	sf_2	637	AF513964.1	hypersaline pond clone LA7-B27N
Deinococcus-Thermus	Unclassified	sf_1	178	AY028380.1	Thermus sp. str. C4
Dictyoglomi	Dictyoglomaceae	sf_9	7579	AF353224.1	marine clone Arctic96B-6
DSS1	Unclassified	sf_2	38	AJ306783.1	DCP-dechlorinating consortium clone SHA-109
Firmicutes	Unclassified	sf_17	2324		
Firmicutes	Unclassified	sf_1	2351	Y11574.1	Desulfotomaculum thermobenzoicum str. DSM 6193
Firmicutes	Unclassified	sf_1	2388	AF465653.1	G+C Gram-positive clone YNPRH70A
Firmicutes	Unclassified	sf_1	2443	Y11573.1	Desulfotomaculum thermoacetoxidans str. DSM 5813
Firmicutes	Unclassified	sf_1	2490	AY084078.1	Desulfotomaculum solfataricum str. V21

Firmicutes	Unclassified	sf_1	77	AF391988.1	thermal soil clone YNPFFP9
Firmicutes	Unclassified	sf_17	3476		
Firmicutes	Unclassified	sf_17	4168		
Firmicutes	Unclassified	sf_4	4503	AB088976.1	termite gut homogenate clone Rs-H83 bacterium
Firmicutes	Unclassified	sf_8	4536	AF507891.1	Mono Lake at depth 35m station 6 July 2000 clone ML635J-14 G+C
Firmicutes	Unclassified	sf_7	4216		
Firmicutes	Unclassified	sf_1	4293	AB089008.1	termite gut homogenate clone Rs-Q01 bacterium
Firmicutes	Unclassified	sf_1	4616	AB185532.1	rumen clone F23-C12
Firmicutes	Streptococcaceae	sf_1	3422	X68418.1	Streptococcus thermophilus str. DSM 20617
Firmicutes	Streptococcaceae	sf_1	3499	AF104676.1	Streptococcus constellatus str. ATCC27823
Firmicutes	Streptococcaceae	sf_1	3685	AF003931.1	Streptococcus gordonii str. ATCC 10558
Firmicutes	Peptostreptococcaceae	sf_5	2694	AY134903.1	oral periodontitis clone FX028
Firmicutes	Peptostreptococcaceae	sf_5	2714	AB088954.2	termite gut homogenate clone Rs-N27 bacterium
Firmicutes	Peptostreptococcaceae	sf_5	2805	AY134904.1	oral periodontitis clone FX033
Firmicutes	Peptostreptococcaceae	sf_5	224	AB109771.1	Finegoldia magna str. ATCC 29328
Firmicutes	Peptostreptococcaceae	sf_5	58	AF481225.1	Peptostreptococcus sp. str. E3_32
Firmicutes	Peptostreptococcaceae	sf_5	393	AF542229.1	Anaerococcus vaginalis str. CCUG 31349
Firmicutes	Peptococc/Acidaminococc	sf_11	709	AB017195.1	Selenomonas ruminantium str.S20
Firmicutes	Peptococc/Acidaminococc	sf_11	131	AF349425.1	pig feces clone
Firmicutes	Peptococc/Acidaminococc	sf_11	992	AJ229198.1	anoxic bulk soil flooded rice microcosm clone BSV43 clone
Firmicutes	Mycoplasmataceae	sf_1	3929	AY191226.1	Mycoplasma gypsbengalensis str. Gb-V33
Firmicutes	Lachnospiraceae	sf_5	2668	AB088998.1	termite gut homogenate clone Rs-G40 bacterium
Firmicutes	Lachnospiraceae	sf_5	2994	AB100463.1	termite gut clone Rs-L15
Firmicutes	Lachnospiraceae	sf_5	2931	AB088994.1	termite gut homogenate clone Rs-G77 bacterium
Firmicutes	Lachnospiraceae	sf_5	3060	AB089002.1	termite gut homogenate clone Rs-B14 bacterium
Firmicutes	Lachnospiraceae	sf_5	3218	AB089000.1	termite gut homogenate clone Rs-N53
Firmicutes	Lachnospiraceae	sf_5	4510	AB089034.1	termite gut homogenate clone Rs-Q53 bacterium
Firmicutes	Lachnospiraceae	sf_5	4540	AB088968.1	termite gut homogenate clone Rs-M18 bacterium
Firmicutes	Lachnospiraceae	sf_5	4571	X85022.1	Faecalibacterium prausnitzii str. ATCC 27766
Firmicutes	Lachnospiraceae	sf_5	4613	AB034003.1	rumen clone 3C0d-3
Firmicutes	Erysipelotrichaceae	sf_3	3952	AB055907.1	Erysipelothrix rhusiopathiae str. Pecs 56
Firmicutes	Erysipelotrichaceae	sf_3	3965	AY133091.1	TCE-contaminated site clone ccslm238
Firmicutes	Erysipelotrichaceae	sf_3	3981	AY128088.1	phototrophic sludge clone PSB-M-3
Firmicutes	Erysipelotrichaceae	sf_3	768		
Firmicutes	Enterococcaceae	sf_1	3288	AY167946.1	Isolation and identification hyper-ammonia producing swine storage pits manure
Firmicutes	Enterococcaceae	sf_1	3433	D88824.1	Tetragenococcus muriaticus
Firmicutes	Enterococcaceae	sf_1	3598	AJ301840.1	Enterococcus solitarius str. DSM 5634
Firmicutes	Enterococcaceae	sf_1	3881	AJ301829.1	Enterococcus dispar str. LMG 13521
Firmicutes	Clostridiaceae	sf_12	4300	AB100493.1	termite gut clone Rs-060
Firmicutes	Clostridiaceae	sf_12	4364	AF481208.1	oral endodontic infection clone MCE3_9
Firmicutes	Clostridiaceae	sf_12	4477	AB089042.1	termite gut homogenate clone Rs-N85 bacterium
Firmicutes	Clostridiaceae	sf_12	4502		
Firmicutes	Clostridiaceae	sf_12	4554	AB100479.1	termite gut clone Rs-068
Firmicutes	Clostridiaceae	sf_12	4266	AB088951.1	termite gut homogenate clone Rs-M86 bacterium
Firmicutes	Clostridiaceae	sf_12	4321	AB089045.1	termite gut homogenate clone Rs-C76 bacterium
Firmicutes	Clostridiaceae	sf_12	4475	AB089035.1	termite gut homogenate clone Rs-N02 bacterium
Firmicutes	Bacillaceae	sf_1	3827	AF547209.1	Bacillus acidogenesis str. 105-2
Firmicutes	Bacillaceae	sf_1	3328	AJ224963.1	Pseudobacillus carolinae
Firmicutes	Alicyclobacillaceae	sf_1	3368	AY529492.1	geothermal site isolate str. G1
Firmicutes	Peptostreptococcaceae	sf_5	3182	AB088970.1	termite gut homogenate clone Rs-Q64 bacterium

Firmicutes	Unclassified	sf_8	546	AF282254.1	Ferribacter thermoautotrophicus
Firmicutes	Unclassified	sf_8	2433	AF282252.1	Ferribacter thermoautotrophicus str. JW/JH-Fiji-2
Firmicutes	Peptococc/Acidaminococc	sf_11	863	AY162469.1	Dialister invisus str. E7_25
Firmicutes	Peptococc/Acidaminococc	sf_11	39	AF523919.1	forested wetland clone RCP2-71
Firmicutes	Lachnospiraceae	sf_5	2961	AB088989.1	termite gut homogenate clone Rs-F92 bacterium
Firmicutes	Lachnospiraceae	sf_5	3036	AB088990.1	termite gut homogenate clone Rs-F27 bacterium
Firmicutes	Lachnospiraceae	sf_5	2834	U41168.1	Butyrivibrio fibrisolvens str. OB156
Firmicutes	Peptostreptococcaceae	sf_5	2679	AB062845.1	termite gut homogenate clone BCf9-13
Firmicutes	Peptostreptococcaceae	sf_5	3080	AB088986.1	termite gut homogenate clone Rs-F43 bacterium
Firmicutes	Peptostreptococcaceae	sf_5	2797	AY167963.1	Isolation and identification hyper-ammonia producing swine storage pits manure
Firmicutes	Bacillaceae	sf_1	3612	AB042060.1	Bacillus schlegelii str. ATCC 43741T
Firmicutes	Bacillaceae	sf_1	3836	AY682096.1	Geobacillus stearothermophilus str. 46
Firmicutes	Halobacillaceae	sf_1	3344	AY881246.1	Halobacillus yeomjeoni str. MSS-402
Firmicutes	Bacillaceae	sf_1	3439	AF071856.1	Bacillus siralis str. 171544
Firmicutes	Bacillaceae	sf_1	1050	AJ717384.1	Bacillus firmus CV93b
Firmicutes	Bacillaceae	sf_1	3579	AB020198.1	Bacillus sp. str. TGS750
Firmicutes	Bacillaceae	sf_1	3675	AY189750.1	Bacillus mojavensis str. M-1
Firmicutes	Bacillaceae	sf_1	3706	AF302119.1	Bacillus sonorensis str. NRRL B-23155
Firmicutes	Bacillaceae	sf_1	3831	AY030328.1	Bacillus licheniformis str. KL-068
Firmicutes	Bacillaceae	sf_1	3909	D26185.1	Bacillus subtilis subsp. Marburg str. 168
Firmicutes	Staphylococcaceae	sf_1	3258	D83358.1	Staphylococcus auricularis str. MAFF911484 ATCC33753T
Firmicutes	Staphylococcaceae	sf_1	3284		
Firmicutes	Staphylococcaceae	sf_1	3545		
Firmicutes	Staphylococcaceae	sf_1	3569	L37596.1	Staphylococcus saprophyticus
Firmicutes	Staphylococcaceae	sf_1	3592	Y12593.1	Staphylococcus caprae str. DSM 20608
Firmicutes	Staphylococcaceae	sf_1	3605		
Firmicutes	Staphylococcaceae	sf_1	3628	X66100.1	Staphylococcus haemolyticus str. CCM2737
Firmicutes	Staphylococcaceae	sf_1	3638	X86641.1	Staphylococcus sp str. AG-30
Firmicutes	Staphylococcaceae	sf_1	3654	AF322002.1	Staphylococcus pettenkoferi str. B3117
Firmicutes	Staphylococcaceae	sf_1	3684	S83569.1	Staphylococcus sciuri
Firmicutes	Staphylococcaceae	sf_1	3794		
Firmicutes	Staphylococcaceae	sf_1	3822	AJ320272.1	Staphylococcus succinus str. SB72
Firmicutes	Staphylococcaceae	sf_1	3494	AB079788.1	Micrococcus luteus B-P 26
Firmicutes	Staphylococcaceae	sf_1	3432	AY188939.1	deep-sea sediment isolate str. P_wp0225
Firmicutes	Caryophanaceae	sf_1	3285	AJ491302.1	Caryophanon latum str. DSM 14151
Firmicutes	Lactobacillaceae	sf_1	3634	AJ417738.1	Lactobacillus letivazi str. JCL3994
Firmicutes	Lactobacillaceae	sf_1	3767	AJ575744.1	Lactobacillus suebicus str. CECT 5917T
Firmicutes	Enterococcaceae	sf_1	3261	AJ301836.1	Enterococcus mundtii str. LMG 10748
Firmicutes	Enterococcaceae	sf_1	3298	AJ301839.1	Enterococcus saccharolyticus str. LMG 11427
Firmicutes	Enterococcaceae	sf_1	3392	Y17152.2	Vagococcus lutrae str. m1134/97/1; CCUG 39187
Firmicutes	Streptococcaceae	sf_1	3250	AF396920.1	Streptococcus bovis str. B315
Firmicutes	Streptococcaceae	sf_1	3253	AF349918.1	derived cheese sample clone 32CR
Firmicutes	Streptococcaceae	sf_1	3313	AY188352.1	Streptococcus salivarius str. ATCC 7073
Firmicutes	Streptococcaceae	sf_1	3397	Z94012.1	Streptococcus macedonicus str. ACA-DC 206 LAB617
Firmicutes	Streptococcaceae	sf_1	3906	AF104114.1	Streptococcus bovis str.ATCC 43143
Firmicutes	Streptococcaceae	sf_1	3446	AY173079.1	Streptococcus bovis str. HJ50
Firmicutes	Streptococcaceae	sf_1	3753	AF009482.1	Streptococcus suis str. 8074
Firmicutes	Streptococcaceae	sf_1	3251	AY188347.1	Streptococcus cristatus str. ATCC 51100
Firmicutes	Streptococcaceae	sf_1	3287	AF432137.1	tongue dorsum scrapings clone FP015
Firmicutes	Streptococcaceae	sf_1	3290	AY518677.1	Streptococcus mitis str. Sm91

Firmicutes	Clostridiaceae	sf_12	4278	AF482434.1	granular sludge clone R1p16
Firmicutes	Clostridiaceae	sf_12	4310	AB100478.1	termite gut clone Rs-056
Firmicutes	Clostridiaceae	sf_12	4584	X71852.1	Clostridium papyrosolvens str. DSM 2782
Firmicutes	Clostridiaceae	sf_12	4272	AB088965.1	termite gut homogenate clone Rs-M34 bacterium
Firmicutes	Clostridiaceae	sf_12	4369	AB089032.1	termite gut homogenate clone Rs-N73 bacterium
Firmicutes	Lachnospiraceae	sf_5	4511	AF376218.1	ckncm314-B7-17 clone
Firmicutes	Lachnospiraceae	sf_5	4514	AB088983.2	termite gut homogenate clone Rs-B34 bacterium
Firmicutes	Lachnospiraceae	sf_5	4533	AB088980.1	termite gut homogenate clone Rs-N06 bacterium
Firmicutes	Clostridiaceae	sf_12	4566	AF371796.1	swine intestine clone p-2657-65A5
Firmicutes	Lachnospiraceae	sf_5	4567	AJ408989.1	human colonic clone HuCB5
Firmicutes	Clostridiaceae	sf_12	4306	AY261814.1	UASB reactor granular sludge clone PD-UASB-4 bacterium
Firmicutes	Lachnospiraceae	sf_5	4525	AB088991.1	termite gut homogenate clone Rs-Q18 bacterium
Firmicutes	Lactobacillaceae	sf_1	3566	X76329.1	Lactobacillus pontis str. LTH 2587
Firmicutes	Aerococcaceae	sf_1	3833	L08623.1	Carnobacterium alterfunditum
Firmicutes	Clostridiaceae	sf_12	4297		
Firmicutes	Clostridiaceae	sf_12	4614	AB093546.1	Clostridium sp. str. JC3
Firmicutes	Lachnospiraceae	sf_5	4212	AB100488.1	termite gut clone Rs-061
Firmicutes	Lachnospiraceae	sf_5	4315	AB089040.1	termite gut homogenate clone Rs-N94 bacterium
Firmicutes	Lachnospiraceae	sf_5	4535	AF376201.1	ckncm297-B1-1 clone
Firmicutes	Peptococc/Acidaminococc	sf_11	304	AB003379.1	Selenomonas ruminantium str.JCM6582
Firmicutes	Peptococc/Acidaminococc	sf_11	710	AF458222.1	Centipeda periodontii str. HB-2
Firmicutes	Peptococc/Acidaminococc	sf_11	940	X84006.1	Veillonella dispar str. DSM 20735
Firmicutes	Peptococc/Acidaminococc	sf_11	428	AJ488090.1	chlorobenzene-degrading consortium clone IIIA-1
Firmicutes	Peptococc/Acidaminococc	sf_11	242	AJ493052.1	Desulfosporosinus orientis str. DSMZ 7493
Firmicutes	Lachnospiraceae	sf_5	2698	AB088950.1	termite gut homogenate clone Rs-B88 bacterium
Firmicutes	Lachnospiraceae	sf_5	3076	AY169415.1	Clostridium nexile
Firmicutes	Lachnospiraceae	sf_5	2825	AF105403.1	Butyrivibrio fibrisolvens str. LP1265
Firmicutes	Lachnospiraceae	sf_5	2844	AF202260.1	Pseudobutyrivibrio ruminis str. pC-XS2
Firmicutes	Lachnospiraceae	sf_5	3059	X89978.1	Butyrivibrio fibrisolvens str. NCDO 2249
Firmicutes	Lachnospiraceae	sf_5	3038	AF371648.1	swine intestine clone p-1594-c5
Firmicutes	Peptostreptococcaceae	sf_5	2729	AJ306754.1	DCP-dechlorinating consortium clone SHA-58
Firmicutes	Peptostreptococcaceae	sf_5	2993	AF538856.1	oral clone P2PB_46 P3
Firmicutes	Clostridiaceae	sf_12	3021	AF458779.1	Clostridium caminithermale str. DVird3
Firmicutes	Clostridiaceae	sf_12	3077	X76750.1	Clostridium glycolicum str. DSM 1288
Firmicutes	Paenibacillaceae	sf_1	3299	AF378230.1	Brevibacillus borstelensis str. LMG 15536
Firmicutes	Bacillaceae	sf_1	3492	AB042061.1	Bacillus subtilis str. IAM 12118T
Firmicutes	Bacillaceae	sf_1	3900	X68416.1	Bacillus licheniformis str. DSM 13
Firmicutes	Bacillaceae	sf_1	3918	AF549498.1	Bacillus subtilis
Firmicutes	Lactobacillaceae	sf_1	3418	AB001836.2	Lactobacillus subsp. aviarius
Firmicutes	Lactobacillaceae	sf_1	3703	AY389803.1	Lactobacillus salivarius str. RA2115
Firmicutes	Enterococcaceae	sf_1	3318	AF539705.1	Enterococcus ratti str. ATCC 700914
Firmicutes	Enterococcaceae	sf_1	3382		
Firmicutes	Enterococcaceae	sf_1	3713	AF061009.1	Enterococcus cecorum str. ATCC43198
Firmicutes	Streptococcaceae	sf_1	3722	NC_002662.1	Lactococcus Il1403 subsp. lactis str. IL1403
Firmicutes	Unclassified	sf_1	3481		
Firmicutes	Streptococcaceae	sf_1	3588	AY188350.1	Streptococcus downei str. ATCC 33748
Firmicutes	Streptococcaceae	sf_1	3629	AF139600.1	Streptococcus mutans str. UA96
Firmicutes	Clostridiaceae	sf_12	4622	AB100475.1	termite gut clone Rs-L36
Firmicutes	Lachnospiraceae	sf_5	4281	AF332721.1	granular sludge clone UASB_brew_B86
Firmicutes	Unclassified	sf_17	4307		
Firmicutes	Lachnospiraceae	sf_5	4331	AF332720.1	granular sludge clone UASB_brew_B84
Firmicutes	Clostridiaceae	sf_12	4357	AF550610.1	Lachnospiraceae bacterium 19gly4

Firmicutes	Clostridiaceae	sf_12	4415	AB089041.1	termite gut homogenate clone Rs-K32 bacterium
Firmicutes	Lachnospiraceae	sf_5	4512	AF332711.1	granular sludge clone UASB_brew_B25
Firmicutes	Clostridiaceae	sf_12	4524	AB100476.1	termite gut clone Rs-093
Firmicutes	Clostridiaceae	sf_12	4169		
Firmicutes	Clostridiaceae	sf_12	2915	AY158079.1	Tepidibacter thalassicus str. SC 562
Firmicutes	Peptococc/Acidaminococc	sf_11	534	AJ488084.1	chlorobenzene-degrading consortium clone IIA-26
Firmicutes	Bacillaceae	sf_1	3283	AB021194.1	Bacillus niacini str. IFO15566
Firmicutes	Clostridiaceae	sf_12	4156	AF407388.1	MCB-contaminated groundwater-treating reactor clone RA9C1
Firmicutes	Lachnospiraceae	sf_5	4434	AB089036.1	termite gut homogenate clone Rs-K11 bacterium
Firmicutes	Clostridiaceae	sf_12	4229		
Firmicutes	Unclassified	sf_3	2373		
Firmicutes	Peptococc/Acidaminococc	sf_11	181	AF548373.1	Allisonella histaminiformans str. MR2
Firmicutes	Peptococc/Acidaminococc	sf_11	59	AF371694.1	swine intestine clone p-1941-s962-3
Firmicutes	Peptococc/Acidaminococc	sf_11	862	AF473834.1	Megasphaera micronuciformis str. AIP 412.00; CIP 107280
Firmicutes	Lachnospiraceae	sf_5	2804	AY353957.1	Clostridium amygdalinum str. BR-10
Firmicutes	Lachnospiraceae	sf_5	3042	AF371584.1	swine intestine clone p-2876-6C5
Firmicutes	Lachnospiraceae	sf_5	3111	AB034059.1	rumen clone 6C3d-11
Firmicutes	Lachnospiraceae	sf_5	2991	AB034063.1	rumen clone 3C3d-8
Firmicutes	Lachnospiraceae	sf_5	3171	AY169414.1	Lachnospira pectinoschiza
Firmicutes	Lachnospiraceae	sf_5	2681	AB088974.1	termite gut homogenate clone Rs-K41 bacterium
Firmicutes	Bacillaceae	sf_1	3661	AB094471.1	Bacillus sp. str. 2216.25.2
Firmicutes	Thermoactinomycetaceae	sf_1	3301	AB088361.1	Thermoactinomyces sp. str. 700375
Firmicutes	Bacillaceae	sf_1	3763	AY672761.1	Geobacillus stearothermophilus
Firmicutes	Bacillaceae	sf_1	3345	AY548955.1	Bacillus pumilus str. S9
Firmicutes	Staphylococcaceae	sf_1	3524	L14326.1	Gemella haemolysans
Firmicutes	Lactobacillaceae	sf_1	3330	AB107637.1	Lactobacillus kitasatonis str. KM9212
Firmicutes	Lactobacillaceae	sf_1	3521	AJ271383.1	Pediococcus inopinatus str. DSM 20285
Firmicutes	Lactobacillaceae	sf_1	3526	AF401673.1	Lactobacillus sakei
Firmicutes	Carnobacteriaceae	sf_1	3536		
Firmicutes	Aerococcaceae	sf_1	3553	Y17300.1	Desemzia incerta str. DSM 20581
Firmicutes	Unclassified	sf_1	3289	AJ302648.1	Isobaculum melis CCUG 37660T
Firmicutes	Streptococcaceae	sf_1	3869	AB104843.1	Streptococcus equi subsp. zooepidemicus str. Tokyo1291 subsp.
Firmicutes	Acholeplasmataceae	sf_1	4044		
Firmicutes	Clostridiaceae	sf_12	4157	AB089043.1	termite gut homogenate clone Rs-A15 bacterium
Firmicutes	Clostridiaceae	sf_12	4225	AB100486.1	termite gut clone Rs-116
Firmicutes	Clostridiaceae	sf_12	4418	AB088966.2	termite gut homogenate clone Rs-H18 bacterium
Firmicutes	Clostridiaceae	sf_12	4507	AB088984.1	termite gut homogenate clone Rs-N21 bacterium
Firmicutes	Paenibacillaceae	sf_1	3641	AJ313027.1	Brevibacillus sp. MN 47.2a
Firmicutes	Bacillaceae	sf_1	283	Z26926.1	Geobacillus thermocatenulatus str. DSM 730
Firmicutes	Bacillaceae	sf_1	3424	AJ532701.1	uranium mill tailings clone Gitt-KF-76
Firmicutes	Bacillaceae	sf_1	3926	X92160.1	Lake Bogoria isolate 64B4
Firmicutes	Lachnospiraceae	sf_5	3066	AF067965.1	Clostridium methoxybenzovorans str. SR3; DSM 12182
Firmicutes	Lachnospiraceae	sf_5	3088	X73449.1	Clostridium sphenoides str. DSM 632
Firmicutes	Lachnospiraceae	sf_5	2937	AF371541.1	swine intestine clone p-2482-18B5
Firmicutes	Lachnospiraceae	sf_5	3089	AY169419.1	Ruminococcus obeum
Firmicutes	Lachnospiraceae	sf_5	3017	AB088993.1	termite gut homogenate clone Rs-D48 bacterium
Firmicutes	Paenibacillaceae	sf_1	3415	AF480937.1	Paenibacillus nematophilus str. NEM1b
Firmicutes	Bacillaceae	sf_1	305	M77488.1	Bacillus thermoleovorans
Firmicutes	Bacillaceae	sf_1	829	AY191842.1	Geobacillus sp. str. YMTC1049

Firmicutes	Bacillaceae	sf_1	3550	AF142677.4	Bacillus megaterium str. QM B1551
Firmicutes	Clostridiaceae	sf_12	4187	AF538854.1	Clostridiales oral clone P4PB_122 P3
Firmicutes	Clostridiaceae	sf_12	4180	AB089028.1	termite gut homogenate clone Rs-M23 bacterium
Firmicutes	Clostridiaceae	sf_12	4555	M59113.1	Clostridium tyrobutyricum
Firmicutes	Clostridiaceae	sf_12	4551	X78070.1	Clostridium acetobutylicum str. ATCC 824 (T)
Firmicutes	Unclassified	sf_1	4298	AY207065.1	human mouth clone P4PA_66
Firmicutes	Peptostreptococcaceae	sf_5	619	AY217429.1	TCE-dechlorinating microbial community clone 1G
Firmicutes	Peptostreptococcaceae	sf_5	1037	AY169425.1	Finegoldia magna
Firmicutes	Peptostreptococcaceae	sf_5	616	AF542230.1	Peptoniphilus lacrimalis str. CCUG 31350
Firmicutes	Bacillaceae	sf_1	3650		
Firmicutes	Peptostreptococcaceae	sf_5	2721	AB088971.1	termite gut homogenate clone Rs-N71 bacterium
Firmicutes	Halobacillaceae	sf_1	3552	AB087828.1	Paraliobacillus ryukyuensis
Firmicutes	Bacillaceae	sf_1	3489	AY167818.1	Bacillus silvestris str. SAFN-010
Firmicutes	Clostridiaceae	sf_12	4339	U51843.1	Clostridium chauvoei str. ATCC 10092T
Firmicutes	Unclassified	sf_1	2359	AB091324.1	UASB granular sludge clone JP
Firmicutes	Unclassified	sf_4	2398	AY093477.1	deep marine sediment clone MB-C2-106
Firmicutes	Peptococc/Acidaminococc	sf_11	1036	AF407698.1	Great Artesian Basin clone G07
Firmicutes	Lachnospiraceae	sf_5	2784	AJ408993.1	human colonic clone HuCB12
Firmicutes	Lachnospiraceae	sf_5	3109	X87151.1	Catonella morbi str. ATCC 51271
Firmicutes	Eubacteriaceae	sf_1	28	AB088988.1	termite gut homogenate clone Rs-H81 bacterium
Firmicutes	Paenibacillaceae	sf_1	3559	AF378696.1	Paenibacillus turicensis str. MOL722
Firmicutes	Bacillaceae	sf_1	385	X57309.1	Geobacillus stearothermophilus str. T10
Firmicutes	Bacillaceae	sf_1	462	Z26927.1	Geobacillus thermodenitrificans str. DSM 466
Firmicutes	Bacillaceae	sf_1	571	Z26922.1	Bacillus caldotenax str. DSM 406
Firmicutes	Halobacillaceae	sf_1	3769	AY121437.1	Gracilibacillus sp. str. YIM-kkny13
Firmicutes	Aerococcaceae	sf_1	3870	AB022027.1	Abiotrophia para-adiacens str. TKT1
Firmicutes	Lactobacillaceae	sf_1	3696	AY253657.1	Lactobacillus kalixensis str. Kx127A2; LMG 22115T; DSM 16043T; CCUG 48459T
Firmicutes	Lactobacillaceae	sf_1	3885	M58834.1	Pediococcus pentosaceus
Firmicutes	Unclassified	sf_6	149	M23730.1	Streptococcus pleomorphus
Firmicutes	Unclassified	sf_1	4261	AB089006.1	termite gut homogenate clone Rs-G04 bacterium
Firmicutes	Lachnospiraceae	sf_5	4539	AB089046.1	termite gut homogenate clone Rs-C61 bacterium
Firmicutes	Lachnospiraceae	sf_5	4623	AJ408957.1	human colonic clone HuCA1
Firmicutes	Unclassified	sf_4	4526	AY133082.1	TCE-contaminated site clone ccslm210
Firmicutes	Syntrophomonadaceae	sf_5	2456	AF482440.1	granular sludge clone R4b14
Firmicutes	Unclassified	sf_4	2716	AB089010.1	termite gut homogenate clone Rs-F76 bacterium
Firmicutes	Halobacillaceae	sf_1	3756	AY121439.1	Salibacillus sp. str. YIM-kkny16
Firmicutes	Bacillaceae	sf_1	3517	AF500007.1	Planococcus maritimus str. TF-9
Firmicutes	Clostridiaceae	sf_12	4598	AB161372.1	Clostridium sardiniense str. DSM 600
Firmicutes	Peptococc/Acidaminococc	sf_11	392	AF481210.1	oral endodontic infection clone MCE7_134
Firmicutes	Unclassified	sf_17	926		
Firmicutes	Lachnospiraceae	sf_5	3152	AF385510.1	tongue dorsa clone DO016
Firmicutes	Lachnospiraceae	sf_5	2709	AY916314.1	human stool clone B065
Firmicutes	Lachnospiraceae	sf_5	3001	AJ408972.1	human colonic clone HuCA20
Firmicutes	Peptostreptococcaceae	sf_5	2796	AF287764.1	human subgingival plaque clone BB142
Firmicutes	Bacillaceae	sf_1	234	AJ293805.1	Bacillus vulcani str. 3S-1
Firmicutes	Bacillaceae	sf_1	3460	AY312404.1	Geobacillus jurassicus str. DS1
Firmicutes	Bacillaceae	sf_1	3540	AB034836.1	Geobacillus thermoleovorans str. B23
Firmicutes	Bacillaceae	sf_1	3589	AF519468.1	Bacillus senegalensis str. RS8; CIP 106 669
Firmicutes	Aerococcaceae	sf_1	3736	Y14650.1	Desemzia incerta str. DSM 20581
Firmicutes	Streptococcaceae	sf_1	3907	U87830.1	aortic heart valve patient with endocarditis clone v6
Firmicutes	Clostridiaceae	sf_12	4265	AB088969.1	termite gut homogenate clone Rs-N70 bacterium
Firmicutes	Clostridiaceae	sf_12	4589	X68176.1	Clostridium butyricum str. ATCC43755

Firmicutes	Lactobacillaceae	sf_1	3768	Y19167.1	Lactobacillus perolens str. L532
Firmicutes	Clostridiaceae	sf_12	4359	AB089047.1	termite gut homogenate clone Rs-C69 bacterium
Firmicutes	Thermoactinomycetaceae	sf_1	3539	AF138738.1	Laceyella sacchari str. KCTC 9789 ()
Firmicutes	Sporolactobacillaceae	sf_1	3879	X92161.1	Lake Elmenteita isolate WE4
Firmicutes	Erysipelotrichaceae	sf_3	144	L34616.1	Eubacterium cylindroides
Firmicutes	Peptococc/Acidaminococc	sf_11	126	AY134907.1	oral periodontitis clone FY011
Firmicutes	Peptococc/Acidaminococc	sf_11	771	X82500.1	Dialister pneumosintes str. ATCC 33048
Firmicutes	Clostridiaceae	sf_12	3049	Z69929.1	Clostridium paradoxum str. DSM 7308T
Firmicutes	Clostridiaceae	sf_12	3108	Z69940.1	Clostridium paradoxum str. DSM 7308T
Firmicutes	Paenibacillaceae	sf_1	3651	AJ011323.1	Paenibacillus borealis KK20
Firmicutes	Bacillaceae	sf_1	3688	AY167821.1	Bacillus sp. str. SAFN-006
Firmicutes	Bacillaceae	sf_1	3894	AJ514408.1	Sporosarcina macmurdoensis str. CMS 21w
Firmicutes	Bacillaceae	sf_1	3383		
Firmicutes	Lactobacillaceae	sf_1	3366	AY255802.1	Lactobacillus saerimneri str. GDA154 LMG 22087 DSM 16049 (T); CCUG 48462 (T)
Firmicutes	Enterococcaceae	sf_1	3680	X75752.1	Melissococcus plutonius str. NCDO 2440
Firmicutes	Clostridiaceae	sf_12	4607	X68188.1	Clostridium novyi str. NCTC538
Firmicutes	Clostridiaceae	sf_12	4427	L08062.1	Clostridium tyrobutyricum str. NIZO 51
Firmicutes	Clostridiaceae	sf_12	4610	AF127024.1	Clostridium putrefaciens str. DSM 1291
Firmicutes	Peptostreptococcaceae	sf_5	3112	CR933145.1	Evry municipal wastewater treatment plant clone 012C11_B_SD_P15
Firmicutes	Bacillaceae	sf_1	3419	AY228462.1	Bacillus algicola str. KMM 3737
Firmicutes	Carnobacteriaceae	sf_1	3792	AF451271.1	Carnobacterium sp. str. D35
Firmicutes	Unclassified	sf_1	2541	AB091328.1	UASB granular sludge clone UT-2
Firmicutes	Lachnospiraceae	sf_5	3236	AF287770.1	Firmicutes sp. oral strain str. FTB41
Firmicutes	Lachnospiraceae	sf_5	2801	AY169412.1	Butyrivibrio fibrisolvens
Firmicutes	Lachnospiraceae	sf_5	3075	AJ312385.1	Roseburia intestinalis str. L1-82
Firmicutes	Lachnospiraceae	sf_5	2693	AB008552.1	ruminantium str. GA195
Firmicutes	Lachnospiraceae	sf_5	2943	AF527773.1	human thigh wound isolate str. MDA2477
Firmicutes	Peptostreptococcaceae	sf_5	2710	AJ306755.1	DCP-dechlorinating consortium clone SHA-74
Firmicutes	Sporolactobacillaceae	sf_1	3365	AF454300.1	Bacillus sp. clone ML615J-19
Firmicutes	Acholeplasmataceae	sf_1	4046	L33735.1	Pigeon pea witches'-broom mycoplasma-like organism
Firmicutes	Erysipelotrichaceae	sf_3	4038	AB031058.1	Bulleidia moorei str. JCM 10647 RCA59-77
Firmicutes	Clostridiaceae	sf_12	4627	AB089030.1	termite gut homogenate clone Rs-A13 bacterium
Firmicutes	Unclassified	sf_4	4325	AB088963.1	termite gut homogenate clone Rs-K21 bacterium
Firmicutes	Peptostreptococcaceae	sf_5	919	AF542234.1	Anaerococcus tetradius str. CCUG 46590
Firmicutes	Aerococcaceae	sf_1	3386	AF317386.1	feedlot manure clone B87
Firmicutes	Lachnospiraceae	sf_5	4335	AB088952.1	termite gut homogenate clone Rs-N86 bacterium
Firmicutes	Peptostreptococcaceae	sf_5	17	AF538859.1	Peptostreptococcus sp. oral clone P4PA_156 P4 oral
Firmicutes	Lachnospiraceae	sf_5	4273	AB089044.1	termite gut homogenate clone Rs-M14 bacterium
Firmicutes	Lachnospiraceae	sf_5	2965	AF481221.1	oral endodontic infection clone MCE9_173
Firmicutes	Peptostreptococcaceae	sf_5	668	AY221992.1	Sedimentibacter sp. str. BRS2
Firmicutes	Sporolactobacillaceae	sf_1	3747	AB043848.1	Bacillus sp. str. C-59-2
Firmicutes	Bacillaceae	sf_1	3848	AB098576.1	Bacillus sp. str. TUT1007
Firmicutes	Bacillaceae	sf_1	3845	AF252326.1	hot synthetic compost clone pPD15
Firmicutes	Leuconostocaceae	sf_1	3497	AY035892.1	Weissella koreensis S-5673
Firmicutes	Lactobacillaceae	sf_1	3490	AY675248.1	Lactobacillus suntoryeus str. LH
Firmicutes	Aerococcaceae	sf_1	3504	AB083413.1	Marinilactibacillus psychrotolerans str. O21
Firmicutes	Acholeplasmataceae	sf_1	3975	AF302841.1	Black raspberry witches'-broom phytoplasma str. BRWB witches'-broom
Firmicutes	Acholeplasmataceae	sf_1	3976		

Firmicutes	Clostridiaceae	sf_12	4275	M59087.1	Clostridium botulinum str. type G
Firmicutes	Peptostreptococcaceae	sf_5	861	AY244779.1	Peptoniphilus sp. str. 2002-2300004
Firmicutes	Peptostreptococcaceae	sf_5	2913	AB088960.2	termite gut homogenate clone Rs-N82 bacterium
Firmicutes	Clostridiaceae	sf_12	3219	AF407695.1	Great Artesian Basin clone R82
Firmicutes	Bacillaceae	sf_1	3898	AB034710.1	compost clone 4-28
Firmicutes	Peptococc/Acidaminococc	sf_11	865	AF287793.1	Selenomonas sputigena str. ATCC 35185
Firmicutes	Unclassified	sf_17	602		
Firmicutes	Peptostreptococcaceae	sf_5	2722	AB088987.2	termite gut homogenate clone Rs-E61 bacterium
Firmicutes	Bacillaceae	sf_1	3635	AJ504797.1	Bacillus aeolius str. 4-1
Firmicutes	Halobacillaceae	sf_1	3849	X94558.1	Halobacillus litoralis str. SL-4
Firmicutes	Lactobacillaceae	sf_1	3547	AJ250074.1	Lactobacillus frumenti str. TMW 1.666
Firmicutes	Streptococcaceae	sf_1	3543		
Firmicutes	Streptococcaceae	sf_1	3637	AF227836.1	str. 37236
Firmicutes	Acholeplasmataceae	sf_1	3961	L33766.1	Clover yellow edge mycoplasma-like organism
Firmicutes	Acholeplasmataceae	sf_1	4045	AY081817.1	Chinaberry yellows phytoplasma
Firmicutes	Acholeplasmataceae	sf_1	3945	AY566302.1	Ash witches'-broom phytoplasma str. AshWB
Firmicutes	Clostridiaceae	sf_12	4459	AB100469.1	termite gut clone Rs-109
Firmicutes	Clostridiaceae	sf_12	4550	AF371790.1	swine intestine clone p-320-a3
Firmicutes	Clostridiaceae	sf_12	4582	AF371783.1	swine intestine clone p-2600-9F5
Firmicutes	Clostridiaceae	sf_12	4296	AB081585.1	Clostridiaceae str. A4d
Firmicutes	Clostridiaceae	sf_12	4575	X68451.1	Clostridium subterminale str. NCIMB 10746
Firmicutes	Peptostreptococcaceae	sf_5	901	Y07841.1	Anaerococcus octavius str. NCTC 9810
Firmicutes	Aerococcaceae	sf_1	3522	M58797.1	Aerococcus viridans
Firmicutes	Lactobacillaceae	sf_1	3829	AJ417500.1	Lactobacillus paralimentarius str. DSM 13238
Firmicutes	Peptococc/Acidaminococc	sf_11	300	AY214183.1	benzene-contaminated groundwater clone ZZ12C8
Firmicutes	Unclassified	sf_1	894	AF351222.1	coal tar waste-contaminated groundwater clone 36-22 G+C
Firmicutes	Lachnospiraceae	sf_5	2893	AY169411.1	Ruminococcus obeum
Firmicutes	Clostridiaceae	sf_12	2786	AY007244.1	Clostridium glycolicum str. CIN5
Firmicutes	Halobacteroidaceae	sf_1	887	X89076.1	Halanaerobacter chitinovorans
Firmicutes	Bacillaceae	sf_1	3467	AJ419629.1	Bacillus luciferensis str. LMG 18422
Firmicutes	Aerococcaceae	sf_1	3866	AF349724.1	Turicibacter sanguinis
Firmicutes	Lactobacillaceae	sf_1	3600	AJ242969.1	Lactobacillus crispatus str. NCTC 4
Firmicutes	Entomoplasmataceae	sf_1	4074	AF371522.1	swine intestine clone p-2013-s959-5
Firmicutes	Clostridiaceae	sf_21	4471	AB100483.1	termite gut clone Rs-058
Firmicutes	Clostridiaceae	sf_12	4587	X68315.1	Clostridium botulinum str. 468; toxin type C
Firmicutes	Clostridiaceae	sf_12	4378		
Firmicutes	Clostridiaceae	sf_12	4560	X68180.1	Clostridium beijerinckii str. NCIMB9362
Firmicutes	Streptococcaceae	sf_1	3560	AJ307888.1	Streptococcus gallinaceus str. CCUG 42692
Firmicutes	Peptococc/Acidaminococc	sf_11	150		
Firmicutes	Clostridiaceae	sf_12	252	AB089014.1	termite gut homogenate clone Rs-A28 bacterium
Firmicutes	Unclassified	sf_1	522	AB091327.1	UASB granular sludge clone UT-1
Firmicutes	Lachnospiraceae	sf_5	3087	AY178635.1	Butyrivibrio hungatei str. Su6
Firmicutes	Paenibacillaceae	sf_1	3630		
Firmicutes	Paenibacillaceae	sf_1	3922	AJ320490.1	Paenibacillus thiaminolyticus str. DSM 7262
Firmicutes	Bacillaceae	sf_1	3730	AF541965.1	Bacillus baekryungensis str. SW-93
Firmicutes	Bacillaceae	sf_1	3370	AB020195.1	Bacillus sp. str. TGS437
Firmicutes	Aerococcaceae	sf_1	3631	D50541.1	Abiotrophia defectiva str. GIFU12707 (ATCC49176)
Firmicutes	Leuconostocaceae	sf_1	3573	AF360736.1	Leuconostoc ficulneum str. FS-1
Firmicutes	Aerococcaceae	sf_1	3326	AF255736.1	Nostocoida limicola I str. Ben206
Firmicutes	Streptococcaceae	sf_1	3699	AE014207.1	Streptococcus agalactiae str. 2603V/R
Firmicutes	Acholeplasmataceae	sf_1	3977	AF495882.1	Chinaberry yellows phytoplasma str. CbY1

Firmicutes	Clostridiaceae	sf_12	4299	AB100466.1	termite gut clone Rs-L02
Firmicutes	Clostridiaceae	sf_12	4406	AB088977.1	termite gut homogenate clone Rs-J39 bacterium
Firmicutes	Clostridiaceae	sf_12	4177	AF241842.1	Clostridium subterminale DSM 2636
Firmicutes	Peptostreptococcaceae	sf_5	840	Y07839.1	Peptoniphilus harei str. DSM 10020; SBH432
Firmicutes	Staphylococcaceae	sf_1	3585		
Firmicutes	Clostridiaceae	sf_12	10457	AJ431218.1	strain isolate str. Dex60-82
Firmicutes	Unclassified	sf_17	2432		
Firmicutes	Syntrophomonadaceae	sf_5	2483	AF529116.1	trichloroethene-contaminated site clone FTLM142 bacterium
Firmicutes	Peptococc/Acidaminococc	sf_11	761	AF338413.1	Anaeroglobus geminatus str. AIP313.00; CIP 106856; CCUG 44773
Firmicutes	Peptococc/Acidaminococc	sf_11	275	AY185322.1	clone AKS21
Firmicutes	Clostridiaceae	sf_12	206	AB089017.1	termite gut homogenate clone Rs-P50 bacterium
Firmicutes	Peptococc/Acidaminococc	sf_11	31	Y10164.1	Dehalobacter restrictus str. TEA
Firmicutes	Peptococc/Acidaminococc	sf_11	562	AF481224.1	oral endodontic infection clone MCE10_265
Firmicutes	Lachnospiraceae	sf_5	2756	AY804149.1	Roseburia faecalis str. M6/1
Firmicutes	Lachnospiraceae	sf_5	2708	AF275914.2	anaerobic digester clone AA02
Firmicutes	Unclassified	sf_17	2659		
Firmicutes	Clostridiaceae	sf_12	2764		
Firmicutes	Peptostreptococcaceae	sf_5	2738	AB037875.1	Mogibacterium neglectum str. ATCC 700924 (=P9a-h)
Firmicutes	Peptostreptococcaceae	sf_5	3153	U13039.1	infirmum str. W 1471
Firmicutes	Peptostreptococcaceae	sf_5	134	AF542228.1	Peptoniphilus asaccharolyticus str. CCUG 9988
Firmicutes	Bacillaceae	sf_1	3506	X92159.1	Lake Nakuru isolate 18N1
Firmicutes	Bacillaceae	sf_1	3861	AJ229201.1	anoxic bulk soil flooded rice microcosm clone BSV46 clone
Firmicutes	Bacillaceae	sf_1	246	AJ509006.1	Bacillus sp. 6160m-C1
Firmicutes	Bacillaceae	sf_1	3820	AY030332.1	Bacillus subtilis str. KL-120
Firmicutes	Aerococcaceae	sf_1	3519	AF016390.1	Granulicatella elegans str. DSM 11693; B1333
Firmicutes	Aerococcaceae	sf_1	3682	X70907.1	Dolosigranulum pigrum str. NCFB 2975
Firmicutes	Aerococcaceae	sf_1	3435	AF275700.1	cf. Alkalibacterium sp. isolate str. F1
Firmicutes	Aerococcaceae	sf_1	3840	X87150.1	Trichococcus pasteurii str. KoTa2
Firmicutes	Acholeplasmataceae	sf_1	3955	AF521672.1	Weeping tea tree witches'-broom phytoplasma tree
Firmicutes	Mycoplasmataceae	sf_1	4014	NC_002771.1	Mycoplasma pulmonis str. UAB CTIP
Firmicutes	Lachnospiraceae	sf_5	4501	AF385563.1	crevicular epithelial cells clone BU014
Firmicutes	Lachnospiraceae	sf_5	4155	AB089039.1	termite gut homogenate clone Rs-K92 bacterium
Firmicutes	Lachnospiraceae	sf_5	4164	AF376226.1	ckncm322-B3-7 clone
Firmicutes	Clostridiaceae	sf_12	4548	AB089029.1	termite gut homogenate clone Rs-Q69 bacterium
Firmicutes	Unclassified	sf_3	4280		
Fusobacteria	Fusobacteriaceae	sf_1	488	NZ_AABF02000111.1	Fusobacterium nucleatum subsp. vincentii str. ATCC 49256
Fusobacteria	Fusobacteriaceae	sf_3	1034	AJ307982.1	Ilyobacter tartaricus str. DSM 2382 T
Fusobacteria	Fusobacteriaceae	sf_3	644	AJ307981.1	Ilyobacter polytropus str. DSM 2926 T
Fusobacteria	Fusobacteriaceae	sf_3	120	AF432138.1	tongue dorsum scrapings clone FP036
Fusobacteria	Fusobacteriaceae	sf_3	558	AJ344093.1	Sneathia sanguinegens str. CCUG 41628T
Fusobacteria	Fusobacteriaceae	sf_3	694	AF385518.1	tongue dorsa clone DR011
Fusobacteria	Fusobacteriaceae	sf_3	387	AY029802.1	Leptotrichia wadeii str. LB16
Fusobacteria	Fusobacteriaceae	sf_3	721	AY207053.1	human mouth clone P2PB_51
Gemmatimonadetes	Unclassified	sf_5	9464	AF432648.1	lodgepole pine rhizosphere soil British Columbia Ministry Forests Long-Term Soil Productivity
Gemmatimonadetes	Unclassified	sf_5	227	AJ519397.1	uranium mining waste pile clone JG37-AG-36
Gemmatimonadetes	Unclassified	sf_5	1127	AJ519396.1	uranium mining waste pile near Johanngeorgenstadt soil clone JG37-AG-21

Gemmatimonadetes	Unclassified	sf_5	2047	AF234148.1	soil clone #0319-7G21
Gemmatimonadetes	Unclassified	sf_5	317	AY218696.1	penguin droppings sediments clone KD8-87
Gemmatimonadetes	Unclassified	sf_5	10112	AF432607.1	forest soil clone NOS7.157WL
Gemmatimonadetes	Unclassified	sf_5	442	AF507712.1	forest soil clone S0134
Gemmatimonadetes	Unclassified	sf_5	1565	AJ532728.1	uranium mining waste pile clone JG34-KF-418
LD1PA group	Unclassified	sf_1	10118	AY114324.1	anoxic marine sediment clone LD1-PA38
Lentisphaerae	Unclassified	sf_5	10027	AJ431234.1	Cytophaga sp. str. Dex80-43
Lentisphaerae	Unclassified	sf_5	10330	AF507900.1	Mono lake clone ML635J-58
Lentisphaerae	Unclassified	sf_5	9704	AJ431235.1	Cytophaga sp. str. Dex80-64
marine group A	Unclassified	sf_1	6344	AF382142.1	bacterioplankton clone ZA3648c
marine group A	Unclassified	sf_1	6408	AACY01094130.1	Sargasso Sea
marine group A	Unclassified	sf_1	6454	U34043.1	marine clone SAR406
Natronoanaerobium	Unclassified	sf_1	769	AJ431345.1	fjord ikaite column clone un-c23
Natronoanaerobium	Unclassified	sf_1	4377	AF507888.1	Mono Lake at depth 35m station 6 July 2000 clone ML635J-65 G+C
Natronoanaerobium	Unclassified	sf_1	3570	AF454298.1	Bacillus sp. clone ML1228J-1
Natronoanaerobium	Unclassified	sf_1	2437	AF507879.2	Mono Lake at depth 23m station 6 July 2000 clone ML623J-19
Natronoanaerobium	Unclassified	sf_1	3745	AF507877.1	Mono Lake at depth 35m station 6 July 2000 clone ML635J-45
NC10	Unclassified	sf_1	10254	AJ519650.1	uranium mill tailings soil sample clone Sh765B-TzT-35
NC10	Unclassified	sf_1	452	AY177763.1	vadose clone 5G01
NC10	Unclassified	sf_1	536	AJ519669.1	uranium mill tailings clone GuBH2-AD-8
NC10	Unclassified	sf_1	2516	AF529103.1	TCE-contaminated site clone FTL22
Nitrospira	Nitrospiraceae	sf_1	984	AJ519405.1	uranium mining waste pile clone JG37-AG-131 sp.
Nitrospira	Nitrospiraceae	sf_2	697	AF524003.1	forested wetland clone FW118
Nitrospira	Nitrospiraceae	sf_2	542	AF524005.1	forested wetland clone FW19
Nitrospira	Nitrospiraceae	sf_1	864	Y14644.1	nitrifying sludge clone GC86
Nitrospira	Nitrospiraceae	sf_1	179	AF407702.1	Great Artesian Basin clone G19
Nitrospira	Nitrospiraceae	sf_2	681		
Nitrospira	Nitrospiraceae	sf_2	544	AF524004.1	forested wetland clone FW5
OD1	Unclassified	sf_1	515		
OP10	Unclassified	sf_1	326	AY222300.1	geothermal clone ST01-SN3H
OP10	Unclassified	sf_4	484	AF524022.1	forested wetland clone FW68
OP10	Unclassified	sf_1	514	AF368184.1	sludge clone SBRA136
OP10	Unclassified	sf_5	9782	AY192275.1	Rocky Mountain alpine soil clone S1a-1H
OP10	Unclassified	sf_1	8413	AJ306784.1	DCP-dechlorinating consortium clone SHA-37
OP3	Unclassified	sf_4	628	AY050598.1	CB-contaminated groundwater clone GOUTB15
OP3	Unclassified	sf_2	349	AJ390463.1	soil clone PBS-25
OP3	Unclassified	sf_3	1015	AY013695.1	polluted aquifer clone BVC56
OP8	Unclassified	sf_3	598	AF419671.1	Guaymas Basin hydrothermal sediment clone a2b010
OP9/JS1	Unclassified	sf_1	726	AF027086.1	hot spring clone OPB72
OP9/JS1	Unclassified	sf_1	969	AJ306782.1	DCP-dechlorinating consortium clone SHA-1
OP9/JS1	Unclassified	sf_1	2489	AY197377.1	Guaymas Basin hydrothermal vent sediments clone B01R005
OP9/JS1	Unclassified	sf_1	2491	AY093469.1	deep marine sediment clone MB-B2-103
Planctomycetes	Pirellulae	sf_3	4670		
Planctomycetes	Planctomycetaceae	sf_3	4948	BX294756.1	anoxic basin clone CY0ARA027D01
Planctomycetes	Pirellulae	sf_3	4677	BX294863.1	aerobic basin clone CY0ARA032A03
Planctomycetes	Anammoxales	sf_4	4694	AF418968.1	USA: Colorado Fort collins Horsetooth Reservoir clone HT2F11

Planctomycetes	Pirellulae	sf_3	4803	X86388.1	Pirellula sp. str. ACM 3181
Planctomycetes	Planctomycetaceae	sf_3	4831	AJ231190.1	Planctomyces brasiliensis
Planctomycetes	Anammoxales	sf_2	4683	BX294785.1	anoxic basin clone CY0ARA028B09
Planctomycetes	Planctomycetaceae	sf_3	4652	BX294789.1	anoxic basin clone CY0ARA028C04
Planctomycetes	Anammoxales	sf_4	9662	AF407728.1	Great Artesian Basin clone B83
Planctomycetes	Unclassified	sf_1	4897	AY093476.1	deep marine sediment clone MB-C2-105
Planctomycetes	Anammoxales	sf_4	4695	AF316773.1	Crater Lake clone CL500-15
Planctomycetes	Pirellulae	sf_3	4692	BX294733.1	aerobic basin clone CY0ARA026G04
Planctomycetes	Planctomycetaceae	sf_3	4855	BX294726.1	aerobic basin clone CY0ARA026D10
Planctomycetes	Pirellulae	sf_3	4769	AY114326.1	anoxic marine sediment clone LD1-PA40
Proteobacteria	Unclassified	sf_1	7382	AF355039.1	marine clone Arctic95C-5
Proteobacteria	Unclassified	sf_3	8339	AY212729.1	water 5 m downstream manure clone 35ds5
Proteobacteria	Unclassified	sf_1	9828	AB089109.1	termite gut homogenate clone Rs-M89 proteobacterium
Proteobacteria	Unclassified	sf_3	9813	AF420340.1	hydrothermal sediment clone AF420340
Proteobacteria	Unclassified	sf_1	10543	U15103.1	hydrothermal vent clone PVB_10
Proteobacteria	Unclassified	sf_1	10427	AY672515.1	hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH3_17_BAC_16SrRNA_9N_EPR
Proteobacteria	Unclassified	sf_1	10530	AY672531.1	hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH5_6_BAC_16SrRNA_9N_EPR
Proteobacteria	Unclassified	sf_20	2520		
Proteobacteria	Sphingomonadaceae	sf_1	6663	AY554010.1	Sphingopyxis flavimaris str. SW-151
Proteobacteria	Ralstoniaceae	sf_1	7778	AJ539233.1	Ralstonia insidiosa str. CCUG 46388
Proteobacteria	Pseudomonadaceae	sf_1	9295		
Proteobacteria	Pseudomonadaceae	sf_1	8474	AJ534672.1	ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A-MN7 proteobacterium
Proteobacteria	Pseudomonadaceae	sf_1	9469	AF290486.1	cf. Pseudomonas sp. clone Llangefni 52
Proteobacteria	Polyangiaceae	sf_3	10249	AJ534629.1	soil sample uranium mining waste pile near town Johanngeorgenstadt clone JG36-TzT-168 proteobacterium
Proteobacteria	Polyangiaceae	sf_3	10298	AY193162.1	marine tidal mat clone BTM36
Proteobacteria	Polyangiaceae	sf_3	10353	AF234747.1	sludge clone A9
Proteobacteria	Pasteurellaceae	sf_1	9237		
Proteobacteria	Oxalobacteraceae	sf_1	7845	AB038368.1	Diaphorina citri symbiont
Proteobacteria	Helicobacteraceae	sf_3	10385		
Proteobacteria	Helicobacteraceae	sf_3	10428	AF034135.1	Flexispira rappini FH 9702248
Proteobacteria	Helicobacteraceae	sf_3	10430	AF506783.1	Helicobacter heilmannii str. MM2
Proteobacteria	Helicobacteraceae	sf_3	10436	AF297868.1	Helicobacter aurati str. MIT 97-5075c
Proteobacteria	Helicobacteraceae	sf_3	10442	AF292378.1	Helicobacter cetorum str. MIT 99-5656
Proteobacteria	Helicobacteraceae	sf_3	10444	AB006148.1	Helicobacter suncus str. Kaz-2
Proteobacteria	Helicobacteraceae	sf_3	10448	U51870.1	Helicobacter felis str. Dog-1
Proteobacteria	Helicobacteraceae	sf_3	10451	AF506779.1	Helicobacter heilmannii str. C4S
Proteobacteria	Helicobacteraceae	sf_3	10454	L36143.1	Helicobacter pullorum str. NCTC 12826
Proteobacteria	Helicobacteraceae	sf_3	10462	U96297.1	Helicobacter rodentium str. MIT 96-1312
Proteobacteria	Helicobacteraceae	sf_3	10548	AF286052.1	Helicobacter rappini W.Tee-Bat
Proteobacteria	Helicobacteraceae	sf_3	10552	AF363062.1	Helicobacter winghamensis str. NLEP 97-1611
Proteobacteria	Helicobacteraceae	sf_3	10562	AF286053.1	Helicobacter rappini W.Tee-Yu
Proteobacteria	Desulfovibrionaceae	sf_1	10248	AF418170.1	Desulfovibrio giganteus str. DSM 4370
Proteobacteria	Desulfobacteraceae	sf_5	10319	AY083017.1	sulfate-reducing habitat clone SLM-CP-116
Proteobacteria	Desulfoarculaceae	sf_2	10227	AY193132.1	marine sediment clone Bol11

Proteobacteria	Coxiellaceae	sf_3	8969	AJ536861.1	uranium mining waste pile soil sample clone JG30-KF-C15 proteobacterium
Proteobacteria	Campylobacteraceae	sf_3	10538	L14624.1	Arcobacter cryaerophilus
Proteobacteria	Campylobacteraceae	sf_3	10447	Y13671.1	Sulfurospirillum deleyianum str. Spirillum 5175
Proteobacteria	Campylobacteraceae	sf_3	10456	L06975.1	Campylobacter showae
Proteobacteria	Alteromonadaceae	sf_1	9324	AF316891.1	Pseudoalteromonas ruthenica str. KMM300
Proteobacteria	Helicobacteraceae	sf_3	10518	X67854.1	Helicobacter pylori str. ATCC 49396T
Proteobacteria	Helicobacteraceae	sf_3	10520	AJ249858.1	Helicobacter sp. blood isolate 964
Proteobacteria	Unclassified	sf_6	7377	AY192273.1	Rocky Mountain alpine soil clone W2b-8C
Proteobacteria	Unclassified	sf_1	7400	AF524861.1	sphagnum peat bog clone K-5b5
Proteobacteria	Unclassified	sf_1	7028		
Proteobacteria	Unclassified	sf_1	7123	AJ518774.1	uranium mining waste pile near Johanngeorgenstadt soil clone JG37-AG-102
Proteobacteria	Unclassified	sf_2	7188	AB089085.1	termite gut homogenate clone Rs-B50 proteobacterium
Proteobacteria	Unclassified	sf_4	7105	AB186982.1	Mariana trough hydrothermal vent water 0.2micro-m filterable fraction clone MT-NB25
Proteobacteria	Caulobacteraceae	sf_1	6781	AB023784.1	Brevundimonas intermedia str. MBIC2712 ATCC15262
Proteobacteria	Caulobacteraceae	sf_1	6904	AB021414.1	Brevundimonas vesicularis str. IAM 12105T
Proteobacteria	Caulobacteraceae	sf_1	6909	X87274.1	Brevundimonas diminuta str. DSM 1635
Proteobacteria	Caulobacteraceae	sf_1	7359	AJ227782.1	Brevundimonas bacteroides str. CB7
Proteobacteria	Caulobacteraceae	sf_1	7366	AJ227784.1	Brevundimonas subvibrioides str. CB81
Proteobacteria	Caulobacteraceae	sf_1	7436	AJ227797.1	Brevundimonas sp. str. FWC40
Proteobacteria	Unclassified	sf_1	7156	AB089097.1	termite gut homogenate clone Rs-M62 proteobacterium
Proteobacteria	Anaplasmataceae	sf_3	6908	M85267.1	Rhinocyllus conicus endosymbiont
Proteobacteria	Nitrosomonadaceae	sf_1	7789		
Proteobacteria	Rhodocyclaceae	sf_1	7956		
Proteobacteria	Rhodocyclaceae	sf_1	7907	AJ315680.1	Thauera aromatica str. LG356
Proteobacteria	Rhodocyclaceae	sf_1	7925	Y17591.1	Thauera selenatis str. ATCC 55363T
Proteobacteria	Unclassified	sf_3	8114		
Proteobacteria	Rhodocyclaceae	sf_1	8156	AY098637.2	industrial-phenol-degrading community clone MM1 sp.
Proteobacteria	Rhodocyclaceae	sf_1	7824	AB089101.1	termite gut homogenate clone Rs-B77 proteobacterium
Proteobacteria	Alcaligenaceae	sf_1	7902	AF155147.1	Alcaligenes faecalis str. M3A
Proteobacteria	Alcaligenaceae	sf_1	8094	AF430122.1	Alcaligenes sp. str. VKM B-2263 dcm6
Proteobacteria	Comamonadaceae	sf_1	7965	X72724.1	Anoxobacterium dechloraticum
Proteobacteria	Oxalobacteraceae	sf_1	7843	U54470.1	Massilia timonae timone
Proteobacteria	Oxalobacteraceae	sf_1	7921	AY593479.1	Collimonas fungivorans str. Ter331
Proteobacteria	Oxalobacteraceae	sf_1	8032	AB074523.1	Aquaspirillum arcticum str. IAM 14963
Proteobacteria	Oxalobacteraceae	sf_1	8034	Y08845.1	Janthinobacterium agaricidamnosum str. W1r3T
Proteobacteria	Oxalobacteraceae	sf_1	8058	Y10146.1	Herbaspirillum seropedicae str. DSM 6445 ATCC 35892
Proteobacteria	Ralstoniaceae	sf_1	8128	M32021.1	Cupriavidus necator
Proteobacteria	Saccharospirillaceae	sf_1	8889	AF452603.1	hypersaline Mono Lake clone ML110J-5
Proteobacteria	Thiotrichaceae	sf_3	8741	AF532771.1	marine sediment clone Limfjorden L10
Proteobacteria	Thiotrichaceae	sf_3	8752	AF110276.1	Beggiatoa sp. str. MS-81-1c
Proteobacteria	Unclassified	sf_1	9418	AJ518784.1	uranium mining waste pile clone JG37-AG-14 proteobacterium
Proteobacteria	Piscirickettsiaceae	sf_3	9291	AF384373.1	Methylophaga alcalica str. M39
Proteobacteria	Xanthomonadaceae	sf_3	8689	AB110496.1	Dyemonas todaii str. XD10

Proteobacteria	Legionellaceae	sf_1	8865	AF468229.1	Arctic pack ice; northern Fram Strait; 80 31.1 N; 01 deg 59.7 min E clone ARKCH2Br2-23
Proteobacteria	Unclassified	sf_3	8587	AF526927.2	Mars Odyssey Orbiter and encapsulation facility clone T5-3
Proteobacteria	Alcanivoraceae	sf_1	8335	AB055205.1	Alcanivorax sp. str. K3-3 (MBIC 4323)
Proteobacteria	Moraxellaceae	sf_3	8727	AY251390.1	Alkanindiges hongkongensis str. HKU9
Proteobacteria	Pseudomonadaceae	sf_1	9056	AB037546.1	Pseudomonas aeruginosa str. #47
Proteobacteria	Pseudomonadaceae	sf_1	9228	AJ297767.1	Pseudomonas stutzeri HY-105
Proteobacteria	Pseudomonadaceae	sf_1	9240	AJ278812.1	Pseudomonas fluorescens str. CHA0
Proteobacteria	Unclassified	sf_6	8780	AJ296549.1	uranium mining mill tailing clone GR-296.II.89 GR-296.II.89
Proteobacteria	Alteromonadaceae	sf_1	8222		
Proteobacteria	Alteromonadaceae	sf_1	8753	AY553079.1	Idiomarina loihiensis str. GSP37
Proteobacteria	Alteromonadaceae	sf_1	8970	AJ295716.1	Arctic seawater isolate str. R9879
Proteobacteria	Alteromonadaceae	sf_1	8978	AF468393.1	Arctic sea ice ARK10108
Proteobacteria	Alteromonadaceae	sf_1	9416	AF539786.1	marine isolate str. R8
Proteobacteria	Pasteurellaceae	sf_1	8409	AF499896.1	human colonic mucosal biopsy clone ABLCf1
Proteobacteria	Enterobacteriaceae	sf_1	8236	AF476110.1	Vryburgia amaryllidis symbiont
Proteobacteria	Enterobacteriaceae	sf_1	8504	AF476104.1	Dysmicoccus neobrevipes symbiont
Proteobacteria	Enterobacteriaceae	sf_1	8283	AF263562.1	Heteropsylla texana symbiont
Proteobacteria	Desulfohalobiaceae	sf_1	9894	AF524933.1	Desulfonauticus submarinus str. 6N
Proteobacteria	Desulfovibrionaceae	sf_1	10262	AF228127.2	Desulfovibrio sp. str. Ac5.2
Proteobacteria	Desulfovibrionaceae	sf_1	9826	AB089108.2	termite gut homogenate clone Rs-M72 proteobacterium
Proteobacteria	Polyangiaceae	sf_3	9874	AJ532714.1	uranium mining waste pile clone JG34-KF-243 proteobacterium
Proteobacteria	Desulfobacteraceae	sf_5	9875	AF420354.1	hydrothermal sediment clone AF420354
Proteobacteria	Unclassified	sf_9	9890	AB089106.1	termite gut homogenate clone Rs-K70 proteobacterium
Proteobacteria	Helicobacteraceae	sf_3	10432	AF449246.1	Riftia pachyptila's tube clone R76-B51
Proteobacteria	Helicobacteraceae	sf_3	10438	AF154101.1	hydrocarbon seep clone GCA014
Proteobacteria	Unclassified	sf_1	10475	AF420359.1	hydrothermal sediment clone AF420359
Proteobacteria	Unclassified	sf_1	10480	AJ441204.1	hydrothermal vent polychaete mucous clone P. palm C 84
Proteobacteria	Campylobacteraceae	sf_3	10464	AY135395.1	Campylobacter sp. str. NO2B
Proteobacteria	Helicobacteraceae	sf_3	10467		
Proteobacteria	Enterobacteriaceae	sf_1	1206	AY265343.1	Dermacentor variabilis symbiont
Proteobacteria	Unclassified	sf_4	8855		
Proteobacteria	Enterobacteriaceae	sf_6	433	AF523903.1	coal effluent wetland clone RCP2-6
Proteobacteria	Enterobacteriaceae	sf_6	646	AY695840.1	Opitutus sp. str. SA-9
Proteobacteria	Alcaligenaceae	sf_1	7838	AB195161.1	Alcaligenes defragrans str. PD-19
Proteobacteria	Oxalobacteraceae	sf_1	7878	AY250094.1	napthalene-contaminated sediment clone 29
Proteobacteria	Ralstoniaceae	sf_1	8110	AF085226.1	Wautersia paucula str. LMG 3413
Proteobacteria	Unclassified	sf_3	8926	AB099937.1	inactive deep-sea hydrothermal vent chimneys clone IheB2-13
Proteobacteria	Alteromonadaceae	sf_1	9562	AF513941.1	Alteromonadaceae clone PH-B55N
Proteobacteria	Desulfobulbaceae	sf_1	9734	AF449229.1	Riftia pachyptila's tube clone R103-B13
Proteobacteria	Campylobacteraceae	sf_3	10446		
Proteobacteria	Caedibacteraceae	sf_4	7157	AF533506.1	acid mine drainage clone ASL45
Proteobacteria	Unclassified	sf_6	7575		
Proteobacteria	Xanthobacteraceae	sf_1	6660	D11342.1	Azorhizobium caulinodans str. ORS 571
Proteobacteria	Unclassified	sf_2	6639		
Proteobacteria	Neisseriaceae	sf_1	7945	AB074518.1	Aquaspirillum serpens str. IAM 13944

Proteobacteria	Rhodocyclaceae	sf_1	7817	AY133064.1	TCE-contaminated site clone ccs265
Proteobacteria	Coxiellaceae	sf_3	7893	AJ252651.1	agricultural soil clone SC-I-71
Proteobacteria	Thiotrichaceae	sf_3	9015	AF110274.1	Beggiatoa alba str. B18LD; ATCC 33555
Proteobacteria	Thiotrichaceae	sf_3	9321	AB108786.1	marine sediment clone Tokyo Bay D
Proteobacteria	Unclassified	sf_1	8957	AF354614.1	marine clone Arctic97C-5
Proteobacteria	Unclassified	sf_1	8605	AF382104.1	bacterioplankton clone ZA2525c
Proteobacteria	Unclassified	sf_1	8654	AB099939.1	inactive deep-sea hydrothermal vent chimneys clone IheB2-31
Proteobacteria	Coxiellaceae	sf_3	8457	AJ240918.1	5' clone CHAB-XI-27
Proteobacteria	Methylococcaceae	sf_1	9438	AJ535221.1	marine sediment above hydrate ridge clone Hyd24-01 proteobacterium
Proteobacteria	Halomonadaceae	sf_1	8514	AJ295144.1	Chromohalobacter israelensis str. ATCC 43985 T
Proteobacteria	Moraxellaceae	sf_3	8838	AJ748267.1	Psychrobacter psychrophilus CMS 28
Proteobacteria	Pseudomonadaceae	sf_1	8691	AE004501.1	Pseudomonas aeruginosa str. PAO1
Proteobacteria	Pseudomonadaceae	sf_1	8777	AB095005.1	Pseudomonas sp. str. KNA6-5
Proteobacteria	Pseudomonadaceae	sf_1	8852	AF063219.1	Pseudomonas stutzeri str. KC
Proteobacteria	Pseudomonadaceae	sf_1	9068	AF143245.1	Pseudomonas stutzeri str. A1501
Proteobacteria	Pseudomonadaceae	sf_1	8725	AJ419674.1	Pseudomonas sp. str. 2N1-1
Proteobacteria	Pseudomonadaceae	sf_1	9238		
Proteobacteria	Pseudomonadaceae	sf_1	9005	AJ278108.1	Pseudomonas sp. str. KY
Proteobacteria	Pseudomonadaceae	sf_1	8513	AF064458.1	Pseudomonas monteilii str. CIP 104883
Proteobacteria	Pseudomonadaceae	sf_1	9493	AF430125.1	Pseudomonas sp. str. dcm7B
Proteobacteria	Pseudomonadaceae	sf_1	8433	AB001441.1	Pseudomonas syringae pv. broussonetiae str. KOZ 8101 pv.
Proteobacteria	Thiotrichaceae	sf_3	8703	AF110275.1	Beggiatoa sp. str. AA5A
Proteobacteria	Pseudomonadaceae	sf_1	9028	AF468452.1	Pseudomonas koreensis str. Ps 9-14
Proteobacteria	Pseudomonadaceae	sf_1	9267	AB001450.1	Pseudomonas syringae pv. theae str. PT1
Proteobacteria	Pseudomonadaceae	sf_1	9310	AJ519791.1	Pseudomonas sp. str. AC-167
Proteobacteria	Pseudomonadaceae	sf_1	8338	AF267911.1	Pseudomonas synxantha str. DSM 13080 G
Proteobacteria	Pseudomonadaceae	sf_1	8561	AF332541.1	Pseudomonas sp. B65
Proteobacteria	Pseudomonadaceae	sf_1	8687	AF094738.1	Pseudomonas putida str. ATCC 17472
Proteobacteria	Pseudomonadaceae	sf_1	8708		
Proteobacteria	Pseudomonadaceae	sf_1	9221	AJ492830.1	Pseudomonas fulgida str. DSM 14938 = LMG 2146 P 515/12
Proteobacteria	Pseudomonadaceae	sf_1	9366	AJ293826.1	Arctic seawater isolate str. R7366
Proteobacteria	Pseudomonadaceae	sf_1	8755	AJ288146.1	Pseudomonas sp. SK-1-3-1
Proteobacteria	Unclassified	sf_3	8327	AF468398.1	Arctic sea ice ARK10148
Proteobacteria	Unclassified	sf_3	8714	AB021372.1	Marinobacter hydrocarbonoclasticus str. ATCC 27132T
Proteobacteria	Alteromonadaceae	sf_1	9239	AF468400.1	Arctic sea ice ARK10228
Proteobacteria	Aeromonadaceae	sf_1	9294	AJ557849.1	Arctic deep sea Isolation common chemoorganotrophic oxygen-respiring polar current d 1210 (50 m above sediment Hakon Mosby Mud Vulcano (HMMV 72N 14E)) via serial dilution series applying 2 g/l yeast or meat extract artifical seawater
Proteobacteria	Alteromonadaceae	sf_1	8174	AF114499.1	attached marine recovered surface clone 17 proteobacterium
Proteobacteria	Alteromonadaceae	sf_1	8318	AY207502.1	Aestuariibacter salexigens str. JC2042
Proteobacteria	Alteromonadaceae	sf_1	8863	AF529060.1	Alteromonas marina str. SW-47
Proteobacteria	Alteromonadaceae	sf_1	9288	AJ295715.1	Alteromonas stellipolaris str. LMG 21861
Proteobacteria	Alteromonadaceae	sf_1	9501	AB086226.1	sea water isolate str. BP-PH
Proteobacteria	Alteromonadaceae	sf_1	8172	AB055791.1	Pseudoalteromonas sp. str. Bdeep-1

Proteobacteria	Alteromonadaceae	sf_1	8336	AF237977.1	Alteromonas sp. str. MS23
Proteobacteria	Alteromonadaceae	sf_1	8580	AJ295713.1	Arctic seawater isolate str. R7076
Proteobacteria	Alteromonadaceae	sf_1	8932	AF045560.1	Pseudoalteromonas antarctica str. N-1
Proteobacteria	Alteromonadaceae	sf_1	8975	AB016268.1	Alteromonas sp. str. NIBH P1M3
Proteobacteria	Alteromonadaceae	sf_1	9058	X82136.1	Pseudoalteromonas carrageenovora str. ATCC 12662T
Proteobacteria	Alteromonadaceae	sf_1	9143	AJ417594.1	Pseudoalteromonas agarivorans str. KMM 255
Proteobacteria	Alteromonadaceae	sf_1	9205	AF354597.1	marine clone Arctic96B-17
Proteobacteria	Alteromonadaceae	sf_1	9218	X67024.1	Pseudoalteromonas haloplanktis str. ATCC 14393
Proteobacteria	Alteromonadaceae	sf_1	9386	AB016267.1	Alteromonas sp. str. NIBH P2M11
Proteobacteria	Pseudoalteromonadaceae	sf_1	9627	AF218245.1	Pseudoalteromonas sp
Proteobacteria	Alteromonadaceae	sf_1	9640	AY028205.1	exposed to diatom detritus isolate str. Tw-10 Tw-10
Proteobacteria	Succinivibrionaceae	sf_1	8822	AF497809.1	Anaerobiospirillum sp. str. 3J102
Proteobacteria	Pasteurellaceae	sf_1	9360	AF224297.1	Pasteurella multocida subsp. gallicida str. MCCM 00021 subsp.
Proteobacteria	Pasteurellaceae	sf_1	8228	AF268964.1	Actinobacillus indolicus str. H1419
Proteobacteria	Pasteurellaceae	sf_1	8861	AB004031.1	Haemophilus parasuis 427
Proteobacteria	Pasteurellaceae	sf_1	8432		
Proteobacteria	Pasteurellaceae	sf_1	8848	AF227858.1	str. 86355
Proteobacteria	Pasteurellaceae	sf_1	9533	AF224299.1	Haemophilus segnis str. MCCM 00337
Proteobacteria	Pasteurellaceae	sf_1	9628	AF549390.1	Histophilus somni str. CCUG 12839
Proteobacteria	Syntrophobacteraceae	sf_1	9661	AJ306805.1	DCP-dechlorinating consortium clone SHD-1
Proteobacteria	Unclassified	sf_1	10489	AF299121.1	S17sBac16 complete clone
Proteobacteria	Rickettsiaceae	sf_1	7556	U11014.1	Rickettsia bellii str. strains 369-C and G2D42
Proteobacteria	Alcaligenaceae	sf_1	7992	AJ509012.1	Alcaligenes faecalis 5659-H
Proteobacteria	Enterobacteriaceae	sf_1	8770		
Proteobacteria	Unclassified	sf_3	468	AJ241004.1	marine sediment clone Sva0515
Proteobacteria	Coxiellaceae	sf_3	9444	AF523974.1	forested wetland clone FW23
Proteobacteria	Alteromonadaceae	sf_1	9111	AF539773.1	Pseudoalteromonas sp. str. E36
Proteobacteria	Alteromonadaceae	sf_1	8579	AJ416756.1	Psychromonas profunda str. 2825
Proteobacteria	Pasteurellaceae	sf_1	8195	NZ_AADP01000001.1	Haemophilus influenzae str. R2866
Proteobacteria	Enterobacteriaceae	sf_1	8173	Z76752.1	Photorhabdus asymbiotica str. ATCC 43949
Proteobacteria	Enterobacteriaceae	sf_1	8642	AF373202.1	Erwinia chrysanthemi str. 580
Proteobacteria	Unclassified	sf_4	9951	AF523973.1	forested wetland clone FW13
Proteobacteria	Unclassified	sf_6	6694	AF523879.1	forested wetland clone RCP2-92
Proteobacteria	Unclassified	sf_1	6732	AF426002.1	Anabaena circinalis AWQC118C isolate str. UNSW7
Proteobacteria	Unclassified	sf_1	7199	AJ532683.1	uranium mill tailings clone Gitt-KF-194
Proteobacteria	Methylobacteriaceae	sf_1	7585	U58018.1	Methylobacterium thiocyanatum str. ALL/SCN-P
Proteobacteria	Unclassified	sf_4	6810	AY033325.1	marine bacterioplankton clone MB13F01
Proteobacteria	Unclassified	sf_6	7312		
Proteobacteria	Phyllobacteriaceae	sf_1	7497	AJ294416.1	Pseudaminobacter salicylatoxidans str. KTC001
Proteobacteria	Rickettsiaceae	sf_1	6809	U11021.1	Rickettsia rickettsii str. Sawtooth
Proteobacteria	Anaplasmataceae	sf_3	6803	AY007547.1	Wolbachia sp. Dlem16SWol
Proteobacteria	Anaplasmataceae	sf_3	7481	AF179630.1	Wolbachia pipientis
Proteobacteria	Sphingomonadaceae	sf_1	7440	AF159257.2	Sphingobium chungbukense str. DJ77
Proteobacteria	Sphingomonadaceae	sf_15	7035	Y09639.1	Sphingomonas asaccharolytica str. IFO 10564-T
Proteobacteria	Neisseriaceae	sf_1	7675	AY157705.1	Neisseria sp. str. CCUG 46910
Proteobacteria	Rhodocyclaceae	sf_1	7800	AY013692.1	sample taken upstream landfill clone BVC77 landfill
Proteobacteria	Methylophilaceae	sf_1	8137	AF289159.1	freshwater clone PRD01a011B
Proteobacteria	Procabacteriaceae	sf_1	8136	AF177426.1	Acanthamoeba sp. UWC6 symbiont
Proteobacteria	Alcaligenaceae	sf_1	8062	AJ277742.1	Brackiella oedipodis str. LMG 1945 R8846
Proteobacteria	Comamonadaceae	sf_1	7856	AY169431.1	Variovorax paradoxus

Proteobacteria	Burkholderiaceae	sf_1	7771	AB021374.1	Burkholderia glathei str. ATCC 29195T
Proteobacteria	Burkholderiaceae	sf_1	7782	AY040365.1	Burkholderia hospita str. LMG 20598T
Proteobacteria	Burkholderiaceae	sf_1	7747		
Proteobacteria	Rhodocyclaceae	sf_1	7762	AF150698.1	Elbe River snow isolate Iso18 Iso18_1411
Proteobacteria	Unclassified	sf_1	8747	AJ536882.1	uranium waste soil clone JG30-KF-CM35
Proteobacteria	Unclassified	sf_1	9246	AY221036.1	Mammoth Cave sediment clone CCD24
Proteobacteria	Acidithiobacillaceae	sf_1	9224	AJ459804.1	Acidithiobacillus albertensis str. DSM 14366
Proteobacteria	Unclassified	sf_3	9568	AF523888.1	forested wetland clone RCP2-96
Proteobacteria	Chromatiaceae	sf_1	8697	AJ401211.1	Thiococcus sp. AT2204
Proteobacteria	Francisellaceae	sf_1	9554	AF206675.1	Tilapia parasite TPT-541
Proteobacteria	Xanthomonadaceae	sf_3	9270	AJ293463.1	Stenotrophomonas rhizophila str. e-p10
Proteobacteria	Xanthomonadaceae	sf_3	9286	AJ131912.1	Stenotrophomonas maltophilia str. LMG 11104
Proteobacteria	Unclassified	sf_1	8962	AF406526.1	bacterioplankton clone AEGEAN_234
Proteobacteria	Coxiellaceae	sf_3	9198	AJ295651.1	uranium mining waste pile clone KF-JG30-B15 KF-JG30-B15
Proteobacteria	Moraxellaceae	sf_3	8366	AJ609556.1	Psychrobacter frigidicola str. DSM 12411
Proteobacteria	Moraxellaceae	sf_3	9466	AF509830.1	Acinetobacter tandoii str. 4N13
Proteobacteria	Pseudomonadaceae	sf_1	8508	AF530073.1	Pseudomonas citronellolis str. TERIDB26
Proteobacteria	Pseudomonadaceae	sf_1	8344	AF425998.1	Anabaena circinalis AWQC118C isolate str. UNSW3
Proteobacteria	Pseudomonadaceae	sf_1	8553	AB046997.1	Pseudomonas fulva str. IAM 1587
Proteobacteria	Pseudomonadaceae	sf_1	9613	U01916.1	Pseudomonas flavescens str. B62
Proteobacteria	Pseudomonadaceae	sf_1	9219	AF181576.1	Pseudomonas cf. monteilii 9
Proteobacteria	Pseudomonadaceae	sf_1	8209	AJ518787.1	uranium mining waste pile clone JG37-AG-122 proteobacterium
Proteobacteria	Pseudomonadaceae	sf_1	8601	AB021401.1	Pseudomonas marginalis str. ATCC 10844T
Proteobacteria	Pseudomonadaceae	sf_1	9175	AF405328.1	Pseudomonas extremorientalis str. KMM3447
Proteobacteria	Pseudomonadaceae	sf_1	9172	AB041885.1	Pseudomonas psychrophila str. E-3
Proteobacteria	Alteromonadaceae	sf_1	8578	AY147906.1	Marinobacter lipolyticus str. SM-19
Proteobacteria	Unclassified	sf_3	8606		
Proteobacteria	Alteromonadaceae	sf_1	8374	AB076560.1	Agarivorans albus str. MKT 89
Proteobacteria	Alteromonadaceae	sf_1	8533		
Proteobacteria	Shewanellaceae	sf_1	8641	AJ252022.1	Moritella abyssi str. 2693
Proteobacteria	Alteromonadaceae	sf_1	9384	AJ132226.1	Moritella viscosa str. NVI 88/478T
Proteobacteria	Pasteurellaceae	sf_1	9349	AF227861.1	Pasteurella sp. str. 91985
Proteobacteria	Pasteurellaceae	sf_1	8614	AF359941.1	Acidithiobacillus thiooxidans str. KCTC 8928P
Proteobacteria	Desulfomicrobiaceae	sf_1	10079	AJ277896.1	Desulfomicrobium baculatum str. DSM 1742
Proteobacteria	Desulfovibrionaceae	sf_1	9709	AB089104.1	termite gut homogenate clone Rs-N31 proteobacterium
Proteobacteria	Unclassified	sf_7	10048		
Proteobacteria	Desulfuromonaceae	sf_1	10020	AJ519664.1	uranium mill tailings soil sample clone GuBH2-AG-114 proteobacterium
Proteobacteria	Desulfobacteraceae	sf_5	9800	AF523960.1	forested wetland clone FW57
Proteobacteria	Campylobacteraceae	sf_3	10397	AB030592.1	groundwater clone 1006
Proteobacteria	Unclassified	sf_1	10407	AF420342.1	hydrothermal sediment clone AF420342
Proteobacteria	Campylobacteraceae	sf_3	10540	AF550655.1	Campylobacter showae str. LMG 12636
Proteobacteria	Nitrospinaceae	sf_2	594	AJ296568.1	uranium mining mill tailing clone GR-296.II.52 GR-296.I.52
Proteobacteria	Oxalobacteraceae	sf_1	7968	U49757.2	Oxalobacter formigenes str. OXB ovinen rumen
Proteobacteria	Ralstoniaceae	sf_1	7761	AF280433.1	Ralstonia detusculanense str. APF11
Proteobacteria	Unclassified	sf_3	9105		
Proteobacteria	Pasteurellaceae	sf_1	8555	AY613451.1	Haemophilus influenzae str. M9741
Proteobacteria	Enterobacteriaceae	sf_1	8607	AF476100.1	Amonostherium lichtensioides symbiont

Proteobacteria	Unclassified	sf_1	6945	AB081581.3	Rhizobiales str. A48
Proteobacteria	Alcaligenaceae	sf_1	7932	AJ278451.1	Achromobacter subsp. denitrificans str. DSM 30026 (T)
Proteobacteria	Unclassified	sf_1	9282		
Proteobacteria	Alteromonadaceae	sf_1	8643	AY771715.1	Pseudoalteromonas porphyrae str. S2-65
Proteobacteria	Pasteurellaceae	sf_1	8876	AF053894.1	Mannheimia sp. R19.2 str. R19.2; CCUG 38463 R19.2
Proteobacteria	Desulfovibrionaceae	sf_1	10016	AB089110.1	termite gut homogenate clone Rs-N35 proteobacterium
Proteobacteria	Unclassified	sf_9	9784	AY177804.1	Antarctic sediment clone LH5_30
Proteobacteria	Syntrophobacteraceae	sf_1	9731	AJ518795.1	uranium mining waste pile clone JG37-AG-90 proteobacterium
Proteobacteria	Acetobacteraceae	sf_1	7529	AJ012698.1	Gluconacetobacter europaeus str. ZIM B028 V3
Proteobacteria	Unclassified	sf_1	7222	AF407727.1	Great Artesian Basin clone B79
Proteobacteria	Hyphomicrobiaceae	sf_1	7646	Y14304.1	Hyphomicrobium aestuarii str. DSM 1564
Proteobacteria	Caulobacteraceae	sf_1	6968	AB021415.1	Brevundimonas diminuta str. IAM 12691T
Proteobacteria	Anaplasmataceae	sf_3	6628	U23709.1	Wolbachia pipientis
Proteobacteria	Anaplasmataceae	sf_3	6648	AF035160.1	Wolbachia sp
Proteobacteria	Sphingomonadaceae	sf_1	7036	AY026916.1	Lutibacterium anuloederans str. LC8
Proteobacteria	Unclassified	sf_6	7572		
Proteobacteria	Unclassified	sf_3	7765		
Proteobacteria	Nitrosomonadaceae	sf_1	7770	BX321856.1	Nitrosomonas europaea str. ATCC 19718
Proteobacteria	Alcaligenaceae	sf_1	7768	AF371864.1	swine intestine clone p-861-a5
Proteobacteria	Thiotrichaceae	sf_3	8321	AF532769.1	Wadden Sea sediment clone Dangast A9
Proteobacteria	Chromatiaceae	sf_1	8546	AJ242772.1	Thiocapsa litoralis
Proteobacteria	Pseudomonadaceae	sf_1	8813	AY150184.1	Lyrodus pedicellatus symbiont
Proteobacteria	Pseudomonadaceae	sf_1	9300	AY150183.1	Lyrodus pedicellatus symbiont
Proteobacteria	Pseudomonadaceae	sf_1	9002	AJ316016.1	Paederus fuscipes endosymbiont
Proteobacteria	Pseudomonadaceae	sf_1	8853	AB021398.1	Pseudomonas cichorii str. ATCC 10857T
Proteobacteria	Pseudomonadaceae	sf_1	9243	Z76670.1	Pseudomonas tolaasii str. LMG 2342T ()
Proteobacteria	Alteromonadaceae	sf_1	9236	AF114501.1	attached marine recovered surface clone 18 proteobacterium
Proteobacteria	Alteromonadaceae	sf_1	9369	X82144.1	Pseudoalteromonas luteoviolacea str. NCIMB 1893T
Proteobacteria	Pasteurellaceae	sf_1	9213	AF224307.1	Haemophilus quentini str. MCCM 02026
Proteobacteria	Pasteurellaceae	sf_1	8952	M75068.1	Actinobacillus lignieresii
Proteobacteria	Enterobacteriaceae	sf_1	8182	X07652.1	Proteus vulgaris str. IFAM 1731
Proteobacteria	Desulfovibrionaceae	sf_1	10071	M34113.1	Desulfovibrio desulfuricans
Proteobacteria	Syntrophaceae	sf_3	9665	X85132.1	Syntrophus gentianae str. HQgoe1
Proteobacteria	Unclassified	sf_1	6830	AF523882.1	coal effluent wetland clone RCP124
Proteobacteria	Ralstoniaceae	sf_1	7823	AF312022.1	Wautersia basilensis str. DSM 11853
Proteobacteria	Unclassified	sf_1	3084	AF523884.1	coal effluent wetland clone RCP216
Proteobacteria	Thiotrichaceae	sf_3	8559	L40998.1	Thioploca ingrica
Proteobacteria	Unclassified	sf_3	8676		
Proteobacteria	Alteromonadaceae	sf_1	9292		
Proteobacteria	Unclassified	sf_1	10076	AF407700.1	Great Artesian Basin clone G13
Proteobacteria	Bradyrhizobiaceae	sf_1	7353	AY216437.1	temperate estuarine mud clone HC65
Proteobacteria	Rhodobacteraceae	sf_1	6701	AF245632.1	Roseobacter clone NAC11-3
Proteobacteria	Rhodobacteraceae	sf_1	6980	AJ582226.1	Loktanella vestfoldensis str. LMG 22003
Proteobacteria	Rhodobacteraceae	sf_1	7263		
Proteobacteria	Nitrosomonadaceae	sf_1	7682	AF363291.1	Nitrosovibrio sp. str. RY6A
Proteobacteria	Nitrosomonadaceae	sf_1	7796	AF080256.1	Nitrosospira sp. str. TYM9
Proteobacteria	Acidithiobacillaceae	sf_1	8320	AF543507.1	acid mine drainage clone BA11

Proteobacteria	Acidithiobacillaceae	sf_1	8552	AJ278723.1	Acidithiobacillus ferrooxidans str. D2
Proteobacteria	Unclassified	sf_1	9128	X95229.1	Lucina nassula gill symbiont
Proteobacteria	Unclassified	sf_1	9316		
Proteobacteria	Unclassified	sf_1	8231	AJ536870.1	uranium waste soil clone JG30a-KF-21
Proteobacteria	Xanthomonadaceae	sf_3	8577	AF442743.1	Xanthomonas axonopodis pv. citri str. MA
Proteobacteria	Unclassified	sf_3	8245		
Proteobacteria	Pseudomonadaceae	sf_1	8850	D88521.1	Agrobacterium agile str. IAM12615
Proteobacteria	Pseudoalteromonadaceae	sf_1	9339	AF284230.1	Pseudoalteromonas sp. str. 05
Proteobacteria	Shewanellaceae	sf_1	8201	AB094597.1	Shewanella surugaensis str. c959
Proteobacteria	Enterobacteriaceae	sf_1	9290	AF465797.1	Baumannia cicadellinicola
Proteobacteria	Unclassified	sf_1	10259		
Proteobacteria	Polyangiaceae	sf_3	9900	AF280857.1	bioreactor clone mle1-27
Proteobacteria	Unclassified	sf_9	10049	AJ306774.1	DCP-dechlorinating consortium clone SHA-72
Proteobacteria	Syntrophobacteraceae	sf_1	10013	AF420341.2	hydrothermal sediment clone AF420341
Proteobacteria	Syntrophobacteraceae	sf_1	10221	AF482439.1	granular sludge clone R3p4
Proteobacteria	Desulfobulbaceae	sf_1	10047	AY355301.1	epibiontic clone C11-D3
Proteobacteria	Syntrophaceae	sf_3	10067	AF323766.1	benzoate-degrading consortium clone BA044
Proteobacteria	Unclassified	sf_1	10084	AF543496.1	acid mine drainage clone AS6
Proteobacteria	Syntrophobacteraceae	sf_1	10021	AJ519630.1	uranium mill tailings soil sample clone Sh765B-TzT-29 proteobacterium
Proteobacteria	Unclassified	sf_1	9945	AF225446.1	acid mine drainage clone BA18
Proteobacteria	Alcaligenaceae	sf_1	7984	AJ318125.1	Waste-gas biofilter clone BIfciii38
Proteobacteria	Unclassified	sf_1	7993	AF423222.1	soil clone 1326-2
Proteobacteria	Unclassified	sf_6	7340	AJ536878.1	uranium mining waste pile soil sample clone JG30-KF-AS50
Proteobacteria	Alcaligenaceae	sf_1	7737	AY081977.1	atrazine-catabolizing microbial presence methanol clone KRA30+06A
Proteobacteria	Thiotrichaceae	sf_3	8477	AF532774.1	marine sediment clone Limfjorden L8
Proteobacteria	Roseococcaceae	sf_1	7500	AF407720.1	Great Artesian Basin clone B35
Proteobacteria	Acetobacteraceae	sf_1	7600	AJ001632.1	Acetobacter pomorum str. LTH2458
Proteobacteria	Unclassified	sf_6	6918	AJ581616.1	soil near uranium mill tailings clone KCM-C-45
Proteobacteria	Bradyrhizobiaceae	sf_1	6887	AB067729.1	Bradyrhizobium str. YB2
Proteobacteria	Phyllobacteriaceae	sf_1	6857	AY195844.1	Mesorhizobium mediterraneum str. PECA20
Proteobacteria	Phyllobacteriaceae	sf_1	7381	AJ011759.1	Aminobacter aminovorans str. DSM7048T
Proteobacteria	Unclassified	sf_20	6763		
Proteobacteria	Unclassified	sf_1	8037	AY323827.1	Chitinimonas taiwanensis str. cf
Proteobacteria	Unclassified	sf_1	9059	AF361096.1	activated sludge clone SBRH10
Proteobacteria	Unclassified	sf_3	9498		
Proteobacteria	Chromatiaceae	sf_1	9054		
Proteobacteria	Methylococcaceae	sf_1	8243	AF521582.1	isolate str. IR
Proteobacteria	Unclassified	sf_1	8403	AF432146.1	Selenate-reducing isolate str. KE4OH1
Proteobacteria	Alcanivoraceae	sf_1	9658	AB053127.1	Alcanivorax sp. str. Haw1
Proteobacteria	Pseudomonadaceae	sf_1	8288		
Proteobacteria	Alteromonadaceae	sf_1	8196		
Proteobacteria	Unclassified	sf_1	10092	AY102330.1	heavy metal-contaminated soil clone a13134
Proteobacteria	Syntrophobacteraceae	sf_1	9864	AJ518801.1	uranium mining waste pile clone JG37-AG-133 proteobacterium
Proteobacteria	Desulfobulbaceae	sf_1	10062	AJ535241.1	marine sediment above hydrate ridge clone Hyd24-11 proteobacterium
Proteobacteria	Desulfobacteraceae	sf_5	10046	AJ237603.1	Desulfobacterium cetonicum str. DSM 7267 oil recovery water
Proteobacteria	Campylobacteraceae	sf_3	10463	AF482990.1	Campylobacter subsp. fetus
Proteobacteria	Burkholderiaceae	sf_1	7720	AY218566.1	penguin droppings sediments clone KD1-79

Proteobacteria	Enterobacteriaceae	sf_1	9309	AJ417833.1	Buchnera sp
Proteobacteria	Campylobacteraceae	sf_3	10484	U03022.1	Campylobacter helveticus
Proteobacteria	Unclassified	sf_2	6697	AB089090.1	termite gut homogenate clone Rs-D84 proteobacterium
Proteobacteria	Unclassified	sf_3	8230		
Proteobacteria	Moraxellaceae	sf_3	9428	AF143841.1	hydrocarbon-degrading consortium clone AF2-1D
Proteobacteria	Pasteurellaceae	sf_1	9030	AY216870.1	Volucribacter amazonae str. B96/5
Proteobacteria	Syntrophobacteraceae	sf_1	9845	AJ518800.1	uranium mining waste pile clone JG37-AG-128 proteobacterium
Proteobacteria	Unclassified	sf_1	7060		
Proteobacteria	Rhizobiaceae	sf_1	7051	D12786.1	Mycoplana dimorpha str. IAM 13154
Proteobacteria	Nitrosomonadaceae	sf_1	7931	L35509.1	Nitrosospira multiformis
Proteobacteria	Alcaligenaceae	sf_1	7788	AY081994.1	atrazine-catabolizing microbial absence methanol clone KRA30-58
Proteobacteria	Chromatiaceae	sf_1	9052		
Proteobacteria	Unclassified	sf_1	8532		
Proteobacteria	Pseudomonadaceae	sf_1	8487		
Proteobacteria	Pseudomonadaceae	sf_1	9343	AF448515.1	Cellvibrio subsp. mixtus str. ACM 2601
Proteobacteria	Alteromonadaceae	sf_1	8368	AJ507251.1	Pseudoalteromonas mariniglutinosa str. KMM 3635
Proteobacteria	Alteromonadaceae	sf_1	9364	U85855.1	Pseudoalteromonas prydzensis str. MB8-11
Proteobacteria	Enterobacteriaceae	sf_1	8286	AF476102.1	Cyphonococcus alpinus symbiont
Proteobacteria	Polyangiaceae	sf_3	9912	AJ532713.1	uranium mining waste pile clone JG34-KF-14 proteobacterium
Proteobacteria	Unclassified	sf_1	9959	AF523965.1	forested wetland clone FW110
Proteobacteria	Unclassified	sf_4	10024	AF420338.1	hydrothermal sediment clone AF420338
Proteobacteria	Oxalobacteraceae	sf_1	7866	AB021375.1	Paucimonas lemoignei str. ATCC 17989T
Proteobacteria	Unclassified	sf_3	9124	AY145601.1	10e-6 dilution marine samples Weser estuary clone DC8-80-1 proteobacterium
Proteobacteria	Unclassified	sf_8	9558		
Proteobacteria	Enterobacteriaceae	sf_1	8282	AF476101.1	Antonina pretiosa symbiont
Proteobacteria	Comamonadaceae	sf_1	8112	AF336312.1	Comamonas testosteroni str. SMCC B329
Proteobacteria	Neisseriaceae	sf_1	7662	AF526930.2	Mars Odyssey Orbiter and encapsulation facility clone T5-1 sp.
Proteobacteria	Oxalobacteraceae	sf_1	8013	AF236013.1	isolate str. A1020
Proteobacteria	Unclassified	sf_9	9876	AY093471.1	deep marine sediment clone MB-B2-106
Proteobacteria	Desulfobulbaceae	sf_1	10187	AF507840.1	Mono Lake at depth 23 m station 6 July 2000 clone ML623J-57 proteobacterium
Proteobacteria	Campylobacteraceae	sf_3	10523	AF449239.1	Riftia pachyptila's tube clone R103-B70
Proteobacteria	Bradyrhizobiaceae	sf_1	7390	U87781.1	Afipia genosp. 10 str. G8996
Proteobacteria	Rhizobiaceae	sf_1	7568	U47303.1	Rhizobium etli str. USDA 2667 ATCC 14483 SEMIA 043
Proteobacteria	Rhodobacteraceae	sf_1	6652	AF353235.1	marine clone Arctic96A-1
Proteobacteria	Sphingomonadaceae	sf_1	7100	D16147.1	Novosphingobium capsulatum str. GIFU11526
Proteobacteria	Unclassified	sf_3	7974		
Proteobacteria	Burkholderiaceae	sf_1	7969	U37342.1	Burkholderia sp.
Proteobacteria	Unclassified	sf_3	8646		
Proteobacteria	Piscirickettsiaceae	sf_3	9557	AF449225.1	Riftia pachyptila's tube clone R76-B23
Proteobacteria	Oceanospirillaceae	sf_1	9351	AF382102.1	bacterioplankton clone ZA2333c
Proteobacteria	Unclassified	sf_3	8959	AF406527.1	bacterioplankton clone AEGEAN_133
Proteobacteria	Enterobacteriaceae	sf_1	8700	AF489427.1	Baumannia cicadellinicola
Proteobacteria	Enterobacteriaceae	sf_1	9293	AJ245598.1	USA clone 14/7
Proteobacteria	Desulfovibrionaceae	sf_1	10244		
Proteobacteria	Unclassified	sf_4	9741	AJ518791.1	uranium mining waste pile clone JG37-AG-30

					proteobacterium
Proteobacteria	Helicobacteraceae	sf_23	10443	U00679.1	Helicobacter pylori str. 85D08
Proteobacteria	Helicobacteraceae	sf_3	10576	AF142585.1	Helicobacter sp. 'liver 3' str. liver 3
Proteobacteria	Geobacteraceae	sf_1	482	AF529120.1	trichloroethene-contaminated site clone FTLM205 proteobacterium
Proteobacteria	Geobacteraceae	sf_1	10171		
Proteobacteria	Chromatiaceae	sf_1	9370	AB010860.1	isolate str. HTB019
Proteobacteria	Shewanellaceae	sf_1	8662		
Proteobacteria	Enterobacteriaceae	sf_1	9135	AJ487029.1	intestine Zophobas mori clone
Proteobacteria	Enterobacteriaceae	sf_1	9157	AF293618.1	Secondary symbiont type-U Acyrthosiphon pisum (rrs) clone 5B type-U
Proteobacteria	Desulfobacteraceae	sf_5	10268		
Proteobacteria	Unclassified	sf_5	7471	AJ347025.1	sponge clone TK03
Proteobacteria	Burkholderiaceae	sf_1	7957	AF476089.1	Maconellicoccus hirsutus symbiont
Proteobacteria	Desulfobulbaceae	sf_1	9739	AJ535252.1	gas hydrate clone Hyd89-51
Proteobacteria	Phyllobacteriaceae	sf_1	7009		
Proteobacteria	Rhizobiaceae	sf_1	6683	D14516.1	Sinorhizobium fredii str. ATCC35423
Proteobacteria	Rhodobacteraceae	sf_1	7433	AF359537.1	Scrippsiella trochoidea NEPCC 15
Proteobacteria	Unclassified	sf_5	6735	AF510192.1	Candidatus Pelagibacter ubique str. HTCC1002
Proteobacteria	Unclassified	sf_1	8035		
Proteobacteria	Rhodocyclaceae	sf_1	8131		
Proteobacteria	Burkholderiaceae	sf_1	8097	AB091761.1	Burkholderia cepacia
Proteobacteria	Chromatiaceae	sf_1	9048	AJ401209.1	Allochromatium sp. AT2202
Proteobacteria	Cardiobacteriaceae	sf_1	8536	M35014.1	Cardiobacterium hominis
Proteobacteria	Moraxellaceae	sf_3	8604	AB087260.2	Moraxella oblonga str. IAM 14971
Proteobacteria	Moraxellaceae	sf_3	9641	X81662.1	Acinetobacter haemolyticus
Proteobacteria	Pseudomonadaceae	sf_1	8754	AB076857.1	Pseudomonas sp. str. P400Y-1
Proteobacteria	Myxococcaceae	sf_1	10358	AJ233917.1	Myxococcus fulvus str. Mx f2
Proteobacteria	Desulfobulbaceae	sf_1	10107	AJ535243.1	marine sediment above hydrate ridge clone Hyd24-30 proteobacterium
Proteobacteria	Unclassified	sf_9	9738	AF354149.1	marine methane seep clone 1513
Proteobacteria	Desulfobacteraceae	sf_5	10239		
Proteobacteria	Helicobacteraceae	sf_3	10602		
Proteobacteria	Unclassified	sf_1	9344	AF005249.1	Shewanella algae str. ATCC 51192
Proteobacteria	Enterobacteriaceae	sf_1	8603	AF476106.1	Melanococcus albizziae symbiont
Proteobacteria	Enterobacteriaceae	sf_1	8627	AF476099.1	Australicoccus grevilleae symbiont
Proteobacteria	Enterobacteriaceae	sf_1	8362	AF453251.1	Klebsiella pneumoniae str. ASR1
Proteobacteria	Beijerinck/Rhodoplan/Methylocyst	sf_3	7239	AF358664.1	Thalassospira lucentensis
Proteobacteria	Unclassified	sf_3	8045		
Proteobacteria	Enterobacteriaceae	sf_1	8467	AB061685.1	Serratia marcescens subsp. sakuensis str. KRED subsp.
Proteobacteria	Enterobacteriaceae	sf_1	8739	AJ233427.1	Serratia entomophila str. DSM 12358
Proteobacteria	Enterobacteriaceae	sf_1	8225		
Proteobacteria	Enterobacteriaceae	sf_1	9337	U90758.1	Rahnella genosp. 3 str. DSM 30078
Proteobacteria	Magnetospirillaceae	sf_1	6922	AY171615.1	Dechlorospirillum sp. str. SN1
Proteobacteria	Beijerinck/Rhodoplan/Methylocyst	sf_3	7153	AJ563928.1	Methylocella tundrae str. Y1
Proteobacteria	Bradyrhizobiaceae	sf_1	7029		
Proteobacteria	Phyllobacteriaceae	sf_1	7216	D88524.1	Ahrensia kielensis str. IAM12618
Proteobacteria	Rhizobiaceae	sf_1	6972	AY040360.1	Ensifer adhaerens str. LMG 20582
Proteobacteria	Rhizobiaceae	sf_1	6974	AF441730.1	India: Himalayas Kaza Spiti Valley Cold Desert isolate str. Kaza-35 Kaza-35
Proteobacteria	Rhizobiaceae	sf_1	6964	AE008265.2	Agrobacterium tumefaciens str. C58 Cereon
Proteobacteria	Rhodobacteraceae	sf_1	7026	AY005463.1	Leisingera methylohalidivorans str. MB2

Proteobacteria	Unclassified	sf_5	7025	AF382105.1	bacterioplankton clone ZA2526c
Proteobacteria	Sphingomonadaceae	sf_1	7548	U87784.1	Afipia genosp. 13 str. G8991
Proteobacteria	Sphingomonadaceae	sf_1	6690	AY048657.1	Porphyrobacter tepidarius str. OK5APO
Proteobacteria	Unclassified	sf_3	8036	AJ519624.1	Uranium mill tailings soil sample clone Sh765B-TzT-132 proteobacterium
Proteobacteria	Comamonadaceae	sf_1	7705	AY218644.1	penguin droppings sediments clone KD4-7
Proteobacteria	Burkholderiaceae	sf_1	8059	Y17010.1	Burkholderia caribensis str. MWAP71
Proteobacteria	Burkholderiaceae	sf_1	8068	X67039.1	Burkholderia caryophylli str. ATCC 25418
Proteobacteria	Piscirickettsiaceae	sf_3	8664	AJ237758.1	Thiomicrospira sp. str. Milos-T2
Proteobacteria	Xanthomonadaceae	sf_3	8983	AF012541.1	Iron oxidising strain ES-1
Proteobacteria	Xanthomonadaceae	sf_3	9320	AJ318204.1	Waste-gas biofilter clone BIyi3
Proteobacteria	Moraxellaceae	sf_3	9359	AB101444.1	Acinetobacter junii str. S33
Proteobacteria	Alteromonadaceae	sf_1	8484	AF513454.1	Alteromonadaceae isolate str. LA50
Proteobacteria	Alteromonadaceae	sf_1	8503	AF468401.1	Arctic sea ice ARK10244
Proteobacteria	Alteromonadaceae	sf_1	9486	AF406617.1	Marine isolate str. GK-2001
Proteobacteria	Alteromonadaceae	sf_1	9067	AF006669.1	Shewanella algae str. ACM 4733
Proteobacteria	Unclassified	sf_3	9473	AF468261.1	Arctic pack ice; northern Fram Strait; 80 31.1 N; 01 deg 59.7 min E clone ARKDMS-58
Proteobacteria	Polyangiaceae	sf_3	9755	AF382126.1	bacterioplankton clone ZA3704c
Proteobacteria	Desulfobacteraceae	sf_5	9666	AJ535229.1	marine sediment above hydrate ridge clone Hyd89-13 proteobacterium
Proteobacteria	Unclassified	sf_9	9798	AJ519663.1	uranium mill tailings soil sample clone GuBH2-AD/TzT-67 proteobacterium
Proteobacteria	Desulfobulbaceae	sf_1	10332	AF099059.1	Psychrophilic sulfate-reducing isolate str. LSv23 bacterium
Proteobacteria	Helicobacteraceae	sf_3	10534	U01329.1	Helicobacter pylori
Proteobacteria	Helicobacteraceae	sf_3	10572	AF057163.1	Helicobacter sp
Proteobacteria	Unclassified	sf_1	10497	AY261811.1	UASB reactor granular sludge clone PD-UASB-2 proteobacterium
Proteobacteria	Helicobacteraceae	sf_3	10614	AJ431216.1	strain isolate str. BHI80-49
Proteobacteria	Helicobacteraceae	sf_3	10417	AY216452.1	temperate estuarine mud clone KM61
Proteobacteria	Unclassified	sf_1	7808	AY221081.1	Mammoth cave clone CCU25
Proteobacteria	Unclassified	sf_1	8023	AF293006.1	ferromanganous micronodule clone MND1
Proteobacteria	Enterobacteriaceae	sf_1	8886	AF170176.1	Salmonella typhimurium LT2 str. SGSC1412
Proteobacteria	Enterobacteriaceae	sf_1	8554	AJ627202.1	Kluyvera ascorbata 69
Proteobacteria	Enterobacteriaceae	sf_1	8885	AB089246.1	Morganella morganii str. AP28
Proteobacteria	Enterobacteriaceae	sf_1	9363	AF025365.1	Citrobacter freundii str. CDC 621-64
Proteobacteria	Enterobacteriaceae	sf_1	8934	AF373188.1	Pectobacterium subsp. carotovorum str. E155 subsp.
Proteobacteria	Enterobacteriaceae	sf_1	9060	AJ853891.1	Enterobacter ludwigii str. EN-119 = DSMZ 16688
Proteobacteria	Enterobacteriaceae	sf_1	8510	AJ233420.1	Klebsiella pneumoniae str. DSM 30104
Proteobacteria	Enterobacteriaceae	sf_1	8473	M59155.1	Hafnia alvei
Proteobacteria	Helicobacteraceae	sf_3	10411	AB089112.2	termite gut homogenate clone Rs-P71 proteobacterium
Proteobacteria	Helicobacteraceae	sf_3	10590	AB089113.1	termite gut homogenate clone Rs-H40 proteobacterium
Proteobacteria	Sphingomonadaceae	sf_1	6650	AY563441.1	Sphingomonas phyllosphaerae str. FA1
Proteobacteria	Nitrosomonadaceae	sf_1	8145	AY123795.1	Nitrosomonas eutropha str. Nm57
Proteobacteria	Comamonadaceae	sf_1	8012	AJ420325.1	Acidovorax konjaci str. DSM 7481
Proteobacteria	Oxalobacteraceae	sf_1	8158	AB006750.1	2-HNA producing isolate MC13289
Proteobacteria	Unclassified	sf_1	7832		
Proteobacteria	Shewanellaceae	sf_1	9081	AB059264.1	Shewanella sp. str. MTW-1
Proteobacteria	Aeromonadaceae	sf_1	8621	AF427150.1	Aeromonas sp. PAR2A

Proteobacteria	Enterobacteriaceae	sf_1	8974	U92197.1	Salmonella subsp. enterica serovar Agona str. Sa1 subsp.
Proteobacteria	Enterobacteriaceae	sf_1	9361	AB004747.1	Enterobacter intermedius str. JCM1238
Proteobacteria	Enterobacteriaceae	sf_1	8529	AF181574.1	Raoultella planticola 7
Proteobacteria	Enterobacteriaceae	sf_1	8892	U93263.1	Aranicola proteolyticus
Proteobacteria	Polyangiaceae	sf_3	9735	AJ518790.1	uranium mining waste pile clone JG37-AG-15 proteobacterium
Proteobacteria	Unclassified	sf_1	9678	AF523883.1	coal effluent wetland clone RCP185
Proteobacteria	Azospirillaceae	sf_1	7539	AJ401217.1	Rhodocista sp. AR2107
Proteobacteria	Unclassified	sf_1	7264	AF508112.1	Bosea thiooxidans TJ1
Proteobacteria	Phyllobacteriaceae	sf_1	7300	AY007683.1	marine isolate JP57
Proteobacteria	Bartonellaceae	sf_1	7415	NC_005955.1	Bartonella quintana str. Toulouse
Proteobacteria	Rhodobacteraceae	sf_1	6888	AF254109.1	hydrothermal vent strain str. TB66
Proteobacteria	Rhodobacteraceae	sf_1	7040	D32238.1	Paracoccus alcaliphilus str. JCM 7364
Proteobacteria	Rhodobacteraceae	sf_1	6991	X53853.1	Rhodobacter sphaeroides str. 2.4.1
Proteobacteria	SAR11	sf_2	7043	AF353223.1	marine clone Arctic95D-8
Proteobacteria	Unclassified	sf_1	6653	AY785128.1	Kaistobacter koreensis str. PB229
Proteobacteria	Neisseriaceae	sf_1	8092	AF487709.1	Neisseria dentiae str. V33
Proteobacteria	Rhodocyclaceae	sf_1	8127	AJ505852.1	Zoogloea resiniphila str. PIV-3A2y
Proteobacteria	Comamonadaceae	sf_1	7986	AF468446.1	Arctic sea ice ARK10281
Proteobacteria	Burkholderiaceae	sf_1	7914	AB021422.1	Burkholderia andropogonis str. ATCC 19311T
Proteobacteria	Unclassified	sf_1	8839	AJ400349.1	f cytometric sorted marine sample subpopulation 3 clone ZD0408 bacterium
Proteobacteria	Xanthomonadaceae	sf_3	9167	AB074619.1	pea aphid symbiont clone APe4_38
Proteobacteria	Pseudomonadaceae	sf_1	9049	AJ296559.1	uranium mining mill tailing clone GR-Sh2-34 GR-Sh2-34
Proteobacteria	Unclassified	sf_3	9044	AF420370.1	hydrothermal sediment clone AF420370
Proteobacteria	Alteromonadaceae	sf_1	9222	X82132.1	Shewanella hanedai str. CIP 103207T
Proteobacteria	Alteromonadaceae	sf_1	8916	U91545.1	Shewanella algae str. 43940
Proteobacteria	Unclassified	sf_3	9367	AF387348.1	USA: Pacific Ocean seawater Naha Vents Hawaii isolate str. PV-4
Proteobacteria	Pasteurellaceae	sf_1	9263	M75067.1	Actinobacillus capsulatus
Proteobacteria	Enterobacteriaceae	sf_1	9151		
Proteobacteria	Enterobacteriaceae	sf_1	9385	AY264673.1	Australiococcus greville symbiont
Proteobacteria	Desulfomicrobiaceae	sf_1	10370	AF030438.1	Desulfomicrobium baculatum str. X; VKM B-1378; DSM 4
Proteobacteria	Polyangiaceae	sf_3	10309	AJ233947.1	Nannocystis exedens str. Na e571
Proteobacteria	Desulfobacteraceae	sf_5	9777	AY197376.1	Guaymas Basin hydrothermal vent sediments clone B01R004
Proteobacteria	Helicobacteraceae	sf_3	10425	AB088432.1	Sulfurimonas autotrophica str. OK5
Proteobacteria	Desulfobacteraceae	sf_5	9940	AY177800.1	Antarctic sediment clone SB2_56
Proteobacteria	Rhodobacteraceae	sf_1	7084	AF359546.1	Scrippsiella trochoidea NEPCC 15
Proteobacteria	Caedibacteraceae	sf_3	7010	AJ428412.1	periodontal pocket clone 10B6
Proteobacteria	Shewanellaceae	sf_1	8581	AB008796.1	Shewanella benthica str. DB21MT-2
Proteobacteria	Vibrionaceae	sf_1	8798	AF172840.1	Vibrio aestuarianus str. KT0901
Proteobacteria	Vibrionaceae	sf_1	8888	AJ845014.1	Vibrio aestuarianus str. 01/151
Proteobacteria	Enterobacteriaceae	sf_1	8742	AF084835.1	USA:New York isolate str. KN4
Proteobacteria	Enterobacteriaceae	sf_6	8783	AF075271.2	Alterococcus agarolyticus str. ADT3; CCRC17102
Proteobacteria	Enterobacteriaceae	sf_1	9358	U92194.1	Salmonella subsp. enterica serovar Waycross str. Swy1 subsp.
Proteobacteria	Enterobacteriaceae	sf_1	9496		
Proteobacteria	Enterobacteriaceae	sf_1	9651	AF373176.1	Pectobacterium subsp. atrosepticum str. GSPB 1710

Proteobacteria	Enterobacteriaceae	sf_1	8379	AF289542.1	Erwinia amylovora EA G-5
Proteobacteria	Enterobacteriaceae	sf_1	9142	AJ233410.1	Erwinia amylovora str. DSM 30165
Proteobacteria	Enterobacteriaceae	sf_1	9345	AF141891.1	Erwinia amylovora str. BC199(=Ea528)
Proteobacteria	Enterobacteriaceae	sf_1	8758	U80201.1	Pectobacterium cypripedii str. ATCC 29267
Proteobacteria	Unclassified	sf_1	8430	AF029226.1	Salmonella bongori str. JEO 4162
Proteobacteria	Enterobacteriaceae	sf_1	8693	AF130912.1	Pantoea agglomerans str. A40
Proteobacteria	Enterobacteriaceae	sf_1	9302	AF373198.1	Pantoea subsp. stewartii str. GSPB 2626
Proteobacteria	Enterobacteriaceae	sf_1	8624	AF476105.1	Erium globosum symbiont
Proteobacteria	Enterobacteriaceae	sf_1	8505	AJ233406.1	Buttiauxella warmboldiae str. DSM 9404
Proteobacteria	Enterobacteriaceae	sf_1	8528	Y17665.1	Enterobacter cloacae Nr. 3
Proteobacteria	Enterobacteriaceae	sf_1	8530	AJ489826.1	Enterobacteriaceae CF01Ent-1
Proteobacteria	Enterobacteriaceae	sf_1	8640		
Proteobacteria	Enterobacteriaceae	sf_1	8936	AF543283.1	Klebsiella oxytoca str. ChDC OS31
Proteobacteria	Enterobacteriaceae	sf_1	9274	AJ550468.1	Enterobacter sp. CC1
Proteobacteria	Enterobacteriaceae	sf_1	9390	Z96077.1	Enterobacter nimipressuralis str. LMG 10245-T
Proteobacteria	Enterobacteriaceae	sf_1	8251	AF214640.1	Nitrogen-fixing isolate str. CANF3
Proteobacteria	Enterobacteriaceae	sf_1	8890	X93216.1	Raoultella planticola str. DR3
Proteobacteria	Enterobacteriaceae	sf_1	8773		
Proteobacteria	Enterobacteriaceae	sf_1	8711	AJ233432.1	Serratia odorifera str. DSM 4582
Proteobacteria	Enterobacteriaceae	sf_1	8712	AJ233434.1	Serratia proteamaculans str. DSM 4543
Proteobacteria	Enterobacteriaceae	sf_1	9417	AJ233429.1	Serratia fonticola str. DSM 4576
Proteobacteria	Enterobacteriaceae	sf_1	8631	AF476108.1	Planococcus ficus symbiont
Proteobacteria	Enterobacteriaceae	sf_1	9265	AY253919.1	Rahnella aquatilis k 8
Proteobacteria	Unclassified	sf_6	6665	AF143830.1	hydrocarbon-degrading consortium clone 4-Org2-22
Proteobacteria	Sphingomonadaceae	sf_1	7535	D16144.1	Sphingomonas paucimobilis str. GIFU2395
Proteobacteria	Neisseriaceae	sf_1	8143	AY005029.1	subgingival dental plaque clone AK105
Proteobacteria	Unclassified	sf_1	7750	AJ518782.1	uranium mining waste pile near Johanngeorgenstadt soil clone JG37-AG-35
Proteobacteria	Comamonadaceae	sf_1	7928	AY218738.1	penguin droppings sediments clone KD5-43
Proteobacteria	Comamonadaceae	sf_1	7919	AB021339.1	strain isolate str. rM4
Proteobacteria	Comamonadaceae	sf_1	7987	AB076844.1	Acidovorax sp. str. OS-6
Proteobacteria	Unclassified	sf_1	7879		
Proteobacteria	Unclassified	sf_1	7766		
Proteobacteria	Unclassified	sf_1	7818	AJ534623.1	soil sample uranium mining waste pile near town Johanngeorgenstadt clone JG36-TzT-215 proteobacterium
Proteobacteria	Burkholderiaceae	sf_1	8011	U96941.1	Burkholderia graminis str. AUS35
Proteobacteria	Unclassified	sf_4	8169	AF523886.1	forested wetland clone RCP2-54
Proteobacteria	Xanthomonadaceae	sf_3	9277	AY188327.1	penguin droppings sediment clone KD8-68
Proteobacteria	Legionellaceae	sf_1	8836	CR628336.1	Legionella pneumophila str. Paris
Proteobacteria	Unclassified	sf_1	9008	AF361092.1	activated sludge clone SBRQ157
Proteobacteria	Oceanospirillaceae	sf_1	8596	AF353238.1	marine clone Arctic95B-7
Proteobacteria	Aeromonadaceae	sf_1	8340	X71120.1	Aeromonas ichthiosmia
Proteobacteria	Aeromonadaceae	sf_1	8364	S39232.1	Aeromonas allosaccharophila str. CECT 4199
Proteobacteria	Aeromonadaceae	sf_1	9026	AJ009860.1	Haemophilus piscium str. NCIMB 1952
Proteobacteria	Aeromonadaceae	sf_1	9440	X60412.1	Aeromonas sobria str. NCIMB 12065
Proteobacteria	Pasteurellaceae	sf_1	9477	AY613549.1	Haemophilus influenzae str. M11105
Proteobacteria	Pasteurellaceae	sf_1	9604	AF224286.1	Mannheimia sp. MCCM 00145
Proteobacteria	Desulfovibrionaceae	sf_1	10212		
Proteobacteria	Polyangiaceae	sf_3	9671	AF420357.1	hydrothermal sediment clone AF420357
Proteobacteria	Unclassified	sf_4	9884	AF523885.1	forested wetland clone RCP2-62
Proteobacteria	Geobacteraceae	sf_1	9956	AF523968.1	forested wetland clone FW140

Proteobacteria	Desulfobacteraceae	sf_5	10364	AY771936.1	marine surface sediment clone SB2
Proteobacteria	Desulfobacteraceae	sf_5	9818	AY216453.1	temperate estuarine mud clone KM62
Proteobacteria	Unclassified	sf_28	10091		
Proteobacteria	Unclassified	sf_1	10384	AF367484.1	deep-sea hydrothermal vent clone VC1.2-cl06
Proteobacteria	Unclassified	sf_1	10405	AF420346.1	hydrothermal sediment clone AF420346
Proteobacteria	Unclassified	sf_1	10414	AY218582.1	penguin droppings sediments clone KD2-34
Proteobacteria	Unclassified	sf_9	244	AY093483.1	deep marine sediment clone MB-C2-152
Proteobacteria	Sphingomonadaceae	sf_1	7215	AF445712.1	travertine hot spring clone SM2B06
Proteobacteria	Rhodocyclaceae	sf_1	8052	AY032610.1	Dechloromonas aromatica str. RCB
Proteobacteria	Methylococcaceae	sf_1	8645	AF307138.1	Methylomicrobium buryatense str. 5B
Proteobacteria	Desulfobacteraceae	sf_5	10031	AY177795.1	Antarctic sediment clone SB1_49
Proteobacteria	Acetobacteraceae	sf_1	6637	X74066.1	Acetobacter aceti str. NCIB8621 DSM3508
Proteobacteria	Unclassified	sf_1	7109	AY189753.1	diesel-polluted Bohai Gulf isolate str. M-5 M-5
Proteobacteria	Beijerinck/Rhodoplan/Methylocyst	sf_3	7401	AF359545.1	Scrippsiella trochoidea NEPCC 15
Proteobacteria	Unclassified	sf_6	7207		
Proteobacteria	Unclassified	sf_6	7647		
Proteobacteria	Xanthobacteraceae	sf_1	6971	AY177367.2	Thiobacillus sp. str. 104
Proteobacteria	Unclassified	sf_1	7067	AB033757.1	Blastochloris sulfoviridis str. GN1
Proteobacteria	Bradyrhizobiaceae	sf_1	6768	M59068.1	Rhodopseudomonas palustris str. GH
Proteobacteria	Bradyrhizobiaceae	sf_1	6636	U35000.3	Bradyrhizobium elkanii str. USDA 76
Proteobacteria	Bradyrhizobiaceae	sf_1	6867	AY102327.1	heavy metal-contaminated soil clone a13131
Proteobacteria	Bradyrhizobiaceae	sf_1	7126	AJ534670.1	ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A-MN96 proteobacterium
Proteobacteria	Bradyrhizobiaceae	sf_1	7522	AF509906.1	Bradyrhizobium sp. str. KKI14
Proteobacteria	Rhizobiaceae	sf_1	7457		
Proteobacteria	Rhizobiaceae	sf_1	6798	AF508099.1	Agrobacterium tumefaciens TG14
Proteobacteria	Rhodobacteraceae	sf_1	7125	AB006899.1	Paracoccus carotinifaciens str. E-396
Proteobacteria	Rickettsiaceae	sf_1	6831		
Proteobacteria	Sphingomonadaceae	sf_1	7528	D16145.1	Sphingobium yanoikuyae str. GIFU9882
Proteobacteria	Sphingomonadaceae	sf_1	7016	AY167834.1	Sphingomonas sp. str. SAFR-027
Proteobacteria	Sphingomonadaceae	sf_1	7537	AY250869.1	lichen-dominated Antarctic cryptoendolithic community clone FBP255 proteobacterium
Proteobacteria	Unclassified	sf_6	6987		
Proteobacteria	Sphingomonadaceae	sf_1	7075	AJ000920.2	Novosphingobium sp. str. K16
Proteobacteria	Methylophilaceae	sf_1	7892	AB193725.1	Methylophilus leisingeri str. DSM 6813
Proteobacteria	Unclassified	sf_17	7819		
Proteobacteria	Nitrosomonadaceae	sf_1	7976	AY123798.1	Nitrosomonas sp. str. Nm86
Proteobacteria	Rhodocyclaceae	sf_1	7951	AF502233.1	EBPR sludge lab scale clone HP1A03
Proteobacteria	Comamonadaceae	sf_1	7949	AF508103.1	Variovorax paradoxus TG27
Proteobacteria	Comamonadaceae	sf_1	8152	AJ543434.1	nephridia Octolasion lacteum clone Ol2-2
Proteobacteria	Ectothiorhodospiraceae	sf_1	9450	AJ318526.1	Halorhodospira neutrophila str. SG 3304
Proteobacteria	Ectothiorhodospiraceae	sf_1	9598	AF507818.1	Mono Lake at depth 2 m station 6 July 2000 clone ML602J-47 proteobacterium
Proteobacteria	Chromatiaceae	sf_1	8408	Y12368.2	Thiorhodovibrio winogradskyi
Proteobacteria	Unclassified	sf_3	8961	M99446.1	Calyptogena magnifica symbiont
Proteobacteria	Piscirickettsiaceae	sf_3	9392	AJ244761.1	Methylophaga sp. str. V4.ME.29 = MM_2343
Proteobacteria	Unclassified	sf_1	9458	AJ518786.1	uranium mining waste pile clone JG37-AG-94 proteobacterium
Proteobacteria	Xanthomonadaceae	sf_3	9211	AY218694.1	penguin droppings sediments clone KD8-80
Proteobacteria	Unclassified	sf_3	9269		
Proteobacteria	Unclassified	sf_8	8247		
Proteobacteria	Halomonadaceae	sf_1	8317	AF211861.1	Chromohalobacter canadensis str. DSM6769

Proteobacteria	Halomonadaceae	sf_1	8598	X92417.1	Halomonas desiderata str. FB2
Proteobacteria	Moraxellaceae	sf_3	8565	Z93454.1	Acinetobacter sp. str. 942 Group BJ17
Proteobacteria	Pseudomonadaceae	sf_1	9588	AF530072.1	Pseudomonas citronellolis str. TERIDB18
Proteobacteria	Pseudomonadaceae	sf_1	8263		
Proteobacteria	Pseudomonadaceae	sf_1	8635		
Proteobacteria	Unclassified	sf_1	8323	AF420363.1	hydrothermal sediment clone AF420363
Proteobacteria	Unclassified	sf_3	9582		
Proteobacteria	Unclassified	sf_1	8483	AJ002006.1	Rheinheimera baltica str. OS140 Baltic # 166
Proteobacteria	Alteromonadaceae	sf_1	8695	AF468296.1	Arctic pack ice; northern Fram Strait; 80 31.1 N; 01 deg 59.7 min E clone ARKIA-34
Proteobacteria	Alteromonadaceae	sf_1	8904	AB059263.1	psychrophile deep-sea sediment south-western Pacific isolate str. PS12-4 PS12-4
Proteobacteria	Alteromonadaceae	sf_1	9586	AY190533.1	Shewanella gaetbuli str. TF-27
Proteobacteria	Vibrionaceae	sf_1	8999	AY292944.1	Photobacterium leiognathi str. LN101
Proteobacteria	Vibrionaceae	sf_1	8665	AY257975.1	Vibrio gallicus str. CIP 107867; HT 3-3
Proteobacteria	Vibrionaceae	sf_1	8267	AJ491290.1	Vibrio pomeroyi str. LMG 20537
Proteobacteria	Aeromonadaceae	sf_1	9000	AF170914.4	Aeromonas culicicola str. MTCC 3249
Proteobacteria	Aeromonadaceae	sf_1	9494	AY532691.1	Aeromonas molluscorum str. 849T
Proteobacteria	Pasteurellaceae	sf_1	8308	M75039.1	Haemophilus actinomycetemcomitans
Proteobacteria	Enterobacteriaceae	sf_1	9391		
Proteobacteria	Enterobacteriaceae	sf_1	8740	AF373201.1	Erwinia chrysanthemi str. 573
Proteobacteria	Enterobacteriaceae	sf_1	9252	AF130971.1	Pantoea cedenensis str. A34
Proteobacteria	Enterobacteriaceae	sf_1	9202	AF189697.1	Activated sludge isolate str. BC55
Proteobacteria	Enterobacteriaceae	sf_1	9594	AB089244.1	Morganella morganii str. ATCC35200
Proteobacteria	Enterobacteriaceae	sf_1	8590	AJ010486.1	Enterobacter pyrinus str. KCTC2520
Proteobacteria	Enterobacteriaceae	sf_1	9420		
Proteobacteria	Enterobacteriaceae	sf_1	9266	Z14096.1	Parasite BEV of E.variegatus
Proteobacteria	Enterobacteriaceae	sf_1	9348		
Proteobacteria	Enterobacteriaceae	sf_1	9368	AJ233424.1	Pragia fontium str. DSM 5563
Proteobacteria	Enterobacteriaceae	sf_1	9029	AY280573.1	Photorhabdus asymbiotica subsp. australis str. MB
Proteobacteria	Enterobacteriaceae	sf_1	9262	AJ871363.1	Yersinia aldovae str. A125
Proteobacteria	Bdellovibrionaceae	sf_1	10010	AJ518802.1	uranium mining waste pile clone JG37-AG-139 proteobacterium
Proteobacteria	Polyangiaceae	sf_3	10082	AJ518792.1	uranium mining waste pile clone JG37-AG-33 proteobacterium
Proteobacteria	Unclassified	sf_9	9760	AY093467.1	deep marine sediment clone MB-A2-137
Proteobacteria	Unclassified	sf_9	9993		
Proteobacteria	Polyangiaceae	sf_4	9733	AF382143.1	bacterioplankton clone ZA3735c
Proteobacteria	Desulfobulbaceae	sf_1	10097	AB100004.1	inactive deep-sea hydrothermal vent chimneys clone IndB2-42
Proteobacteria	Desulfobacteraceae	sf_5	10267	AJ535249.1	marine sediment above hydrate ridge clone Hyd89-61 proteobacterium
Proteobacteria	Desulfobacteraceae	sf_5	9939	AF354163.1	marine methane seep clone 1427
Proteobacteria	Desulfobacteraceae	sf_5	10136	AY197382.1	Guaymas Basin hydrothermal vent sediments clone B01R011
Proteobacteria	Unclassified	sf_1	10622		
Proteobacteria	Unclassified	sf_1	10473	U29081.1	Rimicaris exoculata ectosymbiont
Proteobacteria	Helicobacteraceae	sf_3	10612	AJ441209.1	hydrothermal vent polychaete mucous clone P. palm C/A 64
Proteobacteria	Campylobacteraceae	sf_3	10563	AF144694.2	Campylobacter sp. str. DSM 806
Proteobacteria	Campylobacteraceae	sf_3	10549	AF497805.1	Campylobacter upsaliensis str. LMG 8850
SPAM	Unclassified	sf_1	705	AJ519639.1	uranium tailings soil clone Sh765B-AG-45
SPAM	Unclassified	sf_1	738	AJ532725.1	uranium mining waste clone JG34-KF-252

Spirochaetes	Spirochaetaceae	sf_1	6479	Y08893.1	Treponema sp
Spirochaetes	Spirochaetaceae	sf_1	6580	AF056341.1	Treponema sp. str. III:C:BA213
Spirochaetes	Spirochaetaceae	sf_1	6562	AF523928.1	forested wetland clone RCP1-96
Spirochaetes	Spirochaetaceae	sf_1	6488	AF093251.1	Treponema primitia str. ZAS-1
Spirochaetes	Spirochaetaceae	sf_1	6491	AB062840.1	termite gut homogenate clone BCf8-03
Spirochaetes	Spirochaetaceae	sf_1	6508	X89050.1	termite hindgut clone mpsp2
Spirochaetes	Spirochaetaceae	sf_1	6523	AB088912.1	termite gut homogenate clone Rs-J64 sp.
Spirochaetes	Leptospiraceae	sf_3	6496	NC_005823.1	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130
Spirochaetes	Spirochaetaceae	sf_1	6476	AB084965.1	termite gut clone NkS50
Spirochaetes	Spirochaetaceae	sf_1	6490	AB062823.1	termite gut homogenate clone BCf4-14
Spirochaetes	Spirochaetaceae	sf_1	6568	AJ419821.1	Spirochaeta sp
Spirochaetes	Spirochaetaceae	sf_3	6558	AF166259.1	Spironema culicis str. BR91
Spirochaetes	Spirochaetaceae	sf_1	6526	AY230217.1	Treponema sp. str. 7CPL208
Spirochaetes	Spirochaetaceae	sf_1	6571	AJ458946.1	Mixotricha paradoxa is flagellate hindgut Mastotermes darwiniensis clone mp4 of
Spirochaetes	Spirochaetaceae	sf_1	6502	AF139203.1	Treponema denticola str. ATCC35405
Spirochaetes	Spirochaetaceae	sf_1	6532	AB084963.1	termite gut clone NkS39
Spirochaetes	Spirochaetaceae	sf_1	6459	AJ431240.1	Spirochaeta sp. str. BHI80-158
Spirochaetes	Spirochaetaceae	sf_1	6506	AB088911.1	termite gut homogenate clone Rs-J58 sp.
Spirochaetes	Spirochaetaceae	sf_1	6575	AY133079.1	TCE-contaminated site clone ccslm226
Spirochaetes	Spirochaetaceae	sf_1	6583	AB088875.1	termite gut homogenate clone Rs-J42 sp.
Spirochaetes	Spirochaetaceae	sf_1	6554	AB088889.1	termite gut homogenate clone Rs-A43 sp.
Spirochaetes	Spirochaetaceae	sf_1	6458	AB084961.1	termite gut clone NkS34
Spirochaetes	Spirochaetaceae	sf_1	6494	AB088890.1	termite gut homogenate clone Rs-C47 sp.
Spirochaetes	Spirochaetaceae	sf_1	6489	AJ458944.1	Mixotricha paradoxa is flagellate hindgut Mastotermes darwiniensis clone mp1 of
Spirochaetes	Spirochaetaceae	sf_1	6565	AB085166.1	termite gut clone NkS-Oxy25
Spirochaetes	Spirochaetaceae	sf_1	6579	AB084968.1	termite gut clone NkS83
Spirochaetes	Spirochaetaceae	sf_1	6507	AB085161.1	termite gut clone NkS-Ste2
Spirochaetes	Spirochaetaceae	sf_1	6529	AB062806.1	termite gut homogenate clone BCf10-21
Spirochaetes	Spirochaetaceae	sf_1	6557	AF454308.1	spirochete clone ML320J-13
Spirochaetes	Spirochaetaceae	sf_1	6460	AB088907.1	termite gut homogenate clone Rs-B69 sp.
Spirochaetes	Spirochaetaceae	sf_1	6465	AF357917.2	Spirochaeta sp. str. Grapes
SR1	Unclassified	sf_1	2900		
Synergistes	Unclassified	sf_3	117	AB089065.2	termite gut homogenate clone Rs-D89
Synergistes	Unclassified	sf_3	353	AY261810.1	UASB reactor granular sludge clone PD-UASB-13 G+C
Synergistes	Unclassified	sf_3	719	AY207056.1	Synergistes sp. P1 str. P4G_18
Synergistes	Unclassified	sf_3	60	AF481216.1	Flexistipes sp. str. E3_33
Synergistes	Unclassified	sf_3	740	AF371930.1	swine intestine clone p-4292-4Wa3
Thermodesulfobacteria	Thermodesulfobacteriaceae	sf_1	667	AF411013.1	Geothermobacterium ferrireducens
Thermotogae	Thermotogaceae	sf_4	51	AJ419874.1	Thermosipho sp. str. MV1063
TM6	Unclassified	sf_1	9803	AF507715.1	forest soil clone S1204
TM7	Unclassified	sf_1	8155	AY134895.1	oral periodontitis clone EW086
TM7	Unclassified	sf_1	5177		
TM7	Unclassified	sf_1	2697	AJ576410.1	midgut homogenate Pachnoda ephippiata larva clone PeM47
TM7	Unclassified	sf_1	3145	AF385520.1	tongue dorsa clone DR034
TM7	Unclassified	sf_1	3679		
TM7	Unclassified	sf_1	2917	AF507686.1	arid soil clone C026
TM7	Unclassified	sf_1	3151	AF513102.1	activated sludge foam clone 71
TM7	Unclassified	sf_1	3025		

TM7	Unclassified	sf_1	5061		
TM7	Unclassified	sf_1	8040	AY005446.1	oral cavity clone BE109
Unclassified	Unclassified	sf_160	226		
Unclassified	Unclassified	sf_160	6430		
Unclassified	Unclassified	sf_95	2545	AB106352.1	anaerobic sludge isolate str. JE
Unclassified	Unclassified	sf_160	6456		
Unclassified	Unclassified	sf_140	6355		
Unclassified	Unclassified	sf_160	10012		
Unclassified	Unclassified	sf_106	243	AF027097.1	hot spring clone OPB25
Unclassified	Unclassified	sf_93	925	AF254404.1	4MB-degrading consortium clone UASB_TL26
Unclassified	Unclassified	sf_160	4410		
Unclassified	Unclassified	sf_160	485	AY193179.1	thermal spring mat clone O1aA90
Unclassified	Unclassified	sf_160	333		
Unclassified	Unclassified	sf_160	651		
Unclassified	Unclassified	sf_160	6360		
Unclassified	Unclassified	sf_160	7767		
Unclassified	Unclassified	sf_160	1914		
Unclassified	Unclassified	sf_34	4668		
Unclassified	Unclassified	sf_156	4291	AF507892.1	Mono Lake at depth 35m station 6 July 2000 clone ML635J-21 G+C
Unclassified	Unclassified	sf_160	2488		
Unclassified	Unclassified	sf_160	7444		
Unclassified	Unclassified	sf_105	1995		
Verrucomicrobia	Xiphinematobacteraceae	sf_3	888	AF217462.1	Candidatus Xiphinematobacter brevicolli
Verrucomicrobia	Unclassified	sf_3	486	AJ401113.1	Elbe river clone DEV045
Verrucomicrobia	Unclassified	sf_5	686	AF419674.1	Guaymas Basin hydrothermal sediment clone a2b018
Verrucomicrobia	Unclassified	sf_4	288	U60012.1	Prosthecobacter dejongeii
Verrucomicrobia	Verrucomicrobia subdivision 5	sf_1	547	AY114329.1	anoxic marine sediment clone LD1-PB1
Verrucomicrobia	Unclassified	sf_3	792	AB089122.1	termite gut homogenate clone Rs-P07 bacterium
Verrucomicrobia	Verrucomicrobia subdivision 7	sf_1	446	AY114322.1	anoxic marine sediment clone LD1-PA34
Verrucomicrobia	Verrucomicrobia subdivision 5	sf_1	533	AY114330.1	anoxic marine sediment clone LD1-PB12
Verrucomicrobia	Verrucomicrobia subdivision 5	sf_1	530	AY114334.1	anoxic marine sediment clone LD1-PB20
Verrucomicrobia	Verrucomicrobia subdivision 7	sf_1	559	AY114314.1	anoxic marine sediment clone LD1-PA20
Verrucomicrobia	Verrucomicrobia subdivision 7	sf_1	760	AF454310.2	Mono lake clone ML316M-1
Verrucomicrobia	Verrucomicrobia subdivision 5	sf_1	629	AY114328.1	anoxic marine sediment clone LD1-PA50
Verrucomicrobia	Unclassified	sf_3	40	AJ401121.1	Elbe river clone DEV055
Verrucomicrobia	Verrucomicrobia subdivision 5	sf_1	885	AJ390455.1	soil clone PBS-III-26
Verrucomicrobia	Unclassified	sf_3	11	AF234711.1	sludge clone H2
Verrucomicrobia	Verrucomicrobiaceae	sf_6	613	AJ441222.1	hydrothermal vent polychaete mucous clone P. palm C 85
Verrucomicrobia	Verrucomicrobiaceae	sf_6	203	AY271254.1	Akkermansia muciniphila
Verrucomicrobia	Verrucomicrobiaceae	sf_6	871		
Verrucomicrobia	Verrucomicrobiaceae	sf_1	1024	AY244959.1	rumen clone BS5
Verrucomicrobia	Verrucomicrobiaceae	sf_7	29	AB073978.1	Fucophilus fucoidanolyticus str. SI-1234
Verrucomicrobia	Unclassified	sf_4	169	AY114317.1	anoxic marine sediment clone LD1-PA26
WS3	Unclassified	sf_1	2537	AY114325.1	anoxic marine sediment clone LD1-PA39
WS3	Unclassified	sf_3	95	AJ535231.1	marine sediment above hydrate ridge clone Hyd24-32
WS5	Unclassified	sf_2	8119	AF419661.1	Guaymas Basin hydrothermal sediment clone a2b013

Table S2. Bacterial taxa detected in significantly altered abundance in CRS patient versus healthy subject sinuses.

Phylum	Family	SF	Taxon ID	prokMSA Name	T value	P value	Q value
Actinobacteria	Corynebacteriaceae	sf_1	1493	Corynebacterium tuberculostearicum str. CIP102346	-2.652	0.034	0.003
TM7	Unclassified	sf_1	5177		2.289	0.045	0.004
Acidobacteria	Acidobacteriaceae	sf_14	208	uranium mill tailings soil sample clone GuBH2-AD-9 sp.	2.348	0.039	0.003
Proteobacteria	Beijerinck/Rhodoplan/Methylocyst	sf_3	7401	Scrippsiella trochoidea NEPCC 15	2.362	0.047	0.004
Actinobacteria	Corynebacteriaceae	sf_1	1820	Corynebacterium jeikeium str. ATCC 43734	2.367	0.049	0.004
Proteobacteria	Enterobacteriaceae	sf_1	8173	Photorhabdus asymbiotica str. ATCC 43949	2.375	0.041	0.003
Actinobacteria	Microbacteriaceae	sf_1	1241	Microbacterium kitamiense CV88	2.378	0.043	0.003
Firmicutes	Aerococcaceae	sf_1	3553	Desemzia incerta str. DSM 20581	2.388	0.036	0.003
Actinobacteria	Pseudonocardiaceae	sf_1	1863		2.405	0.044	0.004
Firmicutes	Bacillaceae	sf_1	3439	Bacillus siralis str. 171544	2.428	0.034	0.003
Proteobacteria	Enterobacteriaceae	sf_1	8504	Dysmicoccus neobrevipes symbiont	2.465	0.042	0.003
Proteobacteria	Neisseriaceae	sf_1	7662	Mars Odyssey Orbiter and encapsulation facility clone T5-1 sp.	2.468	0.035	0.003
Actinobacteria	Pseudonocardiaceae	sf_1	1402		2.469	0.045	0.004
Actinobacteria	Rubrobacteraceae	sf_1	1901	earthworm burrow isolate B33D1	2.486	0.046	0.004
Actinobacteria	Frankiaceae	sf_1	1644	Frankia sp. M16467	2.501	0.042	0.003
Proteobacteria	Pseudomonadaceae	sf_1	8508	Pseudomonas citronellolis str. TERIDB26	2.515	0.044	0.004
Cyanobacteria	Chloroplasts	sf_5	5006		2.517	0.030	0.002
Firmicutes	Lachnospiraceae	sf_5	2961	termite gut homogenate clone Rs-F92 bacterium	2.518	0.029	0.002
Proteobacteria	Unclassified	sf_3	9367	USA: Pacific Ocean seawater Naha Vents Hawaii isolate str. PV-4	2.521	0.037	0.003

Bacteroidetes	Crenotrichaceae	sf_11	6143	Toolik Lake main station at 3 m depth clone TLM09/TLMdgge12a	2.541	0.032	0.003
Actinobacteria	Frankiaceae	sf_1	1161	Frankia sp. MRn2-2	2.547	0.028	0.002
Cyanobacteria	Chloroplasts	sf_13	5000	Mitrastema yamamotoi	2.566	0.027	0.002
Actinobacteria	Mycobacteriaceae	sf_1	1175	Mycobacterium cf. xenopi 'Hymi_Wue Tb_939/99' str. Hymi_Wue Tb_939/99	2.574	0.036	0.003
Proteobacteria	Piscirickettsiaceae	sf_3	8664	Thiomicrospira sp. str. Milos-T2	2.597	0.031	0.003
Proteobacteria	Alteromonadaceae	sf_1	9288	Alteromonas stellipolaris str. LMG 21861	2.597	0.033	0.003
Firmicutes	Unclassified	sf_1	4293	termite gut homogenate clone Rs-Q01 bacterium	2.600	0.025	0.002
Actinobacteria	Nocardiaceae	sf_1	1769	Nocardia sp. str. DSM 46067	2.618	0.029	0.002
Firmicutes	Bacillaceae	sf_1	3661	Bacillus sp. str. 2216.25.2	2.626	0.025	0.002
Bacteroidetes	Flavobacteriaceae	sf_1	5589		2.638	0.034	0.003
Actinobacteria	Actinomycetaceae	sf_1	1227	Actinomyces naeslundii	2.639	0.031	0.003
Firmicutes	Bacillaceae	sf_1	283	Geobacillus thermocatenulatus str. DSM 730	2.640	0.029	0.002
Firmicutes	Bacillaceae	sf_1	3894	Sporosarcina macmurdoensis str. CMS 21w	2.645	0.023	0.002
Firmicutes	Bacillaceae	sf_1	3635	Bacillus aeolius str. 4-1	2.650	0.023	0.002
Proteobacteria	Enterobacteriaceae	sf_1	8236	Vryburgia amaryllidis symbiont	2.654	0.023	0.002
Proteobacteria	Bradyrhizobiaceae	sf_1	7353	temperate estuarine mud clone HC65	2.670	0.025	0.002
Actinobacteria	Rubrobacteraceae	sf_1	1739		2.678	0.021	0.002
Bacteroidetes	Unclassified	sf_15	5355	DCP-dechlorinating consortium clone SHA-5	2.682	0.022	0.002
Proteobacteria	Alteromonadaceae	sf_1	9292		2.691	0.028	0.002
Proteobacteria	Methylophilaceae	sf_1	7892	Methylophilus leisingeri str. DSM 6813	2.696	0.029	0.002
Actinobacteria	Micrococcaceae	sf_1	2019	Micrococcus luteus str. HN2-11	2.706	0.028	0.002

Actinobacteria	Nocardiaceae	sf_1	1834	Nocardia transvalensis str. DSM 43405	2.713	0.031	0.003
Firmicutes	Unclassified	sf_17	602		2.725	0.020	0.002
Actinobacteria	Nocardiaceae	sf_1	1432	Nocardia veterana str. DSM 44445	2.726	0.030	0.002
NC10	Unclassified	sf_1	536	uranium mill tailings clone GuBH2-AD-8	2.735	0.021	0.002
Actinobacteria	Dietziaceae	sf_1	1872	Dietzia maris	2.736	0.031	0.003
Actinobacteria	Streptosporangiaceae	sf_1	1158	Streptosporangium roseum str. DSM43021T	2.739	0.032	0.003
Actinobacteria	Microbacteriaceae	sf_1	1106		2.743	0.025	0.002
Proteobacteria	Unclassified	sf_8	8247		2.743	0.032	0.003
Proteobacteria	Rhodobacteraceae	sf_1	7084	Scrippsiella trochoidea NEPCC 15	2.747	0.028	0.002
Proteobacteria	Methylococcaceae	sf_1	8645	Methylomicrobium buryatense str. 5B	2.748	0.025	0.002
Firmicutes	Bacillaceae	sf_1	3283	Bacillus niacini str. IFO15566	2.754	0.021	0.002
Proteobacteria	Desulfovibrionaceae	sf_1	9826	termite gut homogenate clone Rs-M72 proteobacterium	2.757	0.020	0.002
Actinobacteria	Nocardiaceae	sf_1	1261	Nocardia caishijiensis str. F829	2.757	0.027	0.002
Actinobacteria	Streptosporangiaceae	sf_1	1189	Streptosporangium subroseum str. 7113	2.771	0.031	0.003
Bacteroidetes	Sphingobacteriaceae	sf_1	5913	Sphingobacteriaceae str. Ellin160	2.786	0.018	0.002
Firmicutes	Lachnospiraceae	sf_5	4501	crevicular epithelial cells clone BU014	2.786	0.018	0.002
Proteobacteria	Caedibacteraceae	sf_3	7010	periodontal pocket clone 10B6	2.796	0.018	0.002
Bacteroidetes	Crenotrichaceae	sf_11	5463	Flexibacter sancti str. IFO 16034	2.807	0.018	0.002
Bacteroidetes	Flexibacteraceae	sf_19	5372		2.807	0.022	0.002
Bacteroidetes	Unclassified	sf_15	5783	Mono Lake at depth 35 m station 6 July 2000 clone ML635J-15 bacterium	2.823	0.019	0.002
Proteobacteria	Alteromonadaceae	sf_1	8753	Idiomarina loihiensis str. GSP37	2.831	0.026	0.002

Firmicutes	Lachnospiraceae	sf_5	3089	Ruminococcus obeum	2.839	0.016	0.001
Proteobacteria	Alteromonadaceae	sf_1	8174	attached marine recovered surface clone 17 proteobacterium	2.844	0.023	0.002
Proteobacteria	Xanthomonadaceae	sf_3	8983	Iron oxidising strain ES-1	2.856	0.016	0.001
Firmicutes	Lachnospiraceae	sf_5	3059	Butyrivibrio fibrisolvens str. NCDO 2249	2.858	0.016	0.001
Actinobacteria	Microbacteriaceae	sf_1	1804	Microbacterium resistens str. 2002-59119	2.859	0.023	0.002
Actinobacteria	Microbacteriaceae	sf_1	1779	Microbacterium sp. str. VKM Ac-2048	2.864	0.024	0.002
Proteobacteria	Enterobacteriaceae	sf_1	8607	Amonostherium lichtensioides symbiont	2.867	0.022	0.002
Proteobacteria	Oceanospirillaceae	sf_1	8596	marine clone Arctic95B-7	2.879	0.027	0.002
Actinobacteria	Cellulomonadaceae	sf_1	1240	Cellulomonadaceae str. WB9	2.887	0.025	0.002
Actinobacteria	Nocardioidaceae	sf_1	1854	Aeromicrobium marinum str. T2	2.888	0.022	0.002
Proteobacteria	Piscirickettsiaceae	sf_3	9557	Riftia pachyptila's tube clone R76-B23	2.892	0.019	0.002
Proteobacteria	Unclassified	sf_3	8230		2.914	0.019	0.002
Dictyoglomi	Dictyoglomaceae	sf_9	7579	marine clone Arctic96B-6	2.914	0.018	0.002
Proteobacteria	Rhodocyclaceae	sf_1	7800	sample taken upstream landfill clone BVC77 landfill	2.915	0.021	0.002
Proteobacteria	Succinivibrionaceae	sf_1	8822	Anaerobiospirillum sp. str. 3J102	2.917	0.026	0.002
Proteobacteria	Enterobacteriaceae	sf_1	9266	Parasite BEV of E.variegatus	2.930	0.020	0.002
Proteobacteria	Shewanellaceae	sf_1	8662		2.932	0.023	0.002
Actinobacteria	Rubrobacteraceae	sf_1	1551	soil isolate Ellin301	2.932	0.020	0.002
Actinobacteria	Microbacteriaceae	sf_1	1404	freshwater isolate str. MWH-Ta3	2.935	0.021	0.002
Actinobacteria	Unclassified	sf_3	1201	sponge clone TK39	2.936	0.021	0.002
Proteobacteria	Ralstoniaceae	sf_1	7778	Ralstonia insidiosa str. CCUG 46388	2.937	0.014	0.001

Proteobacteria	Alteromonadaceae	sf_1	8975	Alteromonas sp. str. NIBH P1M3	2.956	0.022	0.002
Firmicutes	Clostridiaceae	sf_12	206	termite gut homogenate clone Rs-P50 bacterium	2.961	0.015	0.001
Actinobacteria	Actinomycetaceae	sf_1	2049	Arcanobacterium haemolyticum str. CIP 103370	2.965	0.019	0.002
Planctomycetes	Anammoxales	sf_4	9662	Great Artesian Basin clone B83	2.988	0.012	0.001
Proteobacteria	Alteromonadaceae	sf_1	9324	Pseudoalteromonas ruthenica str. KMM300	2.991	0.024	0.002
Proteobacteria	Alteromonadaceae	sf_1	9501	sea water isolate str. BP-PH	2.992	0.019	0.002
Proteobacteria	Unclassified	sf_6	7207		2.994	0.021	0.002
Proteobacteria	Rhodocyclaceae	sf_1	7956		2.997	0.014	0.001
Chloroflexi	Unclassified	sf_2	818		2.998	0.016	0.001
Proteobacteria	Enterobacteriaceae	sf_1	9252	Pantoea cedenensis str. A34	2.999	0.020	0.002
Firmicutes	Bacillaceae	sf_1	3836	Geobacillus stearothermophilus str. 46	3.001	0.016	0.001
Nitrospira	Nitrospiraceae	sf_1	864	nitrifying sludge clone GC86	3.005	0.018	0.002
Firmicutes	Bacillaceae	sf_1	3492	Bacillus subtilis str. IAM 12118T	3.009	0.014	0.001
Spirochaetes	Spirochaetaceae	sf_1	6575	TCE-contaminated site clone ccslm226	3.014	0.013	0.001
Actinobacteria	Microbacteriaceae	sf_1	1098		3.017	0.015	0.001
Bacteroidetes	Prevotellaceae	sf_1	5718	Prevotella tannerae str. 29-1	3.023	0.014	0.001
Proteobacteria	Polyangiaceae	sf_3	10249	soil sample uranium mining waste pile clone JG36-TzT-168 proteobacterium	3.033	0.011	0.001
Firmicutes	Lachnospiraceae	sf_5	2834	Butyrivibrio fibrisolvens str. OB156	3.034	0.012	0.001
Proteobacteria	Alteromonadaceae	sf_1	8172	Pseudoalteromonas sp. str. Bdeep-1	3.034	0.020	0.002
Proteobacteria	Unclassified	sf_1	7879		3.034	0.016	0.001
Actinobacteria	Thermomonosporaceae	sf_1	1546	Actinomadura fulvescens str. DSM 43923T	3.044	0.020	0.002

Proteobacteria	Enterobacteriaceae	sf_1	8283	Heteropsylla texana symbiont	3.054	0.018	0.002
Proteobacteria	Enterobacteriaceae	sf_1	9151		3.065	0.019	0.002
Proteobacteria	Unclassified	sf_3	9124	10e-6 dilution marine clone DC8-80-1 proteobacterium	3.071	0.013	0.001
Actinobacteria	Gordoniaceae	sf_1	1567		3.074	0.016	0.001
Proteobacteria	Shewanellaceae	sf_1	8641	Moritella abyssi str. 2693	3.081	0.017	0.001
Bacteroidetes	Crenotrichaceae	sf_11	6249	Haliscomenobacter hydrossis	3.089	0.010	0.001
Proteobacteria	Alteromonadaceae	sf_1	9384	Moritella viscosa str. NVI 88/478T	3.093	0.017	0.001
Firmicutes	Clostridiaceae	sf_12	252	termite gut homogenate clone Rs-A28 bacterium	3.094	0.012	0.001
Firmicutes	Peptostreptococcaceae	sf_5	1037	Finegoldia magna	3.102	0.010	0.001
Firmicutes	Bacillaceae	sf_1	3550	Bacillus megaterium str. QM B1551	3.102	0.014	0.001
Firmicutes	Peptostreptococcaceae	sf_5	616	Peptoniphilus lacrimalis str. CCUG 31350	3.102	0.010	0.001
Proteobacteria	Desulfovibrionaceae	sf_1	10262	Desulfovibrio sp. str. Ac5.2	3.103	0.015	0.001
Firmicutes	Clostridiaceae	sf_12	4551	Clostridium acetobutylicum str. ATCC 824 (T)	3.133	0.013	0.001
Proteobacteria	Alteromonadaceae	sf_1	8579	Psychromonas profunda str. 2825	3.134	0.017	0.001
Proteobacteria	Unclassified	sf_1	8432		3.137	0.018	0.002
Proteobacteria	Unclassified	sf_17	7819		3.140	0.013	0.001
Actinobacteria	Streptosporangiaceae	sf_1	1587	Nonomuraea subsp. roseoviolacea str. SF 2303	3.140	0.019	0.002
Firmicutes	Lachnospiraceae	sf_5	3076	Clostridium nexile	3.142	0.012	0.001
Proteobacteria	Oxalobacteraceae	sf_1	8034	Janthinobacterium agaricidamnosum str. W1r3T	3.151	0.014	0.001
Actinobacteria	Intrasporangiaceae	sf_1	1674	Janibacter terrae str. DSM 13953T	3.170	0.011	0.001
Proteobacteria	Moraxellaceae	sf_3	9359	Acinetobacter junii str. S33	3.172	0.016	0.001

Crenarchaeota	Unclassified	sf_1	2587	hydrothermal vent clone pIVWA11	3.172	0.009	0.001
Proteobacteria	Pseudoalteromonadaceae	sf_1	9627	Pseudoalteromonas sp	3.172	0.016	0.001
Deinococcus-Ther	Unclassified	sf_3	920		3.180	0.009	0.001
Proteobacteria	Alteromonadaceae	sf_1	8932	Pseudoalteromonas antarctica str. N-1	3.190	0.018	0.002
Proteobacteria	Alteromonadaceae	sf_1	9205	marine clone Arctic96B-17	3.196	0.013	0.001
Firmicutes	Clostridiaceae	sf_12	4299	termite gut clone Rs-L02	3.205	0.010	0.001
Proteobacteria	Pasteurellaceae	sf_1	9477	Haemophilus influenzae str. M11105	3.206	0.008	0.001
Proteobacteria	Pseudomonadaceae	sf_1	8725	Pseudomonas sp. str. 2N1-1	3.208	0.017	0.001
Proteobacteria	Moraxellaceae	sf_3	8368	Pseudoalteromonas mariniglutinosa str. KMM 3635	3.213	0.017	0.001
Gemmatimonadet	Unclassified	sf_5	10112	forest soil clone NOS7.157WL	3.217	0.014	0.001
Proteobacteria	Alteromonadaceae	sf_1	9364	Pseudoalteromonas prydzensis str. MB8-11	3.217	0.017	0.001
Proteobacteria	Alteromonadaceae	sf_1	8970	Arctic seawater isolate str. R9879	3.220	0.016	0.001
Proteobacteria	Unclassified	sf_1	8962	bacterioplankton clone AEGEAN_234	3.220	0.011	0.001
Actinobacteria	Actinomycetaceae	sf_1	1672	Actinomyces odontolyticus str. CCUG 28084	3.220	0.014	0.001
Proteobacteria	Enterobacteriaceae	sf_1	8700	Baumannia cicadellinicola	3.221	0.012	0.001
Proteobacteria	Anaplasmataceae	sf_3	7481	Wolbachia pipientis	3.226	0.009	0.001
Nitrospira	Nitrospiraceae	sf_2	542	forested wetland clone FW19	3.227	0.009	0.001
Proteobacteria	Pseudomonadaceae	sf_1	9219	Pseudomonas cf. monteilii 9	3.229	0.016	0.001
Chlorobi	Unclassified	sf_8	5822	Saltmarsh mud clone K-790	3.231	0.009	0.001
Firmicutes	Peptostreptococcaceae	sf_5	861	Peptoniphilus sp. str. 2002-2300004	3.235	0.008	0.001
Acidobacteria	Unclassified	sf_1	87	activated sludge clone 2951	3.235	0.008	0.001

Firmicutes	Bacillaceae	sf_1	3820	Bacillus subtilis str. KL-120	3.237	0.008	0.001
Proteobacteria	Pseudomonadaceae	sf_1	8553	Pseudomonas fulva str. IAM 1587	3.237	0.016	0.001
Actinobacteria	Coriobacteriaceae	sf_1	1800	Tomsk-7 clone S15A-MN100	3.238	0.009	0.001
Firmicutes	Peptococc/Acidaminococc	sf_11	863	Dialister invisus str. E7_25	3.239	0.012	0.001
Proteobacteria	Alcaligenaceae	sf_1	7984	Waste-gas biofilter clone BIfciii38	3.240	0.015	0.001
Proteobacteria	Chromatiaceae	sf_1	8409	human colonic mucosal biopsy clone ABLCf1	3.249	0.017	0.001
Proteobacteria	Alteromonadaceae	sf_1	9218	Pseudoalteromonas haloplanktis str. ATCC 14393	3.249	0.017	0.001
Firmicutes	Unclassified	sf_1	894	coal tar waste-contaminated groundwater clone 36-22 G+C	3.251	0.013	0.001
Verrucomicrobia	Xiphinematobacteraceae	sf_3	888	Candidatus Xiphinematobacter brevicolli	3.251	0.010	0.001
Firmicutes	Peptostreptococcaceae	sf_5	2913	termite gut homogenate clone Rs-N82 bacterium	3.255	0.008	0.001
Bacteroidetes	Crenotrichaceae	sf_11	6123	Flexibacter japonensis str. IFO 16041	3.259	0.010	0.001
Proteobacteria	Phyllobacteriaceae	sf_1	7009		3.261	0.008	0.001
Proteobacteria	Alteromonadaceae	sf_1	8695	Arctic pack ice clone ARKIA-34	3.264	0.014	0.001
Verrucomicrobia	Unclassified	sf_4	288	Prosthecobacter dejongeii	3.276	0.009	0.001
Proteobacteria	Alteromonadaceae	sf_1	9143	Pseudoalteromonas agarivorans str. KMM 255	3.293	0.016	0.001
Firmicutes	Peptostreptococcaceae	sf_5	3153	infirmum str. W 1471	3.294	0.012	0.001
Chlorobi	Unclassified	sf_6	5294	Mammoth cave clone CCM9b	3.304	0.010	0.001
Firmicutes	Lachnospiraceae	sf_5	2825	Butyrivibrio fibrisolvens str. LP1265	3.306	0.008	0.001
Proteobacteria	Unclassified	sf_5	6735	Candidatus Pelagibacter ubique str. HTCC1002	3.309	0.013	0.001
Chlamydiae	Chlamydiaceae	sf_1	4820	Chlamydophila pneumoniae str. AR39	3.314	0.011	0.001
Actinobacteria	Unclassified	sf_3	1296	termite gut homogenate clone Rs-M66 bacterium	3.320	0.010	0.001

Actinobacteria	Streptomycetaceae	sf_1	1436	Streptomyces malaysiensis str. ATB-11	3.321	0.014	0.001
Proteobacteria	Unclassified	sf_4	7105	Mariana trough hydrothermal vent clone MT-NB25	3.322	0.007	0.001
Proteobacteria	Xanthomonadaceae	sf_3	9320	Waste-gas biofilter clone BIyi3	3.324	0.007	0.001
Verrucomicrobia	Verrucomicrobia subdivision 5	sf_1	533	anoxic marine sediment clone LD1-PB12	3.327	0.010	0.001
Firmicutes	Sporolactobacillaceae	sf_1	3879	Lake Elmenteita isolate WE4	3.332	0.007	0.001
Proteobacteria	Alteromonadaceae	sf_1	8580	Arctic seawater isolate str. R7076	3.333	0.015	0.001
Actinobacteria	Microbacteriaceae	sf_1	1667	Microbacterium lacticum	3.333	0.010	0.001
Bacteroidetes	Rikenellaceae	sf_5	5947	hydrothermal vent polychaete mucous clone P. palm C/A 221	3.334	0.012	0.001
Proteobacteria	Pasteurellaceae	sf_1	8952	Actinobacillus lignieresii	3.336	0.014	0.001
Chloroflexi	Unclassified	sf_1	2370	Dehalococcoides ethenogenes str. strain 195	3.340	0.009	0.001
Bacteroidetes	Unclassified	sf_15	5890	penguin droppings sediments clone KD1-125	3.345	0.009	0.001
Proteobacteria	Enterobacteriaceae	sf_1	1206	Dermacentor variabilis symbiont	3.345	0.011	0.001
Fusobacteria	Fusobacteriaceae	sf_3	120	tongue dorsum scrapings clone FP036	3.346	0.009	0.001
Proteobacteria	Unclassified	sf_3	9582		3.348	0.011	0.001
Firmicutes	Peptostreptococcaceae	sf_5	2805	oral periodontitis clone FX033	3.365	0.006	0.001
Proteobacteria	Pasteurellaceae	sf_1	8555	Haemophilus influenzae str. M9741	3.367	0.013	0.001
Proteobacteria	Desulfovibrionaceae	sf_1	10244		3.371	0.007	0.001
Proteobacteria	Alteromonadaceae	sf_1	9369	Pseudoalteromonas luteoviolacea str. NCIMB 1893T	3.371	0.013	0.001
Actinobacteria	Coriobacteriaceae	sf_1	1258	ground water Tomsk-7 clone S15A-MN25	3.371	0.015	0.001
Firmicutes	Halobacillaceae	sf_1	3756	Salibacillus sp. str. YIM-kkny16	3.374	0.009	0.001
Bacteroidetes	Flexibacteraceae	sf_19	6297	EBPR sludge lab scale clone HP1A92	3.382	0.008	0.001

Firmicutes	Clostridiaceae	sf_12	4587	Clostridium botulinum str. 468; toxin type C	3.396	0.006	0.001
Proteobacteria	Unclassified	sf_1	7993	soil clone 1326-2	3.399	0.011	0.001
Proteobacteria	Alcaligenaceae	sf_1	7737	atrazine-catabolizing microbial presence methanol clone KRA30+06A	3.400	0.013	0.001
Proteobacteria	Alteromonadaceae	sf_1	9640	exposed to diatom detritus isolate str. Tw-10 Tw-10	3.400	0.014	0.001
Proteobacteria	Oxalobacteraceae	sf_1	7921	Collimonas fungivorans str. Ter331	3.403	0.010	0.001
Proteobacteria	Moraxellaceae	sf_3	8565	Acinetobacter sp. str. 942 Group BJ17	3.406	0.006	0.001
Firmicutes	Bacillaceae	sf_1	3506	Lake Nakuru isolate 18N1	3.412	0.006	0.001
Acidobacteria	Acidobacteriaceae	sf_14	6424	sphagnum peat bog clone K-5b10	3.413	0.008	0.001
Firmicutes	Lachnospiraceae	sf_5	2844	Pseudobutyrivibrio ruminis str. pC-XS2	3.421	0.006	0.001
Firmicutes	Paenibacillaceae	sf_1	3651	Paenibacillus borealis KK20	3.425	0.007	0.001
Proteobacteria	Alcaligenaceae	sf_1	7838	Alcaligenes defragrans str. PD-19	3.427	0.012	0.001
Proteobacteria	Pseudomonadaceae	sf_1	9238		3.428	0.014	0.001
Actinobacteria	Mycobacteriaceae	sf_1	1365	Mycobacterium chelonae str. CIP 104535T	3.430	0.010	0.001
Proteobacteria	Unclassified	sf_3	8606		3.432	0.012	0.001
Proteobacteria	Pseudomonadaceae	sf_1	9343	Cellvibrio subsp. mixtus str. ACM 2601	3.436	0.012	0.001
Proteobacteria	Pseudomonadaceae	sf_1	9228	Pseudomonas stutzeri HY-105	3.437	0.008	0.001
Proteobacteria	Pseudomonadaceae	sf_1	8344	Anabaena circinalis AWQC118C isolate str. UNSW3	3.438	0.014	0.001
Proteobacteria	Rickettsiaceae	sf_1	6831		3.440	0.007	0.001
Proteobacteria	Alteromonadaceae	sf_1	9058	Pseudoalteromonas carrageenovora str. ATCC 12662T	3.442	0.013	0.001
Actinobacteria	Streptomycetaceae	sf_1	1375	soil clone 228-1	3.451	0.009	0.001
Actinobacteria	Unclassified	sf_3	1900		3.452	0.006	0.001

Proteobacteria	Rhodocyclaceae	sf_1	7817	TCE-contaminated site clone ccs265	3.453	0.013	0.001
Proteobacteria	Alteromonadaceae	sf_1	8904	psychrophile deep-sea Pacific isolate str. PS12-4 PS12-4	3.460	0.011	0.001
Proteobacteria	Pseudomonadaceae	sf_1	8687	Pseudomonas putida str. ATCC 17472	3.467	0.011	0.001
Proteobacteria	Pasteurellaceae	sf_1	9237		3.468	0.013	0.001
Bacteroidetes	Prevotellaceae	sf_1	6066	human mouth isolate str. P4P_62	3.469	0.011	0.001
Proteobacteria	Alteromonadaceae	sf_1	8336	Alteromonas sp. str. MS23	3.470	0.012	0.001
Bacteroidetes	Flammeovirgaceae	sf_5	6084	Microscilla arenaria str. IFO 15982	3.471	0.008	0.001
Firmicutes	Clostridiaceae	sf_12	2915	Tepidibacter thalassicus str. SC 562	3.473	0.006	0.001
Firmicutes	Peptococc/Acidaminococc	sf_11	940	Veillonella dispar str. DSM 20735	3.481	0.012	0.001
Proteobacteria	Azospirillaceae	sf_1	7539	Rhodocista sp. AR2107	3.484	0.006	0.001
Proteobacteria	Pasteurellaceae	sf_1	9263	Actinobacillus capsulatus	3.487	0.013	0.001
Proteobacteria	Unclassified	sf_6	6694	forested wetland clone RCP2-92	3.487	0.005	0.001
Proteobacteria	Anaplasmataceae	sf_3	6628	Wolbachia pipientis	3.489	0.007	0.001
Firmicutes	Streptococcaceae	sf_1	3699	Streptococcus agalactiae str. 2603V/R	3.490	0.006	0.001
Firmicutes	Bacillaceae	sf_1	3419	Bacillus algicola str. KMM 3737	3.492	0.006	0.001
Bacteroidetes	Unclassified	sf_1	5951	CFB group clone ML615J-4	3.493	0.010	0.001
Proteobacteria	Comamonadaceae	sf_1	7965	Anoxobacterium dechloraticum	3.495	0.007	0.001
Gemmatimonadet	Unclassified	sf_5	9464	lodgepole pine rhizosphere soil	3.495	0.010	0.001
Proteobacteria	Pasteurellaceae	sf_1	8195	Haemophilus influenzae str. R2866	3.496	0.013	0.001
Proteobacteria	Comamonadaceae	sf_1	7919	strain isolate str. rM4	3.497	0.005	0.001
Firmicutes	Lachnospiraceae	sf_5	3088	Clostridium sphenoides str. DSM 632	3.499	0.005	0.001

Proteobacteria	Unclassified	sf_20	6763		3.499	0.005	0.001
Proteobacteria	Oxalobacteraceae	sf_1	7968	Oxalobacter formigenes str. OXB ovinen rumen	3.499	0.008	0.001
Verrucomicrobia	Verrucomicrobia subdivision 5	sf_1	885	soil clone PBS-III-26	3.501	0.007	0.001
Acidobacteria	Acidobacteriaceae	sf_14	508	uranium mining waste pile clone JG37-AG-81 sp.	3.508	0.005	0.001
Proteobacteria	Unclassified	sf_3	7974		3.510	0.007	0.001
Bacteroidetes	Blattabacteriaceae	sf_1	5828	Blattabacterium species	3.511	0.012	0.001
Proteobacteria	Burkholderiaceae	sf_1	7914	Burkholderia andropogonis str. ATCC 19311T	3.511	0.005	0.001
Proteobacteria	Pasteurellaceae	sf_1	8228	Actinobacillus indolicus str. H1419	3.511	0.012	0.001
Actinobacteria	Acidimicrobiaceae	sf_1	2014	marine sediment clone MB-A2-100	3.513	0.006	0.001
Proteobacteria	Pseudomonadaceae	sf_1	9175	Pseudomonas extremorientalis str. KMM3447	3.515	0.012	0.001
Unclassified	Unclassified	sf_34	4668		3.516	0.005	0.001
Proteobacteria	Moraxellaceae	sf_3	9641	Acinetobacter haemolyticus	3.517	0.009	0.001
Firmicutes	Clostridiaceae	sf_12	4169		3.521	0.005	0.001
Proteobacteria	Pseudomonadaceae	sf_1	8853	Pseudomonas cichorii str. ATCC 10857T	3.522	0.007	0.001
Acidobacteria	Unclassified	sf_1	500	soil clone RB24	3.525	0.005	0.001
Acidobacteria	Unclassified	sf_1	435	anaerobic VC-degrading enrichment clone VC47 bacterium	3.527	0.006	0.001
Proteobacteria	Alteromonadaceae	sf_1	8863	Alteromonas marina str. SW-47	3.527	0.008	0.001
Proteobacteria	Pseudomonadaceae	sf_1	8852	Pseudomonas stutzeri str. KC	3.539	0.012	0.001
Proteobacteria	Unclassified	sf_1	8533		3.545	0.008	0.001
Firmicutes	Unclassified	sf_4	4503	termite gut homogenate clone Rs-H83 bacterium	3.548	0.006	0.001
NC10	Unclassified	sf_1	10254	uranium mill tailings soil sample clone Sh765B-TzT-35	3.551	0.005	0.001

Proteobacteria	Pasteurellaceae	sf_1	9628	Histophilus somni str. CCUG 12839	3.553	0.010	0.001
Proteobacteria	Alteromonadaceae	sf_1	8222		3.557	0.007	0.001
Actinobacteria	Kineosporiaceae	sf_1	1581	Cryptosporangium aurantiacum str. IMSNU 22120	3.557	0.009	0.001
Firmicutes	Sporolactobacillaceae	sf_1	3747	Bacillus sp. str. C-59-2	3.563	0.006	0.001
Actinobacteria	Unclassified	sf_3	1348	lichen-dominated Antarctic cryptoendolithic community clone FBP406	3.564	0.005	0.001
Proteobacteria	Unclassified	sf_3	9498		3.575	0.005	0.001
Proteobacteria	Alteromonadaceae	sf_1	8978	Arctic sea ice ARK10108	3.577	0.009	0.001
Proteobacteria	Methylophilaceae	sf_1	8137	freshwater clone PRD01a011B	3.577	0.006	0.001
Firmicutes	Bacillaceae	sf_1	3730	Bacillus baekryungensis str. SW-93	3.580	0.005	0.001
Cyanobacteria	Unclassified	sf_5	270	drinking water system simulator clone HOClCi9	3.581	0.004	0.000
Proteobacteria	Alteromonadaceae	sf_1	9386	Alteromonas sp. str. NIBH P2M11	3.583	0.010	0.001
Actinobacteria	Microbacteriaceae	sf_1	1921	Firmicutes isolate str. d8	3.584	0.009	0.001
Proteobacteria	Oxalobacteraceae	sf_1	8032	Aquaspirillum arcticum str. IAM 14963	3.589	0.009	0.001
Firmicutes	Peptostreptococcaceae	sf_5	134	Peptoniphilus asaccharolyticus str. CCUG 9988	3.590	0.004	0.000
Proteobacteria	Oxalobacteraceae	sf_1	8058	Herbaspirillum seropedicae str. DSM 6445 ATCC 35892	3.597	0.009	0.001
Proteobacteria	Pseudomonadaceae	sf_1	9028	Pseudomonas koreensis str. Ps 9-14	3.601	0.010	0.001
Firmicutes	Enterococcaceae	sf_1	3392	Vagococcus lutrae str. m1134/97/1; CCUG 39187	3.601	0.011	0.001
Proteobacteria	Desulfobulbaceae	sf_1	10047	epibiontic clone C11-D3	3.603	0.005	0.001
Bacteroidetes	Porphyromonadaceae	sf_1	5454	Dysgonomonas wimpennyi str. ANFA2	3.606	0.006	0.001
Proteobacteria	Oxalobacteraceae	sf_1	8158	2-HNA producing isolate MC13289	3.611	0.008	0.001
Fusobacteria	Fusobacteriaceae	sf_3	558	Sneathia sanguinegens str. CCUG 41628T	3.612	0.007	0.001

Proteobacteria	Hyphomicrobiaceae	sf_1	7646	Hyphomicrobium aestuarii str. DSM 1564	3.614	0.005	0.000
Proteobacteria	Pasteurellaceae	sf_1	9349	Pasteurella sp. str. 91985	3.620	0.008	0.001
Firmicutes	Aerococcaceae	sf_1	3631	Abiotrophia defectiva str. GIFU12707 (ATCC49176)	3.629	0.012	0.001
Proteobacteria	Burkholderiaceae	sf_1	8059	Burkholderia caribensis str. MWAP71	3.629	0.006	0.001
Proteobacteria	Oxalobacteraceae	sf_1	7878	napthalene-contaminated sediment clone 29	3.632	0.008	0.001
Planctomycetes	Anammoxales	sf_4	4694	USA: Colorado Fort collins Horsetooth Reservoir clone HT2F11	3.632	0.008	0.001
Actinobacteria	Nocardiaceae	sf_1	1917	Nocardia otitidiscaviarum str. DSM43242	3.634	0.007	0.001
Proteobacteria	Pseudomonadaceae	sf_1	8754	Pseudomonas sp. str. P400Y-1	3.634	0.011	0.001
Actinobacteria	Unclassified	sf_2	1652	marine sediment clone Bol7	3.634	0.007	0.001
Proteobacteria	Pseudomonadaceae	sf_1	9366	Arctic seawater isolate str. R7366	3.637	0.009	0.001
Proteobacteria	Desulfomicrobiaceae	sf_1	10370	Desulfomicrobium baculatum str. X; VKM B-1378; DSM 4	3.638	0.005	0.001
Actinobacteria	Unclassified	sf_1	1676		3.639	0.007	0.001
Nitrospira	Nitrospiraceae	sf_1	179	Great Artesian Basin clone G19	3.640	0.005	0.001
Proteobacteria	Rhodobacteraceae	sf_1	7433	Scrippsiella trochoidea NEPCC 15	3.640	0.006	0.001
Actinobacteria	Streptomycetaceae	sf_3	1743	Streptomyces scabiei str. DNK-G01	3.640	0.007	0.001
Proteobacteria	Alcaligenaceae	sf_1	7992	Alcaligenes faecalis 5659-H	3.642	0.009	0.001
Proteobacteria	Unclassified	sf_1	9008	activated sludge clone SBRQ157	3.644	0.005	0.001
Proteobacteria	Pseudomonadaceae	sf_1	8777	Pseudomonas sp. str. KNA6-5	3.644	0.011	0.001
Proteobacteria	Unclassified	sf_1	8323	hydrothermal sediment clone AF420363	3.648	0.008	0.001
Firmicutes	Unclassified	sf_17	2659		3.648	0.005	0.001
Proteobacteria	Desulfobacteraceae	sf_5	9777	Guaymas Basin hydrothermal vent sediments clone B01R004	3.649	0.005	0.000

Proteobacteria	Moraxellaceae	sf_3	9428	hydrocarbon-degrading consortium clone AF2-1D	3.652	0.008	0.001
Proteobacteria	Ralstoniaceae	sf_1	7823	Wautersia basilensis str. DSM 11853	3.652	0.007	0.001
Proteobacteria	Pseudomonadaceae	sf_1	8708		3.657	0.010	0.001
Acidobacteria	Acidobacteriaceae	sf_14	6410		3.659	0.004	0.000
Proteobacteria	Pasteurellaceae	sf_1	8433	Pseudomonas syringae pv. broussonetiae str. KOZ 8101 pv.	3.662	0.009	0.001
Actinobacteria	Streptomycetaceae	sf_1	1786	Streptomyces bikiniensis str. DSM40581	3.670	0.004	0.000
Firmicutes	Bacillaceae	sf_1	3763	Geobacillus stearothermophilus	3.674	0.005	0.001
Proteobacteria	Pseudomonadaceae	sf_1	8601	Pseudomonas marginalis str. ATCC 10844T	3.675	0.009	0.001
Proteobacteria	Pseudomonadaceae	sf_1	8338	Pseudomonas synxantha str. DSM 13080 G	3.677	0.009	0.001
Firmicutes	Bacillaceae	sf_1	3589	Bacillus senegalensis str. RS8; CIP 106 669	3.679	0.004	0.000
Proteobacteria	Unclassified	sf_3	8327	Arctic sea ice ARK10148	3.681	0.009	0.001
Proteobacteria	Unclassified	sf_1	9316		3.682	0.004	0.000
Proteobacteria	Pasteurellaceae	sf_1	9030	Volucribacter amazonae str. B96/5	3.683	0.010	0.001
Actinobacteria	Streptomycetaceae	sf_1	1983	Streptomyces cinnabarinus str. ISP 5467	3.686	0.004	0.000
Proteobacteria	Alteromonadaceae	sf_1	8196		3.686	0.006	0.001
Actinobacteria	Unclassified	sf_4	1337	Sturt arid-zone soil clone #0425-2M17	3.691	0.007	0.001
Cyanobacteria	Chloroplasts	sf_11	5123	Lepocinclis fusiformis str. ACOI 1025	3.693	0.006	0.001
Proteobacteria	Pseudomonadaceae	sf_1	9221	Pseudomonas fulgida str. DSM 14938 = LMG 2146 P 515/12	3.695	0.009	0.001
Proteobacteria	Acidithiobacillaceae	sf_1	9224	Acidithiobacillus albertensis str. DSM 14366	3.697	0.007	0.001
Proteobacteria	Pseudomonadaceae	sf_1	9056	Pseudomonas aeruginosa str. #47	3.698	0.010	0.001
Proteobacteria	Moraxellaceae	sf_3	9466	Acinetobacter tandoii str. 4N13	3.698	0.010	0.001

Proteobacteria	Xanthomonadaceae	sf_3	8577	Xanthomonas axonopodis pv. citri str. MA	3.700	0.004	0.000
Proteobacteria	Acetobacteraceae	sf_1	6637	Acetobacter aceti str. NCIB8621 DSM3508	3.701	0.007	0.001
Proteobacteria	Ralstoniaceae	sf_1	8128	Cupriavidus necator	3.701	0.007	0.001
Actinobacteria	Cellulomonadaceae	sf_1	1589	Oerskovia turbata str. DSM 20577T	3.702	0.006	0.001
Verrucomicrobia	Unclassified	sf_3	11	sludge clone H2	3.706	0.005	0.001
Actinobacteria	Acidimicrobiaceae	sf_1	1856	forested wetland clone RCP2-105	3.706	0.005	0.001
Firmicutes	Peptococc/Acidaminococc	sf_11	150		3.707	0.013	0.001
Firmicutes	Peptostreptococcaceae	sf_5	2710	DCP-dechlorinating consortium clone SHA-74	3.709	0.005	0.001
Chloroflexi	Unclassified	sf_5	1051	forest soil clone DUNssu055 (-2B) (OTU#087)	3.710	0.003	0.000
Proteobacteria	Desulfobulbaceae	sf_1	10062	marine sediment above hydrate ridge clone Hyd24-11 proteobacterium	3.710	0.004	0.000
Proteobacteria	Enterobacteriaceae	sf_1	8286	Cyphonococcus alpinus symbiont	3.717	0.008	0.001
Acidobacteria	Acidobacteriaceae	sf_6	6362	grassland soil clone DA052	3.717	0.006	0.001
Proteobacteria	Pseudomonadaceae	sf_1	9172	Pseudomonas psychrophila str. E-3	3.722	0.008	0.001
Proteobacteria	Moraxellaceae	sf_3	8604	Moraxella oblonga str. IAM 14971	3.725	0.005	0.001
Firmicutes	Unclassified	sf_4	2716	termite gut homogenate clone Rs-F76 bacterium	3.730	0.004	0.000
Proteobacteria	Alteromonadaceae	sf_1	8503	Arctic sea ice ARK10244	3.730	0.005	0.001
Proteobacteria	Ralstoniaceae	sf_1	7761	Ralstonia detusculanense str. APF11	3.730	0.008	0.001
Actinobacteria	Brevibacteriaceae	sf_1	1745	Brevibacterium iodinum str. DSM 2062T	3.731	0.007	0.001
Unclassified	Unclassified	sf_160	226		3.732	0.005	0.001
Cyanobacteria	Unclassified	sf_1	5057	Nodularia sphaerocarpa str. UTEX B 2093	3.735	0.004	0.000
Proteobacteria	Pseudomonadaceae	sf_1	8561	Pseudomonas sp. B65	3.736	0.009	0.001

Proteobacteria	Alteromonadaceae	sf_1	9486	Marine isolate str. GK-2001	3.739	0.007	0.001
Firmicutes	Halobacillaceae	sf_1	3552	Paraliobacillus ryukyuensis	3.739	0.005	0.000
OP8	Unclassified	sf_3	598	Guaymas Basin hydrothermal sediment clone a2b010	3.742	0.006	0.001
Aquificae	Unclassified	sf_1	2364	Thermovibrio ammoniificans str. HB-1	3.743	0.005	0.001
Unclassified	Unclassified	sf_95	2545	anaerobic sludge isolate str. JE	3.746	0.008	0.001
Spirochaetes	Spirochaetaceae	sf_1	6465	Spirochaeta sp. str. Grapes	3.749	0.003	0.000
Verrucomicrobia	Verrucomicrobia subdivision 5	sf_1	629	anoxic marine sediment clone LD1-PA50	3.750	0.004	0.000
Proteobacteria	Saccharospirillaceae	sf_1	8889	hypersaline Mono Lake clone ML110J-5	3.751	0.009	0.001
Proteobacteria	Pseudomonadaceae	sf_1	8691	Pseudomonas aeruginosa str. PAO1	3.753	0.009	0.001
Proteobacteria	Pseudomonadaceae	sf_1	9493	Pseudomonas sp. str. dcm7B	3.755	0.008	0.001
Actinobacteria	Streptomycetaceae	sf_1	1771	Streptomyces setonii str. ATCC25497	3.758	0.003	0.000
Chloroflexi	Unclassified	sf_1	1071	denitrifying reactor clone 131	3.761	0.004	0.000
Proteobacteria	Alteromonadaceae	sf_1	9068	Pseudomonas stutzeri str. A1501	3.764	0.009	0.001
Proteobacteria	Unclassified	sf_6	6987		3.768	0.007	0.001
Bacteroidetes	Porphyromonadaceae	sf_1	5800	Porphyromonas endodontalis str. ATCC 35406	3.776	0.008	0.001
OP9/JS1	Unclassified	sf_1	726	hot spring clone OPB72	3.777	0.006	0.001
Proteobacteria	Unclassified	sf_1	9282		3.779	0.004	0.000
Firmicutes	Lachnospiraceae	sf_5	3066	Clostridium methoxybenzovorans str. SR3; DSM 12182	3.780	0.003	0.000
Cyanobacteria	Chloroplasts	sf_11	5098	Euglena tripteris str. UW OB	3.786	0.006	0.001
Proteobacteria	Pasteurellaceae	sf_1	8861	Haemophilus parasuis 427	3.788	0.009	0.001
Proteobacteria	Rhodobacteraceae	sf_1	6991	Rhodobacter sphaeroides str. 2.4.1	3.789	0.004	0.000

Actinobacteria	Unclassified	sf_3	1130	Georgenia muralis str. 1A-C	3.791	0.004	0.000
LD1PA group	Unclassified	sf_1	10118	anoxic marine sediment clone LD1-PA38	3.792	0.004	0.000
Proteobacteria	Shewanellaceae	sf_1	8201	Shewanella surugaensis str. c959	3.792	0.007	0.001
Firmicutes	Thermoactinomycetaceae	sf_1	3539	Laceyella sacchari str. KCTC 9789 ()	3.794	0.003	0.000
Proteobacteria	Burkholderiaceae	sf_1	8011	Burkholderia graminis str. AUS35	3.797	0.004	0.000
Cyanobacteria	Chloroplasts	sf_5	5166		3.798	0.004	0.000
Firmicutes	Erysipelotrichaceae	sf_3	4038	Bulleidia moorei str. JCM 10647 RCA59-77	3.803	0.004	0.000
Actinobacteria	Dermabacteraceae	sf_1	1504	Brachybacterium sacelli str. LMG 20338	3.812	0.006	0.001
Firmicutes	Paenibacillaceae	sf_1	3559	Paenibacillus turicensis str. MOL722	3.816	0.004	0.000
Actinobacteria	Streptomycetaceae	sf_1	1617	soil clone 41-1	3.818	0.004	0.000
Firmicutes	Bacillaceae	sf_1	3540	Geobacillus thermoleovorans str. B23	3.818	0.003	0.000
Proteobacteria	Xanthomonadaceae	sf_3	9286	Stenotrophomonas maltophilia str. LMG 11104	3.818	0.005	0.001
Proteobacteria	Xanthobacteraceae	sf_1	6660	Azorhizobium caulinodans str. ORS 571	3.819	0.003	0.000
Firmicutes	Streptococcaceae	sf_1	3446	Streptococcus bovis str. HJ50	3.820	0.008	0.001
Bacteroidetes	Prevotellaceae	sf_1	6011	rumen clone F24-B03	3.821	0.008	0.001
Bacteroidetes	Unclassified	sf_15	6233	oral periodontitis clone FX069	3.825	0.006	0.001
Proteobacteria	Desulfobulbaceae	sf_1	10107	marine sediment above hydrate ridge clone Hyd24-30 proteobacterium	3.830	0.007	0.001
Proteobacteria	Pseudomonadaceae	sf_1	9295		3.830	0.009	0.001
Firmicutes	Peptostreptococcaceae	sf_5	3112	Evry municipal wastewater treatment plant clone 012C11_B_SD_P15	3.832	0.003	0.000
Proteobacteria	Nitrosomonadaceae	sf_1	7931	Nitrosospira multiformis	3.832	0.005	0.001
Proteobacteria	Pseudomonadaceae	sf_1	9588	Pseudomonas citronellolis str. TERIDB18	3.832	0.008	0.001

Actinobacteria	Streptomycetaceae	sf_1	1690	Streptomyces galbus str. DSM40480	3.832	0.003	0.000
Proteobacteria	Rhodobacteraceae	sf_1	7263		3.834	0.004	0.000
Firmicutes	Clostridiaceae	sf_12	4157	termite gut homogenate clone Rs-A15 bacterium	3.836	0.004	0.000
Proteobacteria	Moraxellaceae	sf_3	8727	Alkanindiges hongkongensis str. HKU9	3.839	0.006	0.001
Proteobacteria	Oxalobacteraceae	sf_1	8013	isolate str. A1020	3.845	0.006	0.001
Thermodesulfobac	Thermodesulfobacteriaceae	sf_1	667	Geothermobacterium ferrireducens	3.847	0.006	0.001
Actinobacteria	Streptomycetaceae	sf_1	1544	Kitasatospora cystarginea str. IFO14836T	3.848	0.004	0.000
Proteobacteria	Oxalobacteraceae	sf_1	7843	Massilia timonae timone	3.852	0.005	0.001
Proteobacteria	Coxiellaceae	sf_3	9444	forested wetland clone FW23	3.859	0.005	0.001
Firmicutes	Streptococcaceae	sf_1	3397	Streptococcus macedonicus str. ACA-DC 206 LAB617	3.862	0.008	0.001
Unclassified	Unclassified	sf_160	1914		3.865	0.003	0.000
Bacteroidetes	Unclassified	sf_15	5257	marine? clone KD3-67	3.869	0.003	0.000
Proteobacteria	Anaplasmataceae	sf_3	6908	Rhinocyllus conicus endosymbiont	3.870	0.003	0.000
Cyanobacteria	Unclassified	sf_5	5030	Hapalosiphon welwitschii	3.871	0.003	0.000
Actinobacteria	Actinomycetaceae	sf_1	2039	Actinomyces cardiffensis str. CCUG 44997	3.875	0.003	0.000
Cyanobacteria	Unclassified	sf_5	5015	Chlorogloeopsis fritschii str. PCC 6912	3.878	0.003	0.000
Chloroflexi	Unclassified	sf_2	789	travertine hot spring clone SM1D10	3.879	0.003	0.000
Proteobacteria	Enterobacteriaceae	sf_1	8513	Pseudomonas monteilii str. CIP 104883	3.881	0.007	0.001
Actinobacteria	Unclassified	sf_3	1243	termite gut homogenate clone Rs-M95 bacterium	3.883	0.004	0.000
Chlorobi	Chlorobiaceae	sf_1	262	Chlorobium ferrooxidans DSM 13031 str. KofoX	3.884	0.003	0.000
Planctomycetes	Anammoxales	sf_4	4695	Crater Lake clone CL500-15	3.885	0.004	0.000

Actinobacteria	Unclassified	sf_1	1666		3.886	0.003	0.000
Proteobacteria	Legionellaceae	sf_1	8865	Arctic pack ice; clone ARKCH2Br2-23	3.889	0.007	0.001
Proteobacteria	Burkholderiaceae	sf_1	8097	Burkholderia cepacia	3.895	0.004	0.000
Firmicutes	Bacillaceae	sf_1	305	Bacillus thermoleovorans	3.898	0.003	0.000
Proteobacteria	Pseudomonadaceae	sf_1	9267	Pseudomonas syringae pv. theae str. PT1	3.898	0.007	0.001
Firmicutes	Mycoplasmataceae	sf_1	4014	Mycoplasma pulmonis str. UAB CTIP	3.899	0.003	0.000
Actinobacteria	Nocardiaceae	sf_1	2048	Nocardia uniformis str. DSM 43136	3.905	0.004	0.000
Proteobacteria	Unclassified	sf_3	8714	Marinobacter hydrocarbonoclasticus str. ATCC 27132T	3.908	0.006	0.001
Firmicutes	Peptococc/Acidaminococc	sf_11	865	Selenomonas sputigena str. ATCC 35185	3.910	0.009	0.001
Proteobacteria	Alteromonadaceae	sf_1	8374	Agarivorans albus str. MKT 89	3.915	0.005	0.001
Proteobacteria	Coxiellaceae	sf_3	8969	uranium mining waste clone JG30-KF-C15 proteobacterium	3.915	0.004	0.000
Cyanobacteria	Unclassified	sf_1	5189	Oscillatoria sancta str. PCC 7515	3.922	0.002	0.000
Bacteroidetes	Flexibacteraceae	sf_19	5542	Cytophaga sp. I-1787	3.923	0.004	0.000
Firmicutes	Lachnospiraceae	sf_5	2804	Clostridium amygdalinum str. BR-10	3.925	0.002	0.000
Proteobacteria	Acidithiobacillaceae	sf_1	8552	Acidithiobacillus ferrooxidans str. D2	3.925	0.005	0.001
NC10	Unclassified	sf_1	452	vadose clone 5G01	3.926	0.003	0.000
Gemmatimonadete	Unclassified	sf_5	2047	soil clone #0319-7G21	3.928	0.004	0.000
Proteobacteria	Pseudomonadaceae	sf_1	9469	cf. Pseudomonas sp. clone Llangefni 52	3.929	0.007	0.001
Firmicutes	Unclassified	sf_6	149	Streptococcus pleomorphus	3.930	0.006	0.001
Acidobacteria	Acidobacteriaceae	sf_14	105	marine sediment above hydrate ridge clone Hyd24-44 sp.	3.931	0.004	0.000
Proteobacteria	Pseudomonadaceae	sf_1	9243	Pseudomonas tolaasii str. LMG 2342T ()	3.934	0.007	0.001

Proteobacteria	Desulfobulbaceae	sf_1	10097	inactive deep-sea hydrothermal vent chimneys clone IndB2-42	3.938	0.004	0.000
Bacteroidetes	Porphyromonadaceae	sf_1	5460	mouse feces clone F8	3.940	0.006	0.001
Proteobacteria	Alteromonadaceae	sf_1	8318	Aestuariibacter salexigens str. JC2042	3.941	0.006	0.001
Proteobacteria	Halomonadaceae	sf_1	8317	Chromohalobacter canadensis str. DSM6769	3.941	0.004	0.000
Proteobacteria	Enterobacteriaceae	sf_1	8532		3.943	0.003	0.000
Firmicutes	Lachnospiraceae	sf_5	4539	termite gut homogenate clone Rs-C61 bacterium	3.951	0.003	0.000
Proteobacteria	Desulfobulbaceae	sf_1	9734	Riftia pachyptila's tube clone R103-B13	3.951	0.004	0.000
Firmicutes	Streptococcaceae	sf_1	3560	Streptococcus gallinaceus str. CCUG 42692	3.952	0.007	0.001
Firmicutes	Lachnospiraceae	sf_5	3001	human colonic clone HuCA20	3.952	0.003	0.000
Proteobacteria	Enterobacteriaceae	sf_1	8182	Proteus vulgaris str. IFAM 1731	3.955	0.005	0.001
Proteobacteria	Burkholderiaceae	sf_1	7771	Burkholderia glathei str. ATCC 29195T	3.955	0.003	0.000
Firmicutes	Lachnospiraceae	sf_5	2784	human colonic clone HuCB12	3.960	0.002	0.000
Gemmatimonadete	Unclassified	sf_5	442	forest soil clone S0134	3.961	0.006	0.001
Firmicutes	Bacillaceae	sf_1	3675	Bacillus mojavensis str. M-1	3.963	0.003	0.000
Firmicutes	Peptostreptococcaceae	sf_5	17	Peptostreptococcus sp. oral clone P4PA_156 P4 oral	3.963	0.002	0.000
Proteobacteria	Beijerinck/Rhodoplan/Methylocyst	sf_3	7153	Methylocella tundrae str. Y1	3.966	0.002	0.000
Firmicutes	Lachnospiraceae	sf_5	2937	swine intestine clone p-2482-18B5	3.967	0.002	0.000
Bacteroidetes	Unclassified	sf_1	5745		3.968	0.007	0.001
Proteobacteria	Polyangiaceae	sf_3	9912	uranium mining waste pile clone JG34-KF-14 proteobacterium	3.969	0.004	0.000
Proteobacteria	Phyllobacteriaceae	sf_1	7497	Pseudaminobacter salicylatoxidans str. KTC001	3.974	0.002	0.000
Firmicutes	Streptococcaceae	sf_1	3313	Streptococcus salivarius str. ATCC 7073	3.978	0.006	0.001

Proteobacteria	Alcaligenaceae	sf_1	7788	atrazine-catabolizing microbial absence methanol clone KRA30-58	3.979	0.004	0.000
Proteobacteria	Anaplasmataceae	sf_3	6803	Wolbachia sp. Dlem16SWol	3.982	0.002	0.000
Firmicutes	Bacillaceae	sf_1	3831	Bacillus licheniformis str. KL-068	3.989	0.004	0.000
Proteobacteria	Rickettsiaceae	sf_1	7556	Rickettsia bellii str. strains 369-C and G2D42	3.989	0.004	0.000
Proteobacteria	Burkholderiaceae	sf_1	8068	Burkholderia caryophylli str. ATCC 25418	3.990	0.004	0.000
Firmicutes	Peptostreptococcaceae	sf_5	2679	termite gut homogenate clone BCf9-13	3.993	0.002	0.000
Unclassified	Unclassified	sf_93	925	4MB-degrading consortium clone UASB_TL26	3.995	0.005	0.001
Proteobacteria	Pseudomonadaceae	sf_1	9310	Pseudomonas sp. str. AC-167	4.000	0.005	0.000
Firmicutes	Lactobacillaceae	sf_1	3768	Lactobacillus perolens str. L532	4.001	0.004	0.000
Proteobacteria	Unclassified	sf_1	10092	heavy metal-contaminated soil clone a13134	4.005	0.002	0.000
Actinobacteria	Unclassified	sf_1	1217	DCP-dechlorinating consortium clone SHA-34	4.007	0.003	0.000
Actinobacteria	Acidimicrobiaceae	sf_1	2030	forested wetland clone RCP1-33	4.007	0.002	0.000
Actinobacteria	Thermomonosporaceae	sf_1	1669	Pseudonocardiaceae str. PA123	4.010	0.002	0.000
Nitrospira	Nitrospiraceae	sf_2	544	forested wetland clone FW5	4.014	0.002	0.000
Proteobacteria	Pseudomonadaceae	sf_1	8484	Alteromonadaceae isolate str. LA50	4.017	0.003	0.000
Proteobacteria	Pseudomonadaceae	sf_1	8263		4.018	0.006	0.001
Proteobacteria	Coxiellaceae	sf_3	9198	uranium mining waste pile clone KF-JG30-B15 KF-JG30-B15	4.022	0.005	0.001
Proteobacteria	Unclassified	sf_1	8605	bacterioplankton clone ZA2525c	4.030	0.002	0.000
Verrucomicrobia	Verrucomicrobia subdivision 5	sf_1	530	anoxic marine sediment clone LD1-PB20	4.030	0.003	0.000
Proteobacteria	Xanthomonadaceae	sf_3	9270	Stenotrophomonas rhizophila str. e-p10	4.031	0.005	0.001
Firmicutes	Unclassified	sf_17	4307		4.031	0.005	0.001

Proteobacteria	Unclassified	sf_3	8245		4.034	0.003	0.000
Bacteroidetes	Prevotellaceae	sf_1	6047	deep marine sediment clone MB-A2-107	4.038	0.006	0.001
Acidobacteria	Acidobacteriaceae	sf_14	6368	soil clone UA2	4.042	0.005	0.001
Firmicutes	Bacillaceae	sf_1	3612	Bacillus schlegelii str. ATCC 43741T	4.042	0.004	0.000
Actinobacteria	Acidimicrobiaceae	sf_1	1360	forested wetland clone RCP2-103	4.042	0.003	0.000
Proteobacteria	Acidithiobacillaceae	sf_1	8320	acid mine drainage clone BA11	4.044	0.005	0.001
Firmicutes	Caryophanaceae	sf_1	3285	Caryophanon latum str. DSM 14151	4.045	0.003	0.000
Actinobacteria	Nocardiaceae	sf_1	1146	Nocardia otitidiscaviarum str. S639	4.048	0.004	0.000
Actinobacteria	Nocardiaceae	sf_1	1142		4.049	0.002	0.000
Proteobacteria	Pasteurellaceae	sf_1	9360	Pasteurella multocida subsp. gallicida str. MCCM 00021 subsp.	4.049	0.006	0.001
Proteobacteria	Thiotrichaceae	sf_3	8487		4.049	0.005	0.001
Proteobacteria	Rhodocyclaceae	sf_1	8156	industrial-phenol-degrading community clone MM1 sp.	4.050	0.004	0.000
Firmicutes	Streptococcaceae	sf_1	3287	tongue dorsum scrapings clone FP015	4.054	0.006	0.001
Bacteroidetes	Prevotellaceae	sf_1	5484	oral periodontitis clone FX046	4.059	0.006	0.001
Proteobacteria	Pseudomonadaceae	sf_1	9005	Pseudomonas sp. str. KY	4.061	0.006	0.001
Proteobacteria	Pseudomonadaceae	sf_1	8755	Pseudomonas sp. SK-1-3-1	4.063	0.006	0.001
Proteobacteria	Unclassified	sf_1	7264	Bosea thiooxidans TJ1	4.063	0.002	0.000
Actinobacteria	Dermatophilaceae	sf_1	1852	Tonsillophilus suis str. HT1-19	4.064	0.002	0.000
Actinobacteria	Streptosporangiaceae	sf_1	1190	Nonomuraea polychroma str. IFO 14345	4.065	0.004	0.000
Firmicutes	Peptococc/Acidaminococc	sf_11	275	clone AKS21	4.065	0.002	0.000
Proteobacteria	Comamonadaceae	sf_1	7949	Variovorax paradoxus TG27	4.067	0.002	0.000

Proteobacteria	Unclassified	sf_1	7808	Mammoth cave clone CCU25	4.069	0.004	0.000
Proteobacteria	Aeromonadaceae	sf_1	8366	Psychrobacter frigidicola str. DSM 12411	4.070	0.003	0.000
Firmicutes	Streptococcaceae	sf_1	3250	Streptococcus bovis str. B315	4.071	0.006	0.001
Firmicutes	Streptococcaceae	sf_1	3906	Streptococcus bovis str.ATCC 43143	4.071	0.006	0.001
Proteobacteria	Burkholderiaceae	sf_1	7969	Burkholderia sp.	4.072	0.003	0.000
WS5	Unclassified	sf_2	8119	Guaymas Basin hydrothermal sediment clone a2b013	4.073	0.002	0.000
Synergistes	Unclassified	sf_3	719	Synergistes sp. P1 str. P4G_18	4.075	0.004	0.000
Proteobacteria	Unclassified	sf_1	7818	soil sample uranium clone JG36-TzT-215 proteobacterium	4.080	0.005	0.001
Coprothermobacte	Unclassified	sf_1	751	Coprothermobacter sp. str. Dex80-3	4.088	0.004	0.000
Proteobacteria	Nitrosomonadaceae	sf_1	7682	Nitrosovibrio sp. str. RY6A	4.088	0.004	0.000
Proteobacteria	Coxiellaceae	sf_3	8474	ground water Tomsk-7 clone S15A-MN7 proteobacterium	4.088	0.006	0.001
Proteobacteria	Alteromonadaceae	sf_1	9236	attached marine recovered surface clone 18 proteobacterium	4.088	0.005	0.001
Proteobacteria	Unclassified	sf_1	10543	hydrothermal vent clone PVB_10	4.089	0.002	0.000
marine group A	Unclassified	sf_1	6454	marine clone SAR406	4.091	0.002	0.000
Synergistes	Unclassified	sf_3	60	Flexistipes sp. str. E3_33	4.091	0.004	0.000
Actinobacteria	Thermomonosporaceae	sf_1	1741	Actinomadura pelletieri str. IMSNU 22169T	4.092	0.002	0.000
Synergistes	Unclassified	sf_3	740	swine intestine clone p-4292-4Wa3	4.094	0.004	0.000
Bacteroidetes	Prevotellaceae	sf_1	5905	swine intestine clone p-2443-18B5	4.096	0.006	0.001
Verrucomicrobia	Verrucomicrobiaceae	sf_6	203	Akkermansia muciniphila	4.097	0.002	0.000
Actinobacteria	Nocardiopsaceae	sf_1	1385	Streptomonospora salina str. YIM90002	4.099	0.002	0.000
Proteobacteria	Thiotrichaceae	sf_3	9321	marine sediment clone Tokyo Bay D	4.100	0.003	0.000

Proteobacteria	Rhizobiaceae	sf_1	7051	Mycoplana dimorpha str. IAM 13154	4.100	0.002	0.000
Firmicutes	Clostridiaceae	sf_12	4187	Clostridiales oral clone P4PB_122 P3	4.101	0.003	0.000
Proteobacteria	Unclassified	sf_1	8654	inactive deep-sea hydrothermal vent chimneys clone IheB2-31	4.107	0.003	0.000
OD1	Unclassified	sf_1	515		4.109	0.002	0.000
Proteobacteria	Xanthomonadaceae	sf_3	9167	pea aphid symbiont clone APe4_38	4.109	0.002	0.000
TM7	Unclassified	sf_1	3145	tongue dorsa clone DR034	4.113	0.002	0.000
Verrucomicrobia	Unclassified	sf_3	40	Elbe river clone DEV055	4.116	0.002	0.000
Firmicutes	Unclassified	sf_1	4298	human mouth clone P4PA_66	4.118	0.002	0.000
Proteobacteria	Unclassified	sf_8	9558		4.120	0.004	0.000
Proteobacteria	Ectothiorhodospiraceae	sf_1	9598	Mono Lake clone ML602J-47 proteobacterium	4.125	0.004	0.000
Firmicutes	Lachnospiraceae	sf_5	3036	termite gut homogenate clone Rs-F27 bacterium	4.126	0.002	0.000
Chloroflexi	Unclassified	sf_1	2485		4.130	0.002	0.000
Bacteroidetes	Unclassified	sf_3	5248	Delaware River estuary clone 1G12	4.136	0.005	0.001
Proteobacteria	Pasteurellaceae	sf_1	8413	DCP-dechlorinating consortium clone SHA-37	4.136	0.002	0.000
Firmicutes	Bacillaceae	sf_1	3706	Bacillus sonorensis str. NRRL B-23155	4.139	0.002	0.000
Proteobacteria	Unclassified	sf_1	7222	Great Artesian Basin clone B79	4.139	0.004	0.000
Proteobacteria	Pasteurellaceae	sf_1	8876	Mannheimia sp. R19.2 str. R19.2; CCUG 38463 R19.2	4.141	0.005	0.001
Proteobacteria	Phyllobacteriaceae	sf_1	7300	marine isolate JP57	4.143	0.003	0.000
Proteobacteria	Moraxellaceae	sf_3	8838	Psychrobacter psychrophilus CMS 28	4.146	0.003	0.000
TM7	Unclassified	sf_1	3151	activated sludge foam clone 71	4.146	0.003	0.000
Proteobacteria	Rhizobiaceae	sf_1	6683	Sinorhizobium fredii str. ATCC35423	4.146	0.002	0.000

Firmicutes	Unclassified	sf_1	4261	termite gut homogenate clone Rs-G04 bacterium	4.146	0.002	0.000
Firmicutes	Halobacillaceae	sf_1	3849	Halobacillus litoralis str. SL-4	4.150	0.003	0.000
Proteobacteria	Alteromonadaceae	sf_1	9111	Pseudoalteromonas sp. str. E36	4.151	0.002	0.000
Proteobacteria	Nitrosomonadaceae	sf_1	7796	Nitrosospira sp. str. TYM9	4.151	0.003	0.000
Proteobacteria	Pasteurellaceae	sf_1	9533	Haemophilus segnis str. MCCM 00337	4.152	0.004	0.000
Proteobacteria	Rhizobiaceae	sf_1	6964	Agrobacterium tumefaciens str. C58 Cereon	4.153	0.002	0.000
Proteobacteria	Xanthomonadaceae	sf_3	8689	Dyemonas todaii str. XD10	4.155	0.002	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	5730		4.155	0.002	0.000
Bacteroidetes	Flexibacteraceae	sf_19	5307	Microscilla sericea str. IFO 16561	4.155	0.004	0.000
Proteobacteria	Pseudomonadaceae	sf_1	9240	Pseudomonas fluorescens str. CHA0	4.156	0.006	0.001
Actinobacteria	Bifidobacteriaceae	sf_1	1444	Bifidobacteriaceae genomosp. C1	4.157	0.002	0.000
Bacteroidetes	Unclassified	sf_4	5787	Mono Lake at depth 35 m station 6 July 2000 clone ML635J-1 bacterium	4.159	0.002	0.000
Firmicutes	Lachnospiraceae	sf_5	4273	termite gut homogenate clone Rs-M14 bacterium	4.160	0.002	0.000
marine group A	Unclassified	sf_1	6408	Sargasso Sea	4.162	0.002	0.000
Planctomycetes	Anammoxales	sf_2	4683	anoxic basin clone CY0ARA028B09	4.162	0.002	0.000
Proteobacteria	Rhodobacteraceae	sf_1	7040	Paracoccus alcaliphilus str. JCM 7364	4.175	0.002	0.000
Firmicutes	Bacillaceae	sf_1	3424	uranium mill tailings clone Gitt-KF-76	4.178	0.002	0.000
Unclassified	Unclassified	sf_160	7767		4.181	0.003	0.000
Proteobacteria	Desulfobacteraceae	sf_5	10268		4.184	0.003	0.000
Firmicutes	Entomoplasmataceae	sf_1	4074	swine intestine clone p-2013-s959-5	4.185	0.002	0.000
Chloroflexi	Unclassified	sf_2	2344	forest soil clone C083	4.189	0.002	0.000

Proteobacteria	Pseudomonadaceae	sf_1	9002	Paederus fuscipes endosymbiont	4.190	0.002	0.000
Proteobacteria	Pseudomonadaceae	sf_1	8209	uranium mining waste pile clone JG37-AG-122 proteobacterium	4.191	0.004	0.000
Proteobacteria	Rhodocyclaceae	sf_1	7925	Thauera selenatis str. ATCC 55363T	4.191	0.003	0.000
Firmicutes	Unclassified	sf_1	4616	rumen clone F23-C12	4.197	0.002	0.000
Proteobacteria	Rhizobiaceae	sf_1	6798	Agrobacterium tumefaciens TG14	4.197	0.002	0.000
Proteobacteria	Nitrosomonadaceae	sf_1	7976	Nitrosomonas sp. str. Nm86	4.197	0.003	0.000
Proteobacteria	Desulfobacteraceae	sf_5	10364	marine surface sediment clone SB2	4.197	0.002	0.000
Actinobacteria	Unclassified	sf_1	1370	forested wetland clone RCP1-37	4.198	0.002	0.000
Proteobacteria	Francisellaceae	sf_1	9554	Tilapia parasite TPT-541	4.201	0.002	0.000
Proteobacteria	Desulfobacteraceae	sf_5	10239		4.201	0.003	0.000
Proteobacteria	Desulfohalobiaceae	sf_1	9894	Desulfonauticus submarinus str. 6N	4.201	0.004	0.000
Proteobacteria	Helicobacteraceae	sf_3	10602		4.206	0.002	0.000
Proteobacteria	Pseudomonadaceae	sf_1	8457	5' clone CHAB-XI-27	4.207	0.003	0.000
Proteobacteria	Halomonadaceae	sf_1	8514	Chromohalobacter israelensis str. ATCC 43985 T	4.210	0.004	0.000
Proteobacteria	Ralstoniaceae	sf_1	8110	Wautersia paucula str. LMG 3413	4.211	0.002	0.000
Acidobacteria	Acidobacteriaceae	sf_14	6366	PCB-polluted soil clone WD228	4.213	0.003	0.000
Proteobacteria	Desulfovibrionaceae	sf_1	10016	termite gut homogenate clone Rs-N35 proteobacterium	4.216	0.003	0.000
Firmicutes	Streptococcaceae	sf_1	3629	Streptococcus mutans str. UA96	4.216	0.004	0.000
Bacteroidetes	Prevotellaceae	sf_1	5940	Prevotella sp. str. E7_34	4.220	0.005	0.001
Proteobacteria	Unclassified	sf_3	8045		4.221	0.002	0.000
Proteobacteria	Alcaligenaceae	sf_1	7902	Alcaligenes faecalis str. M3A	4.224	0.003	0.000

Firmicutes	Clostridiaceae	sf_12	4306	UASB reactor granular sludge clone PD-UASB-4 bacterium	4.225	0.001	0.000
BRC1	Unclassified	sf_1	5051	soil clone PBS-III-24	4.226	0.002	0.000
Proteobacteria	Unclassified	sf_3	9044	hydrothermal sediment clone AF420370	4.226	0.004	0.000
Chloroflexi	Unclassified	sf_9	727	forest soil clone S0208	4.230	0.002	0.000
Firmicutes	Clostridiaceae	sf_12	4406	termite gut homogenate clone Rs-J39 bacterium	4.232	0.001	0.000
Proteobacteria	Rhodobacteraceae	sf_1	7026	Leisingera methylohalidivorans str. MB2	4.233	0.002	0.000
Actinobacteria	Cellulomonadaceae	sf_1	1450		4.235	0.002	0.000
Proteobacteria	Rhodobacteraceae	sf_1	6701	Roseobacter clone NAC11-3	4.236	0.002	0.000
Actinobacteria	Promicromonosporaceae	sf_1	1711	Promicromonospora sukumoe str. DSM 44121	4.238	0.002	0.000
Proteobacteria	Rhodobacteraceae	sf_1	7125	Paracoccus carotinifaciens str. E-396	4.240	0.002	0.000
Firmicutes	Peptostreptococcaceae	sf_5	619	TCE-dechlorinating microbial community clone 1G	4.242	0.002	0.000
Unclassified	Unclassified	sf_160	6430		4.243	0.002	0.000
Proteobacteria	Unclassified	sf_1	10414	penguin droppings sediments clone KD2-34	4.245	0.002	0.000
Proteobacteria	Caulobacteraceae	sf_1	6904	Brevundimonas vesicularis str. IAM 12105T	4.248	0.004	0.000
Proteobacteria	Rhizobiaceae	sf_1	7568	Rhizobium etli str. USDA 2667 ATCC 14483 SEMIA 043	4.248	0.001	0.000
Proteobacteria	Unclassified	sf_5	7025	bacterioplankton clone ZA2526c	4.249	0.003	0.000
Proteobacteria	Enterobacteriaceae	sf_6	433	coal effluent wetland clone RCP2-6	4.250	0.002	0.000
Firmicutes	Unclassified	sf_1	77	thermal soil clone YNPFFP9	4.251	0.003	0.000
Firmicutes	Erysipelotrichaceae	sf_3	3952	Erysipelothrix rhusiopathiae str. Pecs 56	4.252	0.003	0.000
Chloroflexi	Unclassified	sf_1	374	forest soil clone S041	4.253	0.002	0.000
Firmicutes	Clostridiaceae	sf_12	3049	Clostridium paradoxum str. DSM 7308T	4.254	0.001	0.000

Firmicutes	Aerococcaceae	sf_1	3386	feedlot manure clone B87	4.255	0.004	0.000
Cyanobacteria	Chloroplasts	sf_5	5182	Epifagus virginiana -- chloroplast	4.256	0.002	0.000
Firmicutes	Streptococcaceae	sf_1	3722	Lactococcus Il1403 subsp. lactis str. IL1403	4.256	0.003	0.000
Firmicutes	Streptococcaceae	sf_1	3290	Streptococcus mitis str. Sm91	4.258	0.005	0.001
Firmicutes	Aerococcaceae	sf_1	3522	Aerococcus viridans	4.262	0.004	0.000
Firmicutes	Streptococcaceae	sf_1	3753	Streptococcus suis str. 8074	4.263	0.005	0.001
Proteobacteria	Helicobacteraceae	sf_3	10614	strain isolate str. BHI80-49	4.263	0.001	0.000
Proteobacteria	Rhizobiaceae	sf_1	6972	Ensifer adhaerens str. LMG 20582	4.264	0.001	0.000
TM7	Unclassified	sf_1	8040	oral cavity clone BE109	4.265	0.004	0.000
Actinobacteria	Streptomycetaceae	sf_1	1354	Streptomyces subrutilus str. DSM 40445	4.266	0.001	0.000
Bacteroidetes	Unclassified	sf_3	6298	travertine hot spring clone SM1C04	4.268	0.002	0.000
Chloroflexi	Unclassified	sf_1	2367	deep marine sediment clone MB-B2-113	4.269	0.003	0.000
Proteobacteria	Caulobacteraceae	sf_1	6781	Brevundimonas intermedia str. MBIC2712 ATCC15262	4.270	0.003	0.000
Bacteroidetes	Porphyromonadaceae	sf_1	5510	sphagnum peat bog clone 26-4b2	4.271	0.005	0.001
Verrucomicrobia	Verrucomicrobia subdivision 5	sf_1	547	anoxic marine sediment clone LD1-PB1	4.277	0.002	0.000
OP10	Unclassified	sf_4	484	forested wetland clone FW68	4.280	0.001	0.000
Proteobacteria	Unclassified	sf_1	7750	uranium mining waste clone JG37-AG-35	4.283	0.001	0.000
Bacteroidetes	Unclassified	sf_15	5874	hydrothermal vent polychaete mucous clone P. palm A 53	4.284	0.003	0.000
Proteobacteria	Beijerinck/Rhodoplan/Methylocyst	sf_3	7239	Thalassospira lucentensis	4.284	0.004	0.000
Acidobacteria	Acidobacteriaceae	sf_6	6359	PCE-contaminated site clone CLi114	4.287	0.002	0.000
Natronoanaerobiu	Unclassified	sf_1	769	fjord ikaite column clone un-c23	4.292	0.002	0.000

Bacteroidetes	Unclassified	sf_4	5703		4.297	0.003	0.000
Actinobacteria	Promicromonosporaceae	sf_1	1671	Cellulosimicrobium cellulans str. NCIMB 11025	4.301	0.002	0.000
Firmicutes	Clostridiaceae	sf_12	4225	termite gut clone Rs-116	4.301	0.002	0.000
Proteobacteria	Caulobacteraceae	sf_1	7359	Brevundimonas bacteroides str. CB7	4.302	0.003	0.000
Proteobacteria	Caulobacteraceae	sf_1	7366	Brevundimonas subvibrioides str. CB81	4.302	0.003	0.000
Proteobacteria	Comamonadaceae	sf_1	8012	Acidovorax konjaci str. DSM 7481	4.304	0.001	0.000
Proteobacteria	Rhodocyclaceae	sf_1	7951	EBPR sludge lab scale clone HP1A03	4.304	0.003	0.000
Unclassified	Unclassified	sf_160	2488		4.307	0.002	0.000
Proteobacteria	Rhodobacteraceae	sf_1	6980	Loktanella vestfoldensis str. LMG 22003	4.308	0.001	0.000
Caldithrix	Caldithraceae	sf_1	2384	saltmarsh clone LCP-89	4.309	0.001	0.000
Bacteroidetes	Prevotellaceae	sf_1	5926	cow rumen clone BF22	4.310	0.004	0.000
Proteobacteria	Caulobacteraceae	sf_1	6909	Brevundimonas diminuta str. DSM 1635	4.310	0.003	0.000
Spirochaetes	Spirochaetaceae	sf_1	6479	Treponema sp	4.312	0.001	0.000
Proteobacteria	Piscirickettsiaceae	sf_3	9291	Methylophaga alcalica str. M39	4.313	0.002	0.000
Proteobacteria	Aeromonadaceae	sf_1	9294	Arctic deep sea (HMMV 72N 14E))	4.314	0.004	0.000
Proteobacteria	Alteromonadaceae	sf_1	8536	Cardiobacterium hominis	4.315	0.002	0.000
Proteobacteria	Alteromonadaceae	sf_1	8578	Marinobacter lipolyticus str. SM-19	4.317	0.003	0.000
Actinobacteria	Cellulomonadaceae	sf_1	1431	Cellulomonadaceae str. W6	4.317	0.001	0.000
Chlamydiae	Parachlamydiaceae	sf_1	4964	neutral pH mine biofilm clone 44a-B1-34	4.318	0.003	0.000
Firmicutes	Streptococcaceae	sf_1	3499	Streptococcus constellatus str. ATCC27823	4.318	0.004	0.000
Acidobacteria	Unclassified	sf_1	523	soil metagenomic library clone 17F9	4.320	0.001	0.000

Firmicutes	Peptostreptococcaceae	sf_5	224	Finegoldia magna str. ATCC 29328	4.323	0.001	0.000
Proteobacteria	Desulfomicrobiaceae	sf_1	10079	Desulfomicrobium baculatum str. DSM 1742	4.324	0.002	0.000
Proteobacteria	Unclassified	sf_3	8959	bacterioplankton clone AEGEAN_133	4.327	0.002	0.000
Bacteroidetes	Prevotellaceae	sf_1	5398	Prevotella ruminicola L16	4.329	0.004	0.000
Proteobacteria	Caulobacteraceae	sf_1	7436	Brevundimonas sp. str. FWC40	4.329	0.003	0.000
Firmicutes	Peptostreptococcaceae	sf_5	668	Sedimentibacter sp. str. BRS2	4.331	0.001	0.000
Actinobacteria	Actinomycetaceae	sf_1	1684	Varibaculum cambriense str. CCUG 44998	4.337	0.001	0.000
Firmicutes	Erysipelotrichaceae	sf_3	144	Eubacterium cylindroides	4.338	0.002	0.000
Proteobacteria	Unclassified	sf_9	244	deep marine sediment clone MB-C2-152	4.339	0.003	0.000
Proteobacteria	Desulfovibrionaceae	sf_1	9709	termite gut homogenate clone Rs-N31 proteobacterium	4.345	0.002	0.000
Actinobacteria	Bifidobacteriaceae	sf_1	1351	Bifidobacterium psychraerophilum str. T16	4.346	0.002	0.000
WS3	Unclassified	sf_1	2537	anoxic marine sediment clone LD1-PA39	4.347	0.003	0.000
Firmicutes	Bacillaceae	sf_1	3650		4.351	0.004	0.000
Firmicutes	Lachnospiraceae	sf_5	3038	swine intestine clone p-1594-c5	4.351	0.002	0.000
Proteobacteria	Thiotrichaceae	sf_3	8321	Wadden Sea sediment clone Dangast A9	4.351	0.002	0.000
Proteobacteria	Comamonadaceae	sf_1	7705	penguin droppings sediments clone KD4-7	4.353	0.002	0.000
Firmicutes	Peptococc/Acidaminococc	sf_11	992	anoxic bulk soil flooded rice microcosm clone BSV43 clone	4.354	0.003	0.000
Acidobacteria	Unclassified	sf_1	516	uranium mining waste pile clone JG34-KF-153	4.354	0.002	0.000
Proteobacteria	Unclassified	sf_1	9828	termite gut homogenate clone Rs-M89 proteobacterium	4.355	0.002	0.000
Firmicutes	Unclassified	sf_8	2433	Ferribacter thermoautotrophicus str. JW/JH-Fiji-2	4.356	0.002	0.000
Proteobacteria	Unclassified	sf_9	9890	termite gut homogenate clone Rs-K70 proteobacterium	4.356	0.002	0.000

Bacteroidetes	Unclassified	sf_15	5544	marine? clone KD3-17	4.357	0.001	0.000
Firmicutes	Streptococcaceae	sf_1	3422	Streptococcus thermophilus str. DSM 20617	4.358	0.003	0.000
Proteobacteria	Phyllobacteriaceae	sf_1	7216	Ahrensia kielensis str. IAM12618	4.359	0.001	0.000
Spirochaetes	Spirochaetaceae	sf_1	6580	Treponema sp. str. III:C:BA213	4.359	0.001	0.000
Planctomycetes	Planctomycetaceae	sf_3	4652	anoxic basin clone CY0ARA028C04	4.369	0.002	0.000
Firmicutes	Bacillaceae	sf_1	3370	Bacillus sp. str. TGS437	4.374	0.001	0.000
Proteobacteria	Bartonellaceae	sf_1	7415	Bartonella quintana str. Toulouse	4.375	0.001	0.000
Acidobacteria	Acidobacteriaceae	sf_6	6423	coal effluent wetland clone FW92	4.376	0.002	0.000
Proteobacteria	Polyangiaceae	sf_3	9735	uranium mining waste pile clone JG37-AG-15 proteobacterium	4.376	0.002	0.000
Proteobacteria	Unclassified	sf_3	8676		4.377	0.003	0.000
AD3	Unclassified	sf_1	2338	uranium mining waste pile soil clone JG30-KF-C12	4.378	0.001	0.000
Cyanobacteria	Chloroplasts	sf_5	5130	travertine hot spring clone SM2B11	4.380	0.001	0.000
Proteobacteria	Unclassified	sf_1	8408	Thiorhodovibrio winogradskyi	4.384	0.003	0.000
Firmicutes	Bacillaceae	sf_1	3898	compost clone 4-28	4.390	0.001	0.000
Chloroflexi	Unclassified	sf_1	266		4.391	0.001	0.000
Bacteroidetes	Prevotellaceae	sf_1	5706	oral cavity clone 3.3	4.391	0.005	0.001
OP3	Unclassified	sf_4	628	CB-contaminated groundwater clone GOUTB15	4.392	0.002	0.000
Proteobacteria	Desulfovibrionaceae	sf_1	10071	Desulfovibrio desulfuricans	4.393	0.001	0.000
Firmicutes	Bacillaceae	sf_1	3688	Bacillus sp. str. SAFN-006	4.394	0.001	0.000
Proteobacteria	Unclassified	sf_4	8855		4.395	0.003	0.000
Firmicutes	Bacillaceae	sf_1	3579	Bacillus sp. str. TGS750	4.395	0.001	0.000

Proteobacteria	Rhodobacteraceae	sf_1	6652	marine clone Arctic96A-1	4.396	0.001	0.000
Proteobacteria	Pasteurellaceae	sf_1	9604	Mannheimia sp. MCCM 00145	4.396	0.003	0.000
Proteobacteria	Piscirickettsiaceae	sf_3	9392	Methylophaga sp. str. V4.ME.29 = MM_2343	4.396	0.001	0.000
Planctomycetes	Pirellulae	sf_3	4692	aerobic basin clone CY0ARA026G04	4.399	0.003	0.000
Proteobacteria	Unclassified	sf_1	9458	uranium mining waste pile clone JG37-AG-94 proteobacterium	4.399	0.002	0.000
Firmicutes	Peptostreptococcaceae	sf_5	3182	termite gut homogenate clone Rs-Q64 bacterium	4.399	0.001	0.000
Bacteroidetes	Unclassified	sf_15	5573	termite gut homogenate clone Rs-D44 bacterium	4.400	0.001	0.000
Acidobacteria	Unclassified	sf_1	572	forested wetland clone FW144	4.401	0.002	0.000
Gemmatimonadete	Unclassified	sf_5	1565	uranium mining waste pile clone JG34-KF-418	4.405	0.001	0.000
Spirochaetes	Spirochaetaceae	sf_1	6459	Spirochaeta sp. str. BHI80-158	4.408	0.002	0.000
Actinobacteria	Rubrobacteraceae	sf_1	1843	uranium mining waste pile soil sample clone JG30-KF-A23	4.408	0.002	0.000
Bacteroidetes	Unclassified	sf_15	5820	cow rumen clone BF24	4.409	0.002	0.000
Proteobacteria	Comamonadaceae	sf_1	7986	Arctic sea ice ARK10281	4.414	0.002	0.000
Proteobacteria	Xanthomonadaceae	sf_3	9277	penguin droppings sediment clone KD8-68	4.415	0.002	0.000
Proteobacteria	Unclassified	sf_1	9246	Mammoth Cave sediment clone CCD24	4.416	0.002	0.000
Firmicutes	Peptostreptococcaceae	sf_5	2721	termite gut homogenate clone Rs-N71 bacterium	4.416	0.001	0.000
Firmicutes	Streptococcaceae	sf_1	3588	Streptococcus downei str. ATCC 33748	4.417	0.003	0.000
Bacteroidetes	Prevotellaceae	sf_1	5916	cow rumen clone BE14	4.419	0.004	0.000
marine group A	Unclassified	sf_1	6344	bacterioplankton clone ZA3648c	4.421	0.001	0.000
Proteobacteria	Unclassified	sf_6	7377	Rocky Mountain alpine soil clone W2b-8C	4.423	0.002	0.000
Proteobacteria	Polyangiaceae	sf_3	9874	uranium mining waste pile clone JG34-KF-243 proteobacterium	4.424	0.001	0.000

Proteobacteria	Desulfobulbaceae	sf_1	10187	Mono Lake at depth 23 m station 6 July 2000 clone ML623J-57 proteobacterium	4.424	0.002	0.000
Bacteroidetes	Prevotellaceae	sf_1	5403	Prevotella bryantii str. B14 (DSM 11371 species)	4.425	0.002	0.000
Proteobacteria	Helicobacteraceae	sf_3	10417	temperate estuarine mud clone KM61	4.425	0.001	0.000
Proteobacteria	Rhodobacteraceae	sf_1	6888	hydrothermal vent strain str. TB66	4.425	0.002	0.000
Unclassified	Unclassified	sf_160	6456		4.426	0.001	0.000
Firmicutes	Clostridiaceae	sf_12	3219	Great Artesian Basin clone R82	4.429	0.001	0.000
Actinobacteria	Streptomycetaceae	sf_1	1639	Streptomyces coelicolor str. M145 ssp. A3(2)	4.432	0.002	0.000
Verrucomicrobia	Unclassified	sf_3	792	termite gut homogenate clone Rs-P07 bacterium	4.438	0.001	0.000
Proteobacteria	Pasteurellaceae	sf_1	8614	Acidithiobacillus thiooxidans str. KCTC 8928P	4.438	0.001	0.000
Gemmatimonadete	Unclassified	sf_5	317	penguin droppings sediments clone KD8-87	4.440	0.002	0.000
Cyanobacteria	Unclassified	sf_1	5001	sponge clone TK09	4.444	0.003	0.000
Proteobacteria	Unclassified	sf_9	9738	marine methane seep clone 1513	4.444	0.002	0.000
Actinobacteria	Streptosporangiaceae	sf_1	1224	Acrocarpospora corrugata str. DSM43316T	4.448	0.002	0.000
Chloroflexi	Unclassified	sf_1	765	anaerobic bioreactor clone SHD-71	4.449	0.001	0.000
Bacteroidetes	Flexibacteraceae	sf_20	10311	Cytophaga sp. str. BHI60-57B	4.450	0.001	0.000
Proteobacteria	Phyllobacteriaceae	sf_1	6857	Mesorhizobium mediterraneum str. PECA20	4.453	0.001	0.000
Proteobacteria	Anaplasmataceae	sf_3	6648	Wolbachia sp	4.454	0.002	0.000
Proteobacteria	Unclassified	sf_4	6810	marine bacterioplankton clone MB13F01	4.454	0.001	0.000
Bacteroidetes	Prevotellaceae	sf_1	5437	cow rumen clone BE1	4.454	0.003	0.000
Gemmatimonadete	Unclassified	sf_5	227	uranium mining waste pile clone JG37-AG-36	4.456	0.001	0.000
Acidobacteria	Acidobacteriaceae	sf_14	6335	forested wetland clone FW45	4.456	0.001	0.000

Bacteroidetes	Prevotellaceae	sf_1	5769	Bacteroidaceae str. A42	4.458	0.004	0.000
Firmicutes	Bacillaceae	sf_1	3926	Lake Bogoria isolate 64B4	4.459	0.001	0.000
Proteobacteria	Unclassified	sf_9	9876	deep marine sediment clone MB-B2-106	4.461	0.002	0.000
Bacteroidetes	Unclassified	sf_3	6168	Toolik Lake main station at 3 m depth clone TLM11/TLMdgge04	4.461	0.003	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	5933	Flavobacterium columnare str. PH-97028 (IAM 14821)	4.462	0.003	0.000
Chloroflexi	Unclassified	sf_1	2497	forested wetland clone FW60	4.464	0.003	0.000
Firmicutes	Acholeplasmataceae	sf_1	3955	Weeping tea tree witches'-broom phytoplasma tree	4.464	0.003	0.000
Chloroflexi	Unclassified	sf_9	946	temperate estuarine mud clone KM87	4.465	0.001	0.000
Proteobacteria	Nitrosomonadaceae	sf_1	7770	Nitrosomonas europaea str. ATCC 19718	4.465	0.001	0.000
Bacteroidetes	Unclassified	sf_15	5957	hydrothermal vent polychaete mucous clone P. palm C/A 20	4.467	0.002	0.000
Bacteroidetes	Unclassified	sf_15	5475	SHA-25 clone	4.468	0.002	0.000
Proteobacteria	Burkholderiaceae	sf_1	7720	penguin droppings sediments clone KD1-79	4.468	0.002	0.000
Firmicutes	Unclassified	sf_17	4168		4.469	0.002	0.000
Proteobacteria	Chromatiaceae	sf_1	8697	Thiococcus sp. AT2204	4.472	0.003	0.000
Actinobacteria	Dermabacteraceae	sf_1	1677	Brachybacterium conglomeratum str. NCIB 9859	4.472	0.001	0.000
Proteobacteria	Chromatiaceae	sf_1	9052		4.473	0.002	0.000
Proteobacteria	Oxalobacteraceae	sf_1	7845	Diaphorina citri symbiont	4.473	0.003	0.000
Bacteroidetes	Flexibacteraceae	sf_19	5366	Flexibacter roseolus str. IFO 16030	4.474	0.001	0.000
Actinobacteria	Micrococcaceae	sf_1	1573	Arthrobacter nicotianae str. SB42	4.474	0.001	0.000
Proteobacteria	Unclassified	sf_1	7766		4.475	0.001	0.000
Verrucomicrobia	Unclassified	sf_3	486	Elbe river clone DEV045	4.475	0.001	0.000

Firmicutes	Paenibacillaceae	sf_1	3922	Paenibacillus thiaminolyticus str. DSM 7262	4.476	0.001	0.000
Firmicutes	Aerococcaceae	sf_1	3736	Desemzia incerta str. DSM 20581	4.482	0.001	0.000
Proteobacteria	Unclassified	sf_1	8839	f cytometric sorted marine sample subpopulation 3 clone ZD0408 bacterium	4.485	0.002	0.000
Proteobacteria	Unclassified	sf_3	9269		4.486	0.001	0.000
Proteobacteria	Rhizobiaceae	sf_1	6974	India: Himalayas Kaza Spiti Valley Cold Desert isolate str. Kaza-35 Kaza-35	4.486	0.001	0.000
Unclassified	Unclassified	sf_140	6355		4.486	0.001	0.000
Actinobacteria	Acidothermaceae	sf_1	1399	uranium mill tailings clone Gitt-KF-183	4.488	0.001	0.000
Bacteroidetes	Unclassified	sf_6	5439	Mono Lake clone ML635J-40 bacterium	4.490	0.001	0.000
Acidobacteria	Acidobacteriaceae	sf_6	6345	clone JG36-TzT-77 bacterium	4.491	0.001	0.000
Firmicutes	Acholeplasmataceae	sf_1	3977	Chinaberry yellows phytoplasma str. CbY1	4.492	0.001	0.000
Actinobacteria	Micrococcaceae	sf_1	2063	Rothia dentocariosa str. ATCC 17931	4.492	0.002	0.000
Proteobacteria	Phyllobacteriaceae	sf_1	7381	Aminobacter aminovorans str. DSM7048T	4.494	0.001	0.000
Actinobacteria	Unclassified	sf_3	1486	deep marine sediment clone MB-A2-108	4.496	0.002	0.000
Planctomycetes	Pirellulae	sf_3	4803	Pirellula sp. str. ACM 3181	4.497	0.002	0.000
Bacteroidetes	Unclassified	sf_15	5511	marine sediment above hydrate ridge clone Hyd-B2-1 bacterium	4.501	0.004	0.000
Thermotogae	Thermotogaceae	sf_4	51	Thermosipho sp. str. MV1063	4.501	0.002	0.000
Verrucomicrobia	Verrucomicrobiaceae	sf_1	1024	rumen clone BS5	4.501	0.001	0.000
Firmicutes	Erysipelotrichaceae	sf_3	768		4.502	0.001	0.000
Firmicutes	Clostridiaceae	sf_12	4584	Clostridium papyrosolvens str. DSM 2782	4.502	0.001	0.000
Proteobacteria	Chromatiaceae	sf_1	8546	Thiocapsa litoralis	4.502	0.002	0.000
Bacteroidetes	Unclassified	sf_15	6324	temperate estuarine mud clone KM02	4.505	0.003	0.000

Cyanobacteria	Chloroplasts	sf_5	5112	Cyanidium caldarium str. 14-1-1	4.505	0.002	0.000
Firmicutes	Carnobacteriaceae	sf_1	3792	Carnobacterium sp. str. D35	4.506	0.002	0.000
Cyanobacteria	Chloroplasts	sf_5	4967	Toolik Lake main station at 3 m depth clone TLM14	4.509	0.003	0.000
Firmicutes	Clostridiaceae	sf_12	10457	strain isolate str. Dex60-82	4.512	0.001	0.000
Chloroflexi	Unclassified	sf_1	1041	Antarctic cryptoendolith clone FBP471	4.513	0.001	0.000
Proteobacteria	Alcanivoraceae	sf_1	9658	Alcanivorax sp. str. Haw1	4.514	0.002	0.000
Firmicutes	Bacillaceae	sf_1	1050	Bacillus firmus CV93b	4.517	0.002	0.000
Proteobacteria	Alteromonadaceae	sf_1	9416	marine isolate str. R8	4.517	0.002	0.000
Firmicutes	Thermoactinomycetaceae	sf_1	3301	Thermoactinomyces sp. str. 700375	4.523	0.004	0.000
Proteobacteria	Unclassified	sf_1	8231	uranium waste soil clone JG30a-KF-21	4.529	0.001	0.000
Firmicutes	Lachnospiraceae	sf_5	3060	termite gut homogenate clone Rs-B14 bacterium	4.530	0.002	0.000
Fusobacteria	Fusobacteriaceae	sf_3	387	Leptotrichia wadeii str. LB16	4.530	0.003	0.000
Proteobacteria	Pseudomonadaceae	sf_1	9049	uranium mining mill tailing clone GR-Sh2-34 GR-Sh2-34	4.531	0.002	0.000
Cyanobacteria	Chloroplasts	sf_5	5040	Solanum nigrum	4.535	0.001	0.000
Firmicutes	Clostridiaceae	sf_12	4357	Lachnospiraceae bacterium 19gly4	4.536	0.001	0.000
Proteobacteria	Comamonadaceae	sf_1	7928	penguin droppings sediments clone KD5-43	4.541	0.001	0.000
Bacteroidetes	Sphingobacteriaceae	sf_1	6158	municipal wastewater treatment bioreactor isolate str. CAGY10	4.545	0.002	0.000
Acidobacteria	Acidobacteriaceae	sf_14	6425	Great Artesian Basin clone B27	4.548	0.001	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	5423	Aequorivita antarctica str. QSSC9-14	4.549	0.001	0.000
Proteobacteria	Unclassified	sf_5	7471	sponge clone TK03	4.551	0.001	0.000
Proteobacteria	Pseudomonadaceae	sf_1	8635		4.552	0.002	0.000

TM7	Unclassified	sf_1	8155	oral periodontitis clone EW086	4.553	0.002	0.000
Proteobacteria	Myxococcaceae	sf_1	10358	Myxococcus fulvus str. Mx f2	4.554	0.002	0.000
Firmicutes	Lachnospiraceae	sf_5	4535	ckncm297-B1-1 clone	4.555	0.001	0.000
Proteobacteria	Chromatiaceae	sf_1	9054		4.556	0.003	0.000
Firmicutes	Syntrophomonadaceae	sf_5	2456	granular sludge clone R4b14	4.557	0.003	0.000
Acidobacteria	Acidobacteriaceae	sf_14	6378	Acidobacterium capsulatum	4.557	0.002	0.000
Firmicutes	Paenibacillaceae	sf_1	3415	Paenibacillus nematophilus str. NEM1b	4.557	0.001	0.000
Firmicutes	Unclassified	sf_8	546	Ferribacter thermoautotrophicus	4.560	0.001	0.000
Firmicutes	Clostridiaceae	sf_12	3108	Clostridium paradoxum str. DSM 7308T	4.561	0.001	0.000
NC10	Unclassified	sf_1	2516	TCE-contaminated site clone FTL22	4.564	0.001	0.000
SPAM	Unclassified	sf_1	705	uranium tailings soil clone Sh765B-AG-45	4.564	0.001	0.000
Proteobacteria	Pseudomonadaceae	sf_1	9613	Pseudomonas flavescens str. B62	4.567	0.002	0.000
Firmicutes	Clostridiaceae	sf_12	4548	termite gut homogenate clone Rs-Q69 bacterium	4.567	0.001	0.000
Proteobacteria	SAR11	sf_2	7043	marine clone Arctic95D-8	4.568	0.001	0.000
Firmicutes	Aerococcaceae	sf_1	3866	Turicibacter sanguinis	4.568	0.001	0.000
Actinobacteria	Micrococcaceae	sf_1	1324	glacial ice isolate str. CanDirty1	4.569	0.001	0.000
Actinobacteria	Micrococcaceae	sf_1	1266	Arthrobacter psychrolactophilus	4.575	0.001	0.000
Actinobacteria	Streptomycetaceae	sf_1	1274	Trichotomospora caesia str. IFO14562	4.578	0.001	0.000
Firmicutes	Lachnospiraceae	sf_5	2709	human stool clone B065	4.580	0.001	0.000
Proteobacteria	Helicobacteraceae	sf_3	10425	Sulfurimonas autotrophica str. OK5	4.587	0.001	0.000
Firmicutes	Unclassified	sf_4	4325	termite gut homogenate clone Rs-K21 bacterium	4.588	0.001	0.000

Proteobacteria	Procabacteriaceae	sf_1	8136	Acanthamoeba sp. UWC6 symbiont	4.588	0.001	0.000
Proteobacteria	Syntrophobacteraceae	sf_1	9845	uranium mining waste pile clone JG37-AG-128 proteobacterium	4.593	0.002	0.000
Proteobacteria	Unclassified	sf_3	8587	Mars Odyssey Orbiter and encapsulation facility clone T5-3	4.594	0.003	0.000
Firmicutes	Lactobacillaceae	sf_1	3829	Lactobacillus paralimentarius str. DSM 13238	4.597	0.002	0.000
Firmicutes	Peptococc/Acidaminococc	sf_11	131	pig feces clone	4.600	0.002	0.000
Proteobacteria	Unclassified	sf_1	6732	Anabaena circinalis AWQC118C isolate str. UNSW7	4.604	0.001	0.000
Proteobacteria	Unclassified	sf_3	8961	Calyptogena magnifica symbiont	4.604	0.002	0.000
Proteobacteria	Sphingomonadaceae	sf_1	7528	Sphingobium yanoikuyae str. GIFU9882	4.606	0.001	0.000
Proteobacteria	Alcaligenaceae	sf_1	8094	Alcaligenes sp. str. VKM B-2263 dcm6	4.609	0.003	0.000
Firmicutes	Streptococcaceae	sf_1	3253	derived cheese sample clone 32CR	4.609	0.003	0.000
Actinobacteria	Micrococcaceae	sf_1	1889	Citricoccus sp. str. 2216.25.22	4.610	0.001	0.000
Firmicutes	Lachnospiraceae	sf_5	4164	ckncm322-B3-7 clone	4.615	0.001	0.000
Actinobacteria	Cellulomonadaceae	sf_1	1586	Cellulomonas gelida str. DSM 20111T	4.615	0.001	0.000
Verrucomicrobia	Verrucomicrobia subdivision 7	sf_1	760	Mono lake clone ML316M-1	4.617	0.001	0.000
Acidobacteria	Acidobacteriaceae	sf_14	964	uranium mining waste pile clone JG37-AG-145 sp.	4.626	0.001	0.000
Proteobacteria	Acetobacteraceae	sf_1	7529	Gluconacetobacter europaeus str. ZIM B028 V3	4.627	0.001	0.000
Proteobacteria	Oceanospirillaceae	sf_1	9351	bacterioplankton clone ZA2333c	4.628	0.003	0.000
Proteobacteria	Unclassified	sf_6	7572		4.629	0.002	0.000
Firmicutes	Bacillaceae	sf_1	3467	Bacillus luciferensis str. LMG 18422	4.632	0.001	0.000
Firmicutes	Clostridiaceae	sf_12	4364	oral endodontic infection clone MCE3_9	4.634	0.001	0.000
Bacteroidetes	Sphingobacteriaceae	sf_1	5513	crevicular epithelial cells clone AZ123	4.636	0.001	0.000

Proteobacteria	Chromatiaceae	sf_1	9048	Allochromatium sp. AT2202	4.637	0.001	0.000
Acidobacteria	Acidobacteriaceae	sf_16	6414	PCE-contaminated site clone CLs73	4.639	0.002	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	6246	crevicular epithelial cells clone BU084	4.641	0.005	0.001
Firmicutes	Unclassified	sf_1	2388	G+C Gram-positive clone YNPRH70A	4.642	0.001	0.000
Proteobacteria	Helicobacteraceae	sf_3	10467		4.642	0.003	0.000
Verrucomicrobia	Verrucomicrobia subdivision 7	sf_1	559	anoxic marine sediment clone LD1-PA20	4.644	0.001	0.000
Actinobacteria	Frankiaceae	sf_1	1286	Frankia sp. Sn5-8	4.645	0.001	0.000
Cyanobacteria	Unclassified	sf_6	5186	geothermal power station discharge drain clone ST01-SN2C	4.645	0.002	0.000
Proteobacteria	Sphingomonadaceae	sf_1	6690	Porphyrobacter tepidarius str. OK5APO	4.647	0.001	0.000
Firmicutes	Clostridiaceae	sf_12	4627	termite gut homogenate clone Rs-A13 bacterium	4.652	0.001	0.000
Proteobacteria	Unclassified	sf_7	10048		4.653	0.002	0.000
Proteobacteria	Neisseriaceae	sf_1	7675	Neisseria sp. str. CCUG 46910	4.656	0.001	0.000
Proteobacteria	Comamonadaceae	sf_1	8112	Comamonas testosteroni str. SMCC B329	4.657	0.001	0.000
Proteobacteria	Oxalobacteraceae	sf_1	7866	Paucimonas lemoignei str. ATCC 17989T	4.658	0.001	0.000
Bacteroidetes	Flexibacteraceae	sf_19	5566	Hongiella mannitolivorans str. IMSNU 14012 JC2050	4.658	0.001	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	5971	Cytophaga uliginosa	4.659	0.001	0.000
Acidobacteria	Unclassified	sf_1	100	soil sample uranium clone JG36-TzT-10	4.659	0.001	0.000
Proteobacteria	Enterobacteriaceae	sf_6	646	Opitutus sp. str. SA-9	4.661	0.001	0.000
Planctomycetes	Unclassified	sf_1	4897	deep marine sediment clone MB-C2-105	4.663	0.001	0.000
Proteobacteria	Nitrosomonadaceae	sf_1	7789		4.664	0.002	0.000
Proteobacteria	Unclassified	sf_2	6639		4.664	0.001	0.000

Actinobacteria	Micrococcaceae	sf_1	1686	Yania halotolerans str. YIM 70085	4.664	0.001	0.000
Bacteroidetes	Porphyromonadaceae	sf_1	5961	chlorobenzene-degrading consortium clone IA-16	4.667	0.003	0.000
Bacteroidetes	Porphyromonadaceae	sf_1	5295	swine intestine clone p-987-s962-5	4.668	0.001	0.000
Firmicutes	Unclassified	sf_1	2443	Desulfotomaculum thermoacetoxidans str. DSM 5813	4.669	0.001	0.000
Bacteroidetes	Porphyromonadaceae	sf_1	6012	mouse feces clone L11-6	4.670	0.001	0.000
Bacteroidetes	Bacteroidaceae	sf_6	5792	activated sludge foam clone 47	4.672	0.001	0.000
TM7	Unclassified	sf_1	2917	arid soil clone C026	4.673	0.002	0.000
Cyanobacteria	Chloroplasts	sf_5	5183	Pisum sativum -- chloroplast	4.675	0.001	0.000
Firmicutes	Clostridiaceae	sf_12	3021	Clostridium caminithermale str. DVird3	4.675	0.001	0.000
Firmicutes	Lachnospiraceae	sf_5	2893	Ruminococcus obeum	4.676	0.002	0.000
Proteobacteria	Alcanivoraceae	sf_1	8335	Alcanivorax sp. str. K3-3 (MBIC 4323)	4.677	0.002	0.000
Actinobacteria	Micrococcaceae	sf_1	1724	Rothia mucilaginosa str. DSM	4.678	0.001	0.000
Proteobacteria	Alteromonadaceae	sf_1	9239	Arctic sea ice ARK10228	4.679	0.002	0.000
Firmicutes	Bacillaceae	sf_1	3328	Pseudobacillus carolinae	4.680	0.002	0.000
Proteobacteria	Polyangiaceae	sf_3	10353	sludge clone A9	4.680	0.001	0.000
Firmicutes	Lachnospiraceae	sf_5	3042	swine intestine clone p-2876-6C5	4.681	0.001	0.000
Firmicutes	Bacillaceae	sf_1	829	Geobacillus sp. str. YMTC1049	4.682	0.001	0.000
Chloroflexi	Unclassified	sf_9	576	DCP-dechlorinating consortium clone SHA-36	4.684	0.001	0.000
Proteobacteria	Halomonadaceae	sf_1	8598	Halomonas desiderata str. FB2	4.686	0.003	0.000
Firmicutes	Peptococc/Acidaminococc	sf_11	59	swine intestine clone p-1941-s962-3	4.686	0.001	0.000
Proteobacteria	Burkholderiaceae	sf_1	7957	Maconellicoccus hirsutus symbiont	4.687	0.001	0.000

Proteobacteria	Comamonadaceae	sf_1	7987	Acidovorax sp. str. OS-6	4.687	0.001	0.000
Acidobacteria	Unclassified	sf_1	4222	forested wetland clone FW105	4.687	0.002	0.000
Deinococcus-Ther	Unclassified	sf_1	563	Vulcanithermus mediatlanticus str. TR	4.687	0.001	0.000
Proteobacteria	Unclassified	sf_9	9784	Antarctic sediment clone LH5_30	4.689	0.002	0.000
Proteobacteria	Thiotrichaceae	sf_3	9015	Beggiatoa alba str. B18LD; ATCC 33555	4.689	0.001	0.000
Nitrospira	Nitrospiraceae	sf_2	681		4.693	0.001	0.000
Firmicutes	Streptococcaceae	sf_1	3869	Streptococcus equi subsp. zooepidemicus str. Tokyo1291 subsp.	4.694	0.002	0.000
Acidobacteria	Unclassified	sf_1	37	soil clone BAC-14A1	4.695	0.001	0.000
Proteobacteria	Unclassified	sf_3	8036	Uranium mill tailings soil sample clone Sh765B-TzT-132	4.698	0.002	0.000
Proteobacteria	Xanthobacteraceae	sf_1	6971	Thiobacillus sp. str. 104	4.699	0.001	0.000
Bacteroidetes	Bacteroidaceae	sf_12	5256	termite gut homogenate clone Rs-D38 bacterium	4.702	0.002	0.000
Proteobacteria	Syntrophobacteraceae	sf_1	9731	uranium mining waste pile clone JG37-AG-90 proteobacterium	4.705	0.001	0.000
Firmicutes	Enterococcaceae	sf_1	3288	hyper-ammonia producing swine storage pits manure	4.709	0.002	0.000
Proteobacteria	Unclassified	sf_1	3084	coal effluent wetland clone RCP216	4.711	0.002	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	6252	Riftia pachyptila's tube clone R103-B20	4.711	0.001	0.000
Planctomycetes	Pirellulae	sf_3	4769	anoxic marine sediment clone LD1-PA40	4.717	0.001	0.000
Proteobacteria	Coxiellaceae	sf_3	7893	agricultural soil clone SC-I-71	4.718	0.002	0.000
Acidobacteria	Unclassified	sf_1	1049	soil clone C112	4.718	0.001	0.000
Synergistes	Unclassified	sf_3	117	termite gut homogenate clone Rs-D89	4.720	0.002	0.000
Verrucomicrobia	Unclassified	sf_5	686	Guaymas Basin hydrothermal sediment clone a2b018	4.722	0.001	0.000
Firmicutes	Erysipelotrichaceae	sf_3	3965	TCE-contaminated site clone ccslm238	4.722	0.001	0.000

Cyanobacteria	Unclassified	sf_5	5064	Oscillatoria neglecta str. M-82	4.724	0.001	0.000
Spirochaetes	Spirochaetaceae	sf_1	6491	termite gut homogenate clone BCf8-03	4.725	0.001	0.000
Actinobacteria	Cellulomonadaceae	sf_1	1748	Beutenbergia cavernosa str. DSM 12333	4.725	0.001	0.000
Firmicutes	Clostridiaceae	sf_12	4502		4.728	0.001	0.000
Firmicutes	Clostridiaceae	sf_12	4427	Clostridium tyrobutyricum str. NIZO 51	4.732	0.003	0.000
Firmicutes	Peptostreptococcaceae	sf_5	58	Peptostreptococcus sp. str. E3_32	4.734	0.001	0.000
Proteobacteria	Unclassified	sf_3	8339	water 5 m downstream manure clone 35ds5	4.735	0.002	0.000
OP3	Unclassified	sf_2	349	soil clone PBS-25	4.736	0.001	0.000
Proteobacteria	Unclassified	sf_1	9128	Lucina nassula gill symbiont	4.738	0.001	0.000
Proteobacteria	Syntrophaceae	sf_3	9665	Syntrophus gentianae str. HQgoe1	4.739	0.002	0.000
WS3	Unclassified	sf_3	95	marine sediment above hydrate ridge clone Hyd24-32	4.740	0.001	0.000
Cyanobacteria	Chloroplasts	sf_5	4966	Adiantum pedatum	4.745	0.001	0.000
Proteobacteria	Unclassified	sf_1	6830	coal effluent wetland clone RCP124	4.748	0.002	0.000
Proteobacteria	Rickettsiaceae	sf_1	6809	Rickettsia rickettsii str. Sawtooth	4.749	0.001	0.000
OP9/JS1	Unclassified	sf_1	2491	deep marine sediment clone MB-B2-103	4.751	0.001	0.000
Cyanobacteria	Unclassified	sf_9	5038	Rumen isolate str. YS2	4.751	0.001	0.000
Natronoanaerobiu	Unclassified	sf_1	3745	Mono Lake at depth 35m station 6 July 2000 clone ML635J-45	4.752	0.001	0.000
Proteobacteria	Desulfobulbaceae	sf_1	10332	Psychrophilic sulfate-reducing isolate str. LSv23 bacterium	4.752	0.001	0.000
Proteobacteria	Unclassified	sf_3	8926	inactive deep-sea hydrothermal vent chimneys clone IheB2-13	4.754	0.002	0.000
Actinobacteria	Unclassified	sf_2	1233		4.760	0.001	0.000
TM7	Unclassified	sf_1	3025		4.763	0.001	0.000

Actinobacteria	Sporichthyaceae	sf_1	1695	lichen-dominated Antarctic cryptoendolithic community clone FBP417	4.763	0.001	0.000
Proteobacteria	Pseudomonadaceae	sf_1	8288		4.765	0.001	0.000
Proteobacteria	Alcaligenaceae	sf_1	7768	swine intestine clone p-861-a5	4.766	0.001	0.000
Chloroflexi	Unclassified	sf_1	927	hydrothermal vent polychaete mucous clone P. palm C 37	4.768	0.001	0.000
Actinobacteria	Microthrixineae	sf_1	1576	actinobacterium clone ML817J-10	4.770	0.001	0.000
Proteobacteria	Desulfobacteraceae	sf_5	9666	marine sediment above hydrate ridge clone Hyd89-13 proteobacterium	4.770	0.001	0.000
Gemmatimonadete	Unclassified	sf_5	1127	uranium mining waste pile near Johanngeorgenstadt soil clone JG37-AG-21	4.771	0.001	0.000
Actinobacteria	Unclassified	sf_3	2045	hypersaline lake clone ML602J-44	4.772	0.001	0.000
Bacteroidetes	Porphyromonadaceae	sf_1	5817	termite gut homogenate clone Rs-N56 bacterium	4.772	0.003	0.000
Proteobacteria	Acetobacteraceae	sf_1	7600	Acetobacter pomorum str. LTH2458	4.774	0.001	0.000
Proteobacteria	Sphingomonadaceae	sf_1	6663	Sphingopyxis flavimaris str. SW-151	4.775	0.001	0.000
Proteobacteria	Unclassified	sf_3	8646		4.776	0.001	0.000
Proteobacteria	Unclassified	sf_9	10049	DCP-dechlorinating consortium clone SHA-72	4.777	0.001	0.000
Proteobacteria	Methylococcaceae	sf_1	9438	marine sediment above hydrate ridge clone Hyd24-01 proteobacterium	4.778	0.001	0.000
Spirochaetes	Spirochaetaceae	sf_1	6494	termite gut homogenate clone Rs-C47 sp.	4.779	0.001	0.000
Proteobacteria	Xanthomonadaceae	sf_3	9211	penguin droppings sediments clone KD8-80	4.780	0.001	0.000
Proteobacteria	Pasteurellaceae	sf_1	8308	Haemophilus actinomycetemcomitans	4.782	0.002	0.000
Verrucomicrobia	Verrucomicrobia subdivision 7	sf_1	446	anoxic marine sediment clone LD1-PA34	4.782	0.001	0.000
Proteobacteria	Unclassified	sf_3	9568	forested wetland clone RCP2-96	4.788	0.001	0.000
Bacteroidetes	Flexibacteraceae	sf_19	5667	penguin droppings sediments clone KD6-118	4.791	0.001	0.000
Proteobacteria	Unclassified	sf_6	7340	uranium mining waste pile soil sample clone JG30-KF-AS50	4.791	0.001	0.000

Proteobacteria	Thiotrichaceae	sf_3	8703	Beggiatoa sp. str. AA5A	4.794	0.001	0.000
Proteobacteria	Pasteurellaceae	sf_1	8848	str. 86355	4.796	0.002	0.000
Spirochaetes	Spirochaetaceae	sf_1	6565	termite gut clone NkS-Oxy25	4.799	0.001	0.000
Unclassified	Unclassified	sf_156	4291	Mono Lake at depth 35m station 6 July 2000 clone ML635J-21 G+C	4.804	0.002	0.000
Proteobacteria	Syntrophobacteraceae	sf_1	9864	uranium mining waste pile clone JG37-AG-133 proteobacterium	4.806	0.001	0.000
Firmicutes	Clostridiaceae	sf_12	4378		4.807	0.001	0.000
Spirochaetes	Spirochaetaceae	sf_1	6502	Treponema denticola str. ATCC35405	4.807	0.001	0.000
Proteobacteria	Caedibacteraceae	sf_4	7157	acid mine drainage clone ASL45	4.810	0.001	0.000
Proteobacteria	Pseudomonadaceae	sf_1	9300	Lyrodus pedicellatus symbiont	4.813	0.001	0.000
Planctomycetes	Pirellulae	sf_3	4677	aerobic basin clone CY0ARA032A03	4.815	0.001	0.000
Proteobacteria	Comamonadaceae	sf_1	8152	nephridia Octolasion lacteum clone Ol2-2	4.827	0.001	0.000
Unclassified	Unclassified	sf_160	485	thermal spring mat clone O1aA90	4.828	0.001	0.000
Lentisphaerae	Unclassified	sf_5	9704	Cytophaga sp. str. Dex80-64	4.829	0.002	0.000
Firmicutes	Peptostreptococcaceae	sf_5	2694	oral periodontitis clone FX028	4.829	0.001	0.000
Deinococcus-Ther	Unclassified	sf_2	637	hypersaline pond clone LA7-B27N	4.831	0.001	0.000
Proteobacteria	Unclassified	sf_1	10259		4.833	0.001	0.000
Bacteroidetes	Flexibacteraceae	sf_19	6261	Arctic sea ice cryoconite clone ARKCRY-50	4.836	0.001	0.000
Proteobacteria	Unclassified	sf_1	9959	forested wetland clone FW110	4.838	0.001	0.000
Firmicutes	Lactobacillaceae	sf_1	3366	Lactobacillus saerimneri str. GDA154 LMG 22087 DSM 16049 (T); CCUG 48462 (T)	4.842	0.001	0.000
Firmicutes	Clostridiaceae	sf_12	4566	swine intestine clone p-2657-65A5	4.845	0.001	0.000
Chloroflexi	Unclassified	sf_1	159	anaerobic bioreactor clone SHD-235	4.847	0.001	0.000

Firmicutes	Unclassified	sf_17	2432		4.851	0.001	0.000
Firmicutes	Acholeplasmataceae	sf_1	3945	Ash witches'-broom phytoplasma str. AshWB	4.856	0.001	0.000
Unclassified	Unclassified	sf_160	7444		4.863	0.001	0.000
Firmicutes	Clostridiaceae	sf_12	4560	Clostridium beijerinckii str. NCIMB9362	4.868	0.001	0.000
Proteobacteria	Unclassified	sf_1	9059	activated sludge clone SBRH10	4.869	0.001	0.000
Firmicutes	Eubacteriaceae	sf_1	28	termite gut homogenate clone Rs-H81 bacterium	4.871	0.001	0.000
Proteobacteria	Rhodocyclaceae	sf_1	8052	Dechloromonas aromatica str. RCB	4.872	0.001	0.000
Proteobacteria	Unclassified	sf_3	468	marine sediment clone Sva0515	4.875	0.001	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	5997	Flavobacterium aquatile	4.879	0.001	0.000
Chloroflexi	Unclassified	sf_1	2397	deep marine sediment clone MB-C2-127	4.879	0.001	0.000
Spirochaetes	Spirochaetaceae	sf_1	6488	Treponema primitia str. ZAS-1	4.879	0.001	0.000
Proteobacteria	Legionellaceae	sf_1	8836	Legionella pneumophila str. Paris	4.879	0.001	0.000
Proteobacteria	Unclassified	sf_2	7188	termite gut homogenate clone Rs-B50 proteobacterium	4.880	0.001	0.000
Proteobacteria	Unclassified	sf_4	9951	forested wetland clone FW13	4.881	0.001	0.000
Firmicutes	Lactobacillaceae	sf_1	3767	Lactobacillus suebicus str. CECT 5917T	4.882	0.001	0.000
Proteobacteria	Magnetospirillaceae	sf_1	6922	Dechlorospirillum sp. str. SN1	4.882	0.001	0.000
Proteobacteria	Methylobacteriaceae	sf_1	7585	Methylobacterium thiocyanatum str. ALL/SCN-P	4.883	0.001	0.000
Proteobacteria	Unclassified	sf_9	9760	deep marine sediment clone MB-A2-137	4.888	0.001	0.000
Proteobacteria	Enterobacteriaceae	sf_1	8747	uranium waste soil clone JG30-KF-CM35	4.888	0.001	0.000
OP10	Unclassified	sf_1	326	geothermal clone ST01-SN3H	4.894	0.001	0.000
SPAM	Unclassified	sf_1	738	uranium mining waste clone JG34-KF-252	4.894	0.001	0.000

Caldithrix	Caldithraceae	sf_2	91	benzoate-degrading consortium clone BA059	4.895	0.001	0.000
Proteobacteria	Bradyrhizobiaceae	sf_1	7126	ground water Tomsk-7 clone S15A-MN96 proteobacterium	4.895	0.001	0.000
Proteobacteria	Alcaligenaceae	sf_1	7932	Achromobacter subsp. denitrificans str. DSM 30026 (T)	4.896	0.001	0.000
Proteobacteria	Unclassified	sf_1	9678	coal effluent wetland clone RCP185	4.897	0.001	0.000
Firmicutes	Bacillaceae	sf_1	234	Bacillus vulcani str. 3S-1	4.902	0.000	0.000
Firmicutes	Unclassified	sf_1	2359	UASB granular sludge clone JP	4.902	0.001	0.000
Proteobacteria	Burkholderiaceae	sf_1	7747		4.905	0.000	0.000
Lentisphaerae	Unclassified	sf_5	10027	Cytophaga sp. str. Dex80-43	4.905	0.001	0.000
Proteobacteria	Unclassified	sf_6	8780	uranium mining mill tailing clone GR-296.II.89 GR-296.II.89	4.911	0.000	0.000
Chloroflexi	Unclassified	sf_9	72	Charon's Cascade near Echo River October 2000 clone CCD21	4.914	0.001	0.000
Proteobacteria	Roseococcaceae	sf_1	7500	Great Artesian Basin clone B35	4.915	0.001	0.000
Proteobacteria	Helicobacteraceae	sf_3	10590	termite gut homogenate clone Rs-H40 proteobacterium	4.919	0.002	0.000
Proteobacteria	Unclassified	sf_1	10384	deep-sea hydrothermal vent clone VC1.2-cl06	4.919	0.000	0.000
Firmicutes	Paenibacillaceae	sf_1	3299	Brevibacillus borstelensis str. LMG 15536	4.925	0.001	0.000
Firmicutes	Unclassified	sf_1	3481		4.926	0.002	0.000
Proteobacteria	Alteromonadaceae	sf_1	9562	Alteromonadaceae clone PH-B55N	4.927	0.001	0.000
Firmicutes	Unclassified	sf_3	4280		4.938	0.000	0.000
Firmicutes	Peptococc/Acidaminococc	sf_11	300	benzene-contaminated groundwater clone ZZ12C8	4.939	0.001	0.000
Firmicutes	Peptococc/Acidaminococc	sf_11	771	Dialister pneumosintes str. ATCC 33048	4.939	0.001	0.000
Firmicutes	Streptococcaceae	sf_1	3251	Streptococcus cristatus str. ATCC 51100	4.943	0.002	0.000
Firmicutes	Lachnospiraceae	sf_5	2943	human thigh wound isolate str. MDA2477	4.944	0.001	0.000

Bacteroidetes	Rikenellaceae	sf_5	5892	anoxic bulk soil flooded rice microcosm clone BSV73	4.945	0.001	0.000
Firmicutes	Lachnospiraceae	sf_5	3171	Lachnospira pectinoschiza	4.946	0.001	0.000
Spirochaetes	Spirochaetaceae	sf_1	6460	termite gut homogenate clone Rs-B69 sp.	4.947	0.001	0.000
Firmicutes	Unclassified	sf_4	4526	TCE-contaminated site clone ccslm210	4.948	0.001	0.000
Firmicutes	Carnobacteriaceae	sf_1	3536		4.949	0.001	0.000
Firmicutes	Peptostreptococcaceae	sf_5	2993	oral clone P2PB_46 P3	4.950	0.001	0.000
Bacteroidetes	Flexibacteraceae	sf_19	5563	Cytophaga sp. I-545	4.953	0.001	0.000
Actinobacteria	Coriobacteriaceae	sf_1	1459	termite gut homogenate clone Rs-J59 bacterium	4.955	0.000	0.000
Lentisphaerae	Unclassified	sf_5	10330	Mono lake clone ML635J-58	4.960	0.001	0.000
Firmicutes	Lachnospiraceae	sf_5	2991	rumen clone 3C3d-8	4.960	0.001	0.000
Proteobacteria	Desulfovibrionaceae	sf_1	10248	Desulfovibrio giganteus str. DSM 4370	4.964	0.001	0.000
Proteobacteria	Polyangiaceae	sf_3	9755	bacterioplankton clone ZA3704c	4.964	0.001	0.000
Proteobacteria	Unclassified	sf_1	7199	uranium mill tailings clone Gitt-KF-194	4.966	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4278	granular sludge clone R1p16	4.969	0.000	0.000
Bacteroidetes	Rikenellaceae	sf_5	5889	termite gut homogenate clone Rs-F73 bacterium	4.970	0.002	0.000
Proteobacteria	Desulfobacteraceae	sf_5	10136	Guaymas Basin hydrothermal vent sediments clone B01R011	4.974	0.001	0.000
Proteobacteria	Burkholderiaceae	sf_1	7782	Burkholderia hospita str. LMG 20598T	4.975	0.001	0.000
Proteobacteria	Nitrosomonadaceae	sf_1	8145	Nitrosomonas eutropha str. Nm57	4.976	0.000	0.000
Firmicutes	Peptococc/Acidaminococc	sf_11	31	Dehalobacter restrictus str. TEA	4.976	0.001	0.000
Planctomycetes	Pirellulae	sf_3	4670		4.985	0.000	0.000
Cyanobacteria	Chloroplasts	sf_5	4976	Calypogeia muelleriana	4.985	0.000	0.000

Actinobacteria	Kineosporiaceae	sf_1	1087	Kineosporia aurantiaca str. JCM3230	4.988	0.000	0.000
Proteobacteria	Unclassified	sf_1	7067	Blastochloris sulfoviridis str. GN1	4.991	0.000	0.000
Proteobacteria	Desulfobacteraceae	sf_5	9800	forested wetland clone FW57	4.993	0.001	0.000
Proteobacteria	Unclassified	sf_6	6918	soil near uranium mill tailings clone KCM-C-45	4.996	0.002	0.000
Firmicutes	Lachnospiraceae	sf_5	2965	oral endodontic infection clone MCE9_173	4.998	0.000	0.000
Firmicutes	Erysipelotrichaceae	sf_3	3981	phototrophic sludge clone PSB-M-3	4.998	0.001	0.000
Proteobacteria	Rhodocyclaceae	sf_1	8131		4.999	0.000	0.000
Cyanobacteria	Unclassified	sf_8	5206		5.000	0.002	0.000
TM6	Unclassified	sf_1	9803	forest soil clone S1204	5.005	0.001	0.000
Proteobacteria	Campylobacteraceae	sf_3	10523	Riftia pachyptila's tube clone R103-B70	5.006	0.001	0.000
Firmicutes	Lactobacillaceae	sf_1	3547	Lactobacillus frumenti str. TMW 1.666	5.009	0.000	0.000
Firmicutes	Syntrophomonadaceae	sf_5	2483	trichloroethene-contaminated site clone FTLM142 bacterium	5.009	0.001	0.000
Verrucomicrobia	Verrucomicrobiaceae	sf_7	29	Fucophilus fucoidanolyticus str. SI-1234	5.011	0.001	0.000
Proteobacteria	Polyangiaceae	sf_3	9900	bioreactor clone mle1-27	5.012	0.000	0.000
Actinobacteria	Microbacteriaceae	sf_1	1135	Rhodoglobus vestalii str. LV3	5.012	0.001	0.000
Nitrospira	Nitrospiraceae	sf_1	984	uranium mining waste pile clone JG37-AG-131 sp.	5.026	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	2764		5.029	0.000	0.000
Firmicutes	Bacillaceae	sf_1	3909	Bacillus subtilis subsp. Marburg str. 168	5.034	0.001	0.000
Firmicutes	Lachnospiraceae	sf_5	3109	Catonella morbi str. ATCC 51271	5.035	0.002	0.000
Bacteroidetes	Prevotellaceae	sf_1	5426	tongue dorsa clone DO014	5.035	0.001	0.000
Bacteroidetes	Prevotellaceae	sf_1	6152	rumen clone RF37	5.035	0.000	0.000

Bacteroidetes	Prevotellaceae	sf_1	5249	Prevotella denticola str. ATCC 35308	5.037	0.001	0.000
Acidobacteria	Acidobacteriaceae	sf_14	541	uranium mill tailings soil sample clone GuBH2-AG-47 sp.	5.037	0.001	0.000
Proteobacteria	Unclassified	sf_6	6665	hydrocarbon-degrading consortium clone 4-Org2-22	5.038	0.000	0.000
Bacteroidetes	Prevotellaceae	sf_1	5946	tongue dorsa clone DO027	5.040	0.002	0.000
Firmicutes	Peptococc/Acidaminococc	sf_11	181	Allisonella histaminiformans str. MR2	5.044	0.000	0.000
Actinobacteria	Unclassified	sf_3	1577	termite gut homogenate clone Rs-N91 bacterium	5.051	0.000	0.000
Actinobacteria	Cellulomonadaceae	sf_1	1923	Actinobacteria str. VeCb6	5.052	0.000	0.000
Spirochaetes	Spirochaetaceae	sf_1	6458	termite gut clone NkS34	5.057	0.000	0.000
Unclassified	Unclassified	sf_160	10012		5.057	0.001	0.000
Firmicutes	Peptostreptococcaceae	sf_5	2796	human subgingival plaque clone BB142	5.058	0.000	0.000
Verrucomicrobia	Verrucomicrobiaceae	sf_6	871		5.062	0.000	0.000
Proteobacteria	Neisseriaceae	sf_1	8143	subgingival dental plaque clone AK105	5.066	0.000	0.000
Proteobacteria	Rhodocyclaceae	sf_1	7824	termite gut homogenate clone Rs-B77 proteobacterium	5.066	0.001	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	5942		5.066	0.001	0.000
Proteobacteria	Unclassified	sf_6	7575		5.067	0.001	0.000
Proteobacteria	Unclassified	sf_1	10622		5.068	0.002	0.000
Firmicutes	Peptostreptococcaceae	sf_5	393	Anaerococcus vaginalis str. CCUG 31349	5.069	0.001	0.000
Firmicutes	Clostridiaceae	sf_12	4296	Clostridiaceae str. A4d	5.070	0.000	0.000
Proteobacteria	Enterobacteriaceae	sf_1	8477	marine sediment clone Limfjorden L8	5.073	0.001	0.000
Proteobacteria	Unclassified	sf_6	7312		5.077	0.000	0.000
Bacteroidetes	Unclassified	sf_15	5481	marine sediment above hydrate ridge clone Hyd89-72 bacterium	5.078	0.001	0.000

Proteobacteria	Desulfobulbaceae	sf_1	9739	gas hydrate clone Hyd89-51	5.083	0.001	0.000
Bacteroidetes	Prevotellaceae	sf_1	6239	tongue dorsa clone DO033	5.091	0.002	0.000
Unclassified	Unclassified	sf_160	6360		5.093	0.000	0.000
Firmicutes	Paenibacillaceae	sf_1	3630		5.096	0.000	0.000
Firmicutes	Sporolactobacillaceae	sf_1	3365	Bacillus sp. clone ML615J-19	5.098	0.000	0.000
Bacteroidetes	Prevotellaceae	sf_1	5331	tongue dorsa clone DO022	5.099	0.001	0.000
Cyanobacteria	Unclassified	sf_1	5219	Synechococcus sp. str. UH7	5.100	0.000	0.000
Natronoanaerobiu	Unclassified	sf_1	2437	Mono Lake at depth 23m station 6 July 2000 clone ML623J-19	5.101	0.000	0.000
Firmicutes	Clostridiaceae	sf_21	4471	termite gut clone Rs-058	5.104	0.000	0.000
Acidobacteria	Unclassified	sf_1	588	TCB-transforming consortium clone SJA-36	5.107	0.000	0.000
Firmicutes	Unclassified	sf_3	2373		5.107	0.001	0.000
Planctomycetes	Planctomycetaceae	sf_3	4855	aerobic basin clone CY0ARA026D10	5.109	0.000	0.000
Bacteroidetes	Sphingobacteriaceae	sf_1	5492	Sphingobacterium sp. str. HC-6155	5.109	0.001	0.000
Proteobacteria	Helicobacteraceae	sf_3	10612	hydrothermal vent polychaete mucous clone P. palm C/A 64	5.113	0.001	0.000
Verrucomicrobia	Unclassified	sf_4	169	anoxic marine sediment clone LD1-PA26	5.114	0.001	0.000
Firmicutes	Peptostreptococcaceae	sf_5	2714	termite gut homogenate clone Rs-N27 bacterium	5.118	0.000	0.000
Firmicutes	Streptococcaceae	sf_1	3685	Streptococcus gordonii str. ATCC 10558	5.124	0.001	0.000
Firmicutes	Leuconostocaceae	sf_1	3573	Leuconostoc ficulneum str. FS-1	5.125	0.000	0.000
Firmicutes	Lactobacillaceae	sf_1	3600	Lactobacillus crispatus str. NCTC 4	5.126	0.001	0.000
Acidobacteria	Acidobacteriaceae	sf_14	6412	acid mine drainage clone TRB82	5.126	0.000	0.000
Firmicutes	Lactobacillaceae	sf_1	3634	Lactobacillus letivazi str. JCL3994	5.127	0.001	0.000

Proteobacteria	Polyangiaceae	sf_3	10298	marine tidal mat clone BTM36	5.131	0.001	0.000
Firmicutes	Lachnospiraceae	sf_5	2693	ruminantium str. GA195	5.135	0.001	0.000
Firmicutes	Bacillaceae	sf_1	3383		5.136	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	3152	tongue dorsa clone DO016	5.138	0.000	0.000
Proteobacteria	Bradyrhizobiaceae	sf_1	6887	Bradyrhizobium str. YB2	5.143	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4477	termite gut homogenate clone Rs-N85 bacterium	5.148	0.001	0.000
Chlorobi	Chlorobiaceae	sf_1	995	Chlorobium limicola str. M1	5.149	0.001	0.000
Firmicutes	Unclassified	sf_8	4536	Mono Lake at depth 35m station 6 July 2000 clone ML635J-14 G+C	5.149	0.001	0.000
Firmicutes	Unclassified	sf_4	2398	deep marine sediment clone MB-C2-106	5.150	0.000	0.000
OP10	Unclassified	sf_5	9782	Rocky Mountain alpine soil clone S1a-1H	5.150	0.000	0.000
Acidobacteria	Unclassified	sf_1	897	Mammoth cave clone CCM8b	5.150	0.000	0.000
Spirochaetes	Spirochaetaceae	sf_1	6579	termite gut clone NkS83	5.151	0.000	0.000
Proteobacteria	Bradyrhizobiaceae	sf_1	6636	Bradyrhizobium elkanii str. USDA 76	5.151	0.001	0.000
Proteobacteria	Bradyrhizobiaceae	sf_1	7522	Bradyrhizobium sp. str. KKI14	5.151	0.001	0.000
Planctomycetes	Planctomycetaceae	sf_3	4948	anoxic basin clone CY0ARA027D01	5.152	0.000	0.000
Firmicutes	Acholeplasmataceae	sf_1	4046	Pigeon pea witches'-broom mycoplasma-like organism	5.152	0.001	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	5955	Flavobacterium sp. str. V4.MS.29 = MM_2747	5.156	0.001	0.000
Spirochaetes	Spirochaetaceae	sf_1	6476	termite gut clone NkS50	5.157	0.000	0.000
Deinococcus-Ther	Unclassified	sf_1	178	Thermus sp. str. C4	5.157	0.000	0.000
Proteobacteria	Unclassified	sf_1	10407	hydrothermal sediment clone AF420342	5.162	0.000	0.000
Bacteroidetes	Unclassified	sf_4	5785	Mono Lake at depth 35 m station 6 July 2000 clone ML635J-56	5.164	0.001	0.000

Proteobacteria	Desulfovibrionaceae	sf_1	10212		5.164	0.000	0.000
Spirochaetes	Spirochaetaceae	sf_1	6506	termite gut homogenate clone Rs-J58 sp.	5.167	0.001	0.000
Firmicutes	Acholeplasmataceae	sf_1	4044		5.168	0.001	0.000
Proteobacteria	Campylobacteraceae	sf_3	10563	Campylobacter sp. str. DSM 806	5.169	0.001	0.000
Spirochaetes	Spirochaetaceae	sf_1	6523	termite gut homogenate clone Rs-J64 sp.	5.173	0.000	0.000
Actinobacteria	Micrococcaceae	sf_1	1610	Arthrobacter sp str. AC-51	5.174	0.001	0.000
Spirochaetes	Spirochaetaceae	sf_1	6526	Treponema sp. str. 7CPL208	5.176	0.001	0.000
Proteobacteria	Pseudomonadaceae	sf_1	8850	Agrobacterium agile str. IAM12615	5.177	0.001	0.000
Verrucomicrobia	Verrucomicrobiaceae	sf_6	613	hydrothermal vent polychaete mucous clone P. palm C 85	5.181	0.001	0.000
Firmicutes	Aerococcaceae	sf_1	3519	Granulicatella elegans str. DSM 11693; B1333	5.184	0.000	0.000
Cyanobacteria	Chloroplasts	sf_5	5192	Cycas revoluta	5.186	0.000	0.000
Proteobacteria	Polyangiaceae	sf_3	10309	Nannocystis exedens str. Na e571	5.186	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	4571	Faecalibacterium prausnitzii str. ATCC 27766	5.187	0.000	0.000
Firmicutes	Unclassified	sf_1	2490	Desulfotomaculum solfataricum str. V21	5.188	0.000	0.000
Actinobacteria	Kineosporiaceae	sf_1	1961	Kineococcus aurantiacus str. IFO 15268	5.188	0.000	0.000
Bacteroidetes	Unclassified	sf_15	5578	ground water Tomsk-7 clone S15A-MN91	5.194	0.000	0.000
Proteobacteria	Ectothiorhodospiraceae	sf_1	9450	Halorhodospira neutrophila str. SG 3304	5.194	0.001	0.000
Cyanobacteria	Unclassified	sf_1	5034	Spirulina subsalsa str. FACHB351	5.196	0.000	0.000
Proteobacteria	Unclassified	sf_1	9418	uranium mining waste pile clone JG37-AG-14 proteobacterium	5.197	0.001	0.000
Proteobacteria	Thiotrichaceae	sf_3	8559	Thioploca ingrica	5.202	0.000	0.000
Proteobacteria	Unclassified	sf_1	6945	Rhizobiales str. A48	5.203	0.001	0.000

Cyanobacteria	Unclassified	sf_5	5188	Acaryochloris marina str. MBIC11017	5.210	0.001	0.000
Firmicutes	Clostridiaceae	sf_12	4418	termite gut homogenate clone Rs-H18 bacterium	5.210	0.000	0.000
Chloroflexi	Unclassified	sf_1	2438	deep marine sediment clone MB-A2-110	5.211	0.001	0.000
Proteobacteria	Unclassified	sf_6	7647		5.212	0.000	0.000
Spirochaetes	Spirochaetaceae	sf_1	6507	termite gut clone NkS-Ste2	5.214	0.000	0.000
SR1	Unclassified	sf_1	2900		5.218	0.001	0.000
Proteobacteria	Campylobacteraceae	sf_3	10538	Arcobacter cryaerophilus	5.221	0.002	0.000
Proteobacteria	Unclassified	sf_9	9993		5.224	0.001	0.000
Proteobacteria	Bradyrhizobiaceae	sf_1	6867	heavy metal-contaminated soil clone a13131	5.227	0.000	0.000
Firmicutes	Peptostreptococcaceae	sf_5	3080	termite gut homogenate clone Rs-F43 bacterium	5.229	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4359	termite gut homogenate clone Rs-C69 bacterium	5.232	0.001	0.000
Spirochaetes	Spirochaetaceae	sf_3	6558	Spironema culicis str. BR91	5.244	0.000	0.000
Proteobacteria	Polyangiaceae	sf_4	9733	bacterioplankton clone ZA3735c	5.248	0.001	0.000
Proteobacteria	Unclassified	sf_1	10489	S17sBac16 complete clone	5.252	0.001	0.000
Proteobacteria	Unclassified	sf_3	9473	Arctic pack ice; clone ARKDMS-58	5.255	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4607	Clostridium novyi str. NCTC538	5.256	0.000	0.000
Proteobacteria	Caulobacteraceae	sf_1	6968	Brevundimonas diminuta str. IAM 12691T	5.256	0.000	0.000
Proteobacteria	Pseudomonadaceae	sf_1	8813	Lyrodus pedicellatus symbiont	5.259	0.001	0.000
Firmicutes	Streptococcaceae	sf_1	3637	str. 37236	5.260	0.000	0.000
BRC1	Unclassified	sf_1	5143	soil clone PBS-II-1	5.260	0.001	0.000
Actinobacteria	Kineosporiaceae	sf_1	1598	lichen-dominated Antarctic cryptoendolithic community clone FBP402	5.263	0.000	0.000

Proteobacteria	Unclassified	sf_1	10076	Great Artesian Basin clone G13	5.269	0.001	0.000
Firmicutes	Peptococc/Acidaminococc	sf_11	126	oral periodontitis clone FY011	5.275	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4610	Clostridium putrefaciens str. DSM 1291	5.284	0.000	0.000
Firmicutes	Streptococcaceae	sf_1	3907	aortic heart valve patient with endocarditis clone v6	5.286	0.000	0.000
Actinobacteria	Acidimicrobiaceae	sf_1	1749	forest soil clone DUNssu275 (-3A) (OTU#188)	5.286	0.000	0.000
Proteobacteria	Helicobacteraceae	sf_3	10438	hydrocarbon seep clone GCA014	5.292	0.001	0.000
Proteobacteria	Unclassified	sf_1	7156	termite gut homogenate clone Rs-M62 proteobacterium	5.300	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	3075	Roseburia intestinalis str. L1-82	5.301	0.000	0.000
Fusobacteria	Fusobacteriaceae	sf_3	1034	Ilyobacter tartaricus str. DSM 2382 T	5.302	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4265	termite gut homogenate clone Rs-N70 bacterium	5.306	0.001	0.000
Firmicutes	Peptostreptococcaceae	sf_5	2729	DCP-dechlorinating consortium clone SHA-58	5.307	0.000	0.000
Nitrospira	Nitrospiraceae	sf_2	697	forested wetland clone FW118	5.309	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	2801	Butyrivibrio fibrisolvens	5.310	0.000	0.000
Actinobacteria	Dermabacteraceae	sf_1	2053	Brachybacterium nesterenkovii str. DSM 9573	5.311	0.000	0.000
Unclassified	Unclassified	sf_160	4410		5.313	0.000	0.000
Bacteroidetes	Bacteroidaceae	sf_12	5320	Bacteroides distasonis	5.313	0.001	0.000
Proteobacteria	Desulfobacteraceae	sf_5	10319	sulfate-reducing habitat clone SLM-CP-116	5.313	0.001	0.000
Actinobacteria	Unclassified	sf_3	1687	Jonesia quinghaiensis str. DSM 15701	5.315	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	3236	Firmicutes sp. oral strain str. FTB41	5.323	0.000	0.000
Proteobacteria	Helicobacteraceae	sf_3	10448	Helicobacter felis str. Dog-1	5.326	0.001	0.000
Planctomycetes	Planctomycetaceae	sf_3	4831	Planctomyces brasiliensis	5.326	0.001	0.000

Actinobacteria	Coriobacteriaceae	sf_1	2021	termite gut homogenate clone Rs-D41 bacterium	5.327	0.001	0.000
Proteobacteria	Helicobacteraceae	sf_3	10518	Helicobacter pylori str. ATCC 49396T	5.329	0.001	0.000
Firmicutes	Peptococc/Acidaminococc	sf_11	1036	Great Artesian Basin clone G07	5.330	0.000	0.000
Proteobacteria	Unclassified	sf_1	10497	UASB reactor granular sludge clone PD-UASB-2 proteobacterium	5.330	0.001	0.000
Proteobacteria	Unclassified	sf_1	7382	marine clone Arctic95C-5	5.333	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4266	termite gut homogenate clone Rs-M86 bacterium	5.334	0.000	0.000
Proteobacteria	Methylococcaceae	sf_1	8243	isolate str. IR	5.336	0.001	0.000
Proteobacteria	Campylobacteraceae	sf_3	10464	Campylobacter sp. str. NO2B	5.337	0.000	0.000
Actinobacteria	Microbacteriaceae	sf_1	1197	Arctic sea ice ARK10173	5.338	0.000	0.000
Proteobacteria	Unclassified	sf_4	9741	uranium mining waste pile clone JG37-AG-30 proteobacterium	5.338	0.000	0.000
OP10	Unclassified	sf_1	514	sludge clone SBRA136	5.340	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	3077	Clostridium glycolicum str. DSM 1288	5.341	0.000	0.000
Chloroflexi	Unclassified	sf_9	205	uranium mining waste pile clone JG34-KF-221	5.342	0.000	0.000
Cyanobacteria	Chloroplasts	sf_5	5147	Emiliania huxleyi str. Plymouth Marine Laborator PML 92	5.344	0.001	0.000
Bacteroidetes	Bacteroidaceae	sf_12	5950		5.346	0.000	0.000
TM7	Unclassified	sf_1	3679		5.347	0.001	0.000
Proteobacteria	Helicobacteraceae	sf_3	10432	Riftia pachyptila's tube clone R76-B51	5.352	0.001	0.000
Firmicutes	Clostridiaceae	sf_12	4622	termite gut clone Rs-L36	5.358	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	2931	termite gut homogenate clone Rs-G77 bacterium	5.359	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	3087	Butyrivibrio hungatei str. Su6	5.362	0.000	0.000
Cyanobacteria	Unclassified	sf_9	5164	termite gut homogenate clone Rs-H34	5.363	0.000	0.000

Proteobacteria	Unclassified	sf_1	10475	hydrothermal sediment clone AF420359	5.364	0.000	0.000
Firmicutes	Bacillaceae	sf_1	571	Bacillus caldotenax str. DSM 406	5.367	0.000	0.000
Firmicutes	Alicyclobacillaceae	sf_1	3368	geothermal site isolate str. G1	5.368	0.000	0.000
Firmicutes	Bacillaceae	sf_1	3460	Geobacillus jurassicus str. DS1	5.369	0.000	0.000
Proteobacteria	Desulfobacteraceae	sf_5	10031	Antarctic sediment clone SB1_49	5.372	0.001	0.000
Proteobacteria	Desulfuromonaceae	sf_1	10020	uranium mill tailings soil sample clone GuBH2-AG-114 proteobacterium	5.372	0.000	0.000
Proteobacteria	Neisseriaceae	sf_1	7945	Aquaspirillum serpens str. IAM 13944	5.373	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	4525	termite gut homogenate clone Rs-Q18 bacterium	5.373	0.000	0.000
Proteobacteria	Unclassified	sf_1	10530	hydrothermal vent clone CH5_6_BAC_16SrRNA_9N_EPR	5.373	0.001	0.000
Firmicutes	Unclassified	sf_1	2351	Desulfotomaculum thermobenzoicum str. DSM 6193	5.377	0.000	0.000
Proteobacteria	Campylobacteraceae	sf_3	10549	Campylobacter upsaliensis str. LMG 8850	5.377	0.001	0.000
Proteobacteria	Helicobacteraceae	sf_3	10444	Helicobacter suncus str. Kaz-2	5.384	0.001	0.000
Firmicutes	Acholeplasmataceae	sf_1	3961	Clover yellow edge mycoplasma-like organism	5.385	0.001	0.000
Firmicutes	Lachnospiraceae	sf_5	2698	termite gut homogenate clone Rs-B88 bacterium	5.386	0.000	0.000
Firmicutes	Bacillaceae	sf_1	3848	Bacillus sp. str. TUT1007	5.387	0.001	0.000
Firmicutes	Clostridiaceae	sf_12	4321	termite gut homogenate clone Rs-C76 bacterium	5.387	0.000	0.000
Proteobacteria	Helicobacteraceae	sf_3	10411	termite gut homogenate clone Rs-P71 proteobacterium	5.391	0.001	0.000
Actinobacteria	Unclassified	sf_3	1405	Arthrobacter ureafaciens str. DSM 20126	5.391	0.000	0.000
Proteobacteria	Unclassified	sf_20	2520		5.396	0.000	0.000
Proteobacteria	Unclassified	sf_1	7400	sphagnum peat bog clone K-5b5	5.399	0.000	0.000
Proteobacteria	Syntrophobacteraceae	sf_1	10221	granular sludge clone R3p4	5.403	0.000	0.000

TM7	Unclassified	sf_1	5061		5.404	0.000	0.000
Proteobacteria	Sphingomonadaceae	sf_1	7535	Sphingomonas paucimobilis str. GIFU2395	5.405	0.000	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	6274		5.406	0.000	0.000
Proteobacteria	Unclassified	sf_3	7765		5.408	0.001	0.000
Actinobacteria	Microbacteriaceae	sf_1	1186	Cryocola antiquus str. VKM 103PF	5.408	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4575	Clostridium subterminale str. NCIMB 10746	5.414	0.000	0.000
Firmicutes	Unclassified	sf_1	522	UASB granular sludge clone UT-1	5.414	0.001	0.000
Firmicutes	Bacillaceae	sf_1	462	Geobacillus thermodenitrificans str. DSM 466	5.417	0.000	0.000
Bacteroidetes	Prevotellaceae	sf_1	5720	Prevotella sp. str. E9_34	5.421	0.001	0.000
Actinobacteria	Micrococcaceae	sf_1	1213	Kocuria roseus	5.423	0.000	0.000
Chlorobi	Chlorobiaceae	sf_1	859	Chlorobium phaeovibrioides str. 2631	5.428	0.000	0.000
Spirochaetes	Spirochaetaceae	sf_1	6508	termite hindgut clone mpsp2	5.430	0.000	0.000
Chloroflexi	Unclassified	sf_9	375	forest soil clone C043	5.436	0.000	0.000
Proteobacteria	Desulfobacteraceae	sf_5	9940	Antarctic sediment clone SB2_56	5.438	0.000	0.000
Proteobacteria	Sphingomonadaceae	sf_1	7537	Antarctic clone FBP255 proteobacterium	5.440	0.000	0.000
Proteobacteria	Unclassified	sf_1	10427	hydrothermal vent clone CH3_17_BAC_16SrRNA_9N_EPR	5.443	0.001	0.000
Firmicutes	Streptococcaceae	sf_1	3543		5.443	0.000	0.000
Actinobacteria	Micrococcaceae	sf_1	1494	Arthrobacter agilis str. DSM 20550	5.451	0.000	0.000
Proteobacteria	Unclassified	sf_1	10480	hydrothermal vent polychaete mucous clone P. palm C 84	5.452	0.001	0.000
Actinobacteria	Corynebacteriaceae	sf_1	1374		5.455	0.000	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	5969	Capnocytophaga ochracea str. ATCC 27872 T	5.457	0.001	0.000

Proteobacteria	Bradyrhizobiaceae	sf_1	7390	Afipia genosp. 10 str. G8996	5.460	0.000	0.000
Proteobacteria	Helicobacteraceae	sf_23	10443	Helicobacter pylori str. 85D08	5.460	0.001	0.000
Proteobacteria	Helicobacteraceae	sf_3	10576	Helicobacter sp. 'liver 3' str. liver 3	5.460	0.001	0.000
Firmicutes	Unclassified	sf_17	2324		5.465	0.000	0.000
Firmicutes	Peptostreptococcaceae	sf_5	2722	termite gut homogenate clone Rs-E61 bacterium	5.466	0.000	0.000
Acidobacteria	Unclassified	sf_1	6426	Great Artesian Basin clone B11	5.467	0.000	0.000
Firmicutes	Peptococc/Acidaminococc	sf_11	534	chlorobenzene-degrading consortium clone IIA-26	5.468	0.001	0.000
Firmicutes	Clostridiaceae	sf_12	4555	Clostridium tyrobutyricum	5.471	0.000	0.000
Proteobacteria	Bradyrhizobiaceae	sf_1	6768	Rhodopseudomonas palustris str. GH	5.473	0.000	0.000
Firmicutes	Peptococc/Acidaminococc	sf_11	39	forested wetland clone RCP2-71	5.474	0.001	0.000
Firmicutes	Clostridiaceae	sf_12	4598	Clostridium sardiniense str. DSM 600	5.477	0.000	0.000
Cyanobacteria	Chloroplasts	sf_5	5039	Cape Hatteras picoplankton clone OM270	5.479	0.000	0.000
Proteobacteria	Polyangiaceae	sf_3	9671	hydrothermal sediment clone AF420357	5.481	0.000	0.000
Spirochaetes	Spirochaetaceae	sf_1	6554	termite gut homogenate clone Rs-A43 sp.	5.481	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	4613	rumen clone 3C0d-3	5.484	0.000	0.000
Firmicutes	Peptostreptococcaceae	sf_5	2797	hyper-ammonia producing swine storage pits manure	5.486	0.000	0.000
Proteobacteria	Sphingomonadaceae	sf_1	7548	Afipia genosp. 13 str. G8991	5.487	0.000	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	5317	Tenacibaculum maritimum str. IFO 15946	5.488	0.000	0.000
Chloroflexi	Unclassified	sf_1	2339	uranium mill tailings soil sample clone Sh765B-TzT-20 bacterium	5.489	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	3218	termite gut homogenate clone Rs-N53	5.492	0.001	0.000
Spirochaetes	Leptospiraceae	sf_3	6496	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	5.493	0.001	0.000

Proteobacteria	Comamonadaceae	sf_1	7856	Variovorax paradoxus	5.495	0.000	0.000
Proteobacteria	Desulfobacteraceae	sf_5	10267	marine sediment clone Hyd89-61 proteobacterium	5.496	0.000	0.000
Proteobacteria	Helicobacteraceae	sf_3	10572	Helicobacter sp	5.499	0.001	0.000
Proteobacteria	Syntrophobacteraceae	sf_1	10013	hydrothermal sediment clone AF420341	5.499	0.000	0.000
Proteobacteria	Unclassified	sf_1	9945	acid mine drainage clone BA18	5.502	0.001	0.000
Proteobacteria	Desulfobacteraceae	sf_5	10046	Desulfobacterium cetonicum str. DSM 7267 oil recovery water	5.503	0.000	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	5915	ground water Tomsk-7 clone S15A-MN27 bacterium	5.503	0.000	0.000
Proteobacteria	Unclassified	sf_1	10405	hydrothermal sediment clone AF420346	5.504	0.001	0.000
Proteobacteria	Helicobacteraceae	sf_3	10385		5.509	0.001	0.000
Proteobacteria	Helicobacteraceae	sf_3	10451	Helicobacter heilmannii str. C4S	5.509	0.001	0.000
DSS1	Unclassified	sf_2	38	DCP-dechlorinating consortium clone SHA-109	5.510	0.000	0.000
Chloroflexi	Unclassified	sf_2	2532	trichloroethene-contaminated site clone FTL276 bacterium	5.511	0.000	0.000
Firmicutes	Peptococc/Acidaminococc	sf_11	242	Desulfosporosinus orientis str. DSMZ 7493	5.511	0.001	0.000
Firmicutes	Lachnospiraceae	sf_5	4623	human colonic clone HuCA1	5.512	0.000	0.000
Spirochaetes	Spirochaetaceae	sf_1	6532	termite gut clone NkS39	5.513	0.000	0.000
Proteobacteria	Rhodocyclaceae	sf_1	8127	Zoogloea resiniphila str. PIV-3A2y	5.514	0.001	0.000
Proteobacteria	Campylobacteraceae	sf_3	10447	Sulfurospirillum deleyianum str. Spirillum 5175	5.518	0.001	0.000
Proteobacteria	Sphingomonadaceae	sf_1	7075	Novosphingobium sp. str. K16	5.523	0.000	0.000
Bacteroidetes	Crenotrichaceae	sf_11	5619	anaerobic VC-degrading enrichment clone VC10 bacterium	5.528	0.000	0.000
BRC1	Unclassified	sf_2	118	penguin droppings sediments clone KD1-1	5.528	0.000	0.000
Proteobacteria	Thiotrichaceae	sf_3	8741	marine sediment clone Limfjorden L10	5.530	0.000	0.000

Bacteroidetes	Flavobacteriaceae	sf_1	5906	Capnocytophaga sputigena str. ATCC 33612	5.534	0.001	0.000
Proteobacteria	Helicobacteraceae	sf_3	10534	Helicobacter pylori	5.536	0.001	0.000
Proteobacteria	Unclassified	sf_1	7060		5.539	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	2994	termite gut clone Rs-L15	5.540	0.001	0.000
Firmicutes	Unclassified	sf_17	3476		5.546	0.000	0.000
Spirochaetes	Spirochaetaceae	sf_1	6489	Mixotricha paradoxa clone mp1	5.552	0.000	0.000
Firmicutes	Peptococc/Acidaminococc	sf_11	304	Selenomonas ruminantium str.JCM6582	5.553	0.000	0.000
Bacteroidetes	Unclassified	sf_15	5784	fruiting body Pleurotus eryngii clone PE01	5.556	0.001	0.000
Bacteroidetes	Prevotellaceae	sf_1	6259		5.556	0.000	0.000
Fusobacteria	Fusobacteriaceae	sf_3	644	Ilyobacter polytropus str. DSM 2926 T	5.568	0.000	0.000
Proteobacteria	Enterobacteriaceae	sf_1	8403	Selenate-reducing isolate str. KE4OH1	5.569	0.000	0.000
Firmicutes	Aerococcaceae	sf_1	3840	Trichococcus pasteurii str. KoTa2	5.571	0.001	0.000
Fusobacteria	Fusobacteriaceae	sf_1	488	Fusobacterium nucleatum subsp. vincentii str. ATCC 49256	5.575	0.001	0.000
Firmicutes	Lachnospiraceae	sf_5	2756	Roseburia faecalis str. M6/1	5.580	0.000	0.000
Firmicutes	Bacillaceae	sf_1	3845	hot synthetic compost clone pPD15	5.584	0.000	0.000
Actinobacteria	Coriobacteriaceae	sf_1	1926	Collinsella aerofaciens str. JCM7791	5.587	0.000	0.000
Spirochaetes	Spirochaetaceae	sf_1	6490	termite gut homogenate clone BCf4-14	5.594	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	4434	termite gut homogenate clone Rs-K11 bacterium	5.596	0.000	0.000
Chloroflexi	Unclassified	sf_1	583	anaerobic bioreactor clone SHD-238	5.600	0.000	0.000
Actinobacteria	Micrococcaceae	sf_1	1593	Arthrobacter globiformis	5.604	0.000	0.000
Firmicutes	Unclassified	sf_1	3289	Isobaculum melis CCUG 37660T	5.605	0.000	0.000

Firmicutes	Unclassified	sf_17	926		5.606	0.000	0.000
Chloroflexi	Unclassified	sf_7	757	DCP-dechlorinating consortium clone SHA-8	5.606	0.000	0.000
OP9/JS1	Unclassified	sf_1	2489	Guaymas Basin hydrothermal vent sediments clone B01R005	5.611	0.000	0.000
Spirochaetes	Spirochaetaceae	sf_1	6557	spirochete clone ML320J-13	5.612	0.001	0.000
Firmicutes	Lachnospiraceae	sf_5	3017	termite gut homogenate clone Rs-D48 bacterium	5.613	0.000	0.000
Firmicutes	Lactobacillaceae	sf_1	3418	Lactobacillus subsp. aviarius	5.618	0.001	0.000
Chlorobi	Unclassified	sf_9	6146	sludge clone A12b	5.626	0.000	0.000
Firmicutes	Lactobacillaceae	sf_1	3566	Lactobacillus pontis str. LTH 2587	5.627	0.001	0.000
Firmicutes	Lachnospiraceae	sf_5	4511	ckncm314-B7-17 clone	5.628	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4275	Clostridium botulinum str. type G	5.629	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4554	termite gut clone Rs-068	5.630	0.000	0.000
Firmicutes	Lactobacillaceae	sf_1	3521	Pediococcus inopinatus str. DSM 20285	5.631	0.000	0.000
Firmicutes	Peptococc/Acidaminococc	sf_11	428	chlorobenzene-degrading consortium clone IIIA-1	5.638	0.000	0.000
Firmicutes	Leuconostocaceae	sf_1	3497	Weissella koreensis S-5673	5.639	0.000	0.000
Firmicutes	Peptococc/Acidaminococc	sf_11	761	Anaeroglobus geminatus str. AIP313.00; CIP 106856; CCUG 44773	5.641	0.001	0.000
Firmicutes	Acholeplasmataceae	sf_1	3975	Black raspberry witches'-broom phytoplasma str. BRWB witches'-broom	5.643	0.001	0.000
Firmicutes	Clostridiaceae	sf_12	4272	termite gut homogenate clone Rs-M34 bacterium	5.647	0.001	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	5367	patient's bronchoalveolar lavage isolate str. MDA2507 sp.	5.650	0.000	0.000
Cyanobacteria	Unclassified	sf_1	5190	Plectonema sp. str. F3	5.653	0.001	0.000
Spirochaetes	Spirochaetaceae	sf_1	6571	Mixotricha paradoxa is flagellate hindgut Mastotermes darwiniensis clone mp4 of	5.653	0.000	0.000
Cyanobacteria	Unclassified	sf_5	4998		5.666	0.000	0.000

Firmicutes	Bacillaceae	sf_1	3900	Bacillus licheniformis str. DSM 13	5.667	0.000	0.000
Cyanobacteria	Unclassified	sf_1	4978	LPP-group isolate str. MBIC10087	5.668	0.000	0.000
Firmicutes	Mycoplasmataceae	sf_1	3929	Mycoplasma gypsbengalensis str. Gb-V33	5.683	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4589	Clostridium butyricum str. ATCC43755	5.685	0.000	0.000
Firmicutes	Peptococc/Acidaminococc	sf_11	562	oral endodontic infection clone MCE10_265	5.687	0.000	0.000
Proteobacteria	Sphingomonadaceae	sf_1	7036	Lutibacterium anuloederans str. LC8	5.687	0.000	0.000
Actinobacteria	Micrococcaceae	sf_1	2020	Rothia dentocariosa str. ChDC B200	5.690	0.001	0.000
Proteobacteria	Unclassified	sf_4	10024	hydrothermal sediment clone AF420338	5.697	0.000	0.000
Proteobacteria	Campylobacteraceae	sf_3	10456	Campylobacter showae	5.698	0.001	0.000
Proteobacteria	Helicobacteraceae	sf_3	10442	Helicobacter cetorum str. MIT 99-5656	5.701	0.001	0.000
Proteobacteria	Unclassified	sf_1	8957	marine clone Arctic97C-5	5.701	0.000	0.000
Spirochaetes	Spirochaetaceae	sf_1	6568	Spirochaeta sp	5.706	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4524	termite gut clone Rs-093	5.711	0.000	0.000
Spirochaetes	Spirochaetaceae	sf_1	6562	forested wetland clone RCP1-96	5.718	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	2668	termite gut homogenate clone Rs-G40 bacterium	5.721	0.001	0.000
Firmicutes	Clostridiaceae	sf_12	4369	termite gut homogenate clone Rs-N73 bacterium	5.724	0.000	0.000
Bacteroidetes	Unclassified	sf_15	5353	trichloroethene-contaminated site clone FTLpost3 bacterium	5.724	0.001	0.000
Firmicutes	Clostridiaceae	sf_12	4614	Clostridium sp. str. JC3	5.727	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	4315	termite gut homogenate clone Rs-N94 bacterium	5.730	0.000	0.000
Unclassified	Unclassified	sf_106	243	hot spring clone OPB25	5.730	0.000	0.000
Chloroflexi	Unclassified	sf_9	2539	penguin droppings sediments clone KD4-96	5.735	0.000	0.000

Chloroflexi	Unclassified	sf_12	2523	sponge clone TK10	5.737	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4229		5.738	0.000	0.000
Firmicutes	Aerococcaceae	sf_1	3326	Nostocoida limicola I str. Ben206	5.743	0.001	0.000
Firmicutes	Clostridiaceae	sf_12	4339	Clostridium chauvoei str. ATCC 10092T	5.745	0.000	0.000
Proteobacteria	Sphingomonadaceae	sf_15	7035	Sphingomonas asaccharolytica str. IFO 10564-T	5.748	0.000	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	5473		5.753	0.000	0.000
Proteobacteria	Desulfobacteraceae	sf_5	9875	hydrothermal sediment clone AF420354	5.755	0.000	0.000
Proteobacteria	Unclassified	sf_1	8037	Chitinimonas taiwanensis str. cf	5.757	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	3111	rumen clone 6C3d-11	5.763	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4507	termite gut homogenate clone Rs-N21 bacterium	5.765	0.000	0.000
Proteobacteria	Syntrophobacteraceae	sf_1	9661	DCP-dechlorinating consortium clone SHD-1	5.774	0.000	0.000
Proteobacteria	Helicobacteraceae	sf_3	10454	Helicobacter pullorum str. NCTC 12826	5.776	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	4567	human colonic clone HuCB5	5.778	0.000	0.000
Proteobacteria	Campylobacteraceae	sf_3	10540	Campylobacter showae str. LMG 12636	5.786	0.001	0.000
Firmicutes	Unclassified	sf_1	2541	UASB granular sludge clone UT-2	5.790	0.000	0.000
Spirochaetes	Spirochaetaceae	sf_1	6529	termite gut homogenate clone BCf10-21	5.791	0.000	0.000
Proteobacteria	Helicobacteraceae	sf_3	10430	Helicobacter heilmannii str. MM2	5.798	0.001	0.000
Firmicutes	Bacillaceae	sf_1	385	Geobacillus stearothermophilus str. T10	5.799	0.000	0.000
Proteobacteria	Bdellovibrionaceae	sf_1	10010	uranium mining waste pile clone JG37-AG-139 proteobacterium	5.811	0.000	0.000
Proteobacteria	Unclassified	sf_1	6653	Kaistobacter koreensis str. PB229	5.812	0.000	0.000
Proteobacteria	Campylobacteraceae	sf_3	10484	Campylobacter helveticus	5.819	0.000	0.000

Firmicutes	Lachnospiraceae	sf_5	4212	termite gut clone Rs-061	5.820	0.000	0.000
Proteobacteria	Unclassified	sf_3	8114		5.827	0.000	0.000
Proteobacteria	Helicobacteraceae	sf_3	10520	Helicobacter sp. blood isolate 964	5.833	0.001	0.000
Proteobacteria	Desulfobacteraceae	sf_5	9818	temperate estuarine mud clone KM62	5.833	0.000	0.000
Actinobacteria	Micrococcaceae	sf_1	1966	TCE-contaminated site clone ccspost2208	5.835	0.000	0.000
Proteobacteria	Geobacteraceae	sf_1	9956	forested wetland clone FW140	5.836	0.000	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	5267	bacterioplankton clone AEGEAN_179	5.843	0.000	0.000
Proteobacteria	Sphingomonadaceae	sf_1	7100	Novosphingobium capsulatum str. GIFU11526	5.845	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4550	swine intestine clone p-320-a3	5.845	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	4335	termite gut homogenate clone Rs-N86 bacterium	5.852	0.000	0.000
Bacteroidetes	Flexibacteraceae	sf_19	5994	Hymenobacter sp. str. NS/50	5.861	0.000	0.000
Proteobacteria	Helicobacteraceae	sf_3	10436	Helicobacter aurati str. MIT 97-5075c	5.863	0.001	0.000
Firmicutes	Clostridiaceae	sf_12	2786	Clostridium glycolicum str. CIN5	5.868	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4177	Clostridium subterminale DSM 2636	5.871	0.000	0.000
Firmicutes	Acholeplasmataceae	sf_1	4045	Chinaberry yellows phytoplasma	5.876	0.000	0.000
Proteobacteria	Rhodocyclaceae	sf_1	7907	Thauera aromatica str. LG356	5.880	0.000	0.000
Actinobacteria	Micrococcaceae	sf_1	1557	Arthrobacter oxydans str. DSM 20119	5.887	0.000	0.000
Firmicutes	Bacillaceae	sf_1	3345	Bacillus pumilus str. S9	5.890	0.000	0.000
Cyanobacteria	Unclassified	sf_1	5210	lichen-dominated Antarctic cryptoendolithic community clone FBP403	5.891	0.000	0.000
Unclassified	Unclassified	sf_160	651		5.897	0.000	0.000
Proteobacteria	Unclassified	sf_1	8035		5.898	0.000	0.000

Proteobacteria	Campylobacteraceae	sf_3	10446		5.899	0.000	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	5521	Flavobacteriaceae str. SW269	5.913	0.000	0.000
Cyanobacteria	Chloroplasts	sf_5	5060	Skeletonema pseudocostatum str. CSIRO CS-76	5.915	0.000	0.000
OP9/JS1	Unclassified	sf_1	969	DCP-dechlorinating consortium clone SHA-1	5.917	0.000	0.000
Spirochaetes	Spirochaetaceae	sf_1	6583	termite gut homogenate clone Rs-J42 sp.	5.931	0.000	0.000
Acidobacteria	Acidobacteriaceae	sf_14	6350	soil isolate Ellin337	5.935	0.000	0.000
Acidobacteria	Acidobacteriaceae	sf_14	6421	PCB-polluted soil clone WD217	5.938	0.000	0.000
Proteobacteria	Nitrospinaceae	sf_2	594	uranium mining mill tailing clone GR-296.II.52 GR-296.I.52	5.947	0.000	0.000
Proteobacteria	Desulfobacteraceae	sf_5	9939	marine methane seep clone 1427	5.956	0.000	0.000
Firmicutes	Peptococc/Acidaminococc	sf_11	710	Centipeda periodontii str. HB-2	5.973	0.000	0.000
Cyanobacteria	Unclassified	sf_1	5049	Oscillatoria spongeliae str. 520bg	5.973	0.000	0.000
Proteobacteria	Unclassified	sf_1	7123	uranium mining waste pile near Johanngeorgenstadt soil clone JG37-AG-102	5.988	0.000	0.000
Proteobacteria	Sphingomonadaceae	sf_1	7016	Sphingomonas sp. str. SAFR-027	5.989	0.000	0.000
Firmicutes	Peptococc/Acidaminococc	sf_11	709	Selenomonas ruminantium str.S20	6.014	0.000	0.000
Proteobacteria	Unclassified	sf_9	9798	uranium mill tailings soil sample clone GuBH2-AD/TzT-67 proteobacterium	6.017	0.000	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	5914	Psychroserpens burtonensis str. S2-64	6.023	0.000	0.000
Proteobacteria	Alcaligenaceae	sf_1	8062	Brackiella oedipodis str. LMG 1945 R8846	6.025	0.000	0.000
Fusobacteria	Fusobacteriaceae	sf_3	721	human mouth clone P2PB_51	6.030	0.000	0.000
Proteobacteria	Unclassified	sf_4	8169	forested wetland clone RCP2-54	6.033	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	4533	termite gut homogenate clone Rs-N06 bacterium	6.035	0.000	0.000
Synergistes	Unclassified	sf_3	353	UASB reactor granular sludge clone PD-UASB-13 G+C	6.037	0.000	0.000

Firmicutes	Clostridiaceae	sf_12	4156	MCB-contaminated groundwater-treating reactor clone RA9C1	6.045	0.000	0.000
Cyanobacteria	Unclassified	sf_5	5027		6.046	0.000	0.000
Proteobacteria	Unclassified	sf_1	10084	acid mine drainage clone AS6	6.051	0.000	0.000
Firmicutes	Unclassified	sf_7	4216		6.051	0.000	0.000
Proteobacteria	Helicobacteraceae	sf_3	10428	Flexispira rappini FH 9702248	6.052	0.001	0.000
Proteobacteria	Syntrophobacteraceae	sf_1	10021	uranium mill tailings soil sample clone Sh765B-TzT-29 proteobacterium	6.057	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4415	termite gut homogenate clone Rs-K32 bacterium	6.083	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	2681	termite gut homogenate clone Rs-K41 bacterium	6.084	0.000	0.000
Firmicutes	Halobacillaceae	sf_1	3769	Gracilibacillus sp. str. YIM-kkny13	6.105	0.000	0.000
Firmicutes	Staphylococcaceae	sf_1	3524	Gemella haemolysans	6.109	0.000	0.000
Proteobacteria	Helicobacteraceae	sf_3	10462	Helicobacter rodentium str. MIT 96-1312	6.109	0.000	0.000
Firmicutes	Acholeplasmataceae	sf_1	3976		6.117	0.000	0.000
Fusobacteria	Fusobacteriaceae	sf_3	694	tongue dorsa clone DR011	6.121	0.000	0.000
Proteobacteria	Helicobacteraceae	sf_3	10562	Helicobacter rappini W.Tee-Yu	6.132	0.000	0.000
Proteobacteria	Helicobacteraceae	sf_3	10548	Helicobacter rappini W.Tee-Bat	6.132	0.001	0.000
Proteobacteria	Bradyrhizobiaceae	sf_1	7029		6.136	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4300	termite gut clone Rs-060	6.138	0.000	0.000
Proteobacteria	Syntrophaceae	sf_3	10067	benzoate-degrading consortium clone BA044	6.154	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4297		6.173	0.000	0.000
Proteobacteria	Helicobacteraceae	sf_3	10552	Helicobacter winghamensis str. NLEP 97-1611	6.184	0.000	0.000
Bacteroidetes	Prevotellaceae	sf_1	5893	tongue dorsa clone DO045	6.185	0.000	0.000

Cyanobacteria	Unclassified	sf_1	5010	LPP-group cyanobacterium isolate str. QSSC5cya QSSC5cya	6.192	0.000	0.000
Proteobacteria	Rhodocyclaceae	sf_1	7762	Elbe River snow isolate Iso18 Iso18_1411	6.195	0.000	0.000
Chloroflexi	Unclassified	sf_1	106	DCP-dechlorinating consortium clone SHD-231	6.229	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4459	termite gut clone Rs-109	6.239	0.000	0.000
Actinobacteria	Acidimicrobiaceae	sf_1	1090		6.244	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4582	swine intestine clone p-2600-9F5	6.244	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	4514	termite gut homogenate clone Rs-B34 bacterium	6.245	0.000	0.000
Actinobacteria	Microthrixineae	sf_1	1964	bacterioplankton clone AEGEAN_247	6.247	0.000	0.000
Unclassified	Unclassified	sf_160	333		6.257	0.000	0.000
Proteobacteria	Sphingomonadaceae	sf_1	6650	Sphingomonas phyllosphaerae str. FA1	6.264	0.000	0.000
Proteobacteria	Geobacteraceae	sf_1	482	trichloroethene-contaminated site clone FTLM205 proteobacterium	6.265	0.000	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	5401	Capnocytophaga gingivalis str. ChDC OS45	6.298	0.000	0.000
Natronoanaerobiu	Unclassified	sf_1	3570	Bacillus sp. clone ML1228J-1	6.313	0.000	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	6104		6.334	0.000	0.000
Firmicutes	Peptococc/Acidaminococc	sf_11	862	Megasphaera micronuciformis str. AIP 412.00; CIP 107280	6.343	0.000	0.000
Proteobacteria	Sphingomonadaceae	sf_1	7440	Sphingobium chungbukense str. DJ77	6.383	0.000	0.000
Firmicutes	Enterococcaceae	sf_1	3680	Melissococcus plutonius str. NCDO 2440	6.384	0.000	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	5301		6.395	0.000	0.000
Proteobacteria	Thiotrichaceae	sf_3	8752	Beggiatoa sp. str. MS-81-1c	6.405	0.000	0.000
Proteobacteria	Geobacteraceae	sf_1	10171		6.408	0.000	0.000
Proteobacteria	Desulfoarculaceae	sf_2	10227	marine sediment clone Bol11	6.414	0.000	0.000

Proteobacteria	Unclassified	sf_4	9884	forested wetland clone RCP2-62	6.432	0.000	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	6269	acidic forest soil clone UC1	6.432	0.000	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	5991	Tenacibaculum ovolyticum str. IAM14318	6.452	0.000	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	5436	Arctic sea ice ARK10004	6.469	0.000	0.000
Bacteroidetes	Porphyromonadaceae	sf_1	5429		6.471	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	4510	termite gut homogenate clone Rs-Q53 bacterium	6.485	0.000	0.000
Natronoanaerobiu	Unclassified	sf_1	4377	Mono Lake at depth 35m station 6 July 2000 clone ML635J-65 G+C	6.490	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4310	termite gut clone Rs-056	6.496	0.000	0.000
Firmicutes	Lactobacillaceae	sf_1	3696	Lactobacillus kalixensis str. Kx127A2;	6.512	0.000	0.000
Proteobacteria	Campylobacteraceae	sf_3	10463	Campylobacter subsp. fetus	6.518	0.000	0.000
Proteobacteria	Unclassified	sf_1	7028		6.518	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	4540	termite gut homogenate clone Rs-M18 bacterium	6.526	0.000	0.000
Proteobacteria	Campylobacteraceae	sf_3	10397	groundwater clone 1006	6.529	0.000	0.000
Firmicutes	Aerococcaceae	sf_1	3504	Marinilactibacillus psychrotolerans str. O21	6.552	0.000	0.000
Chlorobi	Unclassified	sf_8	636	consortium clone Cart-N3 bacterium	6.599	0.000	0.000
TM7	Unclassified	sf_1	2697	midgut homogenate Pachnoda ephippiata larva clone PeM47	6.637	0.000	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	6248	Capnocytophaga sp. oral strain str. S3	6.647	0.000	0.000
Chloroflexi	Unclassified	sf_1	2534	forest soil clone S085	6.647	0.000	0.000
Firmicutes	Enterococcaceae	sf_1	3433	Tetragenococcus muriaticus	6.660	0.000	0.000
Proteobacteria	Neisseriaceae	sf_1	8092	Neisseria dentiae str. V33	6.666	0.000	0.000
Proteobacteria	Unclassified	sf_3	9813	hydrothermal sediment clone AF420340	6.688	0.000	0.000

Firmicutes	Lactobacillaceae	sf_1	3885	Pediococcus pentosaceus	6.692	0.000	0.000
Firmicutes	Enterococcaceae	sf_1	3298	Enterococcus saccharolyticus str. LMG 11427	6.697	0.000	0.000
Firmicutes	Lactobacillaceae	sf_1	3490	Lactobacillus suntoryeus str. LH	6.699	0.000	0.000
Firmicutes	Enterococcaceae	sf_1	3382		6.700	0.000	0.000
Chloroflexi	Unclassified	sf_1	76	DCP-dechlorinating consortium clone SHA-147	6.703	0.000	0.000
Firmicutes	Paenibacillaceae	sf_1	3641	Brevibacillus sp. MN 47.2a	6.736	0.000	0.000
Acidobacteria	Acidobacteriaceae	sf_14	6364	Solibacter usitatus Ellin6076	6.754	0.000	0.000
Chloroflexi	Unclassified	sf_1	258	DCP-dechlorinating consortium clone SHD-14	6.765	0.000	0.000
Firmicutes	Lactobacillaceae	sf_1	3330	Lactobacillus kitasatonis str. KM9212	6.780	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	4155	termite gut homogenate clone Rs-K92 bacterium	6.800	0.000	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	5836	Capnocytophaga granulosa str. LMG 12119; FDC SD4	6.803	0.000	0.000
Actinobacteria	Unclassified	sf_1	1898	termite gut homogenate clone Rs-J10 bacterium	6.839	0.000	0.000
Firmicutes	Peptococc/Acidaminococc	sf_11	392	oral endodontic infection clone MCE7_134	6.843	0.000	0.000
Firmicutes	Lactobacillaceae	sf_1	3703	Lactobacillus salivarius str. RA2115	6.858	0.000	0.000
Bacteroidetes	Porphyromonadaceae	sf_1	5713	Porphyromonas catoniae str. ATCC 51270	6.878	0.000	0.000
Bacteroidetes	Flexibacteraceae	sf_19	5602		6.893	0.000	0.000
Firmicutes	Enterococcaceae	sf_1	3318	Enterococcus ratti str. ATCC 700914	6.926	0.000	0.000
Firmicutes	Enterococcaceae	sf_1	3261	Enterococcus mundtii str. LMG 10748	6.954	0.000	0.000
Bacteroidetes	Flexibacteraceae	sf_19	6124	Flexibacter flexilis subsp. pelliculosus str. IFO 16028 subsp.	6.993	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4180	termite gut homogenate clone Rs-M23 bacterium	7.013	0.000	0.000
Firmicutes	Lactobacillaceae	sf_1	3526	Lactobacillus sakei	7.059	0.000	0.000

Firmicutes	Lachnospiraceae	sf_5	4281	granular sludge clone UASB_brew_B86	7.083	0.000	0.000
Firmicutes	Enterococcaceae	sf_1	3713	Enterococcus cecorum str. ATCC43198	7.091	0.000	0.000
Firmicutes	Aerococcaceae	sf_1	3833	Carnobacterium alterfunditum	7.119	0.000	0.000
Firmicutes	Clostridiaceae	sf_12	4475	termite gut homogenate clone Rs-N02 bacterium	7.217	0.000	0.000
Acidobacteria	Unclassified	sf_1	6367	TCE-contaminated site clone FTL227	7.324	0.000	0.000
Acidobacteria	Unclassified	sf_1	6357	anaerobic benzene-degrading clone Cart-N4	7.498	0.000	0.000
Firmicutes	Enterococcaceae	sf_1	3881	Enterococcus dispar str. LMG 13521	7.614	0.000	0.000
Proteobacteria	Pasteurellaceae	sf_1	9213	Haemophilus quentini str. MCCM 02026	7.728	0.000	0.000
Chlorobi	Unclassified	sf_8	549	consortium clone Cart-N2 bacterium	7.762	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	4331	granular sludge clone UASB_brew_B84	7.854	0.000	0.000
Firmicutes	Aerococcaceae	sf_1	3870	Abiotrophia para-adiacens str. TKT1	7.870	0.000	0.000
Firmicutes	Lachnospiraceae	sf_5	4512	granular sludge clone UASB_brew_B25	7.902	0.000	0.000
Bacteroidetes	Flavobacteriaceae	sf_1	5726	Bergeyella sp. oral AK152 clone	8.319	0.000	0.000
Firmicutes	Enterococcaceae	sf_1	3598	Enterococcus solitarius str. DSM 5634	8.419	0.000	0.000

Table S3. Bacterial taxa significantly correlated with sinus symptom severity.

Phylum	Family	SF	Taxon ID	prokMSA Name	Estimate	P value	Q value
Actinobacteria	Corynebacteriaceae	sf_1	1493	Corynebacterium tuberculostearicum str. CIP102346	0.622	0.018	0.035
Actinobacteria	Corynebacteriaceae	sf_1	1192	Corynebacterium segmentosum str. CIP107068 (CCUG37878)	0.551	0.041	0.035
Firmicutes	Lactobacillaceae	sf_1	3547	Lactobacillus frumenti str. TMW 1.666	-0.532	0.050	0.035
Proteobacteria	Helicobacteraceae	sf_3	10520	Helicobacter sp. blood isolate 964	-0.533	0.050	0.035
Proteobacteria	Campylobacteraceae	sf_3	10538	Arcobacter cryaerophilus	-0.533	0.050	0.035
Unclassified	Unclassified	sf_106	243	hot spring clone OPB25	-0.533	0.050	0.035
Proteobacteria	Nitrospinaceae	sf_2	594	uranium mining mill tailing clone GR-296.II.52 GR-296.I.52	-0.533	0.049	0.035
Firmicutes	Acholeplasmataceae	sf_1	3977	Chinaberry yellows phytoplasma str. CbY1	-0.534	0.049	0.035
Bacteroidetes	Porphyromonadaceae	sf_1	5429		-0.534	0.049	0.035
Cyanobacteria	Chloroplasts	sf_5	5040	Solanum nigrum	-0.534	0.049	0.035
Proteobacteria	Bradyrhizobiaceae	sf_1	7390	Afipia genosp. 10 str. G8996	-0.534	0.049	0.035
Firmicutes	Lachnospiraceae	sf_5	2994	termite gut clone Rs-L15	-0.534	0.049	0.035
Synergistes	Unclassified	sf_3	117	termite gut homogenate clone Rs-D89	-0.534	0.049	0.035
Bacteroidetes	Flavobacteriaceae	sf_1	5401	Capnocytophaga gingivalis str. ChDC OS45	-0.534	0.049	0.035
Proteobacteria	Desulfobacteraceae	sf_5	10046	Desulfobacterium cetonicum str. DSM 7267 oil recovery water	-0.534	0.049	0.035
Verrucomicrobia	Verrucomicrobiaceae	sf_6	613	hydrothermal vent polychaete mucous clone P. palm C 85	-0.534	0.049	0.035
Proteobacteria	Unclassified	sf_1	10427	hydrothermal vent clone CH3_17_BAC_16SrRNA_9N_EPR	-0.534	0.049	0.035
Actinobacteria	Micrococcaceae	sf_1	1686	Yania halotolerans str. YIM 70085	-0.535	0.049	0.035
Unclassified	Unclassified	sf_160	4410		-0.535	0.049	0.035

Cyanobacteria	Unclassified	sf_1	5010	LPP-group cyanobacterium isolate str. QSSC5cya QSSC5cya	-0.535	0.049	0.035
Acidobacteria	Unclassified	sf_1	6357	anaerobic benzene-degrading clone Cart-N4	-0.535	0.049	0.035
Proteobacteria	Unclassified	sf_3	8961	Calyptogena magnifica symbiont	-0.535	0.049	0.035
Firmicutes	Acholeplasmataceae	sf_1	3945	Ash witches'-broom phytoplasma str. AshWB	-0.535	0.049	0.035
Firmicutes	Lachnospiraceae	sf_5	2693	ruminantium str. GA195	-0.535	0.048	0.035
Firmicutes	Peptococc/Acidaminococc	sf_11	865	Selenomonas sputigena str. ATCC 35185	-0.535	0.048	0.035
Firmicutes	Paenibacillaceae	sf_1	3641	Brevibacillus sp. MN 47.2a	-0.536	0.048	0.035
Planctomycetes	Planctomycetaceae	sf_3	4855	aerobic basin clone CY0ARA026D10	-0.536	0.048	0.035
Firmicutes	Lactobacillaceae	sf_1	3696	Lactobacillus kalixensis str. Kx127A2; LMG 22115T; DSM 16043T; CCUG 48459T	-0.537	0.048	0.035
Proteobacteria	Unclassified	sf_1	10259		-0.537	0.048	0.035
Firmicutes	Unclassified	sf_1	2541	UASB granular sludge clone UT-2	-0.537	0.048	0.035
Firmicutes	Lachnospiraceae	sf_5	2681	termite gut homogenate clone Rs-K41 bacterium	-0.537	0.048	0.035
Proteobacteria	Bradyrhizobiaceae	sf_1	7126	ground water Tomsk-7 clone S15A-MN96 proteobacterium	-0.537	0.048	0.035
Firmicutes	Syntrophomonadaceae	sf_5	2483	trichloroethene-contaminated site clone FTLM142 bacterium	-0.538	0.047	0.035
Firmicutes	Peptococc/Acidaminococc	sf_11	131	pig feces clone	-0.538	0.047	0.035
Proteobacteria	Unclassified	sf_3	8587	Mars Odyssey Orbiter and encapsulation facility clone T5-3	-0.538	0.047	0.035
Bacteroidetes	Flavobacteriaceae	sf_1	5906	Capnocytophaga sputigena str. ATCC 33612	-0.538	0.047	0.035
Bacteroidetes	Flavobacteriaceae	sf_1	5933	Flavobacterium columnare str. PH-97028 (IAM 14821)	-0.538	0.047	0.035
Firmicutes	Lachnospiraceae	sf_5	2965	oral endodontic infection clone MCE9_173	-0.538	0.047	0.035
Actinobacteria	Micrococcaceae	sf_1	1494	Arthrobacter agilis str. DSM 20550	-0.538	0.047	0.035
BRC1	Unclassified	sf_1	5143	soil clone PBS-II-1	-0.538	0.047	0.035

Firmicutes	Enterococcaceae	sf_1	3298	Enterococcus saccharolyticus str. LMG 11427	-0.539	0.047	0.035
Cyanobacteria	Unclassified	sf_9	5038	Rumen isolate str. YS2	-0.539	0.047	0.035
Firmicutes	Lachnospiraceae	sf_5	4335	termite gut homogenate clone Rs-N86 bacterium	-0.539	0.047	0.035
Firmicutes	Aerococcaceae	sf_1	3504	Marinilactibacillus psychrotolerans str. O21	-0.540	0.046	0.035
Bacteroidetes	Unclassified	sf_15	5257	marine? clone KD3-67	-0.540	0.046	0.035
Firmicutes	Peptococc/Acidaminococc	sf_11	534	chlorobenzene-degrading consortium clone IIA-26	-0.540	0.046	0.035
Spirochaetes	Spirochaetaceae	sf_1	6526	Treponema sp. str. 7CPL208	-0.540	0.046	0.035
Actinobacteria	Micrococcaceae	sf_1	1573	Arthrobacter nicotianae str. SB42	-0.541	0.046	0.035
Proteobacteria	Desulfoarculaceae	sf_2	10227	marine sediment clone Bol11	-0.541	0.046	0.035
Firmicutes	Clostridiaceae	sf_12	4278	granular sludge clone R1p16	-0.541	0.046	0.035
Proteobacteria	Unclassified	sf_1	7060		-0.541	0.046	0.035
Bacteroidetes	Unclassified	sf_4	5785	Mono Lake at depth 35 m station 6 July 2000 clone ML635J-56	-0.541	0.046	0.035
Firmicutes	Streptococcaceae	sf_1	3499	Streptococcus constellatus str. ATCC27823	-0.542	0.045	0.035
Firmicutes	Clostridiaceae	sf_12	4177	Clostridium subterminale DSM 2636	-0.542	0.045	0.035
Bacteroidetes	Rikenellaceae	sf_5	5889	termite gut homogenate clone Rs-F73 bacterium	-0.542	0.045	0.035
Proteobacteria	Bdellovibrionaceae	sf_1	10010	uranium mining waste pile clone JG37-AG-139 proteobacterium	-0.542	0.045	0.035
Firmicutes	Peptococc/Acidaminococc	sf_11	392	oral endodontic infection clone MCE7_134	-0.542	0.045	0.035
Bacteroidetes	Sphingobacteriaceae	sf_1	5513	crevicular epithelial cells clone AZ123	-0.543	0.045	0.035
Firmicutes	Mycoplasmataceae	sf_1	3929	Mycoplasma gypsbengalensis str. Gb-V33	-0.543	0.045	0.035
Firmicutes	Clostridiaceae	sf_12	4300	termite gut clone Rs-060	-0.543	0.045	0.035
Proteobacteria	Campylobacteraceae	sf_3	10484	Campylobacter helveticus	-0.543	0.045	0.035

OP10	Unclassified	sf_1	514	sludge clone SBRA136	-0.543	0.045	0.035
Proteobacteria	Syntrophobacteraceae	sf_1	10221	granular sludge clone R3p4	-0.543	0.045	0.035
Firmicutes	Lactobacillaceae	sf_1	3330	Lactobacillus kitasatonis str. KM9212	-0.544	0.044	0.035
BRC1	Unclassified	sf_2	118	penguin droppings sediments clone KD1-1	-0.544	0.044	0.035
Firmicutes	Peptococc/Acidaminococc	sf_11	39	forested wetland clone RCP2-71	-0.544	0.044	0.035
Proteobacteria	Pasteurellaceae	sf_1	9213	Haemophilus quentini str. MCCM 02026	-0.544	0.044	0.035
Firmicutes	Streptococcaceae	sf_1	3629	Streptococcus mutans str. UA96	-0.544	0.044	0.035
Proteobacteria	Unclassified	sf_9	9760	deep marine sediment clone MB-A2-137	-0.545	0.044	0.035
Firmicutes	Unclassified	sf_17	926		-0.546	0.044	0.035
Firmicutes	Staphylococcaceae	sf_1	3524	Gemella haemolysans	-0.546	0.043	0.035
Proteobacteria	Syntrophobacteraceae	sf_1	10021	uranium mill tailings soil sample clone Sh765B-TzT-29 proteobacterium	-0.546	0.043	0.035
Actinobacteria	Micrococcaceae	sf_1	1593	Arthrobacter globiformis	-0.546	0.043	0.035
Proteobacteria	Desulfobacteraceae	sf_5	9875	hydrothermal sediment clone AF420354	-0.546	0.043	0.035
Cyanobacteria	Chloroplasts	sf_5	4966	Adiantum pedatum	-0.547	0.043	0.035
Bacteroidetes	Prevotellaceae	sf_1	5893	tongue dorsa clone DO045	-0.547	0.043	0.035
Firmicutes	Peptococc/Acidaminococc	sf_11	562	oral endodontic infection clone MCE10_265	-0.547	0.043	0.035
Chlorobi	Unclassified	sf_8	636	benzene-degrading nitrate-reducing consortium clone Cart-N3 bacterium	-0.547	0.043	0.035
Firmicutes	Carnobacteriaceae	sf_1	3536		-0.548	0.043	0.035
Bacteroidetes	Flavobacteriaceae	sf_1	5473		-0.548	0.043	0.035
Proteobacteria	Syntrophobacteraceae	sf_1	9845	uranium mining waste pile clone JG37-AG-128 proteobacterium	-0.548	0.042	0.035
Proteobacteria	Campylobacteraceae	sf_3	10540	Campylobacter showae str. LMG 12636	-0.549	0.042	0.035

Proteobacteria	Sphingomonadaceae	sf_1	7100	Novosphingobium capsulatum str. GIFU11526	-0.549	0.042	0.035
Proteobacteria	Bradyrhizobiaceae	sf_1	6887	Bradyrhizobium str. YB2	-0.549	0.042	0.035
Chloroflexi	Unclassified	sf_1	76	DCP-dechlorinating consortium clone SHA-147	-0.550	0.042	0.035
Firmicutes	Clostridiaceae	sf_12	4265	termite gut homogenate clone Rs-N70 bacterium	-0.550	0.042	0.035
Bacteroidetes	Flavobacteriaceae	sf_1	5436	Arctic sea ice ARK10004	-0.550	0.042	0.035
Actinobacteria	Unclassified	sf_1	1898	termite gut homogenate clone Rs-J10 bacterium	-0.550	0.041	0.035
Firmicutes	Aerococcaceae	sf_1	3631	Abiotrophia defectiva str. GIFU12707 (ATCC49176)	-0.550	0.041	0.035
Firmicutes	Streptococcaceae	sf_1	3753	Streptococcus suis str. 8074	-0.551	0.041	0.035
Bacteroidetes	Flexibacteraceae	sf_19	6124	Flexibacter flexilis subsp. pelliculosus str. IFO 16028 subsp.	-0.551	0.041	0.035
Firmicutes	Enterococcaceae	sf_1	3382		-0.551	0.041	0.035
Firmicutes	Leuconostocaceae	sf_1	3573	Leuconostoc ficulneum str. FS-1	-0.551	0.041	0.035
Firmicutes	Streptococcaceae	sf_1	3422	Streptococcus thermophilus str. DSM 20617	-0.551	0.041	0.035
Firmicutes	Lachnospiraceae	sf_5	4315	termite gut homogenate clone Rs-N94 bacterium	-0.551	0.041	0.035
Unclassified	Unclassified	sf_160	7444		-0.551	0.041	0.035
Bacteroidetes	Flexibacteraceae	sf_19	6261	Arctic sea ice cryoconite clone ARKCRY-50	-0.552	0.041	0.035
Planctomycetes	Planctomycetaceae	sf_3	4948	anoxic basin clone CY0ARA027D01	-0.552	0.040	0.035
Firmicutes	Streptococcaceae	sf_1	3253	derived cheese sample clone 32CR	-0.553	0.040	0.035
Firmicutes	Clostridiaceae	sf_12	4614	Clostridium sp. str. JC3	-0.553	0.040	0.035
Bacteroidetes	Flavobacteriaceae	sf_1	5267	bacterioplankton clone AEGEAN_179	-0.554	0.040	0.035
Natronoanaerobium	Unclassified	sf_1	4377	Mono Lake at depth 35m station 6 July 2000 clone ML635J-65 G+C	-0.554	0.040	0.035
OP9/JS1	Unclassified	sf_1	2489	Guaymas Basin hydrothermal vent sediments clone B01R005	-0.554	0.040	0.035

Chloroflexi	Unclassified	sf_1	2534	forest soil clone S085	-0.554	0.040	0.035
Bacteroidetes	Unclassified	sf_15	5957	hydrothermal vent polychaete mucous clone P. palm C/A 20	-0.554	0.040	0.035
Firmicutes	Lactobacillaceae	sf_1	3521	Pediococcus inopinatus str. DSM 20285	-0.555	0.039	0.035
Firmicutes	Unclassified	sf_1	77	thermal soil clone YNPFFP9	-0.555	0.039	0.035
Firmicutes	Clostridiaceae	sf_12	4550	swine intestine clone p-320-a3	-0.556	0.039	0.035
Firmicutes	Lachnospiraceae	sf_5	2668	termite gut homogenate clone Rs-G40 bacterium	-0.556	0.039	0.035
Actinobacteria	Micrococcaceae	sf_1	1557	Arthrobacter oxydans str. DSM 20119	-0.556	0.039	0.035
Firmicutes	Clostridiaceae	sf_12	4459	termite gut clone Rs-109	-0.557	0.039	0.035
Bacteroidetes	Flavobacteriaceae	sf_1	5521	Flavobacteriaceae str. SW269	-0.557	0.039	0.035
Proteobacteria	Campylobacteraceae	sf_3	10397	groundwater clone 1006	-0.557	0.039	0.035
Proteobacteria	Unclassified	sf_9	9876	deep marine sediment clone MB-B2-106	-0.557	0.039	0.035
Firmicutes	Lachnospiraceae	sf_5	4514	termite gut homogenate clone Rs-B34 bacterium	-0.557	0.039	0.035
Proteobacteria	Polyangiaceae	sf_4	9733	bacterioplankton clone ZA3735c	-0.557	0.038	0.035
Firmicutes	Unclassified	sf_1	522	UASB granular sludge clone UT-1	-0.558	0.038	0.035
Firmicutes	Streptococcaceae	sf_1	3722	Lactococcus Il1403 subsp. lactis str. IL1403	-0.558	0.038	0.035
Firmicutes	Peptococc/Acidaminococc	sf_11	304	Selenomonas ruminantium str.JCM6582	-0.558	0.038	0.035
Firmicutes	Lactobacillaceae	sf_1	3885	Pediococcus pentosaceus	-0.558	0.038	0.035
Proteobacteria	Sphingomonadaceae	sf_1	7440	Sphingobium chungbukense str. DJ77	-0.558	0.038	0.035
Firmicutes	Aerococcaceae	sf_1	3326	Nostocoida limicola I str. Ben206	-0.558	0.038	0.035
Bacteroidetes	Flexibacteraceae	sf_19	5602		-0.559	0.038	0.035
Proteobacteria	Polyangiaceae	sf_3	10298	marine tidal mat clone BTM36	-0.559	0.038	0.035

Firmicutes	Bacillaceae	sf_1	3900	Bacillus licheniformis str. DSM 13	-0.559	0.038	0.035
Bacteroidetes	Rikenellaceae	sf_5	5892	anoxic bulk soil flooded rice microcosm clone BSV73	-0.559	0.038	0.035
Proteobacteria	Pasteurellaceae	sf_1	8195	Haemophilus influenzae str. R2866	-0.559	0.038	0.035
Chlorobi	Chlorobiaceae	sf_1	859	Chlorobium phaeovibrioides str. 2631	-0.560	0.037	0.035
Firmicutes	Clostridiaceae	sf_12	4477	termite gut homogenate clone Rs-N85 bacterium	-0.560	0.037	0.035
Proteobacteria	Unclassified	sf_9	244	deep marine sediment clone MB-C2-152	-0.560	0.037	0.035
Bacteroidetes	Flavobacteriaceae	sf_1	6248	Capnocytophaga sp. oral strain str. S3	-0.560	0.037	0.035
Proteobacteria	Unclassified	sf_1	10084	acid mine drainage clone AS6	-0.561	0.037	0.035
Firmicutes	Streptococcaceae	sf_1	3588	Streptococcus downei str. ATCC 33748	-0.561	0.037	0.035
Firmicutes	Peptococc/Acidaminococc	sf_11	1036	Great Artesian Basin clone G07	-0.561	0.037	0.035
Chloroflexi	Unclassified	sf_1	2397	deep marine sediment clone MB-C2-127	-0.561	0.037	0.035
Actinobacteria	Micrococcaceae	sf_1	2020	Rothia dentocariosa str. ChDC B200	-0.561	0.037	0.035
Bacteroidetes	Unclassified	sf_15	5353	trichloroethene-contaminated site clone FTLpost3 bacterium	-0.561	0.037	0.035
Bacteroidetes	Flavobacteriaceae	sf_1	5991	Tenacibaculum ovolyticum str. IAM14318	-0.562	0.037	0.035
Proteobacteria	Sphingomonadaceae	sf_1	7036	Lutibacterium anuloederans str. LC8	-0.562	0.036	0.035
Cyanobacteria	Chloroplasts	sf_5	5147	Emiliania huxleyi str. Plymouth Marine Laborator PML 92	-0.562	0.036	0.035
Actinobacteria	Acidimicrobiaceae	sf_1	1090		-0.562	0.036	0.035
Proteobacteria	Unclassified	sf_3	9813	hydrothermal sediment clone AF420340	-0.562	0.036	0.035
Firmicutes	Enterococcaceae	sf_1	3433	Tetragenococcus muriaticus	-0.563	0.036	0.035
Firmicutes	Acholeplasmataceae	sf_1	4044		-0.563	0.036	0.035
TM7	Unclassified	sf_1	8040	oral cavity clone BE109	-0.563	0.036	0.035

Bacteroidetes	Porphyromonadaceae	sf_1	5295	swine intestine clone p-987-s962-5	-0.563	0.036	0.035
Bacteroidetes	Flavobacteriaceae	sf_1	5914	Psychroserpens burtonensis str. S2-64	-0.564	0.036	0.035
Firmicutes	Lachnospiraceae	sf_5	4613	rumen clone 3C0d-3	-0.564	0.036	0.035
Firmicutes	Acholeplasmataceae	sf_1	4046	Pigeon pea witches'-broom mycoplasma-like organism	-0.564	0.036	0.035
Bacteroidetes	Flavobacteriaceae	sf_1	6269	acidic forest soil clone UC1	-0.564	0.036	0.035
OP9/JS1	Unclassified	sf_1	969	DCP-dechlorinating consortium clone SHA-1	-0.564	0.036	0.035
Firmicutes	Clostridiaceae	sf_12	4180	termite gut homogenate clone Rs-M23 bacterium	-0.564	0.036	0.035
Cyanobacteria	Chloroplasts	sf_5	4976	Calypogeia muelleriana	-0.564	0.036	0.035
Firmicutes	Enterococcaceae	sf_1	3261	Enterococcus mundtii str. LMG 10748	-0.565	0.035	0.035
Actinobacteria	Micrococcaceae	sf_1	1324	glacial ice isolate str. CanDirty1	-0.566	0.035	0.035
Firmicutes	Peptococc/Acidaminococc	sf_11	761	Anaeroglobus geminatus str. AIP313.00; CIP 106856; CCUG 44773	-0.566	0.035	0.035
Bacteroidetes	Unclassified	sf_15	5475	SHA-25 clone	-0.566	0.035	0.035
Planctomycetes	Planctomycetaceae	sf_3	4831	Planctomyces brasiliensis	-0.566	0.035	0.035
Firmicutes	Lachnospiraceae	sf_5	4510	termite gut homogenate clone Rs-Q53 bacterium	-0.566	0.035	0.035
Firmicutes	Lactobacillaceae	sf_1	3767	Lactobacillus suebicus str. CECT 5917T	-0.567	0.035	0.035
Firmicutes	Peptococc/Acidaminococc	sf_11	709	Selenomonas ruminantium str.S20	-0.567	0.034	0.035
Proteobacteria	Unclassified	sf_4	9884	forested wetland clone RCP2-62	-0.567	0.034	0.035
Firmicutes	Leuconostocaceae	sf_1	3497	Weissella koreensis S-5673	-0.567	0.034	0.035
Firmicutes	Enterococcaceae	sf_1	3713	Enterococcus cecorum str. ATCC43198	-0.568	0.034	0.035
Firmicutes	Lactobacillaceae	sf_1	3566	Lactobacillus pontis str. LTH 2587	-0.569	0.034	0.035
Firmicutes	Unclassified	sf_8	4536	Mono Lake at depth 35m station 6 July 2000 clone ML635J-14 G+C	-0.569	0.034	0.035

Firmicutes	Unclassified	sf_1	3481		-0.569	0.034	0.035
Proteobacteria	Syntrophobacteraceae	sf_1	9661	DCP-dechlorinating consortium clone SHD-1	-0.570	0.033	0.035
Proteobacteria	Desulfobacteraceae	sf_5	10364	marine surface sediment clone SB2	-0.570	0.033	0.035
Firmicutes	Lachnospiraceae	sf_5	2943	human thigh wound isolate str. MDA2477	-0.571	0.033	0.035
Firmicutes	Enterococcaceae	sf_1	3318	Enterococcus ratti str. ATCC 700914	-0.571	0.033	0.035
Bacteroidetes	Porphyromonadaceae	sf_1	6012	mouse feces clone L11-6	-0.571	0.033	0.035
Firmicutes	Clostridiaceae	sf_12	4554	termite gut clone Rs-068	-0.571	0.033	0.035
Firmicutes	Lactobacillaceae	sf_1	3490	Lactobacillus suntoryeus str. LH	-0.571	0.033	0.035
Firmicutes	Clostridiaceae	sf_12	4582	swine intestine clone p-2600-9F5	-0.573	0.032	0.035
Firmicutes	Peptococc/Acidaminocc	sf_11	242	Desulfosporosinus orientis str. DSMZ 7493	-0.573	0.032	0.035
Firmicutes	Streptococcaceae	sf_1	3907	aortic heart valve patient with endocarditis clone v6	-0.573	0.032	0.035
Firmicutes	Peptococc/Acidaminocc	sf_11	710	Centipeda periodontii str. HB-2	-0.573	0.032	0.035
Cyanobacteria	Chloroplasts	sf_5	5183	Pisum sativum -- chloroplast	-0.576	0.031	0.035
Cyanobacteria	Chloroplasts	sf_5	5192	Cycas revoluta	-0.576	0.031	0.035
Firmicutes	Lachnospiraceae	sf_5	2991	rumen clone 3C3d-8	-0.576	0.031	0.035
Firmicutes	Enterococcaceae	sf_1	3881	Enterococcus dispar str. LMG 13521	-0.576	0.031	0.035
Bacteroidetes	Flavobacteriaceae	sf_1	5836	Capnocytophaga granulosa str. LMG 12119; FDC SD4	-0.577	0.031	0.035
Firmicutes	Peptococc/Acidaminocc	sf_11	300	benzene-contaminated groundwater clone ZZ12C8	-0.579	0.030	0.035
Bacteroidetes	Unclassified	sf_15	5784	fruiting body Pleurotus eryngii clone PE01	-0.579	0.030	0.035
Firmicutes	Bacillaceae	sf_1	3848	Bacillus sp. str. TUT1007	-0.579	0.030	0.035
Firmicutes	Carnobacteriaceae	sf_1	3792	Carnobacterium sp. str. D35	-0.580	0.030	0.035

Firmicutes	Lachnospiraceae	sf_5	4533	termite gut homogenate clone Rs-N06 bacterium	-0.581	0.029	0.035
Unclassified	Unclassified	sf_160	651		-0.581	0.029	0.035
Bacteroidetes	Flavobacteriaceae	sf_1	6246	crevicular epithelial cells clone BU084	-0.581	0.029	0.035
Firmicutes	Lachnospiraceae	sf_5	4434	termite gut homogenate clone Rs-K11 bacterium	-0.581	0.029	0.035
Firmicutes	Lactobacillaceae	sf_1	3418	Lactobacillus subsp. aviarius	-0.581	0.029	0.035
Firmicutes	Clostridiaceae	sf_12	4297		-0.582	0.029	0.035
Proteobacteria	Polyangiaceae	sf_3	9671	hydrothermal sediment clone AF420357	-0.582	0.029	0.035
Firmicutes	Acholeplasmataceae	sf_1	3976		-0.583	0.029	0.035
Firmicutes	Acholeplasmataceae	sf_1	3961	Clover yellow edge mycoplasma-like organism	-0.583	0.028	0.035
Bacteroidetes	Flavobacteriaceae	sf_1	5301		-0.584	0.028	0.035
Firmicutes	Streptococcaceae	sf_1	3685	Streptococcus gordonii str. ATCC 10558	-0.584	0.028	0.035
Actinobacteria	Micrococcaceae	sf_1	2063	Rothia dentocariosa str. ATCC 17931	-0.585	0.028	0.035
Firmicutes	Clostridiaceae	sf_12	4272	termite gut homogenate clone Rs-M34 bacterium	-0.586	0.028	0.035
Synergistes	Unclassified	sf_3	353	UASB reactor granular sludge clone PD-UASB-13 G+C	-0.586	0.028	0.035
Fusobacteria	Fusobacteriaceae	sf_3	721	human mouth clone P2PB_51	-0.586	0.028	0.035
Firmicutes	Clostridiaceae	sf_12	4524	termite gut clone Rs-093	-0.587	0.027	0.035
Firmicutes	Acholeplasmataceae	sf_1	4045	Chinaberry yellows phytoplasma	-0.587	0.027	0.035
Firmicutes	Lachnospiraceae	sf_5	4155	termite gut homogenate clone Rs-K92 bacterium	-0.588	0.027	0.035
Firmicutes	Lactobacillaceae	sf_1	3703	Lactobacillus salivarius str. RA2115	-0.590	0.026	0.035
Firmicutes	Clostridiaceae	sf_12	4622	termite gut clone Rs-L36	-0.591	0.026	0.035
Firmicutes	Aerococcaceae	sf_1	3833	Carnobacterium alterfunditum	-0.591	0.026	0.035

Firmicutes	Lachnospiraceae	sf_5	4540	termite gut homogenate clone Rs-M18 bacterium	-0.592	0.026	0.035
Firmicutes	Streptococcaceae	sf_1	3251	Streptococcus cristatus str. ATCC 51100	-0.592	0.026	0.035
TM7	Unclassified	sf_1	2697	midgut homogenate Pachnoda ephippiata larva clone PeM47	-0.592	0.026	0.035
Chloroflexi	Unclassified	sf_1	258	DCP-dechlorinating consortium clone SHD-14	-0.593	0.026	0.035
Firmicutes	Aerococcaceae	sf_1	3840	Trichococcus pasteurii str. KoTa2	-0.593	0.026	0.035
Proteobacteria	Neisseriaceae	sf_1	8143	subgingival dental plaque clone AK105	-0.594	0.025	0.035
Firmicutes	Acholeplasmataceae	sf_1	3975	Black raspberry witches'-broom phytoplasma str. BRWB witches'-broom	-0.594	0.025	0.035
Firmicutes	Streptococcaceae	sf_1	3543		-0.598	0.024	0.035
Chloroflexi	Unclassified	sf_1	2339	uranium mill tailings soil sample clone Sh765B-TzT-20 bacterium	-0.602	0.023	0.035
Firmicutes	Unclassified	sf_1	3289	Isobaculum melis CCUG 37660T	-0.602	0.023	0.035
Firmicutes	Clostridiaceae	sf_12	4475	termite gut homogenate clone Rs-N02 bacterium	-0.604	0.022	0.035
Firmicutes	Enterococcaceae	sf_1	3598	Enterococcus solitarius str. DSM 5634	-0.607	0.021	0.035
Firmicutes	Clostridiaceae	sf_12	4310	termite gut clone Rs-056	-0.607	0.021	0.035
Firmicutes	Enterococcaceae	sf_1	3680	Melissococcus plutonius str. NCDO 2440	-0.610	0.021	0.035
Firmicutes	Peptococc/Acidaminococc	sf_11	150		-0.617	0.019	0.035
Chlorobi	Unclassified	sf_8	549	benzene-degrading nitrate-reducing consortium clone Cart-N2 bacterium	-0.618	0.018	0.035
Firmicutes	Lactobacillaceae	sf_1	3526	Lactobacillus sakei	-0.620	0.018	0.035
Firmicutes	Lachnospiraceae	sf_5	4281	granular sludge clone UASB_brew_B86	-0.627	0.016	0.035
Bacteroidetes	Flavobacteriaceae	sf_1	5726	Bergeyella sp. oral AK152 clone	-0.628	0.016	0.035
Firmicutes	Lachnospiraceae	sf_5	4512	granular sludge clone UASB_brew_B25	-0.632	0.015	0.035
Firmicutes	Lachnospiraceae	sf_5	4331	granular sludge clone UASB_brew_B84	-0.638	0.014	0.035

Table S6. Kolmogorov-Smirnov assessment of data distribution.

OTU ID	**635**	**5769**	**5822**	**5130**	**6732**	**7878**	**612**	**1233**	**1711**	**2497**
FI[a] values	534	215	2620	115	516	686	732	974	1144	1716
	657	185	1586	330	1086	2441	1341	1246	1337	2145
	401	1064	1138	455	869	2279	1641	716	1012	1987
	419	2895	3411	1069	1515	3589	2784	1760	1796	4049
	497	2259	2801	848	1395	1915	2238	1574	1787	3146
	410	3143	2782	1086	1658	2841	2615	1653	1527	3759
	770	3958	4192	1464	2616	3551	3571	2737	2615	4639
	395	3051	2900	1106	2016	2516	2778	1796	1450	3543
	808	4146	3324	1493	2424	3436	3230	2512	2209	4312
	184	2515	2263	878	1356	2314	2422	1198	1229	2930
	274	4026	3125	1436	1971	3341	3104	2014	1848	4325
	547	4478	4388	2519	2629	4122	4171	2915	2594	5002
	416	3913	3514	1687	2230	3648	3274	2305	1900	4748
	456	3985	3372	1685	2057	3579	3203	2055	2005	4416
p statistic	p = 0.7	p=0.72	p=0.74	p=0.71	p=0.95	p=0.68	p=0.84	p=0.74	p=0.89	p=0.87
Mean	492.8	2736	2931	1182	1711	2821	2609	1822	1769	3560
Standard deviation	205.2	1758	1113	753.6	762.1	1209	1155	751.7	562.6	1263

[a]Fluorescence intensity values reported for each sample