

Supporting on-line material**Table DR1** Final H₂ and acetate concentrations in mineral:sediment slurries at the end of Thermal Gradient incubation, plus maximum CH₄ concentrations and temperature range.

Mineral	Acetate	H ₂	Days	Max Methane	
	μmol/l	μmol/l*		μmol/l*	Temperature °C
Haematite	9999	271	100	123	47-66, 66-89
Labradorite	8757	344	108	396	36-94
Pyrite	8503	525	110	443	39-97
Basalt	7117	300	83	159	35-60, 60-80
Ilmenite	6793	480	83	230	37-69, 82-95
Quartz	6679	638	97	120	32-51, 57-70
Hornblende	6238	720	61	282	33-71, 71-90
Olivine	5841	704	61	335	42-74, 74-94
Magnetite	3757	0	92	536	13-33, 33-58
No mineral	3850	0	93	531	6-35, 35-60
Sterile Basalt	2500	0	130	2	-

*Headspace

Table DR2. Mineral composition by ICP-OES in order of decreasing SiO₂ concentration.

Mineral	SiO ₂ wt%	TiO ₂ wt%	Al ₂ O ₃ wt%	Fe ₂ O ₃ wt%	MnO wt%	MgO wt%	CaO wt%	Na ₂ O wt%	K ₂ O wt%	P ₂ O ₅ wt%	Total wt%
Quartz Sand	100.2	0.02	0.06	0.04	0	0	0.01	0.01	0.02	0	100.36
Labradorite	52.57	0.14	28.24	0.62	0.02	0.63	12.94	3.53	0.24	0.02	98.94
Hornblende	49.95	0.30	8.25	7.87	0.09	15.91	12.55	2.33	0.83	0.00	98.07
Basalt	47.50	1.61	15.52	12.62	0.17	7.45	9.91	1.96	0.23	0.13	97.11
Olivine	41.82	0.01	0.55	7.94	0.09	49.35	0.10	0.08	0.03	0.00	99.98
Hematite	20.53	0.79	17.76	54.12	0.04	1.81	4.94	0.29	0.90	0.23	101.41
Magnetite	2.57	0.05	1.05	99.49	0.18	0.36	0.25	0.23	0.30	0.00	104.48
Ilmenite	1.06	47.31	1.28	50.75	0.22	3.41	0.19	0.04	0.00	0.01	104.27

Table DR3 Prokaryotic 16S rRNA gene sequence matches to excised DGGE bands from basalt amended sediment slurries incubated in a thermal gradient for 83 days.

PCR-DGGE analysis	DGGE band	Phyla/Subphyla (order) ^a	Nearest match by BLASTN search (accession number)	Environment of nearest sequence match	% Sequence similarity	Thermal gradient temperature range (°C) ^b
Bacteria 16S rRNA gene (357FGC-518R)	Bact-23	<i>Thermotogae</i> (<i>Thermotogales</i>)	<i>Thermotoga neapolitana</i> DSM 4359 (CP000916)		98	66
	Bact-34	<i>Firmicutes</i> (<i>Clostridiales</i>)	<i>Bacterium Yos55</i> (AB260040)	Black rust on borehole CORK 1026B exposed to hot crustal fluids, Juan de Fuca Ridge	87	60
	Bact-35	<i>Delta proteobacteria</i>	Uncultured bacterium clone MS-A219 (FJ949267)	Calcareous sandy sediment, Mallorca, Spain	95	15-60
	Bact-37	<i>Firmicutes</i> (<i>Clostridiales</i>)	<i>Tepidimicrobium ferriphilum</i> ^T DSM 16624 (GQ461826)		98	47-66
	Bact-39	<i>Firmicutes</i> (<i>Clostridiales</i>)	<i>Clostridium litorale</i> ^T DSM 5388 (NR_029270)		95	66-92
	Bact-42	<i>Beta proteobacteria</i> (<i>Burkholderiales</i>)	<i>Delftia</i> sp. LP2MM (GU272362)	Wastewater treatment membrane bioreactor, Korea	98	66-98
	Bact-43	<i>Firmicutes</i> (<i>Clostridiales</i>)	<i>Veillonella parvula</i> ^T strain JCM 12972 (AB538437)		86	60-92
	Bact-44	<i>Gammaproteobacteria</i> (<i>Xanthomonadales</i>)	Uncultured bacterium clone (FN555655)	Deteriorated stone, Granada, Spain	97	92-98
	Bact-46	<i>Firmicutes</i> (<i>Lactobacillales</i>)	Uncultured bacterium clone GI-10-A05 (GQ130056)	Spacecraft assembly clean room floor, California, USA	89	98
	Bact-49	<i>Beta proteobacteria</i> (<i>Burkholderiales</i>)	<i>Delftia</i> sp. LP2MM (GU272362)	Wastewater treatment membrane bioreactor, Korea	96	92-98
Archaea 16S rRNA gene (SAF-Parch519R) 30-60% denaturant gradient	Arch-26	<i>Euryarchaeota</i> (<i>MBG-D/Thermoplasmatales</i>)	Uncultured archaeon clone GoM87_Arch341 (FN421133)	Seep sediments, Gulf of Mexico	98	15-60
	Arch-27	<i>Euryarchaeota</i> (<i>MBG-D/Thermoplasmatales</i>)	Uncultured archaeon clone GoM87_Arch341 (FN421133)	Seep sediments, Gulf of Mexico	97	15-60

	Arch-31	<i>Euryarchaeota</i> (MBG-D/ <i>Thermoplasmatales</i>)	Uncultured archaeon clone GoM87_Arch341 (FN421133)	Seep sediments, Gulf of Mexico	97	15-60
	Arch-40	<i>Euryarchaeota</i> (MBG-D/ <i>Thermoplasmatales</i>)	Uncultured archaeon clone GoM87_Arch341 (FN421133)	Seep sediments, Gulf of Mexico	96	15-60
	Arch-41	<i>Euryarchaeota</i> (MBG-D/ <i>Thermoplasmatales</i>)	Uncultured archaeon clone K8MV-C26-08 (AB362545)	Seep sediments, Nankai Trough	97	60-66
	Arch-44	<i>Euryarchaeota</i> (MBG-D/ <i>Thermoplasmatales</i>)	Uncultured archaeon clone 48H-0S-29 (GU270215)	Seep sediments, Okhotsk Sea	97	47, 66
	Arch-45	<i>Euryarchaeota</i> (MBG-D/ <i>Thermoplasmatales</i>)	Uncultured archaeon clone GNA10H07 (EU731608)	Hypersaline microbial mat, Guerrero Negro pond	99	15-66
Archaea 16S rRNA gene (SAF-Parch519R) 30-80% denaturant gradient	Arch-37	<i>Euryarchaeota</i> (MBG-D/ <i>Thermoplasmatales</i>)	Uncultured archaeon clone K8MV-C26-08 (AB362545)	Seep sediments, Nankai Trough	97	60
	Arch-38	<i>Euryarchaeota</i> (MBG-D/ <i>Thermoplasmatales</i>)	Uncultured archaeon clone K8MV-C26-08 (AB362545)	Seep sediments, Nankai Trough	97	60
	Arch-43	<i>Euryarchaeota</i> (<i>Methanococcales</i>)	Uncultured archaeon clone II26B6 (AM268700)	Vent fluid, Logatchev Hydrothermal Vent Field, Mid-Atlantic- Ridge	90	92-98
	Arch-44	<i>Euryarchaeota</i> (MBG-D/ <i>Thermoplasmatales</i>)	Uncultured archaeon clone 48H-0S-29 (GU270215)	Seep sediments, Okhotsk Sea	90	66-98
	Arch-45	<i>Euryarchaeota</i> (MBG-D/ <i>Thermoplasmatales</i>)	Uncultured archaeon clone GoM87_Arch341 (FN421133)	Seep sediments, Gulf of Mexico	94	66-98
	Arch-50	<i>Euryarchaeota</i> (MBG-D/ <i>Thermoplasmatales</i>)	Uncultured archaeon clone GoM87_Arch341 (FN421133)	Seep sediments, Gulf of Mexico	93	92-98
	Arch-51	<i>Euryarchaeota</i> (<i>Methanococcales</i>)	<i>Methanocaldococcus</i> <i>fervens</i> strain AG86	Deep-sea hydrothermal chimney, East Pacific Rise (2600m)	88	66-98

See Supplementary Figures DR1 and DR2 for DGGE gel images, numbers refer to bands on the DGGE Gels Figs DR1- DR2.

a: MBG-D Marine benthic Group D (Vetriani *et al.*, 1999)

b: Determined by sequencing and extrapolation of DGGE band position.

References

1. G. Webster, C. J. Newberry, J. C. Fry, A. J. Weightman, *J. Microbiol. Methods* **55**, 155 (Oct, 2003).
2. C. Vetriani, H. W. Jannasch, B. J. MacGregor, D. A. Stahl, A. L. Reysenbach, *Applied and Environmental Microbiology* **65**, 4375 (Oct, 1999).

Supplementary Figure Legends

Supplementary Figure DR1 PCR-DGGE analysis of bacterial 16S rRNA gene diversity in basalt amended sediment slurries incubated in a thermal gradient (0-100°C) for 83 days. Lanes marked M = DGGE marker (Webster et al., 2003); lanes marked with numbers = slurry incubation temperature (°C). Numbered bands indicate those bands that were excised and sequenced (see Table DR2).

Supplementary Figure DR2 PCR-DGGE analysis of archaeal 16S rRNA gene diversity in basalt amended sediment slurries heated in a thermal gradient (0-100°C) for 83 days. Gels run with a DGGE gradient of (a) 30-60% (b) 30-80%. Lanes marked M = DGGE marker (Webster et al., 2003); lanes marked with numbers = slurry incubation temperature (°C). Numbered bands indicate those bands that were excised and sequenced (see Table DR2).

Supplementary Figure DR3 Phylogenetic tree showing the diversity of *Crenarchaeota* 16S rRNA gene sequences in an ilmenite amended sediment slurry incubated at 63°C for 83 days. Tree was constructed from 410 bases of aligned 16S rRNA gene sequences using Minimum Evolution with LogDet distance analysis implemented in MEGA 4 (Tamura et al., 2007). Bootstrap support values over 50% (1000 replicates) are shown. Representative sequences of the *Korarchaeota* were used as outgroups; hot spring clone pBA5 (AF176347), hot spring clone pJP27 (L25852), and hot spring clone SRI-306 (AF255604). MCG, Miscellaneous Crenarchaeotic Group; MBG-C, Marine Benthic Group C; MBG-D, Marine Benthic Group D (see Teske and Sørensen (2008) for novel archaeal lineage classification).

Supplementary Figure DR4 Phylogenetic tree showing the diversity of *Euryarchaeota* 16S rRNA gene sequences in an ilmenite amended sediment slurry incubated at 89°C for 83 days. Tree was constructed from 410 bases of aligned 16S rRNA gene sequences using Minimum Evolution with LogDet distance analysis implemented in MEGA 4 (Tamura et al., 2007). Bootstrap support values over 50% (1000 replicates) are shown. Representative sequences of the *Korarchaeota* were used as outgroups; hot spring clone pBA5 (AF176347), hot spring clone pJP27 (L25852), and hot spring clone SRI-306 (AF255604). DHVEG, Deep Hydrothermal Vent Euryarchaeotic Group (see Teske and Sørensen (2008) for novel archaeal lineage classification).

Supplementary Figure DR5 Phylogenetic tree showing the diversity of *Euryarchaeota* 16S rRNA gene sequences in a pyrite amended sediment slurry incubated at 65°C for 110 days. Tree was constructed from 602 bases of aligned 16S rRNA gene sequences using Minimum Evolution with LogDet distance analysis implemented in MEGA 4 (Tamura et al., 2007). Bootstrap support values over 50% (1000 replicates) are shown. Representative sequences of the *Korarchaeota* were used as outgroups; hot spring clone pBA5 (AF176347), hot spring clone pJP27 (L25852), and hot spring clone SRI-306 (AF255604). DHVEG, Deep-Sea Hydrothermal Vent Euryarchaeotal Group (see Teske and Sørensen (2008) for novel archaeal lineage classification).

Supplementary Figure DR6 Phylogenetic tree showing the diversity of *Crenarchaeota* 16S rRNA gene sequences in a pyrite amended sediment slurry incubated at 65°C (blue) and 90°C (red) for 110 days. Tree was constructed from 700 bases of aligned 16S rRNA gene sequences using Minimum Evolution with LogDet distance analysis implemented in MEGA 4 (Tamura et

al., 2007). Bootstrap support values over 50% (1000 replicates) are shown. Representative sequences of the *Korarchaeota* were used as outgroups; hot spring clone pBA5 (AF176347), hot spring clone pJP27 (L25852), and hot spring clone SRI-306 (AF255604). MCG, Miscellaneous Crenarchaeotic Group; C3, Crenarchaeota Group 3; MBG-C, Marine Benthic Group C; MBG-D, Marine Benthic Group D (see Teske and Sørensen (2008) for novel archaeal lineage classification).

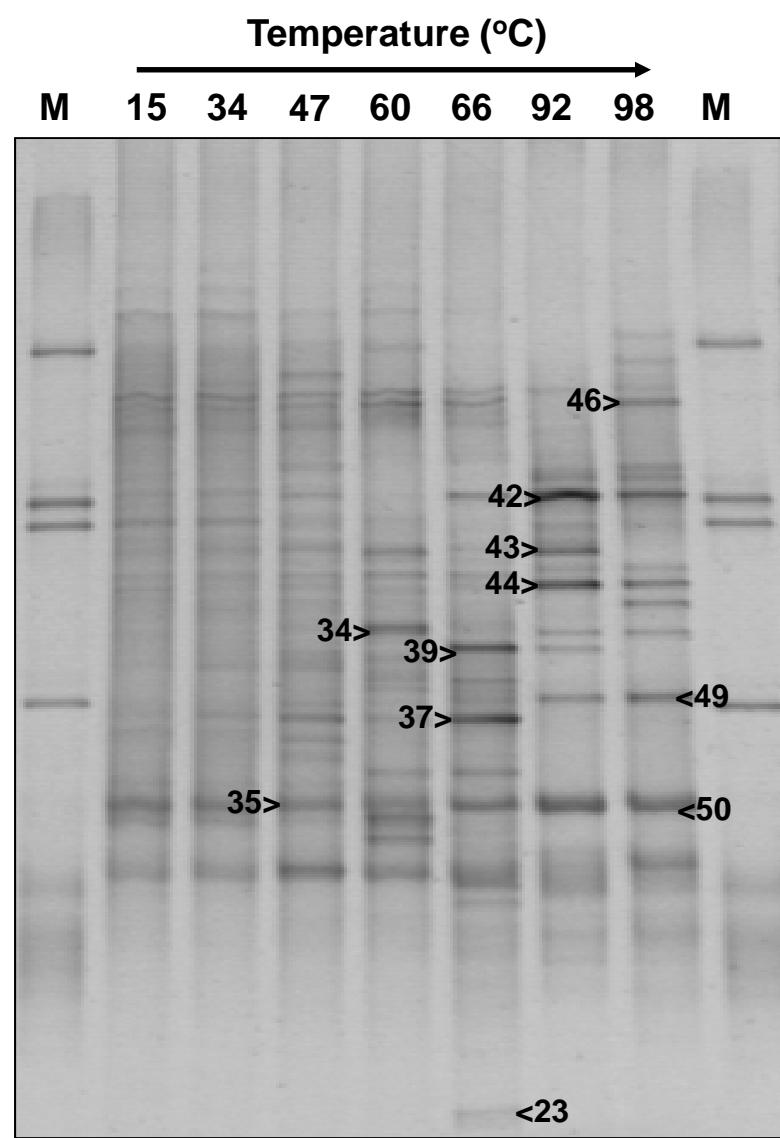
Supplementary Figure DR7 Phylogenetic tree showing the diversity of *Euryarchaeota* 16S rRNA gene sequences in a pyrite amended sediment slurry incubated at 90°C for 110 days. Tree was constructed from 605 bases of aligned 16S rRNA gene sequences using Minimum Evolution with LogDet distance analysis implemented in MEGA 4 (Tamura et al., 2007). Bootstrap support values over 50% (1000 replicates) are shown. Representative sequences of the *Korarchaeota* were used as outgroups; hot spring clone pBA5 (AF176347), hot spring clone pJP27 (L25852), and hot spring clone SRI-306 (AF255604). DHVEG, Deep-Sea Hydrothermal Vent Euryarchaeotal Group (see Teske and Sørensen (2008) for novel archaeal lineage classification). Vent Chimney Euryarchaeotal Group (Kormas et al., 2006).

Supplementary Figure DR8 RockEval analysis of organic matter in pressurised sequential heating experiments with basalt sediment slurries. DR1 is free hydrocarbons and DR2 the labile fraction of the macromolecular organic matter.

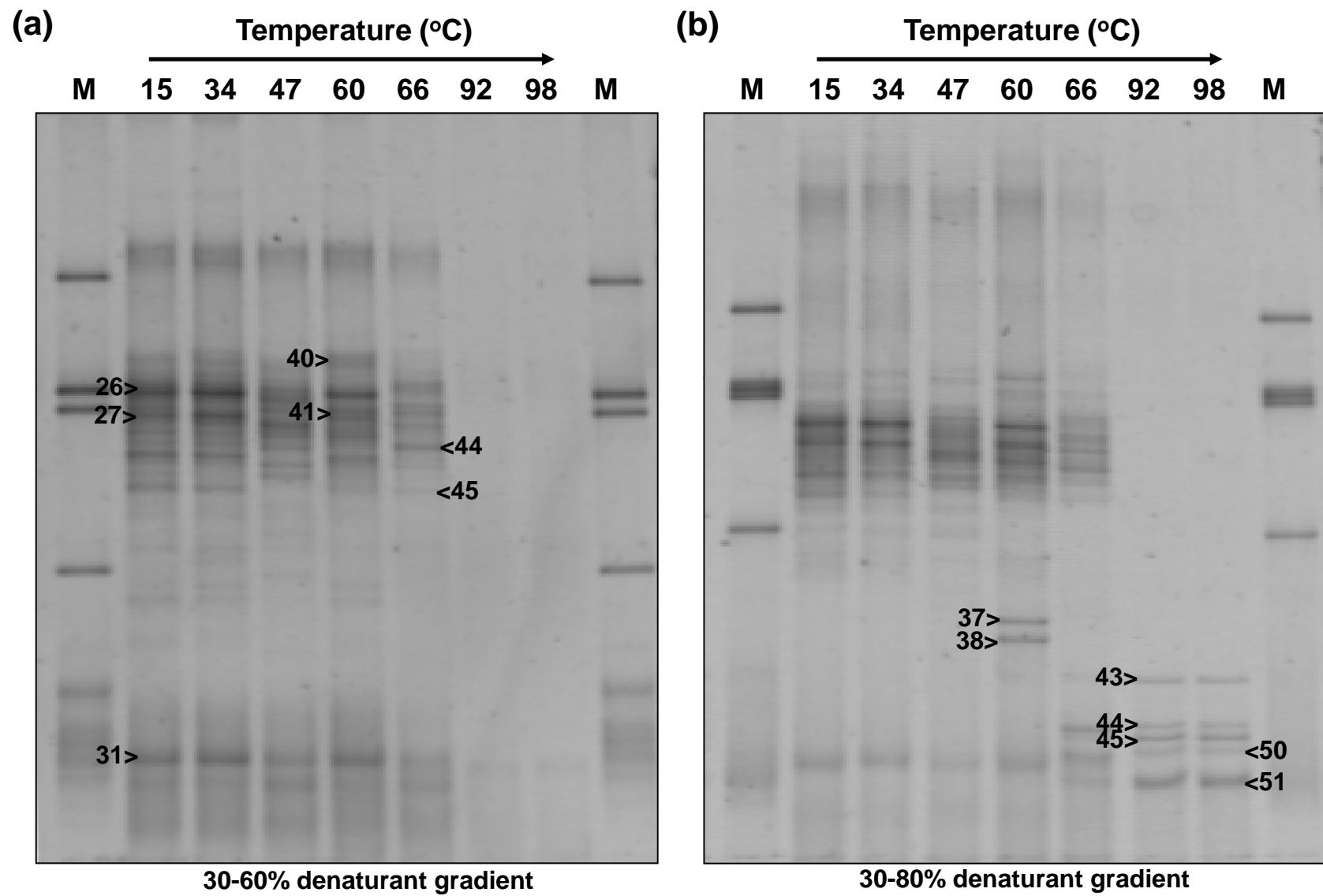
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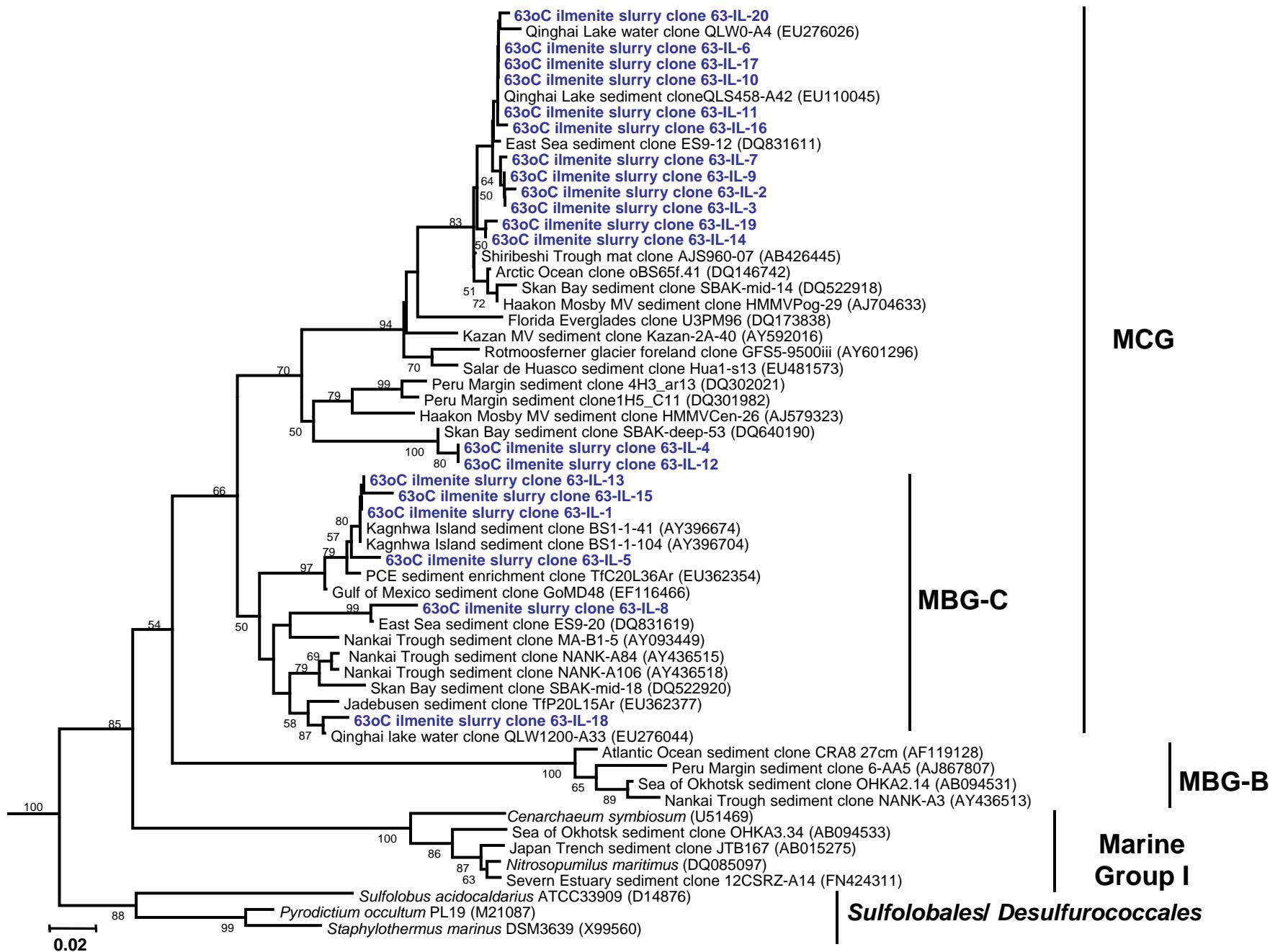
Supplementary Figure DR1



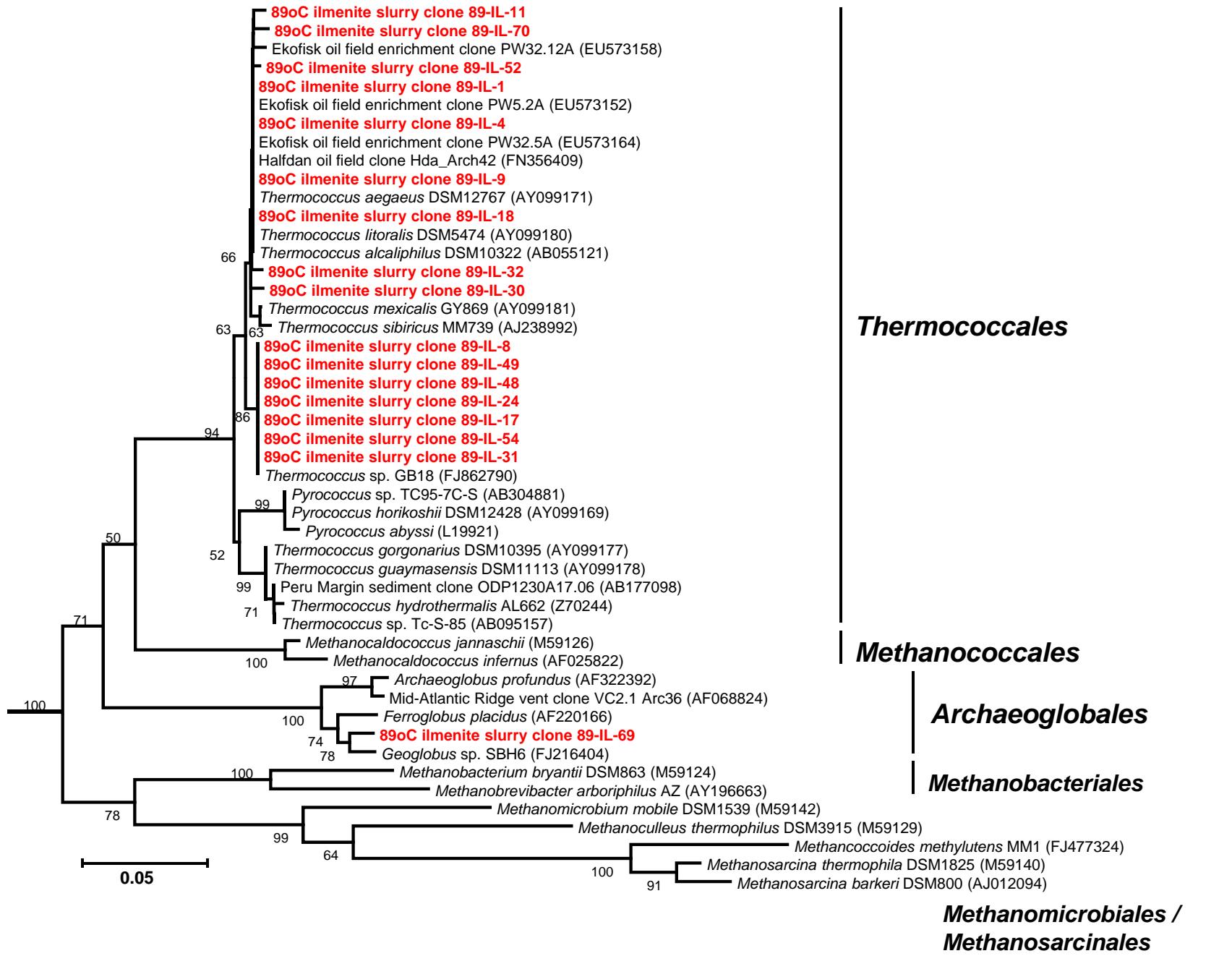
Supplementary Figure DR2



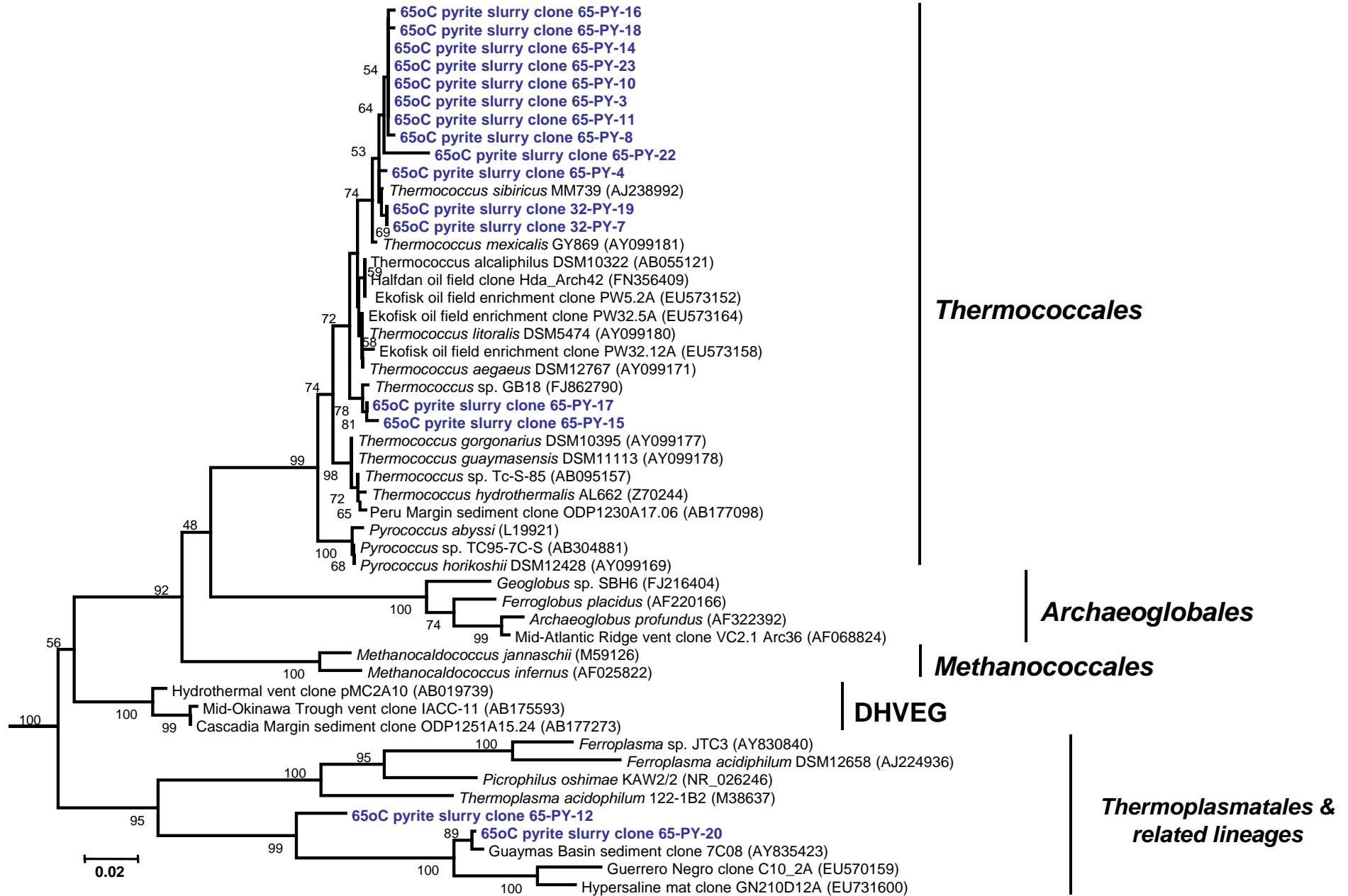
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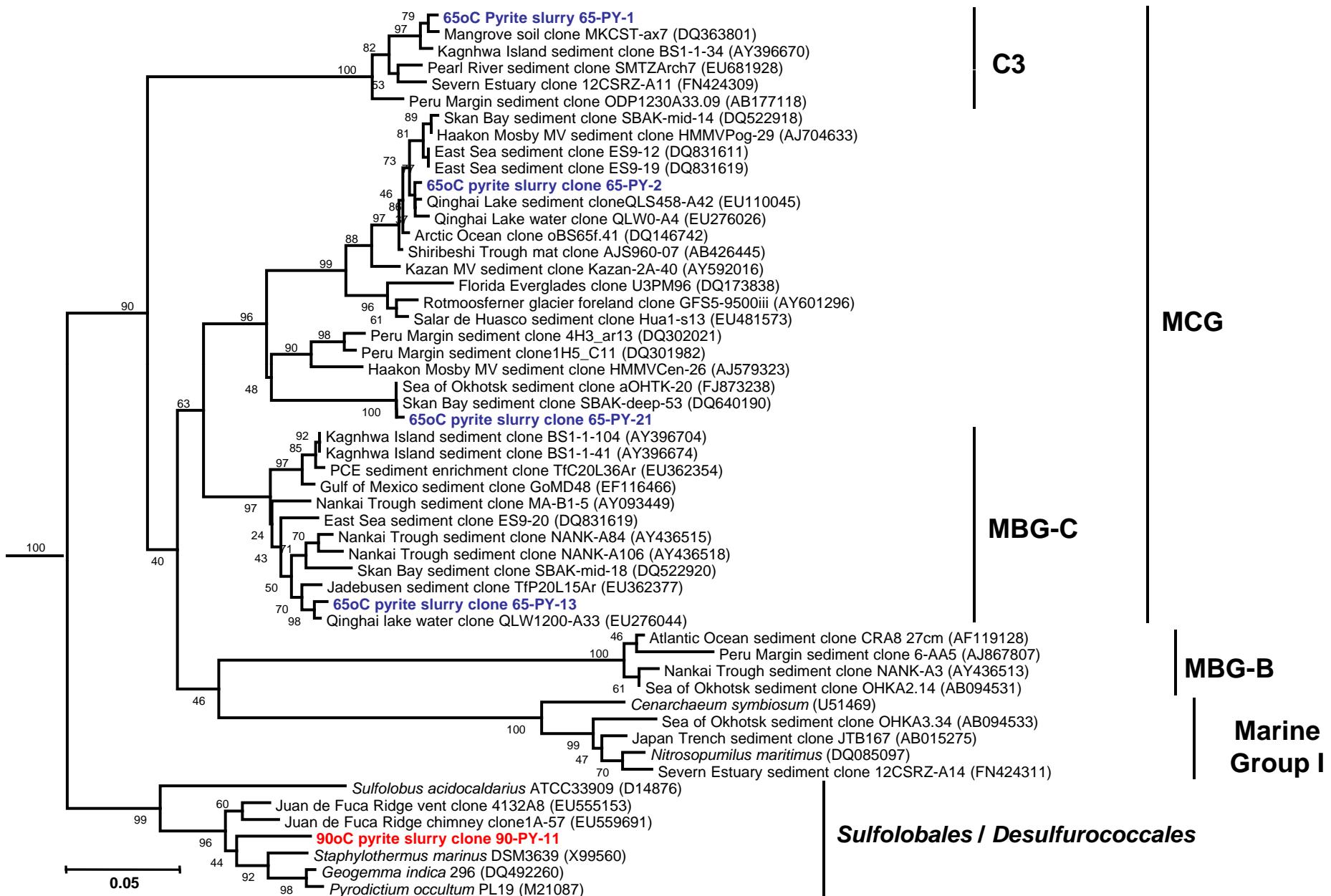
Supplementary Figure DR4



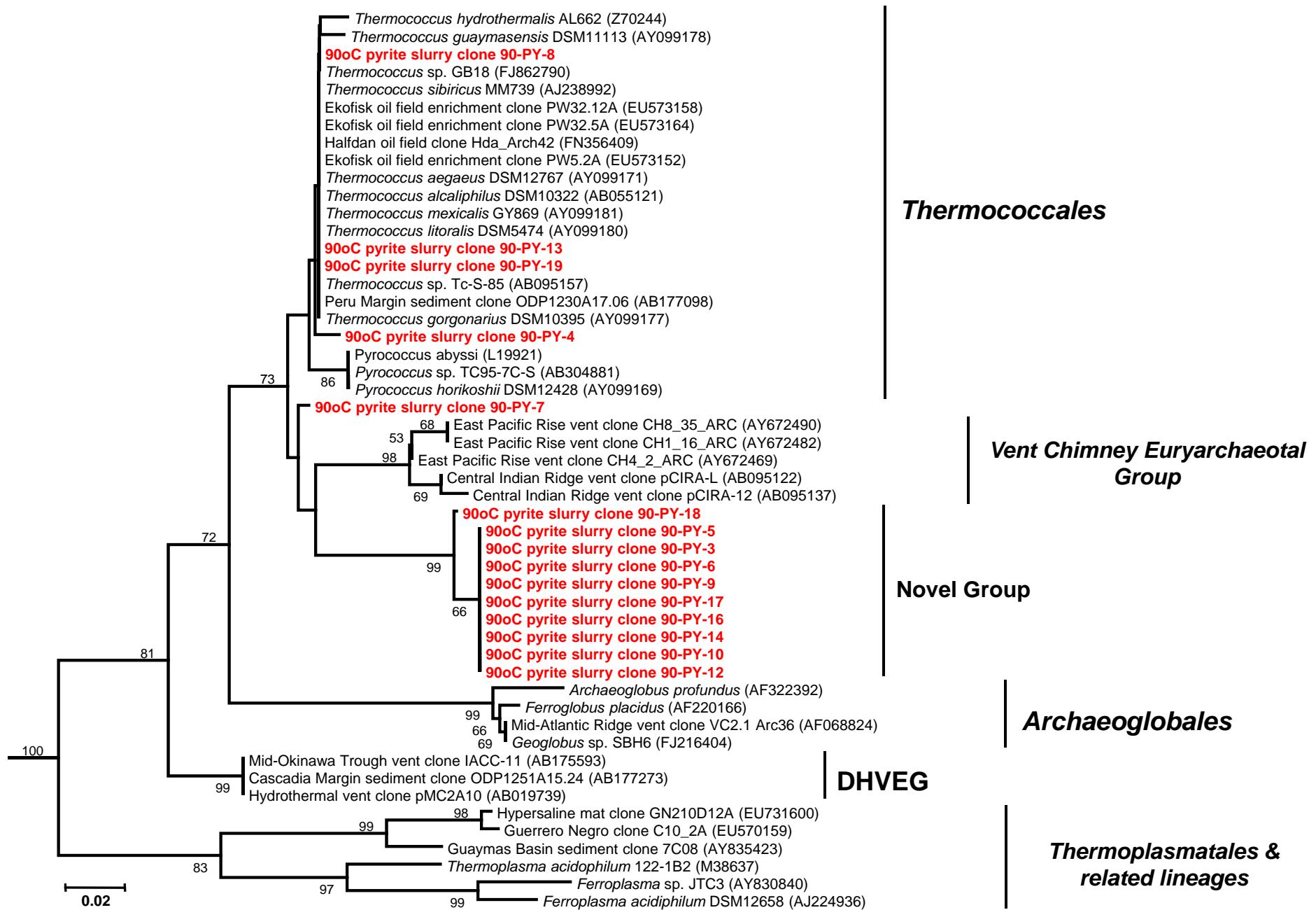
Supplementary Figure DR5



Supplementary Figure DR6



Supplementary Figure DR7



Supplementary Figure DR8

