

**Table S1.** Environmental parameters. DIN: Dissolved inorganic nitrogen; DIP: Dissolved inorganic phosphorus; DSi: Dissolved silica; Chl *a*: Chlorophyll *a*; SPM: Suspended particulate matter.

Sample	Date	Longitude	Latitude	Salinity	Temperature (°C)	DIN (μM)	DIP (μM)	DSi (μM)	Chl <i>a</i> (μg/L)	SPM (g/L)	pH
C1	2019.9.1	121.0561	31.7805	0	28.92	106.97	0.55	118.17	1.23	0.04	7.80
C2	2019.9.1	121.3199	31.5931	0	28.67	101.96	0.55	110.78	1.14	0.03	7.85
C3	2019.9.1	121.5695	31.4020	0.1	28.79	105.24	0.49	112.52	1.38	0.10	7.90
C4	2019.9.1	121.6567	31.3686	0.1	28.87	109.66	0.77	104.90	1.55	0.10	7.89
C5	2019.9.1	121.7494	31.2883	0	28.92	110.83	0.45	101.92	1.91	0.20	7.84
C6	2019.9.1	121.9116	31.1529	0.1	-	110.59	0.68	97.55	2.06	0.58	7.97
C6-1	2019.9.2	121.9674	31.0939	1.0	28.13	113.18	1.18	100.56	2.88	-	7.84
C6-2	2019.9.2	121.9860	31.0852	2.8	27.77	117.72	1.62	108.50	1.86	0.38	7.83
C6-3	2019.9.2	121.9850	31.0843	9.1	26.86	89.48	1.55	83.46	2.08	0.48	7.83
C7	2019.9.1	122.1541	31.0283	12.5	27.25	63.30	1.11	53.95	1.75	1.14	7.81
C8	2019.8.31	122.2495	31.0217	15.1	27.47	50.69	0.81	48.75	1.83	-	7.84
C9	2019.8.31	122.3643	31.0019	18.8	-	60.40	1.10	62.57	2.06	-	7.84
C10	2019.8.31	122.4508	30.9693	22.1	26.88	36.17	0.23	37.53	10.30	0.02	8.08
C11	2019.8.31	122.6159	30.9224	24.6	26.39	33.55	0.21	32.53	9.71	0.02	8.06
C12	2019.8.31	122.7435	30.9422	22.1	-	27.46	0.15	25.84	4.27	-	8.11
C13	2019.8.30	122.8865	30.8135	25.8	26.40	23.69	0.22	20.46	2.75	0.02	8.16
C14	2019.8.29	123.2532	30.6707	23.1	27.42	25.78	0.11	16.21	7.79	0.01	8.28
C15	2019.8.29	123.4979	30.5105	25.6	27.13	15.74	0.10	4.07	9.13	-	8.28
C16	2019.8.29	123.9998	30.2962	25.6	27.43	14.51	0.08	4.55	14.49	0.01	8.24
C18	2019.8.29	124.9874	29.8646	32.1	-	1.00	0.03	2.36	0.21	0.01	8.17
Y1	2019.8.28	122.4656	29.8048	28.8	27.14	26.90	0.76	23.94	1.42	0	7.98
Y2	2019.8.28	122.5940	29.7635	27.8	29.07	29.75	0.83	24.38	1.27	0.02	8.00
Y3	2019.8.28	122.7637	29.6961	29.5	29.46	18.67	0.62	18.84	1.67	0.02	8.08
Y4	2019.8.28	122.9979	29.7627	28.4	28.82	12.94	0.24	6.48	10.90	0.02	8.15
Y5	2019.8.28	123.2539	29.7732	28.4	28.84	4.95	0.06	0.53	9.36	-	8.25
Y6	2019.8.28	123.5106	29.7962	30.4	29.00	1.74	0.05	0.51	6.24	0.01	8.24
Y7	2019.8.28	123.9998	29.8367	30.6	27.63	2.04	0.06	0.91	6.74	0.02	8.23

**Table S2.** Pearson correlation coefficient between environmental variables. ‘\*\*’ represented the significance level (\* $P < 0.05$ ; \*\* $P < 0.01$ ; \*\*\* $P < 0.001$ ). Bold face values indicated significant correlations at  $P < 0.05$ .

	Salinity	Temperature	DIN	DIP	DSi	Chl <i>a</i>	SPM	pH
Salinity	1							
Temperature	-0.22	1						
DIN	<b>-0.98***</b>	0.2	1					
DIP	<b>-0.55**</b>	-0.02	<b>0.66***</b>	1				
DSi	<b>-0.97***</b>	0.23	<b>0.99***</b>	<b>0.63***</b>	1			
Chl <i>a</i>	<b>0.48*</b>	-0.28	<b>-0.54**</b>	<b>-0.58**</b>	<b>-0.57**</b>	1		
SPM	-0.41	-0.21	0.41	<b>0.62**</b>	0.34	-0.29	1	
pH	<b>0.79***</b>	-0.14	<b>-0.84***</b>	<b>-0.81***</b>	<b>0.86***</b>	<b>0.69***</b>	<b>-0.53*</b>	1

**Table S3.** Results of simple and Partial Mantel tests demonstrated spearman's correlations of environmental factors (Euclidean), total environmental variability (Euclidean) and geographic distance with bacterial and protistan beta-diversity dissimilarity (Bary-Curtis) against all sampled sites (n=27, with 9,999 permutations). Env referred to the Euclidean distance of the set of all environmental parameters including salinity, temperature, DIN, DIP, DSI, Chl *a*, SPM and pH. Geo referred to the geographic distance.  $r_{env}$  referred to the correlation coefficient between abiotic drivers and microbial dissimilarity controlled by set of all environmental parameters derived from Mantel test.  $r_{geo}$  referred to the correlation coefficient between abiotic drivers and microbial dissimilarity controlled by geographic distance derived from Partial Mantel tests. \* $P < 0.05$ ; \*\* $P < 0.01$ ; \*\*\* $P < 0.001$ .

Variation  Source	Bacteria			Protists		
	$r$	$r_{env}$	$r_{geo}$	$r$	$r_{env}$	$r_{geo}$
Salinity	0.884***	0.703***	0.778***	0.864***	0.710***	0.819***
Temperature	0.069	-0.083	0.045	0.027	-0.116	0
DIN	0.866***	0.624***	0.754***	0.816***	0.586***	0.740***
DIP	0.263**	-0.414	0.208**	0.226**	-0.347	0.167*
DSi	0.854***	0.595***	0.719***	0.814***	0.581***	0.739***
Chl <i>a</i>	0.265**	-0.092	0.093	0.097	-0.292	-0.061
SPM	0.238**	-0.316	0.335***	0.343**	-0.038	0.399**

<b>pH</b>	0.623***	0.044	0.360***	0.516***	-0.067	0.307***
<b>Env</b>	0.780***	-	0.615***	0.703***	-	0.571***
<b>Geo</b>	0.707***	0.454***	-	0.513***	0.138*	-

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**Table S4.** The Nearest Sequenced Taxon Index (NSTI) scores calculated from PICRUST2 of each sample.

Sample	Metric	Value
C1	Weighted NSTI	0.0551609
C10	Weighted NSTI	0.03150826
C11	Weighted NSTI	0.04724264
C12	Weighted NSTI	0.07872932
C13	Weighted NSTI	0.05352921
C14	Weighted NSTI	0.03476975
C15	Weighted NSTI	0.07232465
C16	Weighted NSTI	0.06565916
C18	Weighted NSTI	0.02740848
C2	Weighted NSTI	0.05182261
C3	Weighted NSTI	0.06716686
C4	Weighted NSTI	0.07140522
C5	Weighted NSTI	0.07202526
C6	Weighted NSTI	0.07911257
C6-1	Weighted NSTI	0.07244714
C6-2	Weighted NSTI	0.11086182
C6-3	Weighted NSTI	0.11971574
C7	Weighted NSTI	0.12988493
C8	Weighted NSTI	0.10011979
C9	Weighted NSTI	0.08623853
Y1	Weighted NSTI	0.05608941
Y2	Weighted NSTI	0.09405516

Y3	Weighted NSTI	0.08174554
Y4	Weighted NSTI	0.03374613
Y5	Weighted NSTI	0.03351958
Y6	Weighted NSTI	0.04643049
Y7	Weighted NSTI	0.04092888

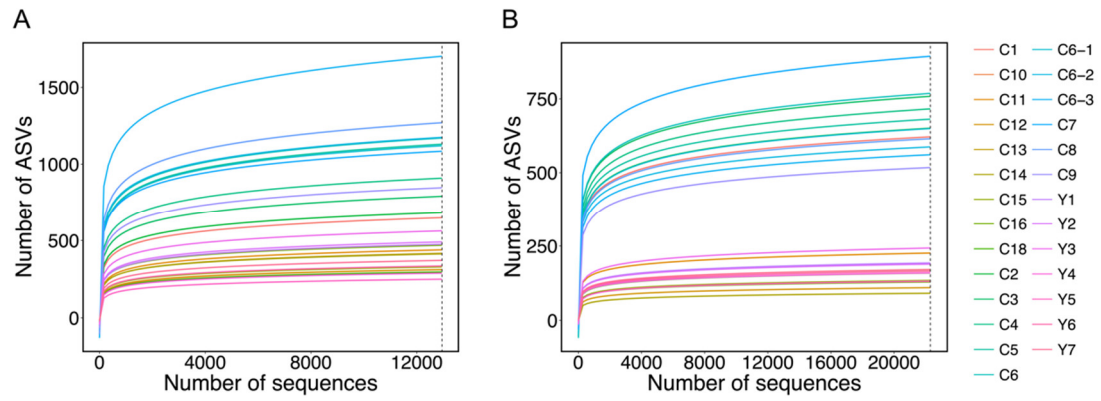
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**Table S5.** The relative abundance of KEGG pathways at the second level and differences between each two groups with different salinity (*t*-test, \**P* < 0.05; \*\**P* < 0.01; \*\*\**P* < 0.001).

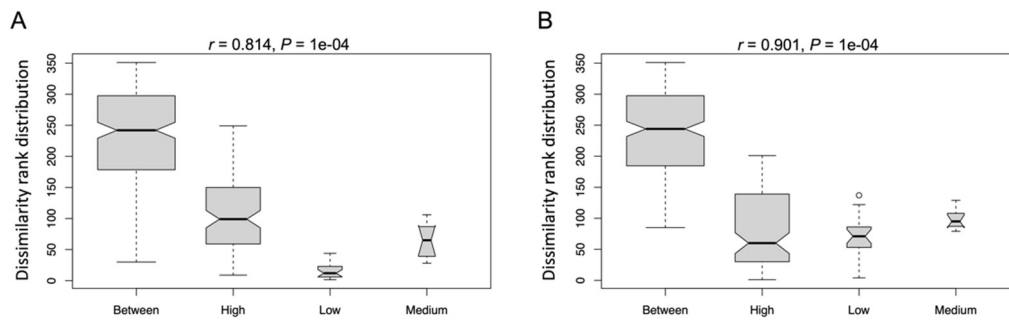
KEGG Level II	Relative Abundances			Spatial Comparisons		
	Low (mean %)	Medium (mean %)	High (mean %)	Low- Medium	Low- High	Medium- High
Amino acid metabolism	13.5093	13.4824	14.1180		**	*
Biosynthesis of other secondary metabolites	2.0923	2.2954	2.1379	**		
Cancer: overview	0.0128	0.0250	0.0047	**	**	***
Carbohydrate metabolism	13.5455	13.3551	13.1513	**	**	
Cardiovascular disease	0.0003	0.0000	0.0010		*	*
Cell growth and death	1.2553	1.3424	1.4722	**	***	*
Cell motility	0.9865	1.5829	1.5607	**	***	
Cellular community - prokaryotes	0.0549	0.0894	0.1013	**	***	
Development and regeneration	0.0000	0.0000	0.0000			
Digestive system	0.0459	0.0308	0.0354	**	*	
Drug resistance: antimicrobial	0.0049	0.0080	0.0056			
Endocrine system	0.0558	0.0677	0.0453	**	*	**
Energy metabolism	5.5475	5.3416	5.9850	**	*	*
Environmental adaptation	0.1463	0.1563	0.1586	**	***	
Excretory system	0.0000	0.0000	0.0000			
Folding, sorting and degradation	3.2082	3.2053	3.1104			
Global and overview maps	1.2361	1.2679	1.0889		*	
Glycan biosynthesis and metabolism	2.3542	2.4845	2.7965		***	*

Immune disease	0.0008	0.0005	0.0001	*	***	
Immune system	0.0092	0.0187	0.0161	**		
Infectious disease: bacterial	0.0149	0.0253	0.0498	**	***	***
Infectious disease: parasitic	0.0570	0.0468	0.0594	**		
Lipid metabolism	6.7192	6.4007	6.0138	*	***	
Membrane transport	1.3767	1.4526	1.5342	*	**	
Metabolism of cofactors and vitamins	11.4776	11.4703	12.3806		**	*
Metabolism of other amino acids	7.4284	7.6852	8.1125	*	***	*
Metabolism of terpenoids and polyketides	9.8915	10.0414	8.6504		***	***
Nervous system	0.0000	0.0000	0.0000			
Neurodegenerative disease	0.0144	0.0592	0.0285	*		
Nucleotide metabolism	1.6957	1.6085	1.7021	**		*
Replication and repair	5.1756	4.8761	4.7302	**	***	
Signal transduction	0.2884	0.3353	0.3298	**	**	
Signaling molecules and interaction	0.0000	0.0000	0.0001		**	
Transcription	0.7250	0.7647	0.7277	*		
Translation	2.9867	2.7896	2.6351	**	***	
Transport and catabolism	0.3221	0.3491	0.3764	**	***	
Xenobiotics biodegradation and metabolism	7.7610	7.3412	6.8801		**	

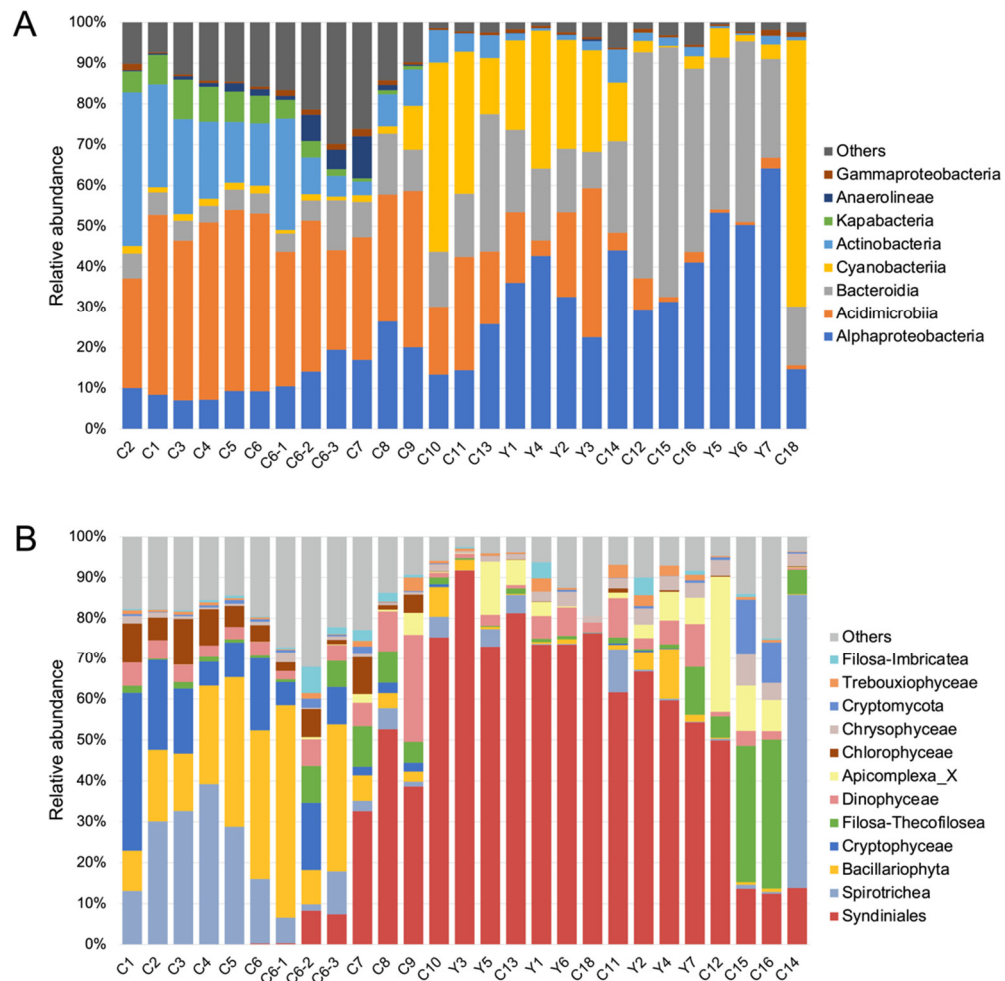
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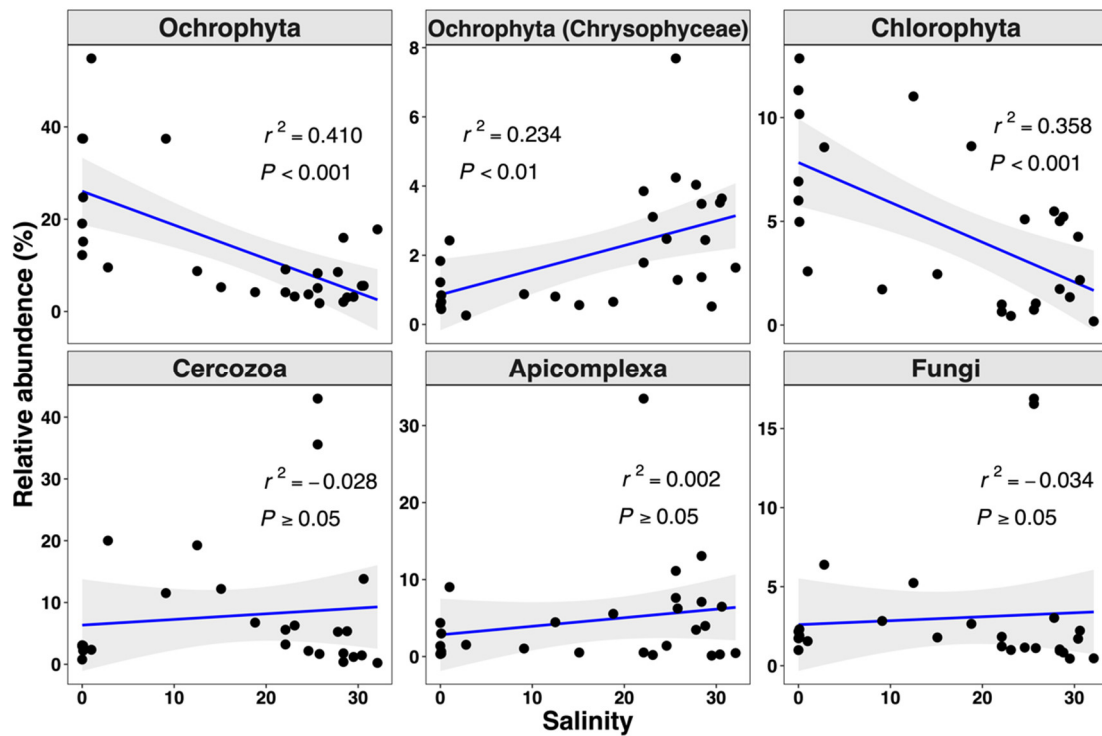
**Figure S1.** Rarefaction curve of bacterial (A) and protistan (B) sequencing.



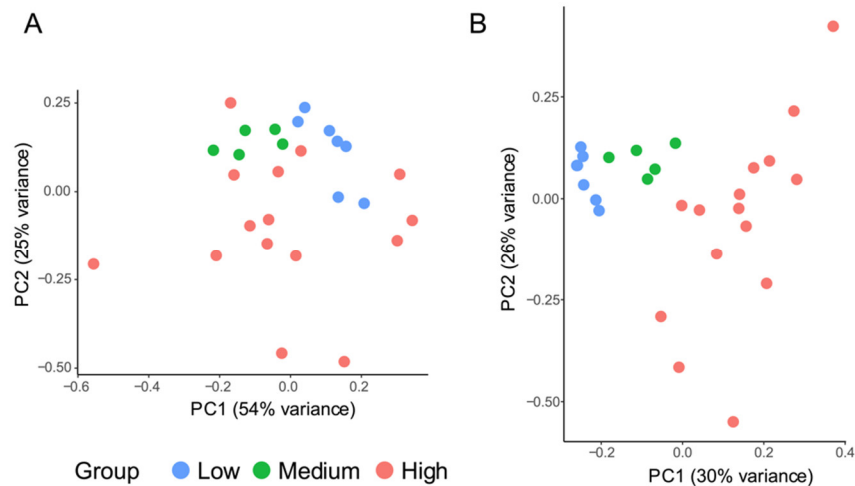
**Figure S2.** Analysis of similarities (ANOSIM) between different salinity groups of bacteria (A) and protists (B).



**Figure S3.** Community composition of bacteria (A) and protists (B) at class level in each sample, respectively. Species with low abundance were assigned to 'Others' (at least less than 1%).



**Figure S4.** Scatter plots showing the relative abundance of some representative phyla(class) of protists as a function of salinity. Blue line = linear regression fit; shaded area = 95% confidence interval.  $r^2$  and  $P$  represented the goodness-of-fit and significance, respectively.



**Figure S5.** PCA plot based on gene functional abundance on level I (A) and III (B) of KEGG predicted by PICRUST2. Each point represented a sample, and the color blue, green and red represented the salinity groups of Low, Medium and High, respectively.