

Table S1 Lists of keystone species in co-occurrence network.

OTU ID	Betweenness centrality	Degree	Modularity classes	Category	Taxonomy
EU132794.1.1350	4824.77	80	I	Other	p_Actinobacteria;c_Acidimicrobiia;o_Acidimicrobiales;f_uncultured
New.ReferenceOTU48	4108.08	80	I	Abundant	p_Gemmatimonadetes;c_S0134 terrestrial group
KR779675.1.1326	4887.82	79	II	Other	p_Chloroflexi;c_KD4-96;o_Ambiguous_taxa;f_Ambiguous_taxa;g_Ambiguous_taxa
AB696516.1.1486	4548.11	76	I	Other	p_Gemmatimonadetes;c_BD2-11terrestrialgroup;o_uncultured;f_uncultured;g_uncultured;
JN417572.1.1515	4203.73	74	I	Abundant	p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae;g_uncultured
EF020094.1.1342	3089.75	74	I	Other	p_Chloroflexi;c_Anaerolineae;o_Anaerolineales;f_Anaerolineaceae;g_uncultured
HG970666.1.1395	4311.19	72	I	Other	p_Bacteroidetes;c_Sphingobacteriia;o_Sphingobacteriales;f_Chitinophagaceae;g_Flavisolibacter
HF548406.1.1395	3719.40	71	I	Other	p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas
New.ReferenceOTU947	3373.32	71	I	Other	p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Sandaracinaceae;g_uncultured
New.ReferenceOTU546	2976.71	71	I	Other	p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_KF-JG30-B3;g_uncultured
FJ479428.1.1498	1251.44	71	I	Other	p_Proteobacteria;c_Betaproteobacteria;o_Nitrosomonadales;f_Nitrosomonadaceae;g_uncultured
JN869200.1.1518	4492.45	70	I	Other	p_Acidobacteria;c_Blastocatellia;o_Blastocatellales;f_Blastocatellaceae(Subgroup4);g_uncultured
HQ119409.1.1418	4017.12	70	I	Other	p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Haliangiaceae;g_Haliangium
KM108700.1.1482	3529.48	70	I	Other	p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae;g_uncultured
HQ697772.1.1470	2037.38	70	I	Other	p_Chloroflexi;c_Anaerolineae;o_Anaerolineales;f_Anaerolineaceae;g_uncultured
AY921851.1.1351	1972.26	70	I	Other	p_Chloroflexi;c_Anaerolineae;o_Anaerolineales;f_Anaerolineaceae;g_Anaerolinea
HM339535.1.1306	1518.54	70	I	Other	p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas

Nodes with high degree (> 70) and low betweenness centrality values (< 5000) are recognized as keystone species in co-occurrence network.

Table S2 Distance-based multivariate linear model of bacterial community variability against the physico-chemical properties of the sediment samples after 999 permutations. Marginal tests: each variable was analyzed individually (ignoring other variables); Sequential tests: forward selection of variables, the percentage of variation explained by each variable added to the model was conditional on the variables already in the model.

Abundant subcommunity:

Marginal tests			
Variable	Pseudo-F	<i>P</i> -value	Percent variation explained
AK	34.3361	0.001	37.19
AP	28.1486	0.001	32.67
Clay	41.3402	0.001	41.61
EC	12.0215	0.001	17.17
Fe _d	39.3916	0.001	40.45
Ammonia	23.1766	0.001	28.55
OC	25.6374	0.001	30.65
pH	31.2531	0.001	35.02
Sand	41.6672	0.001	41.81
Silt	41.6577	0.001	41.8
TN	18.545	0.001	24.23

Sequential tests				
Variable	Pseudo-F	<i>P</i> -value	Percent variation explained	Cumulative variation explained
Sand	41.6672	0.001	41.81	41.81
EC	27.027	0.001	18.72	60.52
OC	3.9346	0.001	2.59	63.12
AK	3.313	0.008	2.10	65.21
pH	2.7045	0.014	1.66	66.87
Ammonia	2.0143	0.041	1.21	68.08
Fe _d	1.921	0.064	1.14	69.22
TN	1.75	0.063	1.02	70.24
AP	1.879	0.082	1.08	71.32
Clay	1.3821	0.157	0.79	72.11
Silt	0.7433	0.649	0.43	72.53

Data in bold are significantly correlated (*P*-value < 0.05).

Rare subcommunity:

Marginal tests			
Variable	Pseudo-F	<i>P</i> -value	Percent variation explained
AK	2.4516	0.001	4.06
AP	2.7619	0.001	4.55
Clay	2.9147	0.001	4.78
EC	2.2821	0.001	3.79
Fe _d	2.8845	0.001	4.74
Ammonia	2.6272	0.001	4.33
OC	2.6345	0.001	4.34
pH	2.7658	0.001	4.55
Sand	2.9196	0.001	4.79
Silt	2.9186	0.001	4.79
TN	2.5071	0.001	4.14

Sequential tests				
Variable	Pseudo-F	<i>P</i> -value	Percent variation explained	Cumulative variation explained
Sand	2.9196	0.001	4.79	4.79
EC	2.2897	0.001	3.68	8.47
pH	1.215	0.002	1.94	10.41
AK	1.1769	0.002	1.88	12.29
Ammonia	1.1223	0.014	1.79	14.08
OC	1.0968	0.044	1.74	15.82
Fe _d	1.0663	0.153	1.69	17.51
AP	1.0475	0.279	1.66	19.17
TN	1.0713	0.186	1.70	20.87
Clay	1.0147	0.48	1.61	22.47
Silt	1.0001	0.545	1.58	24.05

Data in bold are significantly correlated (P -value < 0.05). AP, available phosphorus; AK, available potassium; TN, total nitrogen; OC, organic carbon; Fe_d, free Fe₂O₃; EC, electrical conductivity.

Table S3 The numbers of all, abundant and rare OTUs which was above and below the neutral model.

	Above	Neutral	Below
All	4996	40592	1092
Abundant	0	52	205
Rare	577	25673	0

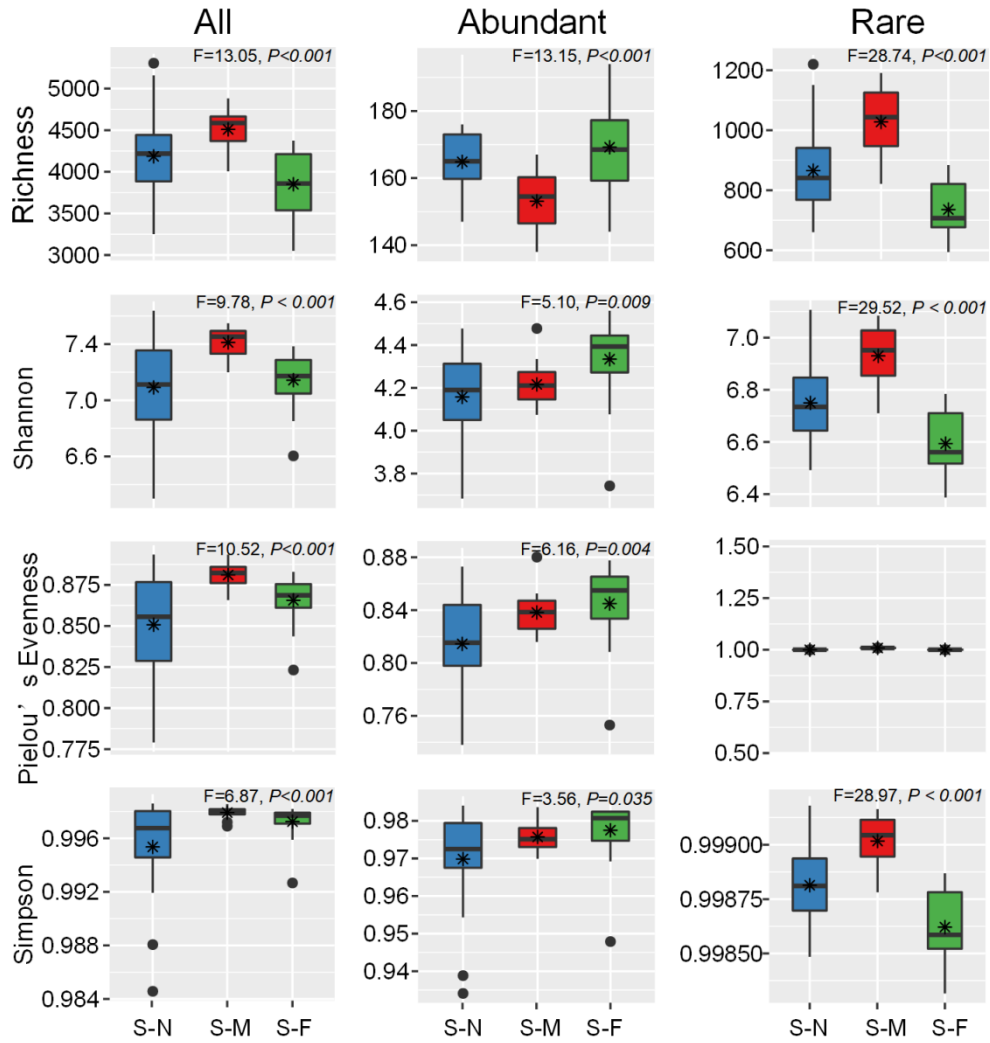


Figure S1 Variation in alpha-diversity of all, abundant and rare bacterial community through sampling transects. One-way ANOVA was used to compare the differences among different transectss. See Table 1 for transect notation.

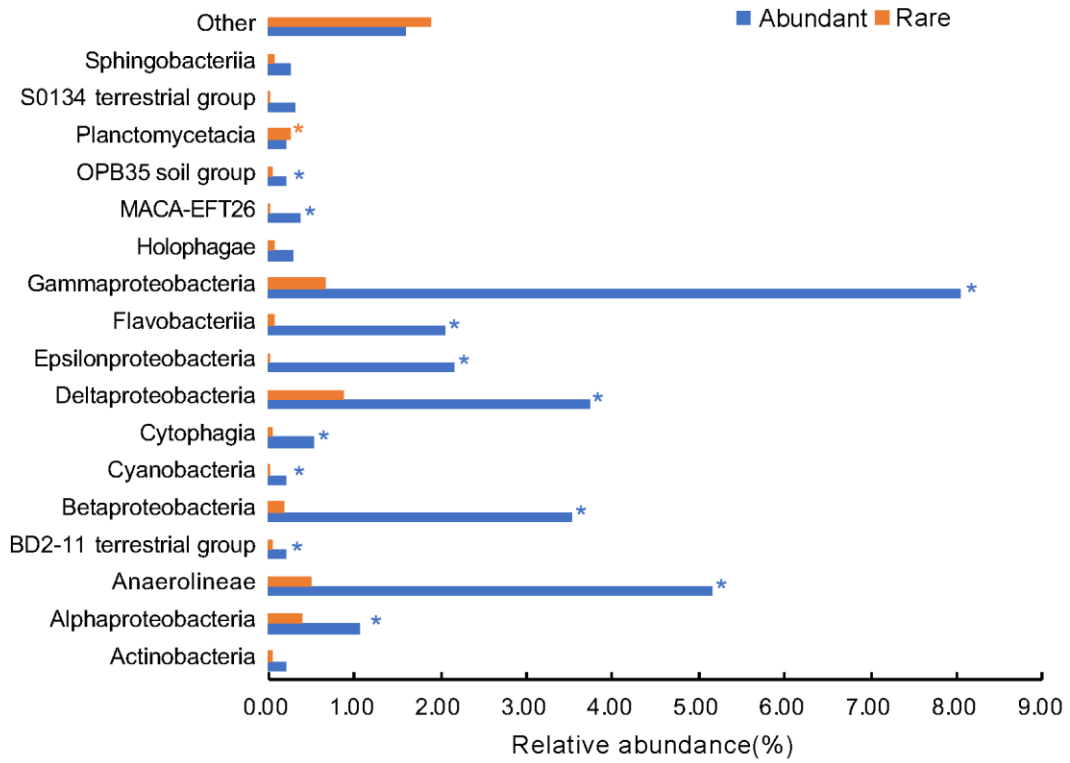


Figure S2 Taxonomic distribution of the 10 most abundant classes (relative abundance) of the abundant and rare bacterial subcommunities in the sediments. * indicates the significant level at P -value < 0.05 level determined by nonparametric Mann-Whitney U test. Abundant: abundant bacterial subcommunity. Rare: rare bacterial subcommunity.

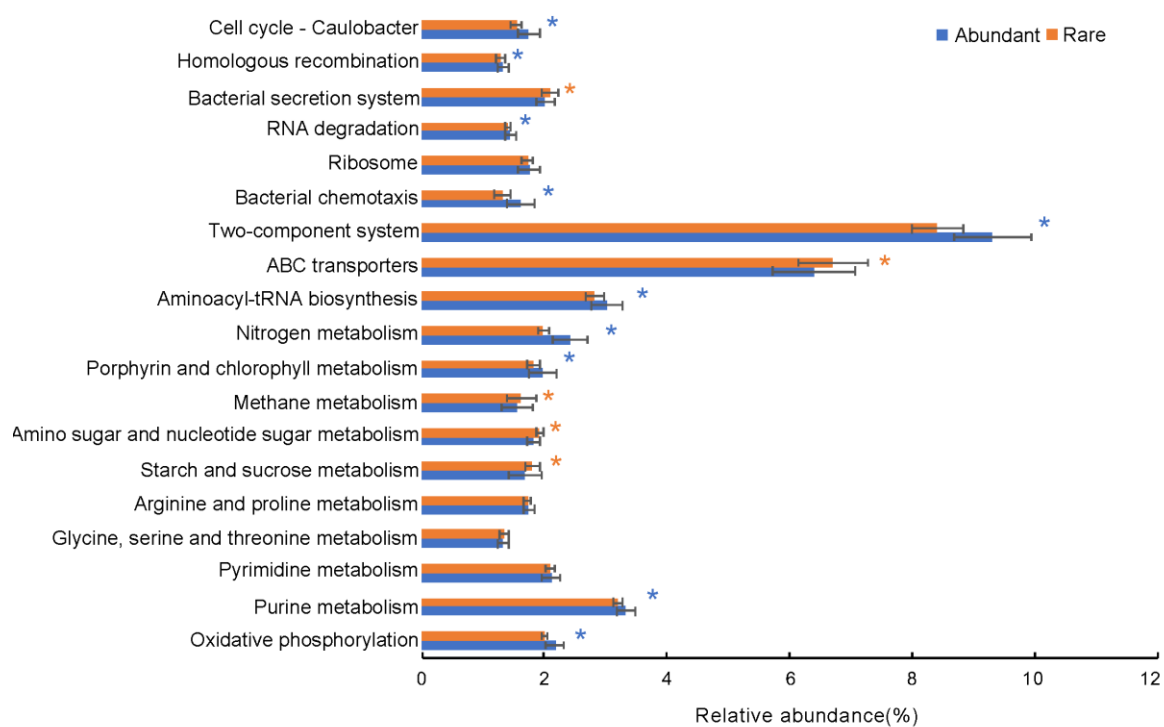


Figure S3 Functional distribution of the 10 most abundant pathways in KEGG (relative abundance) of the abundant and rare bacterial subcommunities in the sediments. * indicates the significant level at P -value < 0.05 level determined by nonparametric Mann-Whitney U test. Abundant: abundant bacterial subcommunity. Rare: rare bacterial subcommunity.

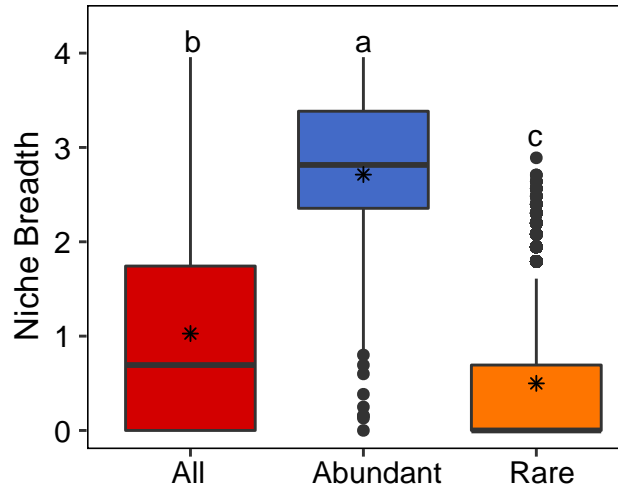


Figure S4 Boxplots showing the mean niche breadth for the all, abundant and rare bacterial communities. The top and bottom boundaries of each box indicate the 75th and 25th quartile values, respectively, and lines and * within each box represent the median values and mean values, respectively ($n = 41,680$ for All, $n = 258$ for Abundant, and $n = 26,250$ for Rare). Different letters indicate the significant level at P -value < 0.05 level. determined by nonparametric Mann-Whitney U test.

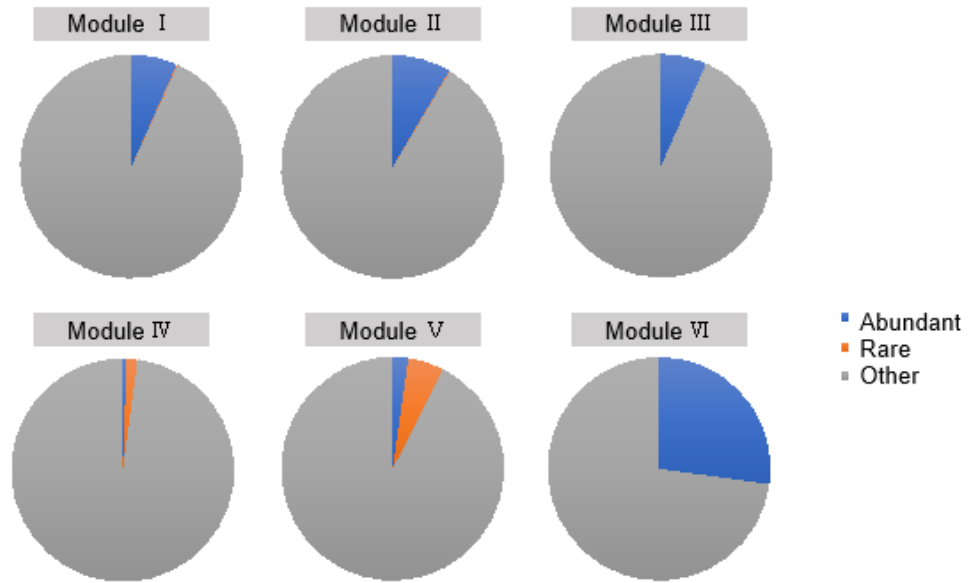


Figure S5 Pie charts showing the richness proportion of different subcommunities in each major module of the co-occurrence network. Abundant: abundant bacterial subcommunity. Rare: rare bacterial subcommunity. Other, other bacterial subcommunity.

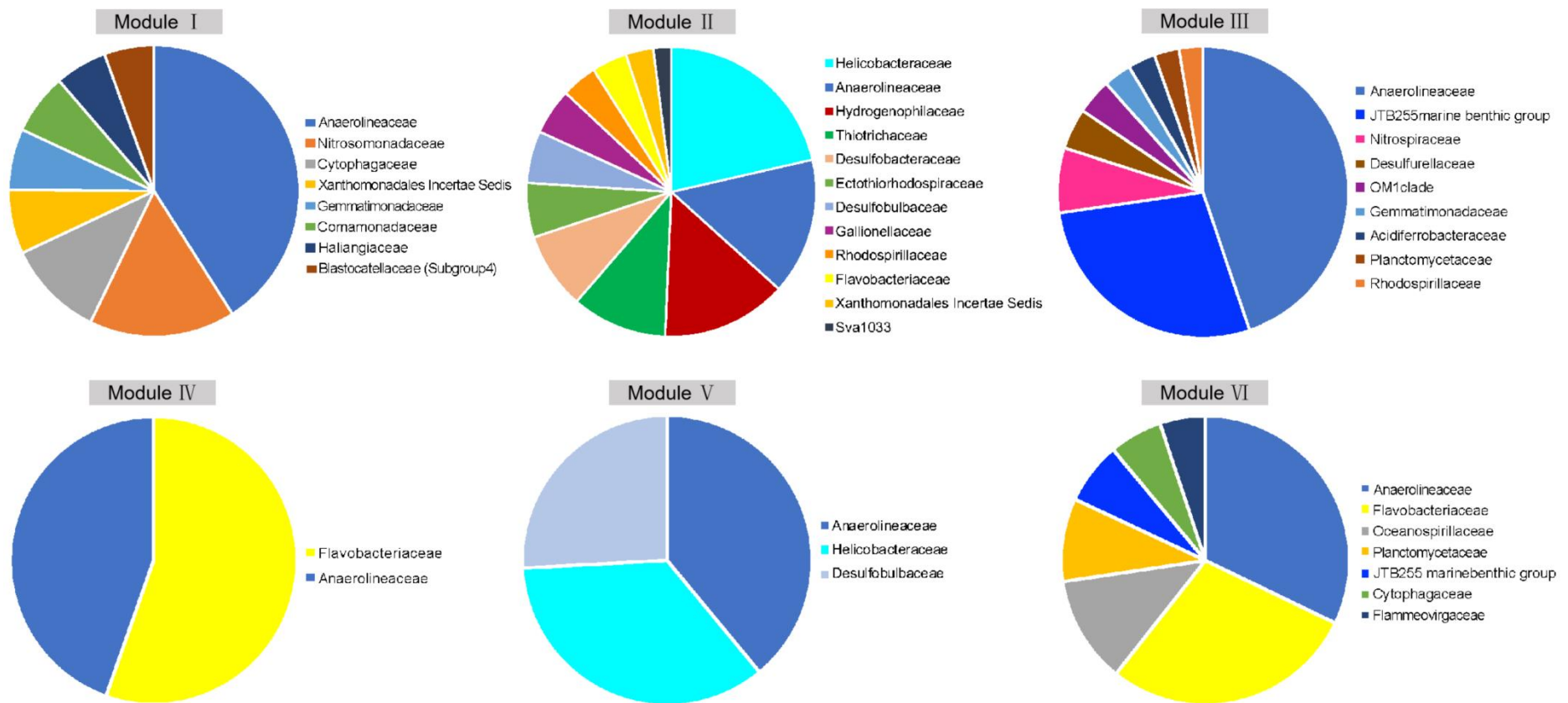


Figure S6 The dominant (relative abundance > 0.5% at least in one sample in Module I, II, III; relative abundance > 0.1% at least in one sample in Module IV, V, VI) taxonomic distribution at family level in each module of the co-occurrence network.

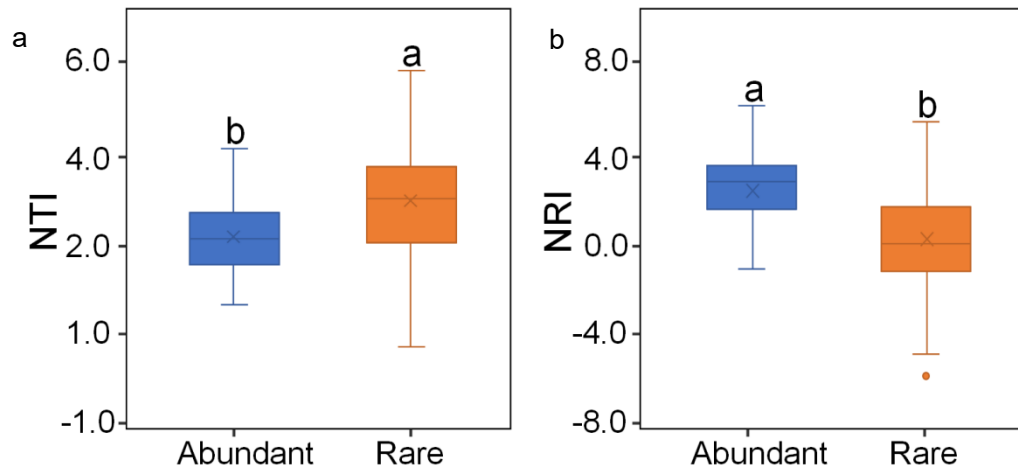


Figure S7 The nearest taxon index (NTI) (a) and net relatedness index (NRI) (b) of abundant and rare bacterial subcommunity. Different letters above bars indicate a significant difference at the P -value < 0.05 level according to nonparametric Mann-Whitney U test.