

Supplementary Materials

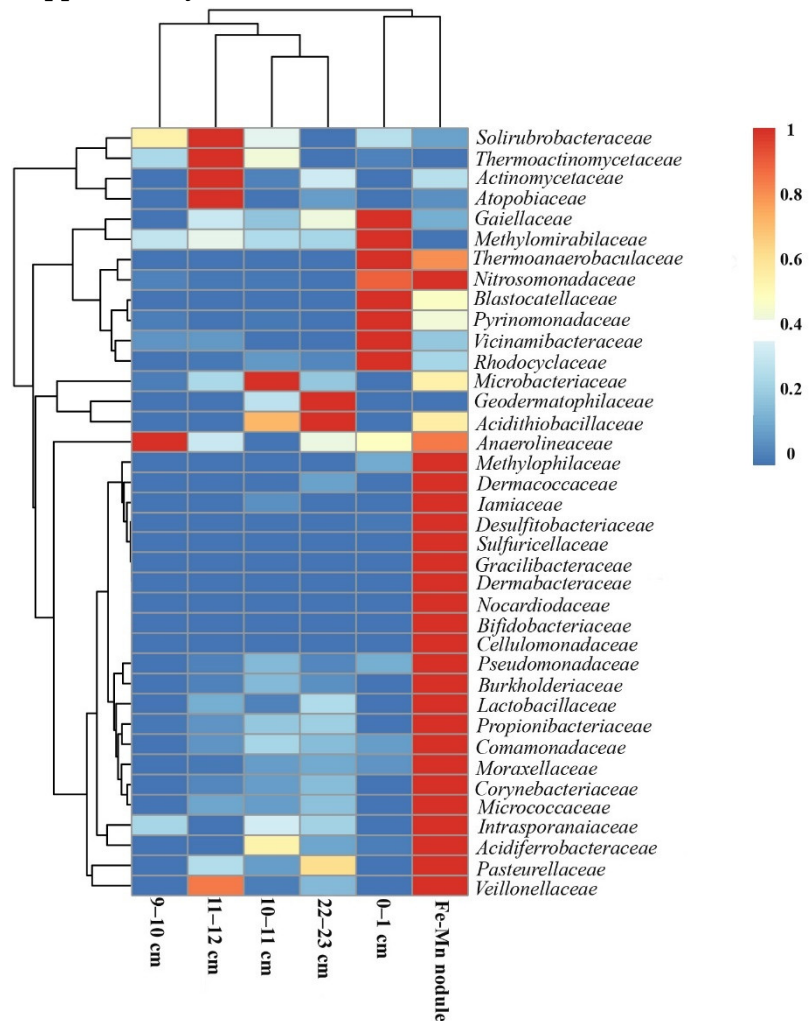


Figure S1. Heat map showing differences in the relative abundance of phyla (classes) in the samples, leading to the formation of two clusters (average linkage clustering) based on the Bray-Curtis distances. The colors mark the normalized relative abundance of taxa across all stations.

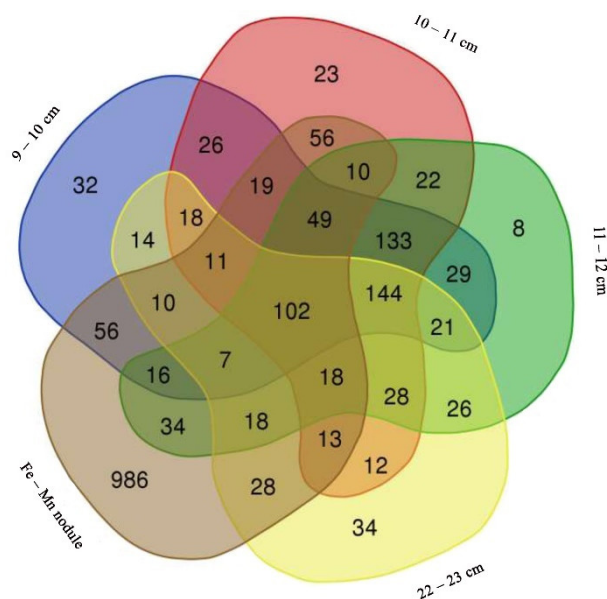


Figure S2. Venn diagram revealed both general and unique OTUs for each community analyzed.

Table S1. Number of reads, OTUs and indices of species hidden richness and evenness in the non-rarefied libraries of bacterial and archaeal 16S rRNA gene fragments (for a cluster distance of 0.03).

Sediment layer, Cmb/f	Reads Bacteria/Arc haea	OTU_{0.03} Bacteria/Arc haea	ACE Bacteria/Arc haea	Chao1 Bacteria/Arc haea	Shannon Bacteria/Arc haea	Inverse Simpson Bacteria/Arc haea
0–1	5785/15144	732/175	889/187.1	941/188.8	5.6/2.2	95.7/4.2
9–10	23884/13808	687/109	764/125.7	771/124.4	4.8/2.5	47.9/8.4
10–11	16922/5979	684/76	767/89.3	761/127	4.9/2.1	61.1/5.0
11–12	16684/8303	665/83	749/102	762/95.2	4.9/2.4	49.7/6.6
22–23	24569/13383	504/60	606/65.8	607/67.2	4.1/1.9	22.9/4.0
Fe-Mn Nodules	64670/-*	1433/-	1439/-	1450/-	4.9/-	15.2/-

* Results are absent.