Supplementary Materials

Occurrence of viable but non-culturable (VBNC) pathogenic bacteria in tap water of public places

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Table S1. Linear distance bewteen each sampling points (Unit: km)

Sites	DWTP	Railway station	Campus	Hospital	Shopping mall	Institute
DWTP	**0**	**3.21**	**1.58**	**3.16**	**4.20**	**3.06**
Railway station		**0**	**3.99**	**3.87**	**6.95**	**2.88**
Campus			**0**	**2.45**	**2.98**	**2.47**
Hospital				**0**	**1.52**	**4.89**
Shopping mall					**0**	**5.01**
Institute						**0**

Table S2. Identification results of suspicious colonies growth on each selective medium

Numbers	Strains	Identities
1	*Pseudomonas putida*	99.93%
2	*Pseudomonas* sp.	99.93%
3	*Pseudomonas putida*	99.93%
4	*Pseudomonas* sp.	99.79%
5	*Stenotrophomonas* sp.	99.86%
6	*Leclercia adecarboxylata*	99.93%
7	*Pseudomonas putida*	99.86%
8	*Bacilus fexus*	99.93%
9	*Pseudomonas putida*	99.86%
10	*Pseudomonas putida*	99.86%
11	*Acinetobacter baumannii*	99.79%
12	*Acinetobacter* sp.	97.01%
13	*Paenibacillus alvei*	99.76%
14	*Staphylococcus epidermidis*	99.93%
15	*Bacterium strain*	100%
16	*P. aeruginosa* (CN medium, May)	99.93%
17	*P. aeruginosa* (CN medium, May)	99.86%
18	*Pseudomonas* sp.	99.86%
19	*P. aeruginosa* (m-TEC medium, May)	100%
20	*Staphylococcus hominis*	100%
21	*Pseudomonas putida*	100%
22	*Bacillus flexus*	100%
23	*P. aeruginosa* PAO1 (CN medium, June)	99.93%
24	*P. aeruginosa* (CN medium, June)	99.93%
25	*Pseudomonas putida*	100%
26	*P. aeruginosa* (m-TEC medium, June)	100%
27	*Pseudomonas putida*	100%
28	*P. aeruginosa* (SS medium, June)	100%
29	*Bacillus* sp.	100%
30	*Bacillus* sp.	100%
31	*Enterobacter tabaci*	100%
32	*Staphylococcus epidermidis*	100%

Table S3. Standard curves of gene plasmid copy numbers and CT values (Guo et al., 2020)**.**

Bacteria	**Standard curve formula**	**R^2**	**Amplification efficiency**
Total bacteria (16S rRNA)	$y=-3.363x+39.055$	0.999	98.31%
E. coli	$y=-2.793x+37.298$	0.997	128.1%
E. faecalis	$y=-3.085x+41.927$	0.990	110.9%
P. aureginosa	$y=-2.962x+42.835$	0.998	117.6%
Salmonella sp.	$y=-3.028x+40.322$	0.996	113.9%
Shigella sp.	$y=-3.030x+39.532$	0.998	113.8%
L. pneumophila	$y=-3.215x+43.782$	0.999	104.7%

Table S4. Standard curves of specific gene copies and viable cell numbers after serial dilutions, by TaqMan-qPCR (Guo et al., 2020).

Bacteria	**Standard curve formula**	**R^2**
E. coli	$y=0.86x+0.83$	0.999
E. faecalis	$y=0.92x-0.29$	0.999
P. aureginosa	$y=0.89x-0.94$	0.998
Salmonella sp.	$y=0.94x+0.57$	0.999
Shigella sp.	$y=0.99x-0.42$	0.988

Table S5. The frequency of detection of each pathogenic bacteira in all tap water samples

Sampling points	**The frequency of detection (FOD) % (total samples n=45)**					
	E. coli	***E. faecalis***	***P. aureginosa***	***Salmonella* sp.**	***Shigella* sp.**	***L. pneumophila***
Railway station	17.78	6.67	4.44	6.67	11.11	2.22
Campus	6.67	8.89	6.67	6.67	13.33	0.00
Hospital	11.11	8.89	0.00	6.67	0.00	0.00
Shopping mall	15.56	17.78	4.44	6.67	13.33	11.11
Institution	13.33	4.44	4.44	6.67	2.22	0.00
Total	64.45	46.67	19.99	33.35	39.99	13.33

Table S6. Corrlelations between target organisms and abiotic parameteris in tap water samples collected from different public places

Physiochemical parameters	**16S rRNA**	**R$_2$A**	***E. coli***	***E. faecalis***	***P. aureginosa***	***Salmonella* sp.**	***Shigella* sp.**	***L. pneumophila***
Resifual chlorine	$r_s = -0.260$	**$r_s = -0.505$**	$r_s = -0.145$	$r_s = 0.127$	**$r_s = -0.301$**	$r_s = -0.076$	$r_s = 0.104$	$r_s = 0.137$
	$P = 0.085$	**$P < 0.001$**	$P = 0.342$	$P = 0.406$	**$P < 0.05$**	$P = 0.622$	$P = 0.498$	$P = 0.371$
TOC	$r_s = -0.119$	**$r_s = -0.390$**	$r_s = -0.046$	$r_s = 0.104$	$r_s = 0.286$	$r_s = -0.028$	$r_s = 0.228$	$r_s = -0.287$
	$P = 0.437$	**$P < 0.05$**	$P = 0.763$	$P = 0.496$	$P = 0.057$	$P = 0.853$	$P = 0.132$	$P = 0.056$
Turbidity	$r_s = -0.242$	$r_s = -0.041$	$r_s = -0.168$	$r_s = -0.220$	$r_s = 0.215$	$r_s = -0.007$	$r_s = -0.126$	**$r_s = -0.357$**
	$P = 0.110$	$P = 0.791$	$P = 0.270$	$P = 0.146$	$P = 0.156$	$P = 0.965$	$P = 0.410$	**$P < 0.05$**
NO_3-N	**$r_s = 0.420$**	$r_s = 0.133$	$r_s = -0.239$	$r_s = -0.161$	$r_s = -0.020$	$r_s = -0.059$	$r_s = 0.014$	**$r_s = 0.403$**
	$P < 0.05$	$P = 0.382$	$P = 0.115$	$P = 0.290$	$P = 0.898$	$P = 0.698$	$P = 0.927$	**$P < 0.05$**
DO	$r_s = 0.237$	$r_s = -0.177$	**$r_s = -0.615$**	$r_s = 0.021$	$r_s = -0.113$	$r_s = 0.199$	$r_s = 0.235$	$r_s = -0.021$
	$P = 0.117$	$P = 0.244$	**$P < 0.001$**	$P = 0.893$	$P = 0.461$	$P = 0.191$	$P = 0.121$	$P = 0.891$
pH	$r_s = -0.056$	$r_s = 0.241$	$r_s = -0.090$	$r_s = 0.076$	$r_s = 0.160$	$r_s = -0.214$	$r_s = -0.006$	$r_s = -0.059$
	$P = 0.717$	$P = 0.111$	$P = 0.557$	$P = 0.619$	$P = 0.294$	$P = 0.158$	$P = 0.968$	$P = 0.701$
Temperature	$r_s = -0.237$	$r_s = 0.063$	**$r_s = 0.619$**	$r_s = 0.075$	$r_s = -0.043$	**$r_s = -0.314$**	$r_s = -0.087$	$r_s = -0.024$
	$P = 0.116$	$P = 0.680$	**$P < 0.001$**	$P = 0.626$	$P = 0.778$	**$P < 0.05$**	$P = 0.571$	$P = 0.878$

Note: Correlations were analyzed using the nonparametric spearman rank correlation method

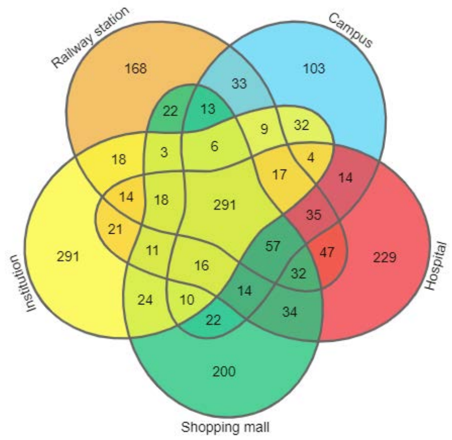

Fig. S1. Venn diagram of detected taxa among each tap water in the five public places.

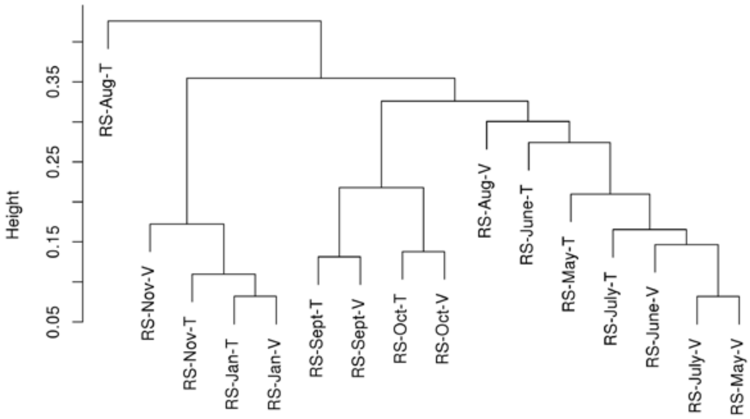

Fig. S2. Hierarchical clustering of the tap water samples for railway station (RS) based on the average linkage clustering method. The branch length describes the difference between the samples. “T” and “V” represented total (non-PMA treatment) and viable (PMA treatment) bacterial communities.

Reference

Guo L, Wan K, Zhu J, Ye C, Chabi K, Yu X (2020). Detection and Distribution of VBNC/Viable Pathogenic Bacteria in Full-Scale Drinking Water Treatment Plants. Journal of Hazardous Materials, 124335