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

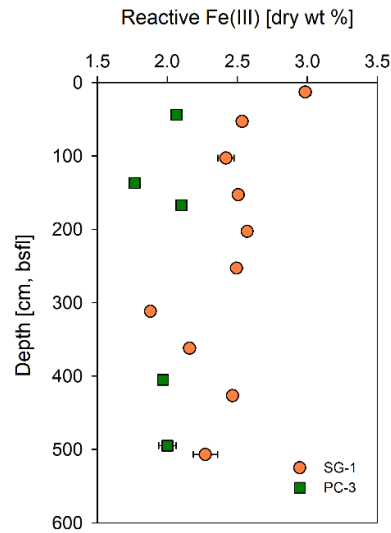* based on 9010 sequences per sample/10 replicates

Figure S1: Measured reactive Fe(III) sedimentary profiles from Station SG-1 from September 2015 (orange circles) and Station PC-3 from January 2015 (green squares). Reactive iron is defined as the sum of so called easily reducible oxides, reducible oxides and magnetite according to Poulton and Canfield (2005). The error bars represent the average deviation between triplicate sediment samples that were taken from the same depth. The error bars are smaller than the symbols if not shown.
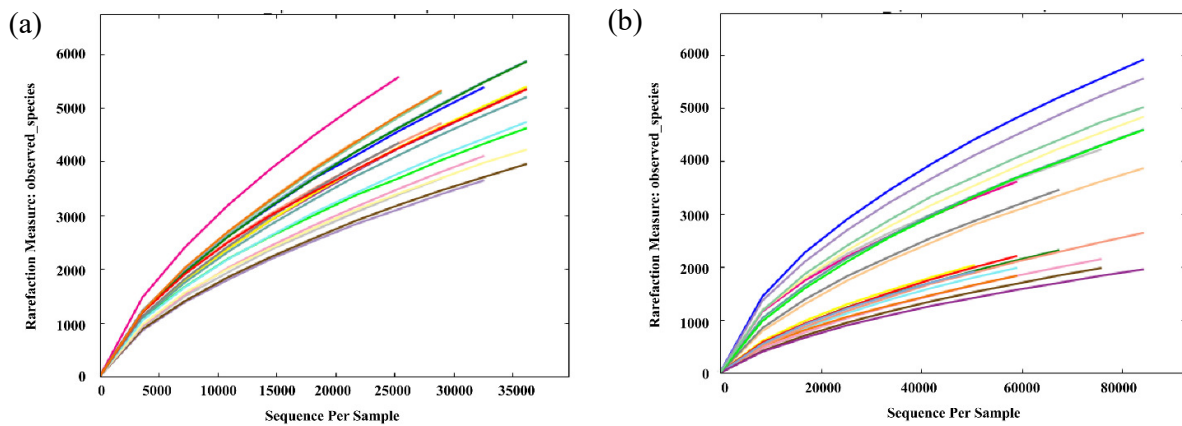

Figure S2: OTU-level rarefaction (observed species) of the measured samples in Station SG-1: Bacterial 16S rRNA gene sequences (a); Archaeal 16S rRNA gene sequences (b).
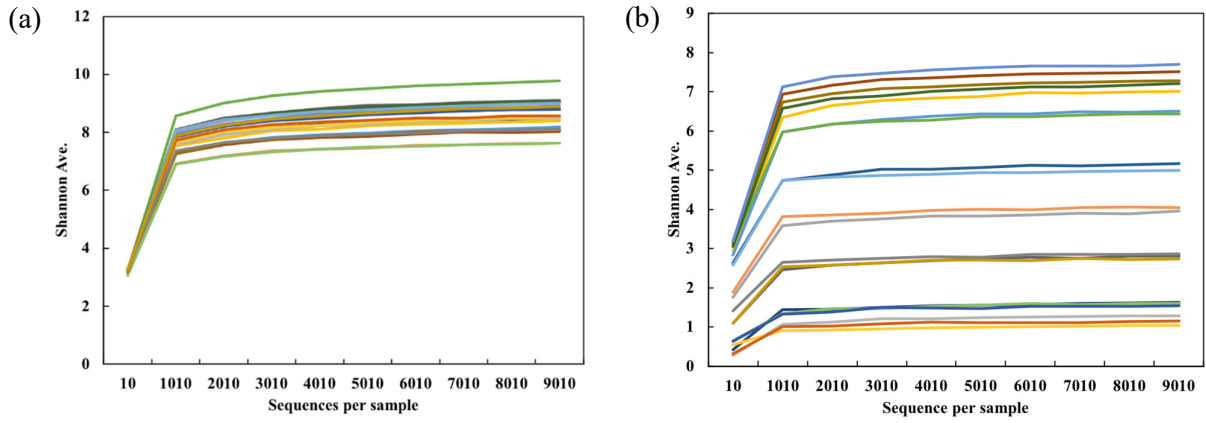
(a)

(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).