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Supplement of

Evidence for microbial iron reduction in the methanic sediments of the oligotrophic southeastern Mediterranean continental shelf

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Supplementary material

Table S1. Alpha diversity indices* of measured sediment samples in Station SG-1 collected on January 2017.

| Depth (cm, bsfl)	Bacterial sequences		Archaeal sequences	
	Shannon	Chao1	Shannon	Chao1
7	9.78	7997.22	7.70	2991.04
35	9.01	5708.70	7.51	2926.27
65	8.51	5009.97	7.29	3009.49
95	8.10	4547.15	1.28	2029.30
125	8.80	6085.62	7.01	3723.54
155	7.62	4427.02	6.51	3414.47
185	8.10	4766.24	2.81	2925.49
215	7.62	4273.17	1.64	1847.72
245	8.03	5039.75	5.17	3358.58
275	8.58	5277.99	3.96	2792.43
315	8.89	7710.27	1.15	1541.96
345	8.91	7340.46	6.43	3232.97
375	9.01	7332.17	1.55	1665.33
400	8.54	6556.15	2.74	1825.71
425	8.49	6772.04	4.04	1972.45
455	9.05	6757.92	1.04	1350.21
485	9.11	6778.52	1.59	1866.84
515	8.19	6172.91	2.87	1571.58
545	8.81	6865.08	7.21	4013.59
575	8.39	6282.57	5.00	1918.03

* based on 9010 sequences per sample/10 replicates

Table S2. Spearman correlation analysis of the qPCR and 16S (only those which correlated significantly) results with the dissolved Fe(II) concentrations in the methanic zone.

	Archaea (copy number)	Bacteria (copy number)	McrA (copy number)	*uncultured Bathyarchaeota sp*.	uncultured bacterium from TK10 class	subgroup 26 class	uncultured bacterium from SBR1093 phylum	depth (cm)	Fe(II) (μM)
	1012219.688	1739020.533	87614.368	87.093%	0.007%	0.000%	0.000%	575	2.263
	7080695.415	2507679.122	123106.601	70.871%	0.009%	0.000%	0.000%	545	1.675
	815428.906	1457344.922	127230.078	84.964%	0.014%	0.000%	0.000%	515	1.350
	2861886.458	2333390.365	594526.823	99.561%	0.025%	0.003%	0.003%	485	33.598
	2911225.982	2131948.770	293744.523	99.740%	0.015%	0.000%	0.000%	455	6.121
	5863148.438	2633319.792	572644.271	89.842%	0.007%	0.000%	0.000%	425	0.596
	4807156.147	2724236.482	977828.369	90.441%	0.017%	0.000%	0.003%	400	0.000
	3200305.469	1621331.250	448280.208	98.650%	0.017%	0.000%	0.003%	375	2.045
	4670232.205	3528446.452	1188747.694	78.944%	0.040%	0.000%	0.003%	345	0.786
	1788323.568	1900948.958	1365189.583	99.169%	0.025%	0.000%	0.000%	315	7.994
	5697072.424	3939200.802	1317183.145	92.635%	0.024%	0.002%	0.017%	275	43.945
	22532928.632	9451375.633	3772965.847	95.084%	0.041%	0.000%	0.032%	245	64.582
	14248938.542	5035076.042	4180939.323	99.028%	0.021%	0.000%	0.009%	215	18.001
	13835269.792	6384697.396	4065646.875	96.017%	0.022%	0.003%	0.035%	185	61.209
Spearman coefficient	0.3143	0.433	0.5429	0.5516	0.5297	0.5841	0.6176		
p-value	0.2735	0.1239	0.04789	0.04388	0.0544	0.02828	0.01859		
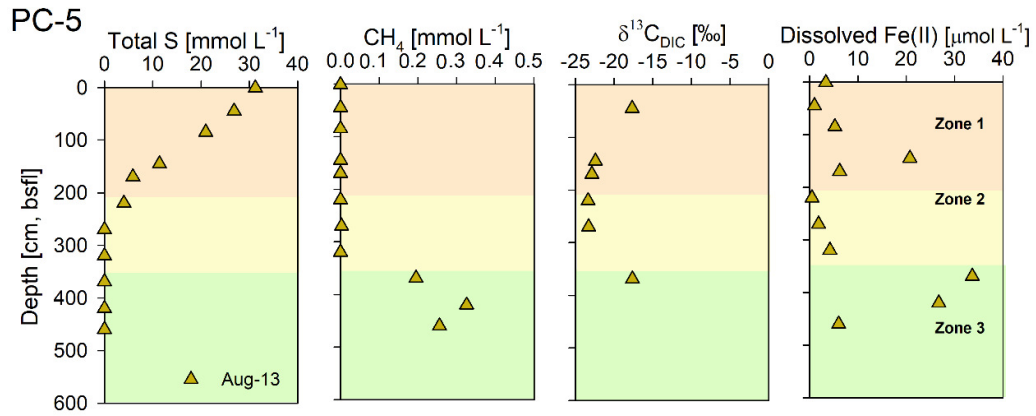
Figure S1: Geochemical pore-water profiles of sediment core collected from Station PC-5 from August 2013. The profiles are divided roughly to three zones according to the dominant processes: upper microbial iron and sulfate reduction, sulfate-methane transition zone, and the methanic zone at the deep part. The error bars for CH_4 are presented where duplicate sediment samples were collected. The analytical errors were smaller than the symbols.

(a)

(b)
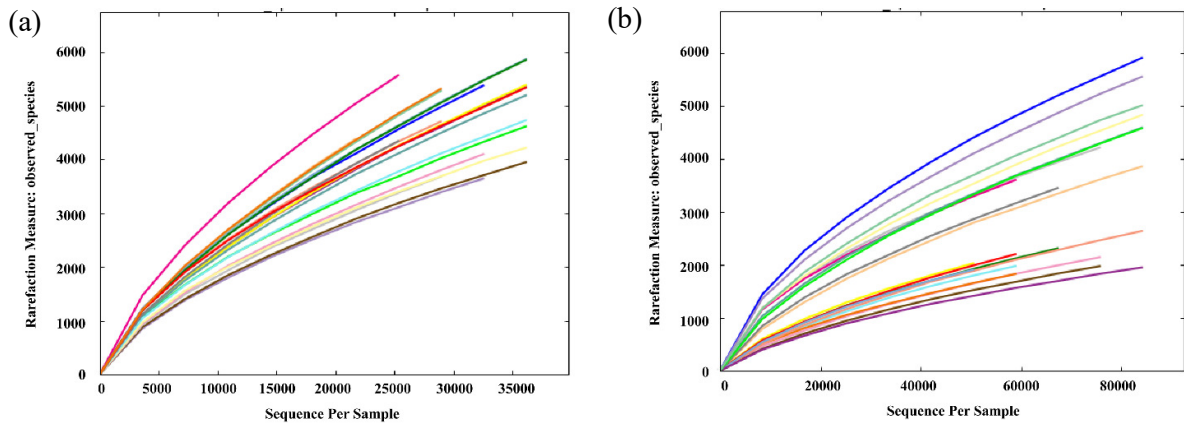
Figure S2: OTU-level rarefaction (observed species) of the measured samples in Station SG-1: Bacterial 16S rRNA gene sequences (a); Archaeal 16S rRNA gene sequences (b).
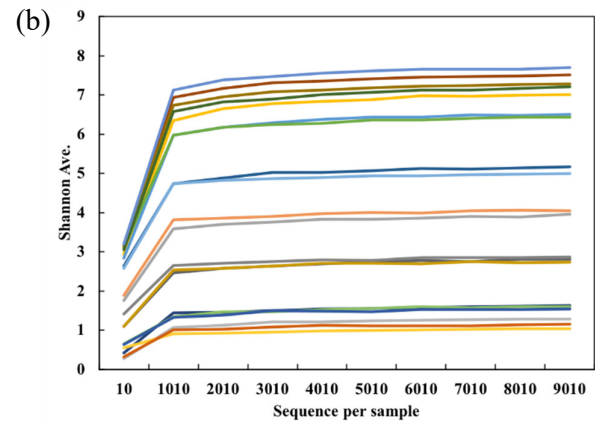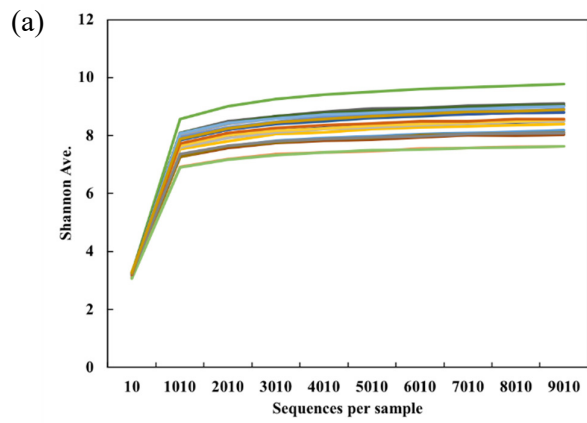
Figure S3: Shannon diversity index curves of measured samples in Station SG-1: Bacterial 16S rRNA gene sequences (a); Archaeal 16S rRNA gene sequences (b).