

1 **Supporting information for**

2 **Enhanced quinoline removal by zero-valent iron coupled novel**

3 **anaerobic processes: performance and underlying function analysis**

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9 Supporting tables

10 Table S1 Alpha diversity parameters

Name	Seq num* ¹	OTU num* ¹	Shannon -index	Simpson	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

11 *¹: “Seq num” indicated the sequence numbers obtained from the high-throughput

12 sequencing analysis;

13 *²: “OTU num” indicated the classified OTU numbers obtained from the gene

14 sequences with the identity of over 97%.

Table S2 Genera (relative abundance >1% in at least one samples)

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