Supplementary

Manucript entitled "Diversity of bacterial communities in sediment in inland water bodies in relation to environmental factors and human impacts: a case study on typical regions in Vietnam" by Bui et al.

Table S1. Detailed location information of the samples

Sample	Coordination	Season	Location information		
			Commune	**District**	**Province/city**
Red river region					
SH15K	21° 8'42.77"N 105°38'50.44"E	Dry	Thọ An	Sơn Tây	Hanoi
SH15M	21° 8'42.77"N 105°38'50.44"E	Rain	Thọ An	Sơn Tây	Hanoi
SH25K	21°41'59.35"N 104°54'0.29"E	Dry	Giới Yên	Yên Bái	Yen Bai
SH25M	21°41'59.35"N 104°54'0.29"E	Rain	Giới Yên	Yên Bái	Yen Bai
SH28K	21°52'49.14"N 104°40'47.45"E	Dry	Mậu A	Văn Yên	Yen Bai
SH28M	21°52'49.14"N 104°40'47.45"E	Rain	Mậu A	Văn Yên	Yen Bai
SH36K	22°19'6.01"N 104°10'49.63"E	Dry	Sơn Hà	Bảo Thắng	Lao Cai
SH36M	22°19'6.01"N 104°10'49.63"E	Rain	Sơn Hà	Bảo Thắng	Lao Cai
Ba river region					
SB02K	13° 4'26.04"N 109°18'22.32"E	Dry	Phường 1	Tuy Hòa	Phu Yen
SB17M	13° 9'45.20"N 108°41'30.26"E	Rain	Phú Cần	Krông Pa	Gia Lai
SB18K	13°13'6.91"N 108°38'57.53"E	Dry	Chư Gu	Krông Pa	Gia Lai
SB18M	13°13'6.91"N 108°38'57.53"E	Rain	Chư Gu	Krông Pa	Gia Lai
SB22K	13°21'38.5"N 108°30'46.8"E	Dry	Ia RSai	Ia Pa	Gia Lai
SB22M	13°21'38.5"N 108°30'46.8"E	Rain	Ia RSai	Ia Pa	Gia Lai
Mekong delta flood zone					
VNL-03	10°48'01.70"N 105°37'43.34"E		Tân Công Sinh	Tam Nông	Dong Thap
VNL-06	10°22'38.4"N 105°33'30.9"E		Bình Thạnh Trung	Lấp Vò	Dong Thap
VNL-07	10°14'36.7"N 105°41'14.5"E		Long Thắng	Lai Vung	Dong Thap
VNL-17	10°26'18.42"N 106° 0'0.40"E		Hậu Mỹ Trinh	Cái Bè	Tien Giang
VNL-18	10°30'9.19"N 106° 4'2.55"E		Phú Cường	Cai Lậy	Tien Giang

*Calculation of human impact scores (presented in Table 1):
The human impact in each site was scored so as to perceive the different levels of human impact in different sites. We assumed that the more a location is affected, the less distant it is to human facilities and that the more facilities or populations it is close to, the more it is affected. Thus, the detailed scoring system is as follows, based on the rationale that the more distant the site is from a facility, the score decreases but in degenerative manner (not linearly).

Table S2. The detailed explanation of how to score the human impacts at the sampling sites

	Criterium	Level of impact		Score
1	Distance to a populated area	0 km (right at the area)		1
		<5 km		0.5
		>5 km and <10km		0.2
		>10km		0
2	Population density of the area of interest	<100 cap/km^2		0
		>100 and <500 cap/km^2		0.2
		>500 and <1000 cap/km^2		0.5
		>1000 cap/km^2		1
3	Distance to a discharing point of a factory or an industrial zone	0 km (right at the point)		1
		<5km		0.5
		>5km and <10km		0.2
		>10km		0
4	Aquaculture activities	Exploitation by deadly means (electricity, mine, chemicals)		1
		Exploitation by traditional methods (using nets, cages, etc.)	Intensive	0,5
			Not intensive	0,2
			No exploitation	0
5	Distance to touristic areas or other service areas	0 km (right at the area)		1
		<5 km		0.5
		>5 km and <10km		0.2
		>10km		0

Note: The total score of each site (presented in Table 1) is the sum of the scores for the 5 criteria above

Table S3. Alpha-diversity indices of the bacterial communities in the studied samples

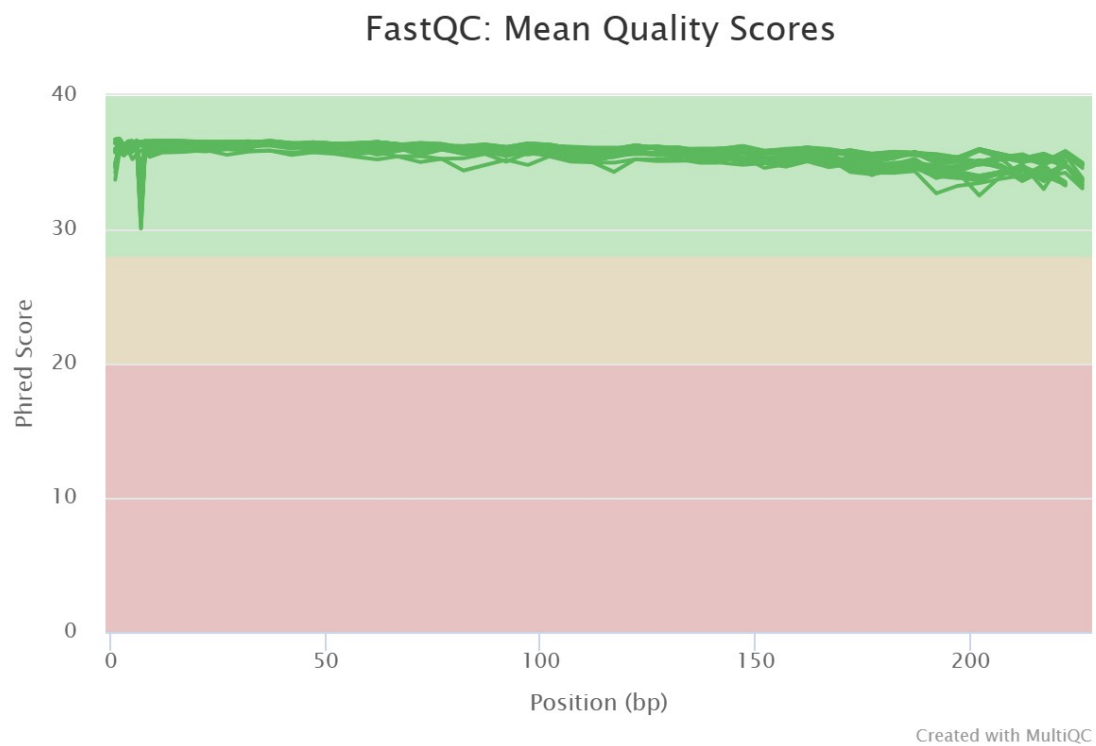| Sample	Chao index	Good's coverage	Simpson index	Shannon index	The number of sequences	The number of OTUs
SH15K	60538.87464	0.955039	0.054473	4.452818	134606	63627
SH15M	36698.19792	0.929572	0.002298	7.743394	135032	58674
SH25K	19203.67500	0.957388	0.001917	7.479667	125410	76671
SH25M	39325.17005	0.909803	0.002974	7.947599	118352	48310
SH28K	19284.35714	0.956177	0.002646	7.526501	118728	67023
SH28M	27474.59176	0.932696	0.002532	7.973241	120037	55413
SH36K	23342.16704	0.949091	0.002573	7.652945	127914	68901
SH36M	18738.23438	0.961874	0.001694	7.655678	127864	71875
SB02K	23722.47128	0.963002	0.129034	3.674820	151738	75044
SB17M	25605.38982	0.937169	0.002717	7.927511	117713	54177
SB18K	17796.30794	0.964813	0.001580	7.686134	126412	80787
SB18M	24068.89356	0.944124	0.001873	7.897387	117976	68438
SB22K	21686.91047	0.955323	0.001534	7.924813	133425	70369
SB22M	31003.52475	0.934875	0.005938	7.225038	123701	52462
VNL03	25425.92788	0.958092	0.036848	5.804995	148014	82362
VNL06	31497.40316	0.934831	0.004942	7.155299	122451	62355
VNL07	33784.20507	0.927867	0.003709	7.352099	121956	60240
VNL17	27164.18118	0.954121	0.002760	7.237795	139431	74415
VNL18	26633.07621	0.960178	0.004473	6.357878	147909	97966

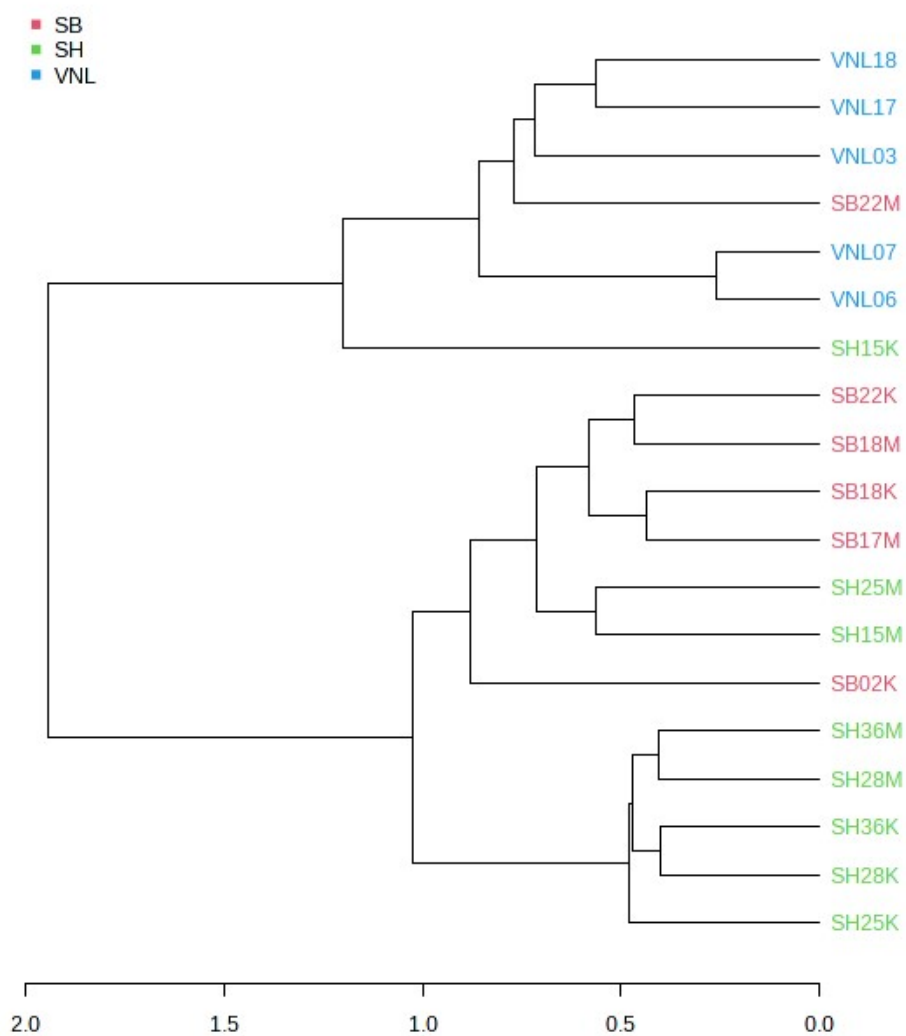**Figure S1. Quality of the sequencing data, as evaluated by FastQC tool.**

Figure S2. Dendrogram displaying the similarity/dissimilarity among the samples (based on Bray-Curtis distance)
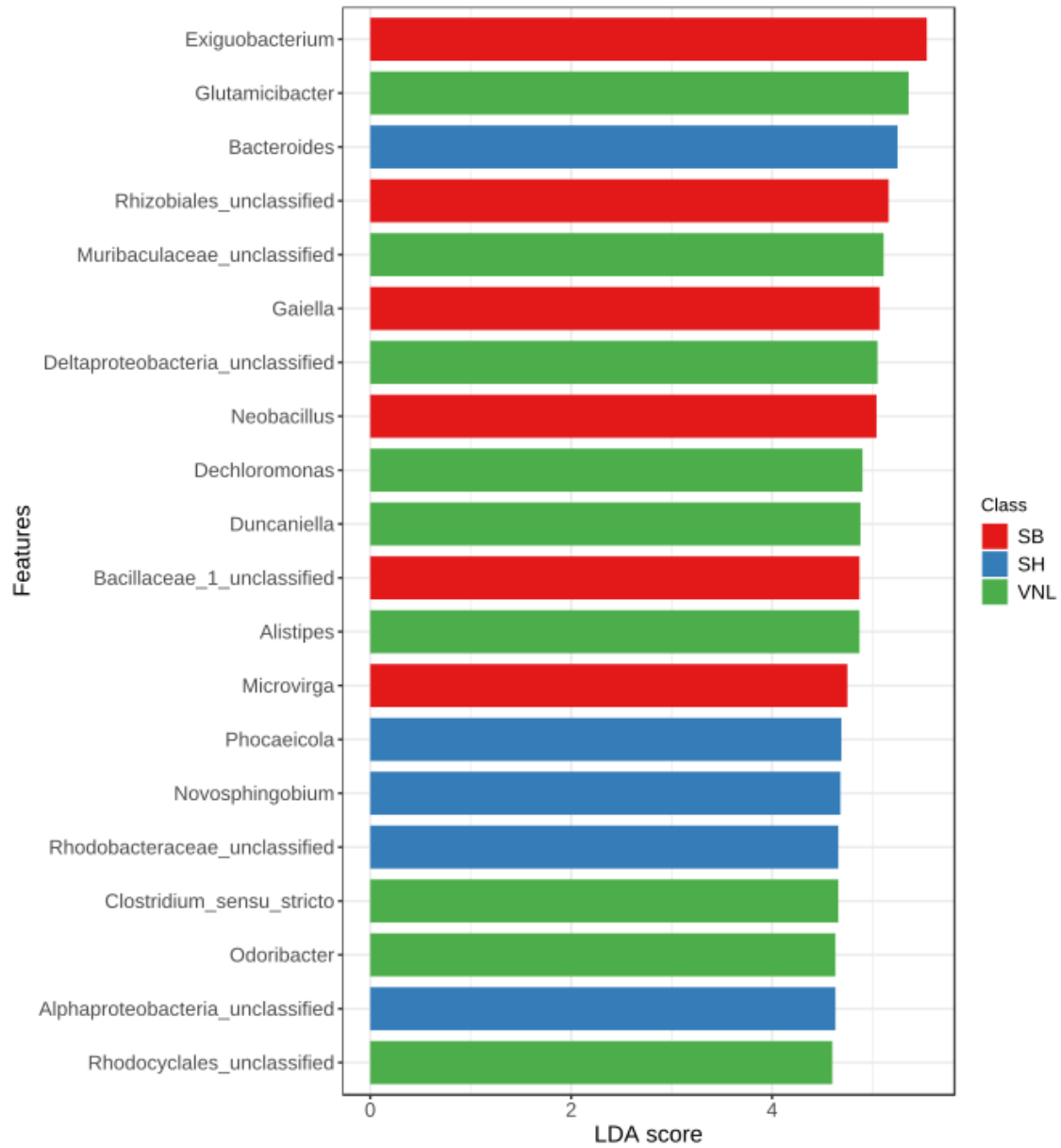
Figure S3. Top 20 genera with the highest LDA scores (the taxonomic biomarkers) when comparing the 3 sample groups from the 3 regions.
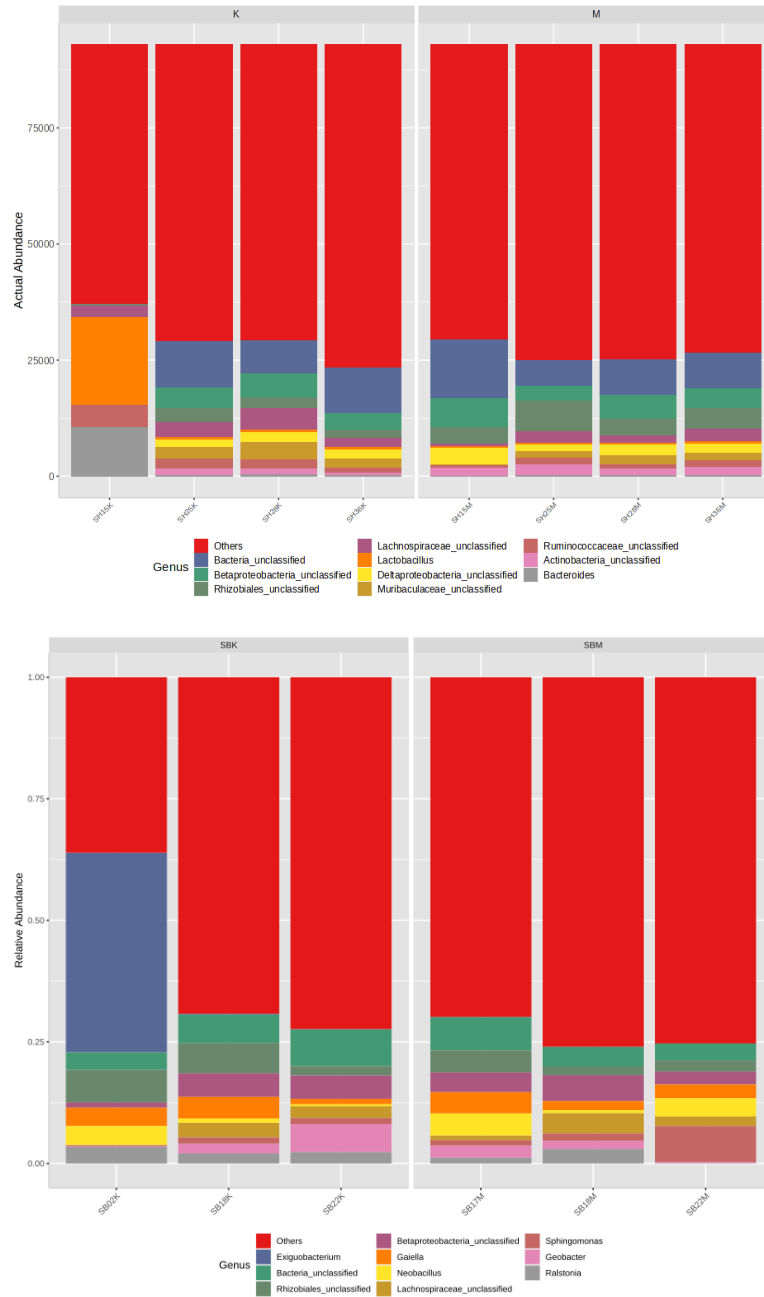
Figure S4. Comparison of the top 10 genera between the dry season sample groups (K) and the rain season sample groups (M) in Red river (top) and in Ba river (bottom)
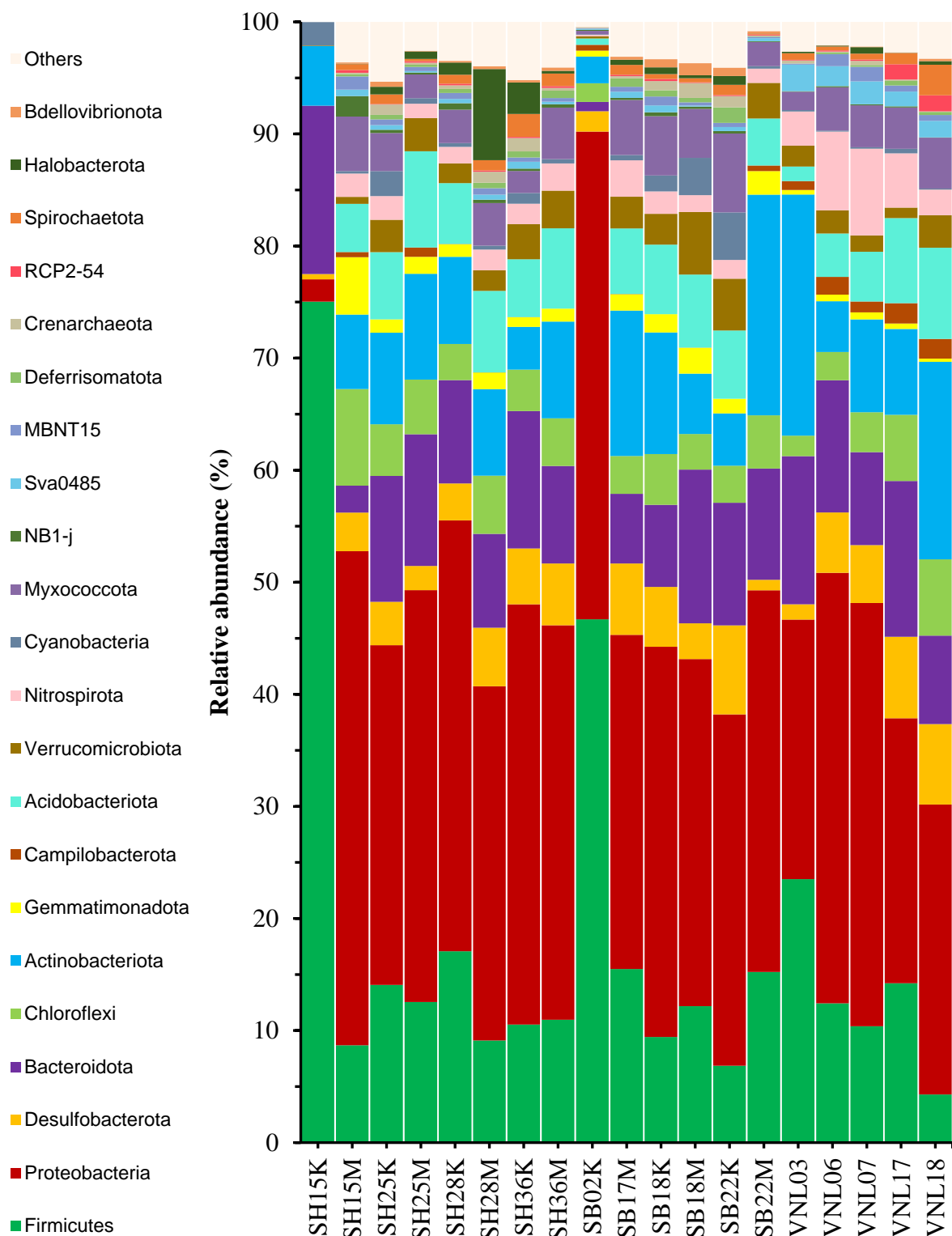
Figure S5. Taxonomic composition of the bacterial communities in the studied samples at phylum level (higher than 1% in relative abundance).
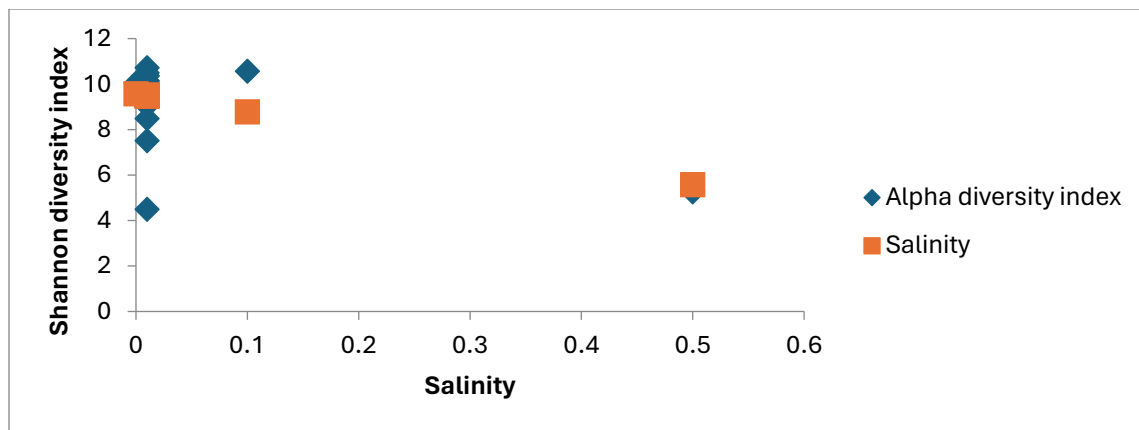
Figure S6. Regression analysis (p<0.01) of the Shannon indices of the bacterial communities in the studied samples versus their salinity levels.