

Supplementary Materials: Abundant and Rare Bacterioplankton in Freshwater Lakes Subjected to Different Levels of Tourism Disturbances

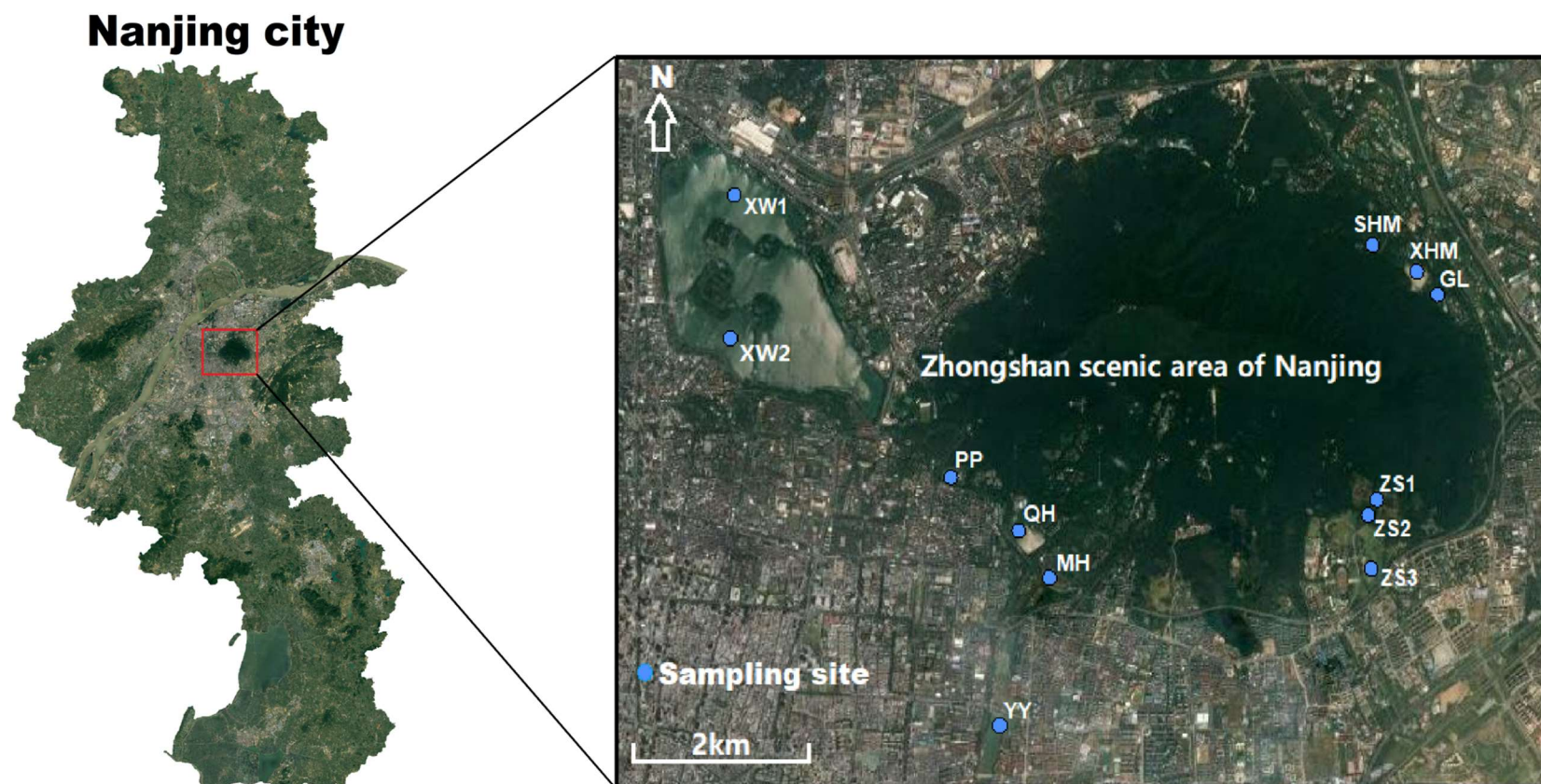


Figure S1. Map of sampling sites in Nanjing, China.

Note: The abbreviations of lake names can be found in Table 1.

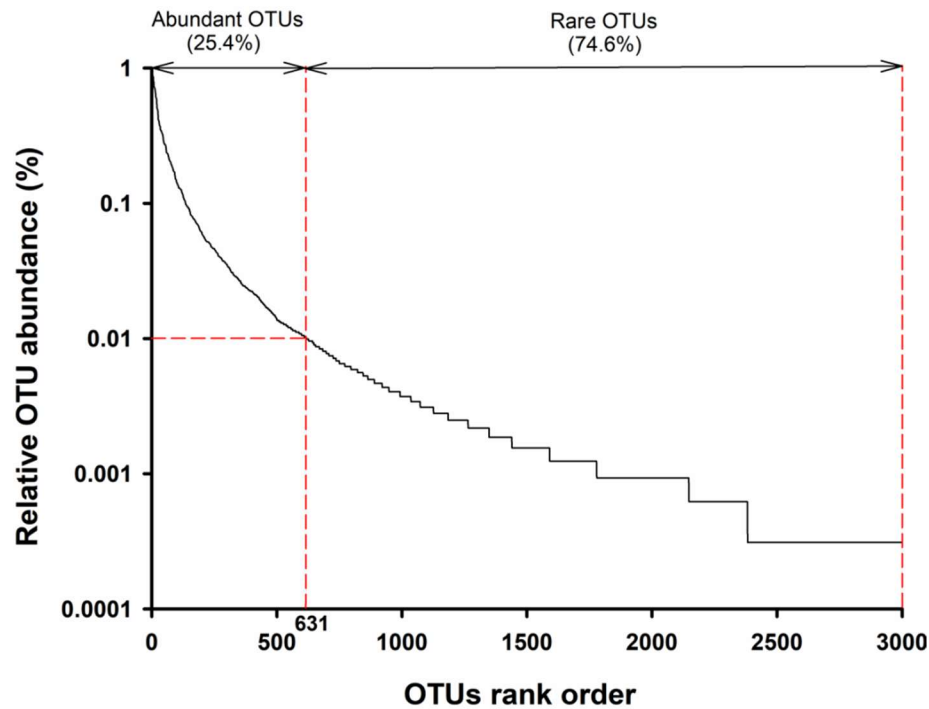


Figure S2. Rank abundance curve for the obtained 2487 OTUs.

Note: The OTUs were defined at the 97% similarity level.

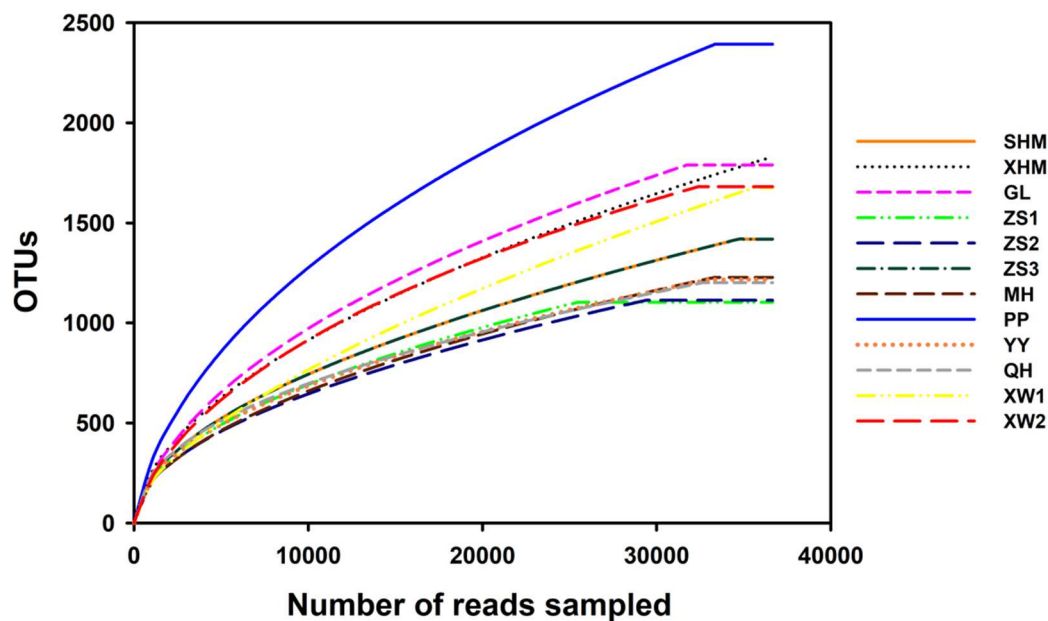


Figure S3. Rarefaction curves of the bacterioplankton.

Note: The OTUs were defined at 97% similarity. The abbreviations of lake names can be seen in Table 1.

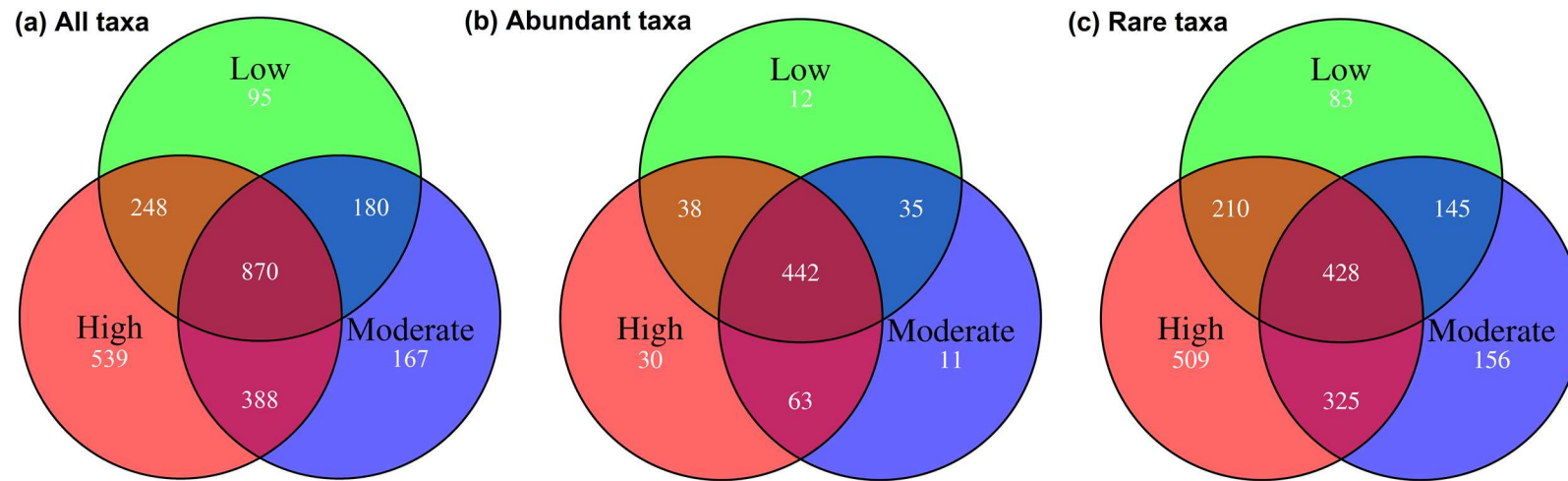


Figure S4. Venn diagrams showing the numbers of unique and shared OTUs between the different analyzed lakes.

Note: Low: low-anthropogenic-disturbance lakes; Moderate: moderate-anthropogenic-disturbance lakes; High: high-anthropogenic-disturbance lakes.

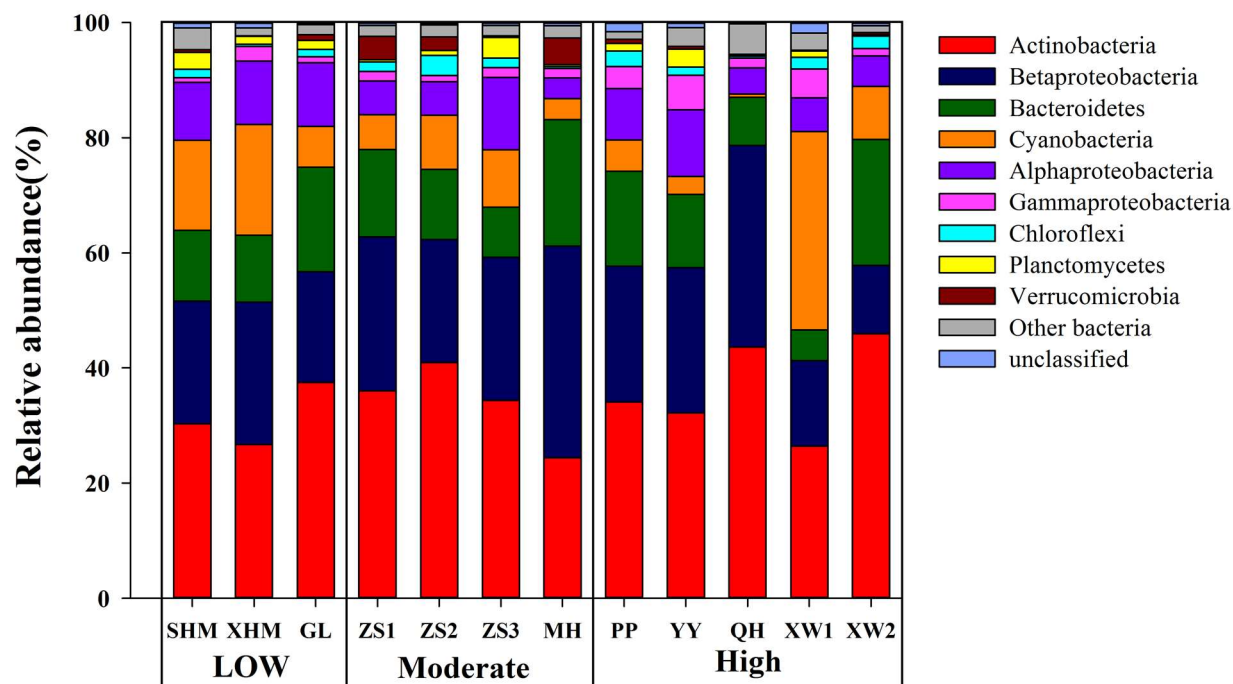


Figure S5. Relative abundance of dominant bacterioplankton phyla/subphyla (average relative abundance >1.0 %) for all bacterial taxa in different sampled lakes from Nanjing.

Note: The abbreviations of lakes name were noted in Table 1. Low: low-anthropogenic-disturbance lakes; Moderate: moderate-anthropogenic-disturbance lakes; High: high-anthropogenic-disturbance lakes.

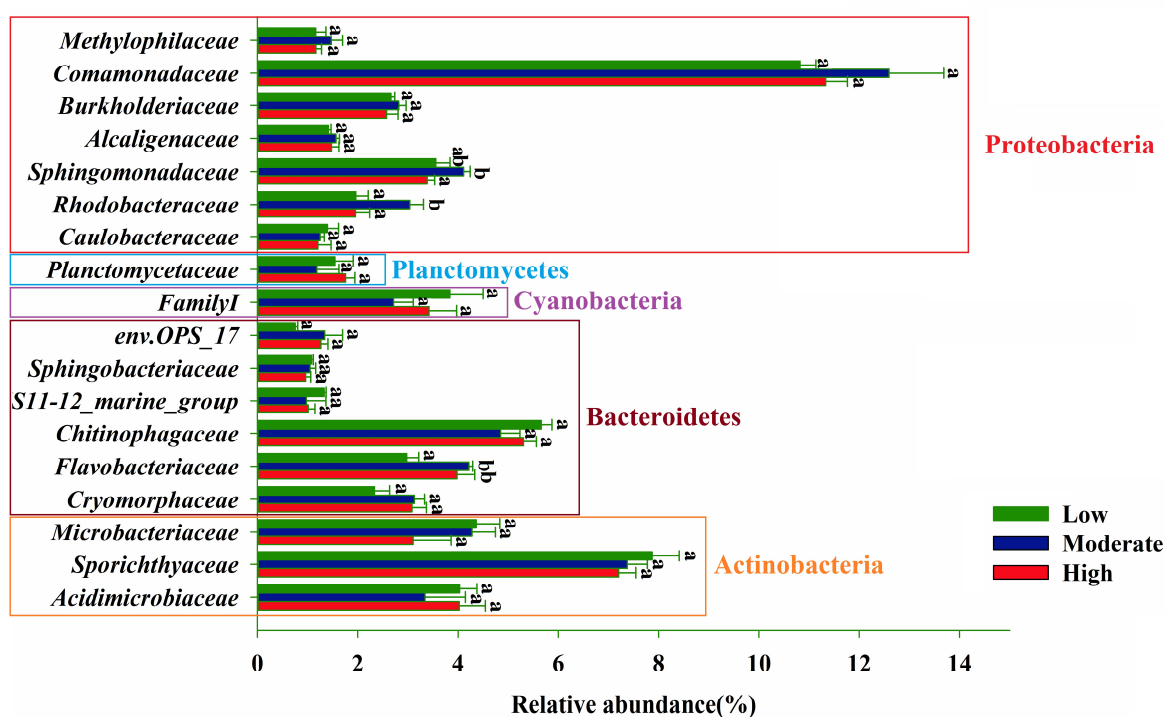
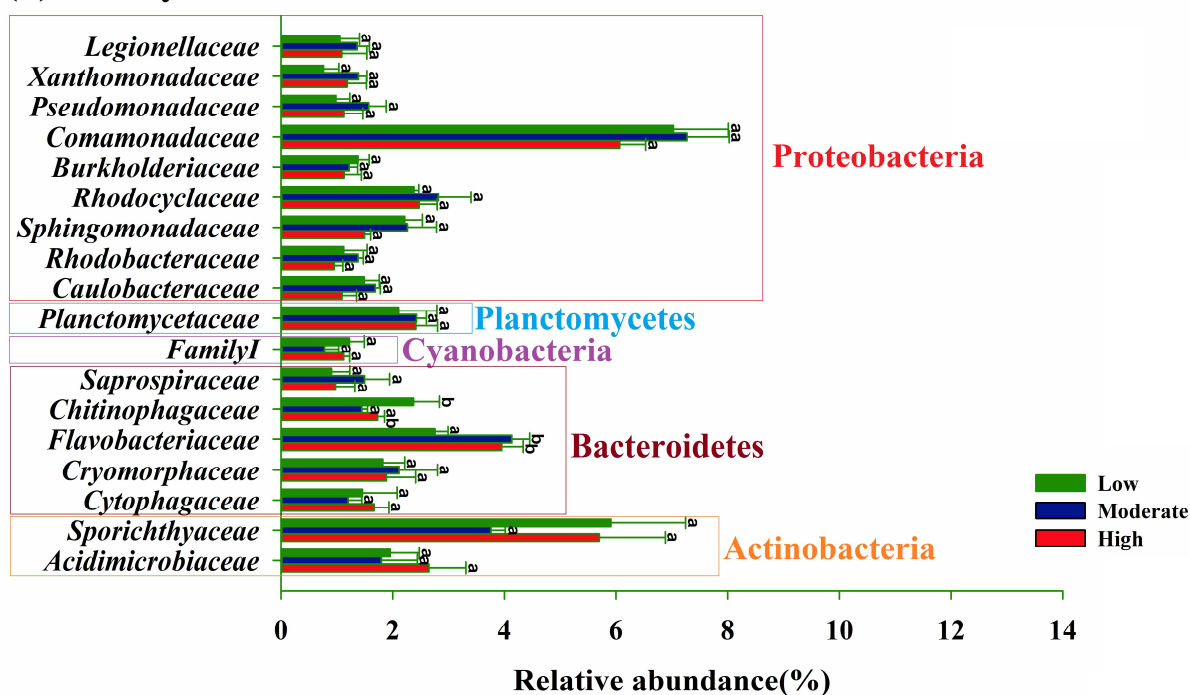
(a) Family in abundant taxa**(b) Family in rare taxa**

Figure S6. Comparison of dominant bacterial family (average relative abundance >1.0 %) among low-, moderate-, and high-anthropogenic-disturbance lakes in (a) abundant and (b) rare taxa, respectively.

Note: Same letter above the error bars indicates no significant difference (One-way ANOVA test, $p > 0.05$).

Table S1. Summary of diversity indices of bacterioplankton community for all, abundant, and rare taxa.

Sample	All Taxa						Abundant Taxa						Rare Taxa			
	Number of filtered sequences	Number of analyzed sequences	OTUs richness	Chao1	Shannon	PD	Number of assigned sequences	OTUs richness	Chao1	Shannon	PD	Number of assigned sequences	OTUs richness	Chao1	Shannon	PD
SHM	36351	26852	818	1167	4.70	46.12	25787	396	444	4.49	25.29	1065	422	688	5.40	36.94
XHM	37688	26852	833	1222	4.44	48.26	25788	407	467	4.23	26.75	1064	426	687	5.39	37.34
GL	32519	26852	762	1078	4.45	45.57	26018	387	424	4.27	24.62	834	375	636	5.53	35.97
ZS1	26852	26852	762	1023	4.53	42.55	25878	359	383	4.32	23.03	974	403	605	5.52	33.38
ZS2	29223	26852	821	1114	4.62	47.45	25714	379	418	4.39	24.59	1138	442	611	5.56	39.53
ZS3	37560	26852	922	1384	4.74	49.03	25746	449	506	4.52	26.00	1106	473	765	5.55	39.15
MH	32290	26852	762	1080	4.31	46.16	25849	342	381	4.09	23.24	1003	420	622	5.58	37.82
PP	36014	26852	875	1218	4.52	49.20	25600	412	446	4.26	24.75	1252	463	670	5.46	39.79
YY	33215	26852	1041	1366	4.96	52.68	24985	475	521	4.62	26.53	1867	566	652	5.50	42.73
QH	33051	26852	889	1165	4.21	51.22	25175	316	371	3.84	19.24	1677	573	676	5.65	43.80
XW1	57195	26852	1081	1482	4.26	57.96	25075	422	466	3.86	25.41	1777	659	781	5.78	48.68
XW2	33633	26852	767	1169	4.14	43.13	26141	383	463	3.97	23.53	711	384	698	5.69	33.23

OTUs: operational taxonomic units; PD: Faith's phylogenetic diversity.

Table S2. Analysis of permutational multivariate analysis of variance (PERMANOVA) testing difference of community composition between abundant and rare bacterial taxa based on Bray–Curtis distance.

Comparison	Pseudo- <i>F</i>	R ²	<i>P</i> (> <i>F</i>)
Abundant taxa versus Rare taxa	11.316	0.3397	0.001***

***: $p < 0.001$.**Table S3.** Taxonomic distribution of the average top ten bacterial genera from all, abundant, and rare bacterial taxa.

All Taxa			Abundant Taxa			Rare Taxa		
Phylum	Genus	Mean±SD(%)	Phylum	Genus	Mean±SD(%)	Phylum	Genus	Mean±SD(%)
Actinobacteria	<i>hgcI_clade</i>	3.12±0.83	Actinobacteria	<i>hgcI_clade</i>	4.14±0.47	Actinobacteria	<i>hgcI_clade</i>	3.65±1.43
	<i>CL500-29_marine_group</i>	2.44±1.15		<i>CL500-29_marine_group</i>	3.80±1.17		<i>CL500-29_marine_group</i>	2.03±1.16
	<i>Candidatus_Planktophila</i>	1.18±0.45		<i>Candidatus_Planktophila</i>	1.54±0.18		<i>Candidatus_Planktophila</i>	1.00±0.74
Bacteroidetes	<i>Flavobacterium</i>	2.68±0.50	Bacteroidetes	<i>Flavobacterium</i>	3.57±0.74	Bacteroidetes	<i>Flavobacterium</i>	3.11±0.78
	<i>Fluviicola</i>	1.66±0.50		<i>Fluviicola</i>	2.62±0.53		<i>Fluviicola</i>	1.82±0.96
Cyanobacteria	<i>Synechococcus</i>	1.13±0.44	Cyanobacteria	<i>Sediminibacterium</i>	1.69±0.60	Proteobacteria	<i>Legionella</i>	1.17±0.71
Proteobacteria	<i>Polynucleobacter</i>	1.17±0.28		<i>Synechococcus</i>	2.94±0.92		<i>Pseudomonas</i>	1.13±0.59
	<i>Legionella</i>	0.97±0.38		<i>Polynucleobacter</i>	1.71±0.22		<i>Polynucleobacter</i>	0.85±0.41
	<i>Aquicella</i>	0.69±0.61		<i>Novosphingobium</i>	1.26±0.37		<i>Dechloromonas</i>	0.75±0.43
	<i>Novosphingobium</i>	0.65±0.20		<i>Limnohabitans</i>	1.11±0.24		<i>Brevundimonas</i>	0.70±0.21

Notes: Different bacterial genera are denoted by different colors. Bacterial genus that was present in all, abundant, and rare taxa is labeled by same color. SD: standard deviation.