Supplementary Information

Microbial communities associated with sediments and polymetallic nodules of the Peru Basin

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Figure S1. Rarefaction curves and diversity coverage in manganese nodules and sediments. a-b) show sample-size-based rarefaction curve for Bacteria and Archaea, respectively; c-d) show coverage-based curves for Bacteria and Archaea, respectively. The solid lines represent the observed accumulation with the number of sequences sampled, and the dashed lines represent the extrapolated accumulation up to double amount of sequences (only in a-b plots). Shaded area showed the 95 % confidence intervals based on 100 bootstrap replications. Knots = 10 for Bacteria, and knots = 40 for Archaea. H0: number of OTUs (q=0); H_1: exponential Shannon (q=1); H_2: inverse Simpson (q=2).
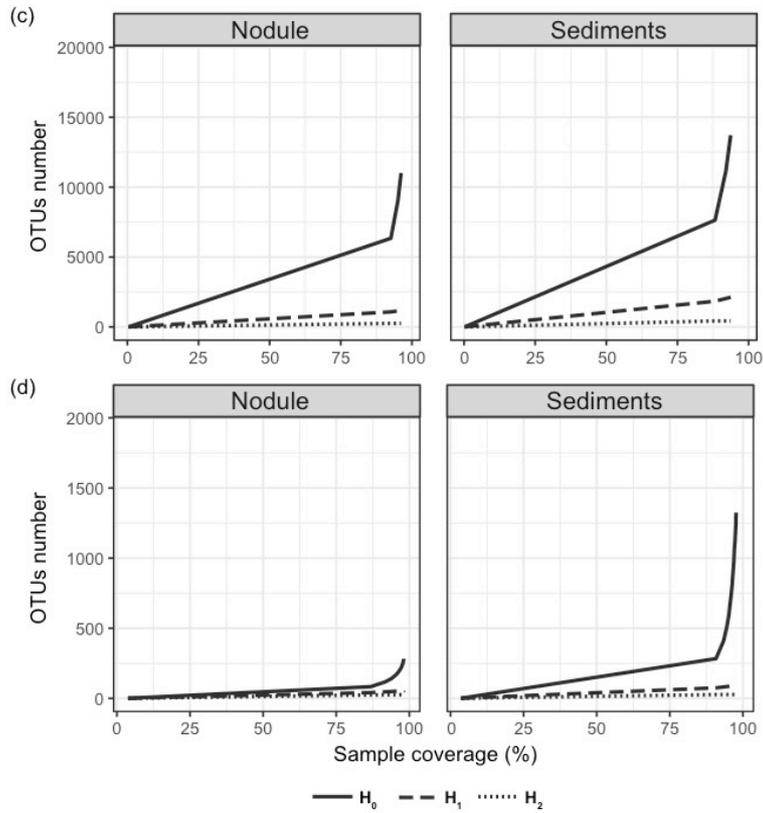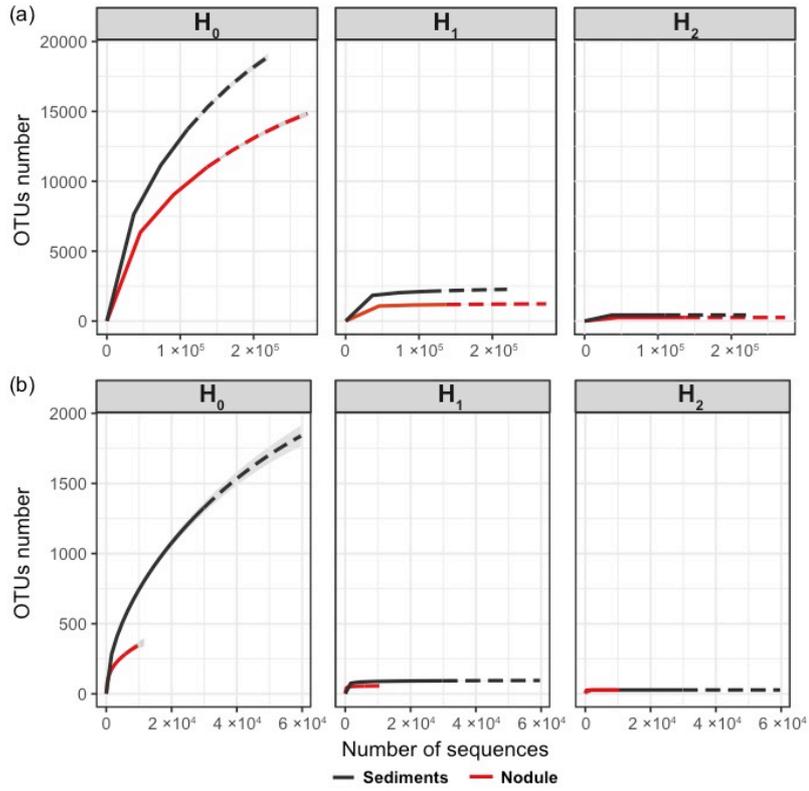
Table S1. Output permutational multivariate analysis of variance on distance matrices

(PERMANOVA).

OTUs CLR transformed and Euclidean distance

		Bacteria						Archaea						
		Df	SS	MS	F	R²	P		Df	SS	MS	F	R²	P
Substrates	Substrates	1	21547	21546.7	3.5043	0.22602	0.001	Substrates	1	3014.5	3014.53	4.9801	0.31164	0.001
	Residuals	12	73783	6148.6		0.77398		Residuals	11	6658.5	605.32		0.68836	
	Total	13	95330			1		Total	12	9673			1	
Sites/Sediment	Sites	2	18360	9180.2	1.8699	0.38397	0.003	Sites	2	2542.1	1271.05	2.3048	0.47969	0.013
	Residuals	6	29458	4909.6		0.61603		Residuals	5	2757.3	551.47		0.52031	
	Total	8	47818			1		Total	7	5299.4			1	
Reference.South/Substrate	Substrates	1	12771	12770.7	2.5848	0.34079	0.023	Substrates	1	3369.1	3369.1	7.5272	0.60087	0.029
	Residuals	5	24703	4940.7		0.65921		Residuals	5	2237.9	447.6		0.39913	
	Total	6	37474			1		Total	6	5607			1	
Sites/Substrates (Strata=Site)	Sites	2	25842	12921	2.4356	0.27108	0.005	Sites	2	1837	918.5	1.8506	0.18991	0.021
	Sites:Substrates	2	21743	10871	2.0492	0.22808	0.005	Sites:Substrate	1	3369.1	3369.1	6.7881	0.3483	0.021
	Residuals	9	47745	5305		0.50084		Residuals	9	4466.9	496.3		0.46179	
	Total	13	95330			1		Total	12	9673			1	

OTUs P/A table and Jaccard dissimilarity [A]

		Bacteria						Archaea						
		Df	SS	MS	F	R²	P		Df	SS	MS	F	R²	P
Substrates	Substrates	1	0.5986	0.59863	2.7963	0.18899	0.002	Substrates	1	0.45274	0.45274	2.2661	0.18474	0.003
	Residuals	12	2.5689	0.21408		0.81101		Residuals	10	1.9979	0.19979		0.81526	
	Total	13	3.1676			1		Total	11	2.45064			1	
Sites/Sediment	Sites	2	0.50624	0.25312	1.3286	0.30693	0.002	Sites	2	0.52048	0.26024	1.4829	0.37231	0.003
	Residuals	6	1.14312	0.19052		0.69307		Residuals	5	0.87749	0.1755		0.62769	
	Total	8	1.64936			1		Total	7	1.39798			1	
Reference.South/Substrate	Substrates	1	0.48253	0.48253	2.2875	0.31389	0.035	Substrates	1	0.41752	0.41752	2.0157	0.33507	0.1
	Residuals	5	1.0547	0.21094		0.68611		Residuals	4	0.82856	0.20714		0.66493	
	Total	6	1.53722			1		Total	5	1.24609			1	
Sites/Substrates (Strata=Site)	Sites	2	0.5954	0.29772	1.4698	0.18798	0.006	Sites	2	0.46094	0.23047	1.2347	0.18809	0.027
	Sites:Substrates	2	0.7492	0.37458	1.8493	0.23651	0.006	Sites:Substrate	2	0.68307	0.34154	1.8297	0.27873	0.027
	Residuals	9	1.823	0.20255		0.57551		Residuals	7	1.30663	0.18666		0.53318	
	Total	13	3.1676			1		Total	11	2.45064			1	

CLR: centered log-ratio; P/A: presence/absence; Df: degrees of freedom; SS: sum of the squares; F: statistic *F-ratio*; P: probability level.

[A] based on 100 sequence re-samplings per sample to the smallest dataset (40613 sequences for Bacteria and 1835 sequences for Archaea).