

Raw Data of Fig.5 High-throughput sequencing analysis of the sediment
after cultivation

genera	the relative abundance
Diaphorobacter	33.82%
Dechloromonas	0.47%
Paracoccus	24.49%
Pleomorphomonas	0.49%
unclassified	5.08%
Trichococcus	0.53%
Thauera	3.85%
Ignavibacterium	0.64%
Cloacibacterium	2.85%
Rhizobium	0.68%
Aquimonas	2.43%
Simplicispira	0.82%
Chiayiivirga	2.14%
Pseudoxanthomonas	1.06%
Flavobacterium	2.13%
Stenotrophomonas	1.43%
Chryseobacterium	1.84%
Petrimonas	1.45%
Brevundimonas	1.84%
Anaerorhabdus	1.45%
Other	10.52%