

TABLE S1. Summary of bacterial 16S rRNA gene sequence-based OTUs detected in Dan and Halfdan PW.

Phylum Sequence representing OTU	No. of clones in OTU	Closest match [†] (Acc. no. %)	Closest cultivated species [‡] (Acc.no., %)	Source of closest match
Dan PW				
Firmicutes				
Dan_Bac67	24	Uncultured <i>Caminicella</i> sp. clone TCB15y (DQ647125, 99)	<i>Clostridium</i> sp. Dex60-4 (AJ431242, 93)	High-temperature oil field
Dan_Bac48	9	Uncultured organism clone MAT-CR-H3-C02 (EU245157, 93)	<i>Caloanaerobacter azorensis</i> (AJ272422, 93)	Solar saltern
Dan_Bac95	4	Uncultured bacterium clone Niigata-25 (AB243993, 98)	<i>Desulfonispira thiosulfatigenes</i> (Y18214, 89)	Oil production well
Dan_Bac42	2	<i>Thermohalobacter berrensii</i> (AF113543, 98)	<i>Thermohalobacter berrensii</i> (AF113543, 98)	Solar saltern
Dan_Bac58	3	<i>Moorella thermoacetica</i> ATCC 39073 (CP000232, 87)	<i>Moorella thermoacetica</i> ATCC 39073 (CP000232, 87)	Horse manure
Dan_Bac50	1	<i>Thermoanaerobacter mathranii</i> (Y11297, 98)	<i>Thermoanaerobacter mathranii</i> (Y11297, 98)	Icelandic hot spring
Dan_Bac26	2	Uncultured bacterium clone 1-9E (EU289466, 96)	<i>Marinilactibacillus piezotolerans</i> (AB294178, 94)	Tropical plant material
Dan_Bac44	1	Uncultured bacterium clone 1-9E (EU289466, 91)	<i>Marinilactibacillus piezotolerans</i> (AB294178, 89)	Tropical plant material
Dan_Bac55	1	Uncultured bacterium clone F2V (DQ860054, 98)	<i>Vagococcus salmoninarum</i> (Y18097, 98)	Aqua culture
Dan_Bac29	1	<i>Desulfotomaculum geothermicum</i> (Y11567, 92)	<i>Desulfotomaculum geothermicum</i> (Y11567, 92)	Geothermal ground water
α-Proteobacteria				
Dan_Bac47	1	Uncultured bacterium clone 96O1 (EU676403, 99)	<i>Skermanella</i> sp. 5416T-32 (DQ672568, 99)	Heavy metal contaminated soils
γ-Proteobacteria				
Dan_Bac63	1	<i>Stenotrophomonas maltophila</i> EC-S105 (AB200253, 99)	<i>Stenotrophomonas maltophila</i> EC-S105 (AB200253, 99)	Rhizoplane
δ-Proteobacteria				
Dan_Bac27	1	Uncultured organism clone MAT-CR-H4-C05 (EU245216, 88)	<i>Desulfonatronum lacustre</i> DSM 10312 (AF418171, 88)	Solar saltern
Dan_Bac76	3	Uncultured bacterium clone E3_10.3_1 (FJ716972, 98)	<i>Desulfovibrio</i> sp. EBD (DQ218320, 98)	Estuarine microbial mat
Dan_Bac73	3	<i>Desulfacinum infernum</i> (L27426, 97)	<i>Desulfacinum infernum</i> (L27426, 97)	High-temperature oil reservoir
ϵ-Proteobacteria				
Dan_Bac25	1	Uncultured <i>Arcobacter</i> sp. clone YJQ-18 (AY569293, 98)	<i>Arcobacter</i> sp. (L42994, 98)	Hot spring
Candidate division OP9				
Dan_Bac65	6	Candidate division OP9 clone OPB47 (AF027082, 93)		Yellowstone hot spring
Thermotogales				
Dan_Bac70	1	<i>Thermotogales</i> bacterium TBF 19.5.1 clone (EU980631, 99)	<i>Thermotogales</i> bacterium Ag70 (AB260048, 99)	Oil production fluid
Synergistes				
Dan_Bac74	3	Bacterium enrichment culture clone PW20.10B (EU573140, 99)	<i>Thermovirga lienii</i> (DQ071273, 99)	Ekofisk oil reservoir
Halfdan PW				
Firmicutes				
Hda_Bac36	22	Uncultured <i>Caminicella</i> sp. clone TCB15y (DQ647125, 99)	<i>Clostridium</i> sp. Dex60-4 (AJ431242, 92)	High-temperature oil field
Hda_Bac1	3	Uncultured <i>Caminicella</i> sp. clone TCB15y (DQ647125, 98)	<i>Clostridium</i> sp. Dex60-4 (AJ431242, 93)	High-temperature oil field
Hda_Bac15	3	Uncultured bacterium clone K2y (DQ647066, 99)	<i>Clostridium</i> sp. Dex60-61 (AJ431243, 94)	High-temperature oil field

Hda_Bac29	1	Uncultured <i>Caminicella</i> sp. clone TCB15y (DQ647125, 96)	<i>Clostridium</i> sp. Dex60-4 (AJ431242, 91)	High-temperature oil field
Hda_Bac43	1	Uncultured <i>Caminicella</i> sp. clone TCB15y (DQ647125, 96)	<i>Clostridium</i> sp. Dex60-4 (AJ431242, 91)	High-temperature oil field
Hda_Bac9	6	<i>Desulfotomaculum geothermicum</i> (Y11567, 90)	<i>Desulfotomaculum geothermicum</i> (Y11567, 90)	Geothermal ground water
<i>γ-Proteobacteria</i>				
Hda_Bac7	1	<i>Stenotrophomonas maltophila</i> EC-S105 (AB200253, 99)	<i>Stenotrophomonas maltophila</i> EC-S105 (AB200253, 99)	Rhizoplane
<i>δ-Proteobacteria</i>				
Hda_Bac14	1	<i>Desulfacinum infernum</i> (L27426, 96)	<i>Desulfacinum infernum</i> (L27426, 96)	High-temperature oil reservoir
Hda_Bac8	1	Bacterium enrichment culture clone PW5.5B (EU573126, 99)	<i>Pelobacter carbinolicus</i> DSM 2380 (CP000142, 96)	Ekofisk oil reservoir
<i>ε-Proteobacteria</i>				
Hda_Bac23	2	Epsilon proteobacterium AN-BI3A (AM157656, 97)	Epsilon proteobacterium AN-BI3A (AM157656, 97)	Deep-sea halocline
<i>Synergistes</i>				
Hda_Bac51	1	Bacterium enrichment culture clone PW20.10B (EU573140, 99)	<i>Thermovirga lienii</i> (DQ071273, 99)	Ekofisk oil reservoir
<i>Deferribacterales</i>				
Hda_Bac32	3	Uncultured <i>Deferribacteres</i> bacterium clone (EU721778, 99)	<i>Flexistipes</i> sp. vp180 (AF220344, 98)	Petroleum reservoir
Hda_Bac26	1	<i>Deferribacter thermophilus</i> (NR_026043, 97)	<i>Deferribacter thermophilus</i> (NR_026043, 97)	Petroleum reservoir
Hda_Bac18	1	<i>Deferribacter thermophilus</i> (NR_026043, 97)	<i>Deferribacter thermophilus</i> (NR_026043, 97)	Petroleum reservoir

† Closest related sequence as revealed from BLAST search, Genbank accession number and percentage of 16S rRNA gene sequence similarity.

TABLE S2. Summary of archaeal 16S rRNA gene sequence-based OTUs detected in Dan and Halfdan PW.

Phylum Sequence representing OTU	No. of clones in OTU	Closest match [†] (Acc. no. %)	Closest cultivated species [†] (Acc.no., %)	Source of closest match
Dan PW				
<i>Thermococcales</i>				
Dan_Arch62	12	<i>Thermococcus aegaeus</i> DSM 12767 (AY099171, 99)	<i>Thermococcus aegaeus</i> DSM 12767 (AY099171, 99)	Hydrothermal deep sea vent
Dan_Arch34	8	<i>Thermococcus aegaeus</i> DSM 12767 (AY099171, 98)	<i>Thermococcus aegaeus</i> DSM 12767 (AY099171, 98)	Hydrothermal deep sea vent
Dan_Arch54	2	<i>Thermococcus aegaeus</i> DSM 12767 (AY099171, 97)	<i>Thermococcus aegaeus</i> DSM 12767 (AY099171, 97)	Hydrothermal deep sea vent
Dan_Arch61	1	<i>Thermococcus litoralis</i> DSM 5474 (AY099180, 95)	<i>Thermococcus litoralis</i> DSM 5474 (AY099180, 95)	Hydrothermal deep sea vent
Dan_Arch50	1	<i>Thermococcus aegaeus</i> DSM 12767 (AY099171, 93)	<i>Thermococcus aegaeus</i> DSM 12767 (AY099171, 93)	Hydrothermal deep sea vent
<i>Methanococcales</i>				
Dan_Arch65	6	<i>Methanococcus thermolithotrophicus</i> (M59128, 97)	<i>Methanococcus thermolithotrophicus</i> (M59128, 97)	Heated sea sediments
Dan_Arch32	2	Archaeon enrichment culture clone EA29.6 (EU573144, 99)	<i>Methanococcus thermolithotrophicus</i> (M59128, 97)	Ekofisk oil reservoir
<i>Archaeoglobales</i>				
Dan_Arch53	7	<i>Archaeoglobus fulgidus</i> DSM 4304 (AE000782, 99)	<i>Archaeoglobus fulgidus</i> DSM 4304 (AE000782, 99)	Submarine hot spring
Dan_Arch46	1	<i>Archaeoglobus fulgidus</i> DSM 4304 (AE000782, 97)	<i>Archaeoglobus fulgidus</i> DSM 4304 (AE000782, 97)	Submarine hot spring
HalfDan PW				
<i>Thermococcales</i>				
Hda_Arch3	26	<i>Thermococcus aegaeus</i> DSM 12767 (AY099171, 99)	<i>Thermococcus aegaeus</i> DSM 12767 (AY099171, 99)	Hydrothermal deep sea vent
Hda_Arch2	5	<i>Thermococcus aegaeus</i> DSM 12767 (AY099171, 98)	<i>Thermococcus aegaeus</i> DSM 12767 (AY099171, 98)	Hydrothermal deep sea vent
<i>Methanococcales</i>				
Hda_Arch35	2	<i>Methanococcus thermolithotrophicus</i> (M59128, 99)	<i>Methanococcus thermolithotrophicus</i> (M59128, 99)	Heated sea sediments
<i>Archaeoglobales</i>				
Hda_Arch9	3	<i>Archaeoglobus fulgidus</i> DSM 4304 (AE000782, 99)	<i>Archaeoglobus fulgidus</i> DSM 4304 (AE000782, 99)	Submarine hot spring

[†] Closest related sequence as revealed from BLAST search, Genbank accession number and percentage of 16S rRNA gene sequence similarity.

TABLE S3. Summary of *dsrAB* gene sequence-based OTUs detected in Dan and Halfdan PW.

Phylum Sequence representing OTU	No. of clones in OTU	Closest match (Acc.no., %) [†]
Dan PW		
<i>Archaeoglobales</i> Dan_dsr69	27	<i>Archaeoglobus fulgidus</i> DSM 4304 (AE000782, 99)
<i>Synthrophobacterales</i> Dan_dsr25T	2	<i>Desulfacinum infernum</i> DSM 9756 (AF418194, 94)
HalfDan PW		
<i>Archaeoglobales</i> Hda_dsr24	23	<i>Archaeoglobus fulgidus</i> DSM 4304 (AE000782, 100)
<i>Synthrophobacterales</i> Hda_dsr20T	5	<i>Desulfacinum infernum</i> DSM 9756 (AF418194, 94)
<i>Clostridiales</i> Hda_dsr92T	3	Uncultured sulfate-reducing bacterium clone B04P001 (AY197448, 82) <i>Desulfotomaculum geothermicum</i> (AF273029, 80)

[†] Closest related sequence as revealed from BLAST search, Genbank accession number and percentage of *dsrAB* gene sequence similarity.