

Supplementary Materials: Effect of Sewage and Industrial Effluents on Bacterial and Archaeal Communities of Creeks Sediments in Taihu Basin

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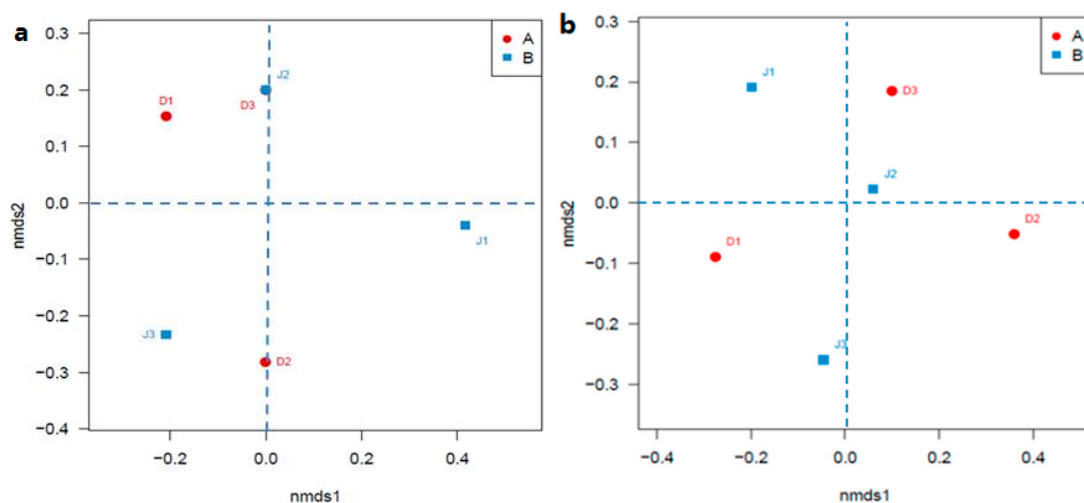


Figure S1. Community analysis based on Bray-Curtis distances of NMDS. (a) Bacterial genes; (b) Archaeal genes.

Table S1. Shared OTUs of bacterial 16S rRNA genes between any two samples.

Class	Shared Reads							
	OTU	D1&D2&D3			OTU	J1&J2&J3		
		D1	D2	D3		J1	J2	J3
Acidimicrobiia	7	53	27	91	4	43	40	11
Actinobacteria	23	267	503	414	30	959	629	261
Anaerolineae	101	593	567	3458	93	3480	593	333
Alphaproteobacteria	59	849	1243	859	49	1241	1026	569
Betaproteobacteria	61	7825	2723	5634	64	4211	2451	1489
Bacilli	17	7072	1457	2106	16	5313	2323	2654
Bacteroidia	15	223	207	629	16	731	12318	350
Caldilineae	30	186	346	390	18	92	116	116
Chloroflexia	30	186	346	390	0	0	0	0
Clostridia	78	2842	3695	2867	67	1997	3293	1749
Coriobacteriia	8	301	29	138	10	542	259	111
Cytophagia	8	59	113	94	4	15	53	40
Deltaproteobacteria	66	2041	868	1199	71	4360	1482	1987
Epsilonproteobacteria	4	297	131	418	4	6836	175	51
Flavobacteria	13	344	403	307	13	499	233	193
Gammaproteobacteria	38	2418	1319	1905	36	3975	2278	1395
Gemmatimonadetes	16	272	296	158	11	47	70	216
Holophagae	5	121	43	58	5	407	142	186
Nitrospira	15	164	504	289	12	169	155	231
Sphingobacteriia	26	191	301	261	18	244	256	105
Total	620	77.1%	71.6%	63.2%	541	74.0%	89.8%	65.9%

Table S2. Shared OTUs of archaeal 16S rRNA genes between any two samples.

Class	Shared Reads							
	OTU	D1&D2&D3			OTU	J1&J2&J3		
		D1	D2	D3		J1	J2	J3
Halobacteria	138	12159	32702	10966	122	23912	13873	26801
Marine_Group_I	1	36	316	35	2	73	76	1135
Methanobacteria	13	1068	603	3999	15	2343	6513	1572
Thermoplasmata	1	22	3	72	1	31	39	4
Soil_Crenarchaeotic_GroupSCG	2	805	39	51	2	38	154	1427
Total	155	43.6%	54.9%	41.5%	142	56.8%	51.7%	58.9%



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