

## Supporting Information

### Effects of disinfectants and particles on occurrence of different microorganisms in drinking water distribution systems

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**Table S1** The primers, probes and amplification programs of opportunistic pathogens

Targeted microbe	Targeted genes	Primer sequences	Size (bp)	Program
<i>Legionella spp</i>	23S rRNA	F: CCCATGAAGCCCGTTGAA R:ACAATCAGCCAATTAGTACGAGTTAGC P:TCCACACCTCGCCTATCAACGTCGTAGT	92	95°C for 2 min, 40 cycles of 95°C for 5 s and 58.5°C for 10 s <sup>1</sup>
<i>Legionella pneumophila</i>	<i>mip</i>	F:AAAGGCATGCAAGACGCTATG R:GAAACTTGTTAAGAACGTCTTTCA TTTG P:TGGCGCTCAATTGGCTTTAACCGA	78	95°C for 2 min, 40 cycles of 95°C for 5 s and 60°C for 10 s <sup>1</sup>
<i>Mycobacteria spp.</i>	16S rRNA	F:CCTGGGAAACTGGGTCTAAT R: CGCACGCTCACAGTTA P:TTTCACGAACAACGCGACAAACT	462	95°C for 2 min, 40 cycles of 95°C for 5 s, 55°C for 15 s and 72°C for 10 s <sup>1</sup>
<i>Mycobacteria avium</i>	16S rRNA	F : AGAGTTTGATCCTGGCTCAG R : ACCAGAAGACATGCGTCTTG	180	98°C for 2 min, 40 cycles of 98°C for 5 s and 68°C for 18 s <sup>1</sup>
<i>Pseudomonas aeruginosa</i>	<i>oprI</i>	F:GACGTACACGCGAAAGACCT R:GCCCAGAGCCATGTTGTA CT	99	95°C for 5 min, 40 cycles: 95°C for 15 s, 60°C for 45 s <sup>2</sup>
<i>Acanthamoeba spp</i>	18S rRNA	F: TTTTCAGTTGGTTTTGGCAG R: GGTCGGCATCGTTTATGG	219	95°C for 2 min, 40 cycles of 95°C for 5 s and 60°C for 10 s <sup>3</sup>
<i>Harmanella vermiformis</i>	18S rRNA	F: TTACGAGGTCAGGACACTGT R: GACCATCCGGAGTTCTCG	512	98°C for 2 min, 40 cycles of 98°C for 5 s, 72°C for 18 s <sup>1</sup>
Total bacteria	16S rRNA	F: CGGTGAATACGTTTCYCGG R: GGYTACCTTGTTACGACTT P: CTTGTACACACCGCCCGTC	124	95°C for 30 s, 35 cycles of 95°C for 15 s and 56°C for 60 s <sup>1</sup>

**Table S2** Quantification limits and amplification efficiencies for qPCR

Target microorganism	Quantification limit (gene copies/ $\mu$ L DNA)	Slope	Amplification efficiency (%)	R <sup>2</sup>
<i>Legionella</i> spp.	4	-3.410	96.43	0.9962
<i>Legionella pneumophila</i>	6	-3.411	96.43	0.9561
<i>Mycobacteria</i> spp.	7	-3.331	99.62	0.9918
<i>Mycobacterium avium</i>	4	-3.388	97.33	0.9779
<i>Pseudomonas aeruginosa</i>	67	-3.420	96.06	0.9921
<i>Acanthamoeba</i> spp.	18	-3.516	92.49	0.9924
<i>Harmanella vermiformis</i>	16	-3.361	98.38	0.9813
Total bacteria (16S rRNA)	8	-3.360	98.43	0.9910

Note: The amplification efficiency was calculated by the formula: Amplification efficiency =  $10^{-1/\text{slope}-1}$

**Table S3** Characteristics of water quality in different regions

Area	Turbidity (NTU)	Temperature (°C)	pH	TOC (mg/L)	DO (mg/L)	Total Fe (µg/L)	particles number
FC	0.30±0.28	18.87±7.12	8.05±0.33	1.88±0.61*	9.37±2.04	63.45±50.12	492±447
TC	0.26±0.15	19.78±6.82	8.06±0.32	2.31±0.45*	9.36±1.5	59.51±40.76	389±535

\*, significant difference with 95% confidence ( $p < 0.05$ ) in two areas.

**Table S4** Number of particles with different sizes

Area	2~3 $\mu\text{m}$	3~5 $\mu\text{m}$	5~7 $\mu\text{m}$	7~10 $\mu\text{m}$	10~15 $\mu\text{m}$	15~20 $\mu\text{m}$	20~25 $\mu\text{m}$	>25 $\mu\text{m}$
FC	164 $\pm$ 149	222 $\pm$ 223	57 $\pm$ 57	30 $\pm$ 32	13 $\pm$ 18	5 $\pm$ 6	1 $\pm$ 2	1 $\pm$ 2
TC	136 $\pm$ 173	168 $\pm$ 236	44 $\pm$ 65	25 $\pm$ 42	10 $\pm$ 19	4 $\pm$ 6	1 $\pm$ 2	2 $\pm$ 2

The value is expressed as mean $\pm$ SD. \*, significant difference with 95% confidence (p < 0.05) in the two areas.

**Table S5** Pearson correlation analysis between the microorganisms in all samples (n = 98).

	16S rRNA	Myc	Ma	Leg	Lp	Ps	Ac	Hv
16S rRNA	1	<b>0.323</b> (p=0.001)	0.149 (p=0.142)	<b>0.477</b> (p=0)	0.109 (p=0.285)	<b>0.382</b> (p=0)	<b>0.408</b> (p=0)	<b>0.228</b> (p=0.024)
Myc		1	<b>0.335</b> (p=0.001)	<b>0.343</b> (p=0.001)	-0.059 (p=0.562)	0.094 (p=0.356)	<b>0.563</b> (p=0)	-0.001 (p=0.99)
Ma			1	0.106 (p=0.301)	-0.023 (p=0.822)	0.19 (p=0.062)	<b>0.286</b> (p=0.004)	0.049 (p=0.63)
Leg				1	<b>0.208</b> (p=0.04)	0.009 (p=0.932)	<b>0.415</b> (p=0)	0.107 (p=0.294)
Lp					1	0.106 (p=0.3)	0.062 (p=0.545)	0.171 (p=0.093)
Ps						1	0.103 (p=0.315)	0.06 (p=0.55)7
Ac							1	0.159 (p=0.119)
Hv	□	□	□	□	□	□	□	1

The bold numbers represented significance under  $p < 0.05$ . Myc: *Mycobacterium* spp., Ma: *M. avium*, Leg: *Legionella* spp., Lp: *L. pneumophila*, Ps: *P. aeruginosa*, Ac: *Acanthamoeba* spp., Hv: *H. vermiformis*.

**Table S6** Pearson correlation analysis between the microorganisms in FC areas  
(n=60).

	16S rRNA	Myc	Ma	Leg	Lp	Ps	Ac	Hv
16S rRNA	1	<b>0.300</b> (p=0.020)	0.157 (p=0.232)	<b>0.489</b> (p=0)	-0.029 (p=0.825)	<b>0.382</b> (p=0.003)	<b>0.460</b> (p=0)	0.213 (p=0.102)
Myc		1	<b>0.417</b> (p=0.001)	<b>0.272</b> (p=0.035)	-0.085 (p=0.517)	0.030 (p=0.818)	<b>0.558</b> (p=0)	-0.030 (p=0.819)
Ma			1	0.122 (p=0.355)	-0.185 (p=0.157)	0.225 (p=0.085)	<b>0.311</b> (p=0.015)	-0.037 (p=0.777)
Leg				1	0.245 (p=0.059)	0.012 (p=0.930)	<b>0.287</b> (p=0.026)	0.166 (p=0.204)
Lp					1	0.064 (p=0.627)	0.036 (p=0.787)	0.150 (p=0.254)
Ps						1	0.143 (p=0.277)	0.216 (p=0.098)
Ac							1	0.078 (p=0.553)
Hv								1

The bold numbers represented significance under  $p < 0.05$ . Myc: *Mycobacterium* spp., Ma: *M. avium*, Leg: *Legionella* spp., Lp: *L. pneumophila*, Ps: *P. aeruginosa*, Ac: *Acanthamoeba* spp., Hv: *H.vermiformis*.

**Table S7** Pearson correlation analysis between the microorganisms in TC areas

(n=38).

	16S rRNA	Myc	Ma	Leg	Lp	Ps	Ac	Hv
16S rRNA	1	0.236 (p=0.154)	0.312 (p=0.056)	0.280 (p=0.089)	<b>0.358</b> <b>(p=0.027)</b>	<b>0.397</b> <b>(p=0.014)</b>	0.123 (p=0.463)	0.152 (p=0.363)
Myc		1	0.314 (p=0.055)	<b>0.348</b> <b>(p=0.032)</b>	-0.070 (p=0.675)	0.186 (p=0.263)	<b>0.498</b> <b>(p=0.001)</b>	-0.064 (p=0.705)
Ma			1	0.228 (p=0.168)	0.259 (p=0.116)	0.161 (p=0.336)	<b>0.392</b> <b>(p=0.015)</b>	0.226 (p=0.173)
Leg				1	0.099 (p=0.555)	-0.047 (p=0.779)	<b>0.500</b> <b>(p=0.001)</b>	-0.108 (p=0.518)
Lp					1	0.164 (p=0.324)	0.048 (p=0.774)	0.170 (p=0.307)
Ps						1	-0.001 (p=0.993)	-0.173 (p=0.300)
Ac							1	0.165 (p=0.323)
Hv								1

The bold numbers represented significance under  $p < 0.05$ . Myc: *Mycobacterium* spp., Ma: *M. avium*, Leg: *Legionella* spp., Lp: *L. pneumophila*, Ps: *P. aeruginosa*, Ac: *Acanthamoeba* spp., Hv: *H. vermiformis*.



**Table S8** Pearson correlation between HPC and other indicators (FC areas: n=60, TC areas: n=38).

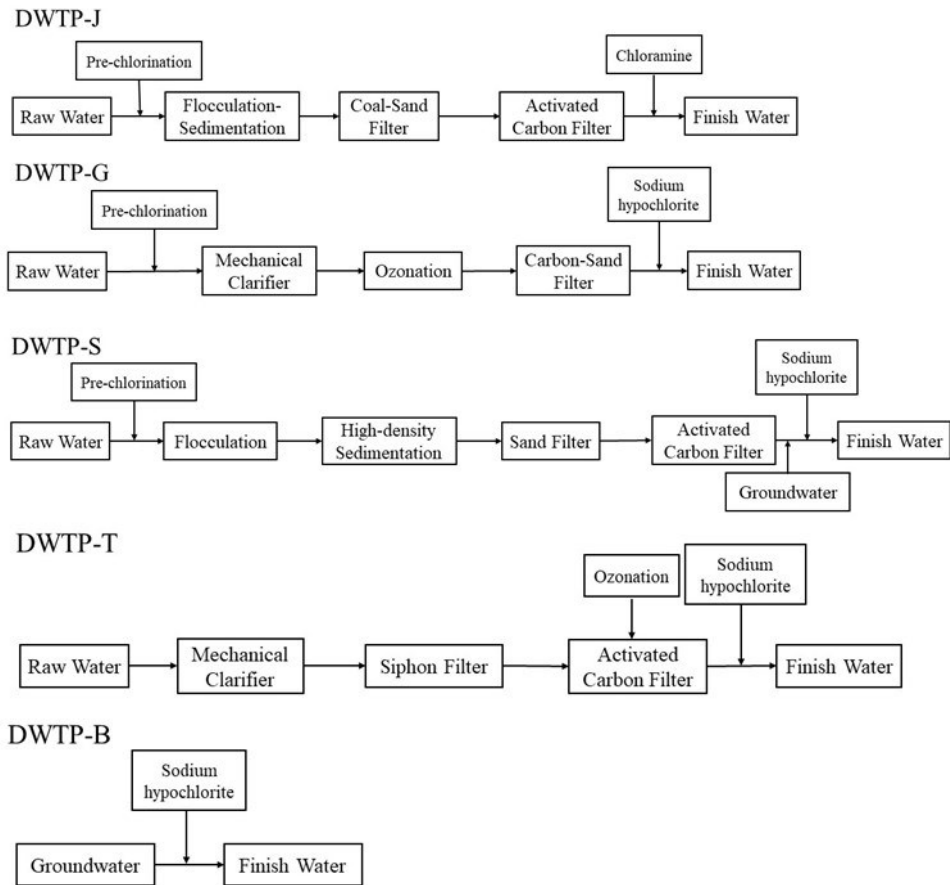
Area	Tur	Temp	pH	TOC	DO	Total Fe	PN
FC	<b>0.279</b>	0.056	-0.091	<b>0.355</b>	0.013	<b>0.417</b>	0.156
	<b>(p=0.031)</b>	(p=0.671)	(p=0.490)	<b>(p=0.005)</b>	(p=0.921)	<b>(p=0.001)</b>	(p=0.232)
TC	<b>0.334</b>	<b>0.348</b>	<b>-0.336</b>	-0.117	<b>0.364</b>	<b>0.482</b>	0.125
	<b>(p=0.040)</b>	<b>(p=0.032)</b>	<b>(p=0.039)</b>	(p=0.485)	<b>(p=0.025)</b>	<b>(p=0.002)</b>	(p=0.455)

Tur: Turbidity, Temp: temperature, PN: particles number.

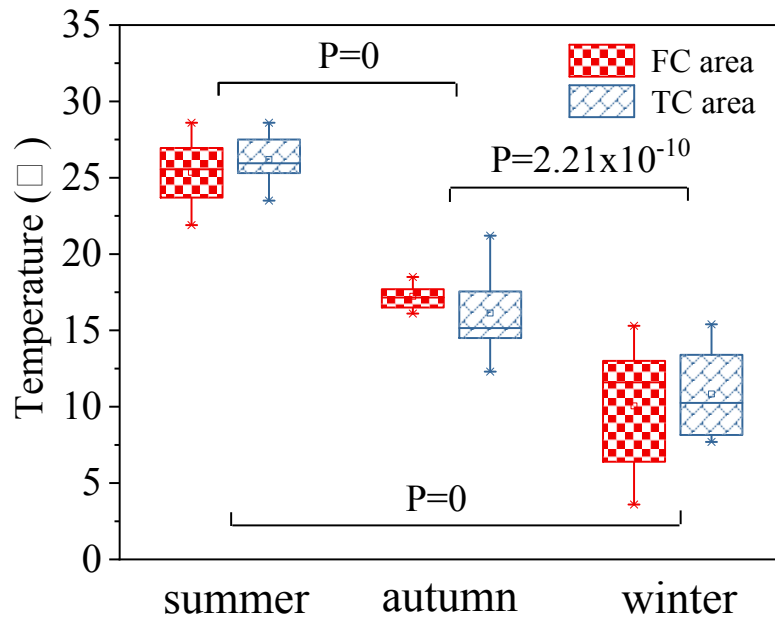
**Table S9** The Pearson correlation between microorganisms and water quality indicators (n=98).

□	Turbidity	Total iron	Particles number	2~3μm	3~5μm	5~7μm	7~10μm	10~15μm	15~20μm	20~25μm	>25μm
16S rRNA	0.196 (p=0.054)	<b>0.349</b> (p=0)	0.026 (p=0.801)	0.004 (p=0.972)	0.024 (p=0.812)	0.04 (p=0.693)	0.08 (p=0.434)	0.078 (p=0.445)	0.052 (p=0.612)	-0.08 (p=0.435)	-0.178 (p=0.079)
Myc	<b>0.203</b> (p=0.045)	0.025 (p=0.806)	0.176 (p=0.084)	0.195 (p=0.055)	0.137 (p=0.179)	0.161 (p=0.114)	<b>0.216</b> (p=0.033)	<b>0.204</b> (p=0.044)	<b>0.219</b> (p=0.031)	<b>0.201</b> (p=0.047)	0.136 (p=0.182)
Ma	<b>0.206</b> (p=0.042)	0.058 (p=0.569)	<b>0.2420</b> (p=0.017)	<b>0.238</b> (p=0.018)	<b>0.217</b> (p=0.032)	<b>0.227</b> (p=0.025)	<b>0.248</b> (p=0.014)	<b>0.260</b> (p=0.01)	<b>0.298</b> (p=0.003)	<b>0.248</b> (p=0.014)	0.103 (p=0.315)
Leg	<b>0.296</b> (p=0.003)	<b>0.230</b> (p=0.022)	0.144 (p=0.158)	0.171 (p=0.093)	0.106 (p=0.299)	0.105 (p=0.302)	<b>0.200</b> (p=0.048)	0.194 (p=0.055)	0.179 (p=0.079)	0.142 (p=0.162)	0.091 (p=0.373)
Lp	-0.032 (p=0.757)	0.056 (p=0.586)	<b>-0.206</b> (p=0.042)	-0.178 (p=0.079)	-0.162 (p=0.111)	<b>-0.220</b> (p=0.03)	<b>-0.348</b> (p=0)	<b>-0.353</b> (p=0)	<b>-0.316</b> (p=0.002)	<b>-0.352</b> (p=0)	<b>-0.336</b> (p=0.001)
Ps	<b>0.214</b> (p=0.034)	<b>0.228</b> (p=0.024)	0.043 (p=0.671)	0.036 (p=0.723)	0.112 (p=0.274)	0.053 (p=0.601)	-0.198 (p=0.051)	<b>-0.273</b> (p=0.007)	-0.185 (p=0.068)	-0.135 (p=0.186)	-0.182 (p=0.072)
Ac	<b>0.314</b> (p=0.002)	0.116 (p=0.257)	<b>0.300</b> (p=0.003)	<b>0.301</b> (p=0.003)	<b>0.285</b> (p=0.005)	<b>0.289</b> (p=0.004)	<b>0.260</b> (p=0.01)	<b>0.203</b> (p=0.045)	0.186 (p=0.067)	0.174 (p=0.086)	0.145 (p=0.155)
Hv	-0.006 (p=0.953)	0.102 (p=0.318)	-0.036 (p=0.724)	-0.02 (p=0.843)	0.02 (p=0.842)	-0.052 (p=0.614)	<b>-0.230</b> (p=0.023)	<b>-0.280</b> (p=0.005)	<b>-0.245</b> (p=0.015)	<b>-0.215</b> (p=0.033)	<b>-0.273</b> (p=0.006)
HPC	<b>0.529</b> (p=0)	<b>0.390</b> (p=0)	0.034 (p=0.742)	0.064 (p=0.533)	0.044 (p=0.665)	0.013 (p=0.902)	-0.062 (p=0.546)	-0.094 (p=0.356)	-0.069 (p=0.498)	-0.086 (p=0.397)	-0.116 (p=0.254)

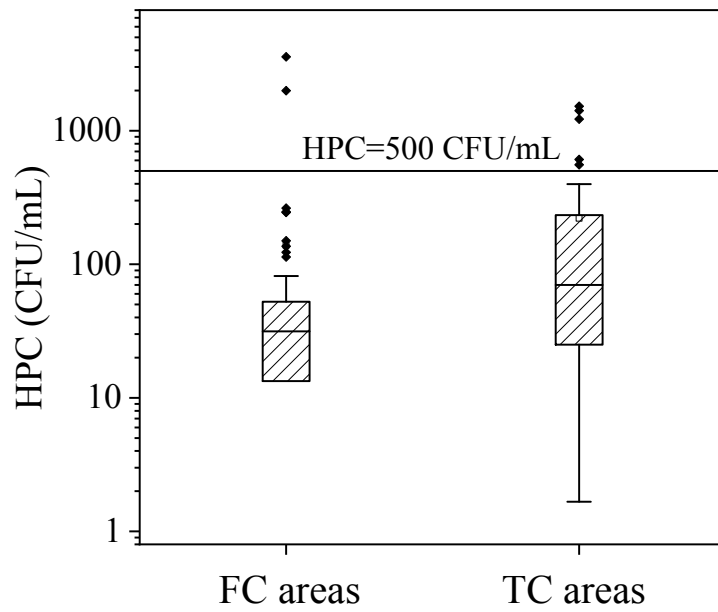
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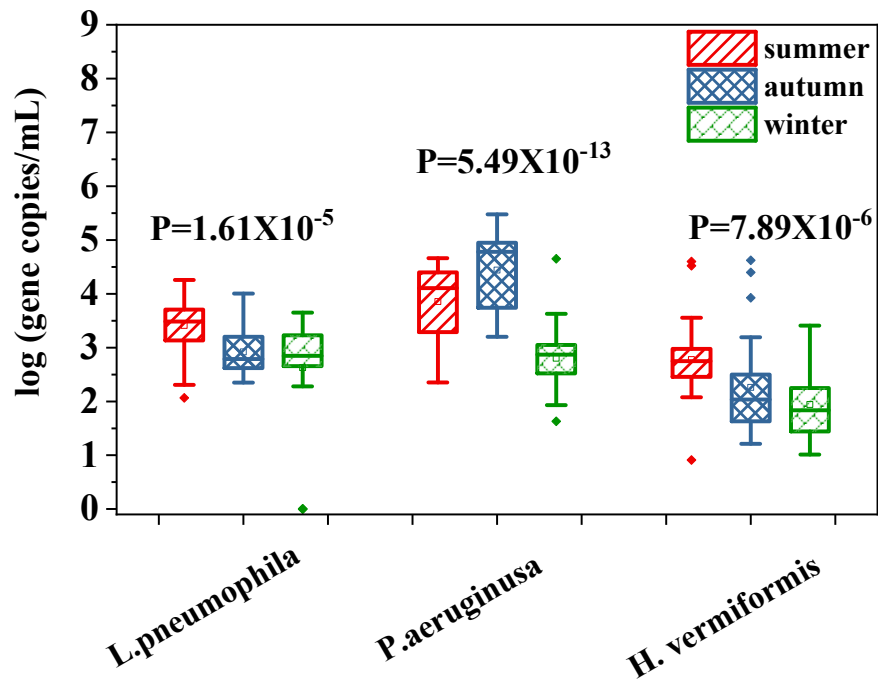
**Fig. S1** The main water treatment processes for the five drinking water treatment plants.



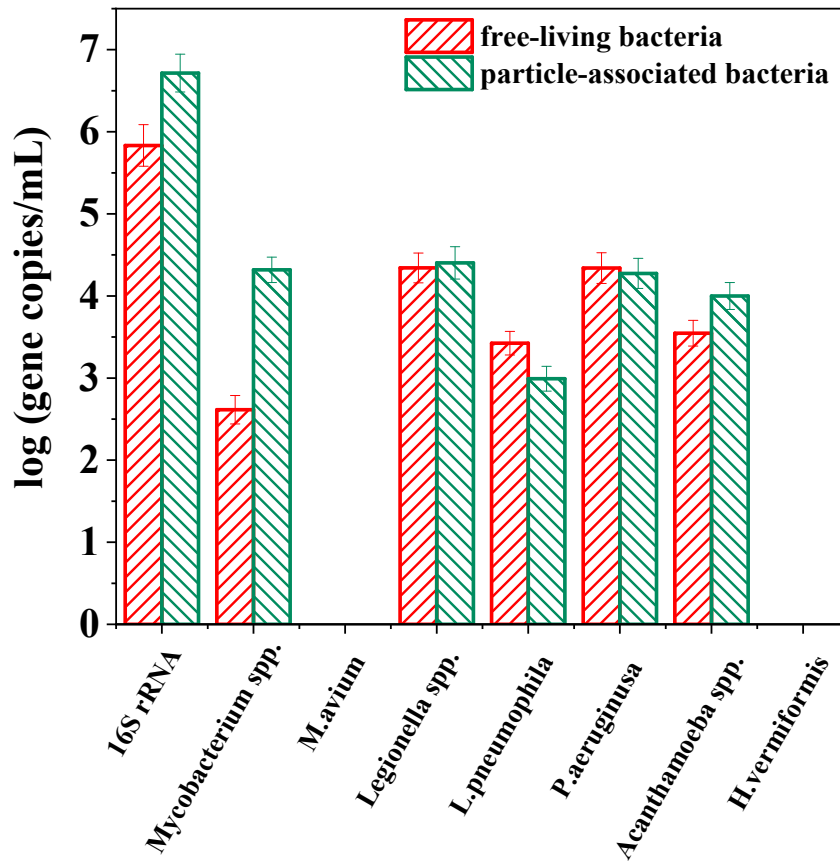
**Fig. S2** Temperature profiles in different seasons of the two areas.



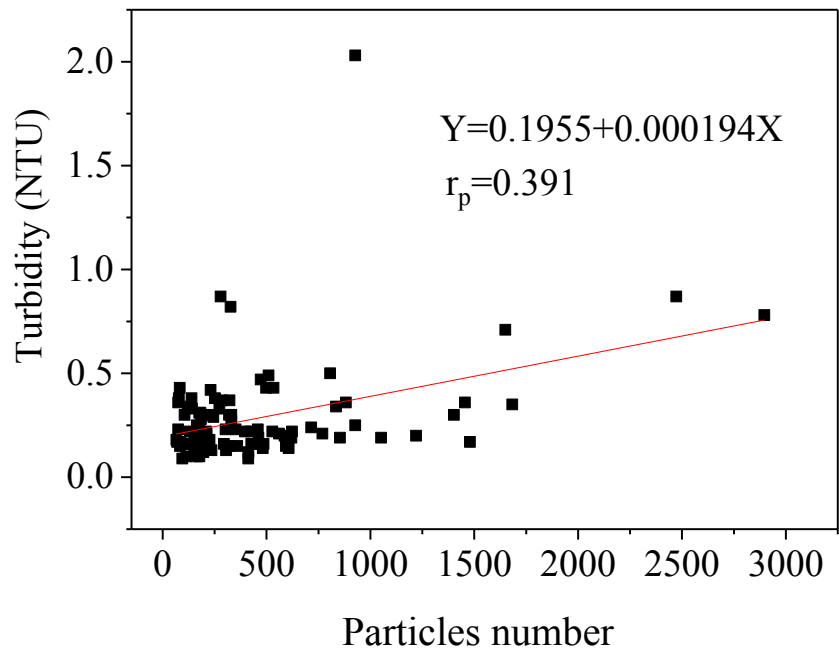
**Fig. S3** The distribution of HPC in free chlorine (FC) areas and total chlorine (TC) areas.



**Fig. S4** The seasonal differences of *L. pneumophila*, *P. aeruginosa*, and *H. vermiformis* for all the samples.



**Fig. S5** The free-living and particle-associated bacteria in tap water of drinking water distribution systems.



**Fig. S6** The Pearson's Rank correlation of particles number and turbidity. ( $r_p$ )



## References

- 1 H. Wang, M. Edwards, J.O. Falkinham and A. Pruden, Molecular survey of the occurrence of *legionella* spp., *mycobacterium* spp., *pseudomonas aeruginosa*, and amoeba hosts in two chloraminated drinking water distribution systems, Appl. Environ. Microbiol, 2012, 78, 6285–6294.
- 2 H.B. Wang, C. Hu, S.N. Zhang, L.Z. Liu and X.C. Xing, Effects of O3/Cl2 disinfection on corrosion and opportunistic pathogens growth in drinking water distribution systems, J. Environ. Sci. (China), 2018, 73, 38–46.
- 3 L.Z. Liu, X.C. Xing, C. Hu and H.B. Wang, One-year survey of opportunistic premise plumbing pathogens and free-living amoebae in the tap-water of one northern city of China, J. Environ. Sci. (China), 2019, 77, 20–31.