

## ***Supporting information***

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**Table S1** Observed richness (Sobs) and water quality parameters of water samples.

	A	B	C	D	E	F	G	H
<b>Observed richness (SOBs)</b>	195	68	142	156	179	185	174	162
<b>pH</b>	6.26	3.98	5.82	5.87	6.45	5.99	6.52	6.66
<b>ORP (MV)</b>	-85.95	-16.4	-125.7	-95.75	-53.95	-80	-52.1	-125.5
<b>TDS (mg/L)</b>	3748.5	2824	1958	1921.5	1149	1649.5	848	799.5
<b>TN (mg/L)</b>	18.03	23.27	12.84	13.03	24.03	24.68	22.03	3.25
<b>NH<sub>4</sub><sup>+</sup>-N (mg/L)</b>	13.69	13.68	10.08	9.56	4.04	12.14	0.66	0.64
<b>NO<sub>3</sub><sup>-</sup>-N (mg/L)</b>	1.33	5.08	1.56	1.27	0.58	0.93	0.43	0.36
<b>NO<sub>2</sub><sup>-</sup>-N (mg/L)</b>	0	0.67	0	0	0	0	0	0
<b>SO<sub>4</sub><sup>2-</sup> (mg/L)</b>	42.9	21.7	40.6	78.5	42.14	57.4	104	2.8
<b>TP (mg/L)</b>	0.65	2.39	1.07	1.19	0.65	0.83	0.55	0.49
<b>COD<sub>cr</sub> (mg/L)</b>	790.4	1111.04	379.36	279.36	513.76	237.12	158.08	39.52
<b>DO (mg/L)</b>	3.76	4.3	3.65	3.82	4.18	4.2	4.15	4.26
<b>T (°C)</b>	20.83	19.25	28.3	25.59	23.66	20.14	20.89	19.46
<b>chromaticity</b>	230.9	1138	1138	478	300.8	227.7	261.79	52.8

**Table S2 Reported the bacterial genera related to Mn and Fe cycle in the environment.**

Elements	Types	Genus	Phylum	Reference	Sites ID (%)							
					A	B	C	D	E	F	G	H
Mn	Mn(II)-oxidizing bacteria	<i>Pseudomonas</i>	<i>Proteobacteria</i>	[1]	2.78	0.00	0.10	4.81	0.14	0.29	3.74	3.07
		<i>Paracoccus</i>	<i>Proteobacteria</i>	[2]	0.14	0.00	0.00	0.00	0.00	0.00	0.01	0.01
		<i>Aeromonas</i>	<i>Proteobacteria</i>	[3]	0.33	0.04	0.04	0.03	0.03	0.10	0.10	0.05
		<i>Acinetobacter</i>	<i>Proteobacteria</i>	[1]	34.27	0.01	4.00	12.29	5.18	2.34	29.66	33.95
		<i>Bosea</i>	<i>Proteobacteria</i>	[4]	0.01	0.00	0.00	0.00	0.00	0.00	0.08	0.04
		<i>Fusobacterium</i>	<i>Fusobacteria</i>	[5]	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00
		<i>Deinococcus</i>	<i>Deinococcus-Thermus</i>	[6]	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.02
		<i>Flavobacterium</i>	<i>Bacteroidetes</i>	[7]	6.75	0.00	0.85	0.39	0.67	0.04	3.41	2.30
	Composite-functional bacteria	<i>Geobacter</i>	<i>Proteobacteria</i>	[8]	0.00	0.00	0.00	0.00	0.02	0.26	0.02	0.00
		<i>Shewanella</i>	<i>Proteobacteria</i>	[9, 10]	0.09	0.00	0.00	0.00	0.00	0.01	0.05	0.01
		<i>Bacillus</i>	<i>Firmicutes</i>	[11, 12]	0.04	0.00	0.00	0.00	0.00	0.02	0.01	0.03
	Mn(IV)-reducing bacteria	<i>Rhodferax</i>	<i>Proteobacteria</i>	[13]	0.22	0.00	5.11	0.02	6.63	0.00	1.37	0.49
		<i>Sulfurospirillum</i>	<i>Proteobacteria</i>	[14]	0.00	0.20	1.67	1.84	1.83	1.47	0.59	0.12
Fe	Fe(II)-oxidizing bacteria	<i>Pseudomonas</i>	<i>Proteobacteria</i>	[15]	2.78	0.00	0.10	4.81	0.14	0.29	3.74	3.07
		<i>Thermomonas</i>	<i>Proteobacteria</i>	[16]	0.65	0.00	0.00	0.00	0.00	0.00	0.01	0.01
		<i>Dechloromonas</i>	<i>Proteobacteria</i>	[17]	0.10	0.00	0.13	0.28	0.10	0.10	0.23	0.12
		<i>Aquabacterium</i>	<i>Proteobacteria</i>	[18]	0.55	0.00	0.07	0.06	0.03	0.01	0.26	0.16
		<i>Acidovorax</i>	<i>Proteobacteria</i>	[18]	5.22	0.00	0.11	0.25	0.14	0.16	0.45	0.37
		<i>Hyphomonas</i>	<i>Proteobacteria</i>	[19]	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.01
		<i>Paracoccus</i>	<i>Proteobacteria</i>	[18]	0.14	0.00	0.00	0.00	0.00	0.00	0.01	0.01
		<i>Geobacter</i>	<i>Proteobacteria</i>	[18]	0.00	0.00	0.00	0.00	0.02	0.26	0.02	0.00
	Fe(III)-reducing bacteria	<i>Desulfovibrio</i>	<i>Proteobacteria</i>	[20]	0.03	0.00	0.30	0.68	0.36	0.49	0.15	0.18
		<i>Desulfobulbus</i>	<i>Proteobacteria</i>	[21]	0.00	0.00	0.08	0.14	0.40	1.52	0.08	0.00
		<i>Shewanella</i>	<i>Proteobacteria</i>	[9]	0.09	0.00	0.00	0.00	0.00	0.01	0.05	0.01
		<i>Aeromonas</i>	<i>Proteobacteria</i>	[22]	0.33	0.04	0.04	0.03	0.03	0.10	0.10	0.05
		<i>Rhodferax</i>	<i>Proteobacteria</i>	[13]	0.22	0.00	5.11	0.02	6.63	0.00	1.37	0.49
		<i>Sulfurospirillum</i>	<i>Proteobacteria</i>	[22]	0.01	0.20	1.67	1.84	1.83	1.47	0.59	0.12
		<i>Clostridium sensu stricto</i>	<i>Firmicutes</i>	[23]	0.10	0.35	0.25	0.47	0.43	8.36	0.08	0.12
		<i>Desulfosporosinus</i>	<i>Firmicutes</i>	[24]	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
		<i>Bacillus</i>	<i>Firmicutes</i>	[22]	0.04	0.00	0.00	0.00	0.00	0.02	0.01	0.03
		<i>Anaeromusa</i>	<i>Firmicutes</i>	[21]	0.01	0.00	0.41	1.38	0.69	2.23	0.04	0.09
		<i>Anaeroarcus</i>										

**Table S3 Reported the bacterial genera related to S cycle in the environment.**

Types	Genus	Phylum	Reference	Site (%)							
				A	B	C	D	E	F	G	H
<b>S-oxidizing bacteria</b>	<i>Acinetobacter</i>	<i>Proteobacteria</i>	[25]	34.27	0.01	4.00	12.29	5.18	2.34	29.66	33.95
	<i>Allochromatium</i>	<i>Proteobacteria</i>	[26]	0.01	0.00	0.00	0.00	0.00	0.01	0.00	0.00
	<i>Azoarcus</i>	<i>Proteobacteria</i>	[27]	0.09	0.00	0.01	0.01	0.00	0.01	0.01	0.00
	<i>Beggiatoa</i>	<i>Proteobacteria</i>	[21]	0.00	0.00	0.00	0.00	0.00	0.06	0.00	0.00
	<i>Bosea</i>	<i>Proteobacteria</i>	[21]	0.01	0.00	0.00	0.00	0.00	0.00	0.08	0.04
	<i>Burkholderia</i>	<i>Proteobacteria</i>	[28]	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
	<i>Candidatus_Thiobios</i>	<i>Proteobacteria</i>	[29]	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Chromatium</i>	<i>Proteobacteria</i>	[29]	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.00
	<i>Paracoccus</i>	<i>Proteobacteria</i>	[21]	0.14	0.00	0.00	0.00	0.00	0.00	0.01	0.01
	<i>Pseudomonas</i>	<i>Proteobacteria</i>	[30]	2.78	0.00	0.10	4.81	0.14	0.29	3.74	3.07
	<i>Sulfuricurvum</i>	<i>Proteobacteria</i>	[31]	0.01	0.00	0.06	0.46	0.04	0.85	0.02	0.00
	<i>Sulfurimonas</i>	<i>Proteobacteria</i>	[32]	0.00	0.05	0.29	0.24	0.53	0.82	0.02	0.00
	<i>Thiocapsa</i>	<i>Proteobacteria</i>	[33]	0.01	0.00	0.00	0.00	0.00	0.01	0.00	0.01
	<i>Thioclava</i>	<i>Proteobacteria</i>	[8]	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Thiothrix</i>	<i>Proteobacteria</i>	[34]	1.21	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<b>Composite-functional bacteria</b>	<i>Bacillus</i>	<i>Firmicutes</i>	[35, 36]	0.04	0.00	0.00	0.00	0.00	0.02	0.01	0.03
	<i>Dechloromonas</i>	<i>Proteobacteria</i>	[17, 37]	0.10	0.00	0.13	0.28	0.10	0.10	0.23	0.12
	<i>Sulfurospirillum</i>	<i>Proteobacteria</i>	[38, 39]	0.01	0.20	1.67	1.84	1.83	1.47	0.59	0.12
	<i>Sulfurovum</i>	<i>Proteobacteria</i>	[40, 41]	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<b>S-reducing bacteria</b>	<i>Clostridium sensu stricto</i>	<i>Firmicutes</i>	[21]	0.10	0.35	0.25	0.47	0.43	8.36	0.08	0.12
	<i>Desulfobacter</i>	<i>Proteobacteria</i>	[21]	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00
	<i>Desulfobacterium</i>	<i>Proteobacteria</i>	[21]	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00
	<i>Desulfobulbus</i>	<i>Proteobacteria</i>	[42]	0.00	0.00	0.08	0.14	0.40	1.52	0.08	0.00
	<i>Desulfomicrobium</i>	<i>Proteobacteria</i>	[43]	0.00	0.00	0.02	0.03	0.03	0.10	0.09	0.07
	<i>Desulfomonile</i>	<i>Proteobacteria</i>	[21]	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Desulfosporosinus</i>	<i>Firmicutes</i>	[24]	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Desulfovibrio</i>	<i>Proteobacteria</i>	[20]	0.03	0.00	0.30	0.68	0.36	0.49	0.15	0.18
	<i>Fusibacter</i>	<i>Firmicutes</i>	[21]	0.00	0.00	0.08	0.03	0.04	0.17	0.15	0.07
	<i>Geobacter</i>	<i>Proteobacteria</i>	[44]	0.00	0.00	0.00	0.00	0.02	0.26	0.02	0.00
	<i>Shewanella</i>	<i>Proteobacteria</i>	[45]	0.09	0.00	0.00	0.00	0.00	0.01	0.05	0.01

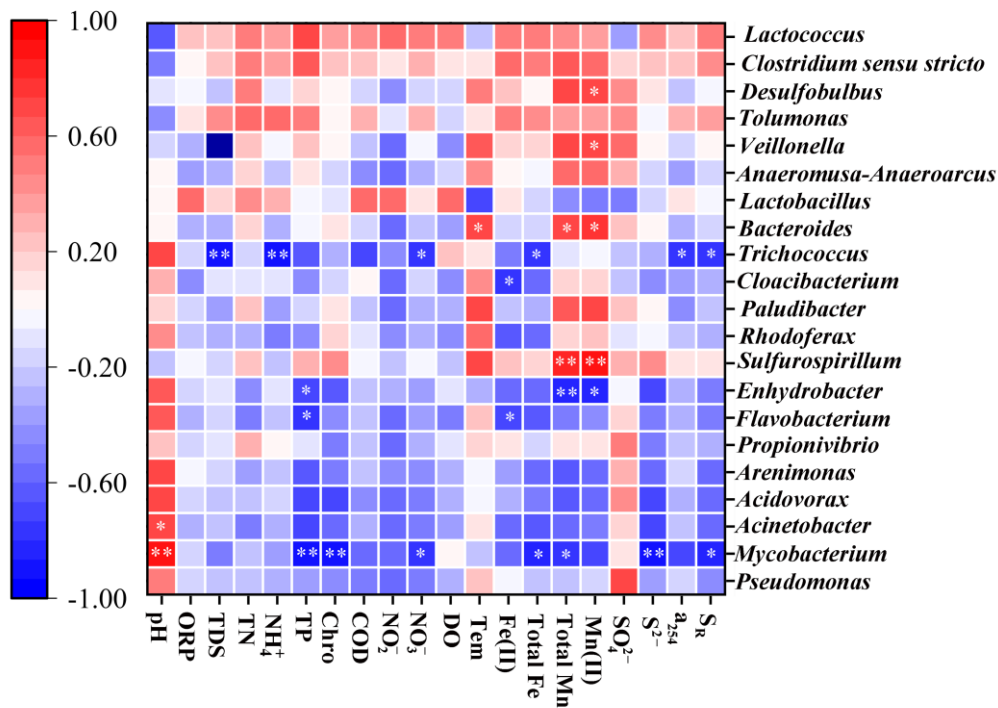
**Table S4 Reported the bacterial genera related to C cycle in the environment.**

Types	Genus	Phylum	Reference	Sites (ID)							
				A	B	C	D	E	F	G	H
Aerobic Chemo- Heterotro- -phic	<i>Acetobacter</i>	<i>Proteobacteria</i>	[46]	0.00	0.35	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Acidovorax</i>	<i>Proteobacteria</i>	[46]	5.22	0.00	0.11	0.25	0.14	0.16	0.45	0.37
	<i>Acinetobacter</i>	<i>Proteobacteria</i>	[46]	34.27	0.01	4.00	12.29	5.18	2.34	29.66	33.95
	<i>Aeromicrobium</i>	<i>Actinobacteriota</i>	[46]	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
	<i>Algoriphagus</i>	<i>Bacteroidota</i>	[46]	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
	<i>Altererythrobacter</i>	<i>Proteobacteria</i>	[46]	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
	<i>Arenimonas</i>	<i>Proteobacteria</i>	[47]	1.53	0.00	0.00	0.01	0.00	0.00	0.07	0.02
	<i>Azoarcus</i>	<i>Proteobacteria</i>	[48]	0.09	0.00	0.01	0.01	0.00	0.01	0.01	0.00
	<i>Bosea</i>	<i>Proteobacteria</i>	[46]	0.01	0.00	0.00	0.00	0.00	0.00	0.08	0.04
	<i>Caulobacter</i>	<i>Proteobacteria</i>	[49]	0.01	0.00	0.00	0.00	0.00	0.00	0.05	0.03
	<i>Chryseobacterium</i>	<i>Bacteroidota</i>	[46]	0.03	0.00	0.00	0.00	0.00	0.00	0.10	0.59
	<i>Dechloromonas</i>	<i>Proteobacteria</i>	[46]	0.10	0.00	0.13	0.28	0.10	0.10	0.23	0.12
	<i>Devosia</i>	<i>Proteobacteria</i>	[50]	0.02	0.00	0.00	0.00	0.00	0.00	0.01	0.00
	<i>Ferruginibacter</i>	<i>Bacteroidota</i>	[51]	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Filomicrobium</i>	<i>Proteobacteria</i>	[50]	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Haliscomenobacter</i>	<i>Bacteroidota</i>	[44]	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Hyphomonas</i>	<i>Proteobacteria</i>	[52]	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.01
	<i>Legionella</i>	<i>Proteobacteria</i>	[46]	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Leucobacter</i>	<i>Actinobacteriota</i>	[46]	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Lewinella</i>	<i>Bacteroidota</i>	[46]	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Lutibacter</i>	<i>Bacteroidota</i>	[46]	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
	<i>Microbacterium</i>	<i>Actinobacteriota</i>	[46]	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.05
	<i>Mycobacterium</i>	<i>Actinobacteriota</i>	[53]	1.91	0.00	0.01	0.04	0.04	0.19	1.72	7.91
	<i>Norank</i>	<i>Verrucomicrobiota</i>	[46]	0.11	0.00	0.00	0.01	0.00	0.00	0.00	0.00
	<i>f Verrucomicrobiaceae</i>										
	<i>Novosphingobium</i>	<i>Proteobacteria</i>	[46]	1.04	0.00	0.05	0.00	0.03	0.04	0.07	0.00
	<i>Paracoccus</i>	<i>Proteobacteria</i>	[46]	0.14	0.00	0.00	0.00	0.00	0.00	0.01	0.01
	<i>Pedobacter</i>	<i>Bacteroidota</i>	[46]	0.21	0.00	0.00	0.00	0.00	0.00	0.03	0.03
	<i>Polymorphobacter</i>	<i>Proteobacteria</i>	[46]	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Porphyrobacter</i>	<i>Proteobacteria</i>	[46]	0.04	0.00	0.02	0.00	0.02	0.00	0.01	0.00
	<i>Prostheco bacter</i>	<i>Verrucomicrobiota</i>	[46]	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Pseudohongiella</i>	<i>Proteobacteria</i>	[46]	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Pseudomonas</i>	<i>Proteobacteria</i>	[46]	2.78	0.00	0.10	4.81	0.14	0.29	3.74	3.07
	<i>Psychrobacter</i>	<i>Proteobacteria</i>	[46]	0.00	0.00	0.01	0.00	0.01	0.01	0.05	0.16
	<i>Reyranella</i>	<i>Proteobacteria</i>	[54]	0.01	0.00	0.00	0.00	0.00	0.00	0.02	0.01
	<i>Rheinheimera</i>	<i>Proteobacteria</i>	[55]	0.13	0.00	0.00	0.01	0.00	0.00	0.00	0.00
	<i>Roseomonas</i>	<i>Proteobacteria</i>	[46]	0.01	0.00	0.00	0.00	0.00	0.00	0.03	0.01
	<i>Sandarakinorhabdus</i>	<i>Proteobacteria</i>	[46]	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
	<i>Shewanella</i>	<i>Proteobacteria</i>	[56]	0.09	0.00	0.00	0.00	0.00	0.01	0.05	0.01
	<i>SN8</i>	<i>Proteobacteria</i>	[46]	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Sphingobium</i>	<i>Proteobacteria</i>	[46]	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Sphingomonas</i>	<i>Proteobacteria</i>	[46]	0.17	0.00	0.00	0.00	0.00	0.00	0.01	0.01
	<i>Sphingopyxis</i>	<i>Proteobacteria</i>	[46]	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Sphingorhabdus</i>	<i>Proteobacteria</i>	[46]	0.03	0.00	0.00	0.00	0.00	0.00	0.02	0.01
	<i>Stenotrophomonas</i>	<i>Proteobacteria</i>	[46]	0.01	0.00	0.00	0.03	0.00	0.00	0.01	0.02
	<i>Thauera</i>	<i>Proteobacteria</i>	[46]	0.00	0.00	0.02	0.00	0.04	0.00	0.04	0.00
	<i>Thermomonas</i>	<i>Proteobacteria</i>	[46]	0.65	0.00	0.00	0.00	0.00	0.00	0.01	0.01
	<i>Zoogloea</i>	<i>Proteobacteria</i>	[54]	0.21	0.00	0.03	0.42	0.02	0.39	0.19	0.25

**Table S4 Reported the bacterial genera related to C cycle in the environment (continued)**

Types	Genus	Phylum	Reference	Sites (ID)							
				A	B	C	D	E	F	G	H
Composite-functional bacteria	<i>Enhydrobacter</i>	<i>Proteobacteria</i>	[55]	0.26	0.00	0.00	0.00	0.00	0.00	0.02	0.02
	<i>Escherichia-Shigella</i>	<i>Proteobacteria</i>	[46]	0.00	0.02	0.01	0.00	0.01	0.07	0.02	0.01
	<i>Flavobacterium</i>	<i>Bacteroidota</i>	[46, 57]	6.91	0.00	0.85	0.48	0.67	0.06	3.45	2.43
	<i>Propionimonas</i>	<i>Actinobacteriota</i>	[46, 58]	0.02	0.00	0.01	0.00	0.03	0.00	0.01	0.01
	<i>Rhodoferrax</i>	<i>Proteobacteria</i>	[13, 46]	0.22	0.00	5.11	0.02	6.63	0.00	1.37	0.49
	<i>Acetoanaerobium</i>	<i>Firmicutes</i>	[46]	0.01	0.00	0.01	0.01	0.02	0.02	0.01	0.05
	<i>Acetobacterium</i>	<i>Firmicutes</i>	[46]	0.00	0.00	0.02	0.01	0.03	0.03	0.01	0.06
	<i>Acidaminobacter</i>	<i>Firmicutes</i>	[46]	0.00	0.00	0.03	0.06	0.05	0.17	0.39	0.09
	<i>Acidaminococcus</i>	<i>Firmicutes</i>	[46]	0.01	0.00	0.00	0.02	0.00	0.04	0.00	0.00
	<i>Aeromonas</i>	<i>Proteobacteria</i>	[46]	0.33	0.04	0.04	0.03	0.03	0.10	0.10	0.05
	<i>Anaerofilum</i>	<i>Firmicutes</i>	[46]	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00
	<i>Anaerovorax</i>	<i>Firmicutes</i>	[46]	0.01	0.00	0.31	0.38	0.73	0.56	0.69	0.22
	<i>Bacteroides</i>	<i>Bacteroidota</i>	[46]	0.03	0.02	0.96	0.66	1.27	0.71	0.36	0.16
	<i>Bifidobacterium</i>	<i>Actinobacteriota</i>	[46]	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Cloacibacterium</i>	<i>Bacteroidota</i>	[46]	1.53	0.00	2.33	0.17	2.19	0.42	0.22	0.82
Fermentative bacteria	<i>Clostridium sensu stricto</i>	<i>Firmicutes</i>	[46]	0.10	0.35	0.25	0.47	0.43	8.36	0.08	0.12
	<i>Desulfobulbus</i>	<i>Desulfobacterota</i>	[46]	0.00	0.00	0.08	0.14	0.40	1.52	0.08	0.00
	<i>Desulfomicrobium</i>	<i>Desulfobacterota</i>	[46]	0.00	0.00	0.02	0.03	0.03	0.10	0.09	0.07
	<i>Enterococcus</i>	<i>Firmicutes</i>	[46]	0.00	0.02	0.01	0.00	0.02	0.03	0.00	0.01
	<i>Formivibrio</i>	<i>Proteobacteria</i>	[46]	0.00	0.00	0.00	0.06	0.00	0.13	0.00	0.00
	<i>Fusobacterium</i>	<i>Fusobacteriota</i>	[46]	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00
	<i>Lactobacillus</i>	<i>Firmicutes</i>	[59]	0.07	1.42	0.02	0.01	0.10	0.05	0.03	0.06
	<i>Lactococcus</i>	<i>Firmicutes</i>	[46]	0.33	91.34	7.41	1.53	15.92	17.16	0.24	0.51
	<i>Lautropia</i>	<i>Proteobacteria</i>	[46]	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
	<i>Leuconostoc</i>	<i>Firmicutes</i>	[46]	0.09	0.43	0.05	0.00	0.19	0.02	0.01	0.00
	<i>Megasphaera</i>	<i>Firmicutes</i>	[46]	0.04	0.00	0.00	0.06	0.00	0.11	0.00	0.00
	<i>Norank f Eubacterium coprostanoligenes</i>	<i>Firmicutes</i>	[46]	0.00	0.00	0.02	0.00	0.03	0.00	0.00	0.00
	<i>Norank f</i>	<i>Bacteroidota</i>	[46]	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Flavobacteriaceae</i>										
	<i>Paludibacter</i>	<i>Bacteroidota</i>	[60]	0.10	0.01	2.18	0.53	3.52	0.79	0.64	0.22
	<i>Parabacteroides</i>	<i>Bacteroidota</i>	[46]	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Pediococcus</i>	<i>Firmicutes</i>	[61]	0.00	0.01	0.00	0.01	0.00	0.05	0.00	0.01
	<i>Propionivibrio</i>	<i>Proteobacteria</i>	[46]	0.01	0.00	0.00	0.14	0.02	0.19	0.01	0.01
	<i>Proteocatella</i>	<i>Firmicutes</i>	[46]	0.00	0.00	0.12	0.00	0.10	0.00	0.03	0.50
	<i>Romboutsia</i>	<i>Firmicutes</i>	[46]	0.05	0.00	0.00	0.00	0.00	0.01	0.00	0.00
	<i>Sedimentibacter</i>	<i>Firmicutes</i>	[46]	0.00	0.00	0.07	0.00	0.09	0.00	0.02	0.01
	<i>Solobacterium</i>	<i>Firmicutes</i>	[46]	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Streptococcus</i>	<i>Firmicutes</i>	[59]	0.01	0.01	0.02	0.01	0.02	0.04	0.02	0.02
	<i>Tolumonas</i>	<i>Proteobacteria</i>	[46]	0.20	0.09	0.08	0.48	0.13	4.82	0.06	0.00
	<i>Trichococcus</i>	<i>Firmicutes</i>	[46]	0.10	0.19	1.35	0.28	3.08	0.47	1.86	8.19
	<i>Veillonella</i>	<i>Firmicutes</i>	[46]	0.01	0.00	0.78	2.03	0.63	10.96	0.02	0.00
	<i>Victivallis</i>	<i>Verrucomicrobiota</i>	[46]	0.00	0.00	0.04	0.00	0.06	0.00	0.00	0.00
	<i>Weissella</i>	<i>Firmicutes</i>	[46]	0.00	0.52	0.28	0.01	0.42	0.04	0.03	0.05

Figure S1 Correlation analysis of different physicochemical parameters; red symbolizes a positive correlation, while blue represents a negative correlation; color intensity indicates correlation strength. Significant difference was denoted with \*\*P<0.01, \*P<0.05.



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