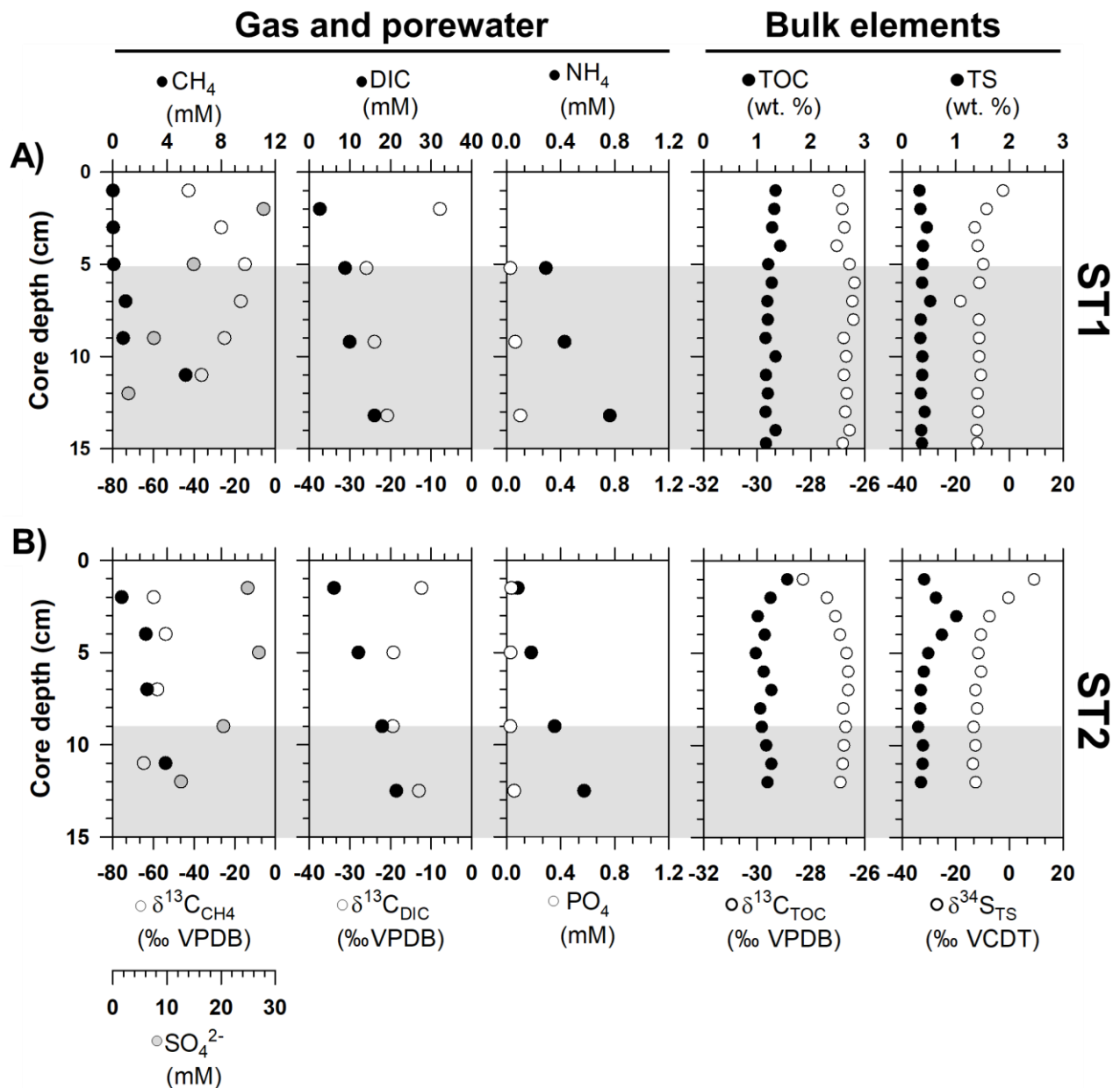
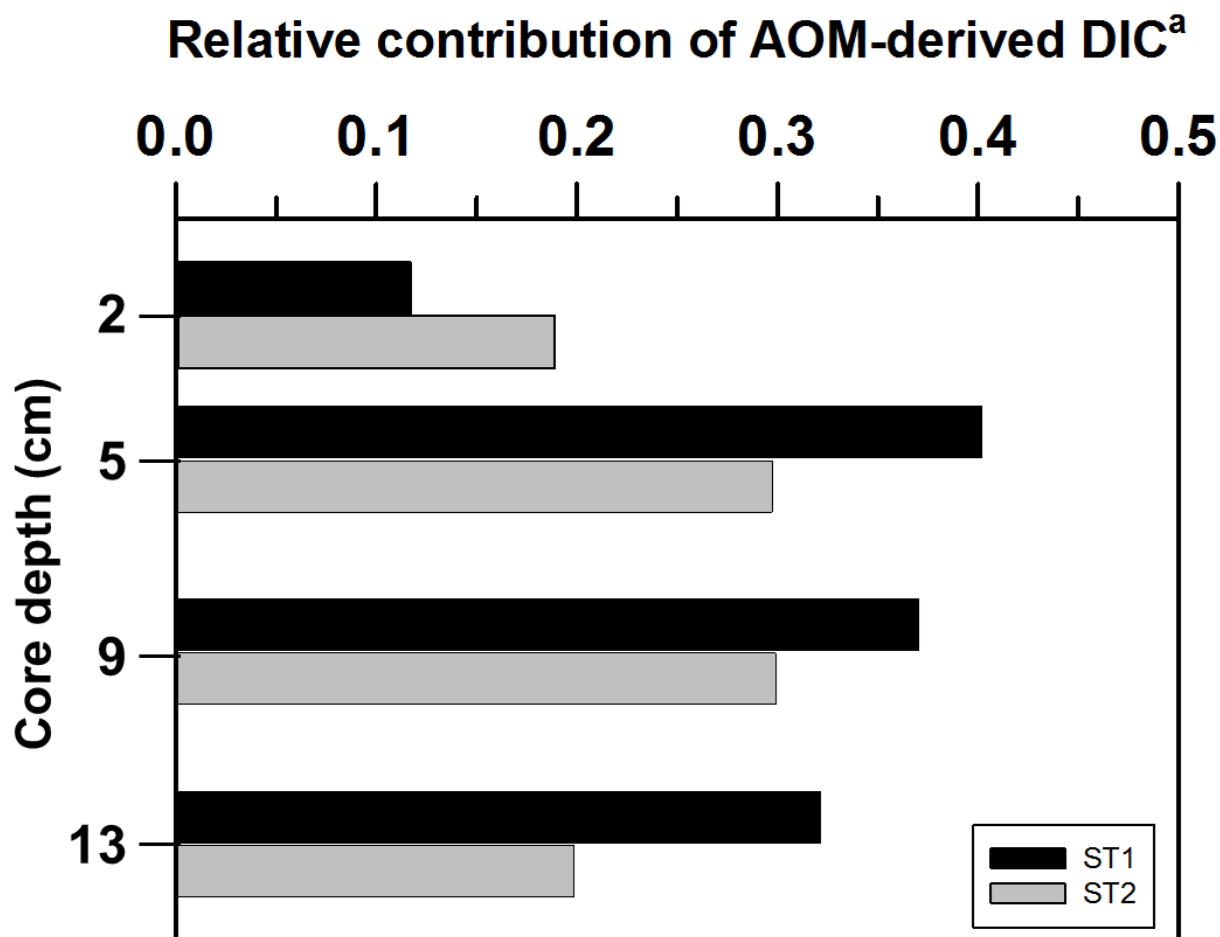


Supplementary Material

Supplementary Figure S1. Depth profiles of gas (methane), porewater (sulfate, dissolved inorganic carbon (DIC), nutrients), and bulk elements (total organic carbon (TOC) and total sulfur (TS) contents) and isotopic compositions of methane, DIC, TOC and TS ($\delta^{13}\text{C}_{\text{CH}_4}$, $\delta^{13}\text{C}_{\text{DIC}}$, $\delta^{13}\text{C}_{\text{TOC}}$ and $\delta^{34}\text{S}_{\text{TS}}$) obtained from a) ST1 and b) ST2 sites. Note that the ST2 data were taken from Lee et al. (2019b). Note that the grey shading indicates potential SMTZ layers.



Supplementary Figure S2. Relative contribution of AOM-derived DIC based on the isotopic mass balance (Coffin et al., 2013).

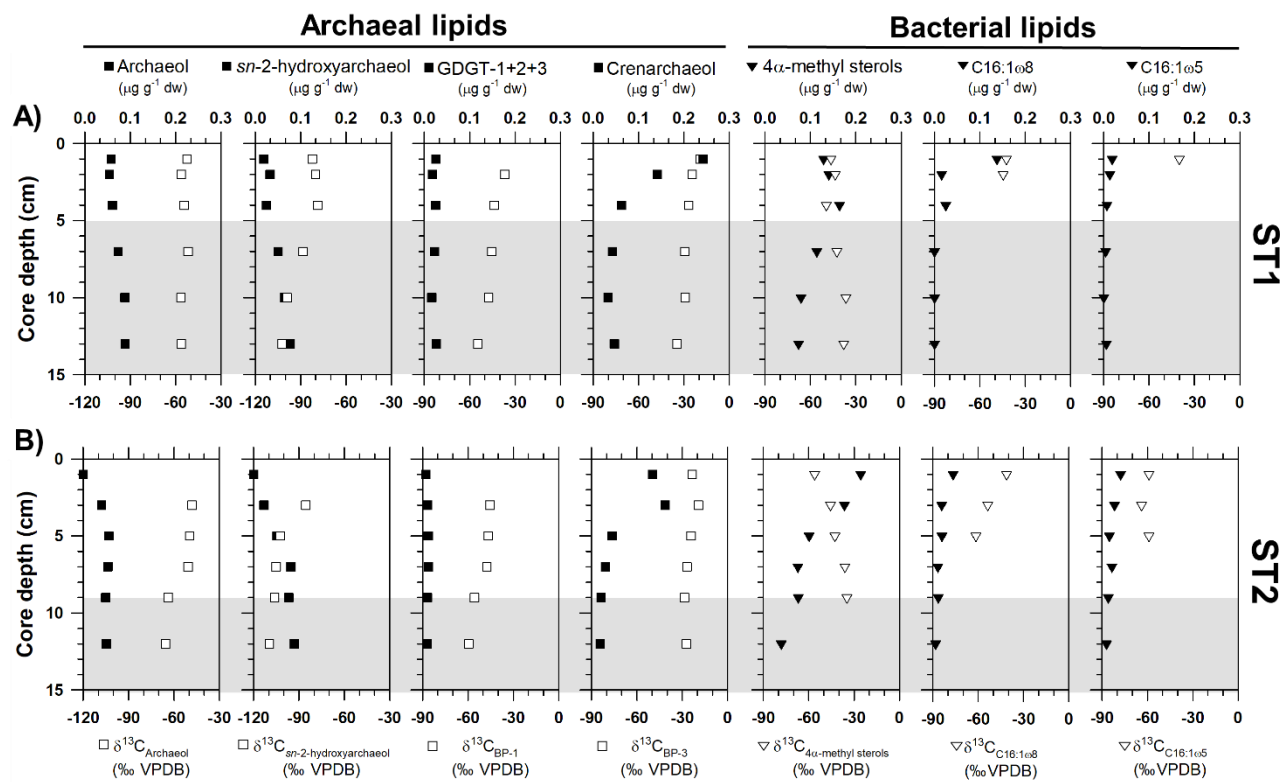


^a calculated based on the isotopic mass balance as follows;

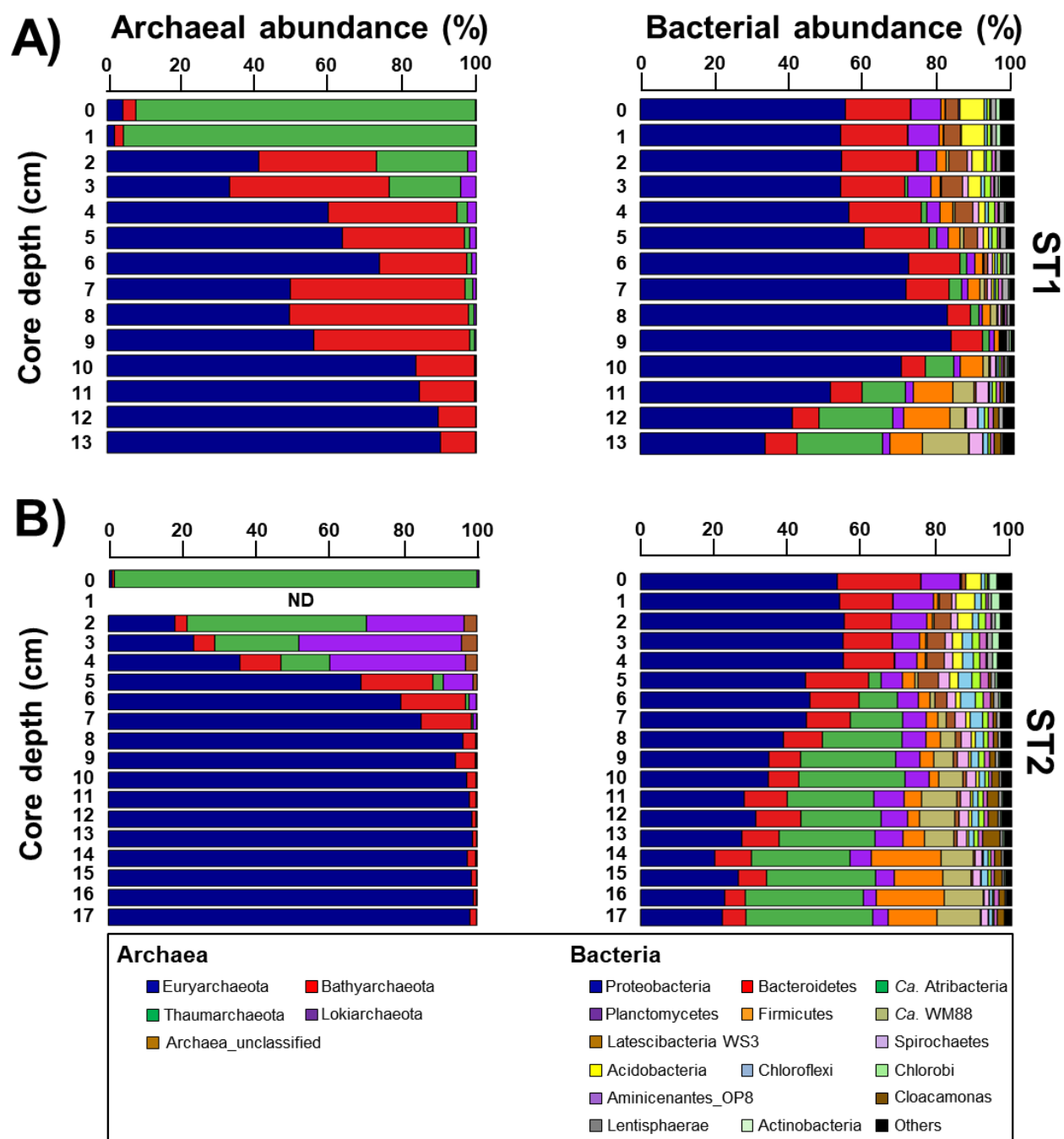
(1) $R_{\text{subsurface CH}_4} + R_{\text{seawater-derived DIC}} = 1$

(2) $R_{\text{subsurface CH}_4} \delta^{13}\text{C}_{\text{subsurface CH}_4} + R_{\text{seawater-derived DIC}} \delta^{13}\text{C}_{\text{seawater-derived DIC}} = \delta^{13}\text{C}_{\text{mixed DIC}}$

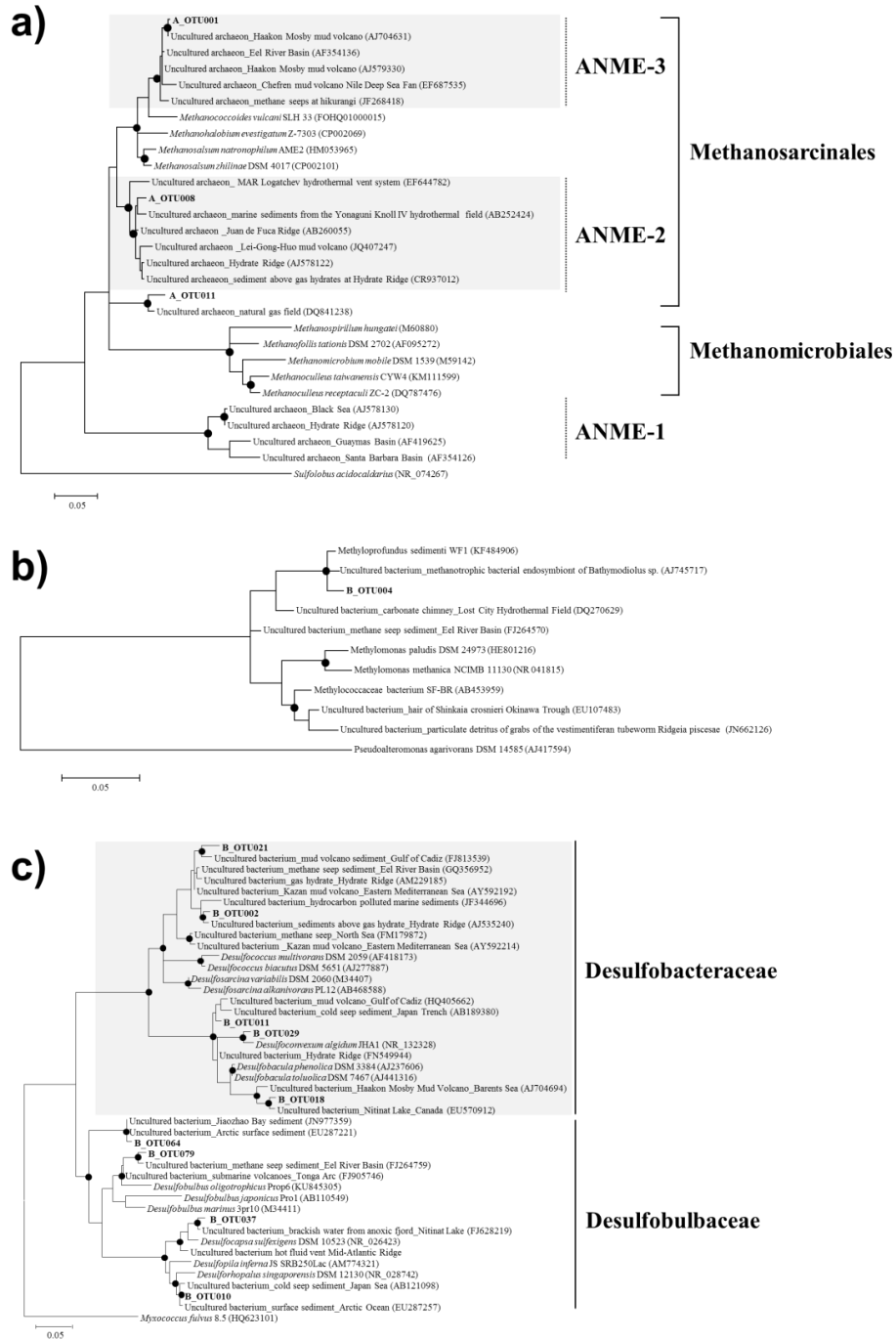
Supplementary Figure S3. Depth profiles of concentrations and isotopic compositions of selected lipid biomarkers (archaeol, *sn*-2-hydroxyarchaeol, GDGTs, 4 α -methyl sterols, and bacterial fatty acids) obtained from a) ST1 and b) ST2 sites. The ST2 data were taken from Lee et al. (2019b). Note that the grey shading indicates potential SMTZ layers.



Supplementary Figure S4. Relative abundances of a) archaea taxa at the class level and b) bacteria taxa at the phylum level but Proteobacteria at the class level along the core depths. The ST2 data were taken from Lee et al. (2019b).



Supplementary Figure S5. Phylogenetic tree of major OTUs of a) *Methanomicrobia*, b) *Methylococcales*, and c) *Deltaproteobacteria*. Major OTUs with greater than 5% relative abundance for each sample were selected and a phylogenetic tree was reconstructed via heuristic search with the maximum likelihood criterion. Filled circles indicate that the corresponding nodes had > 70% bootstrap values based on 1,000 resamplings. Bars indicate five nucleotide substitutions per 100 nucleotides.



Supplementary Table S1. Results of concentration and isotopic compositions of gas (methane) and porewater (sulfate, dissolved inorganic carbon (DIC), nutrients).

Core depth (cm)	Gas and porewater							Bulk elements			
	Methane		Sulfate	DIC		Ammonia	Phosphate	TOC		TS	
	mM	‰ VPDB	μg g ⁻¹ dw	mM	‰ VPDB	mM	mM	wt. %	‰ VPDB	wt. %	‰ VCDT
Siboglinid tubeworm field 1 (ST1)											
1	0.0	-42.8	-	-	-	-	-	1.3	-27.0	0.3	-2.4
2	-	-	27.8	2.6	-7.8	-	-	1.3	-26.8	0.3	-8.5
3	0.0	-26.7	-	-	-	-	-	1.3	-26.7	0.5	-12.9
4	-	-	14.9	8.8	-25.9	0.3	0.0	1.4	-27.0	0.4	-11.8
5	0.1	-15.0	-	-	-	-	-	1.2	-26.6	0.4	-9.8
6	-	-	-	-	-	-	-	1.3	-26.4	0.4	-11.2
7	0.9	-17.0	-	-	-	-	-	1.2	-26.4	0.5	-18.3
8	-	-	-	-	-	-	-	1.2	-26.4	0.3	-11.4
9	0.8	-25.0	7.6	9.9	-23.9	0.4	0.1	1.2	-26.8	0.3	-11.3
10	-	-	-	-	-	-	-	1.3	-26.7	0.4	-11.3
11	5.4	-36.3	-	-	-	-	-	1.2	-26.8	0.4	-10.7
12	-	-	2.9	16.1	-20.8	0.8	0.1	1.2	-26.7	0.3	-11.9
13	-	-	-	-	-	-	-	1.2	-26.7	0.4	-11.7
14	-	-	-	-	-	-	-	1.3	-26.6	0.4	-12.2
15	-	-	-	-	-	-	-	1.2	-26.8	0.4	-12.0
Siboglinid tubeworm field 2 (ST2)											
1	-	-	-	-	-	-	-	1.6	-28.3	0.4	9.2
2	0.7	-59.9	24.9	6.1	-12.4	0.1	0.0	1.2	-27.4	0.6	-0.4
3	-	-	-	-	-	-	-	1.0	-27.1	1.0	-7.5
4	2.4	-54.0	-	-	-	-	-	1.1	-26.9	0.7	-10.7
5			-	12.1	-19.3	0.2	0.0	1.0	-26.7	0.5	-11.6
6	-	-	-	-	-	-	-	1.1	-26.6	0.4	-10.6
7	2.5	-58.1	-	-	-	-	-	1.3	-26.6	0.3	-12.6
8	-	-	-	-	-	-	-	1.1	-26.8	0.3	-12.0
9			20.4	17.9	-19.4	0.4	0.0	1.1	-26.7	0.3	-13.4
10	-	-	-	-	-	-	-	1.2	-26.8	0.4	-12.6
11	3.9	-64.8	-	-	-	-	-	1.3	-26.8	0.4	-13.6
12	-	-	12.6	21.4	-13.0	0.6	0.1	1.2	-26.9	0.4	-12.6

Supplementary Table S2. Results of concentrations and $\delta^{13}\text{C}$ values of selected lipid biomarkers, such as archaeol, *sn*-2-hydroxyarchaeol, GDGTs, and 4 α -methyl sterols.

Core depth (cm)	Archaeol		<i>sn</i> -2-hydroxyarchaeol		GDGT-0	GDGT-1	GDGT-2	GDGT-3	Crenarchaeol	Biphytane-0	Biphytane-1	Biphytane-2	Biphytane-3	4 α -methyl sterols	
	$\mu\text{g g}^{-1}$ dw	‰ VPDB	$\mu\text{g g}^{-1}$ dw	‰ VPDB	$\mu\text{g g}^{-1}$ dw	$\mu\text{g g}^{-1}$ dw	$\mu\text{g g}^{-1}$ dw	$\mu\text{g g}^{-1}$ dw	$\mu\text{g g}^{-1}$ dw	‰ VPDB	‰ VPDB	‰ VPDB	‰ VPDB	$\mu\text{g g}^{-1}$ dw	‰ VPDB
Siboglinid tubeworms field 1 (ST1)															
1	0.06	-52.5	0.02	-82.3	0.19	0.01	0.01	0.01	0.24	-23.7	-	-26.7	-19.2	0.13	-46.4
2	0.05	-56.2	0.03	-80.1	0.08	0.01	0.01	0.01	0.14	-27.9	-36.7	-39.1	-24.5	0.14	-43.6
4	0.06	-54.4	0.02	-78.6	0.08	0.01	0.01	0.01	0.06	-31.2	-43.9	-31.7	-26.9	0.16	-49.5
7	0.07	-51.7	0.05	-88.5	0.06	0.01	0.01	0.01	0.04	-30.6	-45.4	-42.9	-29.5	0.11	-42.5
10	0.09	-56.5	0.06	-99.0	0.05	0.01	0.01	0.01	0.03	-31.3	-47.5	-43.9	-29.2	0.08	-36.5
13	0.09	-56.2	0.08	-102.3	0.07	0.01	0.01	0.01	0.05	-33.3	-54.7	-48.9	-39.3	0.07	-38.0
Siboglinid tubeworms field 2 (ST2)															
1	0.01	-	-	-	0.10	0.00	0.00	0.00	0.13	-22.7	-	-37.0	-23.4	0.21	-56.11
3	0.04	-48.0	0.02	-85.6	0.07	0.01	0.01	0.00	0.16	-26.2	-45.5	-19.4	-19.2	0.18	-45.61
5	0.06	-49.7	0.05	-102.5	0.04	0.01	0.01	0.00	0.05	-37.7	-46.7	-30.6	-24.2	0.10	-42.71
7	0.05	-50.7	0.08	-105.2	0.04	0.01	0.01	0.00	0.03	-30.6	-47.5	-35.5	-33.6	0.08	-36.10
9	0.05	-63.8	0.08	-106.1	0.03	0.01	0.01	0.00	0.02	-32.9	-55.8	-48.9	-36.7	0.08	-34.77
12	0.05	-65.5	0.09	-109.6	0.03	0.01	0.01	0.00	0.02	-26.1	-59.5	-34.6	-27.3	0.04	-

- indicates not determined

Supplementary Table S3. Heat map of major OTUs with taxonomy. The ST2 data were taken from Lee et al. (2019b).

OTU_ID	Taxonomy							Siboglinid tubeworm field 1 (ST1)													Siboglinid tubeworm field 2 (ST2)																			
								Core depth (cm)													Core depth (cm)																			
	Domain	Phylum	Class	Order	Family	Genus	Species	0	1	2	3	4	5	6	7	8	9	10	11	12	13	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	
A_OTU001	Archaea	Euryarchaeota	Methanomicrobia	Methanosarcinales	Methanosarcinaceae	Methanococoides	Methanococoides_unclassified	3.71	1.14	27.75	15.00	51.80	59.15	66.99	42.17	42.30	48.29	95.12	92.49	95.14	96.41	0.28	ND	4.86	9.72	19.69	53.52	79.00	78.69	91.05	95.75	92.45	95.12	96.41	96.14	96.28	94.62	96.93	95.29	
A_OTU008	Archaea	Euryarchaeota	Methanomicrobia	Methanosarcinales	ANME2_f	ANME2_f_unclassified	ANME2_f_unclassified	0.00	0.01	0.00	0.01	0.03	0.09	0.16	0.18	0.15	0.22	0.30	0.19	0.35	0.37	0.00	ND	0.07	0.90	5.39	8.67	3.61	3.12	2.36	2.29	1.79	1.42	0.56	0.68	0.13	0.03	0.04	0.00	
A_OTU013	Archaea	Euryarchaeota	Methanomicrobia	Methanosarcinales	NSM41238_f	NSM41238_g	NSM41238_s	0.03	0.33	8.75	19.43	3.83	0.81	0.90	0.12	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
B_OTU002	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacteriales	Desulfobacteraceae	XXL_g	XXL_g_unclassified	0.02	0.07	0.02	0.01	0.07	0.09	0.16	0.24	0.36	0.23	3.24	3.70	9.37	8.70	0.02	0.04	0.01	0.02	0.05	1.33	6.49	12.61	16.31	16.15	26.90	15.13	18.02	15.08	10.54	17.24	16.44	13.74	
B_OTU021	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacteriales	Desulfobacteraceae	XXL_g	XXL_g_unclassified	0.00	0.00	0.03	0.00	0.06	0.09	0.11	0.29	0.11	0.06	0.38	0.36	0.83	0.39	0.00	0.01	0.00	0.01	0.01	0.06	0.30	0.24	1.26	2.00	1.63	1.79	2.59	3.70	2.04	1.39	0.82	0.46	
B_OTU029	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacteriales	Desulfobacteraceae	Desulfocoryneum	Desulfocoryneum_unclassified	0.04	0.01	0.22	0.29	0.24	0.53	0.34	0.97	0.41	0.44	1.13	2.28	2.97	3.28	0.01	0.11	0.09	0.08	0.09	0.33	0.23	0.33	0.27	0.12	0.19	0.14	0.09	0.10	0.04	0.10	0.06	0.09	
B_OTU011	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacteriales	Desulfobacteraceae	Desulfobacteraceae_unclassified	Desulfobacteraceae_unclassified	0.00	0.02	0.08	0.06	0.10	0.12	0.16	0.25	0.32	0.22	2.11	3.06	7.16	5.89	0.02	0.19	0.47	0.32	0.37	1.42	2.70	4.84	5.58	6.69	4.95	4.54	5.05	3.96	4.40	4.31	3.20	4.79	
B_OTU018	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacteriales	Desulfobacteraceae	Desulfobacula	Desulfobacula_unclassified	0.62	0.40	1.81	1.59	2.00	2.30	1.01	0.80	0.50	0.12	0.57	0.41	0.32	0.08	0.14	1.69	4.30	5.46	3.98	7.05	7.23	5.63	3.04	1.32	1.02	0.67	0.61	0.41	0.15	0.05	0.02	0.05	
B_OTU010	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacteriales	Desulfobacteraceae	Desulfofurax	Desulfofurax_unclassified	2.49	2.40	4.69	4.53	5.01	6.49	7.04	5.39	2.63	1.83	3.48	3.63	2.16	1.55	2.46	5.88	6.76	7.56	5.21	4.85	4.60	4.59	2.58	1.10	0.63	0.35	0.30	0.12	0.06	0.03	0.01	0.02	
B_OTU037	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacteriales	Desulfobacteraceae	Desulfocapsa	Desulfocapsa_unclassified	0.00	0.81	1.55	1.24	1.29	1.88	1.37	0.94	0.86	0.36	0.94	0.34	0.15	0.03	0.24	2.67	4.13	4.13	2.41	1.67	1.40	0.85	0.42	0.16	0.05	0.02	0.02	0.00	0.01	0.01	0.00	0.02	
B_OTU064	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacteriales	Desulfobacteraceae	U1287221_g	U1287221_s	0.83	1.96	1.17	1.44	0.32	0.20	0.13	0.17	0.02	0.02	0.03	0.03	0.05	0.01	3.13	5.07	5.11	2.39	2.05	0.32	0.13	0.03	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
B_OTU079	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacteriales	Desulfobacteraceae	U264759_g	U264759_g_unclassified	0.14	0.06	0.38	0.29	0.28	0.30	0.22	0.18	0.09	0.01	0.06	0.04	0.01	0.01	0.18	0.05	0.05	0.02	0.01	0.00	0.00	0.00	0.00	0.01	1.52	3.73	1.32	0.56	0.46	0.13	0.24	0.13	
B_OTU004	Bacteria	Proteobacteria	Lamnaproteobacteria	Methylococcales	Methylococcaceae_f	Methyloprofundus	Methyloprofundus_unclassified	1.08	1.01	1.67	1.81	4.11	1.83	0.30	0.27	0.16	0.20	0.15	0.09	0.05	0.00	0.97	0.98	0.87	2.29	3.23	3.17	2.33	1.94	0.67	0.24	0.20	0.15	0.14	0.08	0.04	0.06	0.00	0.03	

ND denotes that the samples were not included due to the low number of sequences.

Major OTUs of *Methanomicrobia*, *Deltaproteobacteria*, and *Methylococcales* were selected based on more than 3% in relative abundance at each sample.

The color gradient from white to red indicates low to high relative abundance values.

Supplementary Table S4. Pearson correlation coefficients between the major OTUs of ANMEs and *Deltaproteobacteria*.

OTU ID	Siboglinid tubeworm field 1 (ST1)				Siboglinid tubeworm field 2 (ST2)			
	A_OTU001		A_OTU008		A_OTU001		A_OTU008	
	<i>r</i>	<i>p</i>	<i>r</i>	<i>p</i>	<i>r</i>	<i>p</i>	<i>r</i>	<i>p</i>
B_OTU002	0.70	0.005	0.78	0.001	0.92	0.000	-0.35	0.172
B_OTU010	0.01	0.962	-0.36	0.205	-0.80	0.000	0.44	0.076
B_OTU011	0.71	0.005	0.76	0.001	0.90	0.000	-0.20	0.447
B_OTU018	-0.18	0.532	-0.56	0.037	-0.45	0.069	0.71	0.002
B_OTU021	0.75	0.002	0.79	0.001	0.68	0.002	-0.33	0.192
B_OTU029	0.77	0.001	0.76	0.001	0.20	0.453	0.70	0.002
B_OTU037	-0.35	0.213	-0.61	0.020	-0.79	0.000	0.23	0.367
B_OTU064	-0.82	0.000	-0.69	0.006	-0.91	0.000	-0.13	0.626
B_OTU079	-0.38	0.186	-0.65	0.011	0.33	0.201	-0.17	0.522