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Letter to the Editor

Man's best friend? The effect of pet ownership on house dust microbial communities

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Methods.

Sample collection.

House dust specimens were available from a population-based birth cohort, a subset of these, collected from participants who had subsequently dropped from the cohort, but were clearly characterized with respect to the presence or absence of a dog or a cat at the time of, and in the preceding six months prior to sample collection, were used for this study. Sixteen dust samples collected from households in the greater Detroit area with ≥1 dogs (D; n = 6), ≥1 cats (C; n = 5) or no furred pets (NP; n = 5) were used. Animal behavior was determined by completion of a questionnaire by the pet owner. Housekeeping Index, using a Likert scale, was based on the following question, “How would you rate the general condition of the dwelling?”, with responses falling under the following categories: 1 extremely poor housekeeping; 2 not as bad as 1; 3 average level of housekeeping; 4 above average; 5 good housekeeping award. Field staff were given defined guidelines for assessing the overall cleanliness of the study participant's home.

They were asked to take into account evidence of cockroaches and mice in the home as well as signs of mold or water damage and to consider whether there was any visible damage to the interior and how cluttered the home was.

Samples were collected using a standardized method of vacuuming 1 m^2 of a home floor or mattress for 2 minutes into a collection sock. Pet ownership was defined as households that housed a dog or cat for at least 45 days before sampling. Samples were filtered through a 300 μM sterile filter to remove large debris, fine dust filtrate was stored at -80 °C until processed.

DNA extraction and processing for PhyloChip analysis.

DNA was extracted from 0.1 g of dust using a modified cetyl trimethylammonium bromide (CTAB) and (polyethylene glycol (PEG) method ([41]; see Online Repository). Details of sample processing for PhyloChip analysis is provided in the Online Repository. Background subtraction and normalization were carried out as previously described[42]. Data sets were conservatively filtered, with taxa (defined as groups of organisms detected by the array that possess at least 97% 16S rRNA sequence homology) deemed present if ≥ 90% of probes per probe set were positive as previously described[42].

Fungal community analysis.

DNA extracted from house dust was used to profile fungal communities present. A total of 10 ng of extracted DNA was used in a 35 cycle PCR reaction using fungal-specific ITS primers [ITS1 5'-TCCGTAGGTGAACCTGCGG-3' and ITS4 5'-TCCTCCGCTTATT GATATGC-3';[43]] to amplify this region from fungal species present in these communities (detailed in Online Repository). A total of 2 μl of PCR product was resolved using an Agilent DNA Chip100 kit for the Agilent 2100 bioanalyzer (Agilent, CA) according to the manufacturers instructions. Sample traces were analyzed using Agilent 2100 Expert software to enumerate the number of peaks (representing fungal richness).

The Invitrogen TOPO TA cloning kit (Carlsbad, CA) was used to generate fungal clone libraries for each sample (detailed in Online Repository). Restriction fragment length polymorphism analysis (detailed in Online Repository) analysis was performed (on 96 clones per library) and plasmids encoding distinct bands representing discreet fungal ribotypes, were purified using the QIAprep Spin Miniprep Kit (Qiagen) prior to bidirectional sequencing (Agencourt Bioscience, MA) using M13 primers. Sequences were trimmed for quality, assembled using Geneious 4.7 (www.geneious.com), and identity assigned by BLAST searching based on the percent homology, E-value, and bit score.

Statistical Analyses.

Bacterial community richness (number of taxa detected by the array), Pielou's evenness (metric describing the relative distribution of taxa in a given community), and Simpson's inverse diversity (calculated based on richness and evenness metrics) were calculated using the *vegan* package[44] in R (http://www.Rproject.org). Wilcoxon or Welch's t-test was used to determine significant differences in community metrics (diversity, richness and evenness) and taxon abundance across comparison groups. Q-value false discovery rates were calculated as previously described[45]. To examine if a relationship existed between fungal and bacterial diversity in house dust samples, Pearson's correlation was assessed using 2-sided *cor.test* in the statistical package in R with a confidence interval of 0.95. PhyloChip fluorescence intensities were square root transformed by the metaMDSdist script, prior to generation of a Bray-Curtis distance matrix in the *vegan* package[44]. Hierarchical cluster analysis (HCA[46]), an exploratory tool to examine community composition dissimilarity, was generated using this distance matrix with the average mean distance option in the *stat* package of R. Results of HCA were illustrated using iTOL[47].

Tables

Table E1. Bacterial community metrics, fungal richness, and pet information of house dust samples.

Sample	*Exposure*	*Bacterial Richness*	*Bacterial Evenness*	*Bacterial Diversity*	*Fungal Richness*	*Pet hours indoors / outdoors*
1	D[a]	1561	0.689	1427.4	2	20/4
2	D	1615	0.689	1505.1	3	23/1
3	D	1660	0.688	1518.6	3	0/24
4	D	1246	0.684	1054.8	5	23/1
5	D	1130	0.686	998.5	4	0/24
6	C[b]	1078	0.683	903.6	5	16/8
7	C	984	0.687	881.7	5	24/0
8	C	1617	0.688	1463.4	4	24/0
9	C	1236	0.688	1119.0	5	12/12
10	C	1236	0.687	1105.8	8	24/0
11	NP	878	0.684	735.7	5	0/0
12	NP	1071	0.686	939.4	6	0/0
13	NP	978	0.685	850.2	8	0/0

D[a]= household with ≥ 1 dog; C[b] = household with ≥ 1 cat; NP[c] = household with no cat or dog.

Shaded samples belong to high bacterial diversity HCA cluster G1.

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Table E2. Bacterial taxa detected in significantly higher abundance in dog vs no pet households.

Phylum	*S-F*[a]	*Taxon ID*[b]	*Representative species*[c]	*p-value*	*q-value*
Bacteroidetes	sf_1	5295	swine intestine clone p-987-s962-5	0.000860288	0.03133258
Actinobacteria	sf_1	1558	*Corynebacterium* sp. str. 61722	0.000915893	0.03133258
Actinobacteria	sf_1	1575	*Corynebacterium matruchotii* str. DSM 20635	0.001730035	0.03133258
Firmicutes	sf_12	3019	*Tepidibacter formicigenes* str. DV1184	0.001819953	0.03133258
Bacteroidetes	sf_1	6011	rumen clone F24-B03	0.00192834	0.03133258
Spirochaetes	sf_1	6575	TCE-contaminated site clone ccslm226	0.002453832	0.03133258
Firmicutes	sf_12	4637	termite gut clone Rs-088	0.002699018	0.03133258
TM7	sf_1	2697	midgut homogenate *Pachnoda ephippiata* larva clone PeM47	0.003250189	0.03133258
Firmicutes	sf_3	2373		0.003584048	0.03133258
Firmicutes	sf_1	4044		0.004042678	0.03133258
Proteobacteria	sf_3	9735	uranium mining waste pile clone JG37-AG-15 proteobacterium	0.004622903	0.03133258
Actinobacteria	sf_3	1114		0.005140712	0.03133258
Verrucomicrobia	sf_1	1024	rumen clone BS5	0.005507634	0.03133258
Actinobacteria	sf_1	1856	forested wetland clone RCP2-105	0.005936504	0.03133258
Firmicutes	sf_1	2388	G+C Gram-positive clone YNPRH70A	0.00646989	0.03133258
Acidobacteria	sf_6	6362	grassland soil clone DA052	0.006729145	0.03133258
Proteobacteria	sf_1	10248	*Desulfovibrio giganteus* str. DSM 4370	0.007208291	0.03133258
Spirochaetes	sf_1	6506	termite gut homogenate clone Rs-J58 sp.	0.007548222	0.03133258
Proteobacteria	sf_3	8114		0.007569625	0.03133258
Spirochaetes	sf_1	6488	*Treponema primitia* str. ZAS-1	0.00757132	0.03133258
Proteobacteria	sf_3	10309	*Nannocystis exedens* str. Na e571	0.007730697	0.03133258
Proteobacteria	sf_3	6628	*Wolbachia pipientis*	0.008279464	0.03133258
Spirochaetes	sf_1	6494	termite gut homogenate clone Rs-C47 sp.	0.008396102	0.03133258
Spirochaetes	sf_1	6491	termite gut homogenate clone BCf8-03	0.00849645	0.03133258
Proteobacteria	sf_1	10084	acid mine drainage clone AS6	0.008748161	0.03133258
Spirochaetes	sf_1	6565	termite gut clone NkS-Oxy25	0.009290302	0.03133258
Firmicutes	sf_1	3975	Black raspberry witches'-broom phytoplasma str. BRWB	0.0108543	0.03133258

			witches'-broom		
Spirochaetes	sf_1	6532	termite gut clone NkS39	0.01093518	0.03133258
Proteobacteria	sf_9	10049	DCP-dechlorinating consortium clone SHA-72	0.01153983	0.03133258
Unclassified	sf_92	9999	termite gut homogenate clone Rs-J96	0.01168807	0.03133258
Actinobacteria	sf_1	1544	*Kitasatospora cystarginea* str. IFO14836T	0.01191364	0.03133258
Spirochaetes	sf_1	6571	Mixotricha paradoxa is flagellate hindgut Mastotermes darwiniensis clone mp4 of	0.01193115	0.03133258
Proteobacteria	sf_3	10417	temperate estuarine mud clone KM61	0.01200276	0.03133258
Proteobacteria	sf_9	9784	Antarctic sediment clone LH5_30	0.01213724	0.03133258
Proteobacteria	sf_3	10534	Helicobacter pylori	0.0124312	0.03133258
Bacteroidetes	sf_1	6269	acidic forest soil clone UC1	0.01248821	0.03133258
Spirochaetes	sf_1	6460	termite gut homogenate clone Rs-B69 sp.	0.01263646	0.03133258
Firmicutes	sf_1	3630		0.01279401	0.03133258
Proteobacteria	sf_1	10497	UASB reactor granular sludge clone PD-UASB-2 proteobacterium	0.01351734	0.03133258
Bacteroidetes	sf_1	6012	mouse feces clone L11-6	0.01354004	0.03133258
Proteobacteria	sf_3	6803	*Wolbachia* sp. Dlem16SWol	0.0135749	0.03133258
Actinobacteria	sf_1	1454	*Nocardia yamanashiensis* str. IFM 0265	0.01379599	0.03133258
Firmicutes	sf_1	3961	Clover yellow edge mycoplasma-like organism	0.01380174	0.03133258
Firmicutes	sf_5	668	*Sedimentibacter* sp. str. BRS2	0.01415744	0.03133258
Spirochaetes	sf_1	6579	termite gut clone NkS83	0.01452437	0.03133258
WS3	sf_1	2537	anoxic marine sediment clone LD1-PA39	0.01461253	0.03133258
Verrucomicrobia	sf_3	792	termite gut homogenate clone Rs-P07 bacterium	0.01464949	0.03133258
Acidobacteria	sf_14	6405	soil sample uranium mining waste pile near town Johanngeorgenstadt clone JG36-TzT-31 bacterium	0.01474821	0.03133258
Actinobacteria	sf_1	1312		0.01498466	0.03133258
Actinobacteria	sf_1	2048	*Nocardia uniformis* str. DSM 43136	0.01539902	0.03133258
Firmicutes	sf_12	4502		0.01543917	0.03133258
Firmicutes	sf_1	3488	*Halobacillus salinus* str. HSL-3	0.01557008	0.03133258
Actinobacteria	sf_1	1893	*Kineosporia aurantiaca* str. NRLL B-16913	0.01560354	0.03133258
Proteobacteria	sf_3	10438	hydrocarbon seep clone GCA014	0.01561483	0.03133258
Bacteroidetes	sf_1	5460	mouse feces clone F8	0.01564666	0.03133258
Proteobacteria	sf_1	10071	*Desulfovibrio desulfuricans*	0.01589283	0.03133258

Spirochaetes	sf_1	6526	*Treponema* sp. str. 7CPL208	0.01589774	0.03133258
Proteobacteria	sf_1	10407	hydrothermal sediment clone AF420342	0.01600835	0.03133258
Spirochaetes	sf_1	6554	termite gut homogenate clone Rs-A43 sp.	0.01608096	0.03133258
Proteobacteria	sf_3	10484	*Campylobacter helveticus*	0.01652224	0.03133258
Proteobacteria	sf_3	9321	marine sediment clone Tokyo Bay D	0.01666009	0.03133258
Bacteroidetes	sf_11	5619	anaerobic VC-degrading enrichment clone VC10 bacterium	0.01666736	0.03133258
Proteobacteria	sf_1	10187	Mono Lake at depth 23 m station 6 July 2000 clone ML623J-57 proteobacterium	0.0168146	0.03133258
Synergistes	sf_3	60	*Flexistipes* sp. str. E3_33	0.01683209	0.03133258
Firmicutes	sf_11	181	*Allisonella histaminiformans* str. MR2	0.01685951	0.03133258
Spirochaetes	sf_1	6523	termite gut homogenate clone Rs-J64 sp.	0.01689763	0.03133258
Proteobacteria	sf_1	8962	bacterioplankton clone AEGEAN_234	0.01693148	0.03133258
Actinobacteria	sf_1	2061	rice straw paddy soil isolate str. WB2	0.01830901	0.03133258
Bacteroidetes	sf_4	5785	Mono Lake at depth 35 m station 6 July 2000 clone ML635J-56	0.01845986	0.03133258
Proteobacteria	sf_1	10475	hydrothermal sediment clone AF420359	0.01855131	0.03133258
Actinobacteria	sf_1	1867	*Amycolatopsis vancoresmycina* str. DSM 44592	0.01863488	0.03133258
Proteobacteria	sf_3	10540	*Campylobacter showae* str. LMG 12636	0.0187843	0.03133258
Proteobacteria	sf_1	9845	uranium mining waste pile clone JG37-AG-128 proteobacterium	0.01906774	0.03133258
Proteobacteria	sf_3	8477	marine sediment clone Limfjorden L8	0.01910501	0.03133258
Unclassified	sf_160	6430		0.01925277	0.03133258
Actinobacteria	sf_1	1180	*Mycobacterium palustre* str. E846	0.0193872	0.03133258
Firmicutes	sf_17	926		0.01941024	0.03133258
Bacteroidetes	sf_1	5828	*Blattabacterium* species	0.01942291	0.03133258
Bacteroidetes	sf_19	5366	*Flexibacter roseolus* str. IFO 16030	0.01944996	0.03133258
Proteobacteria	sf_1	9240	*Pseudomonas fluorescens* str. CHA0	0.01957325	0.03133258
Bacteroidetes	sf_1	5401	*Capnocytophaga gingivalis* str. ChDC OS45	0.01968287	0.03133258
Actinobacteria	sf_1	1517	*Corynebacterium xerosis* str. DSM 20743	0.0201329	0.03133258
Verrucomicrobia	sf_1	547	anoxic marine sediment clone LD1-PB1	0.02034385	0.03133258
Proteobacteria	sf_1	9828	termite gut homogenate clone Rs-M89 proteobacterium	0.02042882	0.03133258
Proteobacteria	sf_3	10428	*Flexispira rappini* FH 9702248	0.02051642	0.03133258
Bacteroidetes	sf_1	5955	*Flavobacterium* sp. str. V4.MS.29 = MM_2747	0.02056903	0.03133258

Proteobacteria	sf_23	10443	*Helicobacter pylori* str. 85D08	0.02062707	0.03133258
Proteobacteria	sf_3	10576	*Helicobacter* sp. 'liver 3' str. liver 3	0.02062707	0.03133258
Actinobacteria	sf_1	1551	soil isolate Ellin301	0.02064116	0.03133258
Proteobacteria	sf_3	9874	uranium mining waste pile clone JG34-KF-243 proteobacterium	0.02064265	0.03133258
Bacteroidetes	sf_1	5473		0.0206658	0.03133258
Firmicutes	sf_12	2764		0.02097036	0.03133258
Bacteroidetes	sf_1	5317	*Tenacibaculum maritimum* str. IFO 15946	0.0210302	0.03133258
Bacteroidetes	sf_1	5459	*Pedobacter* sp. An13	0.02112996	0.03133258
Firmicutes	sf_12	2898	*Dorea longicatena* str. III-35	0.02114346	0.03133258
Unclassified	sf_160	10012		0.02160459	0.03133258
Synergistes	sf_3	719	*Synergistes* sp. P1 str. P4G_18	0.02181174	0.03133258
Spirochaetes	sf_1	6490	termite gut homogenate clone BCf4-14	0.02185341	0.03133258
Actinobacteria	sf_1	1239	*Mycobacterium ratisbonense* str. SD4	0.0218987	0.03133258
Proteobacteria	sf_3	10562	*Helicobacter rappini* W.Tee-Yu	0.02194198	0.03133258
Proteobacteria	sf_2	7188	termite gut homogenate clone Rs-B50 proteobacterium	0.02204712	0.03133258
Proteobacteria	sf_3	10538	*Arcobacter cryaerophilus*	0.02217458	0.03133258
Bacteroidetes	sf_15	6046	chlorobenzene-degrading consortium clone IIIB-1	0.02228797	0.03133258
marine group A	sf_1	6454	marine clone SAR406	0.0223979	0.03133258
Proteobacteria	sf_1	10079	*Desulfomicrobium baculatum* str. DSM 1742	0.02250462	0.03133258
Bacteroidetes	sf_1	5991	*Tenacibaculum ovolyticum* str. IAM14318	0.0229782	0.03133258
Acidobacteria	sf_1	790	soil clone 11-25	0.023016	0.03133258
Proteobacteria	sf_2	6639		0.0231442	0.03133258
Firmicutes	sf_12	2736	*Alkaliphilus metalliredigenes* str. QYMF	0.02324827	0.03133258
Acidobacteria	sf_1	87	activated sludge clone 2951	0.02336796	0.03133258
Firmicutes	sf_8	4536	Mono Lake at depth 35m station 6 July 2000 clone ML635J-14 G+C	0.02350543	0.03133258
Proteobacteria	sf_3	10436	*Helicobacter aurati* str. MIT 97-5075c	0.02353168	0.03133258
Gemmatimonadetes	sf_5	10112	forest soil clone NOS7.157WL	0.02396072	0.03133258
Bacteroidetes	sf_1	5961	chlorobenzene-degrading consortium clone IA-16	0.02397067	0.03133258
Proteobacteria	sf_1	9469	cf. *Pseudomonas* sp. clone Llangefni 52	0.0240601	0.03133258
Unclassified	sf_160	4410		0.02413371	0.03133258
Verrucomicrobia	sf_3	40	Elbe river clone DEV055	0.02419767	0.03133258

Firmicutes	sf_12	4638		0.02421994	0.03133258
Proteobacteria	sf_3	10456	*Campylobacter showae*	0.02444631	0.03133258
Spirochaetes	sf_1	6508	termite hindgut clone mpsp2	0.02446658	0.03133258
OP9/JS1	sf_1	2491	deep marine sediment clone MB-B2-103	0.02450183	0.03133258
Bacteroidetes	sf_1	5267	bacterioplankton clone AEGEAN_179	0.024632	0.03133258
Proteobacteria	sf_4	6810	marine bacterioplankton clone MB13F01	0.02470768	0.03133258
Verrucomicrobia	sf_1	559	anoxic marine sediment clone LD1-PA20	0.02480777	0.03133258
Proteobacteria	sf_1	9458	uranium mining waste pile clone JG37-AG-94 proteobacterium	0.02481064	0.03133258
Proteobacteria	sf_3	10518	*Helicobacter pylori* str. ATCC 49396T	0.02490654	0.03133258
Actinobacteria	sf_1	1888	*Mycobacterium brisbanense* str. W6743; ATCC 49938	0.02510079	0.03133258
Firmicutes	sf_5	2710	DCP-dechlorinating consortium clone SHA-74	0.02512473	0.03133258
Chloroflexi	sf_1	2485		0.02516776	0.03133258
Proteobacteria	sf_28	10091		0.025177	0.03133258
TM6	sf_1	9803	forest soil clone S1204	0.02520617	0.03133258
Proteobacteria	sf_3	7010	periodontal pocket clone 10B6	0.02526757	0.03133258
Bacteroidetes	sf_4	5703		0.02558316	0.03133258
Firmicutes	sf_5	3066	*Clostridium methoxybenzovorans* str. SR3; DSM 12182	0.02576891	0.03133258
Proteobacteria	sf_4	7105	Mariana trough hydrothermal vent water 0.2micro-m filterable fraction clone MT-NB25	0.0258226	0.03133258
Proteobacteria	sf_3	10463	*Campylobacter* subsp. fetus	0.02586973	0.03133258
Proteobacteria	sf_6	6986	bacterioplankton clone AEGEAN_167	0.02601555	0.03133258
Firmicutes	sf_1	77	thermal soil clone YNPFFP9	0.02609314	0.03133258
OP9/JS1	sf_1	2489	Guaymas Basin hydrothermal vent sediments clone B01R005	0.02646754	0.03133258
Proteobacteria	sf_4	9733	bacterioplankton clone ZA3735c	0.02654204	0.03133258
Actinobacteria	sf_1	1428	*Corynebacterium simulans* National Microbiology Laboratory Special identifier 00-0186	0.02696231	0.03133258
Actinobacteria	sf_1	1183	*Actinomyces europaeus* str. CCUG 32789A	0.02698892	0.03133258
Firmicutes	sf_5	2804	*Clostridium amygdalinum* str. BR-10	0.0271011	0.03133258
Firmicutes	sf_12	2915	*Tepidibacter thalassicus* str. SC 562	0.02712509	0.03133258
Proteobacteria	sf_3	10430	*Helicobacter heilmannii* str. MM2	0.02723718	0.03133258
Proteobacteria	sf_3	10425	*Sulfurimonas autotrophica* str. OK5	0.02725193	0.03133258
Actinobacteria	sf_3	2045	hypersaline lake clone ML602J-44	0.02733284	0.03133258

Proteobacteria	sf_3	7275	Mammoth cave clone CCU18	0.0275147	0.03133258
Proteobacteria	sf_1	6974	India: Himalayas Kaza Spiti Valley Cold Desert isolate str. Kaza-35 Kaza-35	0.02761887	0.03133258
Spirochaetes	sf_1	6476	termite gut clone NkS50	0.02778509	0.03133258
Acidobacteria	sf_14	208	uranium mill tailings soil sample clone GuBH2-AD-9 sp.	0.02791697	0.03133258
Proteobacteria	sf_1	10530	hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH5_6_BAC_16SrRNA_9N_EPR	0.02833535	0.03133258
Caldithrix	sf_2	91	benzoate-degrading consortium clone BA059	0.02859993	0.03133258
Aquificae	sf_1	737	*Sulfurihydrogenibium azorense*	0.02881639	0.03133258
Firmicutes	sf_12	4610	*Clostridium putrefaciens* str. DSM 1291	0.02895756	0.03133258
Chloroflexi	sf_9	94	DCP-dechlorinating consortium clone SHA-2	0.02900021	0.03133258
Proteobacteria	sf_5	10267	marine sediment above hydrate ridge clone Hyd89-61 proteobacterium	0.0290736	0.03133258
Firmicutes	sf_5	2937	swine intestine clone p-2482-18B5	0.02916053	0.03133258
Firmicutes	sf_12	10457	strain isolate str. Dex60-82	0.02916651	0.03133258
Proteobacteria	sf_3	10442	*Helicobacter cetorum* str. MIT 99-5656	0.02941819	0.03133258
Proteobacteria	sf_1	7768	swine intestine clone p-861-a5	0.02971797	0.03133258
Bacteroidetes	sf_1	6274		0.02977329	0.03133258
Proteobacteria	sf_1	9709	termite gut homogenate clone Rs-N31 proteobacterium	0.02985348	0.03133258
Chloroflexi	sf_9	72	sediments collected at Charon's Cascade near Echo River October 2000 clone CCD21	0.02986605	0.03133258
Bacteroidetes	sf_1	5914	*Psychroserpens burtonensis* str. S2-64	0.03006146	0.03133258
LD1PA group	sf_1	10118	anoxic marine sediment clone LD1-PA38	0.03018487	0.03133258
Bacteroidetes	sf_1	6272	*Sphingobacterium heparinum*	0.03025171	0.03133258
Actinobacteria	sf_1	1146	*Nocardia otitidiscaviarum* str. S639	0.03030156	0.03133258
Actinobacteria	sf_1	1119	*Amycolatopsis tolypomycina* str. DSM 44544	0.03030195	0.03133258
Bacteroidetes	sf_1	5492	*Sphingobacterium* sp. str. HC-6155	0.03034372	0.03133258
Acidobacteria	sf_6	6359	PCE-contaminated site clone CLi114	0.03042882	0.03133258
Actinobacteria	sf_1	1917	*Nocardia otitidiscaviarum* str. DSM43242	0.03053111	0.03133258
Chloroflexi	sf_1	765	anaerobic bioreactor clone SHD-71	0.03057939	0.03133258
Proteobacteria	sf_3	8741	marine sediment clone Limfjorden L10	0.03061989	0.03133258
Bacteroidetes	sf_1	6158	municipal wastewater treatment bioreactor isolate str. CAGY10	0.03062312	0.03133258
Proteobacteria	sf_1	8896	silica sinter depositing geothermal power station discharge	0.03063729	0.03133258

OD1	sf_1	515	drain clone ST01-SN4A proteobacterium	0.0309065	0.03133258
Spirochaetes	sf_1	6568	*Spirochaeta* sp	0.0309648	0.03133258
Actinobacteria	sf_1	1834	*Nocardia transvalensis* str. DSM 43405	0.03096922	0.03133258
Proteobacteria	sf_3	10548	*Helicobacter rappini* W.Tee-Bat	0.03101991	0.03133258
Bacteroidetes	sf_1	5521	Flavobacteriaceae str. SW269	0.03106279	0.03133258
Actinobacteria	sf_1	1104	*Amycolatopsis mediterranei* str. NRRL B-3240	0.0310754	0.03133258
Proteobacteria	sf_3	10432	*Riftia pachyptila*'s tube clone R76-B51	0.03113299	0.03133258
Bacteroidetes	sf_19	5728	*Cytophaga* sp. str. MBIC04693	0.03150707	0.03133258
Proteobacteria	sf_3	10572	*Helicobacter* sp	0.03167141	0.03133258
Proteobacteria	sf_3	10385		0.03167843	0.03133258
Proteobacteria	sf_3	10451	*Helicobacter heilmannii* str. C4S	0.03167843	0.03133258
Actinobacteria	sf_1	1355	*Amycolatopsis mediterranei* str. IMSNU 20056T	0.03181102	0.03133258
Spirochaetes	sf_1	6529	termite gut homogenate clone BCf10-21	0.03188088	0.03133258
Proteobacteria	sf_3	6908	*Rhinocyllus conicus* endosymbiont	0.03193098	0.03133258
Bacteroidetes	sf_1	5901	Arctic sea ice ARK10159	0.03199243	0.03133258
Actinobacteria	sf_1	1360	forested wetland clone RCP2-103	0.0320137	0.03133258
Lentisphaerae	sf_5	10027	*Cytophaga* sp. str. Dex80-43	0.03205003	0.03133258
Actinobacteria	sf_1	1860	*Mycobacterium marinum*	0.03209162	0.03133258
Actinobacteria	sf_1	1111	*Kitasatospora setae* str. KM-6054	0.03211718	0.03133258
Acidobacteria	sf_1	435	anaerobic VC-degrading enrichment clone VC47 bacterium	0.03224751	0.03133258
Actinobacteria	sf_1	1781	*Mycobacterium rhodesiae* str. JS60	0.03238783	0.03133258
Actinobacteria	sf_1	1885	*Mycobacterium neoaurum* str. ATCC 25795	0.03238783	0.03133258
Chlorobi	sf_6	5294	Mammoth cave clone CCM9b	0.03275735	0.03133258
Actinobacteria	sf_1	1187	*Mycobacterium aichiense* str. JS618	0.032761	0.03133258
Firmicutes	sf_5	3017	termite gut homogenate clone Rs-D48 bacterium	0.03279771	0.03133258
Actinobacteria	sf_1	1639	*Streptomyces coelicolor* str. M145 ssp. A3(2)	0.03288446	0.03133258
Proteobacteria	sf_3	10447	*Sulfurospirillum deleyianum* str. Spirillum 5175	0.03295985	0.03133258
Proteobacteria	sf_1	9598	Mono Lake at depth 2 m station 6 July 2000 clone ML602J-47 proteobacterium	0.03302136	0.03133258
Actinobacteria	sf_1	1404	freshwater isolate str. MWH-Ta3	0.03304374	0.03133258
Actinobacteria	sf_1	1872	*Dietzia maris*	0.03304396	0.03133258

Actinobacteria	sf_1	1286	*Frankia* sp. Sn5-8	0.03313284	0.03133258
Proteobacteria	sf_1	9267	*Pseudomonas syringae* pv. theae str. PT1	0.03318664	0.03133258
Chloroflexi	sf_1	927	hydrothermal vent polychaete mucous clone P. palm C 37	0.03327361	0.03133258
Proteobacteria	sf_4	9741	uranium mining waste pile clone JG37-AG-30 proteobacterium	0.03331343	0.03133258
Bacteroidetes	sf_1	5915	ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A-MN27 bacterium	0.03358885	0.03133258
Actinobacteria	sf_1	1567		0.03387427	0.03133258
Proteobacteria	sf_3	10397	groundwater clone 1006	0.03394335	0.03133258
Bacteroidetes	sf_1	5946	tongue dorsa clone DO027	0.03398571	0.03133258
Firmicutes	sf_1	3955	Weeping tea tree witches'-broom phytoplasma tree	0.03403613	0.03133258
Proteobacteria	sf_3	10050	DCP-dechlorinating consortium clone SHA-51	0.034379	0.03133258
Firmicutes	sf_17	2324		0.03439084	0.03133258
Firmicutes	sf_5	3111	rumen clone 6C3d-11	0.03491031	0.03133258
Actinobacteria	sf_1	1261	*Nocardia caishijiensis* str. F829	0.03493306	0.03133258
Proteobacteria	sf_1	8131		0.03505097	0.03133258
Spirochaetes	sf_1	6502	*Treponema denticola* str. ATCC35405	0.03518012	0.03133258
Proteobacteria	sf_1	10480	hydrothermal vent polychaete mucous clone P. palm C 84	0.03541466	0.03133258
Proteobacteria	sf_2	7043	marine clone Arctic95D-8	0.0354164	0.03133258
Cyanobacteria	sf_1	5008	*Synechococcus* sp. str. PCC 7502	0.03544292	0.03133258
Proteobacteria	sf_1	10543	hydrothermal vent clone PVB_10	0.03547007	0.03133258
Proteobacteria	sf_3	7481	*Wolbachia pipientis*	0.03565544	0.03133258
Firmicutes	sf_17	3476		0.03565828	0.03133258
Firmicutes	sf_1	3289	*Isobaculum melis* CCUG 37660T	0.03567713	0.03133258
Firmicutes	sf_12	3219	Great Artesian Basin clone R82	0.03573643	0.03133258
Actinobacteria	sf_1	1770	*Dactylosporangium roseum* str. DSM 43916	0.03581177	0.03133258
marine group A	sf_1	6408	Sargasso Sea	0.0359321	0.03133258
Actinobacteria	sf_1	1901	earthworm burrow isolate B33D1	0.03609328	0.03133258
Bacteroidetes	sf_19	5563	*Cytophaga* sp. I-545	0.03618804	0.03133258
Bacteroidetes	sf_1	5480	ED5 earthworm gut	0.03621907	0.03133258
Proteobacteria	sf_20	2520		0.03669873	0.03133258
Firmicutes	sf_12	3049	*Clostridium paradoxum* str. DSM 7308T	0.03693858	0.03133258
Proteobacteria	sf_1	9486	Marine isolate str. GK-2001	0.03714535	0.03133258

Planctomycetes	sf_3	4704	aerobic basin clone CY0ARA025E11	0.03750463	0.03133258
Proteobacteria	sf_5	10136	Guaymas Basin hydrothermal vent sediments clone B01R011	0.0377474	0.03133258
Proteobacteria	sf_6	7252	bacterioplankton clone AEGEAN_108	0.03778427	0.03133258
Bacteroidetes	sf_1	5482		0.03790595	0.03133258
Actinobacteria	sf_1	1552	*Nocardia cyriacigeorgica* str. D1627T	0.03807711	0.03133258
Proteobacteria	sf_1	7762	Elbe River snow isolate Iso18 Iso18_1411	0.0380896	0.03133258
Actinobacteria	sf_1	1432	*Nocardia veterana* str. DSM 44445	0.03811564	0.03133258
Spirochaetes	sf_1	6562	forested wetland clone RCP1-96	0.038254	0.03133258
Proteobacteria	sf_1	8755	*Pseudomonas* sp. SK-1-3-1	0.03854822	0.03133258
Bacteroidetes	sf_1	5942		0.03874601	0.03133258
Firmicutes	sf_5	3033	human colonic clone HuCA15	0.03904052	0.03133258
Verrucomicrobia	sf_3	486	Elbe river clone DEV045	0.03904737	0.03133258
Firmicutes	sf_12	4548	termite gut homogenate clone Rs-Q69 bacterium	0.03935779	0.03133258
Actinobacteria	sf_1	1637	*Mycobacterium austroafricanum* str. IFP2173	0.03946653	0.03133258
Proteobacteria	sf_3	8457	5' clone CHAB-XI-27	0.03962898	0.03133258
Bacteroidetes	sf_1	5436	Arctic sea ice ARK10004	0.03979708	0.03133258
Actinobacteria	sf_1	1492	*Corynebacterium tuscaniae* str. ISS-5309	0.03984708	0.03133258
Proteobacteria	sf_3	10444	*Helicobacter suncus* str. Kaz-2	0.03992517	0.03133258
Firmicutes	sf_5	4212	termite gut clone Rs-061	0.03994182	0.03133258
Actinobacteria	sf_1	1766	*Dactylosporangium salmoneum* str. DSM 43910	0.04012421	0.03133258
Firmicutes	sf_1	3297	*Aerococcus urinae* str. 1656-92	0.04018357	0.03133258
Firmicutes	sf_5	2693	ruminantium str. GA195	0.04027324	0.03133258
Proteobacteria	sf_1	10069		0.04042032	0.03133258
Bacteroidetes	sf_1	5479	*Flavobacterium frigoris* str. LMG 21471	0.04076238	0.03133258
Proteobacteria	sf_1	7126	ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A-MN96 proteobacterium	0.0408119	0.03133258
Actinobacteria	sf_1	1317	USA: Colorado Fort collins Horsetooth Reservoir clone HTDD3	0.04088223	0.03133258
Actinobacteria	sf_1	1698	*Corynebacterium* subsp. afermentans str. CIP 103499T	0.04099147	0.03133258
Proteobacteria	sf_2	594	uranium mining mill tailing clone GR-296.II.52 GR-296.I.52	0.04106073	0.03133258
Unclassified	sf_160	6456		0.04114194	0.03133258
Proteobacteria	sf_1	8433	*Pseudomonas syringae* pv. broussonetiae str. KOZ 8101	0.04119676	0.03133258

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Proteobacteria	sf_1	7390	*Afipia genosp*. 10 str. G8996	0.04136049	0.03133258
Bacteroidetes	sf_1	5367	patient's bronchoalveolar lavage isolate str. MDA2507 sp.	0.04154043	0.03133258
Spirochaetes	sf_1	6580	*Treponema* sp. str. III:C:BA213	0.04160631	0.03133258
Proteobacteria	sf_4	7157	acid mine drainage clone ASL45	0.04161215	0.03133258
Bacteroidetes	sf_6	5792	activated sludge foam clone 47	0.0416564	0.03133258
Proteobacteria	sf_1	10414	penguin droppings sediments clone KD2-34	0.04170286	0.03133258
Proteobacteria	sf_1	8062	*Brackiella oedipodis* str. LMG 1945 R8846	0.04201794	0.03133258
Proteobacteria	sf_4	8169	forested wetland clone RCP2-54	0.04228357	0.03133258
Firmicutes	sf_5	4315	termite gut homogenate clone Rs-N94 bacterium	0.04232885	0.03133258
Cyanobacteria	sf_5	5221	picoplankton clone OM20	0.04249394	0.03133258
Proteobacteria	sf_1	9310	*Pseudomonas* sp. str. AC-167	0.04255034	0.03133258
Actinobacteria	sf_1	1304	*Nocardia* sp. str. 99-08-244A	0.04266145	0.03133258
Proteobacteria	sf_3	9498		0.04270053	0.03133258
Actinobacteria	sf_1	2014	marine sediment clone MB-A2-100	0.0428089	0.03133258
Proteobacteria	sf_1	9351	bacterioplankton clone ZA2333c	0.04293982	0.03133258
Proteobacteria	sf_3	8321	Wadden Sea sediment clone Dangast A9	0.0429748	0.03133258
Actinobacteria	sf_1	1227	*Actinomyces naeslundii*	0.04304712	0.03133258
Bacteroidetes	sf_1	5903	marine bacterioplankton clone MB11E04	0.04322598	0.03133258
Cyanobacteria	sf_5	4984	Cape Hatteras picoplankton clone OM164	0.04322788	0.03133258
Bacteroidetes	sf_15	5511	marine sediment above hydrate ridge clone Hyd-B2-1 bacterium	0.04337386	0.03133258
Proteobacteria	sf_1	10427	hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH3_17_BAC_16SrRNA_9N_EPR	0.04345438	0.03133258
Actinobacteria	sf_1	1970	*Dietzia* sp. str. E9_2	0.0436654	0.03133258
Deinococcus-Thermus	sf_2	637	hypersaline pond clone LA7-B27N	0.04372637	0.03133258
Actinobacteria	sf_1	1161	*Frankia* sp. MRn2-2	0.04433727	0.03133258
Bacteroidetes	sf_1	5997	*Flavobacterium aquatile*	0.04477501	0.03133258
TM7	sf_1	3025		0.0448083	0.03133258
Verrucomicrobia	sf_1	530	anoxic marine sediment clone LD1-PB20	0.04490774	0.03133258
Firmicutes	sf_5	3089	*Ruminococcus obeum*	0.04492827	0.03133258
Proteobacteria	sf_1	7139	*Mesorhizobium loti* str. R8CS USDA 3467	0.04495827	0.03133258
AD3	sf_1	2338	uranium mining waste pile soil clone JG30-KF-C12	0.04498748	0.03133258

Proteobacteria	sf_3	9269		0.04499476	0.03133258
Unclassified	sf_160	6360		0.04500369	0.03133258
Actinobacteria	sf_1	1884	*Corynebacterium tuberculostearicum* str. ATCC 33035	0.04504225	0.03133258
Firmicutes	sf_5	2844	*Pseudobutyrivibrio ruminis* str. pC-XS2	0.04527833	0.03133258
Actinobacteria	sf_1	1262	*Mycobacterium holsaticum* str. 1406	0.0454355	0.03133258
Actinobacteria	sf_1	1229	*Streptacidiphilus carbonis* str. JL 415; DSM 41754	0.04547963	0.03133258
Firmicutes	sf_5	3088	*Clostridium sphenoides* str. DSM 632	0.0455199	0.03133258
Firmicutes	sf_5	1037	*Finegoldia magna*	0.04577731	0.03133258
Proteobacteria	sf_3	9167	pea aphid symbiont clone APe4_38	0.04601092	0.03133258
Proteobacteria	sf_1	8513	*Pseudomonas monteilii* str. CIP 104883	0.0460157	0.03133258
Proteobacteria	sf_1	8561	*Pseudomonas* sp. B65	0.04618102	0.03133258
Actinobacteria	sf_1	1569	*Streptomyces sampsonii* str. ATCC25495	0.04630371	0.03133258
Proteobacteria	sf_1	8546	*Thiocapsa litoralis*	0.04631959	0.03133258
Firmicutes	sf_4	2398	deep marine sediment clone MB-C2-106	0.04657659	0.03133258
Proteobacteria	sf_1	8140	*Schlegelella* sp. str. KB1a	0.0465991	0.03133258
Firmicutes	sf_5	4623	human colonic clone HuCA1	0.04664543	0.03133258
Spirochaetes	sf_3	6470	neutral pH mine biofilm clone 44a-B1-48	0.04670421	0.03133258
Actinobacteria	sf_1	1105	*Frankia* sp	0.04674021	0.03133258
Bacteroidetes	sf_1	5601	*Sphingobacterium multivorum* str. OM-A8	0.04684498	0.03133258
Actinobacteria	sf_1	1581	*Cryptosporangium aurantiacum* str. IMSNU 22120	0.0469576	0.03133258
Proteobacteria	sf_1	9282		0.04704916	0.03133258
Proteobacteria	sf_1	8012	*Acidovorax konjaci* str. DSM 7481	0.04789895	0.03133258
Proteobacteria	sf_3	10520	*Helicobacter* sp. blood isolate 964	0.04825001	0.03133258
Actinobacteria	sf_1	1116	*Gordona terrae*	0.04834643	0.03133258
Proteobacteria	sf_1	7788	atrazine-catabolizing microbial absence methanol clone KRA30-58	0.04848511	0.03133258
Acidobacteria	sf_14	6335	forested wetland clone FW45	0.04852058	0.03133258
Firmicutes	sf_1	4046	Pigeon pea witches'-broom mycoplasma-like organism	0.04852821	0.03133258
Unclassified	sf_95	2545	anaerobic sludge isolate str. JE	0.04874113	0.03133258
Proteobacteria	sf_1	8196		0.04874598	0.03133258
Actinobacteria	sf_1	1274	*Trichotomospora caesia* str. IFO14562	0.04879441	0.03133258
Proteobacteria	sf_1	7067	*Blastochloris sulfoviridis* str. GN1	0.04882702	0.03133258
Proteobacteria	sf_1	6964	*Agrobacterium tumefaciens* str. C58 Cereon	0.04899273	0.03133258

Proteobacteria	sf_1	7568	*Rhizobium etli* str. USDA 2667 ATCC 14483 SEMIA 043	0.04901525	0.03133258
Actinobacteria	sf_1	1723	*Corynebacterium* sp str. CDC G5911	0.0493076	0.03133258
Actinobacteria	sf_1	1803	*Corynebacterium spheniscorum* str. CCUG 45512	0.04936733	0.03133258
Actinobacteria	sf_1	1545		0.04946945	0.03133258
Actinobacteria	sf_1	1668	*Corynebacterium ulcerans* str. NCTC 7910	0.0495858	0.03133258
Proteobacteria	sf_1	6822		0.04960075	0.03133258
Proteobacteria	sf_1	7101		0.04960075	0.03133258
Proteobacteria	sf_3	10298	marine tidal mat clone BTM36	0.04967707	0.03133258

[a]S-F = subfamily; [b]Taxon ID = Phylochip taxon identification number; [c]Representative species = bacterial species identifier.

Man’s best friend?

The effect of pet ownership on house-dust microbial communities.

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Table E3. Bacterial taxa detected in significantly higher abundance in Group 1 vs. Group 2

Phylum	***S-F*[a]**	***Taxon ID*[b]**	***Representative species*[c]**	***p-value***	***q-value***
Proteobacteria	sf_3	9044	hydrothermal sediment clone AF420370	2.30E-05	0.0114236
Proteobacteria	sf_1	8553	*Pseudomonas fulva* str. IAM 1587	3.20E-05	0.0114236
Proteobacteria	sf_1	7892	*Methylophilus leisingeri* str. DSM 6813	6.84E-05	0.0114236
Proteobacteria	sf_1	8513	*Pseudomonas monteilii* str. CIP 104883	8.64E-05	0.0114236
Proteobacteria	sf_3	9332	wetland ecosystem constructed to remediate mine drainage isolate str. WJ2 WJ2	8.66E-05	0.0114236
Proteobacteria	sf_1	7817	TCE-contaminated site clone ccs265	9.58E-05	0.0114236
Proteobacteria	sf_1	9052		0.000102978	0.0114236
Proteobacteria	sf_1	9243	*Pseudomonas tolaasii* str. LMG 2342T ()	0.000122719	0.01191188
Proteobacteria	sf_1	7390	*Afipia genosp*. 10 str. G8996	0.000151696	0.01308847
Proteobacteria	sf_1	9219	*Pseudomonas* cf. monteilii 9	0.000223641	0.01478585
Proteobacteria	sf_1	8697	*Thiococcus* sp. AT2204	0.000280521	0.01478585
Proteobacteria	sf_1	8140	*Schlegelella* sp. str. KB1a	0.000295271	0.01478585
Proteobacteria	sf_1	8708		0.000321705	0.01478585
Proteobacteria	sf_1	8561	*Pseudomonas* sp. B65	0.00033454	0.01478585
Proteobacteria	sf_1	9221	*Pseudomonas fulgida* str. DSM 14938 = LMG 2146 P 515/12	0.000359384	0.01478585
Proteobacteria	sf_1	10407	hydrothermal sediment clone AF420342	0.000378004	0.01478585
Proteobacteria	sf_3	10444	*Helicobacter suncus* str. Kaz-2	0.000387748	0.01478585
Proteobacteria	sf_1	8209	uranium mining waste pile clone JG37-AG-122 proteobacterium	0.000395645	0.01478585
Proteobacteria	sf_3	10397	groundwater clone 1006	0.00039895	0.01478585
Proteobacteria	sf_1	8338	*Pseudomonas synxantha* str. DSM 13080 G	0.000423269	0.01478585
Proteobacteria	sf_3	9735	uranium mining waste pile clone JG37-AG-15 proteobacterium	0.000440574	0.01478585
Proteobacteria	sf_3	10523	*Riftia pachyptila*'s tube clone R103-B70	0.000458299	0.01478585
Proteobacteria	sf_1	9493	*Pseudomonas* sp. str. dcm7B	0.000458852	0.01478585
Proteobacteria	sf_1	8433	*Pseudomonas syringae* pv. broussonetiae str. KOZ 8101 pv.	0.000480885	0.01478585
Actinobacteria	sf_1	2018	*Curtobacterium herbarum* str. P 420/07	0.000485694	0.01478585
Proteobacteria	sf_1	8813	*Lyrodus pedicellatus* symbiont	0.000495063	0.01478585
Proteobacteria	sf_1	7871		0.000552475	0.01489686
Proteobacteria	sf_1	8263		0.00055849	0.01489686

Proteobacteria	sf_1	8578	*Marinobacter lipolyticus* str. SM-19	0.000600307	0.01489686
Proteobacteria	sf_1	9446	*Halomonas* sp. str. IB-I6	0.000614844	0.01489686
Proteobacteria	sf_1	9267	*Pseudomonas syringae* pv. theae str. PT1	0.000627379	0.01489686
Proteobacteria	sf_1	9028	*Pseudomonas koreensis* str. Ps 9-14	0.000628216	0.01489686
Synergistes	sf_3	719	*Synergistes* sp. P1 str. P4G_18	0.000640356	0.01489686
Proteobacteria	sf_1	6799	*Rhodopseudomonas palustris* str. ATCC 17001	0.000652251	0.01489686
Proteobacteria	sf_1	6768	*Rhodopseudomonas palustris* str. GH	0.000682337	0.01513873
Proteobacteria	sf_1	8723	*Vibrio calviensis* str. RE35F/12	0.000724233	0.01538183
Synergistes	sf_3	60	*Flexistipes* sp. str. E3_33	0.000732911	0.01538183
Proteobacteria	sf_1	9294	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	0.000792741	0.01619968
Proteobacteria	sf_1	9175	*Pseudomonas extremorientalis* str. KMM3447	0.00082506	0.0163176
Proteobacteria	sf_1	8687	*Pseudomonas putida* str. ATCC 17472 [d]	0.000840538	0.0163176
Proteobacteria	sf_3	9277	penguin droppings sediment clone KD8-68	0.000878008	0.01662927
Proteobacteria	sf_3	10428	*Flexispira rappini* FH 9702248	0.00091954	0.01700123
Gemmatimonadetes	sf_5	1127	uranium mining waste pile near Johanngeorgenstadt soil clone JG37-AG-21	0.000967447	0.01711058
Proteobacteria	sf_1	8853	*Pseudomonas cichorii* str. ATCC 10857T	0.00097848	0.01711058
Proteobacteria	sf_3	8714	Marinobacter hydrocarbonoclasticus str. ATCC 27132T	0.001009519	0.01711058
Proteobacteria	sf_1	8957	marine clone Arctic97C-5	0.001013593	0.01711058
Proteobacteria	sf_1	7087	*Bradyrhizobium japonicum* HA1	0.001056936	0.01733955
Proteobacteria	sf_1	8288		0.001114327	0.01733955
Proteobacteria	sf_1	8546	*Thiocapsa litoralis*	0.001127095	0.01733955
Proteobacteria	sf_1	7982	marine? clone KD1-99	0.001129272	0.01733955
Proteobacteria	sf_1	9141	*Halomonas* sp. SK1	0.00115496	0.01733955
Actinobacteria	sf_1	1544	*Kitasatospora cystarginea* str. IFO14836T	0.00119345	0.01733955
Bacteroidetes	sf_19	5366	*Flexibacter roseolus* str. IFO 16030	0.00125056	0.01733955
Proteobacteria	sf_3	8321	Wadden Sea sediment clone Dangast A9	0.001253997	0.01733955
Proteobacteria	sf_1	10248	*Desulfovibrio giganteus* str. DSM 4370	0.001317424	0.01733955
Proteobacteria	sf_3	10562	*Helicobacter rappini* W.Tee-Yu	0.001321901	0.01733955
Proteobacteria	sf_1	7316		0.00136099	0.01733955

Proteobacteria	sf_1	7333	*Afipia genosp*. 4 str. G3644	0.00136099	0.01733955
Proteobacteria	sf_1	8012	*Acidovorax konjaci* str. DSM 7481	0.001387645	0.01733955
Proteobacteria	sf_1	7782	*Burkholderia hospita* str. LMG 20598T	0.001394009	0.01733955
Proteobacteria	sf_1	6917	*Bradyrhizobium japonicum* str. IAM 12608	0.001412753	0.01733955
Firmicutes	sf_12	4415	termite gut homogenate clone Rs-K32 bacterium	0.001424065	0.01733955
Proteobacteria	sf_3	8477	marine sediment clone Limfjorden L8	0.001427925	0.01733955
Bacteroidetes	sf_1	5991	*Tenacibaculum ovolyticum* str. IAM14318	0.001446612	0.01733955
Proteobacteria	sf_1	7705	penguin droppings sediments clone KD4-7	0.001472363	0.01733955
Proteobacteria	sf_3	9270	*Stenotrophomonas rhizophila* str. e-p10	0.001493223	0.01733955
Proteobacteria	sf_1	6887	*Bradyrhizobium* str. YB2	0.001532529	0.01733955
Actinobacteria	sf_3	2045	hypersaline lake clone ML602J-44	0.001572554	0.01733955
Proteobacteria	sf_3	10442	*Helicobacter cetorum* str. MIT 99-5656	0.001576091	0.01733955
Proteobacteria	sf_1	7398	*Bradyrhizobium japonicum* str. USDA 38	0.001593938	0.01733955
Proteobacteria	sf_1	8136	*Acanthamoeba* sp. UWC6 symbiont	0.001606682	0.01733955
Bacteroidetes	sf_1	5473		0.001627847	0.01733955
Acidobacteria	sf_1	572	forested wetland clone FW144	0.001712876	0.01733955
Proteobacteria	sf_1	7319	*Anabaena circinalis* AWQC118C isolate str. UNSW1	0.001720231	0.01733955
Unclassified	sf_140	6355		0.001759842	0.01733955
Proteobacteria	sf_1	6959	*Rhodocista pekingensis* str. 3-p	0.001762273	0.01733955
Proteobacteria	sf_3	8874	hydrothermal sediment clone AF420367	0.001762766	0.01733955
Proteobacteria	sf_1	7720	penguin droppings sediments clone KD1-79	0.001763131	0.01733955
Gemmatimonadetes	sf_5	10112	forest soil clone NOS7.157WL	0.001778436	0.01733955
Proteobacteria	sf_8	9558		0.00181305	0.01733955
Proteobacteria	sf_1	9182	*Methylobacter marinus* str. A45	0.001821519	0.01733955
Proteobacteria	sf_1	9172	*Pseudomonas psychrophila* str. E-3	0.00183102	0.01733955
Proteobacteria	sf_1	7768	swine intestine clone p-861-a5	0.001868532	0.0174816
Proteobacteria	sf_1	7403	*Oligotropha carboxidovorans* str. S23	0.001894307	0.01751176
Proteobacteria	sf_1	6867	heavy metal-contaminated soil clone a13131	0.002058109	0.01880218
Proteobacteria	sf_6	7252	bacterioplankton clone AEGEAN_108	0.002101981	0.01884486
Proteobacteria	sf_3	8230		0.002111317	0.01884486
Proteobacteria	sf_1	9469	cf. *Pseudomonas* sp. clone Llangefni 52	0.002211911	0.01940181
Proteobacteria	sf_3	9167	pea aphid symbiont clone APe4_38	0.002245827	0.01940181
Proteobacteria	sf_3	10456	*Campylobacter showae*	0.002275645	0.01940181

Proteobacteria	sf_3	8577	*Xanthomonas axonopodis* pv. citri str. MA	0.002286618	0.01940181
Proteobacteria	sf_1	6927	*Nitrobacter hamburgensis* str. X14	0.002298642	0.01940181
Proteobacteria	sf_1	10244		0.002350172	0.01962345
Proteobacteria	sf_3	8349	Norway:(Svalbard)Hornsund clone Sva0864	0.002403202	0.01964942
TM6	sf_1	9803	forest soil clone S1204	0.002428388	0.01964942
Proteobacteria	sf_1	6941	*Rhodopseudomonas rhenobacensis* str. Klemme Rb	0.002453911	0.01964942
Proteobacteria	sf_3	10448	*Helicobacter felis* str. Dog-1	0.002454498	0.01964942
Proteobacteria	sf_1	10427	hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH3_17_BAC_16SrRNA_9N_EPR	0.002519605	0.01996481
Nitrospira	sf_2	697	forested wetland clone FW118	0.002585947	0.02028351
Proteobacteria	sf_3	10436	*Helicobacter aurati* str. MIT 97-5075c	0.002633955	0.02045347
Proteobacteria	sf_1	6922	*Dechlorospirillum* sp. str. SN1	0.00268269	0.02062566
Proteobacteria	sf_1	6878	*Bradyrhizobium japonicum* SD5	0.002734541	0.02070931
Proteobacteria	sf_1	6732	*Anabaena circinalis* AWQC118C isolate str. UNSW7	0.002754673	0.02070931
Proteobacteria	sf_1	10332	Psychrophilic sulfate-reducing isolate str. LSv23 bacterium	0.002777805	0.02070931
Proteobacteria	sf_3	10430	*Helicobacter heilmannii* str. MM2	0.002800246	0.02070931
Proteobacteria	sf_3	8741	marine sediment clone Limfjorden L10	0.002842241	0.02078562
Proteobacteria	sf_3	9584		0.003012041	0.02078562
Acidobacteria	sf_6	6345	soil sample uranium mining waste pile near town Johanngeorgenstadt clone JG36-TzT-77 bacterium	0.003018016	0.02078562
Proteobacteria	sf_1	7902	*Alcaligenes faecalis* str. M3A	0.003026214	0.02078562
Acidobacteria	sf_6	6359	PCE-contaminated site clone CLi114	0.003027789	0.02078562
Proteobacteria	sf_3	10050	DCP-dechlorinating consortium clone SHA-51	0.003079084	0.02078562
Proteobacteria	sf_3	10385		0.003108651	0.02078562
Proteobacteria	sf_3	10451	*Helicobacter heilmannii* str. C4S	0.003108651	0.02078562
Proteobacteria	sf_1	9230	Antarctic pack ice Lasarev Sea Southern Ocean clone ANTXI/4_14-62 sea	0.003126135	0.02078562
Actinobacteria	sf_1	1513	*Microbacterium gubbeenense* str. DPC 5284	0.003131395	0.02078562
Proteobacteria	sf_3	10540	*Campylobacter showae* str. LMG 12636	0.003147308	0.02078562
Actinobacteria	sf_1	1771	*Streptomyces setonii* str. ATCC25497	0.003151965	0.02078562
Proteobacteria	sf_3	8327	Arctic sea ice ARK10148	0.003158539	0.02078562
Proteobacteria	sf_1	9239	Arctic sea ice ARK10228	0.003277816	0.02115563
Proteobacteria	sf_1	9300	*Lyrodus pedicellatus* symbiont	0.003294756	0.02115563

Cyanobacteria	sf_8	5206		0.003312486	0.02115563
Proteobacteria	sf_1	8564	*Rahnella aquatilis* str. ATCC 33989	0.003323739	0.02115563
Proteobacteria	sf_1	7135	*Rhizobium gallicum* str. FL27	0.003381379	0.0212033
Proteobacteria	sf_1	9224	*Acidithiobacillus albertensis* str. DSM 14366	0.003393428	0.0212033
Proteobacteria	sf_3	10534	*Helicobacter pylori*	0.003413144	0.0212033
Proteobacteria	sf_5	10239		0.003490004	0.0215087
Proteobacteria	sf_1	7539	*Rhodocista* sp. AR2107	0.00355369	0.02172874
Proteobacteria	sf_3	6908	*Rhinocyllus conicus* endosymbiont	0.003598215	0.0218291
Proteobacteria	sf_1	6981	*Ochrobactrum gallinifaecis* str. Iso 196	0.003651522	0.02198077
Proteobacteria	sf_1	6871	*Rhizobium mongolense* str. USDA 1832	0.003728244	0.02217303
Proteobacteria	sf_3	10463	*Campylobacter* subsp. fetus	0.003747718	0.02217303
Proteobacteria	sf_1	7497	*Pseudaminobacter salicylatoxidans* str. KTC001	0.003769122	0.02217303
Proteobacteria	sf_1	8725	*Pseudomonas* sp. str. 2N1-1	0.003842237	0.02218252
Bacteroidetes	sf_1	5758	*Tenacibaculum* sp. str. MGP-10	0.003867949	0.02218252
Proteobacteria	sf_1	6804	*Rhizobium* sp. str. SH19312	0.003905162	0.02218252
Proteobacteria	sf_3	10548	*Helicobacter rappini* W.Tee-Bat	0.003906924	0.02218252
Proteobacteria	sf_1	8474	ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A-MN7 proteobacterium	0.003913566	0.02218252
Proteobacteria	sf_3	10484	*Campylobacter helveticus*	0.003968936	0.02233335
Proteobacteria	sf_1	8601	*Pseudomonas marginalis* str. ATCC 10844T	0.004041503	0.02242878
Actinobacteria	sf_1	1294		0.004043664	0.02242878
Proteobacteria	sf_1	8508	*Pseudomonas citronellolis* str. TERIDB26	0.004102135	0.0224338
Firmicutes	sf_12	4637	termite gut clone Rs-088	0.004112177	0.0224338
Proteobacteria	sf_1	7381	*Aminobacter aminovorans* str. DSM7048T	0.004131236	0.0224338
Chloroflexi	sf_1	583	anaerobic bioreactor clone SHD-238	0.004199961	0.02253068
Proteobacteria	sf_1	6798	*Agrobacterium tumefaciens* TG14	0.004260194	0.02253068
Proteobacteria	sf_1	7995	*Ottowia thiooxydans* str. K11	0.004263479	0.02253068
Proteobacteria	sf_1	8037	*Chitinimonas taiwanensis* str. cf	0.004265136	0.02253068
Proteobacteria	sf_1	8336	*Alteromonas* sp. str. MS23	0.004308208	0.02255022
Actinobacteria	sf_1	1558	*Corynebacterium* sp. str. 61722	0.004326915	0.02255022
Proteobacteria	sf_1	6964	*Agrobacterium tumefaciens* str. C58 Cereon	0.004447959	0.02282787
Proteobacteria	sf_23	10443	*Helicobacter pylori* str. 85D08	0.004468381	0.02282787
Proteobacteria	sf_3	10576	*Helicobacter* sp. 'liver 3' str. liver 3	0.004468381	0.02282787

Proteobacteria	sf_4	7157	acid mine drainage clone ASL45	0.004550428	0.02300867
Proteobacteria	sf_1	6789	*Shinella zoogloeoides* str. ATCC 19623	0.004603607	0.02300867
Actinobacteria	sf_1	1111	*Kitasatospora setae* str. KM-6054 [d]	0.004611849	0.02300867
Proteobacteria	sf_1	9438	marine sediment above hydrate ridge clone Hyd24-01 proteobacterium	0.004632794	0.02300867
Proteobacteria	sf_1	8211	*Colwellia maris* str. ABE-1	0.004667326	0.02300867
Proteobacteria	sf_1	9005	*Pseudomonas* sp. str. KY	0.004681551	0.02300867
Firmicutes	sf_17	2683		0.004726423	0.0230831
Proteobacteria	sf_1	6869	*Azospirillum* sp. str. Mat2-1a	0.00476124	0.02310781
Proteobacteria	sf_3	9286	*Stenotrophomonas maltophilia* str. LMG 11104 [d]	0.004844135	0.02335979
Proteobacteria	sf_1	7334	*Agrobacterium tumefaciens* C4	0.004882342	0.02335979
Proteobacteria	sf_3	10572	*Helicobacter* sp	0.004916687	0.02335979
Proteobacteria	sf_1	6673	*Nitratireductor aquibiodomus* str. NL21	0.004958027	0.02335979
Proteobacteria	sf_1	7568	*Rhizobium etli* str. USDA 2667 ATCC 14483 SEMIA 043	0.00496357	0.02335979
Spirochaetes	sf_1	6460	termite gut homogenate clone Rs-B69 sp.	0.005009598	0.02337854
Proteobacteria	sf_1	6636	*Bradyrhizobium elkanii* str. USDA 76	0.005074693	0.02337854
Proteobacteria	sf_1	7522	*Bradyrhizobium* sp. str. KKI14	0.005074693	0.02337854
Planctomycetes	sf_3	4652	anoxic basin clone CY0ARA028C04	0.005123257	0.02337854
Proteobacteria	sf_1	7392		0.005124577	0.02337854
Bacteroidetes	sf_1	5492	*Sphingobacterium* sp. str. HC-6155	0.005166728	0.02337854
Deferribacteres	sf_1	797	*Deferribacter abyssi* str. DR	0.005178298	0.02337854
Proteobacteria	sf_1	10016	termite gut homogenate clone Rs-N35 proteobacterium	0.00522264	0.0234062
Proteobacteria	sf_3	10447	*Sulfurospirillum deleyianum* str. Spirillum 5175	0.005244709	0.0234062
Acidobacteria	sf_6	6423	coal effluent wetland clone FW92	0.00529358	0.02348931
Proteobacteria	sf_6	6986	bacterioplankton clone AEGEAN_167	0.005375701	0.02367751
Bacteroidetes	sf_1	5267	bacterioplankton clone AEGEAN_179	0.005396977	0.02367751
Bacteroidetes	sf_15	5511	marine sediment above hydrate ridge clone Hyd-B2-1 bacterium	0.005499922	0.02377873
Proteobacteria	sf_1	7747		0.005508831	0.02377873
Proteobacteria	sf_3	8339	water 5 m downstream manure clone 35ds5	0.005525395	0.02377873
Proteobacteria	sf_1	9554	*Tilapia parasite* TPT-541	0.005542537	0.02377873
Proteobacteria	sf_1	7233		0.005722598	0.02433577
Actinobacteria	sf_1	2048	*Nocardia uniformis* str. DSM 43136	0.005735054	0.02433577
Proteobacteria	sf_1	6683	*Sinorhizobium fredii* str. ATCC35423	0.005807952	0.02444203

Proteobacteria	sf_1	7761	*Ralstonia detusculanense* str. APF11	0.005850434	0.02444203
Proteobacteria	sf_1	6972	*Ensifer adhaerens* str. LMG 20582	0.005944931	0.02444203
Proteobacteria	sf_1	10384	deep-sea hydrothermal vent clone VC1.2-cl06	0.006046435	0.02444203
Proteobacteria	sf_1	6770	*Rhizobium tropici* str. LMG 9517	0.006050366	0.02444203
Proteobacteria	sf_3	10520	*Helicobacter* sp. blood isolate 964	0.006053488	0.02444203
Proteobacteria	sf_1	10497	UASB reactor granular sludge clone PD-UASB-2 proteobacterium	0.006092647	0.02444203
Bacteroidetes	sf_1	5317	*Tenacibaculum maritimum* str. IFO 15946	0.006097862	0.02444203
Proteobacteria	sf_1	9282		0.006115072	0.02444203
Proteobacteria	sf_1	9351	bacterioplankton clone ZA2333c	0.006145238	0.02444203
Proteobacteria	sf_1	7718	*Lampropedia hyalina* str. DSM 15336	0.006281971	0.02444203
Actinobacteria	sf_1	1668	*Corynebacterium ulcerans* str. NCTC 7910	0.006285961	0.02444203
Proteobacteria	sf_1	7044	*Afipia genosp.* 2 str. G4438	0.00631418	0.02444203
Unclassified	sf_132	9820		0.006322822	0.02444203
Proteobacteria	sf_1	6995		0.006341602	0.02444203
Proteobacteria	sf_1	6916	lake microbial mat isolate str. R-9219	0.006357691	0.02444203
Proteobacteria	sf_6	6898	heavy metal-contaminated soil clone a13113	0.006388324	0.02444203
Proteobacteria	sf_1	9048	*Allochromatium* sp. AT2202	0.006407799	0.02444203
Proteobacteria	sf_1	7509		0.00641009	0.02444203
Proteobacteria	sf_1	7600	*Acetobacter pomorum* str. LTH2458	0.006414788	0.02444203
Firmicutes	sf_5	3036	termite gut homogenate clone Rs-F27 bacterium	0.006452047	0.02444203
Proteobacteria	sf_1	7641	*Hyphomicrobium facile* str. H-526	0.006480594	0.02444203
Proteobacteria	sf_1	7467	*Azospirillum* sp. str. ASP-1	0.00648404	0.02444203
Proteobacteria	sf_1	6966	*Mesorhizobium tianshanense* str. -1BS; USDA 3592	0.006562086	0.02452944
Firmicutes	sf_1	4044		0.006570407	0.02452944
Proteobacteria	sf_3	9483		0.006605095	0.02454096
Proteobacteria	sf_5	9821		0.006639166	0.02455008
Proteobacteria	sf_1	8131		0.006827414	0.02488471
Proteobacteria	sf_1	7051	*Mycoplana dimorpha* str. IAM 13154	0.00686309	0.02488471
Proteobacteria	sf_3	9473	Arctic pack ice; northern Fram Strait; 80 31.1 N; 01 deg 59.7 min E clone ARKDMS-58	0.006875842	0.02488471
Proteobacteria	sf_1	10097	inactive deep-sea hydrothermal vent chimneys clone IndB2-42	0.006944132	0.02488471
Proteobacteria	sf_1	8320	acid mine drainage clone BA11	0.00696593	0.02488471
Proteobacteria	sf_1	8202		0.00697489	0.02488471

Actinobacteria	sf_1	1839	*Kribbella solani* str. DSA1	0.007017727	0.02488471
Proteobacteria	sf_3	9321	marine sediment clone Tokyo Bay D	0.007020095	0.02488471
Bacteroidetes	sf_1	6269	acidic forest soil clone UC1	0.007110014	0.02488471
Firmicutes	sf_12	3019	*Tepidibacter formicigenes* str. DV1184	0.007146135	0.02488471
Proteobacteria	sf_1	8552	*Acidithiobacillus ferrooxidans* str. D2	0.007148079	0.02488471
Proteobacteria	sf_1	8068	*Burkholderia caryophylli* str. ATCC 25418	0.007171416	0.02488471
Proteobacteria	sf_1	8283	*Heteropsylla texana* symbiont	0.007263198	0.02488471
Actinobacteria	sf_1	1567		0.007324653	0.02488471
Proteobacteria	sf_1	7041	*Rhizobium huautlense* str. SO2 ()	0.007334955	0.02488471
Spirochaetes	sf_1	6491	termite gut homogenate clone BCf8-03	0.00734572	0.02488471
Actinobacteria	sf_3	1130	*Georgenia muralis* str. 1A-C	0.00735748	0.02488471
Proteobacteria	sf_1	7139	*Mesorhizobium loti* str. R8CS USDA 3467	0.00735907	0.02488471
Proteobacteria	sf_1	10187	Mono Lake at depth 23 m station 6 July 2000 clone ML623J-57 proteobacterium	0.007405174	0.02488471
Proteobacteria	sf_1	8747	uranium waste soil clone JG30-KF-CM35	0.007408697	0.02488471
Proteobacteria	sf_3	9105		0.007408902	0.02488471
Proteobacteria	sf_1	8009	denitrifying reactor clone 81	0.007434673	0.02488471
Proteobacteria	sf_1	7126	ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A-MN96 proteobacterium	0.00749277	0.02493521
Proteobacteria	sf_1	8641	*Moritella abyssi* str. 2693	0.007513981	0.02493521
Proteobacteria	sf_1	10489	S17sBac16 complete clone	0.007600108	0.0251137
Proteobacteria	sf_3	10464	*Campylobacter* sp. str. NO2B	0.007767836	0.0254769
Proteobacteria	sf_1	7907	*Thauera aromatica* str. LG356	0.007775642	0.0254769
Bacteroidetes	sf_15	6046	chlorobenzene-degrading consortium clone IIIB-1	0.007846844	0.02560217
Proteobacteria	sf_4	9884	forested wetland clone RCP2-62	0.00794414	0.02563411
Proteobacteria	sf_1	8201	*Shewanella surugaensis* str. c959	0.007944244	0.02563411
Firmicutes	sf_12	2915	*Tepidibacter thalassicus* str. SC 562	0.007955667	0.02563411
Proteobacteria	sf_1	8011	*Burkholderia graminis* str. AUS35	0.008177084	0.02580294
Proteobacteria	sf_3	10507	termite gut homogenate clone Rs-M59 proteobacterium	0.008184612	0.02580294
Proteobacteria	sf_1	6692	*Phyllobacterium trifolii* str. PETP02	0.008197356	0.02580294
Proteobacteria	sf_1	7929	hydrothermal vent clone VC2.1 Bac29	0.008225679	0.02580294
Spirochaetes	sf_1	6565	termite gut clone NkS-Oxy25	0.008247427	0.02580294
Proteobacteria	sf_4	8855		0.008269412	0.02580294

Bacteroidetes	sf_1	5946	tongue dorsa clone DO027	0.008304323	0.02580294
Bacteroidetes	sf_1	5521	Flavobacteriaceae str. SW269	0.008311553	0.02580294
Nitrospira	sf_2	681		0.008408407	0.02580294
Actinobacteria	sf_1	1241	*Microbacterium kitamiense* CV88	0.00840994	0.02580294
Proteobacteria	sf_1	9864	uranium mining waste pile clone JG37-AG-133 proteobacterium	0.008458665	0.02580294
Proteobacteria	sf_1	6726		0.008463527	0.02580294
Proteobacteria	sf_1	7477	*Bradyrhizobium elkanii* str. SEMIA 6028	0.008466443	0.02580294
Proteobacteria	sf_3	10518	*Helicobacter pylori* str. ATCC 49396T	0.008473262	0.02580294
Proteobacteria	sf_6	6954		0.00857599	0.02597359
Proteobacteria	sf_1	9386	*Alteromonas* sp. str. NIBH P2M11	0.008610834	0.02597359
Proteobacteria	sf_3	9900	bioreactor clone mle1-27	0.008629645	0.02597359
Spirochaetes	sf_1	6557	spirochete clone ML320J-13	0.008704728	0.02609842
Proteobacteria	sf_3	8926	inactive deep-sea hydrothermal vent chimneys clone IheB2-13	0.008832028	0.02624189
Proteobacteria	sf_1	6971	*Thiobacillus* sp. str. 104	0.008923912	0.02624189
Proteobacteria	sf_1	9240	*Pseudomonas fluorescens* str. CHA0	0.008996402	0.02624189
Proteobacteria	sf_1	10262	*Desulfovibrio* sp. str. Ac5.2	0.008996836	0.02624189
Proteobacteria	sf_1	8755	*Pseudomonas* sp. SK-1-3-1	0.009014411	0.02624189
Bacteroidetes	sf_15	5353	trichloroethene-contaminated site clone FTLpost3 bacterium	0.009057943	0.02624189
Cyanobacteria	sf_5	5039	Cape Hatteras picoplankton clone OM270	0.009099153	0.02624189
Proteobacteria	sf_1	9035	*Microbulbifer* sp. str. JAMB-A94	0.009109084	0.02624189
Proteobacteria	sf_1	7634	*Bartonella henselae* str. Houston-1	0.0091277	0.02624189
Proteobacteria	sf_4	7105	Mariana trough hydrothermal vent water 0.2micro-m filterable fraction clone MT-NB25	0.009129833	0.02624189
Bacteroidetes	sf_1	5903	marine bacterioplankton clone MB11E04	0.009134657	0.02624189
Proteobacteria	sf_1	6821	*Sphingomonas echinoides*	0.009158106	0.02624189
Actinobacteria	sf_1	1454	*Nocardia yamanashiensis* str. IFM 0265	0.009230422	0.02626853
Proteobacteria	sf_1	10071	*Desulfovibrio desulfuricans*	0.00923506	0.02626853
Proteobacteria	sf_1	6974	India: Himalayas Kaza Spiti Valley Cold Desert isolate str. Kaza-35 Kaza-35	0.009332126	0.02637742
Actinobacteria	sf_1	1969	hydrocarbon seep clone BPC090	0.009381686	0.02637742
Proteobacteria	sf_1	7987	*Acidovorax* sp. str. OS-6	0.0093864	0.02637742
Proteobacteria	sf_1	9238		0.009461489	0.02637742
Proteobacteria	sf_1	9049	uranium mining mill tailing clone GR-Sh2-34 GR-Sh2-34	0.00947015	0.02637742

Proteobacteria	sf_1	10530	hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH5_6_BAC_16SrRNA_9N_EPR	0.009507547	0.02637742
Proteobacteria	sf_1	9384	*Moritella viscosa* str. NVI 88/478T	0.009531498	0.02637742
Firmicutes	sf_5	668	*Sedimentibacter* sp. str. BRS2	0.009545086	0.02637742
Gemmatimonadetes	sf_5	1565	uranium mining waste pile clone JG34-KF-418	0.009619234	0.02645881
Proteobacteria	sf_1	8852	*Pseudomonas stutzeri* str. KC	0.009642687	0.02645881
Bacteroidetes	sf_4	5703		0.009914083	0.02710772
Proteobacteria	sf_1	8097	*Burkholderia cepacia*	0.009976895	0.02718365
Firmicutes	sf_5	3017	termite gut homogenate clone Rs-D48 bacterium	0.0100523	0.02718365
Proteobacteria	sf_15	6700	*Porphyrobacter tepidarius* str. DSM 10594	0.01008887	0.02718365
Proteobacteria	sf_5	7025	bacterioplankton clone ZA2526c	0.01010292	0.02718365
Proteobacteria	sf_1	7470	*Novosphingobium* sp. str. J30	0.01011689	0.02718365
Proteobacteria	sf_1	7300	marine isolate JP57	0.01017927	0.02725696
Proteobacteria	sf_1	7478		0.01025966	0.02736726
Proteobacteria	sf_3	7481	*Wolbachia pipientis*	0.0103391	0.02736726
Unclassified	sf_92	9999	termite gut homogenate clone Rs-J96	0.01036608	0.02736726
Proteobacteria	sf_1	6757	*Ochrobactrum anthropi* str. ESC1	0.0103743	0.02736726
Unclassified	sf_160	4410		0.01041783	0.02736726
Firmicutes	sf_5	2928	pig feces clone	0.01043192	0.02736726
Proteobacteria	sf_1	9411	*Shewanella waksmanii* str. KMM 3823	0.010475	0.02738776
Proteobacteria	sf_1	6836		0.01056649	0.02753424
Proteobacteria	sf_1	7990	isolate str. A0640	0.01066681	0.0277027
Spirochaetes	sf_1	6488	*Treponema primitia* str. ZAS-1	0.01079274	0.02785052
Proteobacteria	sf_3	10425	*Sulfurimonas autotrophica* str. OK5	0.01080638	0.02785052
Proteobacteria	sf_1	6857	*Mesorhizobium mediterraneum* str. PECA20	0.01083132	0.02785052
Proteobacteria	sf_1	7216	*Ahrensia kielensis* str. IAM12618	0.01086771	0.02785186
Proteobacteria	sf_1	7379	*Phyllobacterium myrsinacearum* HM35	0.01098101	0.02804964
Proteobacteria	sf_3	9320	Waste-gas biofilter clone BIyi3	0.01102908	0.02808007
Bacteroidetes	sf_6	5792	activated sludge foam clone 47	0.01107385	0.02810192
Proteobacteria	sf_1	6660	*Azorhizobium caulinodans* str. ORS 571	0.01114088	0.02817993
Acidobacteria	sf_14	105	marine sediment above hydrate ridge clone Hyd24-44 sp.	0.01119293	0.02821967
Actinobacteria	sf_1	1843	uranium mining waste pile soil sample clone JG30-KF-A23	0.01139416	0.02853671
Proteobacteria	sf_1	8484	Alteromonadaceae isolate str. LA50	0.01144982	0.02853671

Firmicutes	sf_4	4325	termite gut homogenate clone Rs-K21 bacterium	0.01148555	0.02853671
Proteobacteria	sf_1	7741	*Leptothrix cholodnii* str. CCM 1827	0.01149707	0.02853671
Actinobacteria	sf_1	1355	*Amycolatopsis mediterranei* str. IMSNU 20056T	0.01152914	0.02853671
Proteobacteria	sf_1	7039		0.0115543	0.02853671
Proteobacteria	sf_1	9228	*Pseudomonas stutzeri* HY-105	0.01164206	0.02853671
Actinobacteria	sf_1	1695	lichen-dominated Antarctic cryptoendolithic community clone FBP417	0.01164529	0.02853671
Proteobacteria	sf_6	6665	hydrocarbon-degrading consortium clone 4-Org2-22	0.01165009	0.02853671
Proteobacteria	sf_1	8023	ferromanganous micronodule clone MND1	0.01168617	0.02853671
Firmicutes	sf_1	28	termite gut homogenate clone Rs-H81 bacterium	0.01185918	0.02886841
Proteobacteria	sf_6	6987		0.01199628	0.02892301
Proteobacteria	sf_1	7056	*Bartonella schoenbuchensis* str. R1	0.01200334	0.02892301
Proteobacteria	sf_1	8754	*Pseudomonas* sp. str. P400Y-1	0.01204112	0.02892301
Proteobacteria	sf_1	8777	*Pseudomonas* sp. str. KNA6-5	0.01206092	0.02892301
Proteobacteria	sf_1	9366	Arctic seawater isolate str. R7366	0.01206784	0.02892301
Proteobacteria	sf_1	7735	soil clone	0.01216071	0.02905591
Proteobacteria	sf_1	7394	*Novosphingobium subterraneum* str. IFO 16086	0.01219986	0.02906002
Actinobacteria	sf_1	1449	Cellulomonadaceae str. WB13	0.01232506	0.02918082
Proteobacteria	sf_1	7800	sample taken upstream landfill clone BVC77 landfill	0.01232573	0.02918082
Proteobacteria	sf_1	7353	temperate estuarine mud clone HC65	0.01238832	0.0292189
Proteobacteria	sf_3	7010	periodontal pocket clone 10B6	0.01245171	0.0292189
Proteobacteria	sf_1	8196		0.01248634	0.0292189
Proteobacteria	sf_1	10189		0.01249429	0.0292189
Proteobacteria	sf_1	8335	*Alcanivorax* sp. str. K3-3 (MBIC 4323)	0.01253134	0.0292189
Actinobacteria	sf_1	1186	*Cryocola antiquus* str. VKM 103PF	0.01262616	0.0292189
Spirochaetes	sf_1	6579	termite gut clone NkS83	0.01263248	0.0292189
Actinobacteria	sf_1	1229	*Streptacidiphilus carbonis* str. JL 415; DSM 41754	0.0126555	0.0292189
Proteobacteria	sf_1	8172	*Pseudoalteromonas* sp. str. Bdeep-1	0.01268046	0.0292189
Proteobacteria	sf_1	7943	*Aquabacterium parvum* str. B6	0.01275005	0.02929233
Actinobacteria	sf_1	1183	*Actinomyces europaeus* str. CCUG 32789A	0.01281476	0.02935415
Proteobacteria	sf_1	7143	*Bosea massiliensis* str. 63287	0.01288964	0.02943883
Proteobacteria	sf_1	7945	*Aquaspirillum serpens* str. IAM 13944	0.01292937	0.02944298
Proteobacteria	sf_1	7415	*Bartonella quintana* str. Toulouse	0.01301173	0.02945337

Proteobacteria	sf_1	9571	*Nitrosococcus oceanus*	0.01301932	0.02945337
Actinobacteria	sf_1	1340	*Streptomyces coelicolor*	0.01306743	0.02945337
Actinobacteria	sf_1	1692	Arctic sea ice ARK10030	0.01308565	0.02945337
Bacteroidetes	sf_19	5667	penguin droppings sediments clone KD6-118	0.01316815	0.0295105
Acidobacteria	sf_14	6405	soil sample uranium mining waste pile near town Johanngeorgenstadt clone JG36-TzT-31 bacterium	0.01324539	0.0295105
Proteobacteria	sf_1	8127	*Zoogloea resiniphila* str. PIV-3A2y	0.01326038	0.0295105
Actinobacteria	sf_1	1676		0.01326304	0.0295105
Thermodesulfobacteria	sf_1	667	*Geothermobacterium ferrireducens*	0.01341533	0.02952151
Acidobacteria	sf_1	516	uranium mining waste pile clone JG34-KF-153	0.01341926	0.02952151
Proteobacteria	sf_1	7914	*Burkholderia andropogonis* str. ATCC 19311T	0.01344525	0.02952151
Proteobacteria	sf_1	8836	*Legionella pneumophila* str. Paris	0.01344621	0.02952151
Proteobacteria	sf_1	7879		0.01350733	0.02952151
Proteobacteria	sf_3	10432	*Riftia pachyptila*'s tube clone R76-B51	0.0135302	0.02952151
Proteobacteria	sf_1	8344	*Anabaena circinalis* AWQC118C isolate str. UNSW3	0.01353411	0.02952151
Proteobacteria	sf_1	7555	derived microbial 'pearl'- community clone sipK48	0.01372561	0.02972761
Proteobacteria	sf_1	9310	*Pseudomonas* sp. str. AC-167	0.0138204	0.02972761
Proteobacteria	sf_3	9291	*Methylophaga alcalica* str. M39	0.01385625	0.02972761
Verrucomicrobia	sf_1	1024	rumen clone BS5	0.01387923	0.02972761
Actinobacteria	sf_1	1893	*Kineosporia aurantiaca* str. NRLL B-16913	0.01394018	0.02972761
Proteobacteria	sf_3	9269		0.01401322	0.02972761
Proteobacteria	sf_1	7029		0.01402301	0.02972761
Proteobacteria	sf_1	8576	*Halomonas* sp. Ko502	0.01404972	0.02972761
Chloroflexi	sf_9	94	DCP-dechlorinating consortium clone SHA-2	0.01405885	0.02972761
Proteobacteria	sf_1	7171	*Azospirillum* species	0.01405913	0.02972761
Proteobacteria	sf_1	7096		0.01407922	0.02972761
Chloroflexi	sf_2	652	uranium mining waste pile soil sample clone JG30-KF-CM45	0.01411216	0.02972761
Proteobacteria	sf_3	7401	*Scrippsiella trochoidea* NEPCC 15	0.01419334	0.02972761
Firmicutes	sf_1	3955	Weeping tea tree witches'-broom phytoplasma tree	0.01419802	0.02972761
Proteobacteria	sf_1	9845	uranium mining waste pile clone JG37-AG-128 proteobacterium	0.01420284	0.02972761
Proteobacteria	sf_1	8512	marine sediment clone B2M54	0.01425426	0.02975504
Proteobacteria	sf_20	6911		0.01430063	0.02977179
Actinobacteria	sf_1	1312		0.01442103	0.02994218

Proteobacteria	sf_1	7264	*Bosea thiooxidans* TJ1	0.01446565	0.02995473
Proteobacteria	sf_3	9568	forested wetland clone RCP2-96	0.01457058	0.03009177
Proteobacteria	sf_1	7543	Waste-gas biofilter clone BIwii1	0.01463866	0.03015218
Actinobacteria	sf_1	1240	Cellulomonadaceae str. WB9	0.01474128	0.03017166
Firmicutes	sf_5	2679	termite gut homogenate clone BCf9-13	0.01482513	0.03017166
Firmicutes	sf_1	3630		0.01486418	0.03017166
Proteobacteria	sf_1	7674	*Azoarcus anaerobius* str. LuFres1; DSM 12081	0.01488188	0.03017166
Proteobacteria	sf_1	7110	*Novosphingobium subarcticum* LH128	0.01489128	0.03017166
Proteobacteria	sf_1	7771	*Burkholderia glathei* str. ATCC 29195T	0.01491847	0.03017166
Actinobacteria	sf_3	1348	lichen-dominated Antarctic cryptoendolithic community clone FBP406	0.01492867	0.03017166
Firmicutes	sf_1	4074	swine intestine clone p-2013-s959-5	0.01495895	0.03017166
Proteobacteria	sf_1	7281	*Fulvimarina pelagi* str. HTCC2506	0.01506779	0.03024421
Proteobacteria	sf_3	9456	deepest cold-seep area Japan Trench clone JTB23 proteobacterium	0.01507282	0.03024421
Firmicutes	sf_12	2764		0.01512349	0.03026768
Proteobacteria	sf_3	9912	uranium mining waste pile clone JG34-KF-14 proteobacterium	0.01526031	0.03046299
Proteobacteria	sf_4	8169	forested wetland clone RCP2-54	0.01535705	0.0305775
Firmicutes	sf_5	3112	Evry municipal wastewater treatment plant clone 012C11_B_SD_P15	0.01540327	0.03059109
Proteobacteria	sf_3	10467		0.01548437	0.03063968
Actinobacteria	sf_1	1884	*Corynebacterium tuberculostearicum* str. ATCC 33035	0.01552279	0.03063968
Proteobacteria	sf_1	8854	Halomonas variabilis str. ANT9112	0.01554611	0.03063968
Firmicutes	sf_12	4548	termite gut homogenate clone Rs-Q69 bacterium	0.015655	0.03071343
Actinobacteria	sf_1	1551	soil isolate Ellin301	0.01567861	0.03071343
Proteobacteria	sf_3	9874	uranium mining waste pile clone JG34-KF-243 proteobacterium	0.01573574	0.03071343
Proteobacteria	sf_3	7024	deep-sea sediment clone P_wp0211	0.01579186	0.03071343
OD1	sf_1	515		0.01581403	0.03071343
Proteobacteria	sf_1	7049		0.01582084	0.03071343
Proteobacteria	sf_1	8145	*Nitrosomonas eutropha* str. Nm57	0.0160352	0.03100811
Proteobacteria	sf_1	7090	*Blastomonas natatoria* str. DSM 3183T	0.0160525	0.03100811
Bacteroidetes	sf_5	6084	*Microscilla arenaria* str. IFO 15982	0.01625047	0.03127817
Actinobacteria	sf_1	1723	*Corynebacterium* sp str. CDC G5911	0.01631204	0.03127817
Proteobacteria	sf_2	594	uranium mining mill tailing clone GR-296.II.52 GR-296.I.52	0.01631314	0.03127817
Proteobacteria	sf_1	8002	*Rubrivivax gelatinosus* str. A3	0.01643426	0.03143279

Bacteroidetes	sf_1	5901	Arctic sea ice ARK10159	0.01650135	0.03148355
Actinobacteria	sf_1	1834	*Nocardia transvalensis* str. DSM 43405	0.01657152	0.03153994
Actinobacteria	sf_1	1456	*Rathayibacter rathayi* str. DSM 7485	0.01676079	0.03182219
Proteobacteria	sf_1	8531	*Vibrio wodanis* str. NVI 88/441T	0.01682138	0.03185931
Actinobacteria	sf_1	1912	*Agromyces rhizospherae* str. IFO 16236	0.01696747	0.03189344
Proteobacteria	sf_1	7829	*Xylophilus ampelinus* str. ATCC 33914	0.01698362	0.03189344
Proteobacteria	sf_3	6762	acidic forest soil clone UP8	0.01698723	0.03189344
Actinobacteria	sf_3	1114		0.01700368	0.03189344
Proteobacteria	sf_1	6649	*Rhizobium giardinii* str. H152	0.01706504	0.0319314
Nitrospira	sf_2	542	forested wetland clone FW19	0.01713684	0.03195631
Proteobacteria	sf_3	10438	hydrocarbon seep clone GCA014	0.01716066	0.03195631
Proteobacteria	sf_4	9741	uranium mining waste pile clone JG37-AG-30 proteobacterium	0.01730112	0.03196273
Spirochaetes	sf_1	6506	termite gut homogenate clone Rs-J58 sp.	0.01730293	0.03196273
Firmicutes	sf_11	39	forested wetland clone RCP2-71	0.01730618	0.03196273
Proteobacteria	sf_1	7199	uranium mill tailings clone Gitt-KF-194	0.01732875	0.03196273
Proteobacteria	sf_1	8889	hypersaline Mono Lake clone ML110J-5	0.01741599	0.03204753
Actinobacteria	sf_1	1779	*Microbacterium* sp. str. VKM Ac-2048	0.01766163	0.03213003
Planctomycetes	sf_3	4677	aerobic basin clone CY0ARA032A03	0.01770411	0.03213003
Proteobacteria	sf_1	7838	*Alcaligenes defragrans* str. PD-19	0.0177164	0.03213003
Firmicutes	sf_12	132	termite gut homogenate clone Rs-J36 bacterium	0.01777202	0.03213003
Proteobacteria	sf_1	7147		0.01777656	0.03213003
Proteobacteria	sf_1	8812	*Oceanisphaera litoralis* str. DSM 15406	0.01786083	0.03213003
Proteobacteria	sf_2	6639		0.01787261	0.03213003
Proteobacteria	sf_3	6651	*Beijerinckia indica*	0.0179012	0.03213003
Proteobacteria	sf_1	7818	soil sample uranium mining waste pile near town Johanngeorgenstadt clone JG36-TzT-215 proteobacterium	0.01790771	0.03213003
Bacteroidetes	sf_1	5479	*Flavobacterium frigoris* str. LMG 21471	0.01791245	0.03213003
Actinobacteria	sf_1	1917	Nocardia otitidiscaviarum str. DSM43242	0.01791597	0.03213003
Actinobacteria	sf_1	1385	*Streptomonospora salina* str. YIM90002	0.01798903	0.03218672
Actinobacteria	sf_1	1694	*Geodermatophilus obscurus* subsp. dictyosporus str. DSM 43161	0.01836634	0.03271108
Proteobacteria	sf_1	8839	f cytometric sorted marine sample subpopulation 3 clone ZD0408 bacterium	0.01837239	0.03271108
Spirochaetes	sf_1	6532	termite gut clone NkS39	0.01840847	0.03271108

Proteobacteria	sf_3	8664	*Thiomicrospira* sp. str. Milos-T2	0.01853539	0.03283825
Proteobacteria	sf_3	8727	*Alkanindiges hongkongensis* str. HKU9	0.01861108	0.03283825
Verrucomicrobia	sf_3	40	Elbe river clone DEV055	0.01865359	0.03283825
Proteobacteria	sf_1	8580	Arctic seawater isolate str. R7076	0.01868788	0.03283825
Actinobacteria	sf_1	1867	*Amycolatopsis vancoresmycina* str. DSM 44592	0.01870126	0.03283825
Firmicutes	sf_1	4261	termite gut homogenate clone Rs-G04 bacterium	0.01873376	0.03283825
Proteobacteria	sf_1	7743	*Herbaspirillum* sp. str. NAH4	0.01890794	0.03304643
Actinobacteria	sf_1	1569	*Streptomyces sampsonii* str. ATCC25495	0.01904289	0.03304643
Proteobacteria	sf_1	7038	pea aphid symbiont clone APe4_19	0.01905533	0.03304643
Proteobacteria	sf_1	9828	termite gut homogenate clone Rs-M89 proteobacterium	0.01908731	0.03304643
Acidobacteria	sf_1	4222	forested wetland clone FW105	0.01910951	0.03304643
Bacteroidetes	sf_1	5942		0.01912679	0.03304643
Proteobacteria	sf_1	9220	unclassified Lamellibrachia sp. 1 symbiont Lamellibrachia	0.01916295	0.03304643
Proteobacteria	sf_3	10298	marine tidal mat clone BTM36	0.01919297	0.03304643
Actinobacteria	sf_1	1983	*Streptomyces cinnabarinus* str. ISP 5467	0.01925763	0.03308439
Actinobacteria	sf_1	1274	*Trichotomospora caesia* str. IFO14562	0.0194212	0.03324521
Proteobacteria	sf_1	7704	freshwater clone PRD01b009B	0.01943686	0.03324521
Proteobacteria	sf_3	10538	*Arcobacter cryaerophilus*	0.0196309	0.0335033
Actinobacteria	sf_1	1666		0.01969365	0.03353669
Proteobacteria	sf_1	7788	atrazine-catabolizing microbial absence methanol clone KRA30-58	0.01977574	0.03357752
Firmicutes	sf_5	1037	*Finegoldia magna*	0.01980411	0.03357752
Proteobacteria	sf_1	8018	*Acidovorax delafieldii* str. ATCC 17505	0.01988654	0.03364382
Chloroflexi	sf_9	72	sediments collected at Charon's Cascade near Echo River October 2000 clone CCD21	0.02000154	0.03376481
Actinobacteria	sf_1	1581	*Cryptosporangium aurantiacum* str. IMSNU 22120	0.02010797	0.03384954
Proteobacteria	sf_1	8503	Arctic sea ice ARK10244	0.02016928	0.03384954
Proteobacteria	sf_1	8654	inactive deep-sea hydrothermal vent chimneys clone IheB2-31	0.02020085	0.03384954
Actinobacteria	sf_1	1849		0.02029062	0.03384954
Proteobacteria	sf_1	9542	*Alishewanella fetalis* str. CCUG 30811	0.02035096	0.03384954
Actinobacteria	sf_1	1667	*Microbacterium lacticum*	0.02036994	0.03384954
Proteobacteria	sf_1	9143	*Pseudoalteromonas agarivorans* str. KMM 255	0.0203909	0.03384954
Proteobacteria	sf_3	468	marine sediment clone Sva0515	0.02040045	0.03384954
Proteobacteria	sf_1	9128	*Lucina nassula* gill symbiont	0.02048751	0.03388949

Proteobacteria	sf_3	8983	Iron oxidising strain ES-1	0.02051181	0.03388949
Proteobacteria	sf_1	8896	silica sinter depositing geothermal power station discharge drain clone ST01-SN4A proteobacterium	0.02060508	0.03392958
Actinobacteria	sf_1	1639	*Streptomyces coelicolor* str. M145 ssp. A3(2)	0.02062347	0.03392958
Proteobacteria	sf_1	7675	*Neisseria* sp. str. CCUG 46910	0.02068587	0.03393297
Proteobacteria	sf_1	7827		0.02071292	0.03393297
Proteobacteria	sf_1	9058	*Pseudoalteromonas carrageenovora* str. ATCC 12662T	0.02082171	0.03403937
Proteobacteria	sf_1	8231	uranium waste soil clone JG30a-KF-21	0.0209011	0.03409738
Chloroflexi	sf_1	927	hydrothermal vent polychaete mucous clone P. palm C 37	0.02095772	0.03411807
Verrucomicrobia	sf_1	559	anoxic marine sediment clone LD1-PA20	0.02102546	0.03415572
Bacteroidetes	sf_1	5955	*Flavobacterium* sp. str. V4.MS.29 = MM_2747	0.02106914	0.03415572
Acidobacteria	sf_6	6362	grassland soil clone DA052	0.02111281	0.03415572
Proteobacteria	sf_1	9709	termite gut homogenate clone Rs-N31 proteobacterium	0.02124676	0.03425383
Bacteroidetes	sf_1	5459	*Pedobacter* sp. An13	0.02126167	0.03425383
Proteobacteria	sf_1	9068	*Pseudomonas stutzeri* str. A1501	0.02130579	0.03425384
Nitrospira	sf_1	984	uranium mining waste pile clone JG37-AG-131 sp.	0.02145823	0.03442764
Proteobacteria	sf_1	8110	*Wautersia paucula* str. LMG 3413	0.02164836	0.03466107
Proteobacteria	sf_1	7339		0.02172257	0.03470485
Proteobacteria	sf_1	10543	hydrothermal vent clone PVB_10	0.02176509	0.03470485
Bacteroidetes	sf_1	5436	Arctic sea ice ARK10004	0.02190373	0.03485435
Firmicutes	sf_5	2456	granular sludge clone R4b14	0.02200337	0.03487656
Firmicutes	sf_5	2483	trichloroethene-contaminated site clone FTLM142 bacterium	0.02200751	0.03487656
Proteobacteria	sf_1	7921	*Collimonas fungivorans* str. Ter331	0.02209018	0.03493627
Proteobacteria	sf_1	7323		0.02220505	0.03504656
Unclassified	sf_160	6430		0.02229884	0.03505372
Proteobacteria	sf_1	8932	*Pseudoalteromonas antarctica* str. N-1	0.02229987	0.03505372
Proteobacteria	sf_1	9369	*Pseudoalteromonas luteoviolacea* str. NCIMB 1893T	0.02254911	0.0353739
Actinobacteria	sf_1	1223	*Sporichthya polymorpha* str. IFO 12702	0.02277701	0.03555934
Proteobacteria	sf_3	7219	*Methylosinus sporium*	0.02279642	0.03555934
Proteobacteria	sf_1	8003	hydrocarbon-degrading consortium clone AF1-8	0.0228047	0.03555934
Proteobacteria	sf_1	6899		0.02288174	0.03560796
Proteobacteria	sf_1	9640	exposed to diatom detritus isolate str. Tw-10 Tw-10	0.02299018	0.03562131
Proteobacteria	sf_1	7550	soil clone 768-2	0.02311962	0.03562131

Bacteroidetes	sf_1	5971	*Cytophaga uliginosa*	0.02319109	0.03562131
Proteobacteria	sf_1	7928	penguin droppings sediments clone KD5-43	0.02322706	0.03562131
Proteobacteria	sf_1	7436	*Brevundimonas* sp. str. FWC40	0.02329121	0.03562131
Proteobacteria	sf_1	9324	*Pseudoalteromonas ruthenica* str. KMM300	0.02330109	0.03562131
Proteobacteria	sf_6	6918	soil near uranium mill tailings clone KCM-C-45	0.02331846	0.03562131
Proteobacteria	sf_1	7801	Toolik Lake main station at 3 m depth clone TLM05/TLMdgge10 proteobacterium	0.02331919	0.03562131
NC10	sf_1	2516	TCE-contaminated site clone FTL22	0.02335703	0.03562131
Proteobacteria	sf_1	7528	*Sphingobium yanoikuyae* str. GIFU9882	0.02337382	0.03562131
Proteobacteria	sf_6	6694	forested wetland clone RCP2-92	0.02339491	0.03562131
Actinobacteria	sf_1	1804	*Microbacterium resistens* str. 2002-59119	0.02346093	0.03565193
Proteobacteria	sf_1	7969	*Burkholderia* sp.	0.02371533	0.0358706
Proteobacteria	sf_1	9203	*Thalassomonas ganghwensis* str. JC2041	0.02371869	0.0358706
Proteobacteria	sf_1	8139	*Delftia tsuruhatensis* str. AD9	0.02374341	0.0358706
Proteobacteria	sf_1	8022	*Acidovorax avenae* subsp. cattleyae str. NCPPB 961 subsp.	0.02395514	0.03612021
Bacteroidetes	sf_1	5997	*Flavobacterium aquatile*	0.02401921	0.03614662
Proteobacteria	sf_1	9491	Boston Harbor surface water isolate str. UMB6D UMB6D	0.02411664	0.03622305
Chloroflexi	sf_1	2485		0.02421448	0.03629979
Proteobacteria	sf_3	9755	bacterioplankton clone ZA3704c	0.02437721	0.03647333
Proteobacteria	sf_1	8021	*Acidovorax facilis* str. CCUG 2113	0.02449907	0.03657992
Proteobacteria	sf_1	7866	*Paucimonas lemoignei* str. ATCC 17989T	0.02459183	0.03657992
Proteobacteria	sf_1	7766		0.02462955	0.03657992
Proteobacteria	sf_1	8581	*Shewanella benthica* str. DB21MT-2	0.02463688	0.03657992
Proteobacteria	sf_1	8579	*Psychromonas profunda* str. 2825	0.02472202	0.03663628
Actinobacteria	sf_1	1769	*Nocardia* sp. str. DSM 46067	0.02491023	0.03684489
Proteobacteria	sf_1	8605	bacterioplankton clone ZA2525c	0.02505779	0.03690997
Proteobacteria	sf_1	7888	*Hydrogenophaga flava* str. DSM 619T	0.02505913	0.03690997
Actinobacteria	sf_1	1698	*Corynebacterium* subsp. afermentans str. CIP 103499T	0.0251071	0.03690997
Proteobacteria	sf_1	9295		0.02516815	0.03690997
Proteobacteria	sf_1	8152	nephridia Octolasion lacteum clone Ol2-2	0.0251956	0.03690997
Actinobacteria	sf_1	1921	Firmicutes isolate str. d8	0.02526816	0.03690997
Firmicutes	sf_5	2722	termite gut homogenate clone Rs-E61 bacterium	0.0253164	0.03690997
Actinobacteria	sf_1	1690	*Streptomyces galbus* str. DSM40480	0.02536669	0.03690997

Actinobacteria	sf_1	1365	*Mycobacterium chelonae* str. CIP 104535T	0.02538202	0.03690997
Actinobacteria	sf_1	1142		0.02560858	0.03703851
Bacteroidetes	sf_1	5482		0.02566416	0.03703851
Proteobacteria	sf_1	8888	*Vibrio aestuarianus* str. 01/151	0.02568965	0.03703851
Proteobacteria	sf_3	7153	*Methylocella tundrae* str. Y1	0.02572308	0.03703851
Spirochaetes	sf_1	6523	termite gut homogenate clone Rs-J64 sp.	0.02573094	0.03703851
Verrucomicrobia	sf_4	169	anoxic marine sediment clone LD1-PA26	0.0257566	0.03703851
Nitrospira	sf_1	864	nitrifying sludge clone GC86	0.02598975	0.03717954
Proteobacteria	sf_1	7007		0.0261618	0.03717954
Cyanobacteria	sf_5	4993	*Oscillatoria* sp	0.02618858	0.03717954
Actinobacteria	sf_1	1633	*Actinoplanes tuftoflagellus* str. IMSNU 22135	0.02621339	0.03717954
Actinobacteria	sf_1	1404	freshwater isolate str. MWH-Ta3	0.02627146	0.03717954
DSS1	sf_2	38	DCP-dechlorinating consortium clone SHA-109	0.02636014	0.03717954
Actinobacteria	sf_3	1743	*Streptomyces scabiei* str. DNK-G01	0.0263789	0.03717954
Actinobacteria	sf_1	1856	forested wetland clone RCP2-105	0.02639574	0.03717954
Firmicutes	sf_1	2388	G+C Gram-positive clone YNPRH70A	0.02639638	0.03717954
Spirochaetes	sf_1	6494	termite gut homogenate clone Rs-C47 sp.	0.02640508	0.03717954
Proteobacteria	sf_1	7165	*Sphingomonas* sp. str. IW3	0.0264169	0.03717954
Proteobacteria	sf_1	9658	*Alcanivorax* sp. str. Haw1	0.02642922	0.03717954
Proteobacteria	sf_3	8703	*Beggiatoa* sp. str. AA5A	0.02656165	0.03723648
Proteobacteria	sf_1	7750	uranium mining waste pile near Johanngeorgenstadt soil clone JG37-AG-35	0.0265656	0.03723648
Proteobacteria	sf_1	7067	*Blastochloris sulfoviridis* str. GN1	0.0267151	0.03737856
Proteobacteria	sf_1	9246	Mammoth Cave sediment clone CCD24	0.02686362	0.03751876
Proteobacteria	sf_1	7754	Waste-gas biofilter clone BIfdi44	0.02702223	0.03767252
Proteobacteria	sf_3	8488		0.02721504	0.03787333
Proteobacteria	sf_1	6756		0.02737569	0.03797076
Bacteroidetes	sf_1	5367	patient's bronchoalveolar lavage isolate str. MDA2507 sp.	0.02748604	0.03797076
Proteobacteria	sf_20	2520		0.0275294	0.03797076
Proteobacteria	sf_1	6822		0.02752954	0.03797076
Proteobacteria	sf_1	7101		0.02752954	0.03797076
OP9/JS1	sf_1	2491	deep marine sediment clone MB-B2-103	0.02800902	0.0385636
Bacteroidetes	sf_19	5307	*Microscilla sericea* str. IFO 16561	0.02805907	0.03856413

Proteobacteria	sf_3	10411	termite gut homogenate clone Rs-P71 proteobacterium	0.02838566	0.03887148
Gemmatimonadetes	sf_5	227	uranium mining waste pile clone JG37-AG-36	0.02842178	0.03887148
Spirochaetes	sf_1	6571	*Mixotricha paradoxa* is flagellate hindgut *Mastotermes darwiniensis* clone mp4 of	0.02849217	0.03887148
Proteobacteria	sf_1	9731	uranium mining waste pile clone JG37-AG-90 proteobacterium	0.02852311	0.03887148
Proteobacteria	sf_1	7384	aortic heart valve patient with endocarditis clone v9	0.02853299	0.03887148
Firmicutes	sf_1	4046	Pigeon pea witches'-broom mycoplasma-like organism	0.02858591	0.03887538
Proteobacteria	sf_9	9975	TCE-contaminated site clone ccslm247	0.02865968	0.03890756
Proteobacteria	sf_1	8112	*Comamonas testosteroni* str. SMCC B329	0.02876742	0.03898568
Actinobacteria	sf_1	1861	*Rhodococcus rhodochrous* str. 11Y	0.02885706	0.03903902
Proteobacteria	sf_1	8046	*Acidovorax defluvii* str. BSB411	0.02915108	0.03936031
Verrucomicrobia	sf_7	29	*Fucophilus fucoidanolyticus* str. SI-1234	0.02922866	0.03936031
Bacteroidetes	sf_19	5563	*Cytophaga* sp. I-545	0.02931803	0.03936031
Proteobacteria	sf_6	6946	Mammoth cave clone CCM12a	0.02932291	0.03936031
Proteobacteria	sf_6	7572		0.02934799	0.03936031
Verrucomicrobia	sf_3	792	termite gut homogenate clone Rs-P07 bacterium	0.02948926	0.03937991
Deinococcus-Thermus	sf_3	920		0.02950827	0.03937991
Cyanobacteria	sf_1	5190	*Plectonema* sp. str. F3	0.02956159	0.03937991
Proteobacteria	sf_1	7978	*Variovorax paradoxus* str. IAM 12373	0.02956545	0.03937991
Proteobacteria	sf_1	8128	*Cupriavidus necator*	0.02970213	0.03949422
Proteobacteria	sf_3	9428	hydrocarbon-degrading consortium clone AF2-1D	0.02986924	0.03964853
Proteobacteria	sf_3	6803	*Wolbachia* sp. Dlem16SWol	0.0299852	0.03970013
Actinobacteria	sf_1	1965	Arctic sea ice ARK10165	0.03001037	0.03970013
Firmicutes	sf_11	771	*Dialister pneumosintes* str. ATCC 33048	0.03031073	0.04000857
Proteobacteria	sf_1	10414	penguin droppings sediments clone KD2-34	0.03034657	0.04000857
Proteobacteria	sf_3	7640	*Methylosinus trichosporium*	0.03042133	0.04003915
Proteobacteria	sf_1	7576	*Novosphingobium stygium* str. IFO 16085	0.03064516	0.04016989
Proteobacteria	sf_5	9800	forested wetland clone FW57	0.03065768	0.04016989
Firmicutes	sf_8	546	*Ferribacter thermoautotrophicus*	0.03067585	0.04016989
Firmicutes	sf_12	4265	termite gut homogenate clone Rs-N70 bacterium	0.03074856	0.04019354
Proteobacteria	sf_5	10267	marine sediment above hydrate ridge clone Hyd89-61 proteobacterium	0.03080415	0.04019354
Proteobacteria	sf_5	6947	termite gut homogenate clone Rs-B60 proteobacterium	0.03085796	0.04019354

Proteobacteria	sf_1	10062	marine sediment above hydrate ridge clone Hyd24-11 proteobacterium	0.03105235	0.04019354
Proteobacteria	sf_1	10069		0.03105289	0.04019354
Proteobacteria	sf_1	9081	*Shewanella* sp. str. MTW-1	0.03105598	0.04019354
Proteobacteria	sf_1	7845	*Diaphorina citri* symbiont	0.03105623	0.04019354
Proteobacteria	sf_1	8596	marine clone Arctic95B-7	0.03114609	0.04024276
Proteobacteria	sf_1	8034	*Janthinobacterium agaricidamnosum* str. W1r3T	0.03137327	0.04041273
NC10	sf_1	536	uranium mill tailings clone GuBH2-AD-8	0.03138172	0.04041273
Actinobacteria	sf_1	2014	marine sediment clone MB-A2-100	0.03174583	0.04065615
Proteobacteria	sf_3	10552	*Helicobacter winghamensis* str. NLEP 97-1611	0.03175567	0.04065615
Actinobacteria	sf_1	1432	*Nocardia veterana* str. DSM 44445	0.03176626	0.04065615
Actinobacteria	sf_1	1739		0.03178742	0.04065615
Cyanobacteria	sf_9	5164	termite gut homogenate clone Rs-H34	0.03189363	0.04065615
Proteobacteria	sf_3	8959	bacterioplankton clone AEGEAN_133	0.0319343	0.04065615
Proteobacteria	sf_1	6749	Arctic sea ice ARK10031	0.03193753	0.04065615
Actinobacteria	sf_1	1106		0.03198959	0.04065615
Firmicutes	sf_5	224	*Finegoldia magna* str. ATCC 29328	0.03205341	0.04067069
Proteobacteria	sf_1	10076	Great Artesian Basin clone G13	0.03248281	0.04110995
Spirochaetes	sf_1	6502	*Treponema denticola* str. ATCC35405	0.03250548	0.04110995
Firmicutes	sf_4	4526	TCE-contaminated site clone ccslm210	0.03296594	0.0416169
Bacteroidetes	sf_1	5914	*Psychroserpens burtonensis* str. S2-64	0.0330214	0.0416169
Actinobacteria	sf_1	2005	*Nocardioides* sp. str. V4.BO.15 = MM_2364	0.03306711	0.0416169
Proteobacteria	sf_20	6763		0.03317703	0.04168768
Bacteroidetes	sf_19	5728	*Cytophaga* sp. str. MBIC04693	0.03326088	0.04172552
Bacteroidetes	sf_1	6158	municipal wastewater treatment bioreactor isolate str. CAGY10	0.03333958	0.04175679
Bacteroidetes	sf_19	6184		0.03375886	0.04221384
Actinobacteria	sf_1	1966	TCE-contaminated site clone ccspost2208	0.03387271	0.04222089
Actinobacteria	sf_1	1104	*Amycolatopsis mediterranei* str. NRRL B-3240	0.03387631	0.04222089
Chlamydiae	sf_1	4702	*Candidatus Rhabdochlamydia porcellionis* clone RKPsHep porcellionis	0.0339276	0.04222089
Actinobacteria	sf_1	1552	*Nocardia cyriacigeorgica* str. D1627T	0.03398679	0.04222687
Actinobacteria	sf_1	1286	*Frankia* sp. Sn5-8	0.03412426	0.04232994
Proteobacteria	sf_1	7875	EBPR sludge clone SA34	0.03418553	0.04233831

Bacteroidetes	sf_1	5480	ED5 earthworm gut	0.03424144	0.04234002
Proteobacteria	sf_1	8137	freshwater clone PRD01a011B	0.03448029	0.04256759
Proteobacteria	sf_1	7865		0.03461404	0.0425806
Proteobacteria	sf_3	9641	*Acinetobacter haemolyticus*	0.03461543	0.0425806
Firmicutes	sf_5	3111	rumen clone 6C3d-11	0.03465534	0.0425806
Proteobacteria	sf_1	7529	*Gluconacetobacter europaeus* str. ZIM B028 V3	0.03475019	0.04258388
Proteobacteria	sf_1	9598	Mono Lake at depth 2 m station 6 July 2000 clone ML602J-47 proteobacterium	0.03476768	0.04258388
Proteobacteria	sf_3	7954		0.03502972	0.04283726
Firmicutes	sf_12	4627	termite gut homogenate clone Rs-A13 bacterium	0.03511209	0.04287048
Proteobacteria	sf_1	7965	*Anoxobacterium dechloraticum*	0.0354646	0.0432329
Firmicutes	sf_5	4500	*Ruminococcus bromii*	0.03557315	0.04326047
Proteobacteria	sf_1	10021	uranium mill tailings soil sample clone Sh765B-TzT-29 proteobacterium	0.03559864	0.04326047
Proteobacteria	sf_1	10475	hydrothermal sediment clone AF420359	0.03568932	0.0433029
Proteobacteria	sf_1	7822	*Polaromonas naphthalenivorans* str. CJ2	0.03578689	0.04330729
Proteobacteria	sf_1	10212		0.03580447	0.04330729
Proteobacteria	sf_6	7107	*Stappia aggregata* str. IAM12614	0.03603092	0.04350618
Cyanobacteria	sf_1	4999	*Geitlerinema* sp. str. PCC 7105	0.03608096	0.04350618
Proteobacteria	sf_3	9392	*Methylophaga* sp. str. V4.ME.29 = MM_2343	0.03624032	0.0436257
Proteobacteria	sf_15	7035	*Sphingomonas asaccharolytica* str. IFO 10564-T	0.0362995	0.0436257
Firmicutes	sf_1	3898	compost clone 4-28	0.03638912	0.0436257
Proteobacteria	sf_3	9359	*Acinetobacter junii* str. S33	0.0364048	0.0436257
WS3	sf_1	2537	anoxic marine sediment clone LD1-PA39	0.03650694	0.04366713
Actinobacteria	sf_1	1542	*Actinoplanes garbadinensis* str. IMSNU 20040	0.0366047	0.04366713
Proteobacteria	sf_6	7647		0.03665377	0.04366713
Proteobacteria	sf_1	8645	*Methylomicrobium buryatense* str. 5B	0.03666431	0.04366713
Actinobacteria	sf_1	1135	*Rhodoglobus vestalii* str. LV3	0.03691018	0.04383607
Cyanobacteria	sf_1	5219	*Synechococcus* sp. str. UH7	0.03691906	0.04383607
Proteobacteria	sf_1	9062	*Aeromonas* subsp. salmonicida str. NCIMB 1102	0.03699263	0.04384416
Unclassified	sf_160	6456		0.0370388	0.04384416
Proteobacteria	sf_3	9211	penguin droppings sediments clone KD8-80	0.03709552	0.04384447
Proteobacteria	sf_1	9339	*Pseudoalteromonas* sp. str. 05	0.03720666	0.04386485

Planctomycetes	sf_3	4670		0.03722574	0.04386485
Firmicutes	sf_5	3218	termite gut homogenate clone Rs-N53	0.03741684	0.04402323
Actinobacteria	sf_1	1315	*Friedmanniella lacustris* str. EL-17a	0.03774783	0.04418384
Actinobacteria	sf_1	1972	*Actinoplanes regularis* str. IFO 12514T	0.03778048	0.04418384
Proteobacteria	sf_1	6661	*Methylarcula* sp. BIO-24	0.03778073	0.04418384
Proteobacteria	sf_4	6810	marine bacterioplankton clone MB13F01	0.03778095	0.04418384
Proteobacteria	sf_1	7130	Gram-negative MM 1	0.03786185	0.04421188
Proteobacteria	sf_1	7984	Waste-gas biofilter clone BIfciii38	0.03798253	0.0442862
Proteobacteria	sf_1	7807	*Aquaspirillum metamorphum* str. DSM 1837	0.03805957	0.0443095
OP10	sf_1	326	geothermal clone ST01-SN3H	0.03826231	0.04447884
Actinobacteria	sf_1	1901	earthworm burrow isolate B33D1	0.03841458	0.04458607
Proteobacteria	sf_1	7527		0.03846939	0.04458607
Actinobacteria	sf_1	1758	glacial ice isolate str. SB12K-2-1	0.03860772	0.04467971
Verrucomicrobia	sf_6	871		0.03893545	0.04499194
Proteobacteria	sf_1	7925	*Thauera selenatis* str. ATCC 55363T	0.03913719	0.04512895
Proteobacteria	sf_3	8676		0.03917026	0.04512895
Proteobacteria	sf_1	9956	forested wetland clone FW140	0.03943973	0.0453721
Proteobacteria	sf_1	7823	*Wautersia basilensis* str. DSM 11853	0.03969289	0.04559579
Proteobacteria	sf_1	6953	*Caulobacter* sp. str. FWC21	0.03984788	0.04565008
Actinobacteria	sf_1	1931	*Actinoplanes utahensis* str. ATCC 31044	0.03985772	0.04565008
Proteobacteria	sf_1	6830	coal effluent wetland clone RCP124	0.0401769	0.04594787
Proteobacteria	sf_1	6888	hydrothermal vent strain str. TB66	0.04023778	0.04594982
Proteobacteria	sf_3	8689	*Dyemonas todaii* str. XD10	0.04034329	0.04595196
Proteobacteria	sf_3	10454	*Helicobacter pullorum* str. NCTC 12826	0.04035801	0.04595196
AD3	sf_1	2338	uranium mining waste pile soil clone JG30-KF-C12	0.04054423	0.04609641
Proteobacteria	sf_3	7275	Mammoth cave clone CCU18	0.04078195	0.04617004
Proteobacteria	sf_3	10417	temperate estuarine mud clone KM61	0.04086477	0.04617004
Proteobacteria	sf_1	9588	*Pseudomonas citronellolis* str. TERIDB18	0.04094763	0.04617004
Proteobacteria	sf_1	7919	strain isolate str. rM4	0.04094931	0.04617004
Verrucomicrobia	sf_1	760	Mono lake clone ML316M-1	0.04097731	0.04617004
Actinobacteria	sf_1	1689	*Actinoplanes yunnanensis* str. IFO 14459T	0.04099249	0.04617004
Proteobacteria	sf_3	8114		0.04114307	0.04617004
Proteobacteria	sf_1	8999	*Photobacterium leiognathi* str. LN101	0.04124415	0.04617004

Firmicutes	sf_12	4267	termite gut clone Rs-114	0.04125015	0.04617004
Cyanobacteria	sf_5	4967	Toolik Lake main station at 3 m depth clone TLM14	0.04126067	0.04617004
Proteobacteria	sf_1	10010	uranium mining waste pile clone JG37-AG-139 proteobacterium	0.04126302	0.04617004
Proteobacteria	sf_1	8662		0.04140996	0.04626779
Proteobacteria	sf_1	8105	*Hydrogenophaga taeniospiralis* str. ATCC 49743	0.04160483	0.04638172
Proteobacteria	sf_1	7140	*Loktanella salsilacus* str. LMG 22000	0.04166576	0.04638172
Actinobacteria	sf_1	1862	endemic to Mojave Desert isolate str. AS3138 AS3138	0.04169111	0.04638172
Proteobacteria	sf_1	8058	*Herbaspirillum seropedicae* str. DSM 6445 ATCC 35892	0.0418595	0.04650242
Proteobacteria	sf_1	7949	Variovorax paradoxus TG27	0.04203866	0.04650639
Firmicutes	sf_5	2681	termite gut homogenate clone Rs-K41 bacterium	0.0420596	0.04650639
Firmicutes	sf_12	4459	termite gut clone Rs-109	0.04208714	0.04650639
Actinobacteria	sf_1	1350	*Rhodococcus ruber* str. DSM43338	0.04213463	0.04650639
Proteobacteria	sf_1	7597	*Sphingomonas* sp. str. DhA-95	0.04216251	0.04650639
Proteobacteria	sf_1	6708	*Roseomonas* sp. str. SAFR-014	0.04238912	0.04658625
Proteobacteria	sf_1	7016	*Sphingomonas* sp. str. SAFR-027	0.04241359	0.04658625
Spirochaetes	sf_1	6568	*Spirochaeta* sp	0.0424149	0.04658625
Actinobacteria	sf_1	1120	*Actinoplanes violaceus* str. IMSNU 22136	0.0425212	0.04660058
Proteobacteria	sf_1	7500	Great Artesian Basin clone B35	0.04254797	0.04660058
Proteobacteria	sf_1	7009		0.04294923	0.04697381
Actinobacteria	sf_1	1209	*Gordonia* sp. str. J4	0.04315743	0.04707322
Firmicutes	sf_4	2398	deep marine sediment clone MB-C2-106	0.04316136	0.04707322
Actinobacteria	sf_1	1787	*Nocardia pseudovaccinii* str. DSM 43406	0.04322812	0.0470799
Firmicutes	sf_17	926		0.0433188	0.04711258
Acidobacteria	sf_14	6424	sphagnum peat bog clone K-5b10	0.04348751	0.04719842
Proteobacteria	sf_3	9671	hydrothermal sediment clone AF420357	0.04351928	0.04719842
Proteobacteria	sf_3	8604	*Moraxella oblonga* str. IAM 14971	0.04365561	0.04728024
Proteobacteria	sf_1	7537	lichen-dominated Antarctic cryptoendolithic community clone FBP255 proteobacterium	0.0437679	0.04731943
Proteobacteria	sf_1	6750	isolate str. '#33 orange'	0.04382619	0.04731943
Actinobacteria	sf_1	1786	*Streptomyces bikiniensis* str. DSM40581	0.04387461	0.04731943
Actinobacteria	sf_1	1598	lichen-dominated Antarctic cryptoendolithic community clone FBP402	0.04405086	0.0473996
Firmicutes	sf_12	4610	*Clostridium putrefaciens* str. DSM 1291	0.0441394	0.0473996

Proteobacteria	sf_1	6783	*Roseomonas genomospecies* 4 strain isolate str. ATCC 49959 4	0.04416002	0.0473996
Proteobacteria	sf_3	10462	*Helicobacter rodentium* str. MIT 96-1312	0.04425957	0.0473996
Fusobacteria	sf_3	1034	*Ilyobacter tartaricus* str. DSM 2382 T	0.04427464	0.0473996
Firmicutes	sf_5	134	*Peptoniphilus asaccharolyticus* str. CCUG 9988	0.04431518	0.0473996
Proteobacteria	sf_1	8062	*Brackiella oedipodis* str. LMG 1945 R8846	0.04477197	0.04782231
Proteobacteria	sf_1	8798	*Vibrio aestuarianus* str. KT0901	0.04485142	0.04784136
Bacteroidetes	sf_19	5891	*Hymenobacter* group clone KL-59-7-9	0.04505183	0.04798921
Chloroflexi	sf_1	765	anaerobic bioreactor clone SHD-71	0.04519066	0.04807116
Firmicutes	sf_12	2786	*Clostridium glycolicum* str. CIN5	0.04528844	0.04810926
Proteobacteria	sf_3	8838	*Psychrobacter psychrophilus* CMS 28	0.04538889	0.0481501
Actinobacteria	sf_1	1443	*Corynebacterium coyleae* National Microbiology Laboratory Special identifier 97-0171	0.04558497	0.04825177
Proteobacteria	sf_1	7786	*Polaromonas vacuolata* str. 34-P	0.045609	0.04825177
Proteobacteria	sf_1	7285	*Sphingopyxis chilensis* str. S37	0.04594248	0.04841221
Bacteroidetes	sf_1	5601	*Sphingobacterium multivorum* str. OM-A8	0.04598246	0.04841221
Actinobacteria	sf_1	1191	*Gordonia amarae* str. DSM43392	0.0459953	0.04841221
Acidobacteria	sf_14	208	uranium mill tailings soil sample clone GuBH2-AD-9 sp.	0.04601746	0.04841221
Proteobacteria	sf_1	7523	*Rhodovulum euryhalinum* str. DSM4868	0.04607237	0.04841221
Proteobacteria	sf_1	7308	EBPR sludge lab scale clone HP1B39	0.04619338	0.04847377
Actinobacteria	sf_1	1852	*Tonsillophilus suis* str. HT1-19	0.0463106	0.04853119
Proteobacteria	sf_6	6920	*Pseudovibrio denitrificans* str. DN34	0.04658114	0.04874892
Firmicutes	sf_5	2797	Isolation and identification hyper-ammonia producing swine storage pits manure	0.04692793	0.04896982
Proteobacteria	sf_1	7262	*Paracoccus pantotrophus* str. TUT1022	0.04700245	0.04896982
Proteobacteria	sf_1	7075	*Novosphingobium* sp. str. K16	0.04706708	0.04896982
Firmicutes	sf_5	393	*Anaerococcus vaginalis* str. CCUG 31349	0.04708812	0.04896982
Unclassified	sf_160	10012		0.04723011	0.04896982
Spirochaetes	sf_1	6476	termite gut clone NkS50	0.04729219	0.04896982
Planctomycetes	sf_4	4694	USA: Colorado Fort collins Horsetooth Reservoir clone HT2F11	0.04734873	0.04896982
Proteobacteria	sf_1	9218	*Pseudoalteromonas haloplanktis* str. ATCC 14393	0.04735076	0.04896982
Acidobacteria	sf_14	6350	soil isolate Ellin337	0.04735978	0.04896982
Bacteroidetes	sf_1	5462	*Flavobacterium omnivorum* str. AS 1.2747; JCM 11313	0.04748781	0.0490369
Firmicutes	sf_1	3975	Black raspberry witches'-broom phytoplasma str. BRWB witches'-	0.04804609	0.04946253

			broom		
Proteobacteria	sf_1	7968	*Oxalobacter formigenes* str. OXB ovinen rumen	0.04805175	0.04946253
Actinobacteria	sf_1	1742	*Blastococcus saxobsidens* str. BC448	0.04809108	0.04946253
Proteobacteria	sf_1	7585	*Methylobacterium thiocyanatum* str. ALL/SCN-P	0.04844701	0.04971796
Proteobacteria	sf_1	7976	*Nitrosomonas* sp. str. Nm86	0.04846748	0.04971796

[a] S-F = subfamily; [b] Taxon ID = Phylochip taxon identification number; [c] Representative species = bacterial species identifier.

Man’s best friend?

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Table E4. BLAST-based identity of fungal phylotypes.

Ribotype	*Accession No.*	*Phylum*	*Family*	*Organism*	*% ID*
1	AY387144	Basidiomycota		*Malassezia restricta* strain CBS8747	99.4
1	AM901797	Basidiomycota		environmental sample	99.6
2	GQ249171	Ascomycota	Dothideomycetidaceae	*Alternaria alternata*	99.8
2	AF502815	Ascomycota		root endophyte	99.2
3	AB273527	Ascomycota	Erysiphaceae	*Blumeria graminis*	100
4	EU035422			*Exophilia* sp.	100
5	FJ235087	Ascomycota	Pleosporomycetidae	*Cochliobolus* sp.	99.8
5	EU568925	Ascomycota	Metschnikowiaceae	*Clavispora lusitaniae*	98.4
6	AB273527	Ascomycota	Erysiphaceae	*Blumeria graminis*	100
6	AJ876482	Ascomycota	Dothideomycetidaceae	*Cladosporium cladosporioides*	99.8
6	FJ213499			Uncultured soil fungus	99.8
6	AM262377			Fungal endophyte	99.5
7	DQ156341	Ascomycota	Dothideomycetidaceae	*Alternaria alternata* group	99.8
7	DQ156337	Ascomycota	Dothideomycetidaceae	*Alternaria longipes*	99.8
8	EF589865	Ascomycota	Dothideomycetidaceae	*Davidiella tassiana*	100
8	EU167591	Ascomycota	Dothideomycetidaceae	*Davidiella macrospora*	100
8	DQ420994			Uncultured fungal clone	100
9	AY843154	Ascomycota	Herpotrichiellaceae	*Phaeococcomyces nigricans*	99.6
10	AM231398	Ascomycota	Pleosporomycetidae	*Leptosphaerulina chartarum*	100
10	EF621565	Basidiomycota	Tremellomycetidae	*Cryptococcus* sp.	91.8
10	EF505566			*Uncultured endophyte*	99.7
11	AJ244257	Ascomycota	Dothideomycetidaceae	*Pringsheimia smilacis*	96.5
12	AF444614	Basidiomycota		*Rhodotorula mucilaginosa*	99.8
13	AM902044	Basidiomycota		*Uncultured basidiomycota*	99.6
13	EU516849	Basidiomycota	Tremellomycetidae	*Cryptococcus* sp./environmental sample	98.1
14	AM901819	Basidiomycota		Uncultured basidiomycota	99.5
15	FJ553803	Basidiomycota	Suillaceae	Uncultured *Suillus* clone	95.3

16	AF393706	Ascomycota	Dothideomycetidaceae	*Davidiella tassiana*	100
16	EU167591	Ascomycota	Dothideomycetidaceae	*Davidiella macrospora*	100
17	AM902044	Basidiomycota		Uncultured basidiomycota	100
17	EU516849	Basidiomycota	Tremellomycetidae	Uncultured *Cryptococcus* clone	100
18	AY573212	Ascomycota	Botryosphaeriaceae	*Botryosphaeria sarmentorum* strain IMI 63581b	99.6
19	AB470831	Ascomycota	Pleosporomycetidae	*Alternaria alternata*	99.6
20	DQ000318	Basidiomycota	Tremellomycetidae	*Cryptococcus tephrensis*	97.9
21	AM231398	Ascomycota	Pleosporomycetidae	*Leptosphaerulina chartarum*	100
21	FJ450002			Fungal endophyte	100
22	AY739113	Ascomycota	Erysiphaceae	*Podosphaera fusca*	100
23	AB470872	Ascomycota	Pleosporomycetidae	*Alternaria alternata*	99.6
24	EU484245	Fungi incertae sedis	Mucoraceae	*Mucor plumbeus* strain FSU	99.7
25	EF619719	Ascomycota	Orbiliaceae	Uncultured Orbiliaceae clone	92.1
25	EU516806			environmental sample	91
26	AM160642	Basidiomycota		*Rhodotorula glutinis*	100
26	AF444638	Basidiomycota		*Rhodotorula* sp. KB 651	100
27	EU516903			uncultured fungal clone	94.4
27	EU810056	Basidiomycota	Ceratobasidiaceae	*Ceratobasidium noxium* strain CBS154-35	91.6
28	AB470823	Ascomycota	Pleosporomycetidae	*Alternaria alternata*	100
29	EF652065	Ascomycota	Eurotiomycetidae	*Aspergillus reptans*	100
29	AF459728	Ascomycota	Eurotiomycetidae	*Eurotium niveoglaucum*	100
29	AY373890	Ascomycota	Eurotiomycetidae	*Eurotium strain* ATCC 66457	100
30	AY213649	Ascomycota	Eurotiomycetidae	*Eurotium rubrum* strain UWFP 756	100
30	AM999715			Uncultured fungus	90
30	FJ758576			Uncultured fungus	99.6
30	AY605709	Basidiomycota		Basidiomycete sp.	83.8
31	EU484245	Ascomycota	Mucoraceae	*Mucor plumbeus* strain FSU 6178	99.7
32	DQ388849			Uncultured fungus	91.2
32	AY035665			Glomeromycota sp.	89.9
32	EF619688	Ascomycota		Ascomycota sp.	89.2
33	EU326196	Ascomycota	Mucoraceae	*Mucor hiemalis* f. *hiemalis* strain CBS 242.35	99.5
34	AB105432	Basidiomycota	Tremellomycetidae	*Cryptococcus carnescens*	100
35	AJ876481	Ascomycota	Dothideomycetidaceae	*Aureobasidium pullulans*	100

35	EU167608	Ascomycota	Dothideomycetidaceae	*Kabatiella microsticta* strain CBS 342.66	100
36	FJ904830	Ascomycota	Eurotiomycetidae	*Eurotium niveoglaucum* strain Gr136B	96.8