Supporting Material

Use of Molecular Probe Technology to Monitor Key and Low Abundance Community Members in Activated Sludge

Weihong Xu[a,b,*], Veronica R. Brand[c,*], Sundari Suresh[a], Michael A. Jensen[a], Ronald W. Davis[a,d,e], Craig S. Criddle[c], Robert P. St.Onge[a,d], and Richard W. Hyman[a,d,#] ORCID 0000-0002-8460-309X

[a]Stanford Genome Technology Center, Palo Alto, CA 94304, USA
[b]Precision Medicine Institute, The First Affiliated Hospital of Sun Yat-sen University, Guangzhou, China
[c]Department of Civil and Environmental Engineering, Stanford University, Stanford CA 94305, USA
[d]Department of Biochemistry, Stanford University Medical College, Stanford, CA 94305, USA
[e]Department of Genetics, Stanford University Medical College, Stanford, CA 94305, USA
*These authors contributed equally to this investigation.
[#]Address correspondence to rhyman@stanford.edu.

Number of Supplementary Figures: 2.

Number of Supplementary Tables: 3.

Supplementary Figures

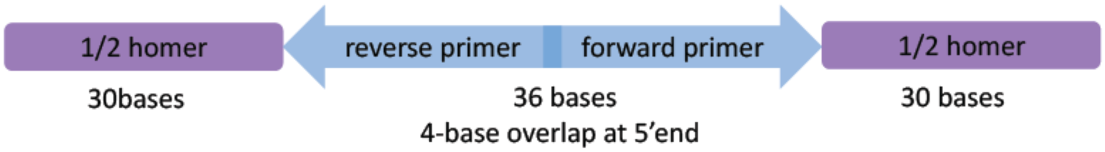

Figure S1. Molecular probe diagram. A diagram of a molecular probe is presented. A molecular probe is a 96 base oligonucleotide that consists of two parts. One part is the Homer (a 60 base sequence unique to the bacterial genome of interest) divided into two 30-base end sequences (purple). The second part is a 36-base internal universal amplification sequence (blue).

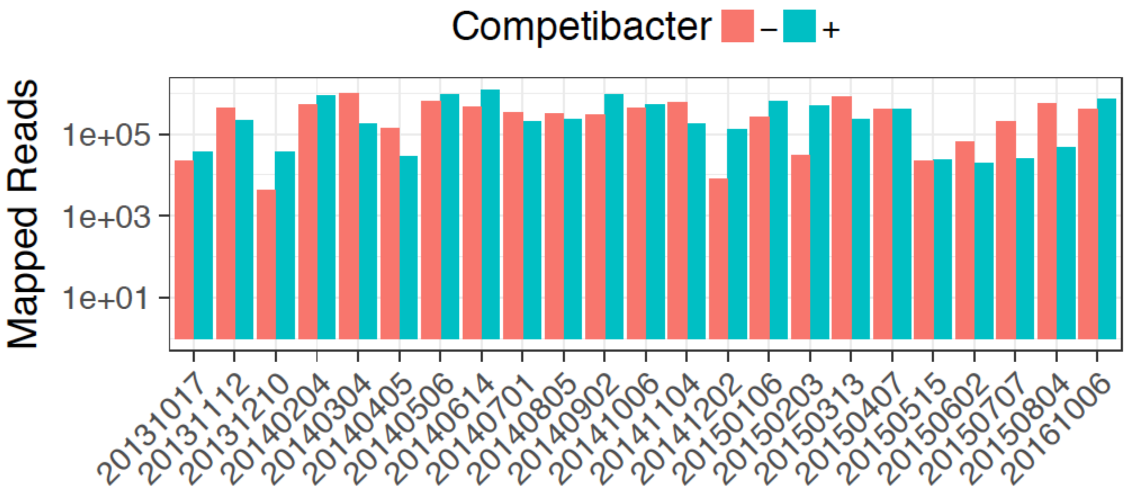

Figure S2. Number of sequence reads per time point. On a log scale, the number of sequence reads per time point for each of the two probe ensembles is presented.

Supplementary Tables

Table S1. Molecular probe base sequences. The final probe ensemble contained 3,316 molecular probes representing 353 bacterial genomes plus 10 toxin genes. The base sequence of each probe is presented. To every design, 5’-TAGACGTAAGCCTGGTCTCA is added to the 5’ end and AGGTAGACTCGATTCCCGAT-3’ is added to the 3’ end. Therefore, with appropriate primers, all of the oligonucleotides can be amplified together such that the group need be ordered only once. Appropriate restriction enzyme cleavage removes these end sequences cleanly.

Bacteria/Toxin Genes	ID	Sequence (X = AGAGTGTACCGACCTCAGTAGCCGTGACTATCGACA)
Achromobacter xylosoxidans	NC_014640_11844	ctaaggcttcgggaatggaatcggctttatXcgccggtggagatcaattcgaatgctagtg
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BFPA	BFPA_371	ccttgaacttaggtacttcagcgaaaggctXtggataaagcggcatgtgttagtcttgcaa

BFPA	BFPA_381	aggtacttcagcgaaaggctacggtgttaaXggcatgtgttagtcttgcaaccttgaactt
BFPA	BFPA_41	cgcttgctgccaccgttaccgcaggtgtgaXtgtctttgattgaatctgcaatggtgcttg
BFPA	BFPA_461	ctgctaaatcgactgctattactcctgctgXttacatcatttggtaatagcgctgatcagg
EAEA	EAEA_1001	taggcgccaagctgatatatgagcagtattXttaatggctatctaccgtcatatccggcat
EAEA	EAEA_1411	ggtctggatcgtatcgtctgggatgatagtXaagattcagttgatcgttaagagcaaatac
EAEA	EAEA_1606	attaccgttctgtcgaatggtcaagttgtcXggcaatagctctaacaatgtacagcttact
EAEA	EAEA_1611	cgttctgtcgaatggtcaagttgtcgaccaXtagctctaacaatgtacagcttactattac
EAEA	EAEA_1846	tcgagtacgccaggacaggtcgtcgtgtctXgctaacggtaaggcaaccgtaacgttgaag
EAEA	EAEA_2401	aaagtcactttgaatggtaaaggcagtgtcXaccagtatcgcgactgtcgatgcatcaggg
EAEA	EAEA_566	cttcgtcacagttgcaggcctggttacaacXataccgctcttggtatcgctggtaaccagg
EAEA	EAEA_576	gttgcaggcctggttacaacattatggaacXtggtatcgctggtaaccaggcttcgtcaca
EAEA	EAEA_586	tggttacaacattatggaacggcagaggttXggtaaccaggcttcgtcacagttgcaggcc
EAEA	EAEA_601	ggaacggcagaggttaatctgcagagtggtXtcacagttgcaggcctggttacaacattat
EAEA	EAEA_721	attgactcccgctttacggcaaatttaggtXctggcatttggtcaggtcggagcgcgttac
EAST1	EAST1_1261	agtgtggccagttccacttctgcacggtttXcgtcgattgttataccagtccacccacgtg
EAST1	EAST1_1341	tagatcactttgcggatgtccgttggataaXctgtttagcgactcgatggcattcgtcgta
EAST1	EAST1_1531	agtccttccatgacacgaagcgcaggctgtXtcgctttcaggtcgcgagtgacggctttgt
EAST1	EAST1_1551	cgcaggctgttgcgcaccatatgcacgatgXacggctttgtagtccttccatgacacgaag
EAST1	EAST1_1557	ctgttgcgcaccatatgcacgatgcataacXttgtagtccttccatgacacgaagcgcagg
EAST1	EAST1_1566	accatatgcacgatgcataactggatgcggXttccatgacacgaagcgcaggctgttgcgc
IPAH	IPAH_1561	tccatccagtcatcggttcgtctgagaatgXgtatcatcagtgtgacgactgcggcggcca
IPAH	IPAH_1801	caacctgttctccggcggccacagcagtaaXtcatggcggcagcaagttcagaggcaggaa
IPAH	IPAH_241	gatgccattcgttataatgctcgaatgcctXgtggcgagcgataatccagcgcactatgcg
IPAH	IPAH_28081	agtacaggcgactcgtatgacaacgcgataXaaggaagccggattactggcatcaacagga
IPAH	IPAH_40321	tccggcttccttaagccgctgtgtgtaggcXgtcgcctgtacttcctgttgatgccagtaa
IPAH	IPAH_47821	gttgatgccagtaatccggcttccttaagcXgcgttgtcatacgagtcgcctgtacttcct
IPAH	IPAH_64621	taacaggcgtaccggcaggacagagatgttXctggagattcctcagcctcatggagcggcg
IPAH	IPAH_70741	caggtactgtaacgctacgcaagcgccgtcXccgaactcatctctcgttgccttgccgaat
IPAH	IPAH_71041	caccggatacaccagagaacgatgcagcctXtgctggctatcgatggtgtgttctggcgca
IPAH	IPAH_72541	taacggattgtcagtactgaggctgtccgcXtccacttctgttccatcagcgtggcaccgg
IPAH	IPAH_82261	ccgtatcatcagtgtgacgactgcggcggcXcgataacatggtgtatacggagaagcacat
IPAH	IPAH_82561	aagacttccttcctggtattgcttacgccaXaacaacctgttctccggcggccacagcagt
IPAH	IPAH_89221	ccggcttccttaagccgctgtgtgtaggccXtcgcctgtacttcctgttgatgccagtaat
LT	LT_151	atgaatccagggttcttctctccaagcttgXtgatgaatttccacaaccttgtggtgcatg
LT	LT_351	cagaaacctcctgttcatatgggtgagggcXatatctgagaatatggtattccacctaacg
LT	LT_361	ctgttcatatgggtgagggctgtatacgccXatatggtattccacctaacgcagaaacctc
LT	LT_371	gggtgagggctgtatacgcctaatacatcaXccacctaacgcagaaacctcctgttcatat
LT	LT_381	tgtatacgcctaatacatcattaacattaaXcagaaacctcctgttcatatgggtgagggc
LT	LT_531	atctgacaaagccggtttgtgttcctctcgXtaagagaagtggaaacatatccgtcatcat
LT	LT_541	gccggtttgtgttcctctcgcgtgatcataXggaaacatatccgtcatcatatctgacaaa

LT	LT_551	gttcctctcgcgtgatcataaagattaataXccgtcatcatatctgacaaagccggtttgt
LT	LT_571	aagattaatattcatttgagttcctctatcXgccggtttgtgttcctctcgcgtgatcata
STH	STH_1021	agcgtttccctgcaatatttcacagtgattXcagcgccaacgtatgctcgtcaacaaagcg
STH	STH_121	agcgcgctcgccaaagcagtgaatacccagXaatcgcctgaccgatatgaataatttcggc
STH	STH_331	agggatatcttcaatcagatgtgcggtggcXgctgatttccgggatggtgtaaataccggt
STH	STH_451	gtaaacgtgtggctgtgcggtctgatacatXgctcggataaccaatcacgtcgcccaccgc
STH	STH_481	gctgttgaccttcagctgtccgcggctgtcXgtaaacgtgtggctgtgcggtctgatacat
STH	STH_511	agtttctagcccaatgttctgtaacgccagXgctgttgaccttcagctgtccgcggctgtc
STH	STH_661	gttgtgacgaatcactacgccactgttccaXgtcacagccttcgatcttctcgtactcttc
STH	STH_691	gaagtgataggagagagaatctgacatctcXgttgtgacgaatcactacgccactgttcca
STH	STH_841	gcgcggttcgtggtgcatgctgagaattgaXgatcactccagcaccatagataagtacatg
STH	STH_871	gtcgctgtcgtaaatgcgtggatgggtgaaXgcgcggttcgtggtgcatgctgagaattga
STH	STH_991	cagcgccaacgtatgctcgtcaacaaagcgXtagtgtttcaacgctgccgtccgggcaatc
STP	STP_1001	ccttcattgtttgttgcatgaacccgaacgXcactatcaattatgttggtatcgctgatca
STP	STP_1021	aacccgaacgcgatttcgatgatttacgcgXtcgctgatcaccttcattgtttgttgcatg
STP	STP_1121	ttaaaccctggcgttccatcggaaatctgaXctacgttgtcaacgtatctgatcccggcgc
STP	STP_121	acatattggccacataaagccttatgccagXtttattactgctctggtcgcctggccttta
STP	STP_21	cggcacagccgttggtgcaggcacgctcttXagaagaaactctgtggagtttcgcgctcta
STP	STP_221	agattggttatctgattaccacgctgtactXcgggcgcagtaacacactactatggcaaga
STP	STP_341	ttcgcatccgtatgttggtgagtctgggtgXaacagctggcaaagcatatggttattgatc
STP	STP_361	agtctgggtgttgtattaatcctgaatctcXgttattgatcttcgcatccgtatgttggtg
STP	STP_41	gcacgctcttccttcctattcagttaggttXtcgcgctctacggcacagccgttggtgcag
STP	STP_541	cttcaccagatatggatatcgattcccgtgXacgacccaggtagagttcaatcagaatacc
STP	STP_741	accttcgtatattgaagcggctaaagaagaXctttgtctttagctgcctgctttctattcc
STP	STP_981	tatgttggtatcgctgatcaccttcattgtXaagtcgtgcatttaaccgcgcactatcaat
STX1	STX1_320	gtagctataccacgttacagcgtgttgcagXgtacaacagcggttacattgtctggtgaca
STX1	STX1_628	ggacaagactctgttcgtgtaggaagaattXaggttgagtagcgtcctgcctgactatcat
STX1	STX1_725	cgcgagttgccagaatggcatctgatgagtXcattaatactgaattgtcatcatcatgcat
STX2	STX2_351	ggtttccatgacaacggacagcagttatacXtacacatatatcagtgcccggtgtgacaac
STX2	STX2_366	ggacagcagttataccactctgcaacgtgtXgcccggtgtgacaacggtttccatgacaac
STX2	STX2_394	gtcgcagcgctggaacgttccggaatgcaaXacggacagcagttataccactctgcaacgt
STX2	STX2_406	gaacgttccggaatgcaaatcagtcgtcacXtataccactctgcaacgtgtcgcagcgctg
STX2	STX2_431	gtcactcactggtttcatcatatctggcgtXcgctggaacgttccggaatgcaaatcagtc
STX2	STX2_461	taatggagttcagtggtaatacaatgaccaXgtcactcactggtttcatcatatctggcgt
STX2	STX2_561	gagagaatttcgtcaggcactgtctgaaacXagcagaagccttacgcttcaggcagataca
STX2	STX2_576	ggcactgtctgaaactgctcctgtgtatacXcttcaggcagatacagagagaatttcgtca
STX2	STX2_731	tgggcactgtggccgttatactgaattgtcXgaatatcctttaataatatatcggcgatac
STX2	STX2_811	gaatgtcagataactggcgacaggcccgttXgttcgcgccgtgaatgaagatagtcaacca

Table S2. Relative Abundance of Genera Detected by Molecular Probes in Shotgun Sequencing Samples as Identified with the Greengenes (2012) Taxonomy.

Taxonomic Identification		**Relative Abundance***					
		3/25/14		**7/21/15**		**10/27/15**	
Phylum	**Genus**	**Raw**	**Adj**	**Raw**	**Adj**	**Raw**	**Adj**
Proteobacteria	*Dechloromonas*	0.00	0.00	0.11	0.05	1.97	1.04
Firmicutes	*Streptococcus*	0.70	0.42	0.63	0.44	0.31	0.20
Actinobacteria	*Bifidobacterium*	0.92	0.90	0.22	0.22	0.17	0.17
Bacteroidetes	*Runella*	0.12	0.11	0.33	0.32	0.43	0.46
Euryarchaeota	*Methanobrevibacter*	0.14	0.13	0.02	0.02	0.01	0.01
Firmicutes	*Lactobacillus*	0.10	0.06	0.02	0.01	0.03	0.01
Synergistetes	*Anaerobaculum*	0.00	0.00	0.03	0.03	0.09	0.10
Proteobacteria	*Enterobacter*	0.00	0.00	0.03	0.01	0.04	0.01
Firmicutes	*Clostridium*	0.01	0.00	0.00	0.00	0.03	0.01
Fusobacteria	*Sebaldella*	0.00	0.00	0.02	0.01	0.01	0.01
Bacteroidetes	*Bacteroides*	0.00	0.00	0.00	0.00	0.03	0.01
Firmicutes	*Leuconostoc*	0.01	0.01	0.00	0.00	0.01	0.01
Firmicutes	*Enterococcus*	0.02	0.01	0.00	0.00	0.00	0.00
Verrucomicrobia	*Akkermansia*	0.01	0.01	0.01	0.01	0.00	0.00
Proteobacteria	*Tolumonas*	0.00	0.00	0.02	0.00	0.00	0.00
Proteobacteria	*Comamonas*	0.00	0.00	0.01	0.01	0.00	0.00

*Raw- uncorrected for copy number; Adj- corrected for 16S rRNA copy number with CopyRighter

Table S3. Relative Abundance of Genera from Shotgun Sequencing Samples as Identified with the MiDAS Taxonomy. OTUs were grouped by genus-level identification if possible. ‘Novel OTU’ represents OTUs not represented in the MiDAS database.

Taxonomic Identification		Relative Abundance		
Phylum	**Genus**	**3/25/14**	**7/21/15**	**10/27/15**
Proteobacteria	CPB_P15	45.72	0.60	0.42
Actinobacteria	Tetrasphaera	8.62	12.84	4.18
Actinobacteria	Mycobacterium	9.66	6.25	3.07
Proteobacteria	CPB_M38**	0.04	6.54	8.17
Proteobacteria	CPB_C95***	0.63	9.18	2.74
Proteobacteria	Zoogloea	0.00	0.18	8.54
Actinobacteria	Propioniciclava	4.22	2.16	0.87
Proteobacteria	Acidovorax	0.90	2.64	1.84
Proteobacteria	Thermomonas	0.44	3.33	1.19
Bacteroidetes	Flavobacterium	0.01	1.49	3.36
Actinobacteria	Gordonia	0.03	1.61	2.95
Actinobacteria	Fodinibacter	1.58	2.03	0.56
Proteobacteria	Rhodobacter	0.93	1.61	1.48
Bacteroidetes	MK04	0.03	2.70	1.17
Unassigned	Unassigned; novel OTU1	0.00	0.01	3.53
Proteobacteria	188up	0.25	1.03	1.93
Firmicutes	Streptococcus	1.21	0.84	0.43
Proteobacteria	Acinetobacter	0.02	1.03	1.23
Proteobacteria	Comamonas	0.15	1.41	0.69
Actinobacteria	Leucobacter	1.11	0.67	0.39
Actinobacteria	f__Propionibacteriaceae_FM872539	0.87	0.47	0.80
Bacteroidetes	Chryseobacterium	0.35	0.79	0.96
Proteobacteria	Bosea	1.05	0.55	0.41
Proteobacteria	GKS98 freshwater group	1.50	0.30	0.18
Proteobacteria	Altererythrobacter	0.62	0.76	0.47
Proteobacteria	Novosphingobium	0.10	0.95	0.66
Unassigned	Unassigned; novel OTU2	0.00	0.00	1.65
Proteobacteria	Reyranella	0.53	0.67	0.39
Bacteroidetes	Sediminibacterium	0.02	0.35	1.19
Proteobacteria	Phenylobacterium	0.05	0.85	0.63
Actinobacteria	Propionicimonas	0.85	0.39	0.18
Proteobacteria	Rhizobium	0.69	0.34	0.33
Proteobacteria	f__Moraxellaceae_DQ640687	0.02	0.08	1.25
Actinobacteria	Microbacterium	0.77	0.29	0.26
Actinobacteria	Bifidobacterium	0.92	0.22	0.17
Actinobacteria	Iamia	0.56	0.50	0.24
Bacteroidetes	Taibaiella	0.02	0.73	0.38
Proteobacteria	Devosia	0.42	0.43	0.25
Proteobacteria	Sphingopyxis	0.00	0.32	0.77
Bacteroidetes	Fluviicola	0.00	0.03	1.05
Proteobacteria	Variovorax	0.11	0.70	0.25
Bacteroidetes	f__env.OPS 17_HM268707	0.00	0.03	1.01
Proteobacteria	Lautropia	0.04	0.49	0.46
Bacteroidetes	f__Chitinophagaceae_EU234264	0.00	0.00	0.98
Proteobacteria	Dechloromonas	0.00	0.04	0.93
Proteobacteria	Thiothrix	0.33	0.19	0.43
Firmicutes	Christensenellaceae R-7 group	0.13	0.66	0.17

Proteobacteria	Candidatus Accumulibacter	0.00	0.02	0.93
Proteobacteria	Ferribacterium	0.00	0.07	0.85
Chloroflexi	Candidatus Defluviifilum	0.00	0.68	0.24
Bacteroidetes	Runella	0.12	0.33	0.43
Actinobacteria	o__Frankiales_EU104204	0.26	0.41	0.18
Proteobacteria	Brachymonas	0.12	0.64	0.09
Proteobacteria	Perlucidibaca	0.00	0.05	0.77
Bacteroidetes	CYCU-0281	0.10	0.68	0.04
Firmicutes	Intestinibacter	0.32	0.23	0.21
Proteobacteria	f__Beijerinckiaceae_CU920741	0.40	0.14	0.22
Actinobacteria	Nocardioides	0.27	0.37	0.12
Actinobacteria	Knoellia	0.36	0.34	0.04
Proteobacteria	Arenimonas	0.00	0.32	0.41
Proteobacteria	Paracocccus	0.05	0.28	0.38
Proteobacteria	f__Comamonadaceae_AF236010	0.02	0.23	0.45
Verrucomicrobia	f__Verrucomicrobiaceae_JN981876	0.00	0.63	0.07
Chloroflexi	o__JG30-KF-CM45_DQ129350	0.40	0.14	0.14
Verrucomicrobia	Prosthecobacter	0.00	0.31	0.37
Actinobacteria	Janibacter	0.35	0.30	0.03
Bacteroidetes	Flavihumibacter	0.03	0.28	0.33
Actinobacteria	Aestuariimicrobium	0.49	0.10	0.05
Bacteroidetes	Cloacibacterium	0.02	0.23	0.38
Bacteroidetes	f__WCHB1-69_HQ178727	0.00	0.12	0.51
Proteobacteria	Roseomonas	0.14	0.21	0.25
Proteobacteria	f__Comamonadaceae_AB286648	0.00	0.00	0.59
Proteobacteria	o__Myxococcales_novel OTU6	0.00	0.18	0.41
Actinobacteria	P58	0.14	0.23	0.21
Proteobacteria	MNG7	0.13	0.29	0.16
Proteobacteria	f__mle1-27_KM016296	0.01	0.47	0.09
Proteobacteria	Methyloversatilis	0.00	0.00	0.55
Proteobacteria	CPB_S18	0.00	0.41	0.12
Proteobacteria	Hydrogenophaga	0.08	0.27	0.18
Proteobacteria	Afipia	0.38	0.10	0.05
Verrucomicrobia	Luteolibacter	0.00	0.48	0.05
Proteobacteria	f__Alcaligenaceae_EU104103	0.24	0.27	0.01
Proteobacteria	Shinella	0.23	0.18	0.10
Bacteroidetes	f__env.OPS 17_novel OTU17	0.01	0.05	0.45
Proteobacteria	f__Methylophilaceae_KC189785	0.00	0.19	0.31
Proteobacteria	Bdellovibrio	0.17	0.22	0.10
Bacteroidetes	PHOS-HE28	0.00	0.05	0.45
Proteobacteria	Leptothrix	0.00	0.10	0.39
Saccharibacteria	p__Saccharibacteria_HM584360	0.00	0.48	0.01
Saccharibacteria	Skagenf80	0.11	0.27	0.10
Bacteroidetes	QEDR3BF09	0.01	0.39	0.08
Proteobacteria	Sphingobium	0.00	0.23	0.24
Proteobacteria	Aeromonas	0.00	0.02	0.43
Proteobacteria	f__Comamonadaceae_EU800316	0.18	0.14	0.12
Firmicutes	Trichococcus	0.35	0.03	0.07
Actinobacteria	Jatrophihabitans	0.13	0.20	0.10
Actinobacteria	rJ14	0.18	0.17	0.08
Proteobacteria	f__Alcaligenaceae_AB516070	0.15	0.25	0.03
Proteobacteria	f__mle1-27_JQ624277	0.00	0.15	0.28
Bacteroidetes	f__WCHB1-69_JQ723668	0.00	0.09	0.33
Verrucomicrobia	f__FukuN18 freshwater group_DQ415853	0.01	0.40	0.00
Proteobacteria	Bordetella	0.29	0.07	0.05
Proteobacteria	f__B142_JQ624330	0.19	0.12	0.09
Verrucomicrobia	f__Verrucomicrobiaceae_GQ396806	0.01	0.34	0.05
Actinobacteria	Collinsella	0.25	0.13	0.01
Bacteroidetes	f__Chitinophagaceae_KC255350	0.00	0.19	0.20

Proteobacteria	Marinobacterium	0.00	0.24	0.14
Bacteroidetes	Paludibacter	0.00	0.07	0.31
Proteobacteria	f__Comamonadaceae_JW950651	0.02	0.19	0.17
Actinobacteria	f__Intrasporangiaceae_EF063716	0.22	0.15	0.01
Bacteroidetes	f__Chitinophagaceae_AB286620	0.00	0.00	0.38
Proteobacteria	Rhodoferax	0.10	0.03	0.25
Proteobacteria	Meganema	0.05	0.14	0.17
Proteobacteria	Azospira	0.00	0.02	0.34
Bacteroidetes	Ferruginibacter	0.00	0.16	0.20
Gracilibacteria	p__Gracilibacteria_EU104071	0.00	0.30	0.05
Actinobacteria	Dietzia	0.08	0.18	0.09
Proteobacteria	Tahibacter	0.00	0.28	0.07
Planctomycetes	Planctomyces	0.04	0.17	0.13
Actinobacteria	f__Propionibacteriaceae_HM773522	0.21	0.08	0.05
Proteobacteria	Aquabacterium	0.00	0.01	0.33
Proteobacteria	Ancalomicrobium	0.14	0.14	0.05
Proteobacteria	Chitinivorax	0.00	0.00	0.33
Firmicutes	Blautia	0.21	0.05	0.07
Firmicutes	Subdoligranulum	0.22	0.06	0.04
Bacteroidetes	Niabella	0.06	0.18	0.07
Gemmatimonadetes	Gemmatimonas	0.00	0.16	0.14
Proteobacteria	f__A0839_JQ624960	0.15	0.11	0.04
Proteobacteria	Simplicispira	0.02	0.08	0.20
Actinobacteria	f__PeM15_KF697453	0.00	0.12	0.17
Proteobacteria	f__Hydrogenophilaceae_JN391552	0.00	0.00	0.29
Firmicutes	f__Eubacteriaceae_KJ881289	0.11	0.10	0.08
Firmicutes	Erysipelothrix	0.00	0.23	0.05
Proteobacteria	Aquimonas	0.00	0.02	0.26
Proteobacteria	f__Methylocystaceae_JF828745	0.05	0.16	0.05
Proteobacteria	Gemmobacter	0.06	0.07	0.13
Firmicutes	Lactococcus	0.19	0.05	0.01
Proteobacteria	Ottowia	0.10	0.13	0.03
Bacteroidetes	c__WCHB1-32_KJ578040	0.00	0.07	0.18
Planctomycetes	Pirellula	0.01	0.16	0.08
Actinobacteria	Marmoricola	0.09	0.11	0.05
Proteobacteria	f__Moraxellaceae_HE650022	0.01	0.00	0.24
Proteobacteria	f__Comamonadaceae_novel OTU16	0.01	0.05	0.18
Planctomycetes	Isosphaera	0.10	0.08	0.07
Bacteroidetes	Hydrotalea	0.00	0.24	0.00
Chlorobi	Ignavibacterium	0.00	0.16	0.08
Proteobacteria	Methylomonas	0.00	0.00	0.24
Proteobacteria	f__Comamonadaceae_AB077038	0.02	0.16	0.05
Proteobacteria	f__Rhodobacteraceae_JN104393	0.06	0.05	0.12
Proteobacteria	12up	0.00	0.01	0.22
Proteobacteria	Arcobacter	0.00	0.00	0.22
Bacteroidetes	f__NS11-12 marine group_AF361199	0.00	0.01	0.21
Proteobacteria	Pseudomonas	0.00	0.01	0.21
Proteobacteria	f__A0839_LN570495	0.08	0.10	0.04
SHA-109	p__SHA-109_KC189732	0.21	0.01	0.00
Firmicutes	Clostridium sensu stricto 1	0.08	0.07	0.07
Euryarchaeota	Methanosarcina	0.15	0.02	0.04
Bacteroidetes	f__Chitinophagaceae_HQ640538	0.00	0.00	0.21
Proteobacteria	Hyphomicrobium	0.04	0.12	0.04
Proteobacteria	Mesorhizobium	0.08	0.07	0.05
Unassigned	Unassigned; novel OTU23	0.00	0.00	0.20
Verrucomicrobia	Opitutus	0.00	0.05	0.14
Proteobacteria	f__Comamonadaceae_HG003356	0.01	0.01	0.17
Proteobacteria	Dokdonella	0.00	0.16	0.03
Saccharibacteria	p__Saccharibacteria_JN398100	0.00	0.16	0.03

Proteobacteria	Defluviimonas	0.03	0.10	0.05
Bacteroidetes	Leadbetterella	0.01	0.16	0.01
Saccharibacteria	p__Saccharibacteria_novel OTU22	0.00	0.17	0.01
Proteobacteria	Sulfuritalea	0.00	0.06	0.12
Bacteroidetes	f__AKYH767_JN679145	0.00	0.07	0.10
Bacteroidetes	f__Saprospiraceae_EU104036	0.00	0.12	0.05
Euryarchaeota	Methanobrevibacter	0.14	0.02	0.01
Proteobacteria	f__Beijerinckiaceae_KC633563	0.04	0.10	0.03
Bacteroidetes	f__Chitinophagaceae_EU104171	0.00	0.00	0.17
Bacteroidetes	f__Chitinophagaceae_JN391913	0.00	0.00	0.17
Proteobacteria	f__Hydrogenophilaceae_KM410434	0.00	0.00	0.17
Bacteroidetes	f__Chitinophagaceae_KC331462	0.00	0.09	0.08
Bacteroidetes	Pedobacter	0.00	0.05	0.12
Proteobacteria	Prosthecomicrobium	0.08	0.04	0.05
Proteobacteria	Moraxella	0.01	0.09	0.07
Proteobacteria	o__Xanthomonadales_EU104062	0.00	0.11	0.05
Proteobacteria	Sorangium	0.01	0.07	0.08
Bacteroidetes	c__WCHB1-32_AY444993	0.00	0.00	0.16
Proteobacteria	f__Nitrosomonadaceae_KJ783141	0.00	0.00	0.16
Bacteroidetes	f__Saprospiraceae_EU104013	0.05	0.05	0.05
Firmicutes	Anaerostipes	0.10	0.02	0.04
Chloroflexi	o__JG30-KF-CM45_DQ130040	0.08	0.04	0.04
Proteobacteria	f__Alcaligenaceae_GQ422442	0.12	0.01	0.03
Proteobacteria	Alicycliphilus	0.01	0.09	0.05
Actinobacteria	f__Microthricaceae_HM339078	0.00	0.10	0.05
Thermotogae	Defluviitoga	0.03	0.04	0.08
Bacteroidetes	Filimonas	0.00	0.11	0.04
Firmicutes	Ruminiclostridium 5	0.14	0.01	0.00
Proteobacteria	CPB_S60	0.00	0.04	0.10
Bacteroidetes	f__NS11-12 marine group_FJ820373	0.00	0.00	0.14
Bacteroidetes	f__Saprospiraceae_JN391687	0.00	0.00	0.14
Firmicutes	Lactobacillus	0.10	0.02	0.03
Actinobacteria	f__Intrasporangiaceae_AF408957	0.08	0.05	0.01
Proteobacteria	Diaphorobacter	0.02	0.11	0.00
Bacteroidetes	o__Sphingobacteriales_novel OTU37	0.00	0.04	0.09
Lentisphaerae	c__PBS-III-20_novel OTU59	0.00	0.04	0.09
Bacteroidetes	o__Sphingobacteriales_EU104024	0.00	0.00	0.13
Proteobacteria	f__Comamonadaceae_HQ158715	0.00	0.00	0.13
Proteobacteria	spb280	0.01	0.04	0.08
Proteobacteria	Chelatococcus	0.00	0.05	0.08
Bacteroidetes	Owenweeksia	0.00	0.01	0.12
Proteobacteria	f__Rickettsiaceae_LC004724	0.00	0.01	0.12
Firmicutes	Succiniclasticum	0.09	0.04	0.00
Saccharibacteria	p__Saccharibacteria_novel OTU25	0.00	0.11	0.01
Candidate division SR1	p__Candidate division SR1_JF917289	0.01	0.06	0.05
Proteobacteria	B63	0.00	0.07	0.05
Saccharibacteria	p__Saccharibacteria_novel OTU61	0.00	0.07	0.05
Actinobacteria	f__PeM15_EU104254	0.03	0.05	0.04
Synergistetes	Anaerobaculum	0.00	0.03	0.09
Proteobacteria	Ideonella	0.01	0.07	0.04
Proteobacteria	Xenophilus	0.01	0.07	0.04
Proteobacteria	f__Comamonadaceae_AF097797	0.00	0.08	0.04
Unassigned	Unassigned; novel OTU139	0.03	0.02	0.07
Bacteroidetes	c__WCHB1-32_JX225892	0.00	0.00	0.12
Proteobacteria	f__Comamonadaceae_KJ147073	0.00	0.00	0.12
Proteobacteria	f__Comamonadaceae_FJ820468	0.00	0.05	0.07
Proteobacteria	Enterobacter	0.00	0.05	0.07
Bacteroidetes	f__Draconibacteriaceae_HQ703849	0.00	0.06	0.05
Firmicutes	Holdemanella	0.09	0.00	0.03

Bacteroidetes	f__env.OPS 17_HQ111163	0.00	0.02	0.09
Firmicutes	Lachnoclostridium	0.08	0.01	0.03
Verrucomicrobia	f__Verrucomicrobiaceae_novel OTU47	0.01	0.07	0.03
Proteobacteria	f__Beijerinckiaceae_CU919262	0.01	0.03	0.07
Proteobacteria	Nannocystis	0.00	0.04	0.07
Proteobacteria	Kaistia	0.06	0.04	0.00
Unassigned	Unassigned; novel OTU28	0.00	0.00	0.10
Lentisphaerae	c__PBS-III-20_novel OTU49	0.00	0.00	0.10
Proteobacteria	Caulobacter	0.01	0.08	0.01
Actinobacteria	f__Propionibacteriaceae_HM264006	0.03	0.07	0.00
Bacteroidetes	c__WCHB1-32_AB244310	0.00	0.05	0.05
Proteobacteria	Steroidobacter	0.00	0.05	0.05
Proteobacteria	f__Bradyrhizobiaceae_HE576382	0.03	0.03	0.04
Saccharibacteria	p__Saccharibacteria_KF771444	0.08	0.00	0.03
Actinobacteria	Micropruina	0.04	0.03	0.03
Firmicutes	Fusicatenibacter	0.09	0.00	0.01
Proteobacteria	f__Comamonadaceae_JX402118	0.00	0.02	0.08
Proteobacteria	Zymomonas	0.01	0.06	0.03
Actinobacteria	f__Microthricaceae_EU104265	0.00	0.07	0.03
Proteobacteria	f__Comamonadaceae_KF441631	0.01	0.02	0.07
Firmicutes	Catenibacterium	0.09	0.01	0.00
Bacteroidetes	G35_D8	0.03	0.05	0.01
Chlamydiae	Candidatus Protochlamydia	0.03	0.05	0.01
Proteobacteria	o__Oligoflexales_JN038860	0.03	0.05	0.01
Bacteroidetes	f__Chitinophagaceae_HM129278	0.00	0.00	0.09
Bacteroidetes	f__NS11-12 marine group_HM921142	0.00	0.00	0.09
Unassigned	Unassigned; novel OTU55	0.00	0.00	0.09
Unassigned	Unassigned; novel OTU706	0.00	0.00	0.09
Proteobacteria	f__Comamonadaceae_JX966536	0.01	0.08	0.00
Proteobacteria	Phreatobacter	0.02	0.03	0.04
Gracilibacteria	p__Gracilibacteria_HQ860703	0.00	0.09	0.00
Proteobacteria	Uruburuella	0.01	0.04	0.04
Proteobacteria	f__Comamonadaceae_KM016257	0.00	0.05	0.04
Proteobacteria	FukuS110	0.00	0.05	0.04
Saccharibacteria	p__Saccharibacteria_LN561157	0.00	0.05	0.04
Firmicutes	Dorea	0.03	0.03	0.03
Proteobacteria	Haematobacter	0.03	0.03	0.03
Proteobacteria	f__Comamonadaceae_JQ323104	0.00	0.01	0.08
Actinobacteria	f__Propionibacteriaceae_EU104308	0.02	0.04	0.03
Proteobacteria	Hirschia	0.00	0.06	0.03
Actinobacteria	f__Microthricaceae_HM007549	0.00	0.07	0.01
Proteobacteria	Sphingomonas	0.00	0.07	0.01
Chloroflexi	f__Anaerolineaceae_CU466712	0.00	0.03	0.05
Proteobacteria	Thauera	0.00	0.03	0.05
Chloroflexi	Kouleothrix	0.01	0.07	0.00
Saccharibacteria	p__Saccharibacteria_AF507686	0.01	0.07	0.00
Proteobacteria	f__Comamonadaceae_AF508103	0.01	0.03	0.04
Actinobacteria	Actinomyces	0.05	0.00	0.03
Bacteroidetes	f__Draconibacteriaceae_FN824888	0.00	0.04	0.04
Unassigned	Unassigned; novel OTU73	0.00	0.04	0.04
Verrucomicrobia	f__Verrucomicrobiaceae_novel OTU38	0.03	0.02	0.03
Bacteroidetes	Phaeodactylibacter	0.00	0.00	0.08
Unassigned	Unassigned; novel OTU67	0.00	0.00	0.08
Proteobacteria	f__mle1-27_novel OTU26	0.00	0.00	0.08
Proteobacteria	f__Moraxellaceae_KF891388	0.00	0.00	0.08
Fusobacteria	f__Leptotrichiaceae_JX040374	0.02	0.03	0.03
Cyanobacteria	c__ML635J-21_novel OTU39	0.01	0.04	0.03
Atribacteria	HAW-R60	0.05	0.01	0.01
Bacteroidetes	f__Saprospiraceae_novel OTU27	0.00	0.05	0.03

Proteobacteria	Limnohabitans	0.04	0.02	0.01
Proteobacteria	f__Comamonadaceae_JQ724322	0.03	0.03	0.01
Proteobacteria	o__Myxococcales_KJ783121	0.00	0.01	0.07
Actinobacteria	Aeromicrobium	0.08	0.00	0.00
Unassigned	Unassigned; novel OTU71	0.08	0.00	0.00
Proteobacteria	f__Burkholderiaceae_LN569635	0.01	0.05	0.01
Actinobacteria	Austwickia	0.00	0.06	0.01
Firmicutes	f__Acidaminococcaceae_GQ406188	0.00	0.06	0.01
Acidobacteria	Bryobacter	0.00	0.02	0.05
Bacteroidetes	f__Chitinophagaceae_JN609315	0.00	0.02	0.05
Proteobacteria	o__DB1-14_AB473970	0.00	0.02	0.05
Saccharibacteria	p__Saccharibacteria_EU104273	0.01	0.06	0.00
Verrucomicrobia	f__FukuN18 freshwater group_AB630657	0.02	0.01	0.04
Unassigned	Unassigned; novel OTU79	0.00	0.07	0.00
Bacteroidetes	Microbacter	0.00	0.03	0.04
Proteobacteria	f__7B-8_JN245869	0.00	0.03	0.04
Proteobacteria	f__Bradyrhizobiaceae_JQ923574	0.01	0.03	0.03
Proteobacteria	32C6	0.00	0.04	0.03
Proteobacteria	f__Comamonadaceae_FQ658779	0.00	0.04	0.03
Proteobacteria	Limnobacter	0.00	0.04	0.03
Proteobacteria	Piscinibacter	0.00	0.04	0.03
Actinobacteria	f__Propionibacteriaceae_FR874241	0.04	0.01	0.01
Proteobacteria	f__Alcaligenaceae_novel OTU82	0.03	0.02	0.01
Bacteroidetes	f__Chitinophagaceae_EU104008	0.00	0.00	0.07
Firmicutes	f__MBA03_EF585997	0.00	0.00	0.07
Unassigned	Unassigned; novel OTU41	0.00	0.00	0.07
Unassigned	Unassigned; novel OTU599	0.00	0.00	0.07
Unassigned	Unassigned; novel OTU62	0.00	0.00	0.07
Proteobacteria	f__Rhodocyclaceae_GX154053	0.00	0.00	0.07
Proteobacteria	f__Rickettsiaceae_novel OTU347	0.00	0.00	0.07
Unassigned	Unassigned; novel OTU30	0.02	0.03	0.01
Proteobacteria	Pseudorhodoferax	0.02	0.03	0.01
Verrucomicrobia	f__Verrucomicrobiaceae_HM332293	0.06	0.00	0.00
Firmicutes	[Ruminococcus] gauvreauii group	0.05	0.01	0.00
Proteobacteria	f__Comamonadaceae_EF626687	0.00	0.05	0.01
Actinobacteria	Atopobium	0.04	0.02	0.00
Actinobacteria	f__Propionibacteriaceae_EF688211	0.04	0.02	0.00
Actinobacteria	Nakamurella	0.04	0.02	0.00
Firmicutes	Acidaminococcus	0.04	0.02	0.00
Firmicutes	Ruminococcaceae UCG-002	0.04	0.02	0.00
Hydrogenedentes	p__Hydrogenedentes_KJ783078	0.00	0.01	0.05
Proteobacteria	Acidocella	0.00	0.01	0.05
Proteobacteria	Denitratisoma	0.00	0.01	0.05
Proteobacteria	Rivicola	0.00	0.01	0.05
Proteobacteria	f__A0839_novel OTU14	0.02	0.04	0.00
Saccharibacteria	Candidatus Saccharimonas	0.01	0.05	0.00
Saccharibacteria	p__Saccharibacteria_AF513103	0.02	0.00	0.04
Actinobacteria	Streptomyces	0.00	0.06	0.00
Unassigned	Unassigned; novel OTU24	0.00	0.06	0.00
Unassigned	Unassigned; novel OTU58	0.00	0.06	0.00
Proteobacteria	f__Alcaligenaceae_KC189690	0.01	0.01	0.04
Actinobacteria	o__Micrococcales_AF226615	0.00	0.02	0.04
Proteobacteria	f__Neisseriaceae_CU927875	0.00	0.02	0.04
Proteobacteria	f__Sandaracinaceae_KF697431	0.00	0.02	0.04
Proteobacteria	Phaselicystis	0.00	0.02	0.04
Bacteroidetes	Chitinophaga	0.01	0.02	0.03
Proteobacteria	Xanthobacter	0.01	0.02	0.03
Bacteroidetes	f__AKYH767_CU466748	0.00	0.03	0.03
Proteobacteria	Bradyrhizobium	0.00	0.03	0.03

Proteobacteria	M05-Pitesti	0.00	0.03	0.03
Proteobacteria	o__DB1-14_novel OTU665	0.00	0.03	0.03
Proteobacteria	Ralstonia	0.00	0.03	0.03
Firmicutes	Lachnospiraceae NK3A20 group	0.04	0.00	0.01
Firmicutes	Coprococcus 3	0.03	0.01	0.01
Actinobacteria	f__Microbacteriaceae_HM265249	0.02	0.02	0.01
Firmicutes	f__Lachnospiraceae_GU559776	0.02	0.02	0.01
Proteobacteria	f__Rhodobacteraceae_AB727354	0.02	0.02	0.01
Verrucomicrobia	f__Verrucomicrobiaceae_novel OTU721	0.02	0.02	0.01
Proteobacteria	Nitrobacter	0.01	0.03	0.01
Proteobacteria	Legionella	0.05	0.00	0.00
Actinobacteria	f__Intrasporangiaceae_novel OTU60	0.00	0.04	0.01
Proteobacteria	f__Comamonadaceae_KM462134	0.00	0.04	0.01
Saccharibacteria	p__Saccharibacteria_novel OTU66	0.04	0.01	0.00
Bacteroidetes	f__Chitinophagaceae_FJ546396	0.00	0.00	0.05
Bacteroidetes	f__Chitinophagaceae_novel OTU697	0.00	0.00	0.05
Bacteroidetes	f__NS11-12 marine group_JQ072894	0.00	0.00	0.05
Bacteroidetes	o__Sphingobacteriales_HQ324879	0.00	0.00	0.05
Unassigned	Unassigned; novel OTU100	0.00	0.00	0.05
Unassigned	Unassigned; novel OTU342	0.00	0.00	0.05
Unassigned	Unassigned; novel OTU742	0.00	0.00	0.05
Miscellaneous Crenarchaeotic Group	p__Misc Crenarchaeotic Group_novel OTU579	0.00	0.00	0.05
Proteobacteria	c__Gammaproteobacteria_EU104106	0.00	0.00	0.05
Proteobacteria	Methylobacter	0.00	0.00	0.05
Firmicutes	Eubacterium	0.01	0.04	0.00
Bacteroidetes	f__Saprospiraceae_novel OTU72	0.00	0.05	0.00
Proteobacteria	f__SD04E11_FM875685	0.00	0.05	0.00
Proteobacteria	o__Oligoflexales_KJ782866	0.00	0.05	0.00
Proteobacteria	o__Oligoflexales_novel OTU15	0.00	0.05	0.00
Proteobacteria	Rhizomicrobium	0.00	0.05	0.00
Verrucomicrobia	f__Verrucomicrobiaceae_novel OTU497	0.00	0.05	0.00
Bacteroidetes	c__WCHB1-32_FR667843	0.00	0.01	0.04
Bacteroidetes	f__Saprospiraceae_EU104080	0.00	0.01	0.04
Proteobacteria	f__Comamonadaceae_HQ385603	0.00	0.01	0.04
Proteobacteria	f__Comamonadaceae_KF441660	0.00	0.01	0.04
Proteobacteria	Paucimonas	0.00	0.01	0.04
Proteobacteria	Propionivibrio	0.00	0.01	0.04
Bacteroidetes	f__Chitinophagaceae_novel OTU807	0.00	0.02	0.03
Bacteroidetes	f__env.OPS 17_JQ941821	0.00	0.02	0.03
Cyanobacteria	c__ML635J-21_novel OTU178	0.00	0.02	0.03
Unassigned	Unassigned; novel OTU817	0.00	0.02	0.03
Proteobacteria	f__Comamonadaceae_HE993549	0.00	0.02	0.03
Proteobacteria	f__Comamonadaceae_HQ232436	0.00	0.02	0.03
Proteobacteria	f__Rhodobacteraceae_HM129109	0.00	0.02	0.03
Actinobacteria	Phycicoccus	0.03	0.00	0.01
Chloroflexi	o__JG30-KF-CM45_JQ624352	0.03	0.00	0.01
Firmicutes	Acetobacterium	0.03	0.00	0.01
Firmicutes	Ruminococcaceae UCG-013	0.03	0.00	0.01
Unassigned	Unassigned; novel OTU11	0.03	0.00	0.01
Chloroflexi	o__JG30-KF-CM45_HM316086	0.02	0.01	0.01
Firmicutes	Coprothermobacter	0.02	0.01	0.01
Proteobacteria	Methylocapsa	0.02	0.01	0.01
Verrucomicrobia	Verrucomicrobium	0.02	0.01	0.01
Proteobacteria	Methylobacterium	0.01	0.02	0.01
Actinobacteria	Actinotignum	0.00	0.03	0.01
Firmicutes	Veillonella	0.00	0.03	0.01
Gracilibacteria	p__Gracilibacteria_HQ860702	0.00	0.03	0.01
Proteobacteria	f__Comamonadaceae_AB200293	0.00	0.03	0.01
Verrucomicrobia	f__Verrucomicrobiaceae_HQ118308	0.00	0.03	0.01

Actinobacteria	o__Micrococcales_CU925140	0.03	0.01	0.00
Firmicutes	Enterococcus	0.03	0.01	0.00
Firmicutes	o__Selenomonadales_AB806235	0.03	0.01	0.00
Proteobacteria	Tabrizicola	0.03	0.01	0.00
Firmicutes	Megasphaera	0.02	0.02	0.00
Verrucomicrobia	f__Verrucomicrobiaceae_KF071300	0.02	0.02	0.00
Actinobacteria	Tessaracoccus	0.01	0.03	0.00
Proteobacteria	Nitratireductor	0.01	0.03	0.00
Proteobacteria	o__Oligoflexales_novel OTU591	0.01	0.03	0.00
Proteobacteria	Rhizobacter	0.01	0.03	0.00
Verrucomicrobia	Akkermansia	0.01	0.03	0.00
Verrucomicrobia	f__Verrucomicrobiaceae_HM329157	0.01	0.03	0.00
Actinobacteria	f__Microthricaceae_AY743693	0.00	0.04	0.00
Bacteroidetes	f__Cytophagaceae_novel OTU76	0.00	0.04	0.00
Unassigned	Unassigned; novel OTU51	0.00	0.04	0.00
Unassigned	Unassigned; novel OTU57	0.00	0.04	0.00
Unassigned	Unassigned; novel OTU585	0.00	0.04	0.00
Bacteroidetes	c__WCHB1-32_JQ723616	0.00	0.00	0.04
Bacteroidetes	Cytophaga	0.00	0.00	0.04
Bacteroidetes	f__Chitinophagaceae_novel OTU19	0.00	0.00	0.04
Bacteroidetes	f__Chitinophagaceae_novel OTU74	0.00	0.00	0.04
Bacteroidetes	f__Draconibacteriaceae_KM410485	0.00	0.00	0.04
Bacteroidetes	f__NS11-12 marine group_FJ546404	0.00	0.00	0.04
Bacteroidetes	Rikenellaceae RC9 gut group	0.00	0.00	0.04
Chlamydiae	o__Chlamydiales_novel OTU343	0.00	0.00	0.04
Firmicutes	Anaerosinus	0.00	0.00	0.04
Fusobacteria	f__Leptotrichiaceae_KC432497	0.00	0.00	0.04
Gracilibacteria	p__Gracilibacteria_novel OTU107	0.00	0.00	0.04
Unassigned	Unassigned; novel OTU21	0.00	0.00	0.04
Unassigned	Unassigned; novel OTU40	0.00	0.00	0.04
Unassigned	Unassigned; novel OTU54	0.00	0.00	0.04
Unassigned	Unassigned; novel OTU81	0.00	0.00	0.04
Unassigned	Unassigned; novel OTU86	0.00	0.00	0.04
Parcubacteria	p__Parcubacteria_novel OTU811	0.00	0.00	0.04
Proteobacteria	Alkanindiges	0.00	0.00	0.04
Proteobacteria	Desulfomicrobium	0.00	0.00	0.04
Proteobacteria	f__mle1-27_AB286342	0.00	0.00	0.04
Proteobacteria	f__Rhodocyclaceae_AF245350	0.00	0.00	0.04
Proteobacteria	f__TK34_novel OTU175	0.00	0.00	0.04
Proteobacteria	o__DB1-14_novel OTU1084	0.00	0.00	0.04
Proteobacteria	Sphaerotilus	0.00	0.00	0.04
Saccharibacteria	p__Saccharibacteria_JQ191024	0.00	0.00	0.04
Candidate division SR1	p__Candidate division SR1_JF917292	0.01	0.00	0.03
Firmicutes	A55_D21	0.01	0.00	0.03
Proteobacteria	f__Comamonadaceae_HQ462550	0.01	0.00	0.03
Saccharibacteria	p__Saccharibacteria_HQ132439	0.01	0.00	0.03
Bacteroidetes	c__WCHB1-32_FM204957	0.00	0.01	0.03
Bacteroidetes	c__WCHB1-32_HM141872	0.00	0.01	0.03
Bacteroidetes	Emticicia	0.00	0.01	0.03
Firmicutes	Phascolarctobacterium	0.00	0.01	0.03
Proteobacteria	f__Comamonadaceae_DQ104935	0.00	0.01	0.03
Proteobacteria	f__Moraxellaceae_novel OTU78	0.00	0.01	0.03
Proteobacteria	f__SM2D12_HM278276	0.00	0.01	0.03
Saccharibacteria	p__Saccharibacteria_KM046964	0.00	0.01	0.03
SHA-109	p__SHA-109_KJ783033	0.00	0.01	0.03
Actinobacteria	f__Actinomycetaceae_HM008736	0.02	0.00	0.01
Proteobacteria	Aminobacter	0.02	0.00	0.01
Proteobacteria	f__Beijerinckiaceae_KJ191883	0.02	0.00	0.01
Proteobacteria	f__Rhodospirillaceae_novel OTU350	0.02	0.00	0.01

Saccharibacteria	p__Saccharibacteria_novel OTU888	0.02	0.00	0.01
Proteobacteria	f__Rhodocyclaceae_LN569631	0.01	0.01	0.01
Saccharibacteria	p__Saccharibacteria_novel OTU954	0.01	0.01	0.01
Actinobacteria	o__Acidimicrobiales_novel OTU159	0.00	0.02	0.01
Bacteroidetes	f__LiUU-11-161_AY509379	0.00	0.02	0.01
Firmicutes	f__Syntrophomonadaceae_EF559046	0.00	0.02	0.01
Fusobacteria	Sebaldella	0.00	0.02	0.01
Proteobacteria	f__A0839_JQ318951	0.00	0.02	0.01
Proteobacteria	o__Sphingomonadales_JQ408099	0.00	0.02	0.01
Proteobacteria	Rubellimicrobium	0.00	0.02	0.01
Proteobacteria	sipK9	0.00	0.02	0.01
Actinobacteria	f__Actinomycetaceae_FJ542912	0.03	0.00	0.00
Actinobacteria	Luteococcus	0.03	0.00	0.00
Chloroflexi	o__JG30-KF-CM45_CU920279	0.03	0.00	0.00
Planctomycetes	f__Planctomycetaceae_FN436058	0.03	0.00	0.00
Proteobacteria	Rhodovarius	0.03	0.00	0.00
Saccharibacteria	p__Saccharibacteria_CU466685	0.03	0.00	0.00
Firmicutes	[Eubacterium] hallii group	0.02	0.01	0.00
Firmicutes	f__Lachnospiraceae_novel OTU110	0.02	0.01	0.00
Firmicutes	Ruminococcaceae NK4A214 group	0.02	0.01	0.00
Proteobacteria	f__Bradyrhizobiaceae_AB486220	0.02	0.01	0.00
Actinobacteria	f__Nocardioidaceae_AB166779	0.01	0.02	0.00
Bacteroidetes	Flavisolibacter	0.01	0.02	0.00
Proteobacteria	f__Comamonadaceae_JX971553	0.01	0.02	0.00
Proteobacteria	MWH-UniP1 aquatic group	0.01	0.02	0.00
Saccharibacteria	p__Saccharibacteria_AF268998	0.01	0.02	0.00
Saccharibacteria	p__Saccharibacteria_novel OTU864	0.01	0.02	0.00
Bacteroidetes	f__Chitinophagaceae_AJ575722	0.00	0.03	0.00
Bacteroidetes	f__env.OPS 17_JN090811	0.00	0.03	0.00
Firmicutes	f__Lachnospiraceae_HM445969	0.00	0.03	0.00
Unassigned	Unassigned; novel OTU447	0.00	0.03	0.00
Unassigned	Unassigned; novel OTU75	0.00	0.03	0.00
Planctomycetes	Singulisphaera	0.00	0.03	0.00
Proteobacteria	c__TA18_novel OTU202	0.00	0.03	0.00
Proteobacteria	f__Rhodobacteraceae_KC189683	0.00	0.03	0.00
Proteobacteria	f__Rhodocyclaceae_GQ844369	0.00	0.03	0.00
Proteobacteria	f__Sphingomonadaceae_HQ436496	0.00	0.03	0.00
Proteobacteria	o__NKB5_EU335403	0.00	0.03	0.00
Proteobacteria	o__Oligoflexales_novel OTU84	0.00	0.03	0.00
Proteobacteria	o__Xanthomonadales_LN570602	0.00	0.03	0.00
Saccharibacteria	p__Saccharibacteria_novel OTU391	0.00	0.03	0.00
Saccharibacteria	p__Saccharibacteria_novel OTU43	0.00	0.03	0.00
Verrucomicrobia	f__Verrucomicrobiaceae_AB247484	0.00	0.03	0.00
Actinobacteria	Brooklawnia	0.00	0.00	0.03
Actinobacteria	o__Frankiales_GQ017242	0.00	0.00	0.03
Actinobacteria	Rhodococcus	0.00	0.00	0.03
Bacteroidetes	Bacteroides	0.00	0.00	0.03
Bacteroidetes	Bergeyella	0.00	0.00	0.03
Bacteroidetes	c__WCHB1-32_FQ660068	0.00	0.00	0.03
Bacteroidetes	f__Chitinophagaceae_JN541148	0.00	0.00	0.03
Bacteroidetes	f__Chitinophagaceae_LK392925	0.00	0.00	0.03
Bacteroidetes	f__Chitinophagaceae_novel OTU261	0.00	0.00	0.03
Bacteroidetes	f__Chitinophagaceae_novel OTU529	0.00	0.00	0.03
Bacteroidetes	f__Chitinophagaceae_novel OTU948	0.00	0.00	0.03
Bacteroidetes	f__env.OPS 17_novel OTU943	0.00	0.00	0.03
Bacteroidetes	f__WCHB1-69_novel OTU494	0.00	0.00	0.03
Fibrobacteres	f__Fibrobacteraceae_novel OTU259	0.00	0.00	0.03
Firmicutes	Acetoanaerobium	0.00	0.00	0.03
Firmicutes	Bacillus	0.00	0.00	0.03

Firmicutes	f__Lachnospiraceae_JX000043	0.00	0.00	0.03
Firmicutes	Fastidiosipila	0.00	0.00	0.03
Firmicutes	Oscillibacter	0.00	0.00	0.03
Firmicutes	Proteiniclasticum	0.00	0.00	0.03
Firmicutes	Ruminococcaceae UCG-014	0.00	0.00	0.03
Hydrogenedentes	p__Hydrogenedentes_FM213068	0.00	0.00	0.03
Unassigned	Unassigned; novel OTU221	0.00	0.00	0.03
Unassigned	Unassigned; novel OTU323	0.00	0.00	0.03
Unassigned	Unassigned; novel OTU45	0.00	0.00	0.03
Unassigned	Unassigned; novel OTU70	0.00	0.00	0.03
Parcubacteria	p__Parcubacteria_JX105635	0.00	0.00	0.03
Proteobacteria	c__SPOTSOCT00m83_JF703353	0.00	0.00	0.03
Proteobacteria	f__Comamonadaceae_AB672262	0.00	0.00	0.03
Proteobacteria	f__Comamonadaceae_GQ008889	0.00	0.00	0.03
Proteobacteria	f__Comamonadaceae_JF681702	0.00	0.00	0.03
Proteobacteria	f__Comamonadaceae_JN128637	0.00	0.00	0.03
Proteobacteria	f__Comamonadaceae_KC286830	0.00	0.00	0.03
Proteobacteria	f__Comamonadaceae_KM035965	0.00	0.00	0.03
Proteobacteria	f__Competibacteraceae_novel OTU698	0.00	0.00	0.03
Proteobacteria	f__Competibacteraceae_novel OTU833	0.00	0.00	0.03
Proteobacteria	f__mle1-27_novel OTU642	0.00	0.00	0.03
Proteobacteria	f__Rhodobacteraceae_CU922876	0.00	0.00	0.03
Proteobacteria	f__Rhodocyclaceae_KC357950	0.00	0.00	0.03
Proteobacteria	f__Rhodospirillaceae_KC551763	0.00	0.00	0.03
Proteobacteria	o__B1-7BS_EU104237	0.00	0.00	0.03
Proteobacteria	Rickettsia	0.00	0.00	0.03
Saccharibacteria	p__Saccharibacteria_EU104337	0.00	0.00	0.03
Saccharibacteria	p__Saccharibacteria_novel OTU1037	0.00	0.00	0.03
Spirochaetae	Turneriella	0.00	0.00	0.03
Actinobacteria	Actinobaculum	0.01	0.00	0.01
Bacteroidetes	f__Chitinophagaceae_EU177675	0.01	0.00	0.01
Firmicutes	Erysipelotrichaceae UCG-003	0.01	0.00	0.01
Firmicutes	f__Family XI_HE650065	0.01	0.00	0.01
Firmicutes	Leuconostoc	0.01	0.00	0.01
Firmicutes	Vagococcus	0.01	0.00	0.01
Unassigned	Unassigned; novel OTU827	0.01	0.00	0.01
Proteobacteria	Citrobacter	0.01	0.00	0.01
Proteobacteria	f__A0839_AF236002	0.01	0.00	0.01
Proteobacteria	f__Rhodobacteraceae_GQ452286	0.01	0.00	0.01
Synergistetes	f__Synergistaceae_FJ375444	0.01	0.00	0.01
Actinobacteria	Olsenella	0.00	0.01	0.01
Bacteroidetes	f__Chitinophagaceae_LN560252	0.00	0.01	0.01
Bacteroidetes	f__Saprospiraceae_HQ827970	0.00	0.01	0.01
Bacteroidetes	f__WCHB1-69_KM410799	0.00	0.01	0.01
Bacteroidetes	f__WCHB1-69_novel OTU874	0.00	0.01	0.01
Firmicutes	[Anaerorhabdus] furcosa group	0.00	0.01	0.01
Firmicutes	Family XIII AD3011 group	0.00	0.01	0.01
Firmicutes	Propionispira	0.00	0.01	0.01
Fusobacteria	Leptotrichia	0.00	0.01	0.01
Planctomycetes	c__vadinHA49_APMI01149768	0.00	0.01	0.01
Proteobacteria	Candidatus Odyssella	0.00	0.01	0.01
Proteobacteria	Curvibacter	0.00	0.01	0.01
Proteobacteria	Escherichia-Shigella	0.00	0.01	0.01
Proteobacteria	f__Comamonadaceae_AB516154	0.00	0.01	0.01
Proteobacteria	f__Comamonadaceae_AF143840	0.00	0.01	0.01
Proteobacteria	f__Comamonadaceae_GQ096191	0.00	0.01	0.01
Proteobacteria	f__Comamonadaceae_KC527620	0.00	0.01	0.01
Proteobacteria	f__Neisseriaceae_AY426973	0.00	0.01	0.01
Proteobacteria	f__Neisseriaceae_JF830238	0.00	0.01	0.01

Proteobacteria	f__Rhodocyclaceae_KC331484	0.00	0.01	0.01
Proteobacteria	Lampropedia	0.00	0.01	0.01
Proteobacteria	o__DB1-14_JF203592	0.00	0.01	0.01
Proteobacteria	o__DB1-14_novel OTU1006	0.00	0.01	0.01
Proteobacteria	o__DB1-14_novel OTU1080	0.00	0.01	0.01
Proteobacteria	o__Oligoflexales_novel OTU479	0.00	0.01	0.01
Proteobacteria	Sulfurospirillum	0.00	0.01	0.01
Saccharibacteria	p__Saccharibacteria_GQ023532	0.00	0.01	0.01
Saccharibacteria	p__Saccharibacteria_novel OTU324	0.00	0.01	0.01
Saccharibacteria	p__Saccharibacteria_novel OTU393	0.00	0.01	0.01
Saccharibacteria	p__Saccharibacteria_novel OTU69	0.00	0.01	0.01
Actinobacteria	f__Coriobacteriaceae_novel OTU64	0.02	0.00	0.00
Euryarchaeota	Methanobacterium	0.02	0.00	0.00
Firmicutes	Dialister	0.02	0.00	0.00
Saccharibacteria	p__Saccharibacteria_novel OTU505	0.02	0.00	0.00
Tenericutes	o__Mollicutes RF9_EU843501	0.02	0.00	0.00
Actinobacteria	f__Intrasporangiaceae_EU090713	0.01	0.01	0.00
Actinobacteria	Senegalimassilia	0.01	0.01	0.00
Euryarchaeota	Methanosphaera	0.01	0.01	0.00
Firmicutes	Turicibacter	0.01	0.01	0.00
Unassigned	Unassigned; novel OTU375	0.01	0.01	0.00
Proteobacteria	o__Rhizobiales_novel OTU222	0.01	0.01	0.00
Saccharibacteria	p__Saccharibacteria_HM262797	0.01	0.01	0.00
Saccharibacteria	p__Saccharibacteria_LN561154	0.01	0.01	0.00
Saccharibacteria	p__Saccharibacteria_novel OTU392	0.01	0.01	0.00
Saccharibacteria	p__Saccharibacteria_novel OTU918	0.01	0.01	0.00
Verrucomicrobia	f__Verrucomicrobiaceae_KC189674	0.01	0.01	0.00
Verrucomicrobia	f__Verrucomicrobiaceae_novel OTU764	0.01	0.01	0.00
Actinobacteria	f__Kineosporiaceae_HM036657	0.00	0.02	0.00
Actinobacteria	f__Microbacteriaceae_FJ542898	0.00	0.02	0.00
Actinobacteria	f__Microbacteriaceae_HF562460	0.00	0.02	0.00
Actinobacteria	o__Micrococcales_EU009865	0.00	0.02	0.00
Actinobacteria	Paraeggerthella	0.00	0.02	0.00
Armatimonadetes	p__Armatimonadetes_novel OTU351	0.00	0.02	0.00
Armatimonadetes	p__Armatimonadetes_novel OTU498	0.00	0.02	0.00
Bacteroidetes	f__Chitinophagaceae_KJ783211	0.00	0.02	0.00
Bacteroidetes	f__Draconibacteriaceae_AY133094	0.00	0.02	0.00
Bacteroidetes	f__Saprospiraceae_KC551756	0.00	0.02	0.00
Candidate division SR1	p__Candidate division SR1_novel OTU627	0.00	0.02	0.00
Candidate division WS6	p__Candidate division WS6_FJ710710	0.00	0.02	0.00
Chloroflexi	f__Caldilineaceae_HQ014651	0.00	0.02	0.00
Cyanobacteria	c__ML635J-21_HJ352604	0.00	0.02	0.00
Euryarchaeota	Methanosaeta	0.00	0.02	0.00
Firmicutes	Anaerococcus	0.00	0.02	0.00
Firmicutes	f__Lachnospiraceae_JQ085718	0.00	0.02	0.00
Gracilibacteria	p__Gracilibacteria_novel OTU622	0.00	0.02	0.00
Unassigned	Unassigned; novel OTU205	0.00	0.02	0.00
Unassigned	Unassigned; novel OTU605	0.00	0.02	0.00
Unassigned	Unassigned; novel OTU606	0.00	0.02	0.00
Unassigned	Unassigned; novel OTU704	0.00	0.02	0.00
Unassigned	Unassigned; novel OTU762	0.00	0.02	0.00
Lentisphaerae	c__PBS-III-20_KM410683	0.00	0.02	0.00
Proteobacteria	Bauldia	0.00	0.02	0.00
Proteobacteria	Candidatus Accumulimonas	0.00	0.02	0.00
Proteobacteria	CPB_CS1	0.00	0.02	0.00
Proteobacteria	f__A0839_HQ433565	0.00	0.02	0.00
Proteobacteria	f__Alcaligenaceae_EF205485	0.00	0.02	0.00
Proteobacteria	f__Beijerinckiaceae_AB690775	0.00	0.02	0.00
Proteobacteria	f__Comamonadaceae_AB672263	0.00	0.02	0.00

Proteobacteria	f__Comamonadaceae_AR381565	0.00	0.02	0.00
Proteobacteria	f__Enterobacteriaceae_KM502221	0.00	0.02	0.00
Proteobacteria	f__Hyphomicrobiaceae_FJ375431	0.00	0.02	0.00
Proteobacteria	f__Methylocystaceae_AB930786	0.00	0.02	0.00
Proteobacteria	f__mle1-27_novel OTU403	0.00	0.02	0.00
Proteobacteria	f__Neisseriaceae_GU199448	0.00	0.02	0.00
Proteobacteria	f__Rhizobiaceae_HQ728398	0.00	0.02	0.00
Proteobacteria	f__Rhodobacteraceae_KC683279	0.00	0.02	0.00
Proteobacteria	f__Rhodobacteraceae_novel OTU101	0.00	0.02	0.00
Proteobacteria	f__Rhodocyclaceae_JN391964	0.00	0.02	0.00
Proteobacteria	f__Rhodospirillaceae_novel OTU537	0.00	0.02	0.00
Proteobacteria	f__Xanthomonadaceae_EF540404	0.00	0.02	0.00
Proteobacteria	Falsirhodobacter	0.00	0.02	0.00
Proteobacteria	Methylophilus	0.00	0.02	0.00
Proteobacteria	mle1-27	0.00	0.02	0.00
Proteobacteria	o__DB1-14_KF963646	0.00	0.02	0.00
Proteobacteria	o__DB1-14_LK392860	0.00	0.02	0.00
Proteobacteria	o__DB1-14_novel OTU117	0.00	0.02	0.00
Proteobacteria	o__Oligoflexales_EU556982	0.00	0.02	0.00
Proteobacteria	o__Oligoflexales_GU444087	0.00	0.02	0.00
Proteobacteria	o__Oligoflexales_novel OTU188	0.00	0.02	0.00
Proteobacteria	o__Oligoflexales_novel OTU29	0.00	0.02	0.00
Proteobacteria	o__Oligoflexales_novel OTU592	0.00	0.02	0.00
Proteobacteria	o__Rhizobiales_novel OTU296	0.00	0.02	0.00
Proteobacteria	o__Rickettsiales_novel OTU349	0.00	0.02	0.00
Proteobacteria	Ramlibacter	0.00	0.02	0.00
Proteobacteria	Stella	0.00	0.02	0.00
Proteobacteria	Tolumonas	0.00	0.02	0.00
Saccharibacteria	p__Saccharibacteria_JF139710	0.00	0.02	0.00
Saccharibacteria	p__Saccharibacteria_KJ783132	0.00	0.02	0.00
Saccharibacteria	p__Saccharibacteria_novel OTU489	0.00	0.02	0.00
SAR	Conthreep	0.00	0.02	0.00
Verrucomicrobia	f__01D2Z36_JN437836	0.00	0.02	0.00
Verrucomicrobia	f__Verrucomicrobiaceae_HM186036	0.00	0.02	0.00
Verrucomicrobia	f__Verrucomicrobiaceae_novel OTU841	0.00	0.02	0.00
Cyanobacteria	c__ML635J-21_AB354619	0.00	0.00	0.01
Gracilibacteria	p__Gracilibacteria_JQ624257	0.00	0.00	0.01
Unassigned	Unassigned; novel OTU563	0.00	0.00	0.01
Unassigned	Unassigned; novel OTU790	0.00	0.00	0.01
Proteobacteria	Aquicella	0.00	0.00	0.01
Proteobacteria	f__Rhodocyclaceae_KF956466	0.00	0.00	0.01
Proteobacteria	Thalassospira	0.00	0.00	0.01
Proteobacteria	Uliginosibacterium	0.00	0.00	0.01
Proteobacteria	Undibacterium	0.00	0.00	0.01
Firmicutes	Saccharofermentans	0.01	0.00	0.00
Unassigned	Unassigned; novel OTU724	0.01	0.00	0.00
Saccharibacteria	p__Saccharibacteria_novel OTU390	0.01	0.00	0.00
Bacteroidetes	Terrimonas	0.00	0.01	0.00
Unassigned	Unassigned; novel OTU576	0.00	0.01	0.00
Proteobacteria	Bacteriovorax	0.00	0.01	0.00
Proteobacteria	f__Comamonadaceae_JN656871	0.00	0.01	0.00
Saccharibacteria	p__Saccharibacteria_novel OTU964	0.00	0.01	0.00

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