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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**

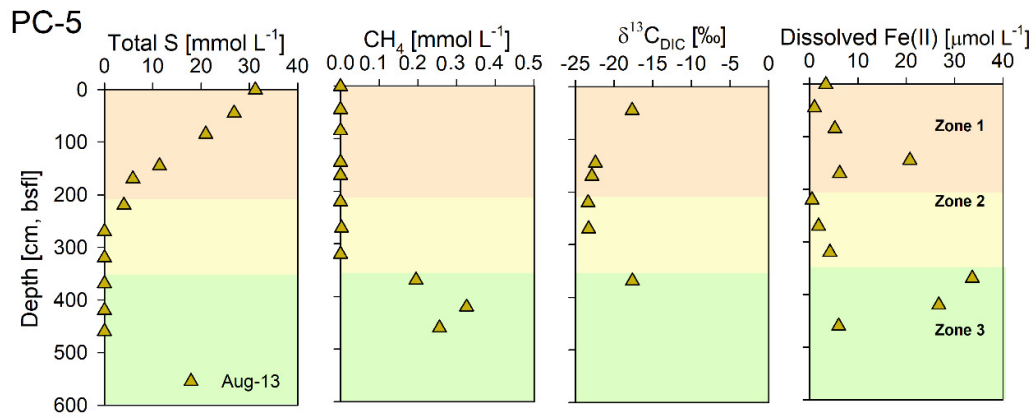
**Table S1.** Alpha diversity indices\* of measured sediment samples in Station SG-1 collected on January 2017.

| 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 |

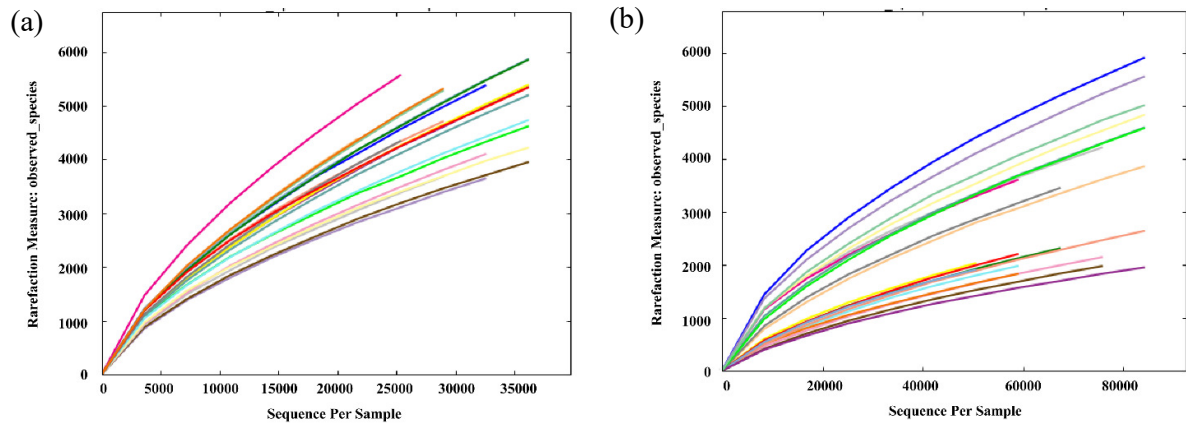
\* based on 9010 sequences per sample/10 replicates

**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.

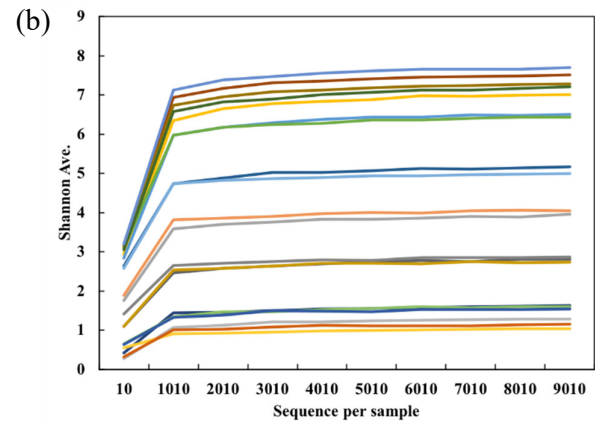
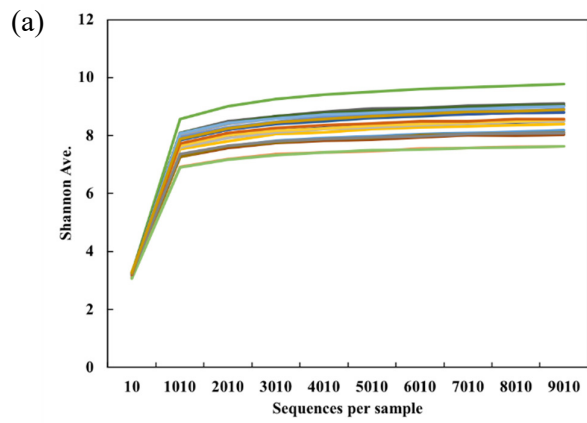
| Archaea (copy number)       | Bacteria (copy number) | McrA (copy number) | <i>uncultured Bathyarchaeota sp.</i> | <i>uncultured bacterium from TK10 class</i> | subgroup 26 class | <i>uncultured bacterium from SBR1093 phylum</i> | depth (cm) | Fe(II) (μM) |
|-----------------------------|------------------------|--------------------|--------------------------------------|---|-------------------|---|------------|-------------|
| 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      |
| <b>Spearman coefficient</b> | 0.3143                 | 0.433              | 0.5429                               | 0.5516                                      | 0.5297            | 0.5841  | 0.6176     |             |
| <b>p-value</b>              | 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<sub>4</sub> are presented where duplicate sediment samples were collected. The analytical errors were smaller than the symbols.



**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).