

Section S1 High-throughput sequencing

The PCR amplification of 16S rRNA gene was performed as follows: initial denaturation at 95 °C for 3 min, followed by 27 cycles of denaturing at 95 °C for 30 s, annealing at 55 °C for 30 s and extension at 72 °C for 45 s, and single extension at 72 °C for 10 min, and end at 4 °C. The PCR mixtures contain 5 × TransStart FastPfu buffer 4 µL, 2.5 mM dNTPs 2 µL, forward primer (5 µM) 0.8 µL, reverse primer (5 µM) 0.8 µL, TransStart FastPfu DNA Polymerase 0.4 µL, template DNA 10 ng, and finally ddH₂O up to 20 µL.

Fig. S1 Attenuation trend of DO under different pH values of the influent

Fig. S2 Attenuation trend of DO under different temperatures of the influent

Fig. S3 Attenuation trend of DO under different nutritional levels of the influent

Fig. S4 Attenuation trend of DO under different concentrations of sodium hypochlorite
(pre-oxidant)

Fig. S5 Decay trend of residual chlorine under different initial residual chlorine
concentrations

Fig. S6 Bacterial distribution of 27 most abundant genera among three biofilm samples.

The color intensity of scale indicates relative abundance of each genus

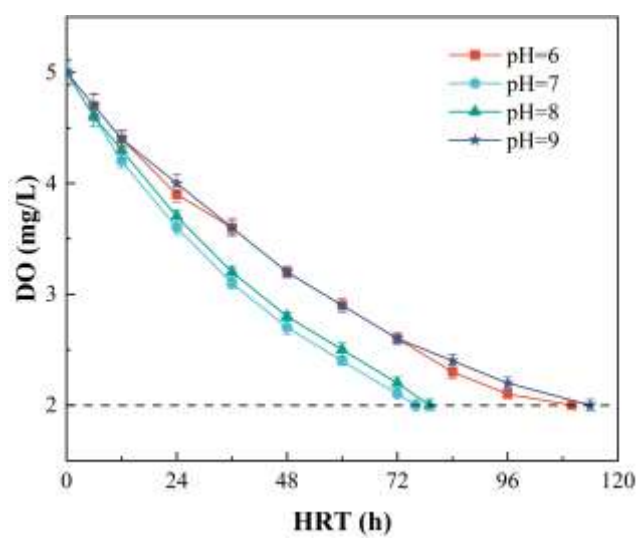


Fig. S1

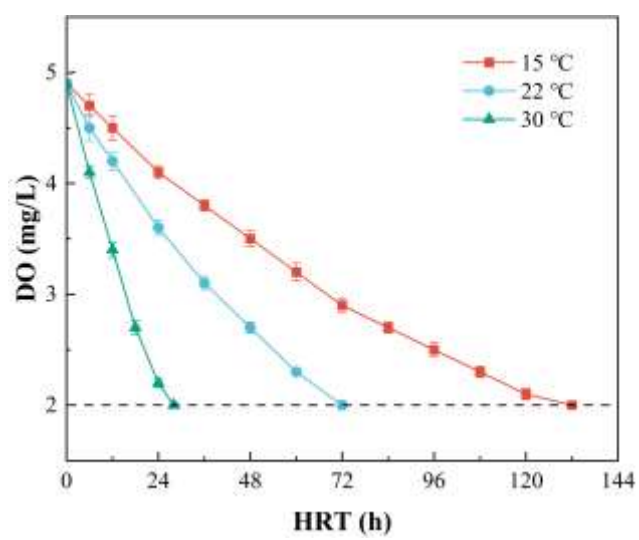


Fig. S2

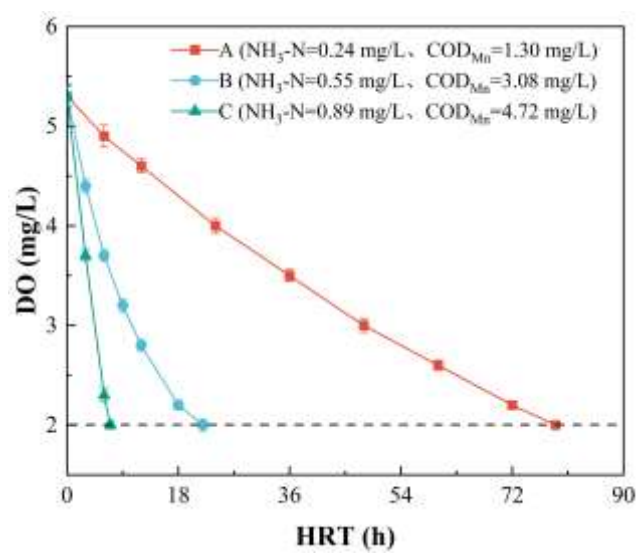


Fig. S3

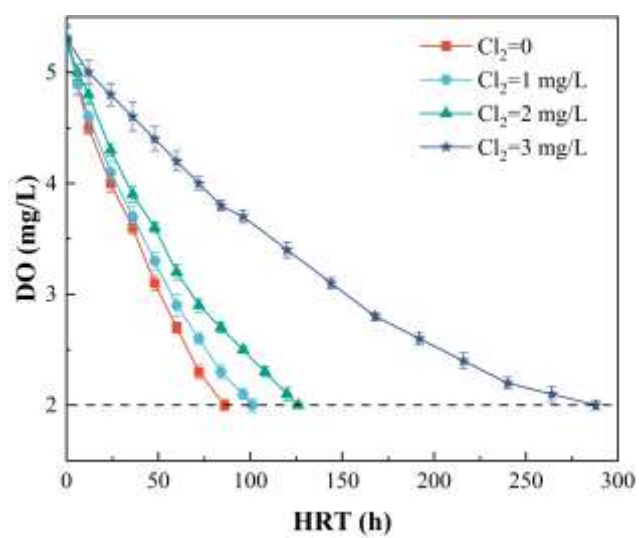


Fig. S4

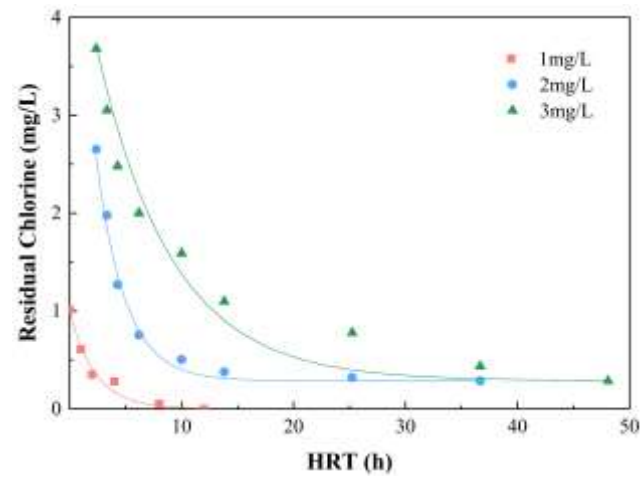


Fig. S5

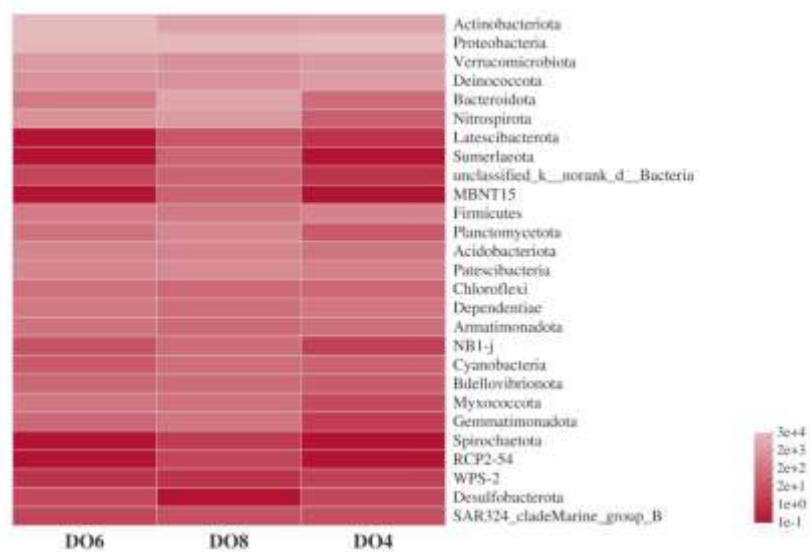


Fig. S6

Table S1

Parameters of the raw water quality

Parameters (units)	Range
Temperature (°C)	14-25
pH value	6.72-7.17
DO (mg/L)	5.1-7.5
HPC (CFU/mL)	7-86
Turbidity (NTU)	0.86-4.15
Total alkalinity (mg/L)	15.4-23.4
Calcium hardness (mg/L)	4.2-21.0
Total manganese (mg/L)	0-0.45
NH ₄ ⁺ (mg/L)	0-0.34
NO ₂ ⁻ (mg/L)	0-0.012
NO ₃ ⁻ (mg/L)	0.603-1.272
COD _{Mn} (mg/L)	0.8-3.2

Table S2

Equation of decay of residual chlorine

Initial concentration of residual chlorine	Equation of decay of residual chlorine
1 mg/L	$y = e^{-0.43793t}$, $R^2 = 0.97543$
2 mg/L	$y = 2e^{-0.14255t}$, $R^2 = 0.95727$
3 mg/L	$y = 3e^{-0.37418t}$, $R^2 = 0.99111$