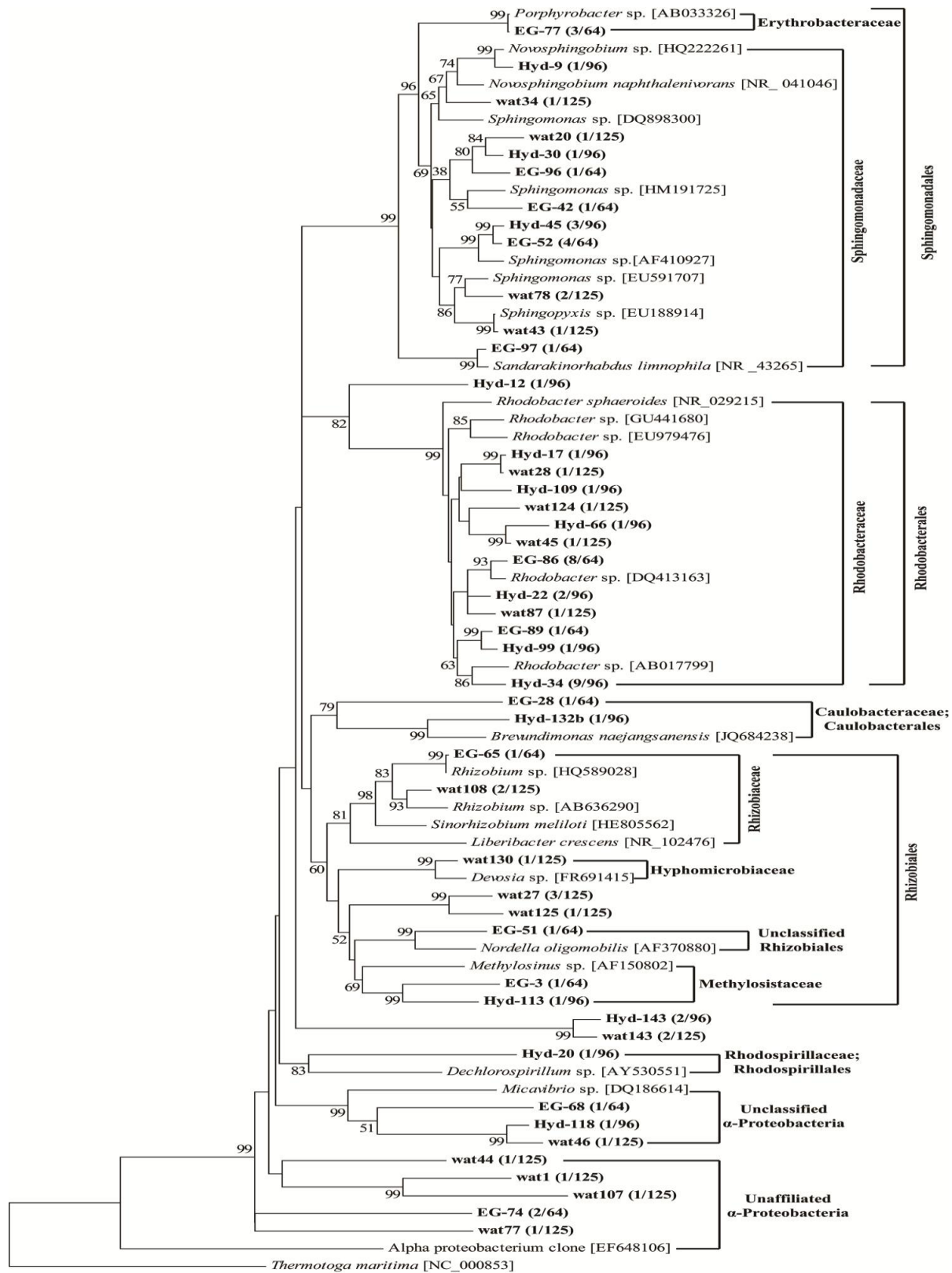


SUPPLEMENTARY MATERIAL

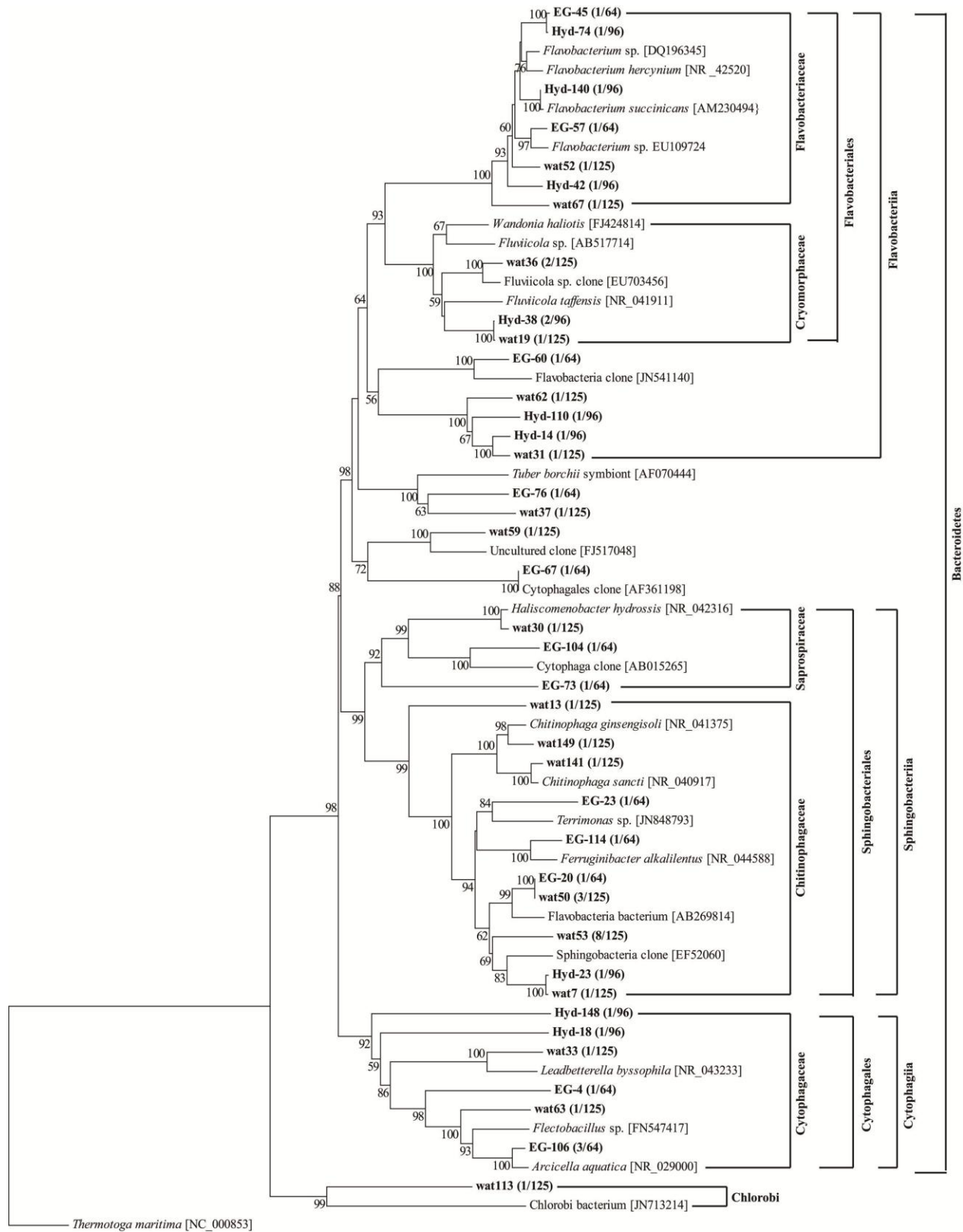
Gordon-Bradley *et al.*, submitted to “Microbes and Environments”



Supplemental Figure S1 Phylogenetic tree of the PCR-amplified 16S rRNA gene (in bold) (c. 1390 bp) of the α -Proteobacteria in the water column and the two plant (*Hydrilla* and eelgrass) libraries of Wakulla Spring, based on the neighbour-joining method as determined by distance Jukes-Cantor analysis. One thousand bootstrap analyses (distance) were conducted and percentages $\geq 50\%$ is indicated at nodes. Clones (bold letters) that have $\geq 97\%$ similar nucleic acid sequences within each sampling site are represented by a single sequence (OTU), with the number of clones out of the total in parentheses. The numbers in brackets are GenBank accession numbers. Scale bar represents 2% estimated distance



Supplemental Figure S2 Phylogenetic tree of the PCR-amplified 16S rRNA gene OTUs (in bold) (c. 1390 bp) of the β -, γ - and δ -Proteobacteria in the water column and the two plant (*Hydrilla* and eelgrass) libraries of Wakulla Spring, based on the neighbour-joining method as determined by distance Jukes-Cantor analysis. Numbers of identical ($\geq 97\%$ sequence similarity) OTUs of the total number OTUs found in each station are shown in parentheses. One thousand bootstrap analyses (distance) were conducted and percentages $\geq 50\%$ is indicated at nodes. Numbers in brackets are GenBank accession numbers. Scale bar represents 2% estimated distance.



Supplemental Figure S3 Phylogenetic tree of the PCR-amplified 16S rRNA gene OTUs (in bold) (c. 1390 bp) of the Bacteroidetes/Chlorobi group in the water column and the two plants (*Hydrilla* and eelgrass) libraries of Wakulla Spring, based on the neighbour-joining method as determined by distance Jukes-Cantor analysis. Numbers of identical ($\geq 97\%$ sequence similarity) OTUs of the total number OTUs found in each station are shown in parentheses. One thousand bootstrap analyses (distance) were conducted and percentages $\geq 50\%$ is indicated at nodes. Numbers in brackets are GenBank accession numbers. Scale bar represents 2% estimated distance.



0.02

Supplemental Figure S4 Phylogenetic tree of the PCR-amplified 16S rRNA gene OTUs (in bold) (c. 1390 bp) of the rest of the retrieved OTUs in the water column and the two plants (*Hydrilla* and eelgrass) libraries of Wakulla Spring, based on the neighbour-joining method as determined by distance Jukes-Cantor analysis. Numbers of identical ($\geq 97\%$ sequence similarity) OTUs of the total number phlotypes found in each station are shown in parentheses. One thousand bootstrap analyses (distance) were conducted and percentages $\geq 50\%$ is indicated at nodes. Numbers in brackets are GenBank accession numbers. Scale bar represents 2% estimated distance.

Supplemental Table S1 Occurrence of bacterial OTUs in the water column and the two plants (*Hydrilla* and eelgrass) libraries of Wakulla Spring

<i>Phylotype</i>	<i>No. of similar (≥97%) clones</i>	<i>Putative affiliation</i>	<i>Closest sequence (similarity) [GenBank accession No.]</i>	<i>Description</i>	<i>Closest organism (similarity) [GenBank accession No.]</i>
EG-3	1	Alphaproteobacteria	Clone D10_29(95.37) [EU266798]	quifer sediments	<i>Hyphomicrobium sulfonivorans</i> 25S (93.86) [AY305006]
EG-4	1	Sphingobacteriia	Clone reservoir-75 16S (87.77) [JF697456]	Stream of Dianchi Lake	<i>Flectobacillus</i> sp. WG3(87.09) [FN547417]
EG-10	1	Gammaproteobacteria	Clone V201-189(98.76) [HQ114204]	Biofilms in a vermifilter	Uncultured <i>Pseudomonadales</i> Plot18-A06(94.26) [FJ889291]
EG-16	1	Bacilli	Clone cpw3b516 (96.88) [HM921122]	Groundwater	<i>Pirellula</i> sp. Schlesner 302 (92.05) [X81942]
EG-20	1	Flavobacteriia	Clone M17-10-B17(97.51) [JQ088393]	Crude oil reservoir	<i>Flavobacterium bacterium</i> KF030 (96.05) [AB269814]
EG-22	1	Planctomycetia	Clone HDB_SIPA613 (99.32) [HM186830]	Subsurface Soil	<i>Gemmata</i> sp. Iol-6 (92.24) [GQ889466]
EG-23	1	Sphingobacteriia	Clone B193(2011) (91.17) [JF830232]	Grass carp intestine	<i>Terrimonas</i> sp. YJ03 (91.07) [JN848793]
EG-28	1	Alphaproteobacteria	Clone Dianchi-17 (98.07) [HQ324864]	Lake water	<i>Pleomorphomonas oryzae</i> F-4 (89.08) [AB159681]
EG-32	1	Planctomycetia	Clone T-29(95.99) [HQ661341]	Tingxi freshwater reservoir	<i>Pirellula</i> sp. Schlesner 302 (92.79) [X81942]
EG-35	1	Cyanobacteria	Clone Rivularia sp. MU24 UAM-305 (92.41) [EU009149]	Rock surface	<i>Calothrix</i> sp. BECID33 (92.49) [AM230683]
EG-37	1	Planctomycetia	Clone Alchichica_AQ2_1_1B_09 (97.02) [JN825597]	Microbialites in aquarium	Uncultured planctomycete QZ-J25 (93.52) [JF776925]
EG-38	1	Gammaproteobacteria	Clone 2\SC\46 (94.55) [EU340183]	Aquatic macrophytes	<i>Dokdonella</i> sp. TSY06 (90.12) [AB663505]
EG-40	1	Gammaproteobacteria	Clone JH-WH38 (98.80) [EF492925]	Soil	<i>Legionella</i> sp. OA32 (91.44) [AB058916]
EG-42	1	Alphaproteobacteria	Clone 3BR-10BB (96.62) [EU937905]	Riparian iron oxidizing biofilm	<i>Sphingomonas</i> sp. SH (95.37) [HM191725]
EG-44	1	Betaproteobacteria	Clone Leptothrix mobilis Feox-1 (96.78) [NR_026333]		<i>Leptothrix</i> sp. G6 (2012) (96.50) [JN820148]
EG-45	1	Flavobacteriia	Clone 3C003394 (97.56) [EU802008]	Chesapeake Bay, MD	<i>Flavobacterium</i> sp. MSY2 (97.16) [DQ196345]
EG-48	1	Unaffiliated	Clone MAT-CR-P3-G08 (83.51) [EU246116]	Hypersaline microbial mat	Uncultured candidate 06D2Y45 (84.61) [DQ330696]
EG-49	1	Betaproteobacteria	Clone ambient_uncontrolled-48 (98.79) [GU454909]	Anaerobic fermentation reactor	<i>Ideonella</i> sp. NS1203 (97.85) [AB636294]
EG-51	1	Alphaproteobacteria	Clone Fr1-9 (98.07) [GU208455]	Dongping Lake sediment	<i>Nordella oligomobilis</i> (92.81) [AF370880]
EG-52	4	Alphaproteobacteria	Clone ZWB4-16 (99.59) [FJ801213]	Zoige Alpine	<i>Sphingomonas</i> sp. B18

				Wetland	(97.45) [AF410927]
EG-57	1	Flavobacteriia	Clone MA-R15 (97.76) [JN038598]	Chongxi wetland soil	Flavobacterium sp. H7 (97.23) [EU109724]
EG-59	1	Cyanobacteria	Clone LI06st1 (98.62) [JF733399]	Genomic DNA	Leptolyngbya sp. FYG (92.84) [FJ933259]
EG-60	1	Flavobacteriia	Clone ASB38 (97.44) [FJ947136]	Activated sludge	Uncultured Flavobacteria CSC8 (94.36) [JN541140]
EG-61	1	Cyanobacteria	Clone EpiUMA6 (91.19) [FJ849244]	Arctic stream epilithon	Chamaesiphon subglobosus PCC 7430 (89.82) [AY170472]
EG-65	1	Alphaproteobacteria	Bacterium NTL215 (99.93) [JQ779044]	Phyllosphere	Rhizobium sp. PRNB-25 (99.93) [HQ589028]
EG-67	1	Cytophagia	Clone cuticle 2.39 (99.45) [HQ111173]	Embryonic stages	Uncultured Cytophagales 17 (99.15) [AF361198]
EG-68	1	Alphaproteobacteria	Clone 3.29h71 (95.85) [JN679095]	Membrane bioreactor	Micavibrio sp. EPC2 (88.99) [DQ186614]
EG-71	1	Actinobacteria	Clone AK4DE1_06E (93.35) [GQ397040]	Soil	Iamia sp. T2-YC6790 (92.18) [GQ369058]
EG-73	1	Sphingobacteriia	Clone 46-2_3 (93.95) [FJ517715]	Epithelium	Haliscomenobacter hydrossis DSM 1100 (84.19) [NR_042316]
EG-74	2	Alphaproteobacteria	Clone DP7.3.17 (87.08) [FJ612212]	Lake water	Ochrobactrum sp. TK14 (86.29) [AJ550273]
EG-75	1	Gammaproteobacteria	Clone HglFeb0118m2 (88.84) [JX016688]	Marine bulk water	Saccharophagus sp. Myt-1 (86.27) [AB566414]
EG-76	1	Unaffiliated	Clone 654995 (88.62) [DQ404664]	Contaminated sediment	Tuber borchii symbiont b-17BO (88.45) [AF070444]
EG-77	3	Alphaproteobacteria	Clone 6-53 (99.86) [JQ923713]	Drinking water distribution system	Porphyrobacter sp. KK351 (99.79) [AB033326]
EG-78	1	Betaproteobacteria	Clone 6'-72 (99.60) [JQ923814]	Drinking water distribution system	Herbaspirillum sp. CHNTR44 (95.46) [DQ337592]
EG-80	1	Gemmatimonadetes	Clone Kas174B (96.70) [EF203205]	Sediment	Gemmatimonas aurantiaca T-27 (95.45) [NR_027529]
EG-84	1	Gammaproteobacteria	Clone BJGMM-t-217 (97.39) [JQ801240]	Soil	Methylbium fulvum Gsoil 328 (96.97) [AB245357]
EG-86	8	Alphaproteobacteria	Clone Chun-s-2 (97.90) [EF632760]	Freshwater sediment	Rhodobacter sp. EMB 174 (97.91) [DQ413163]
EG-88	1	Betaproteobacteria	Clone MACA-EFT44 (97.39) [GQ500809]	Cave stream	Uncultured Methylothera sp. sh-xj122 (95.66) [JQ327997]
EG-89	1	Alphaproteobacteria	Clone 14-95 (99.15) [JF697347]	Stream of Dianchi Lake	Rhodobacter sp. TCRI (97.06) [AB017799]
EG-90	1	Gammaproteobacteria	Clone JN11 (98.74) [JN868991]	Lake water	Dokdonella fugitiva type A3T (92.93) [AJ969432]
EG-96	1	Alphaproteobacteria	Clone SN101 (95.99) [JQ824989]	Saline-alkali soil	Sphingomonas sp. MTR-71 (95.36) [DQ898300]
EG-97	1	Alphaproteobacteria	Clone 6-45 (99.10) [JQ923705]	Drinking water distribution system	Sandarakinorhabdus limnophila so42 (99.18) [NR_043265]

EG-104	1	Cytophagia	Uncultured Verrucomicrobia OTU-1_PBA (93.91) [JN981899]	Aerosols from orbal oxidation ditch	Uncultured Cytophaga sp. JTB251 (91.23) [AB015265]
EG-106	3	Sphingobacteriia	Uncultured Sphingobacteriales Holab_1.7 (97.47) [EF667893]	Epithelium	Arcicella aquatica NO-502 (97.51) [NR_029000]
EG-110	1	Deltaproteobacteria	Clone BN1 (88.88) [HQ190262]	Zhongyuan oil field	Uncultured Desulfocurvus sp. H-169 (85.63) [HM565023]
EG-113	1	Betaproteobacteria	Clone 61 (99.13) [FJ623322]	Aerobic sequencing batch reactor	Hydrogenophaga sp. AH-24 (98.79) [AB300163]
EG-114	1	Sphingobacteriia	Clone KWK6S.61 (95.91) [JN656817]	Thaw pond	Ferruginibacter alkalilentus HU1-GD23 (95.86) [NR_044588]
EG-117	1	Betaproteobacteria	Clone Q7346-HYSA (95.50) [JN391845]	Sludge in anoxic tank	Rubrivivax gelatinosus TUT3906 (95.11) [AB250625]
EG-119	2	Betaproteobacteria	Clone 3.29h30 (93.68) [JN679082]	Membrane bioreactor	Ralstonia solanacearum LYP (90.87) [HQ176322]
Hyd-1	1	Betaproteobacteria	Clone 2C229148 (95.06) [EU800906]	Delaware Bay, NJ	Herbaspirillum sp. G8A1 (92.75) [AJ012069]
Hyd-4	1	Gammaproteobacteria	Clone 6'-12 (99.80) [JQ923767]	Drinking water distribution system	Pseudomonas peli M-T-TSA_17 (99.58) [JQ795777]
Hyd-5	1	Unaffiliated	Clone ZR106 (90.95) [JN713458]	Oral cavity subgingival plaque	Amphiprora paludosa C52 (73.71) [FJ002240]
Hyd-6	1	Alphaproteobacteria	Clone GOM WB10-31 (84.86) [GQ250609]	Sea water column in Gulf of Mexico	Methylosinus sp. PW1 (80.84) [AF150802]
Hyd-8	1	Verrucomicrobiae	Clone C2A (96.59) [DQ856525]	Intestinal microflora in Chinese mitten crab	Uncultured Verrucomicrobiaceae B07-05G (95.36) [FJ543030]
Hyd-9	1	Alphaproteobacteria	Sphingomonas sp. YT0136 (98.76) [AB362778]	Genomic DNA	Novosphingobium sp. Van61 (97.72) [HQ222277]
Hyd-11	4	Betaproteobacteria	Clone MSB19A (98.74) [DQ069200]	SA Au mine	Methylophilus leisingeri (98.13) [AB193725]
Hyd-12	1	Alphaproteobacteria	Clone MACA-OC42 (91.52) [GQ500891]	Cave stream	Sphingomonas sp. MTR-71 (91.41) [DQ898300]
Hyd-14	1	Flavobacteriia	Clone OTU-30-AW (93.42) [JQ624271]	Wastewater treatment plant	Wandonia haliotis Haldis-1 (85.04) [FJ424814]
Hyd-17	1	Alphaproteobacteria	Clone C20 (96.08) [JQ323113]	Cooling water system	Rhodobacter sp. TCRI 14 (94.84) [AB017799]
Hyd-18	1	Sphingobacteriia	Clone SM1C08 (91.67) [AF445665]	Genomic DNA	Algoriphagus sp. KJF5-15 (83.59) [JQ800092]
Hyd-20	1	Alphaproteobacteria	Clone B1NR70D6 (97.43) [AY957891]	Drinking water biofilm	Dechlorospirillum sp. DB (86.41) [AY530551]
Hyd-22	2	Alphaproteobacteria	Clone FGL7S_B42 (97.76) [FJ437987]	Green Lake surface sediments	Rhodobacter sp. EMB 174 (97.91) [DQ413163]

Hyd-23	1	<i>Sphingobacteriia</i>	Clone ZBAF-R4 (94.18) [HQ011389]	Biofilm in a wastewater treatment	Uncultured Bacteroidetes SW11 (94.07) [AJ575719]
Hyd-30	1	<i>Alphaproteobacteria</i>	Clone BF2C07 (97.45) [JN820204]	Ferromanganese deposit	<i>Sphingomonas</i> sp. MTR-71 (96.25) [DQ898300]
Hyd-34	9	<i>Alphaproteobacteria</i>	Clone B5 (99.09) [HQ697418]	Drinking water treatment	<i>Rhodobacter</i> sp. TUT3732 (97.06) [AB251408]
Hyd-38	1	<i>Flavobacteriia</i>	Clone SGUS1259 (97.76) [FJ202110]	Montastraea faveolata kept in aquarium	<i>Fluviicola taffensis</i> DSM 16823
Hyd-41	1	<i>Armatimonadia</i>	Clone MC20 (93.20) [JN868914]	Lake water	RW262 (91.88) [NR_041911]
Hyd-42	1	<i>Flavobacteriia</i>	Clone ATB-LH-7198 (97.22) [FJ535191]	Water of carrot washing plant	<i>Armatimonas rosea</i> (92.26) [AB529679]
Hyd-43	1	<i>Betaproteobacteria</i>	Clone 3.29h30 (98.40) [JN679082]	Membrane bioreactor	<i>Flavobacterium aquatile</i> DSM 1132 (96.94) [NR_042495]
Hyd-45	2	<i>Alphaproteobacteria</i>	Clone F0813 (100) [AF235997]	Genomic DNA	<i>Denitratisoma oestradiolicum</i> AcBE2-1 (91.97) [NR_043249]
Hyd-48	2	<i>Betaproteobacteria</i>	<i>Acidovorax</i> sp. Van23 (99.26) [HQ222268]	Vanillin enrichment culture	<i>Sphingomonas</i> sp. PLS3 (97.25) [AJ620200]
Hyd-49	1	<i>Betaproteobacteria</i>	Uncultured bacterium 0317 (98.33) [AB286389]	Activated sludge	Endosymbiont of <i>Nilaparvata lugens</i> M400 (98.86) [JQ975881]
Hyd-51	1	<i>Alphaproteobacteria</i>	Clone DUP6D09 (99.64) [HQ178928]	Sediment	Uncultured Rhodocyclaceae Amb_16S_876 (94.87) [EF018601]
Hyd-56	1	<i>Betaproteobacteria</i>	Clone JS05 (98.46) [JN869110]	Lake water	<i>Sphingomonas</i> sp. HTCC500 (98.39) [AY584571]
Hyd-57	2	<i>Gammaproteobacteria</i>	Clone ncd1965g04c1 (99.41) [JF166553]	Skin, volar forearm	<i>Leptothrix</i> sp. S1.1 (97.19) [DQ241397]
Hyd-58	1	<i>Deinococci</i>	Clone Alchichica_AL31_2_1B_168 (92.41) [JN825642]	Lake	<i>Silanimonas</i> sp. AK13 (89.75) [HE573746]
Hyd-60	1	<i>Betaproteobacteria</i>	Clone 1H_31 (99.20) [AY546500]	Soda lake sediment	<i>Truepera radiovictrix</i> TU-8 (88.32) [DQ022077]
Hyd-66	1	<i>Alphaproteobacteria</i>	Clone XZXXH70 (96.28) [EU703428]	Freshwater lake	<i>Methylophilus leisingeri</i> (95.34) [AB193725]
Hyd-67	1	<i>Flavobacteriia</i>	Bacterium SH1-3 (96.17) [JQ269247]	Biofilm on antifouling paint-summer	<i>Rhodobacter</i> sp. Cr5-50 (95.18) [GU441680]
Hyd-69	1	<i>Deltaproteobacteria</i>	Clone A90 (93.24) [FJ660578]	Activated sludge	<i>Fluviicola taffensis</i> DSM 16823 (92.33) [NR_041911]
Hyd-72	1	<i>Betaproteobacteria</i>	Clone glb343c (92.85) [EU978831]	Glacier ice	Uncultured Polyangiaceae Amb_16S_1127 (90.95) [EF018495]
					Uncultured Candidatus <i>Accumulibacter</i> sp. 4.6h71 (89.08) [JN679133]

Hyd-73	1	Gammaproteobacteria	Clone B04-06F(97.56) [FJ542988]	High ergovaline treatment gut	Legionella sp. W10-070(86.21) [HE613855]
Hyd-74	1	Flavobacteriia	Clone 3C003394(97.63) [EU802008]	Chesapeake Bay, MD	Flavobacterium sp. MSY2(97.22) [DQ196345]
Hyd-78	3	Betaproteobacteria	Clone MACA-EFT44(96.67) [GQ500809]	Cave stream	Uncultured Methylothermobacter sp. sh-xj122(94.95) [JQ327997]
Hyd-79	9	Betaproteobacteria	Clone reservoir-137(99.74) [JF697518]	Stream of Dianchi Lake	Curvibacter sp. IMCC12707(98.52) [JF715440]
Hyd-81	1	Betaproteobacteria	Beta proteobacterium A1004(95.83) [AF236009]	Genomic DNA	Inhella inkyongensis IMCC1713(94.91) [NR_043920]
Hyd-82	2	Gammaproteobacteria	Cellvibrio sp. KY-YJ-1(98.66) [EF692634]	Genomic DNA	Cellvibrio fibrivorans R-4079(99.05) [NR_025420]
Hyd-83	1	Deltaproteobacteria	Clone FOOS7B_64(95.78) [EU431712]	Percolating waters	Bdellovibrio exovorans JSS(95.74) [EF687743]
Hyd-87	2	Alphaproteobacteria	Uncultured Rhizobiales bacterium Sto3-1(95.43) [AY138237]	human stomach biopsy	Prosthecomicrobium hirschii ATCC:27832(94.63) [HM037994]
Hyd-94	1	Deltaproteobacteria	Clone fjc-58(98.81) [JQ278802]	Groundwater	Chondromyces pediculatus Cm p51(92.64) [GU207875]
Hyd-97	1	Unaffiliated	Clone V201-13(91.04) [HQ114028]	Biofilms in a full-scale vermifilter	Candidate division OP10(86.73) [GQ339893]
Hyd-99	1	Alphaproteobacteria	Clone 14-95(99.15) [JF697347]	Stream of Dianchi Lake	Rhodobacter sp. TUT3732(96.43) [AB251408]
Hyd-109	1	Alphaproteobacteria	Clone MN03(98.18) [JN869015]	Lake water	Rhodobacter sp. Cr5-50(95.67) [GU441680]
Hyd-110	1	Flavobacteriia	Clone AGS-HB2-1(95.57) [HQ403245]	Aerobic granular sludge	Wandonia haliotis Haldis-1(84.57) [FJ424814]
Hyd-113	1	Alphaproteobacteria	Clone J52(96.61) [HQ697493]	Biologically activated carbon	Hyphomicrobium sp. KC-IT-W2(95.57) [FJ711209]
Hyd-118	1	Alphaproteobacteria	Clone: UTFS-OF08-d36-35(97.51) [AB200296]	Activated sludge	Sinorhizobium meliloti GR67(86.19) [HE805562]
Hyd-132	1	Alphaproteobacteria	Asticcacaulis excentricus CB48(98.24) [CP002396]	Pond water	Brevundimonas naejangsansensis HWG-A15(93.14) [JQ684238]
Hyd-133	1	Betaproteobacteria	Clone 8-105(94.98) [JQ923988]	Drinking water distribution system	Limnobacter thiooxidans CS-K2(94.79) [AJ289885]
Hyd-140	1	Flavobacteriia	Flavobacterium succinicans DSM4001(99.25) [AM230494]	Genomic DNA	Flavobacterium sp. WB4.3-96(97.41) [AM177633]
Hyd-141	1	Gammaproteobacteria	Clone FGL7S_B125(99.66) [FJ437965]	Green Lake surface sediments	Steroidobacter sp. ZUMI37(93.93) [AB548216]
Hyd-142	9	Betaproteobacteria	Clone S25_1448(95.85) [EF575104]	Coco's Island	Piscinibacter aquaticus IMCC1728(95.71) [NR_043921]
Hyd-143	2	Alphaproteobacteria	Clone: SWB04(97.86) [AB294315]	Stream	Novosphingobium sp.

					Van61 (84.40) [HQ222277]
Hyd-145	4	Betaproteobacteria	Clone R15-71 (98.07) [JF808901]	Activated sludge	Methylobacillus glycogenes DSM5685T (95.62) [FR733701]
Hyd-148	1	Cytophagia	Clone MA-R29 (98.25) [JN038610]	Chongxi wetland soil	Uncultured Flexibacter sp. EFT307_D08 (92.51) [GU2015 55]
Hyd-152	1	Gammaproteobacteria	Clone 2\SC\46 (96.89) [EU340183]	Aquatic macrophytes	Dokdonella sp. TSY06 (89.94) [AB663505]
wat1	1	Alphaproteobacteria	Clone sdm114 (87.77) [JQ798469]	Decomposed maize straw	Rhizobium sp. PRNB- 25 (84.96) [HQ589028]
wat2	2	Planctomycetia	Uncultured Planctomyces sp. Joinville4 (98.33) [FJ236055]	Drinking water	Planctomyces sp. Schlesner 130 (87.06) [X81952]
wat5	13	Betaproteobacteria	Clone reservoir- 93 (99.73) [JF697474]	Stream of Dianchi Lake	Acidovorax sp. R- 24667 (99.60) [AM084010]
wat6	1	Actinobacteria	Clone D23 (99.19) [EU234313]	Upstream of Wang Yang River	Uncultured actinobacterium STH11- 15 (98.85) [DQ316377]
wat7	1	Sphingobacteriia	Clone ZBAF-R4 (94.25) [HQ011389]	Biofilm in a wastewater treatment	Uncultured Sphingobacteriia ADK- MOe02- 08 (93.87) [EF520606]
wat8	1	Alphaproteobacteria	Clone FGL7S_B145 (93.59) [FJ437978]	Green Lake surface sediments	Uncultured alpha proteobacterium HB125 (92.32) [EF648106]
wat10	2	Deltaproteobacteria	Isolate 1112864242226 (99.54) [HQ120302]	Loamy sand	Phaselicystis flava SBKo001 (87.98) [NR_044523]
wat12	1	Unaffiliated	Clone S39 (99.19) [JF775633]	Pond sediment	Uncultured Acidobacteria bacterium JH46 (94.78) [JQ861336]
wat13	1	Sphingobacteriia	Clone sdm140 (98.38) [JQ798482]	Decomposed maize straw buried	Chitinophaga ginsengisoli Gsoil 052 (87.36) [NR_041375]
wat14	2	Gammaproteobacteria	Uncultured Legionella sp.2H7 (97.21) [HQ003528]	Carrizo shallow lake	Legionella sp. LLAP11 (96.86) [X97362]
wat18	1	Gammaproteobacteria	Clone 12TCLN056 (98.86) [AB636982]	Soil	Cellvibrio gandavensis R-4069 (99.19) [NR_025419]
wat19	1	Flavobacteriia	Clone SGUS1259 (97.47) [FJ202110]	Montastraea faveolata	Fluviicola sp. NBRC 101268 (93.52) [AB517714]
wat20	1	Alphaproteobacteria	Clone BF2C07 (98.62) [JN820204]	Ferromanganese deposit	Sphingomonas sp. D31C2 (95.18) [AY162145]
wat22	1	Planctomycetia	Uncultured Planctomycetales (99.17) [JN825563]	Lake	Gemmata sp. Wal- 6 (99.16) [GQ889484]
wat24	1	Betaproteobacteria	Clone mv13.2 (98.80) [AY424823]	Genomic DNA	Methylotenera versatilis 301 (95.61) [CP002056]
wat26	3	Actinobacteria	Clone AK4DE1_06E (97.04) [GQ397040]	Soil	Iamia sp. T2- YC6790 (94.56) [GQ369058]

wat27	3	Alphaproteobacteria	Clone L65 (96.88) [EU834774]	Lab scale EBPR-activated sludge	Rhodobium marinum C3 (89.41) [EU445270]
wat28	1	Alphaproteobacteria	Clone C20 (96.64) [JQ323113]	Cooling water system	Rhodobacter sp. TCRI (95.26) [AB017799]
wat30	1	Sphingobacteriia	Clone BF2B08 (99.66) [JN820194]	Ferromanganese deposit	Haliscomenobacter hydrossis DSM 1100 (98.78) [NR_042316]
wat31	1	Flavobacteriia	Clone SINN629 (94.76) [HM128667]	Tanggulha Lake	Flavobacterium sp. 1-C-1 (84.97) [GU593613]
wat33	1	Cytophagia	Clone Dianchi-34 (98.84) [HQ324880]	Lake water	Leadbetterella byssophila DSM 17132 4M15 (93.24) [NR_043233]
wat34	1	Alphaproteobacteria	Uncultured Novosphingobium sp. fjc-77 (97.53) [JQ278820]	Groundwater	Novosphingobium naphthalenivorans TUT562 (96.22) [NR_041046]
wat36	2	Flavobacteriia	Clone 3C003181 (97.24) [EU801804]	Chesapeake Bay, MD	Uncultured Fluviicola sp. XZXXH2 (96.98) [EU703456]
wat37	1	Unaffiliated	Clone 654995 (91.06) [DQ404664]	Contaminated sediment	Tuber borchii symbiont b-17B0 (90.37) [AF070444]
wat38	1	Unaffiliated	Uncultured candidate TM7 D116231C09 (97.08) [GU180006]	Oil well	TM7 phylum sp. canine oral taxon 250 ZL096 (92.81) [JN713414]
wat43	1	Alphaproteobacteria	Sphingopyxis sp. M2R2 (99.79) [EU188914]	PAH polluted site	Sphingopyxis chilensis R9-594 (99.58) [JQ660012]
wat41	1	Betaproteobacteria	Clone 6'-72 (99.58) [JQ923814]	Drinking water distribution system	Undibacterium sp. M4-14 (99.03) [HE616176]
wat44	1	Alphaproteobacteria	Clone ncd2177c08c1 (99.16) [JF189806]	Skin, volar forearm	Devosia geojensis BD-c194 (87.97) [NR_044291]
wat45	1	Alphaproteobacteria	Uncultured Rhodobacteraceae XZXXH70 (97.13) [EU703428]	Freshwater lake	Rhodobacter sp. Cr5-50 (95.81) [GU441680]
wat46	1	Alphaproteobacteria	Clone UTFS-OF08-d36-35 (98.13) [AB200296]	Activated sludge	Micavibrio sp. EPC2 (86.06) [DQ186614]
wat48	1	Unaffiliated	Clone Run-SP58 (95.52) [AB247481]	Activated sludge	clone B1Q1E-91f-JRD28 (96.38) [JF917288]
wat50	3	Flavobacteriia	Clone M17-10-B17 (97.38) [JQ088393]	Crude oil reservoir	Flavobacteria bacterium KF030 (95.98) [AB269814]
wat52	1	Flavobacteriia	Clone reservoir-60 (98.31) [JF697441]	Stream of Dianchi Lake	Flavobacterium succinicans DSM 4002 (97.01) [NR_042498]
wat53	8	Sphingobacteriia	Uncultured bacterium FukuS59 (94.13) [AJ290042]	Genomic DNA	Uncultured Sphingobacteria ADK-MOe02-08 (92.99) [EF520606]
wat54	1	Verrucomicrobiae	Uncultured Tolumonas sp. R40-25 (99.27) [JF808981]	Activated sludge	Prostheco bacter vanneervanii 12252 (96.67) [AJ966883]
wat59	1	Sphingobacteriia	Clone RS06101_B100 (96.97) [EU101214]	Frasassi sulfidic cave stream biofilm	clone TDNP_Wbc97_206_1_92 (92.75) [FJ517048]

wat62	1	Flavobacteriia	Clone SINN629(95.72) [HM128667]	Tanggulha Lake	Flavobacterium sp. WB 4.4-22(84.45) [AM177636]
wat63	1	Cytophagia	Clone reservoir-107(99.66) [JF697488]	Stream of Dianchi Lake	Uncultured Arcicella sp. XZXXH12(99.39) [EU703452]
wat64	3	Verrucomicrobiae	Uncultured bacterium Kas152B(98.80) [EF203197]	Sediment	Luteolibacter sp. CCTCC AB 2010415(96.67) [JN630810]
wat65	1	Planctomycetia	Pirellula sp. Schlesner 302(94.17) [X81942]	Genomic DNA	planctomycete str. 535(93.17) [AJ231176]
wat67	1	Flavobacteriia	Clone MC1_16S_47(94.44) [EU662615]	Floating microbial mat from sulfidic water	Flavobacterium hercynium WB 4.2-33(93.95) [NR_042520]
wat70	1	Betaproteobacteria	Uncultured bacterium FOOS7B_45(96.44) [EU431699]	Alcium carbonate muds	Herbaspirillum seropedicae Z67(96.12) [NR_029329]
wat77	1	Alphaproteobacteria	Clone 214(98.09) [JF828749]	Waste water	Rickettsia heilongjiangii HLJ-054(93.52) [NR_041770]
wat78	2	Alphaproteobacteria	Clone MP104-SW-b24(97.79) [DQ088789]	Crustal biotome	Sphingomonas sp. EZ41(96.76) [EU591707]
wat79	1	Cyanobacteria	Uncultured Oscillatoriales cyanobacterium LI06st1(98.48) [JF733399]	Genomic DNA	Leptolyngbya sp. FYG(92.70) [FJ933259]
wat80	1	Actinobacteria	Uncultured actinobacterium LT1G10(99.66) [EU117848]	Lake epilimnion	Candidatus Planktophilia MWH-EgelM2-3.acI(99.66) [FJ428831]
wat81	1	Unaffiliated	Clone A11(88.50) [HM773452]	Food-wastewater treatment plant	Uncultured candidate division TM7 E1B-B5-114(87.31) [EF016808]
wat83	1	Gammaproteobacteria	Cellvibrio sp. KY-YJ-1(97.40) [EF692634]	Genomic DNA	Cellvibrio fibrivorans R-4079(97.75) [NR_025420]
wat84	1	Cyanobacteria	Clone EpiNCA39(97.30) [FJ849099]	Arctic stream epilithon	Oscillatoria sp. PCC 8927(90.12) [GQ351575]
wat87	1	Alphaproteobacteria	Clone C-78(97.62) [HQ860594]	Stream water	Rhodobacter sphaeroides 2.4.1(96.22) [NR_029215]
wat91	1	Betaproteobacteria	Clone 2C228284(99.07) [EU800248]	Delaware Bay, NJ	Uncultured Rhodocyclaceae Elev_16S_475(97.56) [EF019288]
wat92	1	Betaproteobacteria	Clone 3C003675(99.40) [EU802237]	Chesapeake Bay, MD	Uncultured Curvibacter sp. sh-xj128(99.06) [JQ327990]
wat93	1	Bacilli	Uncultured bacterium, SRODG012(95.33) [FM995177]	Genomic DNA	Streptococcus suis S735(79.64) [NR_036918]
wat95	1	Betaproteobacteria	Clone VW-86(96.58) [FM994919]	hot spring Mizinka	Curvibacter delicatus 146(96.95) [NR_028713]
wat97	1	Unaffiliated	Uncultured candidate Pav-SR4(98.37) [FJ482217]	Lake Pavin water column	Uncultured candidate B1Q1E-91f-E070(98.72) [JF917287]
wat99	1	Unaffiliated	Uncultured Chloroflexi	Volcano 1, South	Caldilineae bacterium

			V1B07b21 (89.28) [GU369915]	Tonga Arc.	PRI 4131 (80.90) [JQ733906]
wat103	2	Unaffiliated	Uncultured Chloroflexi MP-R51 (87.42) [JN038723]	Chongxi wetland soil	Uncultured Chloroflexi P-R16 (85.40) [JN038805]
wat104	1	Deltaproteobacteria	Clone ASB26 (86.53) [FJ947130]	Activated sludge	Geobacter thiogenes K1 (79.89) [NR_028775]
wat106	1	Betaproteobacteria	Clone MACA-EFT44 (96.74) [GQ500809]	Bio-Sep beads in base level cave stream	Methylotenera versatilis 301 (95.22) [CP002056]
wat107	1	Alphaproteobacteria	Clone TDNP_LSbc97_232_1_69 (86.88) [FJ516840]	Lower sediment	Dichotomicrobium thermohalophilum DSM5002T (83.35) [FR733679]
wat108	2	Alphaproteobacteria	Alpha proteobacterium A0721 (99.51) [AF235998]	Genomic DNA	Rhizobium sp. Rb122 (96.82) [AB636290]
wat109	1	Actinobacteria	Clone OTU_22 (93.19) [EU083500]	Hexadecane-degrading denitrifying consortium	Uncultured actinobacterium FAC31 (91.75) [DQ451470]
wat111	1	Actinobacteria	Clone thermophilic alkaline-17 (98.78) [GU455257]	Anaerobic fermentation reactor	Iamia sp. T2- YC6790 (93.86) [GQ369058]
wat113	1	Unaffiliated	Uncultured Chlorobi BLC04 (97.34) [JN820218]	Ferromanganese deposit	Chlorobi bacterium canine oral taxon 046 1F061 (81.30) [JN713214]
wat116	2	Unaffiliated	Clone p22k16ok (96.31) [FJ478864]	Undisturbed tall grass prairie	Uncultured candidate division MP-R126 (95.51) [JN038791]
wat117	6	Gammaproteobacteria	Vibrio parahaemolyticus RIMD 2210633 (99.67) [BA000031]	Genomic DNA	Vibrio sp. SBP (99.47) [HQ123984]
wat119	2	Unaffiliated	Clone a-86 (96.45) [JX040386]	Waste water	GN02 bacterium canine oral taxon 291 ZR106 (82.82) [JN713458]
wat120	2	Betaproteobacteria	Clone 6'-72 (99.33) [JQ923814]	Drinking water distribution system	Herminiimonas arsenicoxydans ULPAs1 (95.46) [NR_043147]
wat121	1	Unaffiliated	Uncultured candidate RB_31f (86.41) [EF123563]	Black band diseased (BBD) coral tissues	Uncultured candidate RII-TR069 (83.19) [JQ580302]
wat124	1	Alphaproteobacteria	Clone PC0810_49 (96.56) [JN983651]	Genomic DNA	Rhodobacter sp. CR07-62 (94.96) [EU979476]
wat125	1	Alphaproteobacteria	Clone D-26 (96.08) [HQ860667]	Stream water	Aquabacter spiritensis DSM9035T (89.23) [FR733686]
wat126	1	Bacilli	Clone cpw3b516 (96.88) [HM921122]	Groundwater	Pirellula sp. Schlesner 302 (92.25) [X81942]
wat127	1	Gammaproteobacteria	Legionella sp. W10-070 (93.64) [HE613855]	Water	Legionella pneumophila Los Angelos-1 (93.37) [HQ287902]
wat129	1	Betaproteobacteria	Clone DR136 (96.86) [JF429180]	Primary drinking water supply	Uncultured Nitrosospira sp.

					Ba204 (93.86) [JQ684443]
wat130	1	Alphaproteobacteria	Clone T1-25 (98.75) [GQ487892]	Soil polluted by heavy metals	<i>Devosia</i> sp. R-43964 (97.69) [FR691415]
wat139	1	Betaproteobacteria	Clone 3C003105 (99.53) [EU801741]	Chesapeake Bay, MD	<i>Polynucleobacter necessarius</i> MWH-LF2-54B (99.39) [AJ964893]
wat140	2	Gammaproteobacteria	Clone KIST-JJY048 (91.15) [EF659421]	Suspended sludge from anammox reactor	<i>Legionella</i> sp. OUB41 (89.83) [AB058918]
wat141	1	Sphingobacteriia	<i>Flexibacter sancti</i> IFO 15057 (98.71) [AB078066]	Genomic DNA	<i>Chitinophaga sancti</i> IFO 15057 (98.71) [NR_040917]
wat143	2	Alphaproteobacteria	Clone: SWB04 (98.50) [AB294315]	Stream	<i>Novosphingobium hassiacum</i> W-51 (84.52) [NR_028962]
wat145	2	Gammaproteobacteria	Clone AW67 (99.39) [JN868837]	Lake water	<i>Pseudomonas</i> sp. N1 (98.99) [EU275166]
wat147	1	Betaproteobacteria	Clone 3C003190 (99.93) [EU801813]	Chesapeake Bay, MD	<i>Methylotenera versatilis</i> 301 (97.93) [CP002056]
wat148	1	Gammaproteobacteria	Clone AW55 (98.87) [JN868834]	Lake water	<i>Silanimonas</i> sp. AK13 (95.17) [HE573746]
wat149	1	Sphingobacteriia	<i>Chitinophaga</i> sp. SaZS3 (99.73) [JQ806450]	Genomic DNA	<i>Flexibacter sancti</i> :IFO 16034 (98.57) [AB078068]