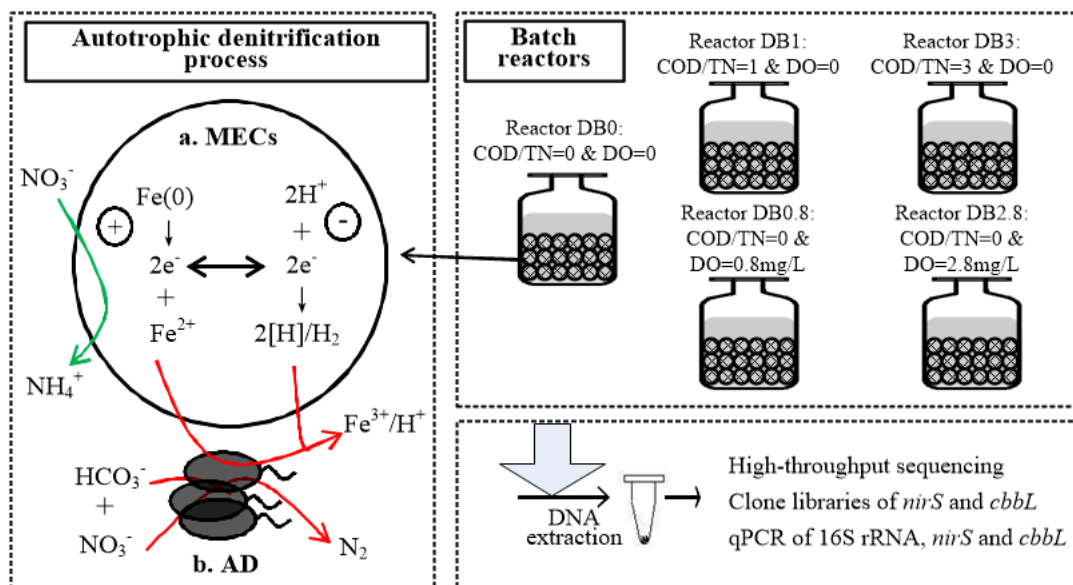


**Table S1** PCR primers and conditions used in this study.

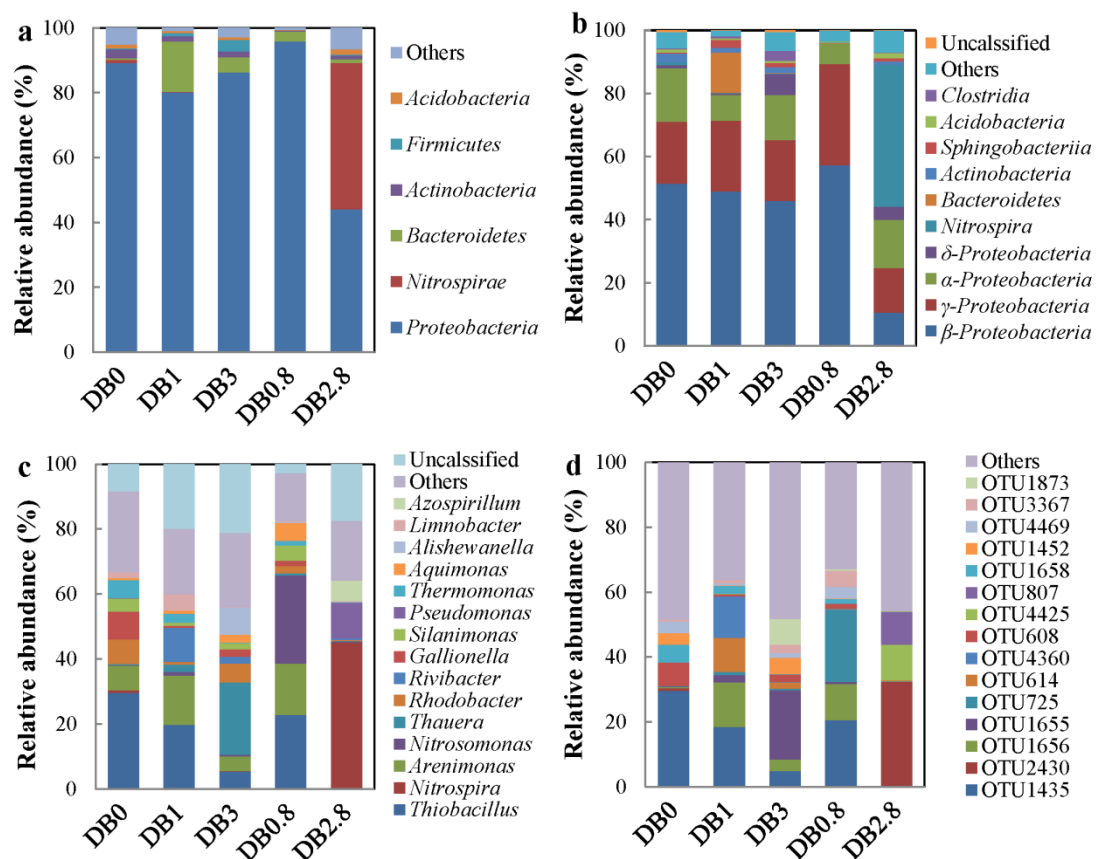
Target gene	Primer name	Primer sequence (5'-3')	Thermal Profile (94 °C 5 min for pre-denaturation)	Purpose
16S rRNA	338F	ACTCCTACGGGAGGCAGCA	28 cycles of 94 °C for 30 s, 55 °C for 30 s, and 72 °C for 60 s, and a final extension cycle at 72 °C for 7 min.	High-throughput sequencing
	806R	GGACTACHVGGGTWTCTAAT		
	341F	CCTACGGGAGGCAGCAG	36 cycles of 94 °C for 30 s, 64 °C for 60 s, with plate read.	qPCR
	515R	ATTACCGCGGCTGCTGG		
<i>nirS</i>	nirS1F	CCTAYTGGCCGCCRCART	36 cycles of 94 °C for 30 s, 56 °C for 30 s, and 72 °C for 60 s, and a final extension cycle at 72 °C for 10 min.	Clone library
	nirS6R	CGTTGAACTTRCCGGT		
	nirS1F	TACCACCCSGARCCGCGCGT	36 cycles of 94 °C for 30 s, 64 °C for 60 s, with plate read.	qPCR
	nirS3R	GCCGCCGTCRTGVAGGAA		
<i>cbbL</i>	168F	CGGCACSTGGACCACSGTSTGGAC	36 cycles of 94 °C for 30 s, 60 °C for 30 s, and 72 °C for 60 s, and a final extension cycle at 72 °C for 7 min (qPCR without extension).	Clone library qPCR
	786R	GTARTCGTGCATGATGATSGG		

**Table S2** Overall analysis of sequencing data for DB0, DB1, DB3, DB0.8 and DB2.8 in the 3% dissimilarity level.

Sample	DB0	DB1	DB3	DB0.8	DB2.8
Numbers of OTUs	340	387	504	190	549
Ace	396	581	897	362	747
Chao1	397	538	749	295	758
Shannon	3.351	3.397	3.673	2.803	3.393
Simpson	0.107	0.085	0.069	0.117	0.132
Coverage	0.997	0.995	0.993	0.998	0.991



**Figure S1** Schematic of the experimental procedures.



**Figure S2** Relative abundances of bacterial community in all five samples based on high-throughput sequencing.