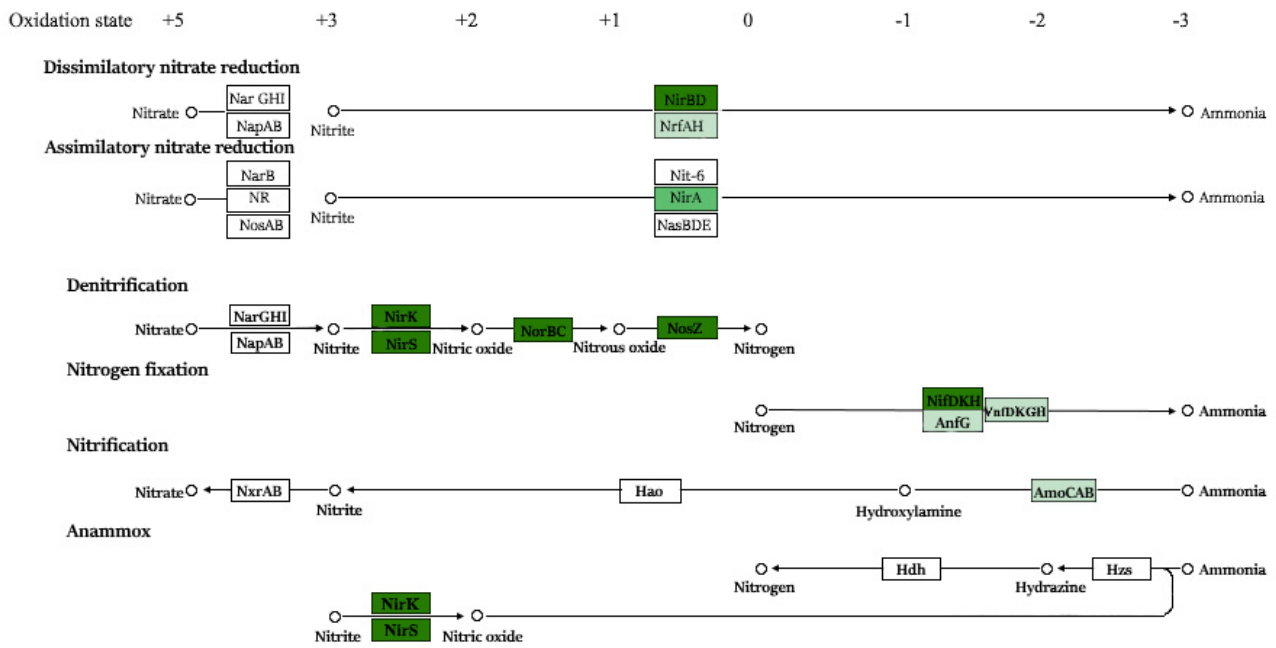
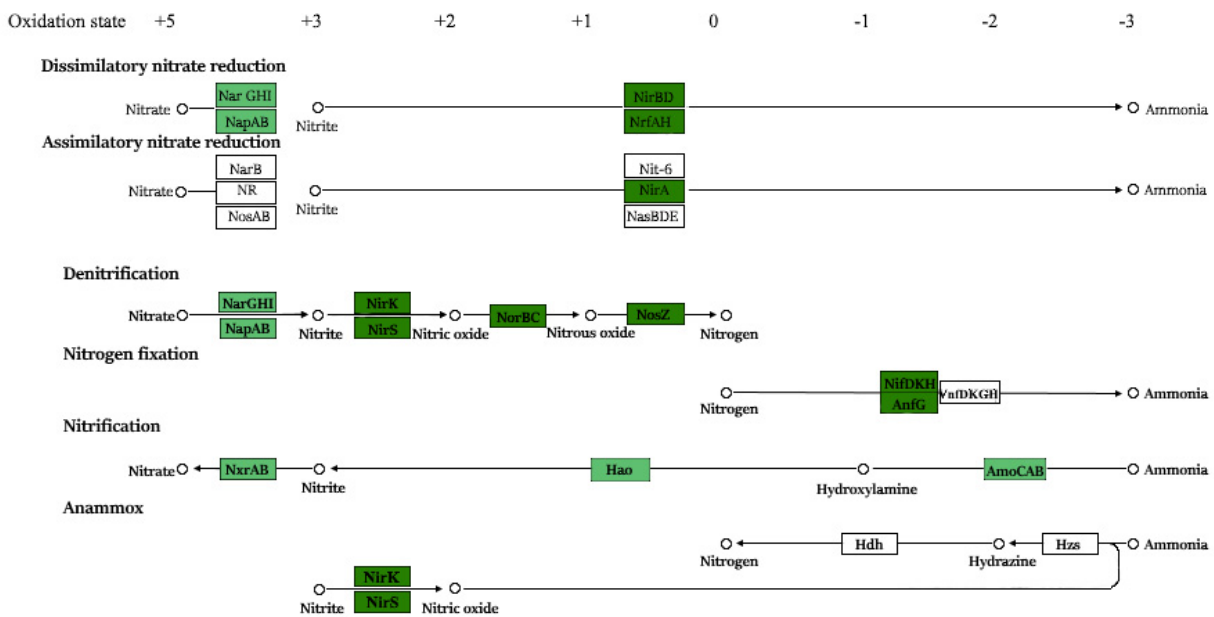


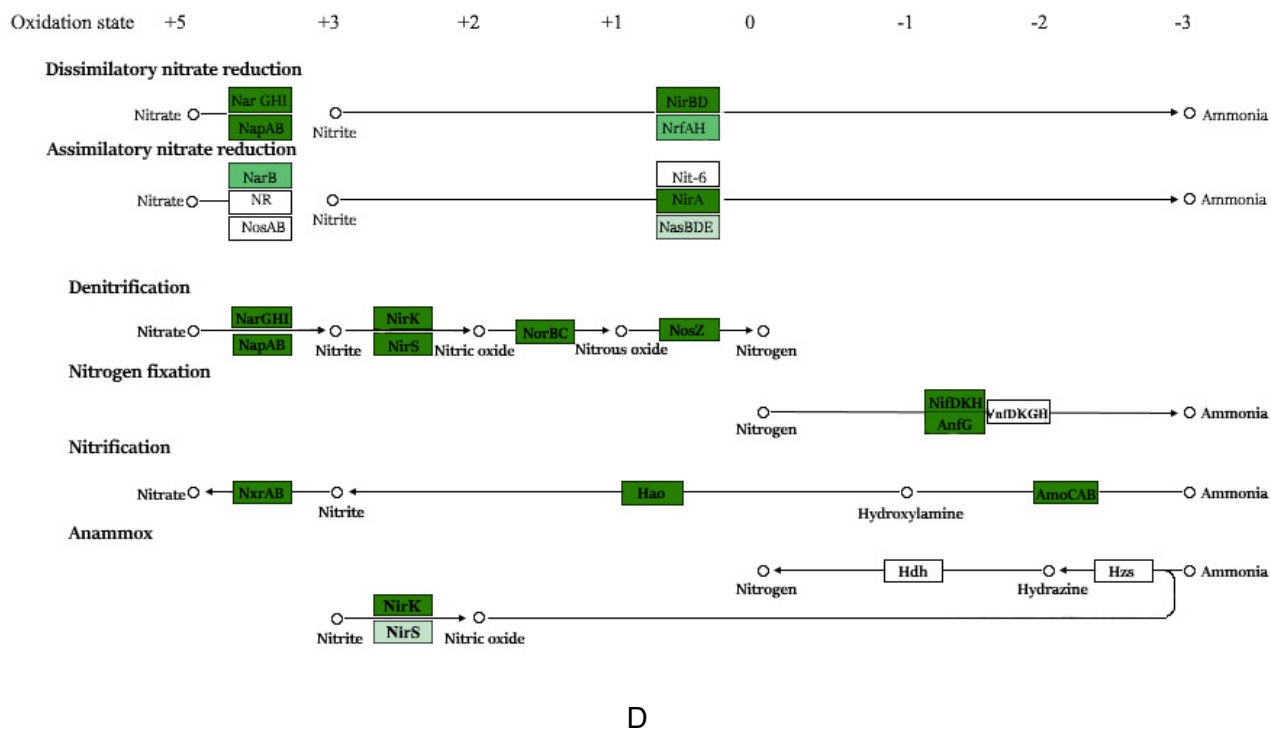
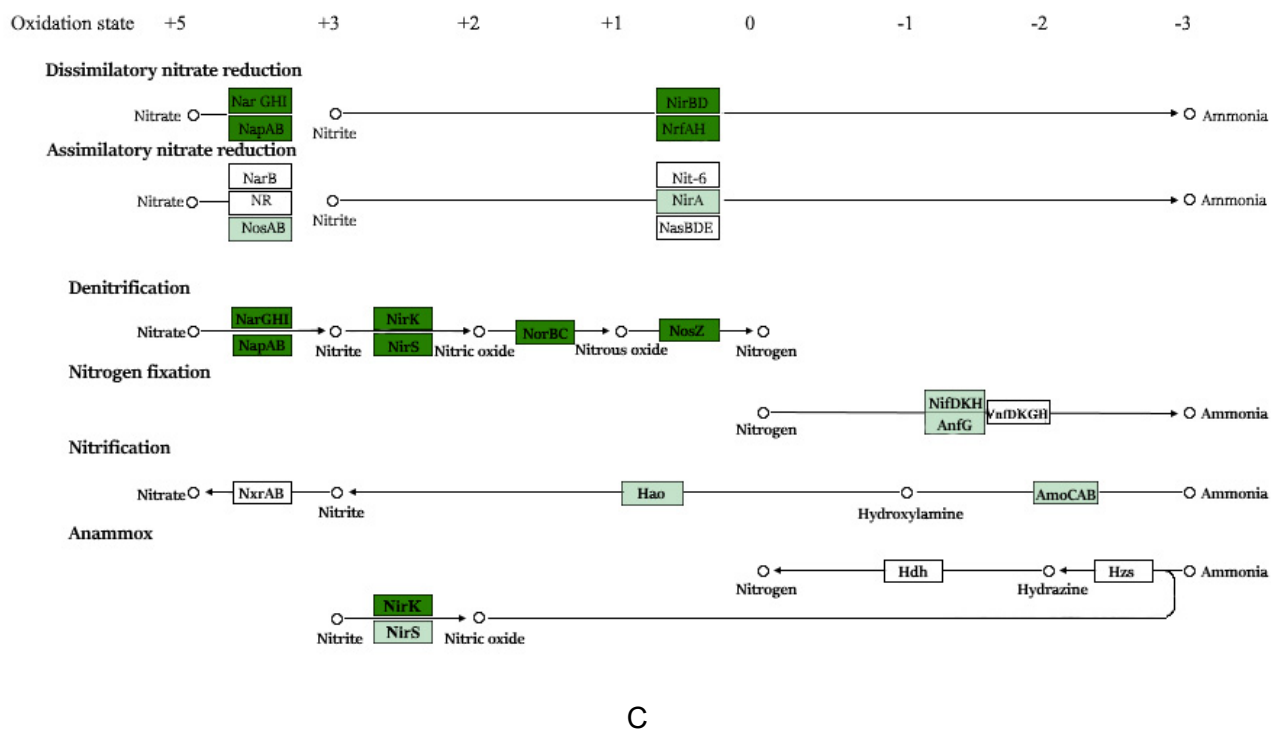
Supplementary



A



B



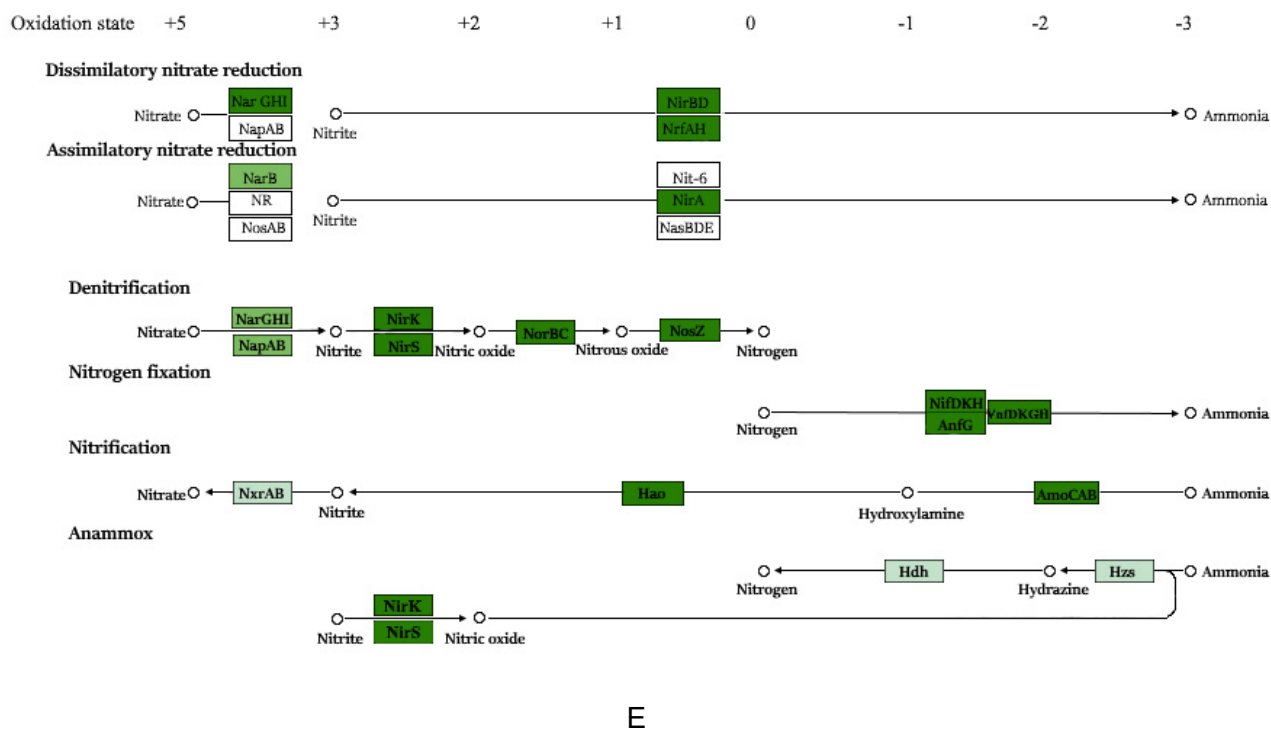


Figure S1. Nitrogen metabolic pathways in fed-batch enrichment cultures and continuous-flow cultivated ABR performed by IVICODAK [83]: (A) AOB, (B) NOB, (C) DB, (D) AnAOB, (E) ABR.

Table S1. The number of gene copies of key N cycle bacteria in phase 4 of the ABR operation.

Gene	Number of copies (per 1 mL)
anammox 16S rRNA	$(2.41 \pm 0.11) \times 10^2$
nirS (denitrifiers)	$(1.07 \pm 0.12) \times 10^8$
nirK (denitrifiers)	$(9.91 \pm 0.41) \times 10^4$
AOB	$(1.22 \pm 0.37) \times 10^8$

Table S2. Bacterial taxon representation in the Venn diagram intersections.

Intersections	Common taxa
A	<i>Mycobacteriaceae</i> , <i>Chitinophagaceae</i> , <i>Microscillaceae</i> , <i>Crocinitomicaceae</i> , <i>NS9 marine group</i> , <i>Weeksellaceae</i> , <i>NS11-12 marine group</i> , <i>Ignavibacteriaceae</i> , <i>A4b</i> , <i>Babeliaceae</i> , <i>Gemmatimonadaceae</i> , <i>Gemmataceae</i> , <i>Isosphaeraceae</i> , <i>Pirellulaceae</i> , <i>Beijerinckiaceae</i> , <i>Hyphomicrobiaceae</i> , <i>Leptospiraceae</i> , <i>Chthoniobacteraceae</i> , <i>Terrimicrobiaceae</i> , <i>WPS-2</i>
B	<i>Flavobacteriaceae</i> , <i>B1-7BS</i> , <i>Methylophilaceae</i> , <i>TRA3-20</i> , <i>Pedosphaeraceae</i>
C	<i>Ferroplasmaceae</i> , <i>Ferrovibrionaceae</i> , <i>Oceanibaculaceae</i>

D	<i>Blastocatellaceae, Streptomycetaceae, Bacteroidaceae, Bacteroidales RF16 group, F082, Prevotellaceae, Rikenellaceae, Nitrososphaeraceae, Gastranaerophilales, Thermaceae Desulfovibrionaceae, Methanobacteriaceae, Acholeplasmataceae, Acidaminococcaceae, Butyricococcaceae, Christensenellaceae, Erysipelotrichaceae, Ethanoligenenaceae, Hungateiclostridiaceae, Lachnospiraceae, Monoglobaceae, Ruminococcaceae, Halanaerobiaceae, Woesearchaeales, Acetobacteraceae, Acidiferrobacteraceae, Methanomethylophilaceae, Thermoplasmataceae, Petrotogaceae, Akkermansiaceae, Victivallaceae, WCHB1-41</i>
E	<i>Carnobacteriaceae, Clostridiaceae, Dysgonomonadaceae, Sedimentibacteraceae, Tannerellaceae</i>
F	<i>Xanthobacteraceae, Burkholderiaceae, Nitrosomonadaceae, Rhodocyclaceae</i>
G	<i>Comamonadaceae, Rhodanobacteraceae</i>
H	<i>Alcaligenaceae</i>
I	<i>Rhizobiaceae</i>
J	<i>Caulobacteraceae</i>
K	<i>Pseudomonadaceae</i>
L	<i>Oscillospiraceae, UCG-010, Sphingomonadaceae</i>
M	<i>Devosiaceae</i>
N	<i>Hydrogenophilaceae</i>

Table S3. Major metabolic pathways in dominant microbial groups (according to KEGG database <https://www.genome.jp/>)

dominant taxa	Dissimilatory nitrate reduction	Denitrification to N ₂	Assimilatory nitrate reduction	Nitrite reduction	N ₂ fixation	Anaerobic ammonium oxidation
Pseudomonadaceae, g:Pseudomonas	+	+	+	+	-	-
Rhodanobacteraceae	NO ₂ to NH ₄	NO ₂ to N ₂ O	NO ₃ to NO ₂	-	+	-
Hydrogenophilaceae	+	NO ₂ to N ₂ O	NO ₃ to NH ₄	NH ₄ to hydroxylamine	-	-
Nitrososphaeraceae	+	NO ₂ to NO	+	+	-	-
Butyricococcaceae	-	-	+	-	-	-
Xanthomonadaceae, g:Thermomonas, Stenotrophomonas	NO ₃ to NO ₂	NO ₃ to N ₂ O	+	NO ₂ to NO ₃	-	-
Rhizobiaceae, g:Aminobacter	NO ₃	+	+	+	+	-

	to NH ₄					
Sphingomonadaceae	-	-	NO ₃ to NH ₄	-	-	-
Oscillospiraceae	-	-	-	-	+	-
Rikenellaceae	-	-	+	-	-	-
Bacteroidaceae	NO ₂ to NH ₄	-	+	+	-	-
Alcaligenaceae, g:Pusillimonas	NO ₃ to NH ₄	NO ₂ to N ₂ O	NO ₃ to NO ₂	+	-	-
Clostridiaceae	+	-	+	-	+	-
Carnobacteriaceae	-	-	+	-	-	-

Note: + means presence, - means absence or unknown

