Supporting information for

Enhanced quinoline removal by zero-valent iron coupled novel anaerobic processes: performance and underlying function analysis

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## Supporting tables

**Table S1 Alpha diversity parameters**

| Name  | Seq num*1 | OTU num*1 | Shannon index | Simpson index | ACE index | Chao1 index |
|-------|-----------|-----------|---------------|----------------|-----------|-------------|
| Control | 56853 | 2134 | 4.08 | 0.059 | 15966.97 | 9584.53 |
| IP | 89490 | 3823 | 5.20 | 0.022 | 9891.16 | 9333.85 |
| IS | 40777 | 1591 | 3.86 | 0.074 | 8319.70 | 5061.21 |
| RIS | 49240 | 1622 | 3.24 | 0.145 | 13072.79 | 6913.01 |

*1: “Seq num” indicated the sequence numbers obtained from the high-throughput sequencing analysis; *2: “OTU num” indicated the classified OTU numbers obtained from the gene sequences with the identity of over 97%.
### Table S2 Genera (relative abundance >1% in at least one samples)

| Genera                      | Control | IP   | IS   | RIS  |
|-----------------------------|---------|------|------|------|
| *Azotobacter*               | 16.33   | 8.88 | 21.81| 4.72 |
| *Thermomonas*               | 0.47    | 0.07 | 0.53 | 36.2 |
| *Alicyciphilus*             | 12.56   | 1.79 | 7.83 | 3.01 |
| *Pseudomonas*               | 3.77    | 2.26 | 4.76 | 12.41|
| *Rhizobium*                 | 10.25   | 2.36 | 6.45 | 0.78 |
| *Novosphingobium*           | 3.32    | 4.76 | 7.91 | 0.44 |
| *Rhizorhabdus*              | 4.78    | 3.35 | 3.45 | 0.64 |
| *Comamonas*                 | 3.6     | 2.85 | 4.17 | 1.75 |
| *Ignavibacterium*           | 5.75    | 0.57 | 5.18 | 2.11 |
| *Acinetobacter*             | 0.28    | 6.9  | 0.27 | 0.5  |
| *Eubacterium*               | 1.98    | 4.24 | 1.17 | 0.02 |
| *Exiguobacterium*           | 0.76    | 4.39 | 0.82 | 1.15 |
| *Sphingopyxis*              | 0.55    | 0.58 | 0.4  | 6.24 |
| *Citrobacter*               | 0.5     | 3.3  | 0.53 | 0.85 |
| *Bacillus*                  | 0.09    | 0.14 | 0.04 | 7.13 |
| *Stenotrophomonas*          | 0.92    | 0.16 | 0.69 | 5.23 |
| *Chelatococcus*             | 1.19    | 2.14 | 1.2  | 0.15 |
| *Thauera*                   | 1.28    | 0.68 | 4.07 | 0.13 |
| *Planctomicrobium*          | 0.1     | 2.96 | 0.06 | 0.03 |
| *Ornatilinea*               | 0.86    | 1.53 | 0.67 | 0.18 |
| *Brevibacillus*             | 0.52    | 1.09 | 1.48 | 0.14 |
| *Limnobacter*               | 1.01    | 0.71 | 0.88 | 0.1  |
| *Clostridium sensu stricto* | 0.04    | 1.28 | 0.03 | 0.73 |
| *Methyloversatilis*         | 1.12    | 0.52 | 0.76 | 0.11 |
| *Hydrotalea*                | 0       | 0    | 0    | 2.67 |
| *Saccharibacteria_genera_in_ | 0.08    | 1.34 | 0.08 | 0.04 |
| certae_sedis                |         |      |      |      |
| *Acetoanaerobium*           | 0.01    | 1.19 | 0.01 | 0    |
| *Lactobacillus*             | 0.02    | 1.02 | 0.03 | 0.02 |