# Supplementary Information

## Enhanced resistance to ciprofloxacin stress in integrated floating film activated sludge system filled with surface-modified carriers for simultaneous nitrification and denitrification

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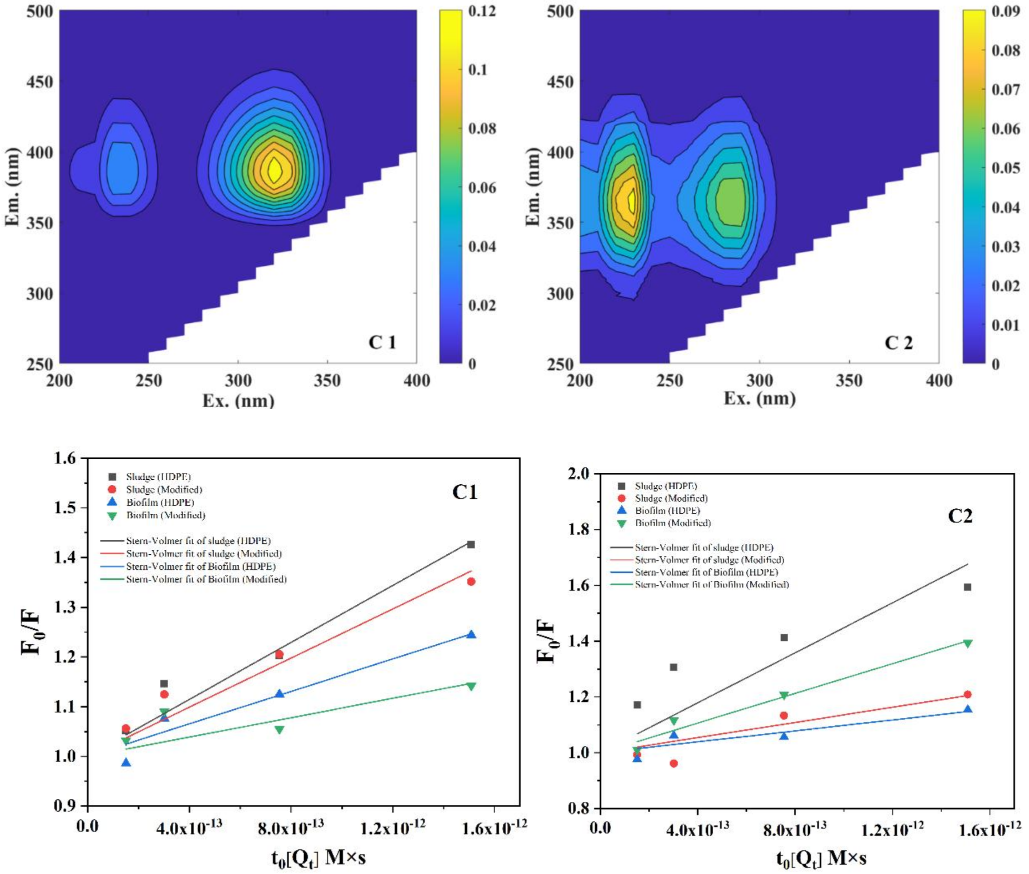

Fig. S1 EEM contours of the two identified decomposed components (C1, C2) under short-term stress of CIP by PARAFAC model; Fitting results for fluorescence intensities of the two main components (C1, C2) using Sterne-Volmer equation.

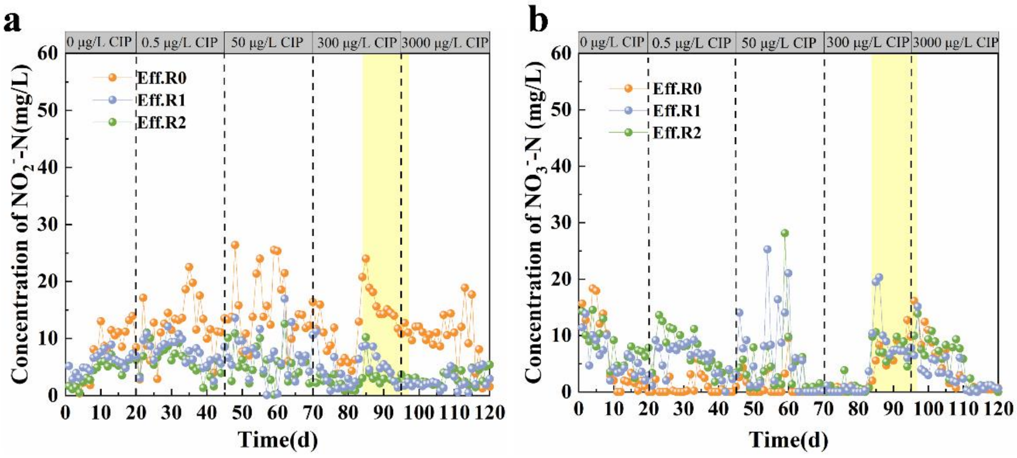

Fig. S2 Effluent $NO_2^-$-N (a) and $NO_3^-$-N (b) concentrations during the long-term exposure of CIP. The time period highlighted by the yellow background represented the aerobic duration was adjusted from 100 min to 120 min.

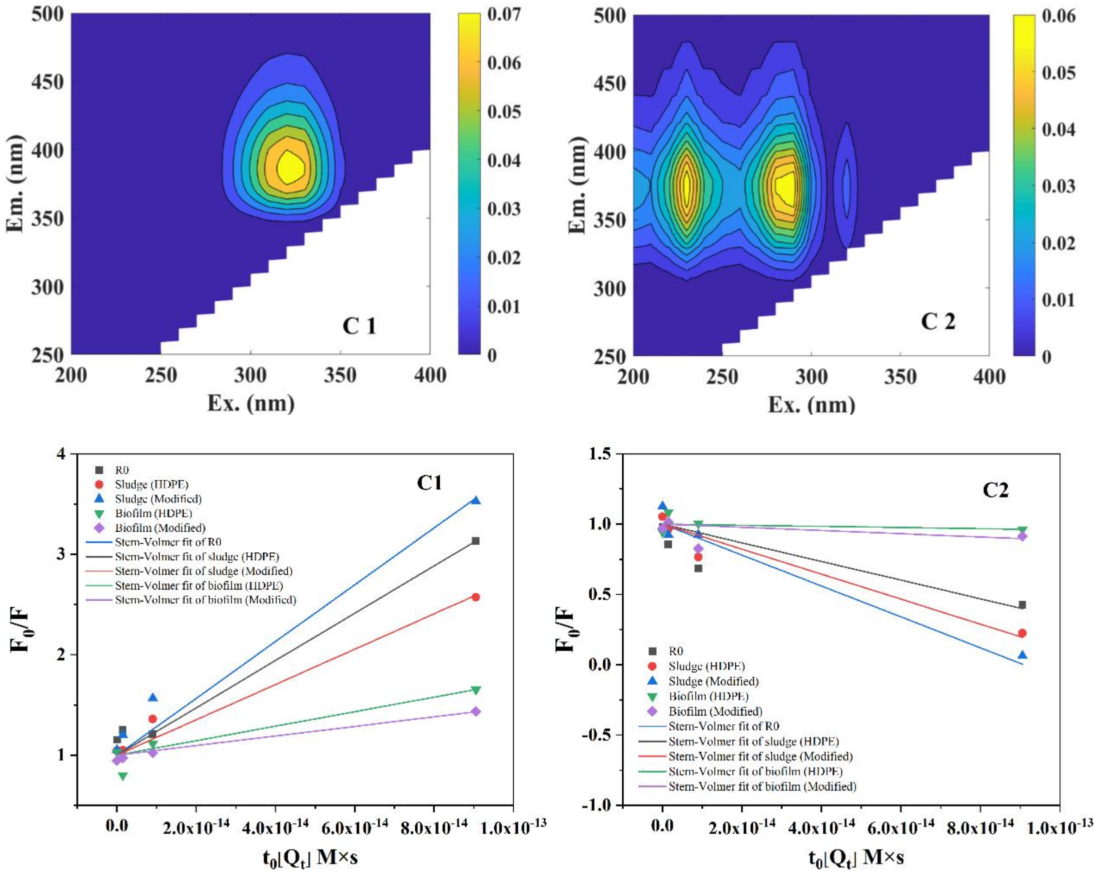

Fig. S3 EEM contours of the two identified decomposed components (C1, C2) under long-term stress of CIP by PARAFAC model; Fitting results for fluorescence intensities of the two main components (C1, C2) using Sterne-Volmer equation.

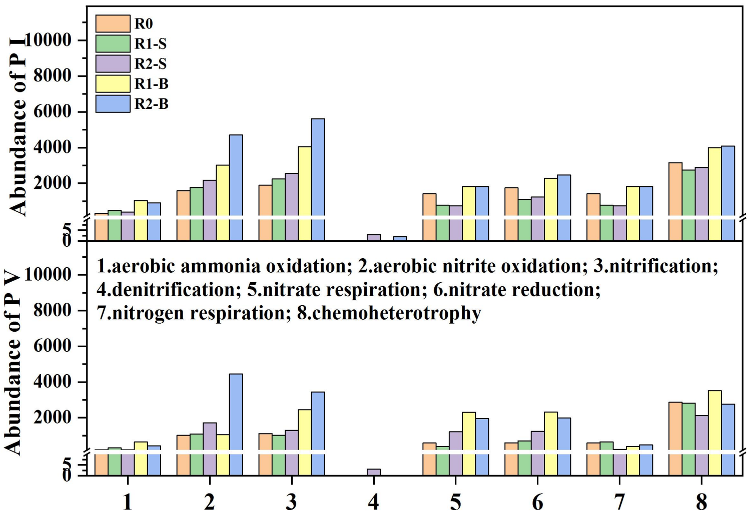

Fig. S4 Function prediction based on FAPROTAX database in phase I and V. R$_i$-S: sludge sample in R$_i$; R$_i$-B: biofilm sample in R$_i$.

Table S1 The primer sequence of ARGs and integrase gene.

| ARGs/integrase gene | Forward primer (5′-3′) | Reverse primer (3′-5′) |
|---|---|---|
| *intI1* | CGAACGAGTGGCGGAGGGTG | TACCCGAGAGCTTGGCACCCA |
| *qepA* | GCCGGTGATGCTGCTGA | CAGRAACAGCGCSCCSA |
| *qnrA* | AGGATTTCTCACGCCAGGATT | CCGCTTTCAATGAAACTGCAA |
| *qnrB* | GGMATHGAAATTCGCCACTG | TTYGCBGYYCGCCAGTCG |
| *qnrC* | ATTACGGGTTGTAATTTGTCTTATG | ATCAGAAAATGATCCCCTACT |

Table S2 The α-diversity index under no CIP stress (phase I) and the CIP stress of 3000 μg/L (phase V) in R0, R1 and R2.

|  | Sample | OTUs | Shannon | Chao | Ace | Simpson | Coverage |
|---|---|---|---|---|---|---|---|
| Phase I | R0-S | 1404 | 3.92 | 1455.54 | 1517.77 | 0.13 | 1.00 |
|  | R1-S | 1432 | 4.34 | 1494.28 | 1554.25 | 0.06 | 1.00 |
|  | R2-S | 1488 | 4.55 | 1566.23 | 1621.38 | 0.04 | 1.00 |
|  | R1-B | 1698 | 5.24 | 1734.44 | 1796.41 | 0.02 | 1.00 |
|  | R2-B | 1578 | 5.08 | 1645.27 | 1696.99 | 0.02 | 1.00 |
| Phase V | R0-S | 1545 | 3.77 | 1581.48 | 1643.23 | 0.06 | 1.00 |
|  | R1-S | 1470 | 3.24 | 1545.39 | 1621.37 | 0.12 | 1.00 |
|  | R2-S | 1365 | 4.54 | 1433.90 | 1503.23 | 0.06 | 0.99 |
|  | R1-B | 1803 | 4.87 | 1854.98 | 1935.15 | 0.04 | 0.99 |
|  | R2-B | 1639 | 5.00 | 1692.4 | 1774.02 | 0.04 | 1.00 |

Table S3 Relative abundances (%) of functional genus under no CIP stress (0 μg/L, phase I) and the CIP stress of 3000 μg/L (phase V) in R0, R1 and R2.

| Key functional groups | | Phase I | | | | | Phase V | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | R0-S | R1-S | R2-S | R1-B | R2-B | R0-S | R1-S | R2-S | R1-B | R2-B |
| AOB | *Nitrosomonas* | 0.52 | 0.80 | 0.67 | 1.88 | 1.62 | 0.00 | 0.02 | 0.02 | 0.00 | 0.03 |
| NOB | *Nitrospira* | 2.65 | 2.96 | 3.73 | 5.46 | 8.41 | 0.01 | 0.02 | 0.07 | 0.21 | 0.85 |
| DNB | *Saccharibacteria incertae sedis* | 47.93 | 46.71 | 40.33 | 15.11 | 13.47 | - | - | - | - | - |
| | *Azospira* | 2.19 | 1.05 | 0.93 | 3.15 | 3.11 | 6.69 | 8.08 | 6.31 | 9.39 | 10.92 |
| | *Thauera* | 1.84 | 3.27 | 1.54 | 1.51 | 1.59 | 1.22 | 3.18 | 2.27 | 1.27 | 1.06 |
| | Unclassified *Comamonadaceae* | 1.25 | 1.49 | 1.67 | 1.19 | 1.13 | 0.23 | 0.15 | 0.33 | 0.42 | 0.34 |
| | Unclassified *Rhodanobacteraceae* | 0.69 | 1.31 | 5.30 | 0.31 | 0.79 | 0.18 | 0.00 | 0.00 | 0.00 | 0.01 |
| | Unclassified *Rhodobacteraceae* | 0.42 | 0.24 | 0.33 | 0.28 | 0.27 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 |
| | Unclassified *Rhodocyclaceae* | 0.20 | 0.14 | 0.09 | 0.17 | 0.21 | 0.05 | 0.07 | 0.26 | 0.43 | 0.48 |
| | *Zoogloea* | 0.60 | 1.50 | 0.77 | 0.70 | 0.77 | 0.02 | 0.12 | 0.05 | 0.21 | 0.01 |
| | *Aeromonas* | 0.43 | 0.53 | 0.78 | 0.35 | 0.75 | - | - | - | - | - |
| | *Rhodobacter* | 0.04 | 0.08 | 0.12 | 0.05 | 0.05 | 0.09 | 0.19 | 0.26 | 0.33 | 0.16 |
| | *Mesorhizobium* | 0.25 | 0.05 | 0.10 | 0.23 | 0.28 | - | - | - | - | - |
| | *Acidovorax* | 0.02 | 0.04 | 0.05 | 0.03 | 0.03 | 0.26 | 0.14 | 0.47 | 0.14 | 0.22 |
| | *Novosphingobium* | 0.01 | 0.01 | 0.05 | 0.10 | 0.09 | 0.01 | 0.01 | 0.03 | 0.06 | 0.10 |
| | *Flavobacterium* | 0.01 | 0.02 | 0.02 | 0.04 | 0.02 | 0.02 | 0.00 | 0.04 | 0.03 | 0.03 |
| | Unclassified *Rhodospirillales* | 0.12 | 0.09 | 0.19 | 0.38 | 0.29 | - | - | - | - | - |
| | Unclassified *Flavobacteriaceae* | 0.01 | 0.00 | 0.02 | 0.02 | 0.00 | 0.01 | 0.01 | 0.03 | 0.05 | 0.01 |