Supporting Information

Table S1. Basic physicochemical and nutrient properties of the sediment samples.

Samples	Longitude/ latitude	pH	redox potential (mV)	T (°C)	OM (%)	HS (g/kg)	HA (g/kg)	FA (g/kg)	humin (g/kg)	NH_4-N (mg/kg)	AN (mg/kg)	AP (mg/kg)
S1	120.5792/ 31.3325	7.16	104	13.72	1.21	5.10	0.26	1.47	3.37	22.60	26.00	8.80
S2	120.5918/ 31.3334	7.23	72	14.06	1.38	4.03	0.21	1.57	2.25	70.50	73.00	28.20
S3	120.5955/ 31.2981	6.95	-122	13.54	9.18	25.38	0.87	7.41	17.10	429.00	440.00	79.20
S4	120.6129/ 31.3193	7.22	27	14.33	8.10	19.02	0.72	5.50	12.80	144.00	208.00	55.20
S5	120.6316/ 31.3233	7.57	-168	14.82	9.37	35.98	1.01	7.37	27.60	347.00	354.00	44.13
S6	120.6350/ 31.3176	7.06	-123	15.21	9.65	19.17	1.00	6.37	11.80	326.00	338.00	72.40
S7	120.6339/ 31.3127	7.53	-90	14.46	11.72	22.15	1.15	9.40	11.60	193.00	197.00	104.00
S8	120.6411/ 31.3005	7.60	10	14.75	14.14	22.07	1.09	8.58	12.40	141.00	144.00	91.00
S9	120.6229/ 31.3011	7.40	118	14.06	8.62	19.36	1.04	7.12	11.20	420.00	424.00	81.50
S10	120.6134/ 31.2967	7.38	134	14.48	13.62	16.62	0.97	5.75	9.90	546.00	550.00	46.00
S11	120.6284/ 31.2928	7.55	-80	15.18	17.76	42.78	1.68	11.50	29.60	779.00	785.00	87.80
S12	120.6345/ 31.2954	7.31	-135	15.15	5.86	10.14	0.67	4.54	4.93	470.00	473.00	54.00
S13	120.6525/ 31.2887	7.34	-55	14.98	30.86	36.38	1.68	10.70	24.00	1000.00	1050.00	54.70

T, temperature; OM, organic matter; HS, humic substance; HA, humic acid; FA, fulvic acid; AN, available nitrogen; AP, available phosphorus.

Table S2. The primers used for amplifying V3-V4 regions of the bacterial 16S RNA gene.

Primer	Primer sequence
338F	5'- ACTCCTACGGGAGGCAGCAG-3'
806R	5'- GGACTACHVGGGTWTCTAAT-3'

Table S3. Summary of Miseq sequencing of 16S rRNA genes in sediment samples.

Sediment samples	High quality sequence number	OTUs number	Coverage	Shannon	Simpson	ACE	Chao1
S1	37909	2400	0.984	5.785	0.034	2872	2843
S2	35171	1910	0.983	5.751	0.012	2536	2564
S3	31017	2441	0.979	6.275	0.009	2968	2967
S4	34984	2320	0.982	6.076	0.010	2838	2826
S5	36935	2623	0.981	6.317	0.009	3207	3235
S6	31963	2234	0.980	5.955	0.014	2816	2777
S7	29624	2255	0.977	6.035	0.013	2889	2898
S8	31429	2007	0.980	5.627	0.018	2623	2592
S9	34898	2210	0.981	5.990	0.009	2800	2808
S10	50243	2888	0.988	6.629	0.004	3344	3391
S11	40389	2103	0.987	5.879	0.010	2525	2521
S12	34865	2655	0.980	6.436	0.006	3241	3264
S13	38573	2479	0.984	6.337	0.006	3011	3044

Table S4. Eigen values, F values and P values obtained from the partial CCA testing the influence of the significant parameters on the bacterial community composition.

Parameters included in the model	Eigen value	% Variation explains solely	F value	*P* value
HS	0.098	9.8	4.5	0.010
AN	0.128	12.8	5.7	0.002
AP	0.123	12.3	5.5	0.004
Hg	0.083	8.3	3.9	0.006
Zn	0.093	9.3	4.3	0.008
Cu	0.071	7.1	3.4	0.028
As	0.062	6.2	3.1	0.016

Partial CCA based on Monte Carlo permutation (n = 499) kept only the significant parameters in the models. For each partial model, the other significant parameters were used as covariables. F and *P* values were estimated using Monte Carlo permutations.

Table S5. The core bacterial genera identified in co-occurrence networks of group 1 and group 2.

Group1		Group2	
Phylum	Genus	Phylum	Genus
AC1	norank_AC1	AC1	norank_AC1
Acetothermia	norank_Acetothermia	Acetothermia	norank_Acetothermia
Acidobacteria	norank_Acidobacteria	Acidobacteria	norank_Acidobacteria
	norank_o__Subgroup_7		norank_o__Subgroup_23
	unclassified_Acidobacteria		Thermoanaerobaculum
	Paludibaculum		norank_o__TPD-58
	Thermoanaerobaculum		Bryobacter
	norank_o__TPD-58		unclassified_Acidobacteria
	norank_o__Subgroup_23		Paludibaculum
	norank_f__ABS-19		norank_o__Subgroup_7
Actinobacteria	norank_o__PeM15		GOUTB8
	norank_o__Gaiellales	Actinobacteria	norank_o__Gaiellales
	Mycobacterium		norank_f__OM1_clade
	norank_f__Propionibacteriaceae		norank_Actinobacteria
	norank_f__Coriobacteriaceae		Brooklawnia
	CL500-29_marine_group		norank_o__PeM15
	Brooklawnia		norank_f__Coriobacteriaceae
	hgcI_clade		Mycobacterium
	norank_Actinobacteria		Microbacterium
	unclassified_o__Frankiales		hgcI_clade
	norank_f__TM146		CL500-29_marine_group
	unclassified_Actinobacteria		Rhodococcus
	Fodinicola		Leucobacter
	Ilumatobacter		Micromonospora
	Microbacterium		norank_f__Propionibacteriaceae
	Gaiella		Fodinicola
	Ornithinibacter	Aminicenantes	norank_Aminicenantes
	norank_f__Geodermatophilaceae	Armatimonadetes	norank_Armatimonadetes
	norank_o__Acidimicrobiales	Atribacteria	Candidatus_Caldatribacterium
	Propionicicella	Bacteroidetes	norank_Bacteroidetes_vadinHA17
	unclassified_f__Acidimicrobiaceae		norank_f__Lentimicrobiaceae
Aminicenantes	norank_Aminicenantes		Flavobacterium
Bacteroidetes	norank_Bacteroidetes_vadinHA17		norank_SB-5
	norank_f__Lentimicrobiaceae		norank_f__Draconibacteriaceae
	Actibacter		Actibacter
	Flavobacterium		norank_f__Saprospiraceae
	norank_f__Draconibacteriaceae		unclassified_Bacteroidetes
	BSV13		BSV13
	norank_SB-5		norank_f__Cytophagaceae
	norank_f__Saprospiraceae	BRC1	norank_BRC1
	norank_Bacteroidetes_BD2-2	Caldiserica	Caldisericum
	Dinghuibacter		norank_f__WCHB1-02
	norank_f__Cytophagaceae	Chlamydiae	unclassified_o__Chlamydiales
	Fluviicola	Chlorobi	norank_f__OPB56
	norank_f__PHOS-HE51	Chloroflexi	norank_f__Anaerolineaceae
	Chitinophaga		unclassified_Chloroflexi
Chlorobi	norank_f__OPB56		norank_SBR2076
Chloroflexi	norank_f__Anaerolineaceae		norank_o__GIF9

Group1		Group2	
Phylum	Genus	Phylum	Genus
Chloroflexi	norank_KD4-96	Chloroflexi	norank_SJA-15
	norank_SJA-15		norank_o__MSBL5
	norank_SBR2076		norank_SJA-68
	norank_f__Caldilineaceae		norank_o__FS117-23B-02
	unclassified_Chloroflexi		norank_KD4-96
	norank_o__JG30-KF-CM45		Anaerolinea
	unclassified_f__Caldilineaceae		unclassified_Dehalococcoidia
	norank_o__FS117-23B-02		unclassified_f__Anaerolineaceae
	norank_o__GIF9		Longilinea
	Anaerolinea		Leptolinea
	norank_o__MSBL5		norank_o__JG30-KF-CM45
	norank_SJA-68		norank_o__Dehalococcoidales
	norank_1-20		norank_o__GIF3
	unclassified_f__Anaerolineaceae		norank_o__vadinBA26
	Longilinea		Levilinea
	Leptolinea		norank_f__Caldilineaceae
	unclassified_Dehalococcoidia		norank_MSB-5E12
	norank_Ardenticatenia		Pelolinea
Cyanobacteria	norank_Cyanobacteria		unclassified_f__Caldilineaceae
Cyanobacteria	unclassified_f__FamilyI_o__SubsectionI		norank_Chloroflexi
Cyanobacteria	Synechococcus		norank_o__FW22
Deferribacteres	Caldithrix		norank_1-20
Firmicutes	Clostridium_sensu_stricto_1		norank_SHA-26
	unclassified_f__Peptostreptococcaceae	Cyanobacteria	norank_Cyanobacteria
	Trichococcus		unclassified_f__FamilyI_o__SubsectionI
	Intestinibacter	Deferribacteres	Caldithrix
	Clostridium_sensu_stricto_13	Deinococcus-Thermus	norank_o__KD3-62
	Turicibacter	Fibrobacteres	norank_f__FD035
	norank_f__TSAC18	Firmicutes	Clostridium_sensu_stricto_1
	unclassified_f__Clostridiaceae_1		unclassified_f__Peptostreptococcaceae
	norank_f__Ruminococcaceae		Turicibacter
	Clostridium_sensu_stricto_3		Intestinibacter
	[Eubacterium]_brachy_group		Syntrophomonas
	Bacillus		Terrisporobacter
	unclassified_f__Ruminococcaceae		Clostridium_sensu_stricto_13
	Christensenellaceae_R-7_group		norank_f__TSAC18
	Terrisporobacter		Bacillus
	Syntrophomonas		unclassified_f__Clostridiaceae_1
Gemmatimonadetes	norank_f__Gemmatimonadaceae		Gelria
Gracilibacteria	norank_Gracilibacteria		norank_f__Ruminococcaceae
Ignavibacteriae	norank_f__BSV26		Clostridium_sensu_stricto_3
	Ignavibacterium		Trichococcus
	norank_f__PHOS-HE36		Cryptanaerobacter
Latescibacteria	norank_Latescibacteria		Clostridium_sensu_stricto_6
Lentisphaerae	norank_f__MVP-94		Clostridium_sensu_stricto_5
Nitrospinae	norank_Belgica2005-10-ZG-3		Hydrogenispora

Nitrospirae	Nitrospira		Ruminiclostridium_1
Omnitrophica	norank_Omnitrophica		Ercella
Parcubacteria	norank_Parcubacteria		Clostridium_sensu_stricto_9
	norank_Candidatus_Moranbacteria		Clostridium_sensu_stricto_11
Planctomycetes	norank_OM190		unclassified_f__Ruminococcaceae
	norank_Pla4_lineage		Proteiniclasticum
	norank_Pla3_lineage		Christensenellaceae_R-7_group
Group1		Group2	
Phylum	Genus	Phylum	Genus
Planctomycetes	norank_f__Planctomycetaceae	Gemmatimonadetes	norank_f__Gemmatimonadaceae
Proteobacteria	Dechloromonas	Ignavibacteriae	norank_f__BSV26
	norank_f__Xanthomonadales_Incertae_Sedis	KSB3__Modulibacteria_	norank_KSB3__Modulibacteria_
	norank_o__SC-I-84	Latescibacteria	norank_Latescibacteria
	norank_f__Alcaligenaceae	LCP-89	norank_LCP-89
	Methylotenera	Lentisphaerae	norank_f__MVP-94
	norank_o__SZB30	Nitrospinae	norank_Belgica2005-10-ZG-3
	Geobacter		Nitrospira
	Sva0081_sediment_group	Omnitrophica	norank_Omnitrophica
	Candidatus_Competibacter	Parcubacteria	norank_Parcubacteria
	norank_o__Sva0485	Planctomycetes	norank_Pla3_lineage
	unclassified_f__Methylocystaceae		norank_Pla4_lineage
	Thiobacillus		norank_OM190
	BD1-7_clade		unclassified_Planctomycetes
	Crenothrix	Proteobacteria	Sulfuricurvum
	unclassified_f__Rhodocyclaceae		norank_f__Xanthomonadales_Incertae_Sedis
	norank_f__MNG7		Dechloromonas
	Anaeromyxobacter		Smithella
	Desulfobacca		norank_f__Syntrophaceae
	Smithella		Syntrophorhabdus
	Geothermobacter		norank_o__Sva0485
	norank_f__Nitrosomonadaceae		Pseudomonas
	Arcobacter		Syntrophus
	Syntrophorhabdus		norank_f__Bacteriovoracaceae
	norank_f__Syntrophaceae		norank_o__SC-I-84
	unclassified_f__Comamonadaceae		norank_f__Alcaligenaceae
	norank_Gammaproteobacteria		norank_o__SZB30
	Pseudomonas		norank_f__MNG7
	Desulfatiglans		Thiobacillus
	norank_f__Rhodocyclaceae		unclassified_f__Methylocystaceae
	norank_f__Syntrophobacteraceae		Crenothrix
	unclassified_f__Rhodobacteraceae		BD1-7_clade
	Arenimonas		Syntrophobacter
	Sulfurisoma		Geobacter
	norank_f__Comamonadaceae		unclassified_f__Comamonadaceae
	norank_f__Methylophilaceae		Desulfatiglans
	Desulfoprunum		Sva0081_sediment_group

	Desulfobulbus		Anaeromyxobacter
	Sulfuricurvum		Aquabacterium
	norank_f__Hydrogenophilaceae		Candidatus_Competibacter
	Syntrophobacter		Desulfobacca
	Syntrophus		Sulfurimonas
	Desulfomonile		unclassified_f__Rhodocyclaceae
	Roseomonas		Arenimonas
	Ferritrophicum		Defluviicoccus
	unclassified_o__Rhizobiales		Geothermobacter
	norank_o__Run-SP154		Methylotenera
	Methylomicrobium		Ferritrophicum
	Acinetobacter		norank_Gammaproteobacteria
	norank_o__43F-1404R		unclassified_o__Rhizobiales
	norank_o__Xanthomonadales		Perlucidibaca
	norank_f__alphaI_cluster		Albidiferax
	unclassified_Betaproteobacteria		Desulforhabdus
Group1		Group2	
Phylum	Genus	Phylum	Genus
Proteobacteria	Halomonas	Proteobacteria	unclassified_f__Rhodobacteraceae
	Desulforhabdus		Desulfomonile
	norank_f__Bacteriovoracaceae		norank_f__Nitrosomonadaceae
	H16		norank_f__Syntrophobacteraceae
	Desulfatirhabdium		norank_f__PS-B29
	Sulfurifustis		Acinetobacter
	Lautropia		Rhodoferax
	Novosphingobium		unclassified_f__Syntrophobacteraceae
	norank_f__P3OB-42		norank_o__Xanthomonadales
	Defluviicoccus		unclassified_Betaproteobacteria
	unclassified_f__Syntrophobacteraceae		Methylomicrobium
	unclassified_o__Myxococcales		norank_f__Hydrogenophilaceae
	Hyphomicrobium		norank_f__Comamonadaceae
	norank_f__Phyllobacteriaceae		unclassified_Deltaproteobacteria
	unclassified_f__Desulfobacteraceae		norank_f__Rhodocyclaceae
	Perlucidibaca		unclassified_f__Desulfobacteraceae
	Albidiferax		norank_f__alphaI_cluster
	Haliangium		Sulfurisoma
	Denitratisoma		Arcobacter
	unclassified_f__Methylococcaceae		Roseomonas
	Methylosarcina		Hyphomicrobium
	norank_f__Arenicellaceae		unclassified_o__Myxococcales
	Aquabacterium		unclassified_f__Syntrophaceae
	Rhodoferax		Sulfurifustis
	norank_f__PS-B29		Novosphingobium
	unclassified_f__Halieaceae		Undibacterium
	Sulfuritalea		Escherichia-Shigella
	Albirhodobacter		Desulfococcus
	Desulfococcus		norank_f__Methylophilaceae
	Deferrisoma		Desulfoprunum
	Phaselicystis		Desulfobulbus

	norank_f__Chromatiaceae		H16
	unclassified_Gammaproteobacteria	RBG-1__Zixibacteria_	norank_RBG-1__Zixibacteria_
	Methyloparacoccus	Spirochaetae	Spirochaeta_2
	unclassified_f__Acetobacteraceae		norank_f__Leptospiraceae
RBG-1__Zixibacteria_	norank_RBG-1__Zixibacteria_		norank_f__Spirochaetaceae
Saccharibacteria	norank_Saccharibacteria	Synergistetes	norank_f__Synergistaceae
Spirochaetae	Spirochaeta_2	Tenericutes	norank_o__NB1-n
	norank_f__Leptospiraceae	Thermotogae	Mesotoga
	norank_f__Spirochaetaceae	unclassified_k__norank	unclassified_k__norank
unclassified_k__norank	unclassified_k__norank	Verrucomicrobia	norank_OPB35_soil_group
Verrucomicrobia	norank_OPB35_soil_group		norank_WCHB1-41
	Luteolibacter		Luteolibacter
	norank_f__Verrucomicrobiaceae	WS2	norank_WS2
	norank_WCHB1-41	WS6	norank_WS6
WS6	norank_WS6	WWE3	norank_WWE3

Table S6. Topological properties of the bacterial networks with key environmental factors in Fig. S4 according to the clusters in Fig. 4c

Category	No. of bacterial nodes	No. of links	No. of selected links [a]	Average degree	Average clustering coefficient
Group 1	200	2097	260	18.87 ± 0.37	0.513 ± 0.001
Group 2	199	1855	229	16.82 ± 0.28	0.562 ± 0.002

[a] The selected links presented the edges connecting key environmental factors to bacterial genera.

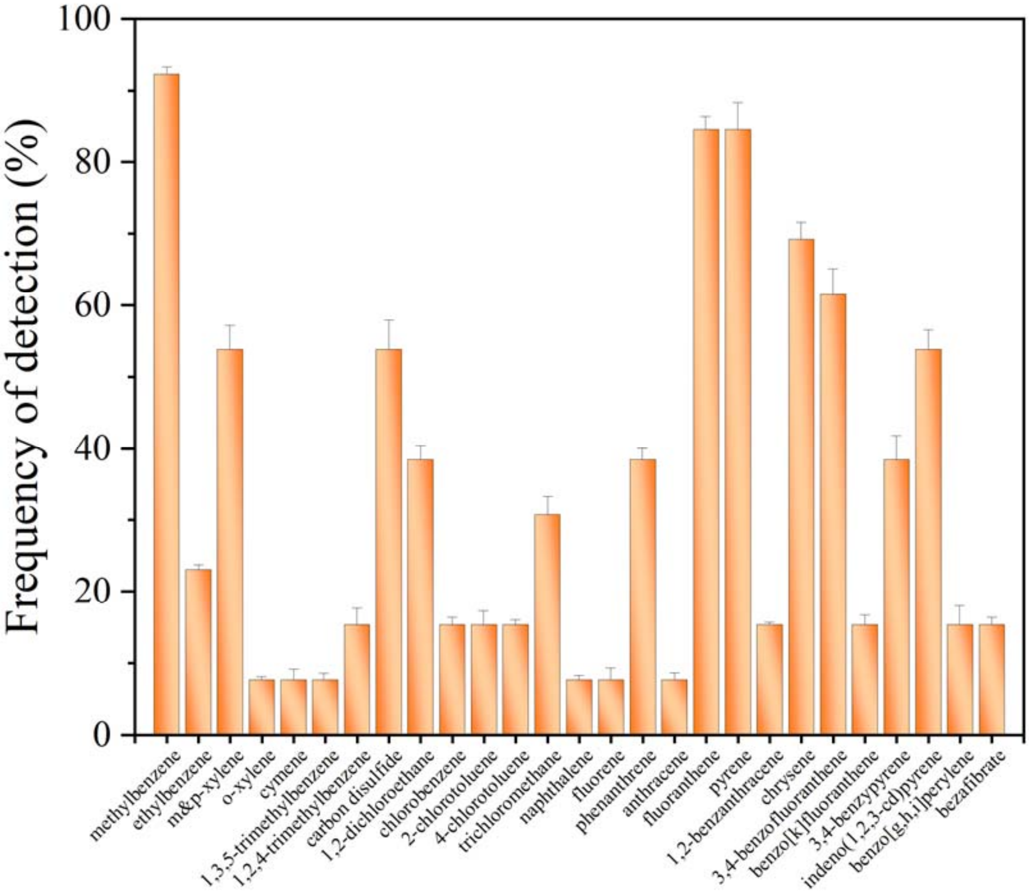

Fig. S1. Frequency of detection of organic pollutants in sediments. The columns indicate the mean values (n=3).

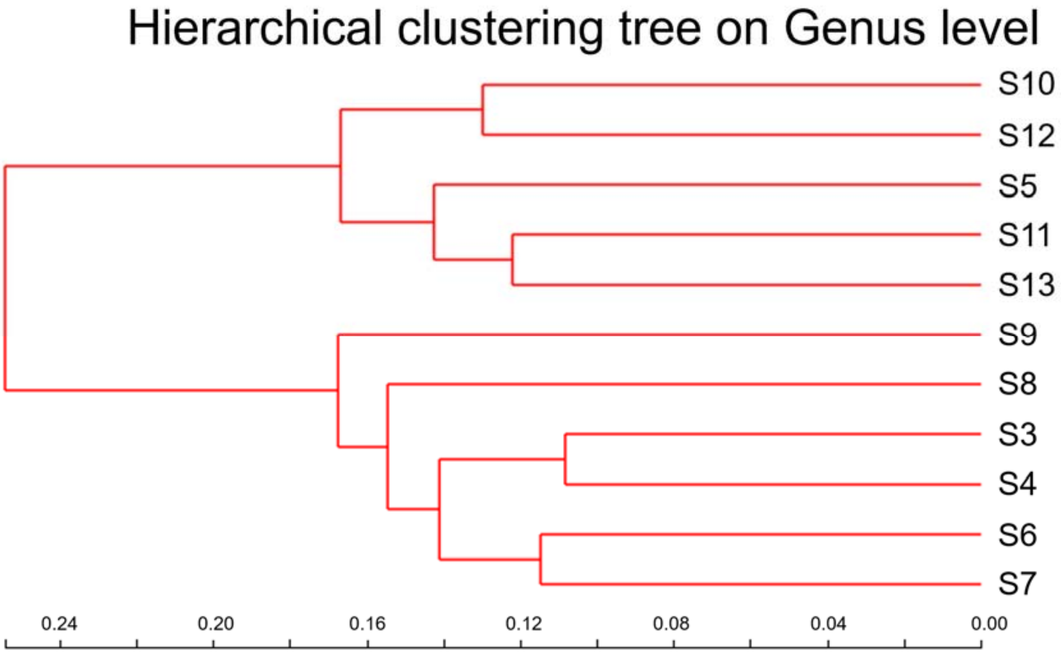

Fig. S2. Hierarchical clustering analysis of bacterial community in sediments samples on Genus level.

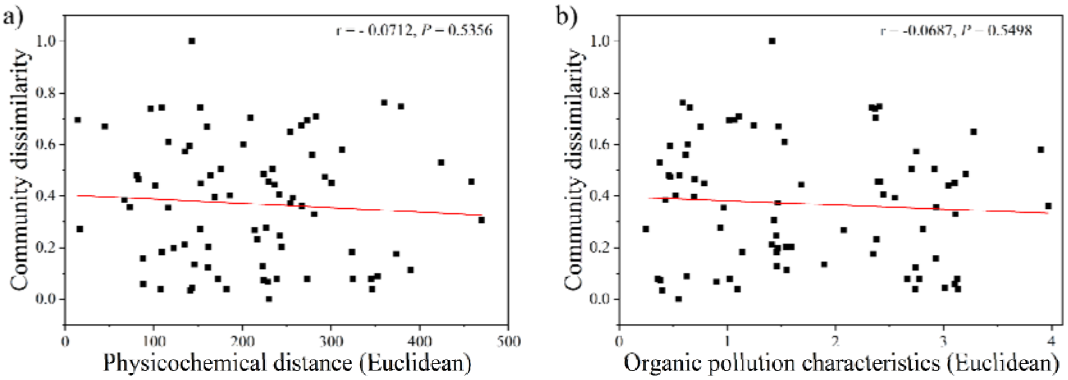

Fig. S3. Relationship between a) Bray-Curtis dissimilarity of bacterial communities and basic physicochemical distance, b) Bray-Curtis dissimilarity of bacterial communities and organic pollution characteristics in the sediment samples of unban river network.

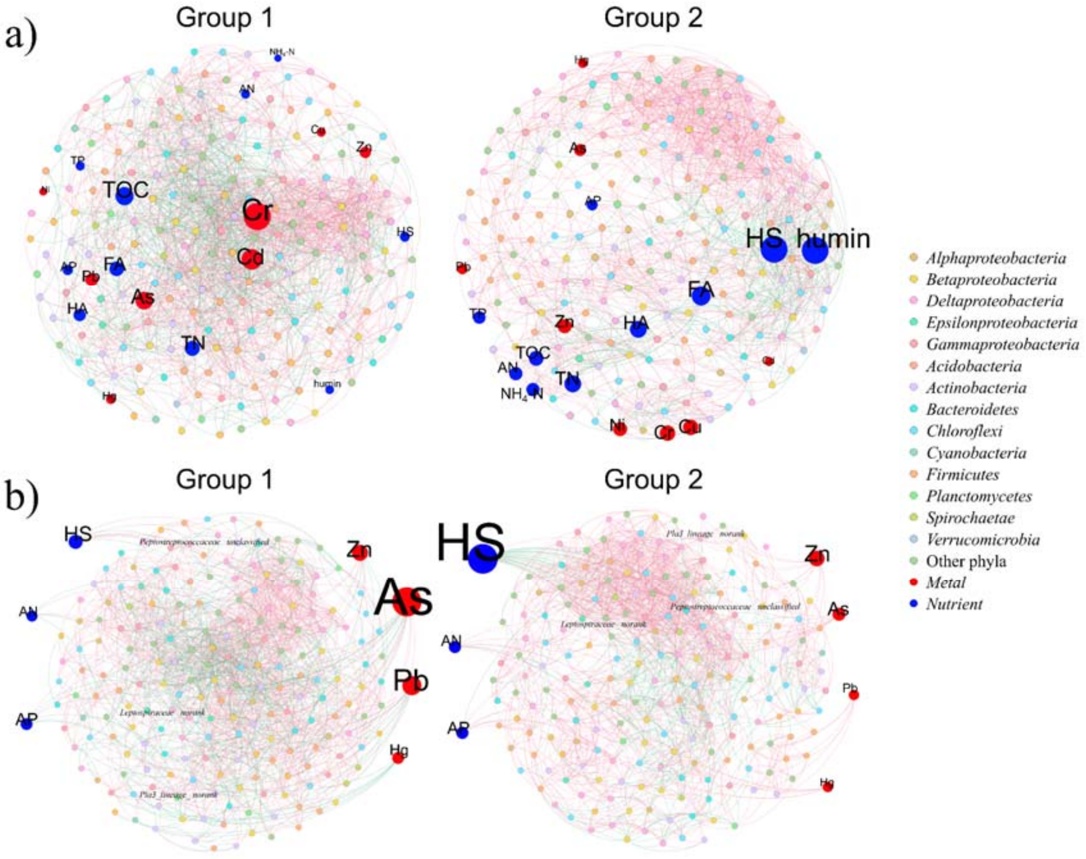

Fig. S4. Network analysis of bacterial community with a) environmental factors related to nutrient and metal, b) key factors of nutrient and metal in diverse groups. Nodes represent individual genus, key factors of nutrient and metal; edges represent significant Spearman correlations ($P < 0.01$). Light green and red lines denote negative and positive correlations, respectively.

Fig. S5. Bubble diagram showing significant differences of genera in bacterial networks in Fig. S4b that were related to the key environmental factors in two groups. The red bubbles in boxes are significantly correlated with the corresponding key environmental factors on the top of boxes.