

Figure S1 The rarefaction curves of Chao1 and Shannon indexes.

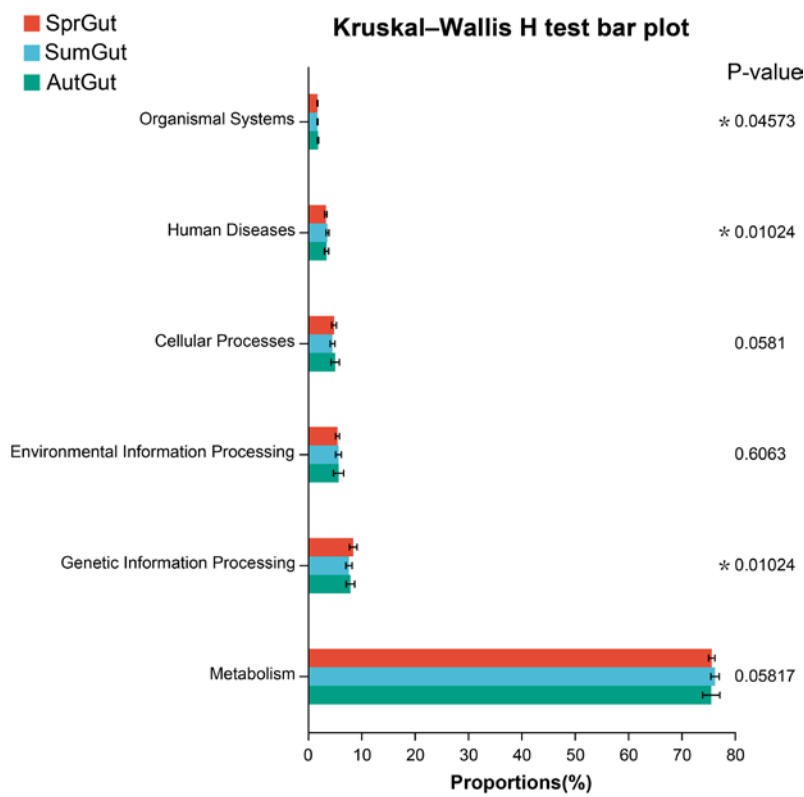


Figure S2 Kruskal-Wallis H test bar plot at level1 KEGG pathways. "*" indicates a significant difference.

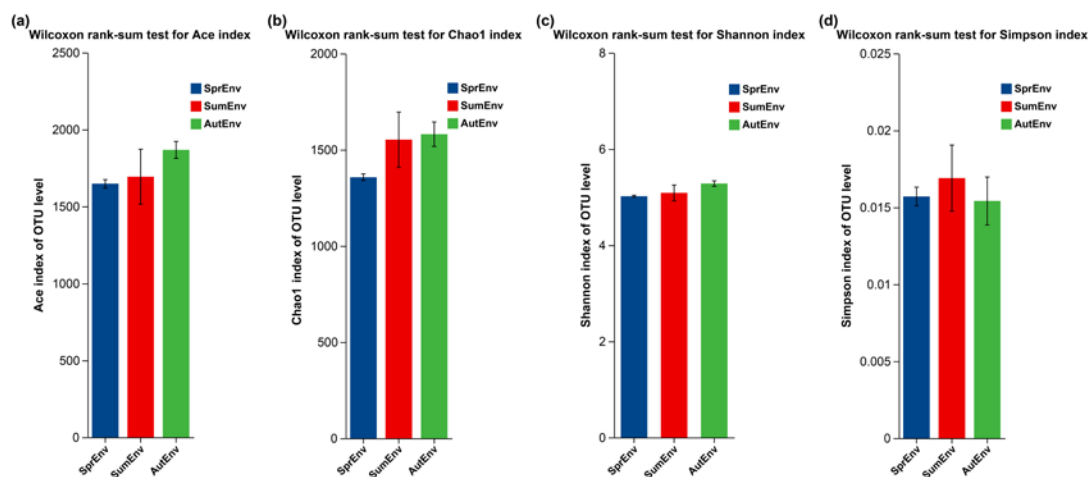


Figure S3 The alpha diversity index of the microbiome in the three seasons of the surrounding water. (a): Ace index; (b): Chao1 index; (c): Shannon index; (d): Simpson index.

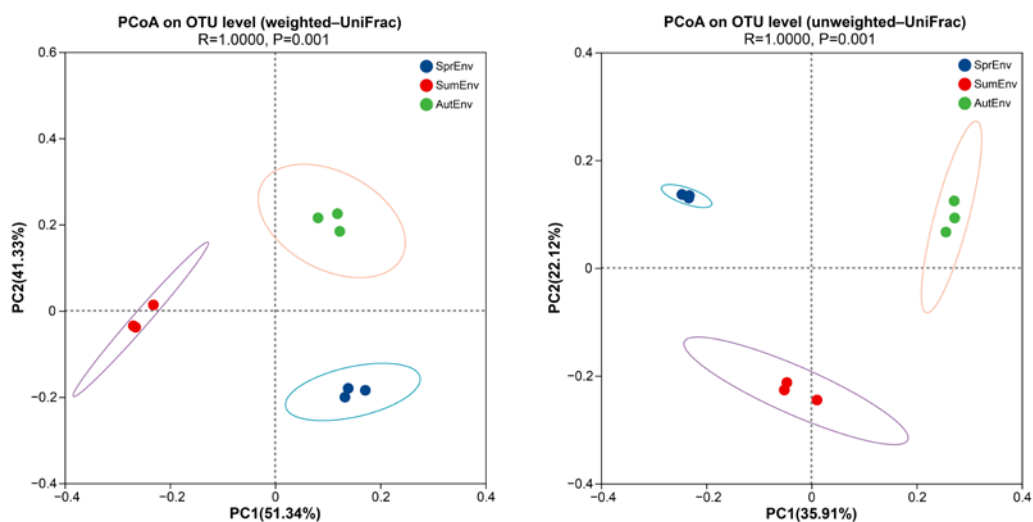


Figure S4 PCoA analysis of microorganisms in the surrounding water in the three studied seasons.

Table S1 The clean sequence number, base number, and sequence mean length for each sample. SprGut1–SprGut20, SprEnv1–SprEnv3 represent the gut and water samples collected in spring, SumGut1–SumGut20, SumEnv1–SumEnv3 represent the gut and water samples collected in summer, AutGut1–AutGut20, AutEnv1–AutEnv3 represent the gut and water samples collected at autumn.

Samples	Seq number	Base number	Mean length (bp)
SprGut1	48,555	20,789,363	428.16
SprGut2	56,315	24,003,365	426.23
SprGut3	57,721	24,647,498	427.01
SprGut4	52,680	22,460,995	426.37
SprGut5	57,483	24,490,609	426.05
SprGut6	63,880	27,350,553	428.16
SprGut7	46,964	20,090,819	427.79
SprGut8	49,498	21,185,045	428.00
SprGut9	39,583	16,946,640	428.13
SprGut10	42,764	18,265,593	427.13
SprGut11	45,250	19,320,505	426.97
SprGut12	62,881	26,667,819	424.10
SprGut13	58,275	24,888,705	427.09
SprGut14	55,873	23,872,437	427.26
SprGut15	47,990	20,508,047	427.34
SprGut16	53,827	22,942,297	426.22
SprGut17	50,028	21,381,659	427.39
SprGut18	58,505	24,969,471	426.79
SprGut19	43,572	18,579,378	426.41
SprGut20	56,161	23,982,215	427.03
SprEnv1	61,170	25,573,689	418.08
SprEnv2	68,162	28,500,965	418.14
SprEnv3	68,253	28,577,397	418.70
SumGut1	38,637	16,509,615	427.30
SumGut2	41,188	17,413,224	422.77
SumGut3	32,690	13,866,943	424.20
SumGut4	30,477	12,951,498	424.96
SumGut5	42,899	18,208,172	424.44
SumGut6	42,330	17,986,558	424.91
SumGut7	47,730	20,093,811	420.99
SumGut8	33,424	14,162,665	423.73
SumGut9	42,145	17,927,944	425.39
SumGut10	40,199	16,919,037	420.88
SumGut11	34,086	14,561,060	427.19
SumGut12	38,849	16,502,765	424.79
SumGut13	41,821	17,738,726	424.16
SumGut14	41,843	17,614,108	420.96
SumGut15	35,509	15,205,550	428.22
SumGut16	44,593	18,831,798	422.30
SumGut17	38,352	16,262,865	424.04
SumGut18	40,710	17,254,241	423.83
SumGut19	38,205	16,171,725	423.29
SumGut20	38,044	16,239,770	426.87

SumEnv1	42,182	17,753,812	420.89
SumEnv2	51,555	21,707,781	421.06
SumEnv3	55,447	23,296,242	420.15
AutGut1	80,140	34,177,525	426.47
AutGut2	75,982	32,414,904	426.61
AutGut3	87,474	37,358,170	427.08
AutGut4	71,990	30,692,184	426.34
AutGut5	78,327	33,206,509	423.95
AutGut6	74,776	32,029,171	428.33
AutGut7	64,550	27,551,281	426.82
AutGut8	52,179	22,104,291	423.62
AutGut9	64,725	27,554,628	425.72
AutGut10	66,762	28,368,498	424.92
AutGut11	103,268	43,931,114	425.41
AutGut12	89,583	38,164,222	426.02
AutGut13	80,990	34,560,635	426.73
AutGut14	82,852	35,016,115	422.63
AutGut15	80,756	34,482,813	427.00
AutGut16	81,971	34,826,094	424.86
AutGut17	59,439	25,293,319	425.53
AutGut18	96,245	40,954,655	425.53
AutGut19	75,313	32,088,391	426.07
AutGut20	96,748	41,253,693	426.40
AutEnv1	52,633	21,965,526	417.33
AutEnv2	67,301	28,100,403	417.53
AutEnv3	69,409	29,004,468	417.88

Table S2 OTUs number, richness indexes(ACE and Chao1), diversity indexes (Shannon and Simpson), and estimated sample Coverage for the different samples. SprGut1–SprGut20, SprEnv1–SprEnv3 represent the gut and water samples collected in spring, SumGut1–SumGut20, SumEnv1–SumEnv3 represent the gut and water samples collected in summer, AutGut1–AutGut20, AutEnv1–AutEnv3 represent the gut and water samples collected in the autumn.

Samples	OTUs	ACE	Chao1	Shannon	Simpson	Coverage
SprGut1	220	607.82	410.57	1.36	0.5020	0.9942
SprGut2	434	898.00	704.43	2.97	0.1387	0.9906
SprGut3	286	759.74	538.98	1.71	0.3263	0.9926
SprGut4	497	1031.21	792.64	2.41	0.2815	0.9887
SprGut5	389	947.34	657.83	2.11	0.2798	0.9907
SprGut6	350	1005.36	704.92	2.47	0.1691	0.9907
SprGut7	246	778.51	520.09	1.73	0.3533	0.9933
SprGut8	104	456.64	231.15	2.01	0.2000	0.9971
SprGut9	148	248.54	213.03	1.27	0.4291	0.9967
SprGut10	384	949.47	691.23	2.52	0.2022	0.9907
SprGut11	380	856.40	696.20	2.55	0.1434	0.9907
SprGut12	525	1114.53	868.50	3.56	0.0733	0.9886
SprGut13	470	1245.18	845.58	2.50	0.1928	0.9880
SprGut14	290	658.22	451.05	2.39	0.1598	0.9932
SprGut15	194	503.29	396.04	1.50	0.4143	0.9949

SprGut16	456	965.02	736.54	1.96	0.4393	0.9897
SprGut17	301	843.42	565.06	1.72	0.3094	0.9919
SprGut18	194	561.73	396.54	1.27	0.5221	0.9947
SprGut19	600	1102.92	907.44	2.59	0.2131	0.9872
SprGut20	337	834.78	559.07	2.92	0.0902	0.9920
SprEnv1	958	1701.80	1391.20	5.04	0.0152	0.9820
SprEnv2	895	1623.12	1332.07	5.04	0.0150	0.9833
SprEnv3	916	1619.01	1348.50	4.98	0.0169	0.9827
SumGut1	385	757.31	608.62	2.26	0.2665	0.9915
SumGut2	993	1316.45	1325.16	5.12	0.0172	0.9844
SumGut3	630	1057.10	865.51	3.89	0.0610	0.9888
SumGut4	695	906.13	916.03	4.09	0.0590	0.9891
SumGut5	388	732.12	635.63	3.70	0.0558	0.9929
SumGut6	365	750.80	643.32	2.94	0.1213	0.9922
SumGut7	713	1210.30	1021.90	4.58	0.0222	0.9870
SumGut8	553	899.27	760.85	3.82	0.0730	0.9908
SumGut9	493	929.73	753.68	2.52	0.2728	0.9897
SumGut10	447	636.91	617.08	3.45	0.0797	0.9922
SumGut11	355	701.00	500.00	2.25	0.2291	0.9928
SumGut12	637	1115.49	964.65	3.79	0.0696	0.9879
SumGut13	769	1324.35	1120.91	4.28	0.0421	0.9858
SumGut14	958	1378.52	1369.62	4.88	0.0260	0.9827
SumGut15	330	780.64	543.13	1.88	0.3569	0.9923
SumGut16	805	1390.97	1228.54	4.94	0.0166	0.9854
SumGut17	638	846.87	823.03	4.72	0.0243	0.9909
SumGut18	506	850.68	765.84	3.93	0.0520	0.9910
SumGut19	474	897.74	776.78	3.91	0.0434	0.9909
SumGut20	310	538.00	467.76	3.77	0.0428	0.9945
SumEnv1	952	1336.95	1299.76	4.92	0.0186	0.9834
SumEnv2	988	1885.63	1559.64	4.93	0.0195	0.9799
SumEnv3	1293	1857.94	1796.75	5.41	0.0126	0.9767
AutGut1	174	425.33	285.86	2.03	0.2413	0.9960
AutGut2	356	779.02	593.37	2.45	0.1723	0.9918
AutGut3	239	617.62	443.84	2.60	0.1429	0.9943
AutGut4	285	576.64	433.17	2.34	0.1827	0.9937
AutGut5	473	967.82	776.24	3.13	0.0858	0.9891
AutGut6	159	404.23	260.94	1.25	0.5462	0.9960
AutGut7	257	562.82	400.29	1.86	0.3612	0.9941
AutGut8	576	854.54	834.62	3.40	0.0906	0.9890
AutGut9	236	494.53	374.18	2.72	0.1347	0.9952
AutGut10	444	915.05	788.08	3.04	0.1026	0.9899
AutGut11	406	849.16	673.00	2.83	0.1693	0.9911
AutGut12	259	646.30	450.05	1.66	0.4808	0.9940
AutGut13	313	683.68	527.50	2.38	0.1807	0.9928
AutGut14	445	776.87	707.89	3.46	0.0685	0.9916
AutGut15	218	707.78	440.68	1.72	0.3393	0.9941
AutGut16	337	775.08	565.00	2.64	0.1587	0.9924

AutGut17	657	930.88	925.90	3.62	0.0858	0.9882
AutGut18	286	798.02	532.75	2.36	0.1912	0.9930
AutGut19	363	715.02	618.13	2.79	0.1452	0.9922
AutGut20	315	597.24	484.33	2.77	0.1167	0.9936
AutEnv1	1130	1880.24	1635.00	5.33	0.0144	0.9798
AutEnv2	1149	1956.18	1653.72	5.35	0.0134	0.9789
AutEnv3	1058	1767.74	1454.31	5.17	0.0185	0.9813

Table S3 Alpha diversity indexes of *Sinopotamon planum* of three gut groups.

	Ace	Chao1	Shannon	Simpson
AutGut-group	703.88±162.94	555.79±182.81	2.5516±0.6298	0.19983±0.13224
SprGut-group	818.41±250.35	594.34±200.62	2.1756±0.61901	0.27198±0.13559
SumGut-group	951.02±258.54	835.4±266.54	3.7361±0.94281	0.096571±0.10024
P-value (AutGut-SprGut)	0.07205	0.4903	0.08103	0.0531
P-value (SprGut-SumGut)	0.2616	0.007712	1.81E-05	4.17E-05
P-value (AutGut-SumGut)	0.00432	0.0009209	0.0002471	0.000622

Table S4 The LEfSe analysis of gut microbiota composition of *Sinopotamon planum* in each group (LDA score > 3.5, P < 0.05).

Taxon	Species name	Group	LDA-value	P-value
Phylum	Campilobacterota	AutGut	4.3325	4.75×10^{-10}
	Fusobacteriota	AutGut	3.8924	1.23×10^{-8}
	Deinococcota	SumGut	4.4821	1.33×10^{-7}
	Firmicutes	SprGut	5.1271	0.000297
	Nitrospirota	SumGut	4.5810	0.001065
genus	<i>Fusobacterium</i>	AutGut	3.7878	1.20×10^{-10}
	<i>unclassified-f-Arcobacteraceae</i>	AutGut	4.2449	1.30×10^{-9}
	<i>TM7a</i>	SumGut	3.7254	1.31×10^{-7}
	<i>Bacteroides</i>	AutGut	4.5532	1.93×10^{-9}
	<i>Comamonas</i>	SumGut	3.8443	2.75×10^{-9}
	<i>Flavobacterium</i>	SumGut	4.2968	1.52×10^{-5}
	<i>unclassified-o-Saccharimonadales</i>	SumGut	3.6606	5.82×10^{-6}
	<i>Pseudomonas</i>	SumGut	3.8654	2.24×10^{-7}
	<i>Proteocatella</i>	SumGut	3.5542	1.31×10^{-10}
	<i>Chryseobacterium</i>	SumGut	4.0877	2.08×10^{-7}
	<i>Acinetobacter</i>	SumGut	4.0109	1.14×10^{-6}
	<i>Macellibacteroides</i>	SumGut	3.5504	9.61×10^{-9}

Table S5 The relative abundance of 24 predicted metabolic functions of three gut groups.

Category	Description	Relative abundance		
		SprGut	AutGut	SumGut
A	RNA processing and modification	< 0.001	< 0.001	< 0.001
B	Chromatin structure and dynamics	< 0.001	< 0.001	< 0.001
C	Energy production and conversion	0.064	0.066	0.064
D	Cell cycle control, cell division, chromosome partitioning	0.012	0.011	0.012
E	Amino acid transport and metabolism	0.081	0.087	0.084
F	Nucleotide transport and metabolism	0.031	0.028	0.030
G	Carbohydrate transport and metabolism	0.061	0.058	0.060
H	Coenzyme transport and metabolism	0.038	0.040	0.040

I	Lipid transport and metabolism	0.035	0.038	0.032
J	Translation, ribosomal structure and biogenesis	0.082	0.065	0.070
K	Transcription	0.061	0.065	0.061
L	Replication, recombination and repair	0.069	0.059	0.063
M	Cell wall/membrane/envelope biogenesis	0.062	0.066	0.067
N	Cell motility	0.018	0.017	0.021
O	Posttranslational modification, protein turnover, chaperones	0.044	0.042	0.042
P	Inorganic ion transport and metabolism	0.065	0.067	0.067
Q	Secondary metabolites biosynthesis, transport and catabolism	0.016	0.018	0.014
R	General function prediction only	0.081	0.082	0.078
S	Function unknown	0.087	0.093	0.091
T	Signal transduction mechanisms	0.051	0.059	0.063
U	Intracellular trafficking, secretion, and vesicular transport	0.023	0.021	0.022
V	Defense mechanisms	0.020	0.018	0.019
W	Extracellular structures	< 0.001	< 0.001	< 0.001
Z	Cytoskeleton	< 0.001	< 0.001	< 0.001
