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Impact of ZnO nanoparticles on the antibiotic resistance genes (ARGs) in estuarine water: ARG variations and their association with the microbial community

Yu-ru Chen[a], Xing-pan Guo[a], Jing-nan Feng[a], Da-pei Lu[a], Zuo-shun Niu[a], Fei-yun Tou[a], Li-jun Hou[b], Min Liu[a,c], Yi Yang[a,b]*

[a] Key Laboratory of Geographic Information Science (Ministry of Education); School of Geographical Sciences, East China Normal University, 500 Dongchuan Road, Shanghai 200241, China

[b] State Key Laboratory of Estuarine and Coastal Research, East China Normal University, 3663 North Zhongshan Road, Shanghai 200062, China

[c] Institute of Eco-Chongming, East China Normal University, 500 Dongchuan Road, Shanghai 200241, China

Corresponding author: yyang@geo.ecnu.edu.cn

Supporting Information

1. Sampling sites and estuarine water sample analysis along the Yangtze Estuary

Water samples were collected along the Yangtze Estuary at three sampling sites (Fig. S1), and the physicochemical properties of these three estuarine samples were shown in Table S1.

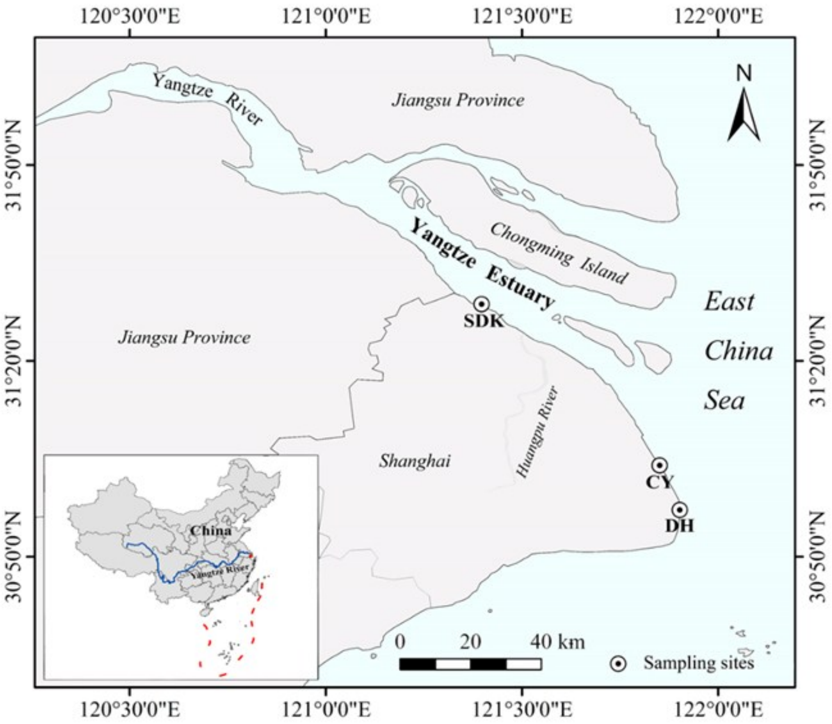

Figure S1. Sampling sites along the Yangtze Estuary.

Table S1. Physicochemical properties of three estuarine samples

Sampling sites	Salinity （‰）	Conductivity (μs/cm)	pH	DO (mg/L)	ORP (mV)	DOC (mg/L)
SDK	0.15	516	7.22	4.03	106.9	15.6
CY	1.44	4128	7.66	5.36	86.4	6.7
DH	3.38	6344.67	7.47	4.45	-142.4	7.4

Notes: DO, dissolved oxide; OPR, oxidation-reduction potential; DOC, dissolved organic carbon.

2. Characterization of ZnO NPs by TEM

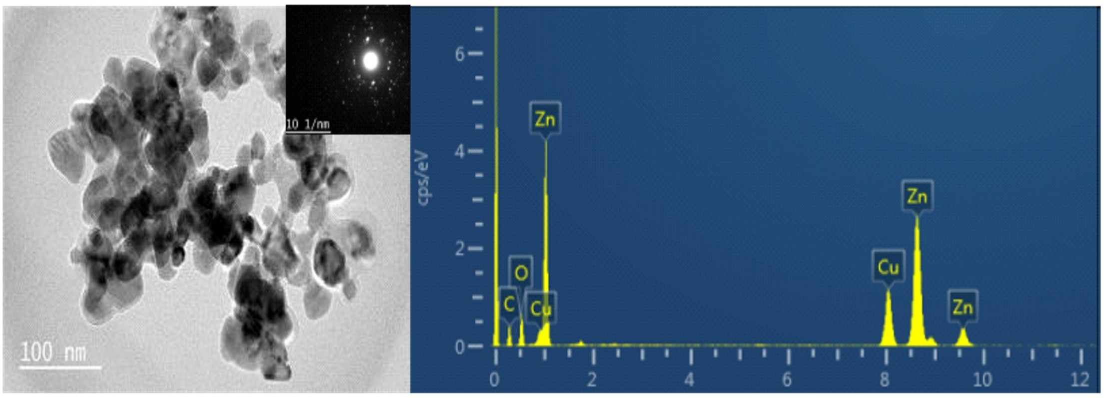

Figure S2. Representative TEM images, EDX and SAED analysis of ZnO NPs particles.

3. Preliminary experiment

Preliminary experiment had been conducted in SDK water samples for long-term effect (up to 84 h) of ZnO NPs on the native cultivable bacteria. The results showed that the total bacteria viability had a clear time-dependent variation (Figure S3). At 12 h, ZnO NPs exhibited strong growth inhibition to bacteria and the viability of the bacteria at ZnO NPs concentration of 7.5mg/L, 25mg/L and 50mg/L were 42%, 19% and 18%, respectively. However, there was a growth recovery trend after 24h exposure time. The dramatic culturability variation of cultivable bacteria at different ZnO NP doses appears within 24h.

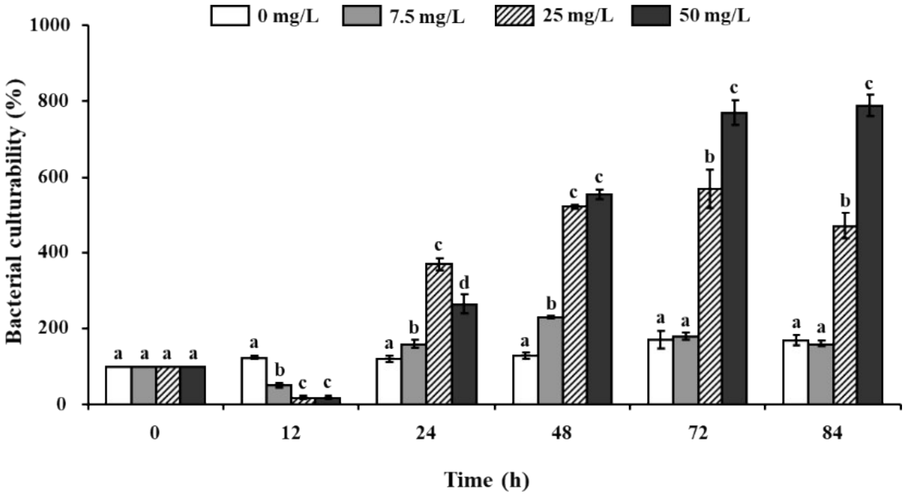

Figure S3. Cell viability assessment of native cultivable bacteria treated with 0, 7.5, 25 and 50 mg/L ZnO NPs at 12, 24, 48, 72 and 84 hours in SDK water sample.

4. Illumina MiSeq sequencing

The V4–V5 region of the 16S rRNA gene was amplified with the forward primer 515F (5′-GTGCCAGCMGCCGCGG-3′) and reverse primer 907R (5′-CCGTCAATTCMTTTRAGTTT-3′), where the barcode is an eight-base sequence unique to each sample.[1] After DNA extraction, Polymerase chain reaction (PCR) was conducted in a 20 μL reaction mixture containing 4 μL of 5× FastPfu Buffer, 2 μL of 2.5 mM dNTPs, 0.8 μL of each primer (5 μM), 0.4 μL of FastPfu Polymerase, and 10 ng of template DNA following the cycling parameters: 2 min for 95 °C, 25 cycles of 95 °C for 30 s, 55 °C for 30 s and 72 °C for 30 s, and a final elongation at 72 °C for 10 min. After being purified using the AxyPrep DNA Gel Extraction Kit (Axygen Biosciences, Union City, CA, USA) and quantified using the QuantiFluor™-ST system (Promega, USA), the amplicons were pooled in equimolar amounts and paired-end sequenced (2 × 250) on an Illumina MiSeq platform at Personal Biotechnology Co., Ltd., Shanghai, China, according to the standard protocols. The original paired Illumina MiSeq reads were deposited in the NCBI sequence read archive (accession number: SRP188045).

5. Quantitative PCR (qPCR)

5.1 PCR amplification and Plasmids construction

The PCR amplification was performed in 25 μL reaction mixture containing 0.5 μL of each primer (10 μM), 1 μL of template DNA, 12.5 μL of Taq PCR Master Mix (2×, with blue dye), and sterile distilled water to a final volume of 25 μL. And thermal cycling was conducted under the following conditions: an initial denaturing step at 94 ℃ for 10min, a touch-down thermal cycling of denaturation at 94 ℃ for 1 min, annealing temperature and time were listed in the Supporting Information (Table S2) and elongation at 72 ℃ for 0.5-1.0 min with 35 cycles. Finally, an extension step was carried out at 72 ℃ for 10 min. PCR products and their sizes were verified by agarose gel electrophoresis (1.0% weight/volume agarose) with ethidium bromide staining in 1× TAE buffer at 120 V for 20 min and visualized using an ultraviolet (UV) transilluminator. After that, the target gene fragments were purified using the Universal DNA purification Kit (Tiangen, China) and connected onto the pMD®19-T Vector, which conjugated into *Escherichia coli* DH5α. Then, plasmids were extracted from *Escherichia coli* DH5α using a SanPrep plasmid Mini Preparation Kit (Sangon, China) for standard curve construction. Plasmid DNA concentrations were measured using a Nanodrop-2000 Spectrophotometer (Thermo, USA), and used as standards in a 10-fold dilution for making qPCR standard curve.

5.2 Copy number calculation

The calculation of the copy number was conducted as follows[2]: (1) The corresponding copy number of the six 10-fold serial dilution series of the target gene plasmid was calculated as follows: copy number μl−1 = (A × 6.022 × 1023) (660 × B) $^{-1}$, where A is the plasmid DNA concentration (g μl−1), B is the plasmid length (bp) containing the cloned sequence, 6.022 × 1023 is Avogadro's number, and 660 is the average molecular weight of one base pair. (2) The six values (copy number of the 10-fold serial dilution series of the target gene plasmid) obtained from step (1) were subjected to log10 transformation. (3) The standard curve was generated through a linear regression of the six log10-transformed copy numbers (x-axis) and their corresponding CT values (y-axis). (4) The absolute number of the target genes in the experimental samples was derived after normalization to the corresponding standard curves.

5.3 qPCR thermocycling steps

qPCR was performed in a total volume of 25 μL reaction volume containing 12.5 μL of 2×SGExcel FastSYBR Mixture (with ROX) (Sangon, China), 1 μL of standard plasmid or DNA extract, 0.5 μL of each primer (10 μM) and 10.5μL sterile distilled water. The thermocycling steps for qPCR amplification were as follows: 2min for 50°C,10 min for 95°C, followed by 40 cycles: 95°C for 30s, 53 -60°C for 30s, and 72°C for 0.5- 1min, the melt curve stage with temperature ramping from 66 to 95 ºC (0.5 ºC/5s). Primer specificity was confirmed by melting curves and gel electrophoresis. Primers, annealing temperature used in qPCR and the corresponding amplification efficiencies were summarized in Tables S2 and S3, respectively. Each gene was quantified in triplicate for each sample using a standard curve and a negative control. Negative controls containing no template DNA were subjected to detect and exclude any possible contamination. The target genes abundance was calculated based on the constructed standard curve (Table S3), and then converted into copies per milliliter of water samples.

5.4 ARGs analysis

Twenty-two ARGs, including sulfonamide resistance genes (*sul*1, *sul*2, *sul*3, *sul*A), fluoroquinolones resistant genes (*qnr*S, *qnr*B, *aac(6')*-Ib), tetracycline resistance genes (*tet*A, *tet*B, *tet*C, *tet*E, *tet*G, *tet*L, *tet*M, *tet*O, *tet*Q, *tet*S, *tet*T, *tet*W, *tet*X), macrolide resistance gene (*erm*B) and chloramphenicol resistance gene (*Chl*), were detected, as they were corresponded to the five classes of antibiotics and had been reported in the various environments. Primers, annealing temperature used in PCR were summarized in Tables S2

Table S2. The primer sequences, expected amplicon size, and annealing temperature for each target gene used in this study.

Target genes	Primer Sequences (5'-3')	Amplicon size(bp)	Annealing temp(℃)	Reference
*sul*1	CACCGGAAACATCGCTGCA AAGTTCCGCCGCAAGGCT	158	55	3
*sul*2	TCCGGTGGAGGCCGGTATCTGG CGGGAATGCCATCTGCCTTGAG	191	55	4
*tet*A	GCTACATCCTGCTTGCCTTC CATAGATCGCCGTGAAGAGG	210	60	5
tetW	GAGAGCCTGCTATATGCCAGC GGGCGTATCCACAATGTTAAC	168	60	6
ermB	CGTTTACGAAATTGGAACAGG GCGTGTTTCATTGCTTGATG	364	58	7
qnrS	TCTAAACCGTCGAGTTCGGCG GCAAGTTCATTGAACAGGGT	428	56	8
*znt*A	TAACGCATTCGCTGTCACCA TCCGCCAGAACATCACCATT	134	60	9
*znt*B	GAAATCGACGCCTGTATAGCA TTGACGCCAAATAACCCTGT	153	60	
*int*I1	CCTCCCGCACGATGATC TCCACGCATCGTCAGGC	280	60	10
Tn*916/1545*	GACAGTATTAAGCCATCAGAC TCTTCCGAACACAATCATCT	142	50	11
16S rRNA	CCTACGGGAGGCAGCAG TTACCGCGGCTGCTGGCAC	193	60	10
*sul*3	CCCATACCCGGATCAAGAATAA CAGCGAATTGGTGCAGCTACTA	143	57/58	12
*sul*A	GCACTCCAGCAGGCTCGTAA CTCTGCCACCTGACTTTTCCA	198	56/57	12
*tet*B	CGAAGTAGGGGTTGAGACGC AGACCAAGACCCGCTAATGAA	192	56	12
*tet*C	CTTGAGAGCCTTCAACCCAG GGCAGGTAGATGACGACCAT	418	55	5
*tet*E	AAACCACATCCTCCATACGC AAATAGGCCACAACCGTCAG	278	55	5
*tet*G	GCAGAGCAGGTCGCTGG	134	65	9

	CCYGCAAGAGAAGCCAGAAG			
*tet*L	TCGTTAGCGTGCTGTCATTC GTATCCCACCAATGTAGCCG	267	58/55	13
*tet*M	CCGTTGGGAAGTGGAATGC TCCGAAAATCTGCTGGGGTA	196	57	5
*tet*O	GATGGCATACAGGCACAGACC GCCCAACCTTTTGCTTCACTA	172	57	5
*tet*Q	AGAATCTGCTGTTTGCCAGTG CGGAGTGTCAATGATATTGCA	167	53	13
*tet*S	ATAGCGGTACAACGAAAACGG GATTAGCAAAATAGCTCCATCCAA	188	56/55	5
*tet*T	ATGCTACAACGACAACGGATTC TCGCTCAACTTCGGCTATGA	149	55	5
*tet*X	AGCCTTACCAATGGGTGTAAA TTC TTA CCT TGG ACA TCC CG	278	60	10
Chl	GGAGTGAATACCACGACGAT ACGGCATGATGAACCTGAAT	268	*55*	9
*qnr*B	GATCGTGAAAGCCAGAAAGG ATGAGCAACGATGCCTGGTA	476	50	9
aac(6')-Ib	TTGCGATGCTCTATGAGTGGCTA CTCGAATGCCTGGCGTGTTT	482	58	9

Table S3. Standard curve and amplification efficiency of selected genes for qPCR.

Target genes	Standard curve	r^2	amplification efficiencies
*sul*1	y = -3.23 x + 34.57	0.999	104%
sul2	y = -3.70 x + 39.45	0.998	86.3%
*tet*A	y = -3.42 x + 34.17	0.999	96.1%
*tet*W	y = -3.33 x + 36.96	0.998	99.7%
*erm*B	y = -3.64 x + 40.65	0.994	88%
*qnr*S	y = -3.39 x + 42.88	0.996	97%
*znt*A	y = -3.61 x + 43.1	0.994	89.3%
*znt*B	y = -3.56 x + 33.98	0.999	91%
*int*I1	y = -3.41 x + 37.48	0.998	96.5%
Tn*916/1545*	y = -3.61 x + 43.16	0.992	89.1%
16s rRNA	y = -3.75 x + 41.94	0.993	84.7%

Notes: “y” means the threshold cycle number (C_T value) determined during the real-time PCR, “x” is the log gene copy number in the PCR mix.

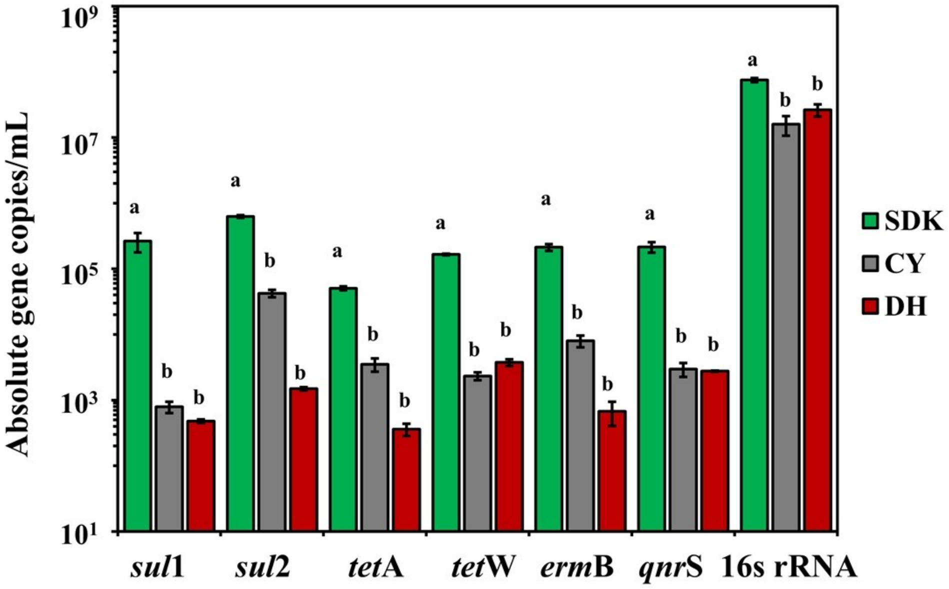

Figure S4. Absolute gene copies of six ARGs and 16S rRNA in raw SDK, CY and DH samples.

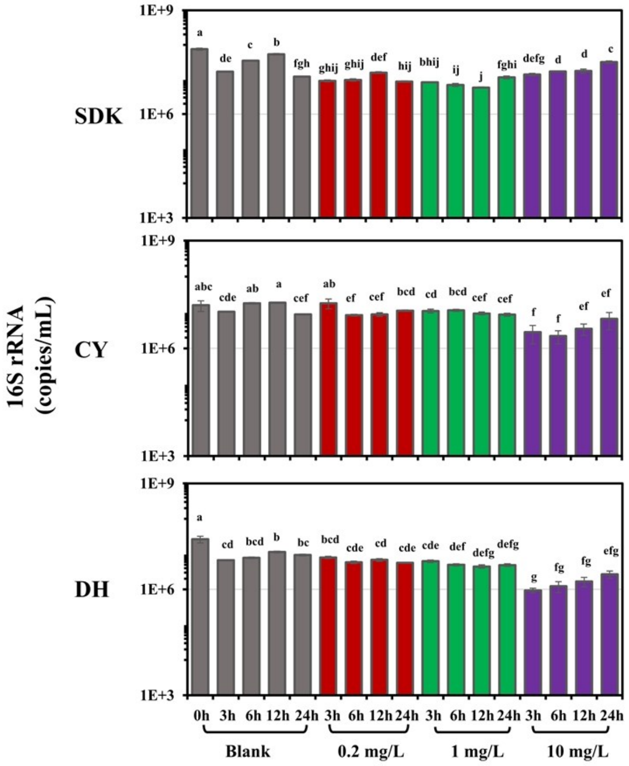

Figure S5. Variations of absolute gene copies of 16S rRNA in SDK, CY and DH samples.

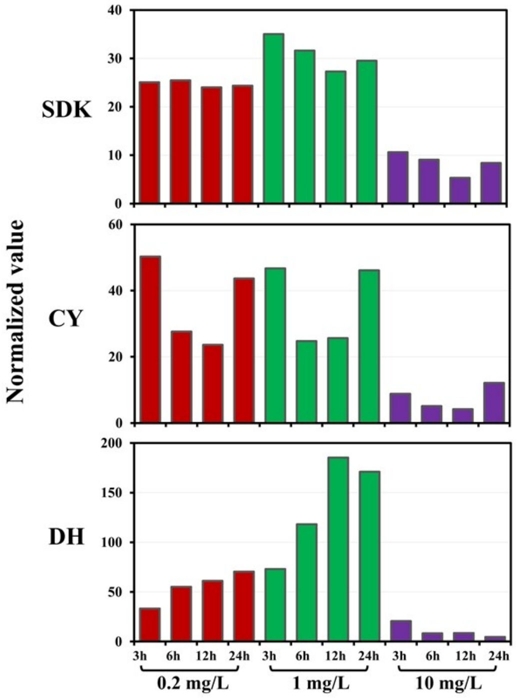

Figure S6. The normalized value (NV) of total ARGs during ZnO NPs exposure in SDK, CY and DH samples. The NV was calculated as relative abundance of total ARGs versus the corresponding blank values. The NV >1 indicated the abundances of ARGs were enhanced when exposed to ZnO NPs, at certain time compared to the corresponding blanks; the NV <1 indicated the abundances of ARGs were reduced when exposed to ZnO NPs, at certain time.

6. Hydrodynamic size and zeta-potential of ZnO NPs

Water samples were filtered through 1-µm glass fiber filters (PAUL, USA) and further ultra-filtered by cross-flow ultrafiltration with a 1-kDa regenerated cellulose Pellicon 2 PLAC ultrafiltration membrane to remove the indigenous colloids and microorganisms.[14] Then, the filtrate (<1 kD) water was used as the aqueous medium for the aggregation test of ZnO NPs. In order to better mimic the real aquatic environmental conditions, ZnO NPs (10mg/L) were added in the filtrate (<1 kD) water samples, and the dynamic size and zeta-potential of ZnO NPs were analyzed using Zeta-Sizer (Malvern, Nano-ZS90, UK).

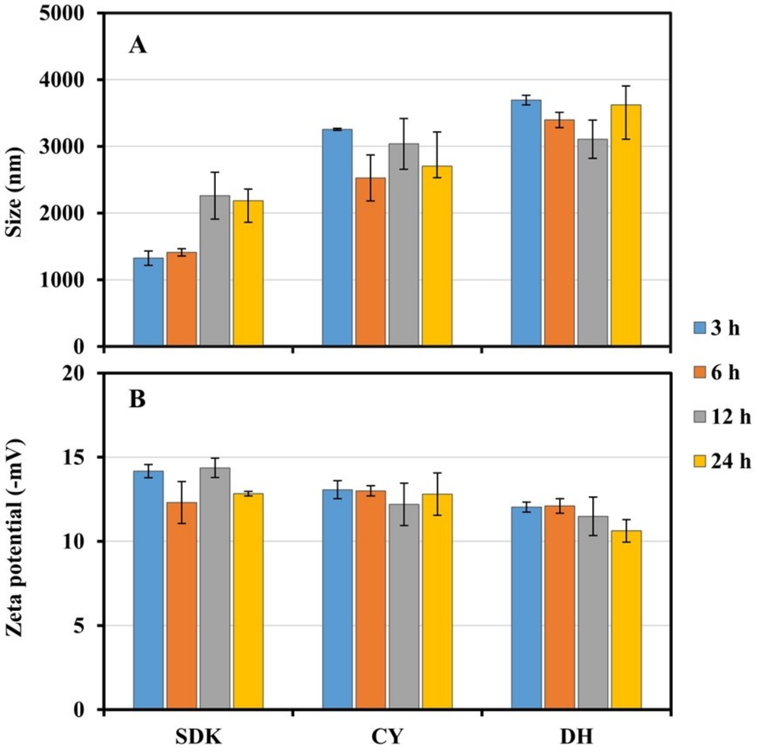

Figure S7. The particle size (A) and Zeta potential (B) of ZnO NPs in three estuarine water samples under the exposure of 10 mg/L ZnO NPs.

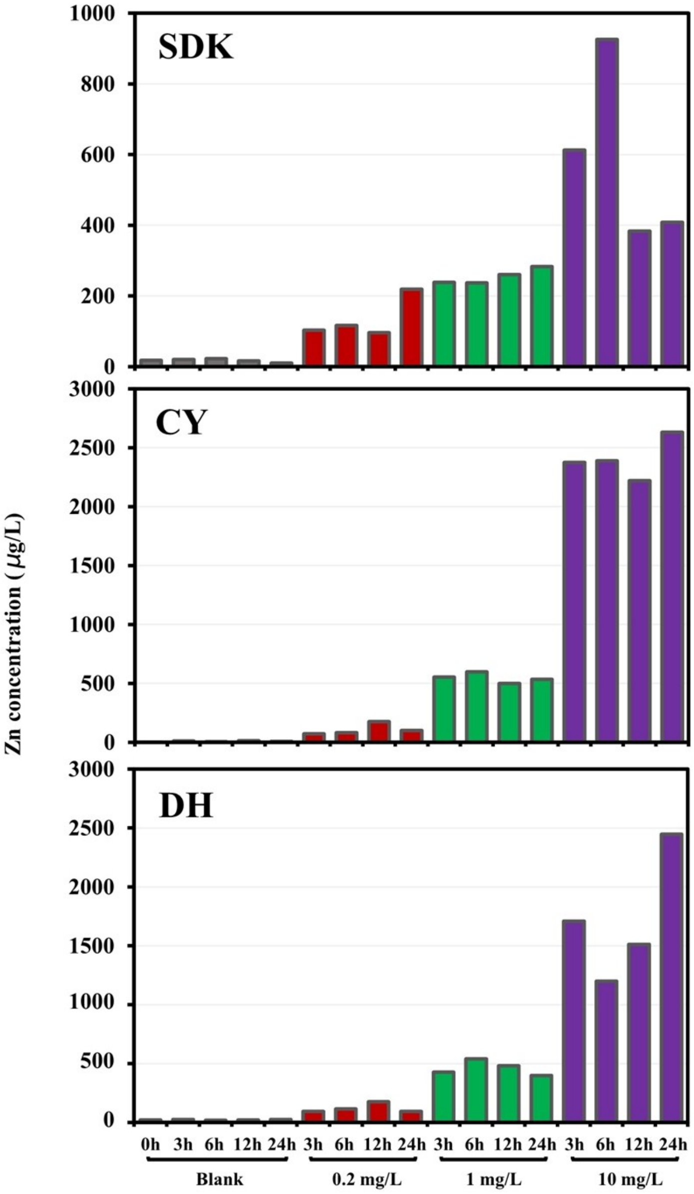

Figure S8. Dissolved Zn concentrations in SDK, CY and DH samples with exposure to ZnO Nos with different doses.

Table S4. The normalized value (NV) of individual ARG, MGE and MRG during ZnO NPs exposure in SDK, CY and DH samples. The NV was calculated as relative abundance of individual ARG, MGE and MRG versus the corresponding blank values. The redder, the higher the NV, and the greener, the lower the NV.

Sampling sites	Treatment	Time	ARGs						MGEs		MRGs	
			*sul*1	*sul*2	*tet*A	*tet*W	*erm*B	*qnr*S	*int*I1	Tn*916/1545*	*znt*A	*znt*B
SDK	0.2 mg/L	3h	46.020	3.534	6402.657	10.774	2581.240	54.562	11.724	641.950	826.801	70.456
		6h	50.013	3.253	3410.704	10.401	3271.448	23.273	5.460	223.630	349.492	90.853
		12h	40.806	3.488	2306.235	19.299	5538.642	22.651	5.409	615.453	428.557	92.571
		24h	29.120	2.700	4707.979	16.856	6462.501	22.301	13.768	439.547	1298.575	37.575
	1 mg/L	3h	53.295	3.006	8104.901	18.006	5960.328	51.079	21.132	514.520	1020.844	75.117
		6h	37.400	1.734	4576.129	25.785	6329.656	25.263	14.454	390.068	6545.967	145.863
		12h	32.152	1.270	4712.155	34.290	4038.256	151.261	12.620	247.576	1919.029	320.530
		24h	46.597	3.728	5053.302	34.331	5855.580	19.115	35.239	452.796	4039.972	19.681
	10 mg/L	3h	2.531	8.587	120.809	59.199	260.269	6.390	4.700	657.113	810.730	49.647
		6h	4.708	7.210	54.051	56.432	248.728	5.831	2.259	560.557	283.961	54.927
		12h	1.955	2.876	87.911	122.363	421.669	9.957	1.869	773.021	632.313	102.491
		24h	3.384	7.299	58.214	111.468	499.418	2.625	3.410	1198.697	2094.161	17.732
CY	0.2 mg/L	3h	25.258	4.867	4018.273	3.873	10204.182	10.990	2.834	110.861	35.297	0.788
		6h	18.107	6.561	7698.584	19.853	1421.160	12.556	6.612	1408.672	1.907	1.627
		12h	34.251	4.003	9786.557	13.466	229.989	4.101	21.200	370.208	0.242	0.778
		24h	24.651	2.566	4021.242	4.003	13159.805	67.493	12.196	705.588	0.603	0.974
	1 mg/L	3h	47.296	8.699	6225.628	9.361	4065.207	12.771	8.940	171.873	56.594	1.218
		6h	25.194	5.671	6207.767	4.964	837.798	8.515	4.252	935.287	1.347	1.160
		12h	42.880	7.908	8228.866	5.482	769.099	6.093	22.209	184.709	0.244	0.904
		24h	57.151	4.594	3446.036	4.818	3281.598	80.963	47.147	462.312	1.750	0.875
	10 mg/L	3h	1.271	10.798	145.483	91.568	56.350	5.123	6.093	1622.249	275.909	6.104
		6h	0.485	9.584	86.029	67.409	196.600	1.788	1.018	13185.085	7.384	6.194
		12h	0.609	9.585	135.129	94.122	140.169	0.546	2.266	2108.750	0.632	2.083
		24h	0.683	5.189	79.581	91.295	233.179	19.847	1.498	528.882	2.445	1.868
DH	0.2 mg/L	3h	22.930	3.057	4206.153	5.189	38.293	57.287	2.738	671.288	55.280	1.024
		6h	58.525	5.882	9517.490	16.835	54.262	34.860	12.639	3589.473	48.404	1.124
		12h	103.471	5.157	6864.698	54.133	130.307	25.312	9.505	793.243	61.790	0.864
		24h	68.395	5.221	23920.918	38.878	734.408	40.231	15.576	2060.491	67.262	1.357
	1 mg/L	3h	75.275	3.387	7965.747	1.494	135.050	74.652	7.318	1030.057	86.302	1.276
		6h	193.393	3.020	10842.900	5.799	236.175	36.329	13.381	2575.133	53.570	1.275
		12h	461.156	16.004	11012.770	20.789	1511.301	48.953	42.798	1876.082	137.521	2.174
		24h	327.609	22.394	22562.248	24.835	306.493	65.385	41.888	1845.516	95.780	1.750
	10 mg/L	3h	2.056	8.133	224.048	127.040	121.579	27.683	0.396	49035.468	633.140	8.139
		6h	1.285	7.920	147.753	58.689	68.432	8.541	0.897	21069.677	330.496	5.778
		12h	4.721	14.845	92.444	114.333	13.788	2.790	3.879	10855.690	333.054	6.751
		24h	1.114	3.701	89.577	51.856	87.245	1.875	0.580	8357.609	307.855	4.193

Table S5. Correlation coefficients between MGEs (gene copies/16S rRNA copies) and Zn^{2+} (mg/L) in SDK, CY and DH respectively.

	SDK		CY		DH	
	intI1	Tn*916/1545*	*intI1*	Tn*916/1545*	*intI1*	Tn*916/1545*
Zn^{2+}	0.502*	0.529*	0.397	0.495*	0.201	0.826**

* Significant at $P < 0.05$.

** Significant at $P < 0.01$.

Table S6. Correlation coefficients between MRGs and ARGs based on their relative abundance (gene copies/16S rRNA copies) in SDK, CY and DH respectively.

	SDK		CY		DH	
	*znt*A	*znt*B	*znt*A	*znt*B	*znt*A	*znt*B
*sul*1	0.620**	0.534*	-0.140	-0.230	0.382	0.370
*sul*2	0.358	0.301	0.189	0.297	0.841**	0.811**
*tet*A	0.779**	0.789**	-0.025	0.056	0.397	0.282
*tet*W	0.581*	0.493*	0.471	0.600*	0.806**	0.696**
*erm*B	0.632**	0.730**	-0.230	-0.186	0.591*	0.461
*qnr*S	0.703**	0.819**	0.091	0.054	0.419	0.390

* Significant at $P < 0.05$.

** Significant at $P < 0.01$.

Table S7. The richness (Chao and Ace), diversity (Shannon and Simpson) and sequencing depth indexes for bacterial community of each sample.

Treatment	Time	SDK						CY						DH					
		reads	OTU	chao1	ACE	simpson	shannon	reads	OTU	chao1	ACE	simpson	shannon	reads	OTU	chao1	ACE	simpson	shannon
Blank	0h	48409	2632	1511	1597	0.99	8.50	67453	2711	1172	1212	0.99	8.25	71766	3890	1698	1797	1.00	9.24
	3h	45012	2463	1532	1589	0.98	8.60	41117	2718	1393	1479	0.99	8.38	42733	2738	1764	1848	0.99	8.77
	6h	42699	2455	1698	1704	0.99	9.00	40216	3065	1586	1690	0.99	8.40	65378	2865	1933	2079	0.99	8.82
	12h	44350	2377	1444	1518	0.99	8.60	47386	3053	1563	1662	0.99	8.71	68531	3071	1823	1966	0.99	8.88
	24h	42811	2454	1506	1531	0.99	8.70	44266	2175	1364	1400	0.91	7.30	35689	2708	1339	1434	0.99	8.02
0.2 mg/L ZnO NPs	3h	35583	2491	1465	1523	0.99	8.80	40660	2552	1376	1482	0.99	8.27	48383	2647	1650	1783	0.99	8.58
	6h	33473	2472	1659	1762	0.99	8.70	41057	2545	1358	1463	0.99	8.15	52267	2720	1656	1797	0.97	8.10
	12h	42356	2588	1686	1820	0.99	8.70	39332	2577	1767	1907	0.99	8.53	37789	2562	1757	1884	0.99	8.39
	24h	43970	2601	1752	1896	0.99	8.70	42814	2649	1609	1741	0.99	8.44	40256	2470	1641	1781	0.99	8.51
1 mg/L ZnO NPs	3h	49230	2792	1738	1758	0.99	9.00	40649	1494	888	959	0.97	6.79	29835	2516	1293	1372	0.98	8.10
	6h	41816	2698	1656	1729	1.00	8.90	37436	2231	1026	1084	0.98	7.38	52162	2525	1453	1535	0.97	7.93
	12h	39842	2309	1621	1699	0.99	8.40	43349	2286	1254	1294	0.99	7.91	37132	2735	1614	1692	0.97	8.21
	24h	34324	2423	1478	1550	0.99	8.90	52072	2009	1223	1303	0.99	7.88	34760	2579	1500	1575	0.98	7.87
10 mg/L ZnO NPs	3h	49227	2181	1446	1510	0.99	8.70	68453	3250	1408	1514	0.98	7.88	73422	3505	1564	1684	0.99	8.18
	6h	46402	2083	1589	1620	0.99	8.90	74768	3346	1598	1731	0.99	8.56	70002	3611	1526	1656	0.99	8.05
	12h	41249	2222	1633	1696	0.99	8.60	60787	3579	1621	1750	0.99	8.60	70473	3532	1689	1804	0.99	8.52
	24h	47495	2345	1659	1765	0.99	8.80	63898	2740	1010	1058	0.98	7.44	69683	3526	1466	1576	0.99	8.09

Notes: The richness, diversity and sequencing depth indexes data for each treatment group are presented as the average values of the replicates.

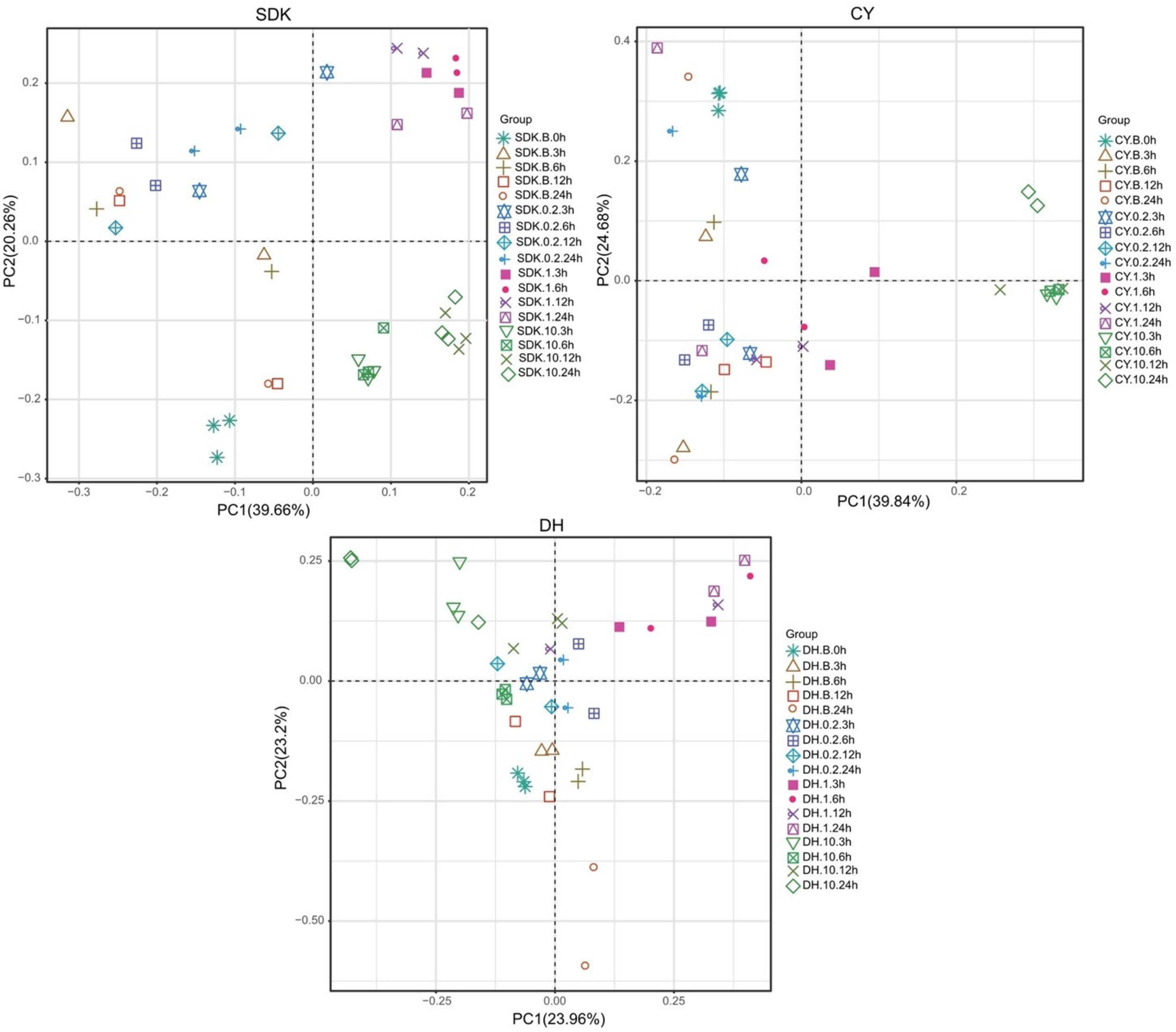

Figure S9. PCA analysis of relative abundance of genera showed the evolution of the microbial community dosed with different concentrations of ZnO NPs at different exposure time.

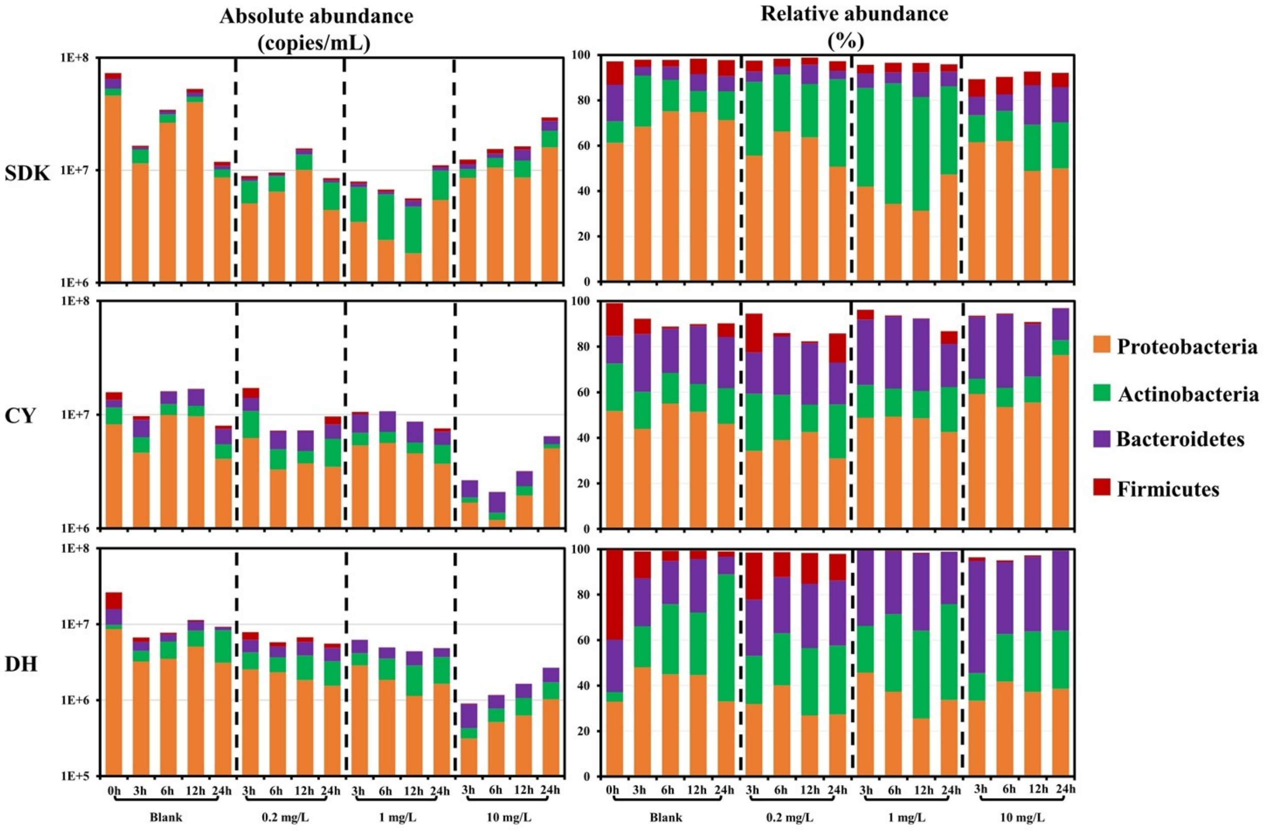

Figure S10. Absolute and relative abundances of top four phyla in microbial community in SDK, CY and DH samples.

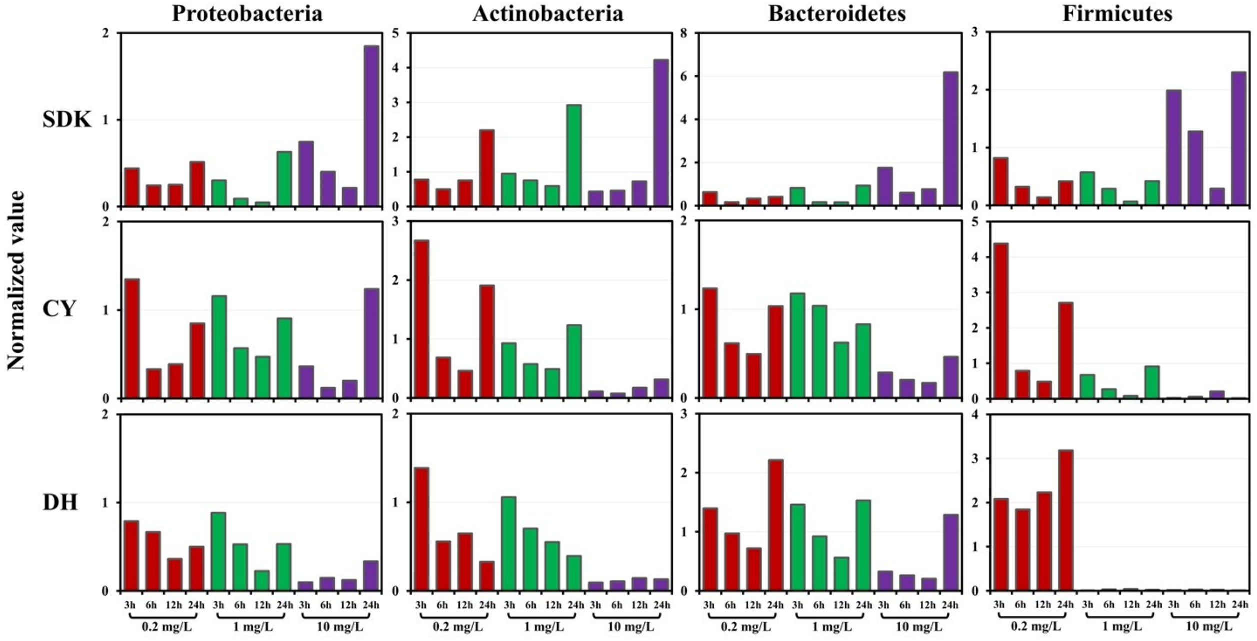

Figure S11. The NVs for the top 4 phyla in SDK, CY and DH samples. The values were calculated as the absolute abundance of each phylum at each treatment normalized by the corresponding blank values.

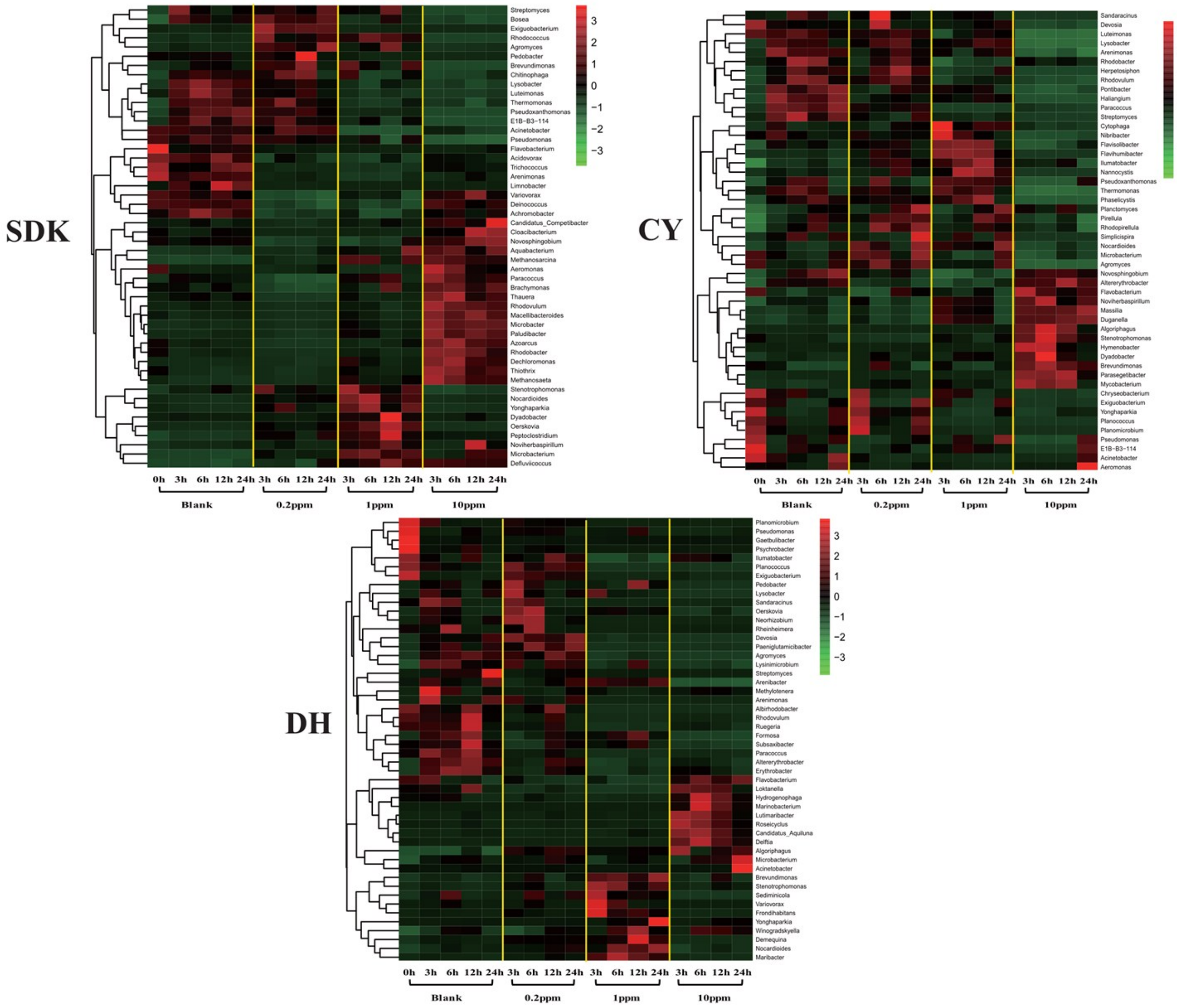

Figure S12. Heatmap of relative abundance of top 50 genera (values were log10- transformed) showed the evolution of the microbial community dosed with different concentration of ZnO NPs at different exposure time.

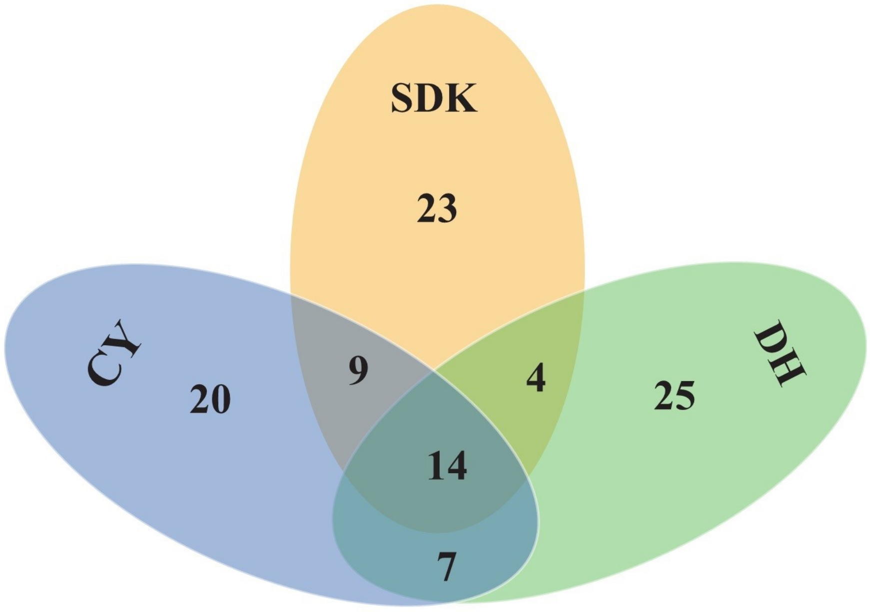

Figure S13. Venn map of the top 50 genera in this study.

Table S8. The normalized values (NVs) for the top 50 genera in SDK, CY and DH samples. The values were calculated as the absolute abundance of each genus at each treatment normalized by the corresponding blank values. The redder, the higher the NV, and the greener, the lower the NV.

Sampling sites	Top 50 genera	Treatment											
		0.2 mg/L				1 mg/L				10 mg/L			
		3h	6h	12h	24h	3h	6h	12h	24h	3h	6h	12h	24h
SDK	***Streptomyces***	**0.2192**	**0.3989**	**0.5659**	**1.8347**	**0.1538**	**0.1453**	**0.5630**	**0.4756**	**0**	**0**	**0**	**0**
	E1B-B3-114	0.5004	0.2485	0.2779	0.3608	0.1243	0.0782	0.0107	0.3553	0	0	0	0.0077
	Microbacterium	**3.3680**	**0.9890**	**1.8943**	**5.0815**	**7.8888**	**3.6860**	**1.7077**	**21.4033**	**2.7299**	**2.2003**	**5.5552**	**49.9009**
	Nocardioides	**1.5619**	**0.7496**	**1.2718**	**2.8292**	**5.1972**	**3.1025**	**0.7665**	**8.1839**	**0.6847**	**0.5135**	**0.5353**	**3.7322**
	Agromyces	**2.6456**	**2.0220**	**1.7031**	**11.7868**	**0.4515**	**0.6408**	**1.6448**	**2.2879**	**0.0618**	**0.1609**	**0.2044**	**1.7647**
	Rhodococcus	3.8544	0.8948	0.9015	4.1094	1.7246	2.1297	0.5927	4.0478	0	0.0073	0.0015	0
	Oerskovia	5.8294	1.6878	2.8293	11.6274	11.4413	5.8860	9.0265	40.5296	0	0	0.0157	0
	Yonghaparkia	**3.2196**	**18.8755**	**2.3300**	**3.5306**	**8.7223**	**22.0537**	**1.2669**	**39.5163**	**0.1265**	**0.1632**	**0.2192**	**6.1766**
	Pedobacter	1.4293	0.2404	1.4705	1.4459	0.2256	0.0029	0.0081	0.5345	0	0	0	0.0420
	Dyadobacter	0.3756	0.2449	0.3419	5.1782	2.0620	2.0236	6.6945	20.8883	0	0.2417	1.6965	2.0589
	Paludibacter	0.5779	0.1754	0.0291	0.2230	2.2596	0.7947	0.0809	1.3291	12.0016	5.4588	2.5319	17.5544
	Cloacibacterium	0.2584	0.0501	0.0099	0.0160	0.6565	0.1244	0.0037	0.0812	5.6520	1.8163	1.7932	17.6473
	Microbacter	1.1499	0.1225	0.2184	0.5946	5.2093	0.5077	0.2157	1.7721	31.4807	5.1852	5.8823	28.6072
	Chitinophaga	0.4817	0.3764	0.5859	0.1341	0.6561	0.0018	0.0051	0.6393	0	0.0058	0.0206	0.9605
	Flavobacterium	**0.3947**	**0.0291**	**0.0604**	**0.0308**	**0.0757**	**0.0178**	**0.0038**	**0.0493**	**0.0851**	**0.0168**	**0.0266**	**0.8471**
	Macellibacteroides	0.3756	0.0661	0.0376	0.0763	3.1400	0.3258	0.0243	0.4803	27.2752	4.7646	3.5287	16.2164
	Deinococcus	0.1931	0.1165	0.1011	0.1553	0.2289	0.0674	0.0492	0.2833	0.8672	0.4859	0.2412	2.2920
	Methanosaeta	1.6098	0.4330	0.3560	3.2481	8.7545	1.3624	0.5152	14.2165	38.3951	16.6899	6.0406	86.1189
	Methanosarcina	3.1525	0.8267	0.7678	3.3737	9.8126	2.8719	0.4999	16.3157	18.3638	6.8235	3.5672	32.9416
	Trichococcus	0.2739	0.0898	0.0432	0.0980	0.0800	0.0547	0.0029	0.0609	0.7184	0.4693	0.0891	0.6019
	Peptoclostridium	1.9931	1.2302	0.5825	3.5508	2.6046	1.5398	1.7984	3.9817	2.2289	1.5035	0.9630	6.3026
	Exiguobacterium	**164.1997**	**12.9511**	**2.8986**	**18.0943**	**0**	**0.2484**	**0.0565**	**1.1691**	**0**	**0**	**0**	**0**
	Acinetobacter	**0.3263**	**0.3945**	**0.3956**	**0.8501**	**0.0037**	**0.0028**	**0.0010**	**0.0356**	**0.3365**	**0.2168**	**0.0653**	**0.4563**
	Thermomonas	0.4930	0.3339	0.2249	0.5346	0.2246	0.0742	0.0428	0.6461	0.3608	0.2080	0.0926	1.4424
	Pseudomonas	**0.6081**	**0.2198**	**0.2091**	**0.4522**	**0.3237**	**0.1340**	**0.0173**	**0.6200**	**0.1681**	**0.0727**	**0.0464**	**0.2330**
	Pseudoxanthomonas	0.6218	0.1857	0.2473	0.2783	0.1518	0.0372	0.0211	0.1927	0.0021	0.0014	0.0000	0.0033

	Lysobacter	**0.3107**	**0.1359**	**0.2357**	**0.3988**	**0.1477**	**0.0284**	**0.0483**	**0.3754**	**0.1810**	**0.1025**	**0.0541**	**0.7084**
	Stenotrophomonas	**2.0898**	**0.3830**	**0.3184**	**0.8096**	**2.5216**	**0.5651**	**0.0893**	**3.2655**	**0.0769**	**0.0419**	**0.0784**	**1.2475**
	Aeromonas	0.3465	0.2774	0.2257	0.9713	0.1679	0.1527	0.0204	0.5407	8.7040	4.2979	0.7831	4.9368
	Bosea	0.5966	0.3044	0.4799	1.1024	0.1487	0.0870	0.1595	0.5249	0.2071	0.1834	0.1204	0.8464
	Acidovorax	0.1227	0.1737	0.0975	0.2267	0.1433	0.0522	0.0429	0.2765	0.4513	0.2965	0.1287	1.2308
	Brevundimonas	1.9094	0.4086	0.8703	0.7227	2.3995	0.1845	0.0403	3.1433	0	0.0007	0.0032	0.0208
	Luteimonas	0.2943	0.0949	0.2230	0.3722	0.0980	0.0109	0.0170	0.1523	0.0735	0.0251	0.0178	0.4788
	Aquabacterium	0.6820	0.3149	0.4381	1.2357	1.3887	0.3564	0.2610	5.9706	5.7126	3.1978	1.6450	15.2969
	Arenimonas	**0.1520**	**0.0700**	**0.0953**	**0.1629**	**0.0380**	**0.0167**	**0.0042**	**0.2075**	**0.1838**	**0.1155**	**0.1515**	**0.6827**
	Paracoccus	**0.2130**	**0.0758**	**0.0953**	**0.2162**	**0.4910**	**0.2807**	**0.2005**	**0.7349**	**1.7778**	**0.9730**	**0.4405**	**4.7180**
	Achromobacter	0.1456	0.0700	0.1057	0.2763	0.2460	0.0340	0.0244	0.4717	0.4799	0.2813	0.1637	2.3172
	Variovorax	0.1459	0.1041	0.0619	0.1698	0.2932	0.1236	0.0552	0.3315	0.7193	0.5802	0.4419	2.8816
	Noviherbaspirillum	0.6778	0.8267	0.3084	0.4783	2.6922	1.6830	1.4715	2.8361	0.7193	0.4607	7.0020	5.1234
	Dechloromonas	0.4188	0.2441	0.0324	0.3455	3.8911	0.7663	0.1677	1.6915	12.4717	9.9673	3.6171	19.3745
	Novosphingobium	0.2576	0.1314	0.1315	0.4119	0.1958	0.1109	0.0475	1.0620	1.3438	0.7438	0.6859	5.5515
	Brachymonas	0.2348	0.1218	0.0615	0.2648	0.4669	0.1756	0.2232	1.0522	1.8417	1.7000	0.4570	7.6839
	Thiothrix	0.5151	0.0882	0.3236	1.0592	1.8030	0.4371	0.5032	2.4785	12.9600	6.5921	6.9418	30.8828
	Defluviicoccus	0.9391	0.4822	0.3137	2.5356	1.8486	0.9338	1.2939	4.4214	4.7831	2.5944	2.5125	11.3905
	Thauera	0.1480	0.0617	0.0906	0.1126	0.5239	0.0890	0.0958	0.4880	2.7784	1.7876	0.7161	5.2942
	Rhodovulum	**0.3389**	**0.0861**	**0.1456**	**0.3531**	**0.7997**	**0.1925**	**0.0359**	**0.6547**	**8.3615**	**2.1416**	**1.7537**	**9.8825**
	Rhodobacter	0.3302	0.0877	0.0539	0.1284	0.9350	0.2890	0.0439	0.7227	12.9652	4.3611	1.9892	11.4708
	Limnobacter	0.0079	0.0056	0.0004	0.0062	0.0089	0.0140	0.0008	0.0207	0.0367	0.0857	0.0034	0.0781
	Azoarcus	0.0826	0	0	0.0235	0.5649	0.0662	0.1120	1.8706	7.8405	3.6483	2.4198	15.0002
	CandidatusCompetibacter	0.1736	0.0204	0	0.2463	0.5660	0.0809	0.4025	0.7178	3.1820	1.4021	1.9291	23.6802
	Nocardioides	**4.0858**	**1.1473**	**0.5868**	**4.2152**	**1.7796**	**1.3607**	**1.1447**	**3.1742**	**0.1057**	**0.0795**	**0.2650**	**0.4467**
	Microbacterium	**2.9667**	**1.1123**	**0.6269**	**2.2078**	**0.8095**	**0.3796**	**0.4181**	**1.2601**	**0.0812**	**0.0665**	**0.2280**	**0.2931**
	Yonghaparkia	**7.9035**	**1.6158**	**0.8478**	**1.0902**	**0.7909**	**0.3433**	**0.1887**	**0.4701**	**0.0645**	**0.0587**	**0.2628**	**0.2328**
	Agromyces	**3.2462**	**1.3451**	**1.0639**	**1.7753**	**1.2113**	**0.6695**	**0.7435**	**1.2406**	**0.0205**	**0.0060**	**0.0276**	**0.0308**
	Ilumatobacter	2.1092	0.8120	0.7431	2.0854	1.8819	1.4509	1.1295	1.7640	0.3203	0.1413	0.2366	0.6142
	Mycobacterium	2.0973	1.7331	1.2922	1.2258	2.3463	1.7104	1.1873	0.8058	1.8875	1.4206	1.7485	0.8198
	E1B-B3-114	0.6353	0.1072	0.4328	0.6435	3.1447	0.6559	0.5702	7.1669	0.0093	0	0	22.6945
	Streptomyces	**0.5841**	**0.0684**	**0.0304**	**0.8720**	**0.1728**	**0.0667**	**0.0685**	**0.2128**	**0**	**0**	**0**	**0.0028**

	Chryseobacterium	4.0022	0.1449	0.2286	1.2729	1.4103	0.5146	0.2163	1.9689	0.0388	0.0158	0.0806	0.2064
	Pontibacter	0.5233	0.1275	0.3417	0.6243	0.5954	0.4666	0.2966	0.1789	0.0189	0.0057	0.0093	0.0915
	Algoriphagus	1.6957	0.7054	0.4527	1.4420	2.6249	1.1520	0.7728	3.4378	6.6957	5.1131	3.6506	3.1158
	Nibribacter	1.2082	0.3742	0.6461	1.5445	1.9507	1.1666	0.7085	0.7631	0.0073	0.0129	0.0289	0.2087
	Flavobacterium	**0.5510**	**0.3657**	**0.9704**	**1.6940**	**1.2785**	**1.0664**	**0.6517**	**0.5298**	**1.1051**	**0.6280**	**0.3027**	**1.7418**
	Flavisolibacter	1.4784	0.6881	0.6485	1.5181	1.9905	1.9370	1.2152	1.1996	0.0334	0.0231	0.0764	1.0033
	Cytophaga	0.6825	0.3882	1.0181	1.8197	2.8745	1.9419	1.7652	2.4370	0.0800	0.0662	0.1110	0.1889
	Parasegetibacter	2.7300	0.6825	0.5121	1.1400	1.9478	0.7659	0.7165	1.1376	5.8296	2.0300	3.7571	5.2767
	Dyadobacter	1.9800	0.7847	0.6066	3.2556	0.9256	1.2963	1.4937	2.2250	1.6879	1.0191	0.9205	1.8413
	Flavihumibacter	4.2526	4.0268	1.5371	0	14.7026	10.7410	4.2174	0	0	0	0	0
	Hymenobacter	0	0	0	0.9653	0.3888	0	0	0.1244	33.1172	0	0	4.4998
	Herpetosiphon	1.0369	0.3810	1.0647	1.4333	0.0982	0.0580	0.0835	0.9208	0	0.0001	0.0003	0
	Exiguobacterium	**4.2490**	**0.4658**	**0.1021**	**3.8165**	**1.1537**	**0.6820**	**0.2956**	**2.0462**	**0.0112**	**0.0284**	**0.5577**	**0.0095**
	Planococcus	4.3455	1.3215	0.7306	1.7555	0.0338	0.0551	0.0066	0.0897	0.0006	0.0018	0	0
	Planomicrobium	8.7198	0.6117	0.4666	3.3492	0.2734	0.1026	0.0135	0.1498	0	0	0	0.0084
	Pirellula	2.6995	0.9100	0.5076	1.8608	1.1090	0.6460	0.6158	1.3552	0.2521	0.0625	0.0923	0.0849
	Rhodopirellula	1.7672	1.0080	0.4000	3.6506	1.0782	0.5030	0.4142	1.4298	0.2836	0.0693	0.0947	0.1423
	Planctomyces	2.1911	0.5784	0.7265	3.5523	0.8233	0.6425	0.5609	2.2828	0.7114	0.1550	0.2735	0.4904
	Thermomonas	1.4241	0.3609	0.3484	1.7131	1.3116	0.4688	0.5666	1.5000	0.0202	0.0044	0.0120	0.2222
	Acinetobacter	**0.7522**	**0.0861**	**0.0793**	**0.0569**	**0.1437**	**0.1629**	**0.0349**	**0.0048**	**0.0244**	**0.0197**	**0.1183**	**0.4461**
	Lysobacter	**1.0715**	**0.5420**	**0.6082**	**1.5487**	**0.5761**	**0.5177**	**0.5921**	**2.0366**	**0.0037**	**0.0013**	**0.0029**	**0.0163**
	Pseudomonas	**1.0003**	**0.0893**	**0.5037**	**0.8170**	**1.1756**	**0.6593**	**0.4577**	**1.5987**	**0.0047**	**0.0050**	**0.0036**	**0.9268**
	Paracoccus	**0.8917**	**0.1596**	**0.2951**	**0.6526**	**0.0405**	**0.0379**	**0.0298**	**0.0533**	**0.0398**	**0.0111**	**0.0193**	**0.0331**
	Luteimonas	1.3667	0.3443	0.4995	1.4898	0.1837	0.2919	0.4063	0.8999	0.0128	0.0051	0.0147	0.0375
	Massilia	5.5094	0.1770	0.2433	1.0643	9.5608	1.9090	0.7565	0.8652	3.1161	0.6753	0.6235	21.0029
	Rhodovulum	**1.7200**	**0.3357**	**0.4368**	**1.3404**	**0.3364**	**0.1867**	**0.1978**	**0.6846**	**0.1043**	**0.0177**	**0.0336**	**0.1813**
	Arenimonas	**0.5756**	**0.3292**	**0.4730**	**0.9443**	**0.5115**	**0.2423**	**0.3631**	**0.8977**	**0.0393**	**0.0194**	**0.0465**	**0.0439**
	Rhodobacter	1.1403	0.2592	0.4075	1.4237	0.3491	0.1797	0.1779	0.5895	0.2638	0.0473	0.0920	0.5640
	Simplicispira	1.0558	0.0389	0.0644	3.4383	0.5670	0.4835	0.1545	1.2656	0.0043	0.0007	0.0065	0.0112
	Devosia	1.0156	1.5680	0.3811	1.0419	0.5720	0.4779	0.5477	1.5326	0.0224	0.0128	0.0470	0.0373
	Aeromonas	0.4331	0	0	0.1902	0.3517	0.0947	0	0	0.0844	0.1419	1.7846	1.3647
	Brevundimonas	1.3765	3.4527	1.2132	0.7275	1.1219	1.1666	0.5178	2.9862	0.6626	1.4429	1.2248	4.4913

	Noviherbaspirillum	2.0790	0.1346	0.3342	1.1326	2.1287	1.0344	0.7536	0.8759	0.6894	0.4573	0.2285	5.4780
	Novosphingobium	1.9751	0.2845	0.3039	0.3592	0.3525	0.1559	0.1781	0.2006	0.4337	0.1432	0.1586	0.4246
	Altererythrobacter	0.6417	0.2341	0.2692	0.2645	0.1728	0.2764	0.1340	0.4091	0.3501	0.1731	0.3974	0.7718
	Pseudoxanthomonas	1.0395	0.5641	0.1394	1.0297	2.3696	0.6407	0.4462	5.9724	0	0	0	4.1476
	Duganella	6.9301	0.2234	0.3680	1.3659	10.0667	1.9871	1.1806	0.8735	2.7800	0.5644	0.7737	13.8147
	Stenotrophomonas	**1.0588**	**0.1911**	**0.1970**	**0.5148**	**1.9007**	**0.8381**	**0.1881**	**6.6692**	**1.4827**	**1.0894**	**0.7598**	**7.6692**
	Sandaracinus	4.0557	0.9365	0.2402	2.2771	1.6493	0.2361	0.3476	0.9571	0	0	0	0
	Haliangium	0.2530	0.1966	0.2514	0.3547	0.3413	0.2595	0.3705	0.3997	0.0014	0	0.0007	0.0082
	Nannocystis	0.9574	0.9830	1.5332	4.3293	1.5278	9.6318	2.7597	8.3251	0	0	0	0
	Phaselicystis	1.6088	0.3984	0.2901	0.9608	1.3329	0.8912	0.6683	0.4486	0	0	0.0034	0
	Microbacterium	**1.2896**	**0.5975**	**0.8004**	**0.8737**	**0.3632**	**0.5531**	**0.3489**	**0.5908**	**0.0730**	**0.2117**	**0.1969**	**1.4769**
	Nocardioides	**2.0148**	**0.7967**	**1.3411**	**1.3563**	**1.7928**	**2.3258**	**1.6017**	**2.7346**	**0.0298**	**0.0743**	**0.1670**	**0.1546**
	Oerskovia	2.1174	2.5717	0.9814	1.4105	0.4306	0.6772	0.7805	1.6743	0.0053	0	0.1998	0
	Agromyces	**1.5638**	**0.3646**	**0.6647**	**0.6126**	**0.0086**	**0.0361**	**0.0622**	**0.0682**	**0.0027**	**0.0027**	**0.0032**	**0.0034**
	Lysinimicrobium	1.0093	0.2164	0.9067	0.9436	0.1260	0.1370	0.6389	0.2474	0.0197	0.0219	0.0539	0.0368
	Ilumatobacter	1.1232	1.0430	0.8145	1.4730	0.1051	0.1000	0.1044	0.0866	0.1832	0.3517	0.0869	0.1842
	Demequina	2.3856	1.2330	1.5493	2.0398	1.8142	1.6089	5.2232	3.2216	0.0371	0.0443	0.0538	0.0272
	Frondihabitans	3.0243	1.7147	1.0222	1.5412	16.7145	5.1235	5.9730	4.5725	0	0	0.0018	0.0600
	Streptomyces	**0.0918**	**0.1460**	**0.2332**	**0.0773**	**0.0616**	**0.0502**	**0.0374**	**0.0031**	**0.0021**	**0.0010**	**0.0008**	**0.0002**
	Candidatus_Aquiluna	0.3470	0.4076	0.3883	0.3268	0.5078	1.0877	0.7423	0.6856	2.8504	6.8498	1.4132	1.3350
	Yonghaparkia	**0.7753**	**0.3925**	**0.5433**	**1.2843**	**0.4054**	**2.5319**	**2.2766**	**30.2720**	**0.0517**	**0.0562**	**0.5271**	**1.8515**
	Paeniglutamicibacter	1.2899	1.1267	2.3125	1.1978	0.0000	0.0069	0.0373	0.0076	0	0.0012	0.0172	0
	Flavobacterium	**0.4154**	**0.5847**	**0.2607**	**1.0837**	**0.2647**	**0.1461**	**0.1019**	**0.7505**	**0.0764**	**0.7701**	**0.3620**	**5.3491**
	Algoriphagus	5.5664	3.0357	1.2265	5.2519	2.8347	2.2505	0.5927	3.3296	1.2141	0.3872	0.2567	3.1357
	Sediminicola	0.7961	0.6449	1.7125	3.0277	6.3231	0.2474	2.4578	1.6826	0.0002	0.0001	0.0006	0.0000
	Arenibacter	0.3702	0.5859	0.7125	0.4806	0.9062	1.0166	0.6454	0.4938	0.0086	0.0243	0.0157	0.0019
	Winogradskyella	0.6305	0.3549	0.6135	1.0725	1.1885	0.8747	0.9010	0.9696	0.1740	0.2277	0.2119	0.6387
	Formosa	0.1434	0.2184	0.2857	0	0.4904	0.4601	0.3159	0	0.0131	0.0099	0.0063	0
	Maribacter	1.0868	0	0	3.9152	5.5194	0	0	10.7274	0.0445	0	0	0.0747
	Subsaxibacter	0.1969	0.1243	0.2542	0.6113	0.5161	0.4220	0.1734	0.2332	0.0246	0.0326	0.0070	0.0322
	Gaetbulibacter	0	0.0923	0.2642	0.3585	0.1886	0.5669	0.1742	0.5470	0.1136	0.2073	0.0230	0.0711
	Pedobacter	4.9394	0.8554	1.0435	0.3600	0.4620	0.0705	7.1915	0.3686	0.0096	0.0046	0.0126	0

	Planococcus	**2.3525**	**1.3769**	**2.2139**	**3.6392**	**0.0000**	**0.0024**	**0.0047**	**0**	**0.0091**	**0.0025**	**0.0005**	**0.0040**
	Exiguobacterium	**11.0284**	**6.4515**	**7.1796**	**4.8097**	**0.0687**	**0.0367**	**0.0229**	**0.0285**	**0.1202**	**0.0136**	**0.0040**	**0.0053**
	Planomicrobium	0.6728	1.5103	1.9853	1.7281	0	0	0	0	0.0072	0.0056	0.0049	0.0090
	Paracoccus	**0.1181**	**0.1015**	**0.1891**	**0.2086**	**0.0047**	**0.0099**	**0.0088**	**0.0116**	**0.0072**	**0.0126**	**0.0061**	**0.0117**
	Methylotenera	0.0394	0.0778	0.5963	0.9334	0.0907	0.0357	1.1468	0.3095	0.0095	0.0671	4.7610	0.2242
	Altererythrobacter	0.4110	0.1399	0.3905	0.5008	0.0479	0.0430	0.0625	0.0554	0.0492	0.0450	0.0216	0.0265
	Sandaracinus	1.0376	0.6421	0	0	0	0	0	0	0	0	0	0
	Lysobacter	**2.0880**	**0.9758**	**0.9938**	**0.4799**	**1.1324**	**0.4366**	**0.8155**	**0.0953**	**0**	**0**	**0**	**0**
	Erythrobacter	0.2794	0.0838	0.2972	0.4260	0.0588	0.0246	0.0762	0.1029	0.0626	0.0511	0.0310	0.0518
	Devosia	3.2318	2.0438	1.2514	0.9284	0.1598	0.0505	0.1234	0.0442	0.0063	0.0122	0.0061	0.0020
	Albirhodobacter	0.3501	0.9831	0.5943	0.3975	0.0065	0.0095	0	0.0064	0.0102	0.0138	0.0017	0.0060
	Rheinheimera	2.2178	0.7184	1.0380	7.6962	0	0	0.0566	0	0.0061	0.0038	0.0748	0.6618
	Arenimonas	**0.5508**	**1.2067**	**0.3237**	**0.4040**	**0**	**0**	**0.0109**	**0**	**0.0005**	**0.0141**	**0.0029**	**0.0010**
	Loktanella	0.1786	0.2139	0.1188	0.3753	0.0696	0.0760	0.0224	0.0472	0.2940	0.5384	0.1103	0.4445
	Rhodovulum	**0.1978**	**0.2463**	**0.2611**	**0.2359**	**0.0317**	**0.0355**	**0.0075**	**0.0445**	**0.0250**	**0.0328**	**0.0089**	**0.0349**
	Brevundimonas	1.8792	2.6019	0.5111	1.6637	6.5188	4.3516	9.3588	7.5399	0.1043	0.0144	3.1787	0.0535
	Ruegeria	0.3880	0.2838	0.2234	0.3451	0.0543	0.0410	0.0161	0.0511	0.0356	0.0533	0.0131	0.0538
	Pseudomonas	**3.9622**	**4.1372**	**0.6992**	**0.3903**	**1.0705**	**1.5631**	**0.6966**	**0.0369**	**0.0302**	**0.0597**	**0.0091**	**0.2918**
	Neorhizobium	3.1197	4.3001	1.0435	0.3310	0	0	0	0	0	0	0	0
	Variovorax	0.7655	0.6832	0	0.7224	42.0104	1.9005	0	4.7198	0.0014	0.0036	0	0.0965
	Acinetobacter	**2.4792**	**2.3395**	**0.7084**	**0.5348**	**0.1943**	**0.1546**	**0.1610**	**0.6849**	**0.0111**	**0.2264**	**0.0463**	**80.6107**
	Hydrogenophaga	0.1150	0.3784	1.2385	1.2385	0.0651	0.0805	0.7351	0.9526	0.2546	0.6419	3.5329	5.8548
	Psychrobacter	0.5169	0.9076	0.2043	0.6192	0	0	0	0	0.0564	0.0030	0.0006	0.0322
	Roseicyclus	0.4880	0.4701	0.2534	0.8515	0.6962	0.5623	0.1625	0.3897	3.0997	5.5321	0.9337	3.3537
	Lutimaribacter	0.8201	0.9499	0.4617	1.2901	1.5204	1.1486	0.2035	0.7361	6.2641	14.4081	0.9345	2.5092
	Stenotrophomonas	**2.2227**	**6.2684**	**1.3119**	**1.3159**	**11.3877**	**20.2319**	**19.0116**	**24.8925**	**0.0898**	**0.0994**	**3.9838**	**1.8698**
	Delftia	0	0	0	0	0	0	0	0	0	0	0	0
	Marinobacterium	0	0	0	0	0	0	2.2936	0	0	0	54.6086	0

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