

Bacterial communities in sediments of Lake Baikal from areas with oil and gas discharge

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Table S1. The most closely related *Actinobacteria* from the GenBank database, according to 16S rRNA gene sequences identified from the discharge areas of gas- and oil-bearing mineralized fluids of Lake Baikal

Number of Station	OTU ID	Number of seqs	Closest 16S rRNA sequence	GenBank ID	16S rRNA identity (%)	Location, setting
#1 a-g, #2 a, b, #3, #4, #5 a-f, #6	2	8933	Unc. <i>Acidimicrobiales</i> bacterium D7N82	KC006228	99	downstream along river ban Jiulong River, Longhai, China
			Unc. bacterium 6016A3 H2	HF558719	99	diesel (petroleum hydrocarbon), the Baltic Sea, Askainen
#1 a-g, #2 a, b, #3, #4, #5 a-f, #6	5	5665	Unc. actinobacterium	AB920866	100	Lake Kanagawa, Japan
			Unc. bacterium clone AK4b2	JN626885	100	Methane seep, ice-free, Lake Qalluuraq, Alaska
#1 a-g, #2 a, b, #3, #4, #5 a-f, #6	6	1930	Unc. actinobacterium DSH4C1-46	KF543148	100	harbor water Duluth-Superior Harbor, USA
			Unc. bacterium BT3900DF 09B	JX448574	100	drilling fluid, Ontario, Canada
#1 a-g, #2 a, b, #4, #5 a-f, #6	9	1724	Unc. <i>Propionibacterium</i> sp. O-22	KF786767	100	deepwater Horizon cofferdam (oil sheens), USA
			Unc. bacterium GS6 E25	KF720836	100	oil reservoirs of Diyarbakir ,Turkey
#1 a-d, f, g, #2, #3, #4, #5 b-f, #6	14	1095	<i>Actinobacterium</i> SCGC AAA044-F19	HQ663471	100	epilimnion of freshwater Lake Damariscotta, isolate (0.5-1 m depth), USA
			Unc. bacterium SD 1 G05	JX564520	100	sediment wastewaters, Germany
#1 a-g, #2 a, b, #3, #4, #5 a-e, #6	15	1108	Unc. <i>Acidimicrobinae</i> bacterium clone YL116	HM856482	100	Lake Yellowstone, USA
			Unc. <i>Actinomycetales</i> bacterium clone YL137	HM856502	100	Lake Yellowstone, USA
#1a, b, c, g, #2 a, b, #5 a, b, #6	22	810	Unc. bacterium clone AK2	JN626625	99	off-seep methane under ice cover Lake Qalluuraq Alaska
			Unc. <i>Ferrimicrobium</i> sp. Pad-78	JX505325	99	soil, Northeast China
			Unc. <i>Acidimicrobidae</i> bacterium AMDE12	AM935602	97	pilot-scale bioremediation process of a hydrocarbon-contaminated soil
#1 e, f, #2 a, b, #3, #4, #5 a, b, #6	25	537	Unc. <i>Rubrobacteridae</i> bacterium RUGL6-316	GQ366590	100	soil, Roopkund Glacier, India
			Unc. bacterium AC16S141	HQ664300	100	arsenic contaminated sediment

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#1 a, b, d-g, #2, #3, #4, #5 a-c, e	28	530	Unc. bacterium 204_284	KF596574	99	E54, Gulf of Gdansk, Baltic Sea
			Unc. <i>Actinomycetales</i> bacterium B3 30 016	JN866285	99	Lake Bangongco, Tibetan Plateau
			Unc. bacterium clone AK4b2	JN626866	97	off-seep methane under ice cover Lake Qalluuraq Alaska
#1 a-g, #2 a, b, #3, #5 a-f, #6	39	342	Unc. <i>Actinomycetales</i> bacterium R1-077	JQ684904	99	Lake Ranwu, southeast of Tibetan Plateau
			Unc. bacterium QCS6_Act_006	JX667974	98	Tibetan cold springs, China
#1 a-g, #2 a, b, #3, #4, #5 a-f, #6	46	278	Unc. <i>Intrasporangiaceae</i> bacterium M7N27	KC006354	100	downstream along river ban Jiulong River, city Longhai China
			Unc. bacterium 55011P2_B4	HF558917	100	diesel, Archipelago Sea in South-West Finland (Baltic Sea)
#1 a-g, #2 a, b, #3, #4, #5 a-f, #6	47	259	Unc. <i>actinobacterium</i> clone CB11A12	EF471696	100	surface water from Chesapeake Bay, USA
#1 a-g, #2 a, b, #3, #4, #5 a-f, #6	58	213	Unc. <i>actinobacterium</i>	FR647614	100	seawater, 2 m depth, Sweden
#1 a-g, #2 a, b, #3, #4, #5 a-f, #6	60	145	Unc. <i>Acidimicrobinae</i> bacterium YL067	HM856436	100	Lake Yellowstone, USA
			Unc. bacterium clone 03-BS78	KF791079	99	deep-water endemic sponge, Lake Baikal, Russia
#1 a-g, #5 a-f	62	205	Unc. bacterium clone bOHTK-56	FJ873263	99	sediments from the Okhotsk Sea
			Unc. <i>actinobacterium</i>	AF351232	99	upgradient of coal tarwaste-contaminated groundwater, USA
#1 a-g, #2 a, b, #3, #4, #5 a-f, #6	68	163	Unc. bacterium SINO606	HM129794	100	Lake Nam Co, Tibet
			Unc. bacterium 62	HG003476	98	former uranium mine, Germany
#1 a-g, #2 a, b, #6	73	167	Unc. <i>Iamibacter</i> RUGL1-322	GQ421063	100	soil, Roopkund Glacier, India
			Unc. <i>actinobacterium</i> lhac3	DQ648928	100	PCB (polychlorinated biphenyl-polluted) contaminated soil, Spain
			Unc. <i>Acidimicrobidae</i> bacterium CM36D6	AM936315	100	pilot-scale bioremediation process of a hydrocarbon-contaminated soil
#1 a-g, #5 a-f, #6	75	174	Unid. marine bacterioplankton E307B 1 39	KC002579	100	surface seawater, China offshore waters and South China Sea
#1 a-g, #2 a, b, #5a-f	80	72	Unc. <i>Actinobacteridae</i> bacterium S2-059	KF182995	100	soil of continuous peanut cropping, China
			Unc. <i>actinobacterium</i> BLAKE3cm23	JQ793055	99	sediment core, arctic oligotrophic lake Char, Canada
			Unc. <i>Rubrobacteridae</i> bacterium glen99 25	AY150872	98	Surface coal mining soil, USA
#1 a-g, #4, #5 a-f	98	114	<i>Microbacterium foliorum</i> strain 7	KF923417	100	permafrost soils, Qinghai-Tibet Plateau, China
#1 a-g, #2 a, b, #3, #4, #5 a-f, #6	103	112	Unc. <i>Actinomycetales</i> bacterium Ac63B5	GU472680	99	Lake Pavin (meromictic lake), France
			Unc. bacterium Munt 2 A7	HE857797	99	high-altitude Pyrenean lakes
#1 a-g, #2 a, b, #3, #5 a-f, #6	123	92	Unc. <i>Micrococcineae</i> bacterium DVPSD110	KF465638	100	marine coastal sediment, India

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#1 a-g, #2 a, b, #3, #5 a-f, #6	124	64	Unc. bacterium 31-1	KF638305	100	water, Kyrgyzstan
			Unc. <i>actinobacterium</i> URO3.3.B03	JX473199	99	URO spring from rift zone of Lake Baikal, Russia
#1 a-g, #2 a, b, #3, #4, #5 a-f, #6	131	96	Unc. <i>Ilumatobacter</i> sp. B3 0 034	JN866200	99	Bangongco Lake, the Tibetan Plateau
#1 a-g	325	40	<i>Brevibacterium linens</i>	KJ019204	99	marine sediment, Dalian, China
#1 a-g, #2 a, b, #4, #5 a-f	654	10	<i>Cryobacterium</i> sp. Cry-k	AB872307	100	glacier cryoconite sediment, Svalbard
			Bacterium enrichment culture Cont28 3131	KJ425069	99	coal-rich sediment, Germany
#1 a-g, #6	1385	5	Unc. <i>actinobacterium</i> Upland 500 9733	JF990432	98	upland cropland soils, reclaimed from salt marshes for 500 years, China

Table S2. The most closely related *Cyanobacteria* from the GenBank database, according to 16S rRNA gene sequences identified from the discharge areas of gas-and oil-bearing mineralized fluids of Lake Baikal

ID of samples	OTU ID	Number of seqs	Closest 16S rRNA sequence	GenBank ID	16S rRNA identity (%)	Site location and characteristics
#1 a-g, #2 a, b, #3, #4, #5 a-f, #6	4	3551	Unc. cyanobacterium OuchyA-62	FN679245	100	lake sediments, Lake Geneva, Switzerland
#1 a-g, #2 a, b, #3, #4, #5 a-f, #6	1	12251	Unc. cyanobacterium BaikallB83	JX570966	100	of sponge-associated Cyanobacteria in Lake Baikal
			Unc. bacterium 26LB-10	JQ272733		
			<i>Synechococcus rubescens</i>	NR125481	99	Culture collection Span
#1 a-g, #2 a, b, #3, #4, #5 a-f	11	1774	Unc.bacterium Espejo_9	KM162361	99	Water, Lake Espejo, Argentina
#1 a, c, f, g, #2 a, #3, #4, #5 a, c-e	127	61	Cyanobacterium sp. MS-M-47	FJ460126	99	marine aquaculture pond
#1 a-g, #2 a, b, #3, #4, #5 a, c, d, e a-f	86	117	Unc. cyanobacterium SLc2.B05_L2	EF555720	99	Silver Lake through flow playa California, USA
#1 a-g, #3	63	7	Unc. organism 6m-51-27F	KC192445	97	Mystic Lake, Winchester, USA
#5 a-f	104	49	Unc. bacterium FMSB13	KF975556	100	mine environment soil Semnan Province, Foroumad chromite mine, Iran
#1 a-g, #2 a, b, #3, #4, #5 a-f, #6	83	71	Unc. bacterium 9	KC297775	98	biofilm on artificial substrates China Lake Taihu, Jiangsu province
#1 a-g, #2 a, b, #3, #4, #5 a-f, #6	34	375	Unc. cyanobacterium GC6m-4-5	EU641986	100	Lake Michigan Wisconsin USA
#1 c, f, g, #2a,b, #3, #4, #5b, c, e	82	77	Unc. cyanobacterium BksYy43000	KC463151	93	Soil, Namibia
#6	3008	1	<i>Cyanobium</i> sp. CENA185	KC695876	98	Soil, Bertioga, Brazil
#1 c, f, #2b, #3, #4, #5b, c, e,f	115	74	Unc. cyanobacterium OTUC14	KC262726	99	ukang Station of Desert Ecology, China, XinJiang province
#2 a	3874	1	Unc. cyanobacterium BNSB02	JF929513	97	Bertioga soil mangrove
#5 c	7816	1	<i>Calothrix</i> sp. LCRSM-1413	JN705664	97	paddy fields, ponds and soils
#1 d	4647	1	Unc. bacterium GB7N87002DOYU4	HM673125	99	unvegetated soil environments on Signy Island, open-top chamber plot W16
#5 f	139	11	<i>Geitlerinema</i> sp. 0BU40S1	DQ264185	99	of planktonic cyanobacteria from Belgium and Luxembourg
#5 f	569	16	<i>Nostoc</i> sp. CAWBG77	JX088107	99	Freshwater lake in Canterbury, New Zealand

Table S3. The most closely related methanotrophs from the GenBank database, according to 16S rRNA gene sequences identified from the discharge areas of gas- and oil-bearing mineralized fluids of Lake Baikal

ID of samples	Phylum	Number of seqs	Closest 16S rRNA sequence	GenBank ID	16S rRNA identity (%)	Site location and characteristics
#1a-g, #3, #4, #5 a-f, #6	<i>Alphaproteobacteria</i>	231	<i>Methylobacterium mesophilicum</i>	AB900968	99	Household biofilms
	<i>Rhizobiales</i>					
	<i>Methylobacteriaceae</i>					
#1 a-g, #2 a, b, #3, #5 a-f, #6	<i>Alphaproteobacteria</i>	49	<i>Methylocystis</i> sp.	FN422003	99	Peat bog
	<i>Rhizobiales</i>		Unc. bacterium	EU546762	99	Lake Washington sediment
	<i>Methylocystaceae</i>					
#1 a-g, #2 a, b, #3, #4, #5 a-f, #6	<i>Betaproteobacteria</i>	166	Unc. bacterium	KF791109	100	Two deep-water endemic sponges of Lake Baikal
	<i>Methylophilales</i>		Unc. <i>Methylophilaceae</i> bacterium	HM856405	100	Yellowstone Lake
	<i>Methylophilaceae</i>		Unc. beta proteobacterium	EU642393	100	Lake Michigan
	LD28					
#1 a-g, #2 a, b, #3, #5 a-f, #6	<i>Betaproteobacteria</i>	89	Beta proteobacterium	HQ663370	100	Epilimnion of freshwater Lake Damariscotta
	<i>Methylophilales</i>		Unc. <i>Methylophilus</i> sp.	AF388908	100	Estuarine bacterioplankton
	<i>Methylophilaceae</i>		Unc. <i>Methylophilus</i> sp.	FN860076	99	Industrial ultra pure supply water plant
			Unc. bacterium	JX406254	99	Water Lake Taihu
			Unc. <i>Methylophilus</i> sp.	JX494012	100	Soil
#1 a-g, #2 a, b, #5 a-f	<i>Betaproteobacteria</i>	14	Unc. bacterium	AB661536	99	Lake sediment, Biwa
	<i>Burkholderiales</i>		Methylibium sp.	HM156141	100	Soil from glacier forefield
	<i>Comamonadaceae</i>					
#1 a-g, #2 a, b, #3, #4, #5 a-f, #6	<i>Gammaproteobacteria</i>	1674	Unc. bacterium	KF791117	100	Deep-water endemic sponges of Lake Baikal
	<i>Methylococcales</i>		Unc. bacterium	EU340166	98	Aquatic macrophytes in a geothermally active area
			Unc. bacterium	HM446109	100	Yellowstone lake sublacustrine hydrothermal vent waters
#1 a-g, #2 a, b, #3, #5 a-f, #6	<i>Gammaproteobacteria</i>	307	Unc. <i>Methylobacter</i> sp.	JQ793373	99	Sediment core from an arctic wetland
	<i>Methylococcales</i>		Unc. bacterium	KC922985	99	Groundwater discharge zone sediment
	<i>Methylococcaceae</i>		Unc. bacterium	AB722196	98	Freshwater iron-rich microbial mat
#1 a-g, #2 a, b, #3, #5 a-f, #6	<i>Gammaproteobacteria</i>	230	Unc. <i>Methylobacter</i> sp.	JQ793046	99	Sediment core from an arctic oligotrophic lake Char
	<i>Methylococcales</i>		Unc. <i>Methylobacter</i> sp.	GQ390219	99	Lake Pavin
	<i>Methylococcaceae</i>		Unc. bacterium	KC922577	100	Groundwater discharge zone sediment
	<i>Methylobacter</i>		Unc. <i>Methylobacter</i> sp.	KC492844	99	Baltic Sea redoxcline, 119 m depth
			Unc. <i>Methylococcaceae</i> bacterium	FN679277	99	Lake Geneva, sediments
#2 a,b	<i>Gammaproteobacteria</i>	1	Unc. <i>Crenothrix</i> sp.	DQ984191	95	Water samples from an artesian well on a farm
	<i>Methylococcales</i>		Unc. <i>Crenothrix</i> sp.	JN936833	95	Sludge of drinking water
	<i>Methylococcaceae</i>					
	<i>Methylosoma</i>					
	unclassified					

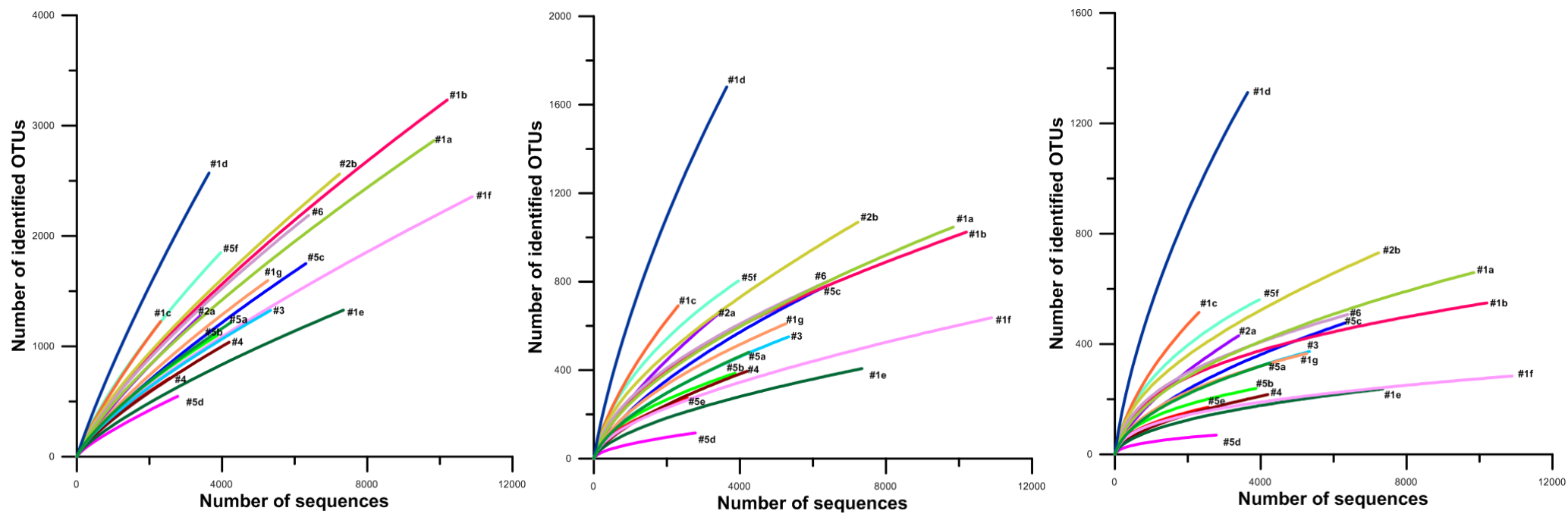


Fig. S1. Rarefaction curves: **a** - 0.01 dissimilarity level, **b** - 0.03 dissimilarity level, **c** - 0.05 dissimilarity level

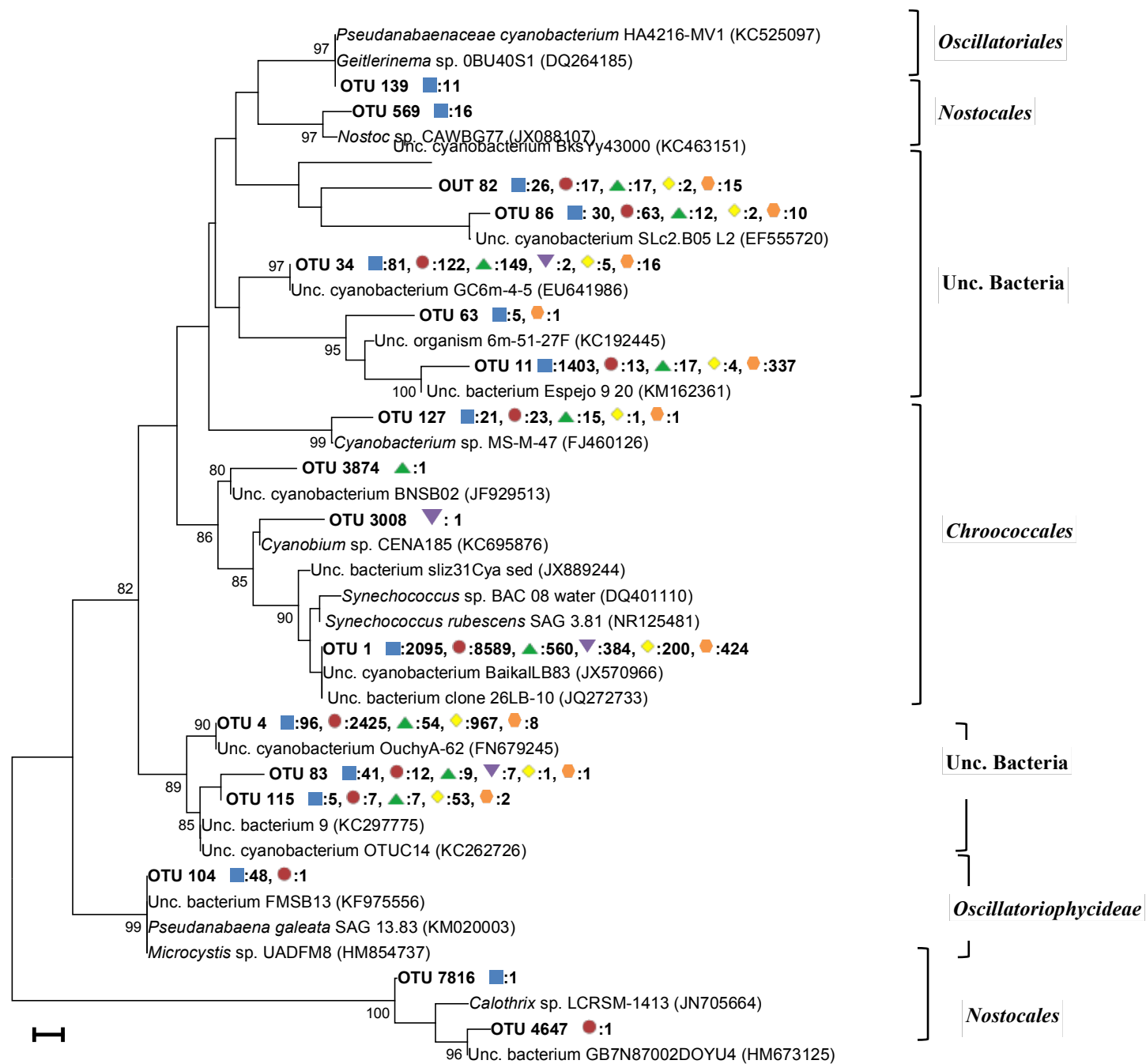


Fig.. S2. Phylogenetic tree of the phylum *Cyanobacteria* based on the analysis of nucleotide sequences of 16S rRNA gene fragments obtained from the total DNA of bottom sediments in the discharge areas of gas- and oil-bearing mineralized fluids. The tree was constructed using the neighbor-joining (NJ) method. Bootstrap analysis provided probability assessment of individual nodes; the values above 70 % are shown. The scale is 0.01.

■ - #5, ● - #1, ▲ - #2, ◆ - #4, ⬡ - #3, ▼ - #6