Supporting Information

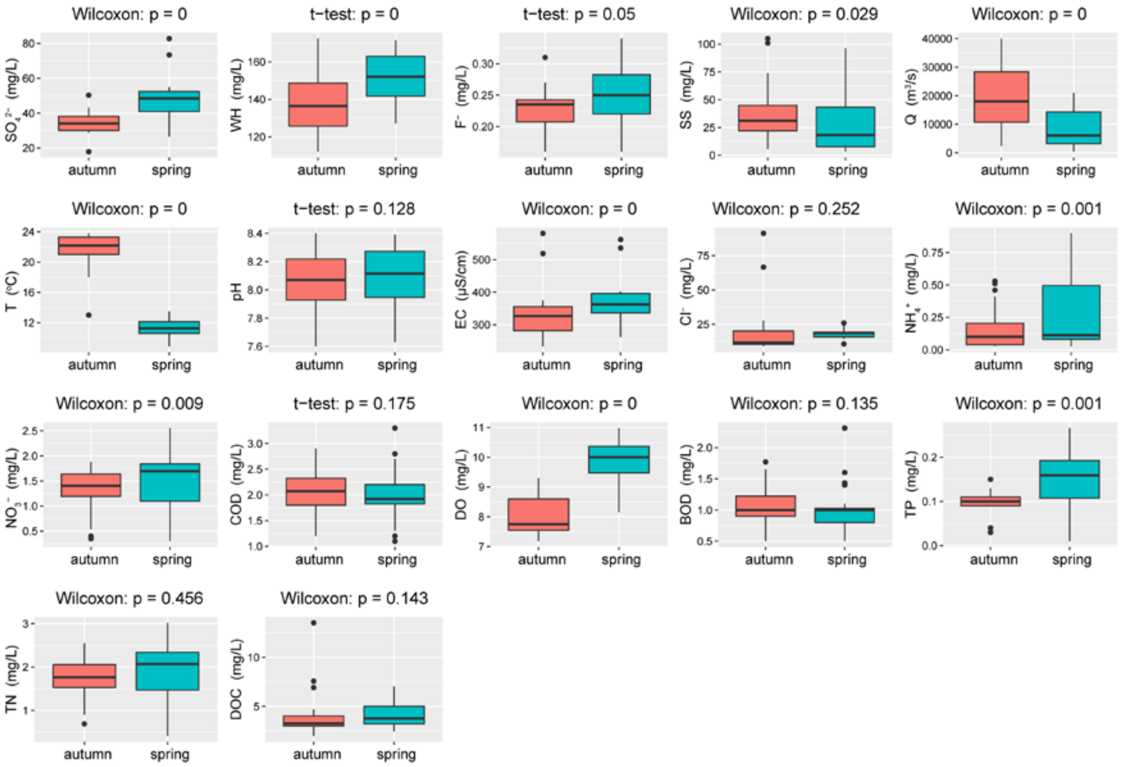

Fig. S1 Paired *t*-test and Wilcoxon signed-rank test for environmental factors between spring and autumn. $p < 0.05$ indicated a significant difference between both seasons. T, water temperature; TN, total nitrogen; SO_4^{2-}, sulfate ion; WH, water hardness; EC, electrical conductivity; Cl^-, chloride ion; DOC, dissolved organic carbon; TP, total phosphorus; F^-, fluoride ion; NO_3^-, nitrate nitrogen; COD, chemical oxygen demand; BOD, biological oxygen demand; NH_4^+, ammonium nitrogen; SS, suspended solids; Q, river flow; DO, dissolved oxygen

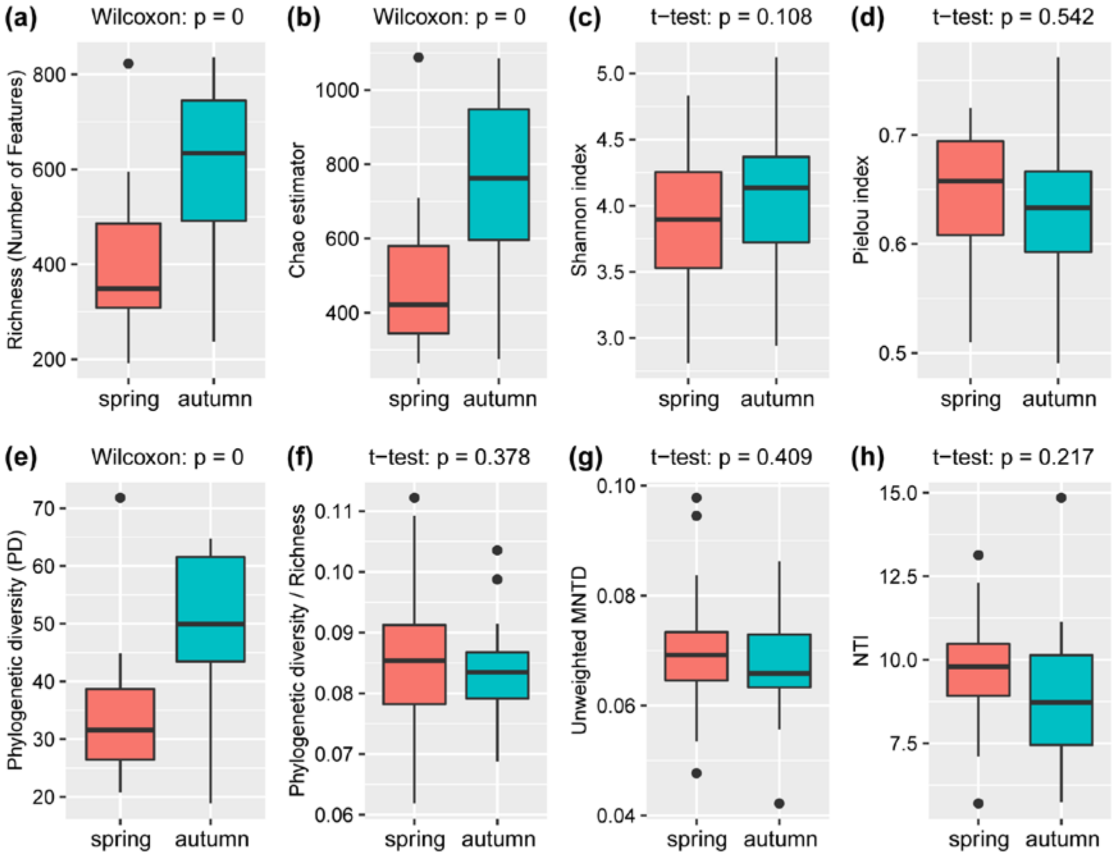

Fig. S2 Paired *t*-test and Wilcoxon signed-rank test for alpha-diversity between spring and autumn. $p < 0.05$ indicated a significant difference between both seasons. (a) Richness (Number of Features); (b) Chao estimator; (c) Shannon index; (d) Pielou index; (e) Phylogenetic diversity (PD); (f) Phylogenetic diversity / Richness; (g) Unweighted MNTD; (h) NTI

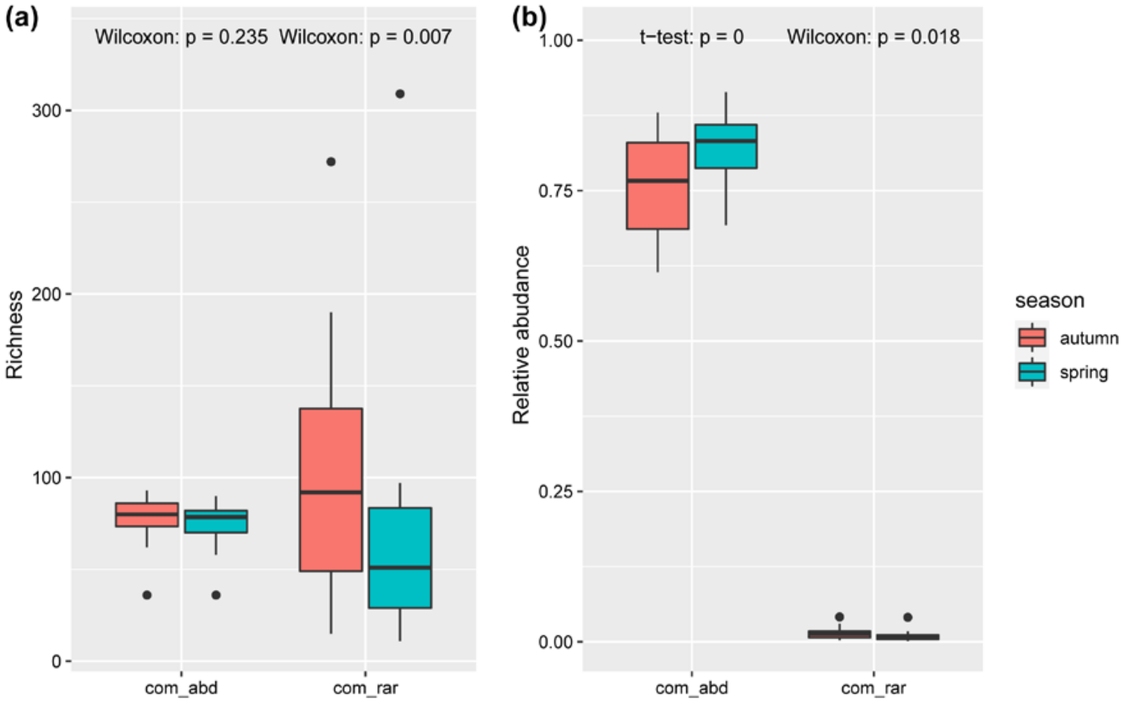

Fig. S3 Paired *t*-test and Wilcoxon signed-rank test for richness (a) and relative abundance (b) of abundant and rare bacterioplankton subcommunities in Yangtze River. $p < 0.05$ indicated a significant difference between both seasons

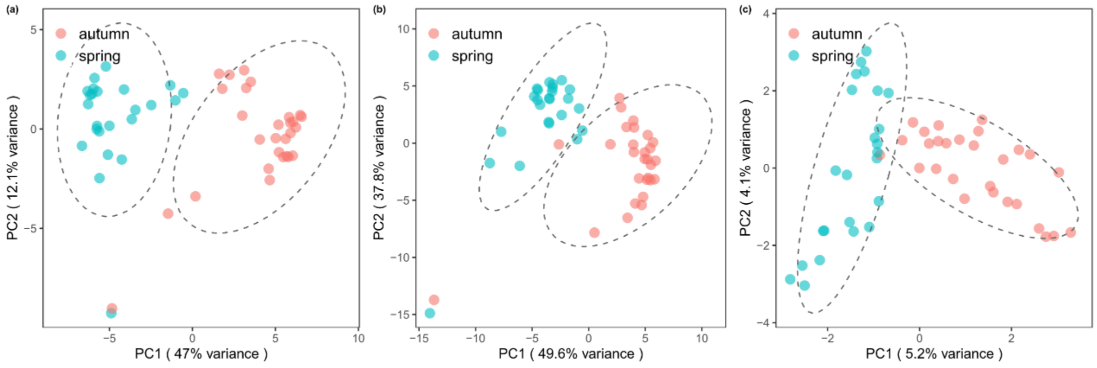

Fig. S4 Principal coordinates analysis of all samples for total (a), abundant (b) and rare (c) bacterial communities. The Sørensen distance is used for quantifying the community compositional variation

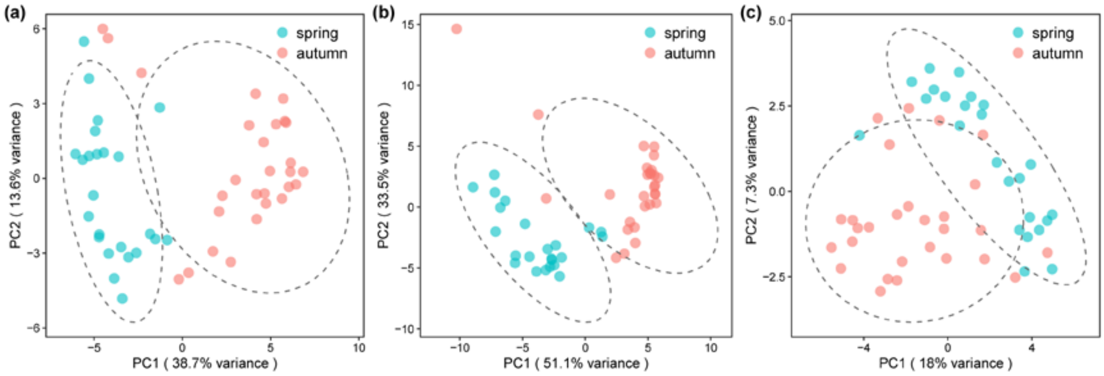

Fig. S5 Principal coordinates analysis of all samples for total (a), abundant (b) and rare (c) bacterial (sub)communities. The unweighted UniFrac distance is used for quantifying the community compositional variation. Red indicates autumn, and blue indicates spring

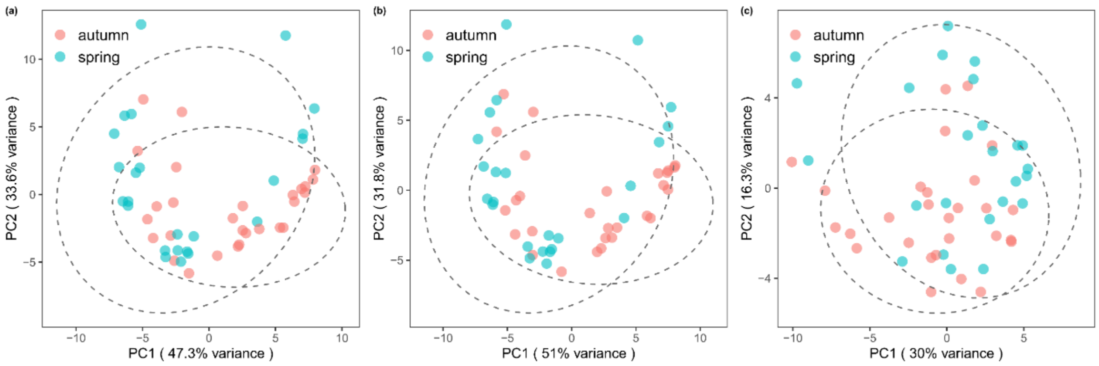

Fig. S6 Principal coordinates analysis of all samples for total (a), abundant (b) and rare (c) bacterial communities. The weighted Unifrac distance is used for quantifying the community compositional variation

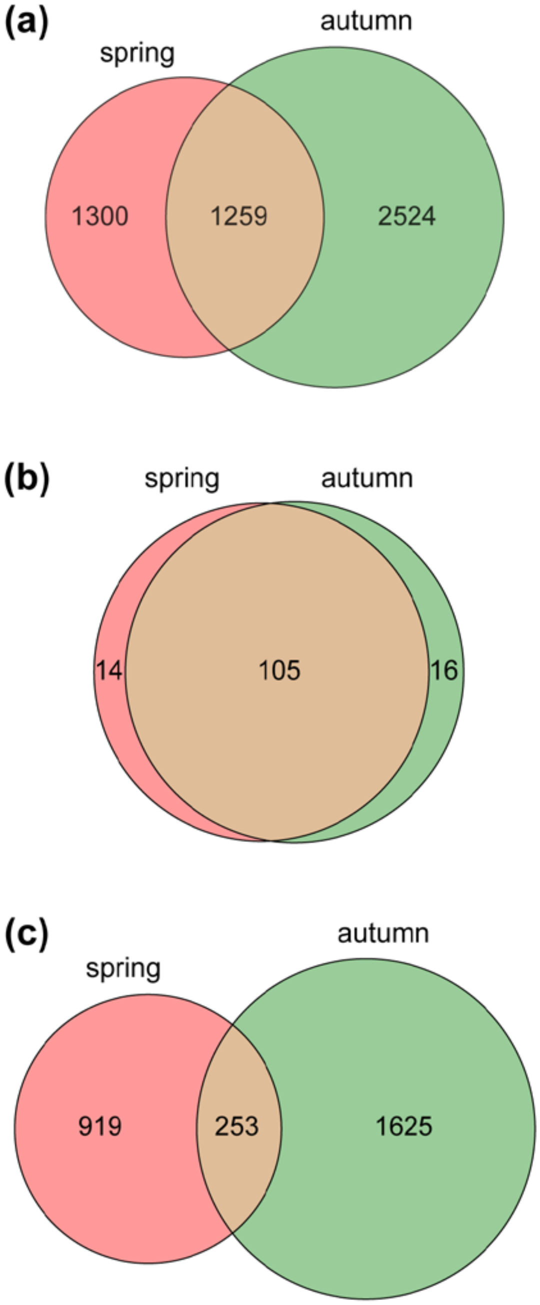

Fig. S7 Shared ASVs analysis of the different seasons for total (a), abundant (b) and rare (c) taxa

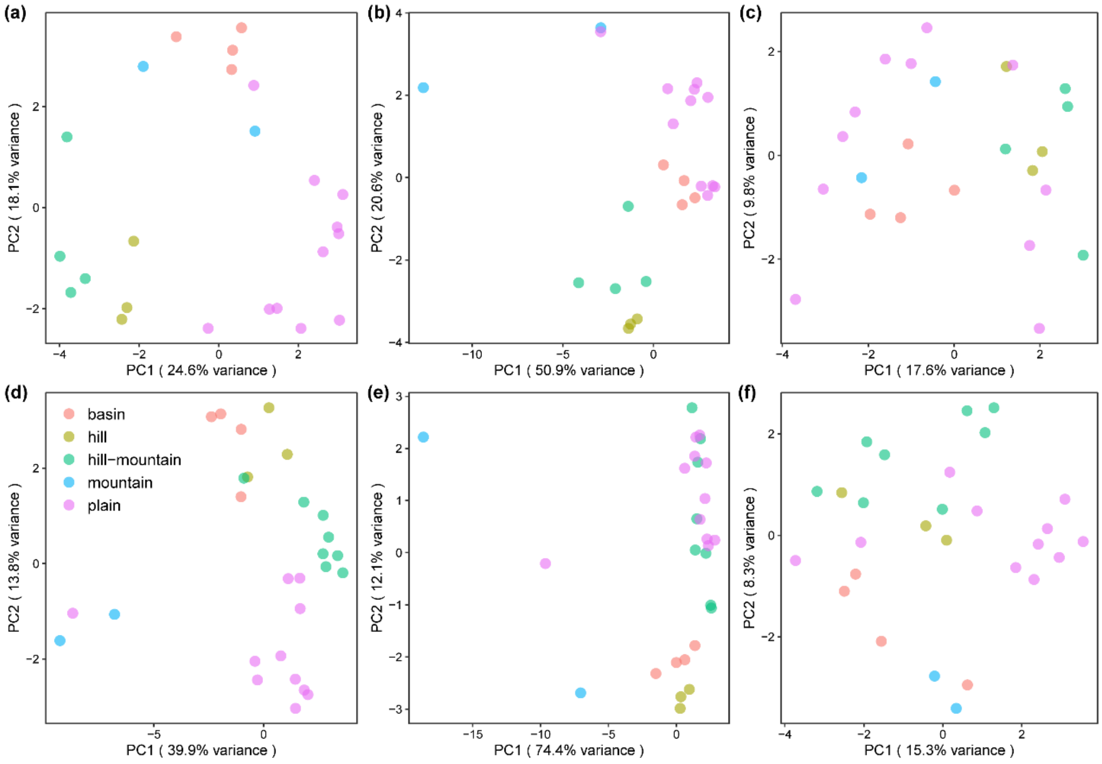

Fig. S8 Principal coordinates analysis showing the bacterioplankton community composition among different landforms in the total-spring (a), abundant-spring (b), rare-spring (c), total-autumn (d), abundant-autumn (e), and rare-autumn (f) samples. The unweighted UniFrac distance is used for quantifying the community compositional variation

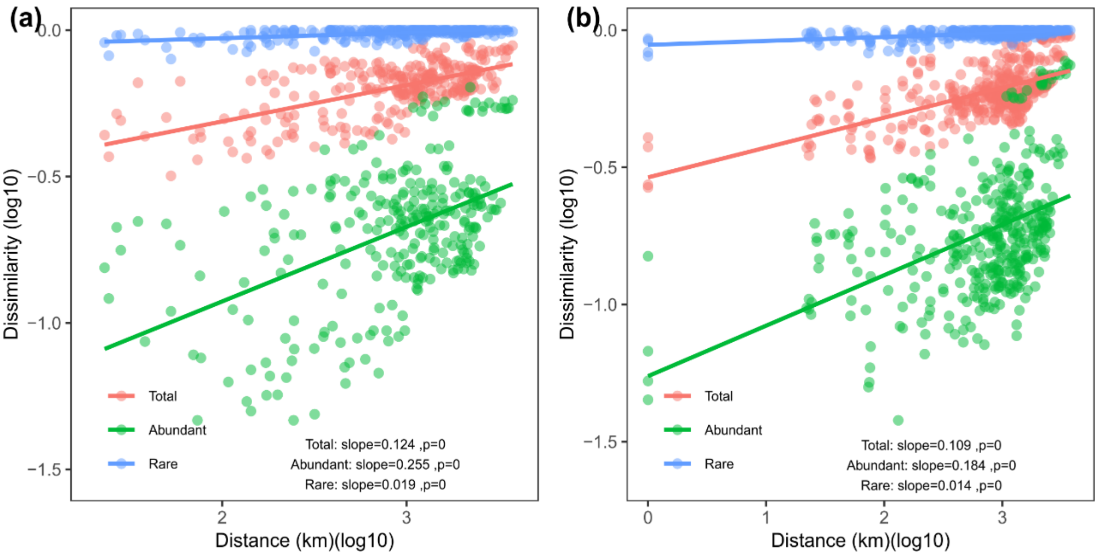

Fig. S9 Distance-decay patterns based on the Sørensen distance of bacterioplankton community composition and river kilometer (rkm) in spring (a) and autumn (b), respectively

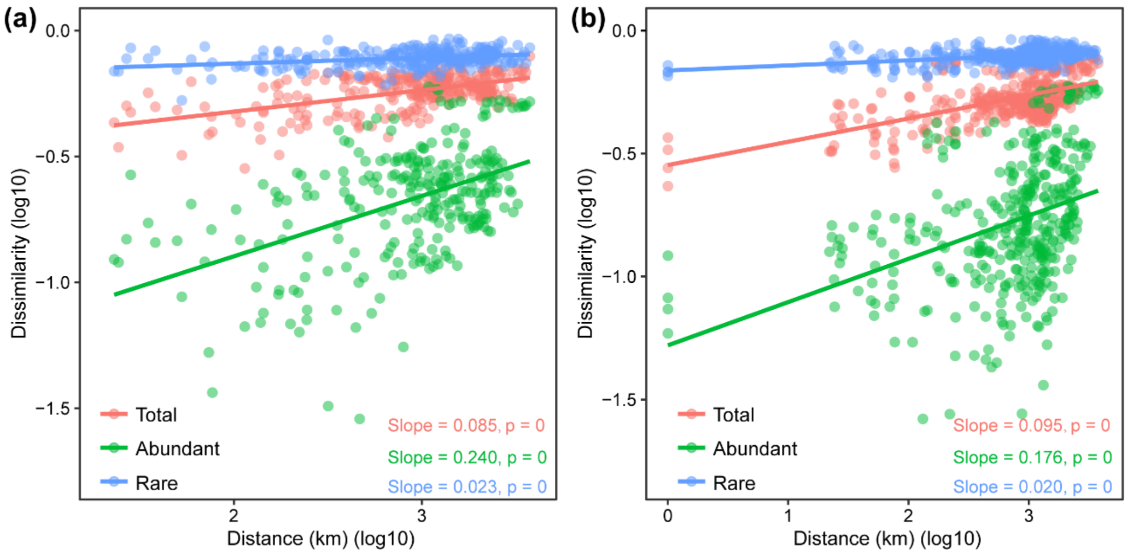

Fig. S10 Distance-decay patterns based on the unweighted UniFrac distance of bacterioplankton community composition and river kilometer (rkm) in spring (a) and autumn (b), respectively

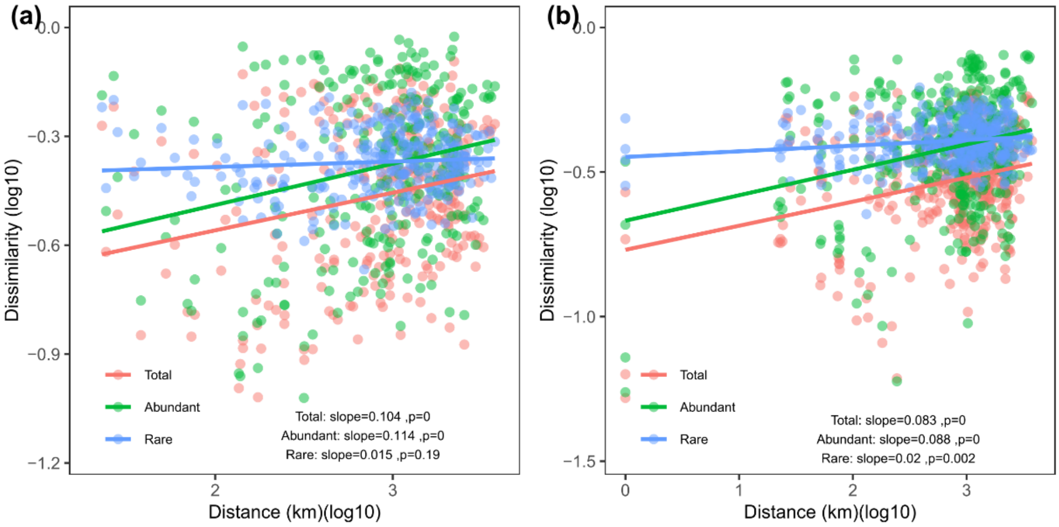

Fig. S11 Distance-decay patterns based on the weighted UniFrac distance of bacterioplankton community composition and river kilometer (rkm) in spring (a) and autumn (b), respectively

Table S1 Analysis of similarities between spring and autumn based Jaccard, Bray-Curtis, unweighted Unifrac and weighted Unifrac dissimilarities

Distance	Type	R	p
Sørensen distance	Total taxa	0.739	0.001
	Abundant taxa	0.698	0.001
	Rare taxa	0.414	0.001
Bray-Curtis distance	Total taxa	0.388	0.001
	Abundant taxa	0.317	0.001
	Rare taxa	0.551	0.001
unweighted Unifrac distance	Total taxa	0.600	0.001
	Abundant taxa	0.628	0.001
	Rare taxa	0.362	0.001
weighted Unifrac distance	Total taxa	0.204	0.001
	Abundant taxa	0.165	0.001
	Rare taxa	0.138	0.002

Table S2 The Mantel test correlating the total community composition with abundant and rare subcommunity composition

Metric	Subcommunity	R	p
Sorensen	Abundant subcommunity	0.867	0.001
	Rare subcommunity	0.623	0.001
Bray Curtis	Abundant subcommunity	0.993	0.001
	Rare subcommunity	0.545	0.001
Unweighted Unifrac	Abundant subcommunity	0.773	0.001
	Rare subcommunity	0.495	0.001
Weighted Unifrac	Abundant subcommunity	0.989	0.001
	Rare subcommunity	0.274	0.001

Table S3 The Bray-Curtis dissimilarities between and within landforms of total taxa in spring. The sample numbers of mountain, hill, basin, hill-mountain, and plain were 2, 3, 4, 4, and 11, respectively

Landform	mountain	hill	basin	hill-mountain	plain
mountain	0.702	NA	NA	NA	NA
hill	0.704 ± 0.276	0.33 ± 0.079	NA	NA	NA
basin	0.585 ± 0.167	0.588 ± 0.208	0.412 ± 0.098	NA	NA
hill-mountain	0.761 ± 0.184	0.593 ± 0.164	0.664 ± 0.18	0.59 ± 0.146	NA
plain	0.559 ± 0.190	0.566 ± 0.185	0.542 ± 0.151	0.61 ± 0.192	0.481 ± 0.160

Table S4 The Bray-Curtis dissimilarities between and within landforms of total taxa in autumn. The sample numbers of mountain, hill, basin, hill-mountain, and plain were 2, 3, 4, 8, and 11, respectively

Landform	mountain	hill	basin	hill-mountain	plain
mountain	0.556	NA	NA	NA	NA
hill	0.714 ± 0.262	0.383 ± 0.131	NA	NA	NA
basin	0.577 ± 0.217	0.496 ± 0.147	0.337 ± 0.07	NA	NA
hill-mountain	0.673 ± 0.245	0.566 ± 0.211	0.579 ± 0.191	0.559 ± 0.236	NA
plain	0.692 ± 0.232	0.599 ± 0.189	0.627 ± 0.18	0.621 ± 0.189	0.599 ± 0.209

Table S5 The Bray-Curtis dissimilarities between and within landforms of abundant taxa in spring. The sample numbers of mountain, hill, basin, hill-mountain, and plain were 2, 3, 4, 4, and 11, respectively

Landform	mountain	hill	basin	hill-mountain	plain
mountain	0.652	NA	NA	NA	NA
hill	0.678 ± 0.289	0.292 ± 0.096	NA	NA	NA
basin	0.541 ± 0.162	0.556 ± 0.217	0.375 ± 0.099	NA	NA
hill-mountain	0.743 ± 0.191	0.562 ± 0.174	0.64 ± 0.188	0.573 ± 0.155	NA
plain	0.518 ± 0.201	0.527 ± 0.197	0.502 ± 0.162	0.577 ± 0.206	0.44 ± 0.175

Table S6 The Bray-Curtis dissimilarities between and within landforms of abundant taxa in autumn. The sample numbers of mountain, hill, basin, hill-mountain, and plain were 2, 3, 4, 8, and 11, respectively

Landform	mountain	hill	basin	hill-mountain	plain
mountain	0.503	NA	NA	NA	NA
hill	0.695 ± 0.273	0.36 ± 0.156	NA	NA	NA
basin	0.526 ± 0.220	0.46 ± 0.158	0.285 ± 0.067	NA	NA
hill-mountain	0.648 ± 0.267	0.529 ± 0.244	0.538 ± 0.217	0.534 ± 0.270	NA
plain	0.669 ± 0.251	0.561 ± 0.212	0.594 ± 0.195	0.59 ± 0.213	0.571 ± 0.229

Table S7 The Bray-Curtis dissimilarities between and within landforms of rare taxa in spring. The sample numbers of mountain, hill, basin, hill-mountain, and plain were 2, 3, 4, 4, and 11, respectively

Landform	mountain	hill	basin	hill-mountain	plain
mountain	0.968	NA	NA	NA	NA
hill	0.951 ± 0.057	0.875 ± 0.033	NA	NA	NA
basin	0.98 ± 0.026	0.966 ± 0.045	0.963 ± 0.033	NA	NA
hill-mountain	0.969 ± 0.042	0.95 ± 0.048	0.97 ± 0.035	0.93 ± 0.042	NA
plain	0.973 ± 0.032	0.972 ± 0.036	0.974 ± 0.029	0.976 ± 0.033	0.965 ± 0.034

Table S8 The Bray-Curtis dissimilarities between and within landforms of rare taxa in autumn. The sample numbers of mountain, hill, basin, hill-mountain, and plain were 2, 3, 4, 8, and 11, respectively

Landform	mountain	hill	basin	hill-mountain	plain
mountain	0.965	NA	NA	NA	NA
hill	0.977 ± 0.025	0.953 ± 0.031	NA	NA	NA
basin	0.963 ± 0.038	0.968 ± 0.037	0.932 ± 0.042	NA	NA
hill-mountain	0.969 ± 0.035	0.967 ± 0.033	0.965 ± 0.033	0.954 ± 0.037	NA
plain	0.971 ± 0.034	0.972 ± 0.033	0.97 ± 0.033	0.97 ± 0.031	0.961 ± 0.037

Table S9 Analysis of similarities across landforms based Bray-Curtis dissimilarities. Asterisks denote significance (*, p < 0.05; **, p < 0.01)

Taxa	Group	Spring R	Autumn R
Total	basin vs hill-mountain	0.958*	0.353
	basin vs plain	0.604**	0.510**
	hill-mountain vs plain	0.882**	0.186*
	hill vs basin	1.000*	1.000*
	hill vs hill-mountain	0.500*	0.234
	hill vs plain	0.794**	0.120
	mountain vs basin	0.857*	1.000
	mountain vs hill	1.000	1.000
	mountain vs hill-mountain	1.000	0.836*
	mountain vs plain	0.789*	0.833*
Abundant	basin vs hill-mountain	0.927*	0.287
	basin vs plain	0.552**	0.410*
	hill-mountain vs plain	0.843**	0.145
	hill vs basin	0.981*	0.981*
	hill vs hill-mountain	0.463	0.118
	hill vs plain	0.752**	−0.002
	mountain vs basin	0.857	1.000
	mountain vs hill	1.000	1.000
	mountain vs hill-mountain	1.000	0.703*
	mountain vs plain	0.724*	0.810*
Rare	basin vs hill-mountain	0.854*	0.728**
	basin vs plain	0.589**	0.565**
	hill-mountain vs plain	0.899**	0.383**
	hill vs basin	0.944*	0.963*
	hill vs hill-mountain	0.852*	0.655**
	hill vs plain	0.806**	0.675**
	mountain vs basin	0.679	0.929
	mountain vs hill	0.917	1.000
	mountain vs hill-mountain	1.000	0.897*
	mountain vs plain	0.645**	0.740*

Table S10 Variation partitioning analysis based on partial RDA (Bray-Curtis distance) illustrating the effects of physicochemical and spatial factors on the bacterial communities in the Yangtze River

Season	Effects	Total taxa		Abundant taxa		Rare taxa	
		R^2	p	R^2	p	R^2	p
Spring	Physicochemical	0.292	0.001	0.242	0.001	0.040	0.001
	Shared	0.086	–	0.103	–	0.004	–
	Spatial	0.124	0.002	0.108	0.002	0.015	0.003
	Residual	0.498	–	0.547	–	0.941	–
Autumn	Physicochemical	0.465	0.001	0.461	0.001	0.031	0.001
	Shared	0.141	–	0.125	–	0.018	–
	Spatial	0.001	0.134	0.001	0.268	0.002	0.350
	Residual	0.393	–	0.413	–	0.949	–
Both season	Physicochemical	0.422	0.001	0.373	0.001	0.043	0.001
	Shared	0.050	–	0.052	–	0.008	–
	Spatial	0.015	0.009	0.016	0.013	0.003	0.031
	Residual	0.513	–	0.559	–	0.945	–

Notes: The selected physicochemical factors were Q, EC, TP, COD for Spring×Total taxa, Q, EC, TP for Spring×Abundant taxa, Q, TP, COD for Spring×Rare taxa, T, F^-, WH, Q, Cl^-, EC, pH, DO for Autumn×Total taxa, T, F^-, WH, Q, Cl^- for Autumn×Abundant taxa, Q, F, NO_3^-, TN for Autumn×Rare taxa, T, EC, Q, TP, COD, F^-, NO_3^-, pH, SO_4^{2-} for Both season×Total taxa, T, EC, F^-, Q, COD, TP, NO_3^- for Both season×Abundant taxa, and T, Q, TN, WH, EC, COD for Both season×Rare taxa

Table S11 Variation partitioning analysis based on partial RDA (unweighted UniFrac distance) illustrating the effects of environmental and spatial factors on the bacterial communities in the Yangtze River

Season	Effects	Total taxa		Abundant taxa		Rare taxa	
		R^2	p	R^2	p	R^2	p
Spring	Physicochemical	0.187	0.001	0.442	0.001	0.031	0.006
	Shared	0.016	–	0.181	–	0.002	–
	PCNM	0.082	0.003	0.067	0.003	0.013	0.048
	Residual	0.716	–	0.311	–	0.953	–
Autumn	Physicochemical	0.360	0.001	0.344	0.001	0.128	0.001
	Shared	0.161	–	0.356	–	0.021	–
	PCNM	0.005	0.073	−0.007	0.296	0.008	0.089
	Residual	0.475	–	0.307	–	0.843	–
Both season	Physicochemical	0.460	0.001	0.651	0.001	0.123	0.001
	Shared	0.043	–	0.054	–	0.012	–
	PCNM	0.012	0.002	0.006	0.056	0.003	0.090
	Residual	0.485	–	0.290	–	0.862	–

Notes: The selected physicochemical factors were Q, TP, T for Spring × Total taxa, DO, Q, EC, Cl^-, TP for Spring × Abundant taxa, NH_4^+ for Spring × Rare taxa, Q, Cl^-, F^-, WH, pH, EC, DO, TP for Autumn × Total taxa, Cl^-, NO_3^-, WH for Autumn × Abundant taxa, Q, F^-, COD, TN, Cl^-, NO_3 for Autumn × Rare taxa, T, Q, Cl^-, TP, DO, COD, EC, F^-, SO_4^{2-}, WH for Both season × Total taxa, T, DO, Cl^-, NH_4^+, TP for Both season × Abundant taxa, and Q, T, F^-, SO_4^{2-}, COD, Cl^-, BOD for Both season × Rare taxa

Table S12 Partial mantel analysis (conditioned on distance along river) of the βNTI of abundant and rare taxa against environmental factors for spring and autumn. Asterisks denote significance (*, $p< 0.05$; **, $p< 0.01$)

Environmental factors	**Abundant (Mantel's r)**		**Rare (Mantel's r)**	
	Spring	**Autumn**	**Spring**	**Autumn**
SO_4^{2-}	−0.186	−0.028	−0.066	0.252*
WH	−0.101	−0.039	0.056	0.101
F^-	−0.090	−0.037	0.014	0.026
SS	−0.141	0.097	0.209*	0.200*
Q	−0.041	0.004	0.234**	0.433**
T	−0.069	−0.011	0.300**	0.171
pH	−0.130	0.155*	0.016	0.106
EC	0.129	−0.014	−0.009	0.363**
Cl^-	−0.052	0.112	−0.113	0.096
NH_4^+	0.034	−0.109	0.156	0.310**
NO_3^-	−0.039	0.065	0.132	0.049
COD	−0.077	0.052	−0.151	0.162
DO	0.077	0.103	0.018	0.045
BOD	0.022	0.054	0.075	0.299**
TP	−0.083	0.004	−0.068	0.034
TN	0.028	0.078	0.134	0.042
DOC	0.063	0.067	−0.042	0.102

Notes: a) These abbreviations of environmental factors are the same as those in Methods and Fig. S1. The significance level is labeled by * when $p \le 0.050$ and by ** when $p \le 0.01$

Table S13 List of studies about assembly processes of abundant and rare taxa

Habitat	Taxon	Primary process		Reference
		Abundant taxa	Rare taxa	
Tibetan Plateau (China) grassland soils	Bacterial community	Stochasticity	Stochasticity	(Ji et al., 2020)
Surface layer of marginal seas	Picoeukaryotic community	Stochasticity	Selection	(Wu et al., 2017)
Subsurface layer of marginal seas	Picoeukaryotic community	Stochasticity	Stochasticity	(Wu et al., 2017)
Agricultural fields across eastern China	Bacterial community	Selection	Selection	(Jiao and Lu, 2020)
Eutrophic Lake Nanhu	Bacterial community	Dispersal limitation	Variable selection	(Wan et al., 2021a)

Salinized Agricultural Soils	Bacterial community	Dispersal limitation	Variable selection	(Wan et al., 2021b)
Coastal Wetlands along an Inundation Gradient	Bacterial community	Dispersal limitation	Homogeneous selection	(Gao et al., 2020)

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Wan W, Grossart H P, He D, Yuan W, Yang Y (2021a). Stronger environmental adaptation of rare rather than abundant bacterioplankton in response to dredging in eutrophic Lake Nanhu (Wuhan, China). Water Research, 190: 116751

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Wu W, Logares R, Huang B, Hsieh C H (2017). Abundant and rare picoeukaryotic sub-communities present contrasting patterns in the epipelagic waters of marginal seas in the northwestern Pacific Ocean. Environmental Microbiology, 19(1): 287–300