Complete genome-centric analysis reveals functional divergence and adaptive evolution of uncultured bacteria in anammox community

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Running title: Complete genome-centric analysis of anammox community

Abstract

Anaerobic ammonium-oxidation (anammox) bacteria play a crucial role in global nitrogen cycling and wastewater nitrogen removal, but they depend on mutualistic symbiosis with various other microorganisms for their survival. Although shotgun metagenomics based on short reads has been widely used in anammox research, metagenome-assembled genomes (MAGs) are often discontinuous and highly contaminated, which limits in-depth analyses of anammox communities. Here, for the first time, we performed Pacific Biosciences high-fidelity (HiFi) sequencing on the anammox granule sludge sample, and obtained 30 accurate and complete metagenome-assembled genomes (cMAGs). These cMAGs were obtained by selecting high-quality circular contigs from initial assemblies of long reads generated by HiFi sequencing, eliminating the need for Illumina short reads, binning, and reassembly. cMAG-centric analysis revealed divergences in general and nitrogen metabolism among members of the anammox community. Furthermore, we identified mobile genetic elements (MGEs) and putative horizontal gene transfer (HGT) events within these cMAGs to explore the adaptive evolution of the community. The results suggest that MGEs and HGT events, particularly transposons containing *tnpA* in anammox bacteria, might play important roles in the adaptive evolution of this anammox community. The cMAGs generated in the present study could be used to establish of a comprehensive database for anammox bacteria and associated microorganisms. Our findings highlight the advantages of HiFi sequencing for the studies of complex cultures such as anammox communities and advance our understanding of anammox communities.

Keywords: anammox community; adaptive evolution; mobile genetic elements; horizontal gene transfer; HiFi metagenomic sequencing

Introduction

Anaerobic ammonium-oxidation (anammox) plays a key role in the global nitrogen cycle and is a cost-effective technique for treating ammonium-rich wastewaters due to no external carbon source requirement, lower oxygen consumption and sludge production (Peeters and van Niftrik, 2019; Adams et al., 2022). Approximately 100 anammox wastewater treatment plants are currently operating worldwide (Lackner et al., 2014). Anammox bacteria affiliated with the phylum Planctomycetota (also known as Planctomycetes) are responsible for catalyzing anammox process, in which anammox bacteria utilize nitrite as electron acceptor to oxidize ammonium to dinitrogen gas (N_2) under anoxic conditions (Kartal et al., 2013). Although anammox bacteria have been discovered for over 20 years, and substantial efforts have been made to isolate them, yet pure cultures of these bacteria are still unavailable to date (Peeters and van Niftrik, 2019; Kuenen, 2020). It is well known that anammox bacteria hardly survive alone and share symbiotic relationships with various other microorganisms affiliated with the phyla Acidobacteriota, Armatimonadota, Bacteroidota, Chloroflexota, Proteobacteria, Patescibacteria, etc. (Bhattacharjee et al., 2017; Lawson et al., 2017; Feng et al., 2018; Zhao et al., 2018a). The co-existing bacteria can provide anammox bacteria with growth factors or stable nitrite under specific C/N ratios, and prevent the inhibition of anammox bacteria by organic matter (Zhao et al., 2018b; Cao et al., 2021). Therefore, comprehensive analysis of the diversity, functional divergence, and adaptive evolution of anammox communities can contribute to advance our understanding of anammox systems and promote the widespread application of this energy-efficient treatment process.

Shotgun metagenomics employing next-generation sequencing (NGS) has been widely used in studies of anammox systems, and the genomes of different anammox bacteria and associated bacteria have been successfully retrieved from samples from

various habitats (Speth et al., 2016; Lawson et al., 2017; Suarez et al., 2022; Yang et al., 2022). However, due to the short reads and PCR requirement of NGS represented by the Illumina platform, leading to some shortcomings such as fragmented assembly and high genome contamination (Meziti et al., 2021). The recovered metagenome-assembled genomes (MAGs) generated by NGS are generally discontinuous because of repetitive, mobile, and conserved sequences, which limits their application in further analyses (Yuan et al., 2015; Sangwan et al., 2016; Meziti et al., 2019; Maguire et al., 2020). Long-read third-generation sequencing (TGS) developed by Pacific Biosciences (PacBio) and Oxford Nanopore Technologies (ONT) is a promising approach for addressing the above problems. The complete circular genomes of anammox bacteria from highly enriched cultures of *Candidatus* Kuenenia stuttgartiensis (> 87% of the total biomass) were previous recovered using only long reads generated by PacBio RS II sequencing (Frank et al., 2018; Ding and Adrian, 2020). Additionally, Liu et al. (2020) employed a combination of Illumina and ONT sequencing to develop an iterative hybrid assembly (IHA) method, which enabled the retrieval of eight circular genomes from one sample of a partial nitrification anammox reactor. However, nucleotide accuracy and assembly bubbles were not reported for these eight circular genomes. Consequently, a simpler and more efficient approach for recovering numerous accurate circular genomes from anammox systems is currently lacking. Furthermore, whether TGS can be employed alone to retrieve accurate and complete prokaryotic genomes, beyond those of dominant species, from anammox communities remains unclear.

Recently, PacBio high-fidelity (HiFi) sequencing, which can yield high-accuracy long reads (accuracy > 99.5% and average read length of 10-25 kb) (Hon et al., 2020), has become popular for the assembly of plant and animal genomes (Hon et al., 2020; Nurk et al., 2022), as well as the analysis of complex microbiomes (from human gut, sheep fecal, chicken cecum, and saline lake sediment samples) (Bickhart et al., 2022; Feng et al., 2022; Kim et al., 2022; Tao et al., 2023). HiFi sequencing has been shown

100 to greatly improve the quality of metagenome assembly (Tao et al., 2023). Most
101 importantly, HiFi sequencing enables the acquisition of accurate and complete
102 prokaryotic genomes from complex microbiomes, without the need for Illumina short
103 reads, binning, and reassembly. Kim et al. (2022) assembled the HiFi reads derived
104 from five human gut samples, and obtained 102 complete metagenome-assembly
105 genomes (cMAGs). One of these cMAGs is almost identical to the genome of pure
106 culture, with an average nucleotide identity (ANI) value exceeding 99.99%. Taken
107 together, HiFi sequencing provides a highly suitable approach for the accurate and
108 comprehensive analysis of environmental microbiomes, such as anammox
109 communities. The utilization of HiFi sequencing enables the retrieval of more reliable
110 cMAGs compared with MAGs. These cMAGs can serve as a valuable resource for
111 subsequent downstream analyses, including the identification of novel species,
112 exploration of genes associated with specific pathways (Parks et al., 2017; Galambos
113 et al., 2019), investigation of functional divergence, and study of the adaptive
114 evolutionary mechanisms of prokaryotes (Douglas and Langille, 2019).

115 To address the aforementioned research gaps and facilitate in-depth analysis of
116 anammox communities, we performed HiFi sequencing on one granular sludge
117 sample obtained from a lab-scale anammox reactor for the first time. The long-read
118 metagenome obtained was *de novo* assembled, and non-redundant 30 cMAGs,
119 including a genome of a novel anammox species and three genomes from novel
120 families, were filtered out without any binning and reassembly processes. Using these
121 reliable cMAGs, functional divergence and adaptive evolution within the anammox
122 community were further explored. Overall, the results of this study provide a valuable
123 workflow for analyzing complex aquatic microbiomes as well as new insights into
124 bacterial interactions and evolution within the anammox community.

125 Materials and methods

126 Sample collection and DNA extraction

127 The anammox granular sludge sample was collected from a lab-scale expanded
128 granular sludge blanket (EGSB) reactor (**Fig. S1**), which has been operated for two
129 years. The composition of the culture medium is shown in **Table S1** and **Table S2**.
130 The EGSB reactor was initially inoculated with commercially purchased anammox
131 granular sludge, and it was used as the parent reactor to generate an ongoing supply of
132 anammox granular sludge in our laboratory. Total genomic DNA was extracted using
133 the E.Z.N.A.® Soil DNA Kit (Omega Bio-Tek, USA) according to the manufacturer's
134 protocol. The purity and quantity of genomic DNA were assessed using the NanoDrop
135 2000 (ThermoFisher Scientific, USA) and the Qubit 3.0 Fluorometer (Invitrogen,
136 USA) respectively, and its integrity was verified using agarose gel electrophoresis.
137 The DNA sample with a high molecular weight and sufficient quantity was used in
138 subsequent procedures.

139 **Metagenomic sequencing**

140 Metagenomic sequencing libraries were prepared and sequenced by Biozeron
141 Biotechnology Co. Ltd. (Shanghai, China). For PacBio HiFi sequencing, 5 μg of DNA
142 was used to construct a SMRTbell library with the SMRTbell Prep Kit (Pacific
143 Biosciences, USA) according to the manufacturer's protocol. Damaged
144 double-stranded DNA in the initial DNA sample was repaired using the PreCR®
145 Repair Mix Kit (New England Biolabs, USA) before library construction. The
146 repaired DNA was then size-selected to obtain molecules larger than 3 kb. The
147 SMRTbell library was sequenced on the PacBio Sequel IIe platform using a single
148 SMRT 8M cell. HiFi reads were generated with the CCS module (–min-passes = 3,
149 and –min-rq = 0.99) of SMRT Link v11.0 (Pacific Biosciences, USA). For Illumina
150 sequencing, the sequencing library was constructed with a fragment length of ~450 bp
151 and sequenced using the PE150 strategy on the Illumina NovaSeq 6000 platform.
152 Basic information of both the HiFi and Illumina reads is shown in **Table S3** and **Table**
153 **S4**, respectively.

De novo assembly and quality assessment

De novo assembly of HiFi reads was performed using three different assemblers: hifiasm-meta v0.3-r063.2 (Feng et al., 2022), Flye v2.9.1-b1780 (Kolmogorov et al., 2020), and Canu v2.2 (Nurk et al., 2020). Both the hifiasm-meta and Flye assembly were conducted using the recommended PacBio HiFi meta mode. The Canu assembly was conducted using the PacBio HiFi mode with recommended parameters. The assembly quality was assessed using QUAST v5.2.0 (Gurevich et al., 2013), and the results are shown in **Table S5**.

Filtering, taxonomic classification, and functional annotation of cMAGs

The HiFi cMAGs were filtered from initial assemblies using an adapted workflow published before (Kim et al., 2022). The workflow is briefly described as follows: (1) the circular contigs without assembly bubbles (assessed by BubbleGun v1.1.6 (Dabbaghie et al., 2022) as required) and repeats were filtered from the three assemblies; (2) contigs with sequence lengths shorter than 100 kb were removed; (3) the completeness and taxonomic classification of remaining contigs were assessed using GTDB-Tk v2.1.1 (Parks et al., 2022), and contigs with bacterial marker genes (bac120) less than 80 were removed (at this step, no archaea genome was found); (4) the SSU rRNA of the remaining contigs was predicted using barrnap v0.9 (https://github.com/tseemann/barrnap), and contigs missing 5S, 16S or 23S rRNA were removed; (5) the tRNA of remaining contigs was identified using tRNAscan-SE v2.0.11 (Chan et al., 2021), and contigs with tRNA types fewer than 18 were filtered out; and (6) ANI values of contigs were calculated using FastANI v1.33 (Jain et al., 2018). Redundant contigs were those with ANI values ≥ 99% and alignment percentages ≥ 95%, and the contigs with the maximal sum of ANI values were selected as the representative sequences. The contigs obtained through above six steps were considered non-redundant cMAGs. The cMAG abundances represented by transcripts per million (TPM) were calculated using salmon v1.10.1 (Patro et al., 2017), by mapping Illumina reads onto these genomes.

182 Gene prediction of cMAGs was performed using Prodigal v2.6.3 (Hyatt et al.,
183 2010), and the predicted genes were comprehensively annotated using MEBS v1.2
184 (De Anda et al., 2017), eggNOG database v5.0.2 (e-value < 1e-5) (Huerta-Cepas et al.,
185 2019), NCycDB (e-value < 1e-5, identity > 40%, and coverage > 40%) (Tu et al.,
186 2019), and KofamKOALA (Aramaki et al., 2020). The gene abundances represented
187 by TPM were also calculated using salmon v1.10.1 (Patro et al., 2017).

188 **Identification of mobile genetic elements (MGEs) and horizontal gene transfer**
189 **(HGT)**

190 MGEs of cMAGs were identified by alignment (--escore = 1e-6, --pidentvalue = 80,
191 and –queryscore = 75) against mobileOG-db beatrix-1.6 (Brown et al., 2022). The
192 HGT events among all cMAGs were identified using MetaCHIP v1.10.12 (Song et al.,
193 2019) with default parameters. All putative transferred genes were further annotated
194 by alignment (e-value < 1e-5) against both the eggNOG database v5.0.2
195 (Huerta-Cepas et al., 2019) and NCBI non-redundant (NR) database.

196 **Comparative genomic analyses**

197 Reference genomes (**Table S6**) of 26 anammox bacteria in eight genera (*Ca.*
198 Anammoxibacter, *Ca.* Anammoxoglobus, *Ca.* Anammoximicrobium, *Ca.* Brocadia,
199 *Ca.* Jettenia, *Ca.* Kuenenia, *Ca.* Loosdrechtia, and *Ca.* Scalindua) were downloaded
200 from both the NCBI and EMBL-EBI databases. JSpeciesWS (Richter et al., 2015) was
201 used to calculate the ANI values (based on blast) between cMAGs representing
202 anammox bacteria and other reference genomes of *Ca.* Jettenia. DNA-DNA
203 hybridization (DDH) *in silico* was performed using GGDC v3.0 (Meier-Kolthoff et al.,
204 2022) with recommended parameters. All reference anammox bacterial genomes were
205 also comprehensively annotated like cMAGs.

Results

Overview of cMAGs from an anammox community

Through HiFi sequencing and assembly, a total of 541 circular contigs were obtained from one anammox granular sludge sample (**Fig. 1)**. These contigs were filtered based on biological features and ANI values, yielding 30 non-redundant contigs known as cMAGs (**Fig. 1)**. The number of cMAGs from the assembly of hifiasm-meta, Canu and Flye was 19, 7, and 4, respectively. The size of these cMAGs ranged from 0.6 to 4.4 Mb, and the number of coding sequences (CDSs) ranged from 629 to 4,388 (**Table 1**). According to the taxonomic classification by GTDB-Tk, only 16 cMAGs were assigned to known species (**Fig. 2**). Three cMAGs could not be assigned to known families, and four cMAGs could not be assigned to known genera. These cMAGs represented nine phyla, with Patescibacteria having the highest number of cMAGs. Notably, more than 75% and 50% of Patescibacteria genomes were not assigned at the species and genus level, respectively. The genomes of Patescibacteria bacteria are very compact, with far fewer CDSs than the genomes of bacteria affiliated with other phyla. The phyla Actinobacteriota, Armatimonadota, Bdellovibrionota, and Proteobacteria each had only one member, but the abundances of cMAG.1 (Actinobacteriota) and cMAG.30 (Proteobacteria) were not low compared with other cMAGs. cMAG.27, cMAG.1, and cMAG.25 were the most abundant in the community of 30 members, and the abundances of nine species (cMAG.10, cMAG.17, cMAG.5, cMAG.26, cMAG.18, cMAG.19, cMAG.2, cMAG.23, and cMAG.13) were less than one-fiftieth of that of cMAG.27. Pure cultures are not available for none of the 16 species assigned at the species level at present, indicating that all cMAGs might represent uncultured species.

A total of three anammox bacteria, namely cMAG.27, cMAG.28, and cMAG.29, were identified and they were all assigned to the genus *Ca.* Jettenia. According to the

classification by GTDB-Tk, cMAG.28 was unclassified at the species level, and cMAG.27 and cMAG.29 were assigned to the species *Ca.* Jettenia sp. AMX2 and *Ca.* Jettenia caeni, respectively. Therefore, we downloaded the 11 available *Ca.* Jettenia genomes from the NCBI database and calculated ANI values among the above three cMAGs and other *Ca.* Jettenia genomes. As shown in **Fig. S2**, ANI values between cMAG.29 and *Ca.* Jettenia caeni (GCA_000296795.1), and between cMAG.27 and *Ca.* Jettenia sp. AMX2 (GCA_900696655.1) were 99.70% and 99.45%, respectively. These results indicate that cMAG.29 and cMAG.27 are same species of *Ca.* Jettenia caeni and *Ca.* Jettenia sp. AMX2, respectively. The ANI value between cMAG.28 and *Ca.* Jettenia sp. AM49 (GCA_021650895.1) was 95.83%, which was just within the threshold of 95–96% species boundary (Richter and Rosselló-Móra, 2009; Palmer et al., 2020). Consequently, we calculated the DDH value between cMAG.28 and *Ca.* Jettenia sp. AM49 (GCA_021650895.1), and the resulting DDH value (66.60%) is less than the species boundary threshold of 70% (Meier-Kolthoff et al., 2013), indicating that cMAG.28 could represent a novel species of *Ca.* Jettenia different from *Ca.* Jettenia sp. AM49.

Functional divergence in general metabolism

Metabolic inference revealed that, aside from members of Patescibacteria, other bacteria in the anammox system might play a crucial role in nitrogen (N) and iron (Fe) cycles (**Fig. 3**). Additionally, members of phyla such as Planctomycetota and Chloroflexota were found to be important for the carbon (C) cycle in this anammox system. These inferences were further supported by the presence of important metabolic genes or pathways in their genome. For instance, members of the phyla Planctomycetota and Chloroflexota harbor a relatively high abundance of carbohydrate enzymes, including glycoside hydrolases and glycosyl transferases (**Fig. S3**).

In this community, there might be 13 species capable of autotrophic growth that utilize three different carbon fixation pathways. Conversely, no known carbon fixation

pathways could be identified in the remaining 17 species, suggesting that they might be heterotrophic. In detail, all the members of the phyla Chloroflexota and Planctomycetota (cMAG.27, cMAG.28, and cMAG.29) harbor the key genes encoding CO dehydrogenase and acetyl-CoA synthase, which are essential for carbon fixation via the Wood-Ljungdahl (WL) pathway. As for the only Proteobacteria bacterium (cMAG.30), the presence of a nearly complete Arnon-Buchanan cycle indicates its potential for autotrophic growth. Moreover, the presence of the complete Embden–Meyerhof pathway (EMP) and the non-oxidative pentose phosphate pathway (PPP) pathways in cMAG.30 reflect its capability for heterotrophic growth. Besides, the presence of genes encoding cytochrome c oxidase (cbb_3-type), cytochrome bc_1 ubiquinol oxidase, and succinate dehydrogenase in cMAG.30 suggests its capability for aerobic respiration. Three members of Patescibacteria (cMAG.18, cMAG.19, and cMAG.26) were found to carry the RubisCO-encoding gene (*rbcL*), suggesting that they might perform carbon fixation through the Calvin-Benson-Bassham cycle (CBB). The presence of complete EMP and the non-oxidative PPP pathways in three *Ca.* Jettenia species (cMAG.27, cMAG.28, and cMAG.29), as well as a complete tricarboxylic acid cycle (TCA cycle) and *pdhA* encoding pyruvate dehydrogenase, suggest their capabilities for fermentation.

Functional divergence in nitrogen metabolism

To further explore functional divergence in nitrogen metabolism of these bacteria, 30 cMAGs were comprehensively annotated using a curated nitrogen cycle database (NCycDB). A total of 24 species were identified as potentially participating in key nitrogen conversion processes, such as anammox, denitrification, nitrification, and dissimilatory nitrate reduction to ammonia (DNRA) (**Fig. 4A** and **B**). Three members of *Ca.* Jettenia harbor the full set of anammox genes, including *nirK*/*nirS*, *hzs*, and *hdh*, but they all lack *nxrA* encoding nitrite oxidoreductase (**Fig. 4A**). In addition, they all harbor *napA, narG*, and *nrfA*, suggesting their capacities for DNRA. Similarly, among the 11 *Ca.* Jettenia species from other habitats, none of them carry the *nxrA*

gene (**Fig. S4**). Only three members, i.e. two members of *Ca.* Jettenia caeni and one member of *Ca.* Jettenia sp. AMX2, harbor both *napA* and *narG*. Nearly all of these *Ca.* Jettenia members (10 out of 11) may be capable of DNRA. Members belonging to the genera *Ca.* Jettenia and *Ca.* Brocadia possess a richer repertoire of nitrogen metabolism marker genes compared with anammox bacteria in other genera (**Fig. S4**).

A total of 20 non-anammox bacteria community members were found to carry denitrification genes (**Fig. 4A**). However, none of them carry the full set of denitrification genes, indicating a potential for cooperative denitrification. In addition, seven members carry the key gene *nrfA* for DNRA, while only five of them harbor the complete DNRA pathway. The Armatimonadota bacterium (cMAG.2) exclusively harbors *nrfA*. According to gene abundance, the denitrification pathway might have not outcompeted both the anammox and DNRA pathways (**Fig. 4B)**. Of note, the majority of Patescibacteria members were not been identified with important known nitrogen metabolism genes, suggesting that they might play other roles in the system. No complete nitrification pathway was identified in any of these cMAGs, and the gene encoding ammonia monooxygenase (*amo*) was not found.

Adaptive evolution

To gain insights into the adaptive evolution of the anammox community, an analysis was conducted to identify MGEs in all cMAGs using the latest MGE database (mobileOG-db) with stringent parameters. Among these cMAGs, eight members were found to carry MGEs, with a total of 63 MGEs identified (**Fig. 5A**). Notably, cMAG.4, cMAG.7, cMAG.28, and cMAG.30 were found to harbor sequences related to phages. The majority of the predicted MGEs were associated with integration or excision processes. Of note, one of the anammox bacteria (cMAG.29) was predicted to harbor a discrete distribution of 28 transposons, all of which contained the transposase-encoding gene *tnpA* (**Fig. S5**). Another anammox bacterium (cMAG.28) also harbors three transposons that containing *tnpA*, while the remaining members (including cMAG.27) did not carry *tnpA*. The same identification procedure was

316 performed on the other 26 reference genomes of anammox bacteria. Approximately
317 half of the anammox bacteria were predicted to carry *tnpA*, with gene counts no less
318 than 18 in *Ca*. Jettenia caeni (only one) and all members of *Ca*. Kuenenia
319 stuttgartiensis, and others carried no more than eight *tnpA* genes (**Fig. 5B**).
320 Furthermore, the upstream and downstream genes of *tnpA* in cMAG.29 were found to
321 be different (**Fig. 6**), indicating that they represent the simple transposon (insertion
322 sequence) without additional functional genes.

323 In addition to MGE analysis, HGT events were identified on all cMAGs. A total of
324 50 putative HGT events along with their transfer direction were identified, involving 6
325 phyla and 14 species (**Fig. 7A**). Most of the putative HGT events occurred within the
326 phylum Chloroflexota, accounting for 66% of the total. Putative HGT events within
327 the phylum Bacteroidetes accounted for 34% of the total, with 24% assumed to occur
328 with members of different phyla. At the species level, putative HGT events were the
329 most abundant in one member of the genus UBA12294 (cMAG.13), with 25 donors
330 and 5 recipients. Surprisingly, a putative HGT event was observed between an
331 anammox bacterium (cMAG.27) and a denitrifying bacterium affiliated with
332 Bacteroidota, suggesting that cMAG.27 might have received a gene from cMAG.8.

333 The donor and recipient genes for putative HGT events were identified. A total of
334 26 genes (> 50% of the total) in both donated and received genes could be annotated
335 using the Clusters of Orthologous Groups (COG) database (**Fig. 7B** and **C**). The
336 donated genes are primarily responsible for energy production and conversion (C, 4
337 genes), posttranslational modification, protein turnover, chaperones (O, 4 genes),
338 while four genes were annotated with unknown functions. For example, cMAG.4
339 donated four genes (*sucD*, *fumC*, *atpA*, and *atpD*) to cMAG.9. Interestingly, the
340 denitrifying bacterium cMAG.13 donated 10 genes to another denitrifying bacterium,
341 cMAG.16, and reciprocally, cMAG.16 donated 5 genes to cMAG.13. It should be
342 noted that cMAG.27 might receive a gene encoding IS200 family transposase. No
343 transfer genes directly related to nitrogen removal were identified. However, nearly

344 half of the genes in both donors and recipients were either unannotated or had
345 unknown functions; thus, additional investigation is required.

346 **Discussion**

347 In this study, a total of 30 complete circular prokaryotic genomes were successfully
348 recovered from an anammox community sample using HiFi sequencing. We made
349 slight adjustments to the filtering criteria compared with a previous study (Kim et al.,
350 2022) to include circular contigs that did not meet all the proposed criteria but
351 exhibited other desirable features. According to the predictions by PlasClass (Pellow
352 et al., 2020) (**Table S7)**, predicted values of these substandard contigs were far lower
353 than the threshold (0.5) for plasmids. More importantly, most of these contigs were
354 assigned to Patescibacteria, which are also referred to as candidate phyla radiation
355 bacteria and are known to have much smaller genomes compared with other
356 prokaryotes (Luef et al., 2015; Castelle and Banfield, 2018; Tian et al., 2020). They
357 might have fewer marker genes than other conventional bacteria. These substandard
358 contigs were therefore retained for downstream analysis. In strict terms, some of the
359 recovered cMAGs from this study or previous studies might represent complete
360 chromosomes rather than complete genomes, as the existence of associated MGEs
361 (e.g., plasmids) remains uncertain. For complex cultures, such as anammox
362 community, accurately resolving the link of MGEs to their host complete
363 chromosomes poses a major challenge. To address this problem, we propose that a
364 combination of the recently developed high-throughput single-microbe sequencing
365 (Microbe-seq) (Zheng et al., 2022) with HiFi sequencing would offer an effective
366 strategy.

367 Although hifiasm-meta did not generate the highest number of circular contigs, it
368 yielded cMAGs that accounted for 63% of the total. This is consistent with previous
369 findings and highlights the advantages of hifiasm-meta for the assembly of HiFi reads

370 (Kim et al., 2022). These cMAGs represent anammox bacteria and associated bacteria,
371 including those with low abundance, and ~47% of them may represent novel species,
372 including a novel species of anammox bacteria. This suggests that a considerable
373 number of anammox-associated bacteria remain poorly characterized. The reliability
374 of the recovered cMAGs was supported by the high ANI values with conspecific
375 genomes from previous studies. Our approach outperformed the IHA method (Liu et
376 al., 2020) in terms of using fewer long reads (26.7 Gb vs. 69.4 Gb) and no need for
377 short reads while ensuring the accuracy of circular genome reconstruction,
378 demonstrating the potential for HiFi sequencing to accurately recover prokaryotic
379 genomes from complex environmental microbiomes.

380 cMAGs provide comprehensive and accurate information on the metabolic
381 potential and genetic interactions within the anammox community. Unlike previous
382 MAGs (Lawson et al., 2017; Liu et al., 2020; Kallistova et al., 2022) that were
383 affected by discontinuity and contamination, these cMAGs offer a more complete
384 picture of the community. The anammox system was thought to be autotrophic due to
385 the absence of additional organic carbon sources, but there are still many heterotrophs
386 in this system. Similar phenomena have been widely observed in previous studies
387 (Speth et al., 2016; Lawson et al., 2017; Zhao et al., 2018b). In light of our culture
388 conditions, these co-existing heterotrophic bacteria might be responsible for granular
389 aggregation, supplying growth factors to anammox bacteria, and consuming organic
390 matter.

391 Approximately 70% of the species in the community were potentially engaged in
392 nitrogen removal processes, either through anammox or denitrification pathways. The
393 remaining 30% might not be directly involved in such nitrogen conversion processes.
394 Nevertheless, some of them could perform carbon fixation, which provides organic
395 matter to other co-existing bacteria. These members of Patescibacteria might also play
396 roles in the degradation of poly-N-acetylglucosamine produced by anammox bacteria
397 (Hosokawa et al., 2021). Three anammox bacteria affiliated with *Ca.* Jettenia could

398 conduct DNRA and carbon fixation through the WL pathway, which is consistent with
399 the results of previous studies (Strous et al., 2006; Lawson et al., 2017; Mardanov et
400 al., 2019). Intriguingly, our results indicate that these three anammox bacteria were
401 capable of respiratory ammonification with oxidation acetate, and similar results were
402 observed for the two other anammox bacteria affiliated with *Ca.* Jettenia (Ali et al.,
403 2015; Mardanov et al., 2019). The DNRA capability of anammox bacteria could be a
404 valuable strategy for survival, as they would no longer dependent on other
405 microorganisms for the supply of ammonium and nitrite (Kartal et al., 2007).
406 Furthermore, not all anammox bacteria are capable of carrying out the DNRA
407 pathway, and it could be speculated that these anammox bacteria with the DNRA
408 pathway might be better adapted to environments with a low concentration of
409 ammonium and a high concentration of nitrite or nitrate.

410 Adaptive evolution plays a crucial role in the adaptation of bacteria to different
411 habitats, and both MGEs and HGT contribute to this process (Brito, 2021; Arnold et
412 al., 2022; Shi et al., 2022). We identified abundant MGEs and putative HGT events
413 within the anammox community. Certain members of the community showed
414 evidence of past phage infections, which led to mutations in their genomes. It is well
415 known that transposons can provide a pool of pre-evolved genes that help bacteria
416 adapt quickly to their environment (Dahlberg and Hermansson, 1995). The
417 transposons containing the *tnpA* gene were prevalent in some anammox bacteria,
418 indicating they might play important roles in their environmental adaptation. As
419 mentioned above, anammox bacteria are not available for pure culture to date; thus,
420 molecular biology methods based on monoclones cannot be used for the identification
421 of metabolic pathways or bioaugmentation. Many questions about the basic metabolic
422 pathways of anammox bacteria have not yet been addressed (Peeters and van Niftrik,
423 2019; Kuenen, 2020), challenges (such as the fast start-up and operation under
424 non-optimal conditions) during the full-scale operation of anammox also require
425 attention (Adams et al., 2020; Kouba et al., 2022), and this will require the

426 development of methods for the genome editing of anammox bacteria. We believe that
427 the transposon containing *tnpA* might be one of the breakthroughs for the genome
428 editing of anammox bacteria in mixed cultures.

429 A considerable number of putative HGT events were predicted, suggesting that
430 HGT might be another important strategy for promoting the adaptive evolution of
431 bacteria in this anammox community. The transferred genes are involved in multiple
432 metabolic pathways rather than antibiotic resistance, showing that these putative HGT
433 events might contribute to the metabolic specialization and competitive advantage of
434 these species (Seeleuthner et al., 2018; Wang et al., 2022). Particularly, the putative
435 HGT events mainly occurred in denitrifying bacteria in the phyla Chloroflexota and
436 Bacteroidota. Similar findings were observed in the previous study of a full-scale
437 anammox systems (Wang et al., 2022). It could be inferred that denitrifying bacteria
438 were probably very active in genetic interactions within anammox communities. The
439 putative HGT event between cMAG.27 and cMAG.8 shows that HGT events could
440 occur between anammox bacteria and co-existing bacteria affiliated with distantly
441 related lineages. Moreover, the transferred gene is a transposase-coding gene, again
442 suggesting that some specific transposons could be utilized for the genome editing of
443 anammox bacteria.

444 In summary, our study demonstrates that HiFi sequencing enables the
445 reconstruction of accurate cMAGs from the complex anammox community without
446 the need for Illumina short reads, binning, and reassembly. These cMAGs represent
447 not only high-abundance species, but also low-abundance species in this anammox
448 community. Additionally, these cMAGs provide valuable insights into microbial
449 diversity, metabolic divergence, and genetic interactions within the community, and
450 they may lay a core foundation for a comprehensive database for anammox bacteria
451 and associated microorganisms. The presence of MGEs and putative HGT events
452 suggests ongoing evolution within the community, and they may play an important
453 role in the domestication of the anammox culture. To our knowledge, this is the first

study to describe the functional divergence and adaptive evolution of uncultured bacteria in an anammox community at the complete genome level. Further studies are warranted to confirm the functional divergence and genetic interactions within anammox communities, employing a combination of HiFi sequencing and other techniques.

Conflict of interest

The authors declare no conflict of interest.

Data availability

The 30 cMAGs generated in this study have been deposited in the GenBank under the accession number PRJNA983097. The raw sequencing data have been deposited in the Sequence Read Archive under the accession number PRJNA981667 and PRJNA981689.

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683 **Table 1.** Characteristics of the 30 cMAGs obtained in this study.

ID	Phylum (Genus)	Genome size (Mb)	GC (%)	CDS	GTDB-Tk marker gene	Types of tRNA	Features (5S/16S/23S)
cMAG.1	Actinobacteriota (Unclassified)	2.2	68.58	2,260	118	23	1/1/1
cMAG.2	Armatimonadota (H1-ARM1)	2.9	60.95	2,651	111	23	1/1/1
cMAG.3	Bacteroidota (OLB6)	3.0	49.64	2,427	119	22	2/2/2
cMAG.4	Bacteroidota (BCD5)	3.3	36.15	2,825	119	22	1/1/1
cMAG.5	Bacteroidota (UTCHB3)	3.4	42.13	2,623	118	23	1/1/1
cMAG.6	Bacteroidota (SURF-28)	3.7	34.47	3,351	118	22	1/1/1
cMAG.7	Bacteroidota (OLB8)	3.9	65.21	3,252	119	22	1/1/1
cMAG.8	Bacteroidota (PHOS-HE28)	4.0	41.08	3,258	119	22	2/2/2
cMAG.9	Bacteroidota (UBA2336)	4.1	43.59	3,752	117	23	2/2/2
cMAG.10	Bdellovibrionota (Unclassified)	2.3	55.04	2,089	93	18	1/1/1
cMAG.11	Chloroflexota (UBA7227)	3.5	59.60	3,200	116	24	1/1/1
cMAG.12	Chloroflexota (UBA7227)	3.6	59.76	3,268	116	24	1/1/1
cMAG.13	Chloroflexota (UBA12294)	3.9	53.51	3,590	111	23	1/1/1
cMAG.14	Chloroflexota (UBA12294)	4.0	53.65	3,738	110	23	1/1/1
cMAG.15	Chloroflexota (OLB14)	4.1	54.13	3,820	113	23	1/1/1
cMAG.16	Chloroflexota (OLB14)	4.4	53.56	4,388	115	24	1/1/1
cMAG.17	Desulfobacterota (UBA5799)	2.8	57.87	2,559	119	23	1/1/1
cMAG.18	Patescibacteria (Unclassified)	1.0	44.78	956	89	20	1/1/1
cMAG.19	Patescibacteria (Unclassified)	1.1	39.76	982	84	21	1/1/1
cMAG.20	Patescibacteria (Unclassified)	1.2	60.26	1,204	95	21	1/1/1

cMAG.21	Patescibacteria (OLB21)	1.2	38.42	1,073	93	21	1/1/1
cMAG.22	Patescibacteria (Unclassified)	0.6	52.17	629	82	21	1/1/1
cMAG.23	Patescibacteria (BOKC01)	0.7	40.37	698	84	22	1/1/2
cMAG.24	Patescibacteria (UBA12026)	0.8	34.42	947	80	20	1/1/1
cMAG.25	Patescibacteria (UBA919)	0.9	36.84	827	90	22	1/2/1
cMAG.26	Patescibacteria (Unclassified)	0.9	41.50	858	87	21	1/1/1
cMAG.27	Planctomycetota (*Ca.* Jettenia)	3.5	41.60	3,145	108	23	2/2/2
cMAG.28	Planctomycetota (*Ca.* Jettenia)	3.8	39.42	3,292	107	24	2/2/2
cMAG.29	Planctomycetota (*Ca.* Jettenia)	4.0	40.01	3,510	107	24	2/2/2
cMAG.30	Proteobacteria (QUBU01)	3.4	66.68	3,021	118	23	1/1/1

Figure legends

Fig. 1. Workflow for filtering the HiFi cMAGs from three assemblies by hifiasm-meta, Flye, and Canu.

Fig. 2. The phylogenetic placement and abundance of cMAGs recovered from anammox granular sludge. The phylogenetic tree was inferred based on the multiple sequence alignments of conserved marker genes from 30 cMAGs using the GTDB-Tk.

Fig. 3. The MEBS scores for the nitrogen (N), iron (Fe), oxygen (O), carbon (C) and sulfur (S) metabolic pathways of 30 cMAGs.

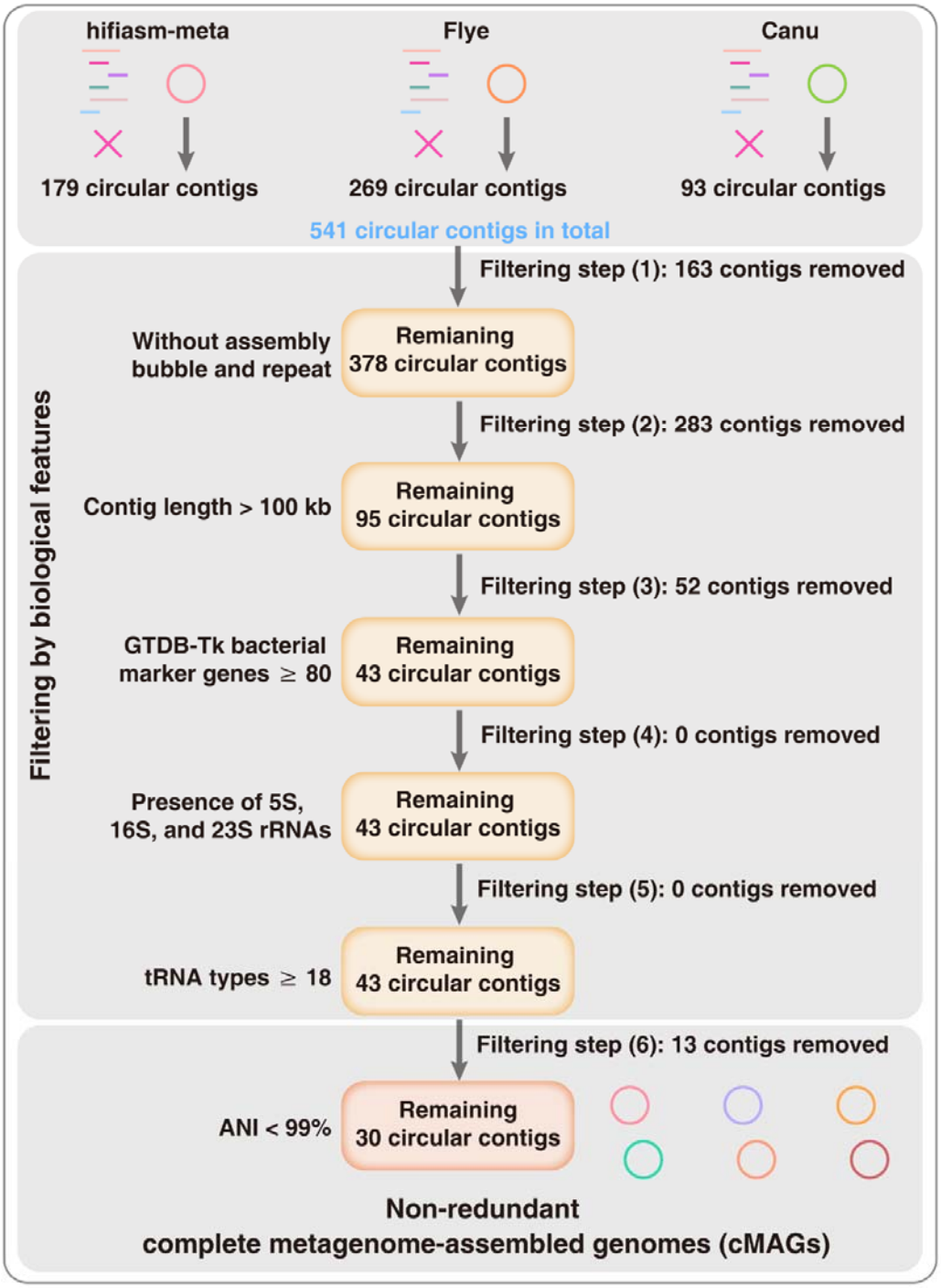
Fig. 4. The potential for nitrogen metabolism of 30 cMAGs. (**A**) Nitrogen metabolism marker genes. (**B**) Proposed pathway for nitrogen conversion in the anammox community. The number indicates the number of species with genes encoding a given step. Colored squares indicate gene abundances.

Fig. 5. Mobile genetic elements (MGEs) identified in the cMAGs and reference genomes. (**A**) MGEs identified in cMAGs. (**B**) The *tnpA* counts identified in two *Ca.* Jettenia species of this study and other anammox species.

Fig. 6. The predicted 28 gene clusters containing *tnpA* of cMAG.29.

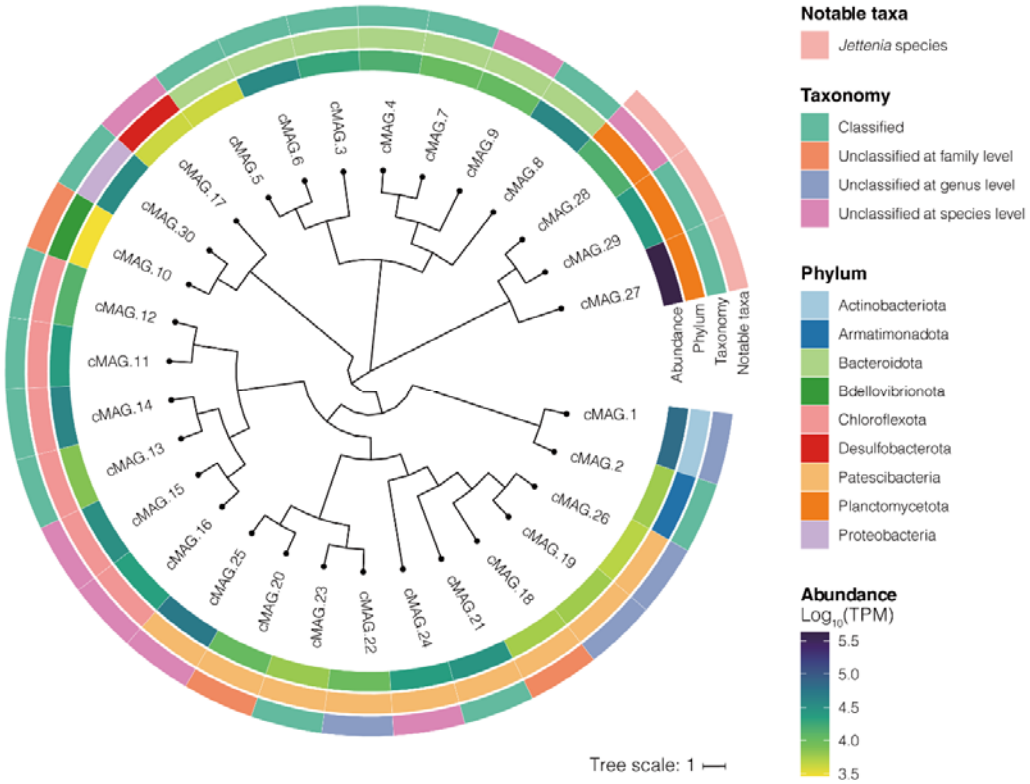
Fig. 7. Network and functions of HGT genes of the anammox community. (**A**) HGT network of the anammox community; the direction and width of blue arrows indicate the direction of transfer and gene counts, respectively; the size of the node represents

710 the count of connected edges. (**B**) and (**C**) Bubble size indicates the count of HGT
711 genes annotated with COG functional categories. C: Energy production and
712 conversion; D: Cell cycle control, cell division, chromosome partitioning; E: Amino
713 acid transport and metabolism; H: Coenzyme transport and metabolism; J: Translation,
714 ribosomal structure and biogenesis; L: Replication, recombination and repair; N: Cell
715 motility; O: Posttranslational modification, protein turnover; S: Function unknown; T:
716 Signal transduction mechanisms.


hifiasm-meta
Flye
Canu
179 circular contigs
269 circular contigs
93 circular contigs
541 circular contigs in total
Filtering step (1): 163 contigs removed
Filtering by biological features
Without assembly bubble and repeat
Remianing 378 circular contigs
Filtering step (2): 283 contigs removed
Contig length > 100 kb
Remaining 95 circular contigs
Filtering step (3): 52 contigs removed
GTDB-Tk bacterial marker genes ≥ 80
Remaining 43 circular contigs
Filtering step (4): 0 contigs removed
Presence of 5S, 16S, and 23S rRNAs
Remaining 43 circular contigs
Filtering step (5): 0 contigs removed
tRNA types ≥ 18
Remaining 43 circular contigs
Filtering step (6): 13 contigs removed
ANI < 99%
Remaining 30 circular contigs
Non-redundant
complete metagenome-assembled genomes (cMAGs)

717

718 **Fig. 1**


Notable taxa
Jettenia species
Taxonomy
Classified
Unclassified at family level
Unclassified at genus level
Unclassified at species level
Phylum
Actinobacteriota
Armatimonadota
Bacteroidota
Bdellovibrionota
Chloroflexota
Desulfobacterota
Patescibacteria
Planctomycetota
Proteobacteria
Abundance
Log10(TPM)
5.5
5.0
4.5
4.0
3.5
Tree scale: 1
Abundance
Phylum
Taxonomy
Notable taxa
cMAG.1
cMAG.2
cMAG.26
cMAG.19
cMAG.18
cMAG.21
cMAG.24
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cMAG.9
cMAG.8
cMAG.28
cMAG.29
cMAG.27

Fig. 2

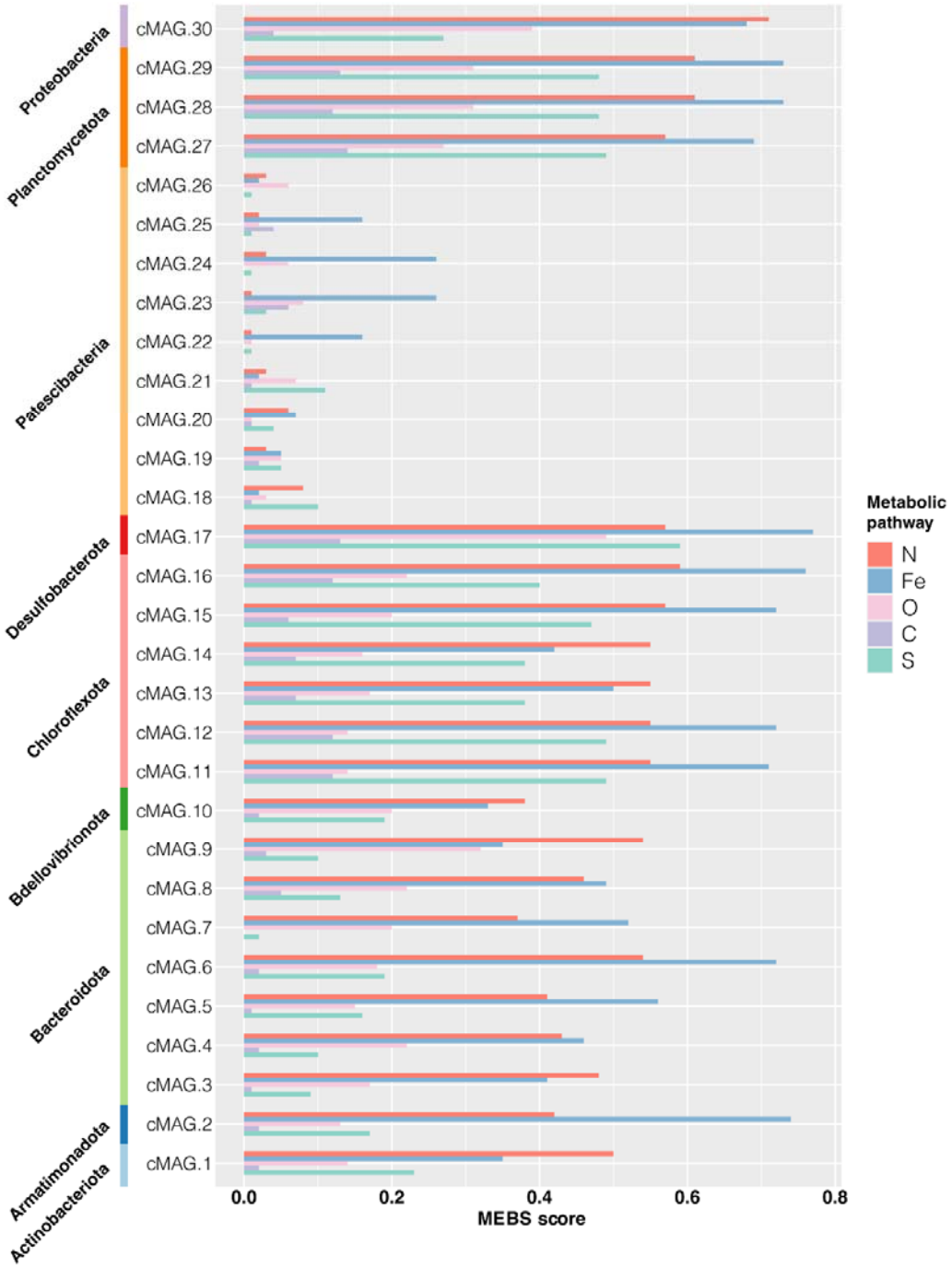
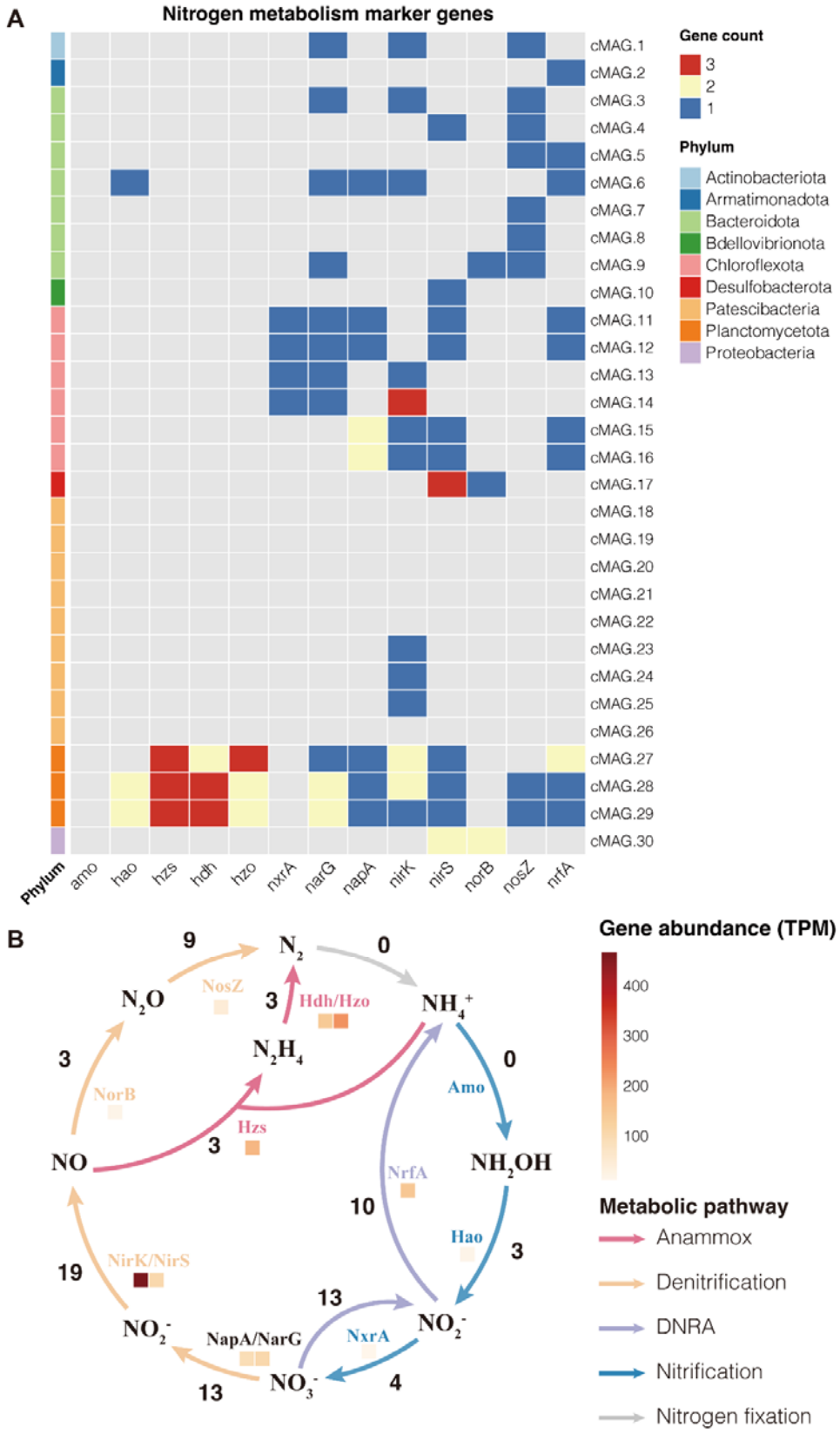

Proteobacteria
Planctomycetota
Patescibacteria
Desulfobacterota
Chloroflexota
Bdellovibrionota
Bacteroidota
Armatimonadota
Actinobacteriota
cMAG.30
cMAG.29
cMAG.28
cMAG.27
cMAG.26
cMAG.25
cMAG.24
cMAG.23
cMAG.22
cMAG.21
cMAG.20
cMAG.19
cMAG.18
cMAG.17
cMAG.16
cMAG.15
cMAG.14
cMAG.13
cMAG.12
cMAG.11
cMAG.10
cMAG.9
cMAG.8
cMAG.7
cMAG.6
cMAG.5
cMAG.4
cMAG.3
cMAG.2
cMAG.1
0.0
0.2
0.4
0.6
0.8
MEBS score
Metabolic pathway
N
Fe
O
C
S

Fig. 3


A
Nitrogen metabolism marker genes
Gene count
3
2
1
Phylum
Actinobacteriota
Armatimonadota
Bacteroidota
Bdellovibrionota
Chloroflexota
Desulfobacterota
Patescibacteria
Planctomycetota
Proteobacteria
cMAG.1
cMAG.2
cMAG.3
cMAG.4
cMAG.5
cMAG.6
cMAG.7
cMAG.8
cMAG.9
cMAG.10
cMAG.11
cMAG.12
cMAG.13
cMAG.14
cMAG.15
cMAG.16
cMAG.17
cMAG.18
cMAG.19
cMAG.20
cMAG.21
cMAG.22
cMAG.23
cMAG.24
cMAG.25
cMAG.26
cMAG.27
cMAG.28
cMAG.29
cMAG.30
Phylum
amo
hao
hzs
hdh
hzo
nxrA
narG
napA
nirK
nirS
norB
nosZ
nrfA
B
Gene abundance (TPM)
400
300
200
100
Metabolic pathway
Anammox
Denitrification
DNRA
Nitrification
Nitrogen fixation
N2
N2O
N2H4
NH4+
NH2OH
NO
NO2-
NO3-
NO2-
9
0
3
3
0
3
10
3
19
13
13
4
NosZ
Hdh/Hzo
NorB
Hzs
Amo
NrfA
Hao
NirK/NirS
NapA/NarG
NxrA

723 **Fig.**

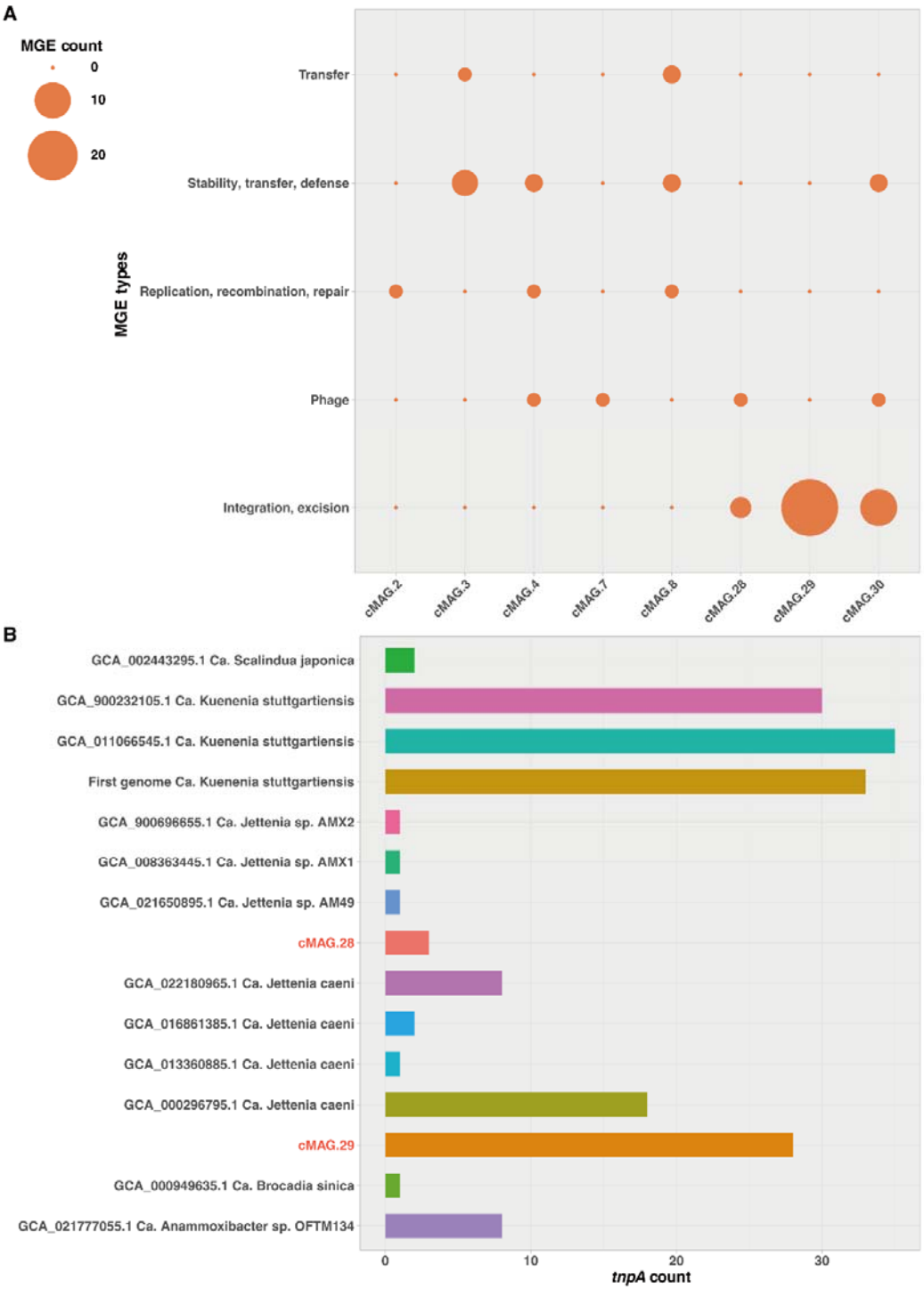

A
MGE count
0
10
20
MGE types
Transfer
Stability, transfer, defense
Replication, recombination, repair
Phage
Integration, excision
cMAG.2
cMAG.3
cMAG.4
cMAG.7
cMAG.8
cMAG.28
cMAG.29
cMAG.30
B
GCA_002443295.1 Ca. Scalindua japonica
GCA_900232105.1 Ca. Kuenenia stuttgartiensis
GCA_011066545.1 Ca. Kuenenia stuttgartiensis
First genome Ca. Kuenenia stuttgartiensis
GCA_900696655.1 Ca. Jettenia sp. AMX2
GCA_008363445.1 Ca. Jettenia sp. AMX1
GCA_021650895.1 Ca. Jettenia sp. AM49
cMAG.28
GCA_022180965.1 Ca. Jettenia caeni
GCA_016861385.1 Ca. Jettenia caeni
GCA_013360885.1 Ca. Jettenia caeni
GCA_000296795.1 Ca. Jettenia caeni
cMAG.29
GCA_000949635.1 Ca. Brocadia sinica
GCA_021777055.1 Ca. Anammoxibacter sp. OFTM134
0
10
20
30
tnpA count

Fig. 5

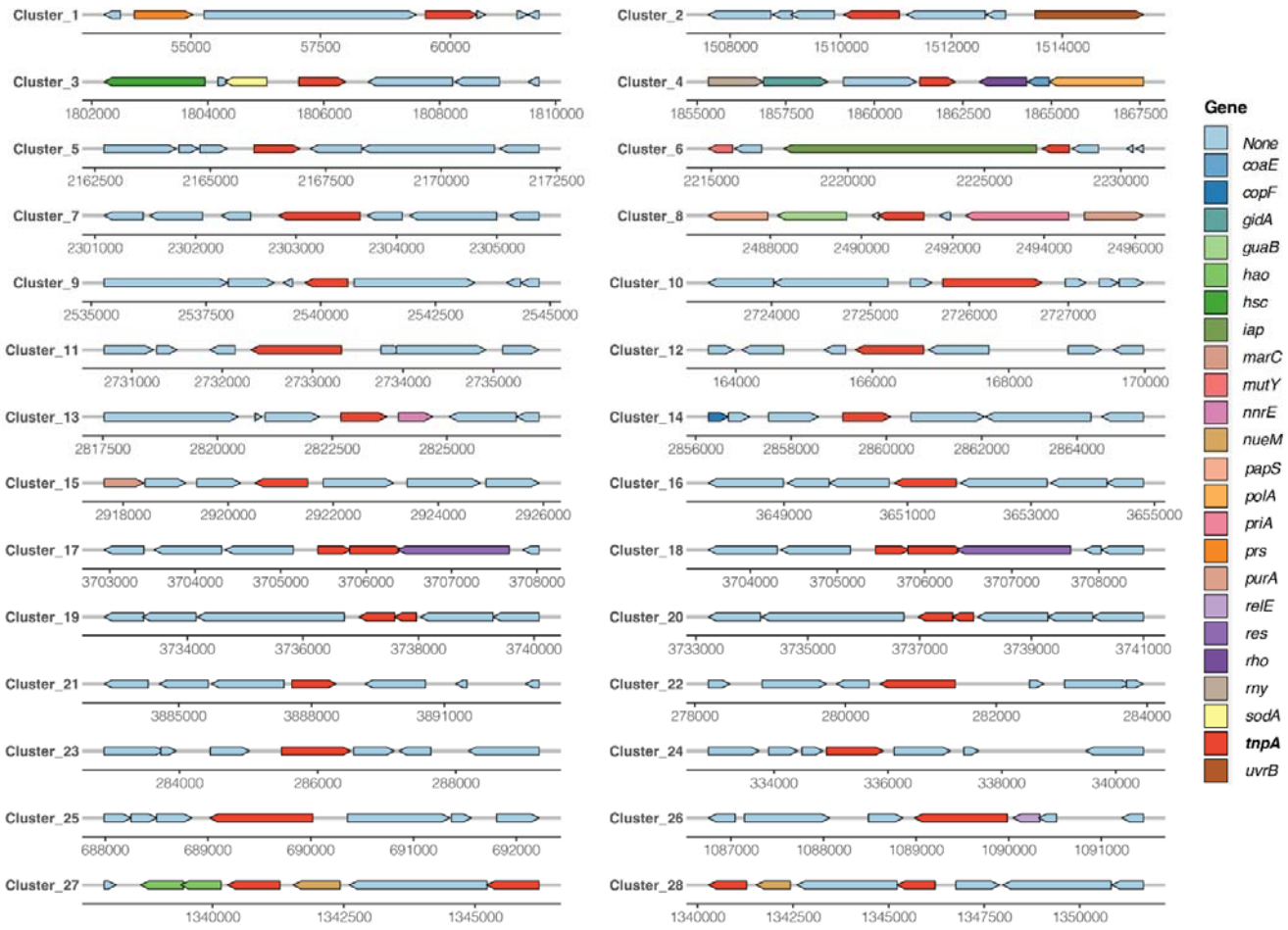

Cluster_1
55000
57500
60000
Cluster_2
1508000
1510000
1512000
1514000
Cluster_3
1802000
1804000
1806000
1808000
1810000
Cluster_4
1855000
1857500
1860000
1862500
1865000
1867500
Cluster_5
2162500
2165000
2167500
2170000
2172500
Cluster_6
2215000
2220000
2225000
2230000
Cluster_7
2301000
2302000
2303000
2304000
2305000
Cluster_8
2488000
2490000
2492000
2494000
2496000
Cluster_9
2535000
2537500
2540000
2542500
2545000
Cluster_10
2724000
2725000
2726000
2727000
Cluster_11
2731000
2732000
2733000
2734000
2735000
Cluster_12
164000
166000
168000
170000
Cluster_13
2817500
2820000
2822500
2825000
Cluster_14
2856000
2858000
2860000
2862000
2864000
Cluster_15
2918000
2920000
2922000
2924000
2926000
Cluster_16
3649000
3651000
3653000
3655000
Cluster_17
3703000
3704000
3705000
3706000
3707000
3708000
Cluster_18
3704000
3705000
3706000
3707000
3708000
Cluster_19
3734000
3736000
3738000
3740000
Cluster_20
3733000
3735000
3737000
3739000
3741000
Cluster_21
3885000
3888000
3891000
Cluster_22
278000
280000
282000
284000
Cluster_23
284000
286000
288000
Cluster_24
334000
336000
338000
340000
Cluster_25
688000
689000
690000
691000
692000
Cluster_26
1087000
1088000
1089000
1090000
1091000
Cluster_27
1340000
1342500
1345000
Cluster_28
1340000
1342500
1345000
1347500
1350000
Gene
None
coaE
copF
gidA
guaB
hao
hsc
iap
marC
mutY
nnrE
nueM
papS
polA
priA
prs
purA
relE
res
rho
rny
sodA
tnpA
uvrB

Fig. 6

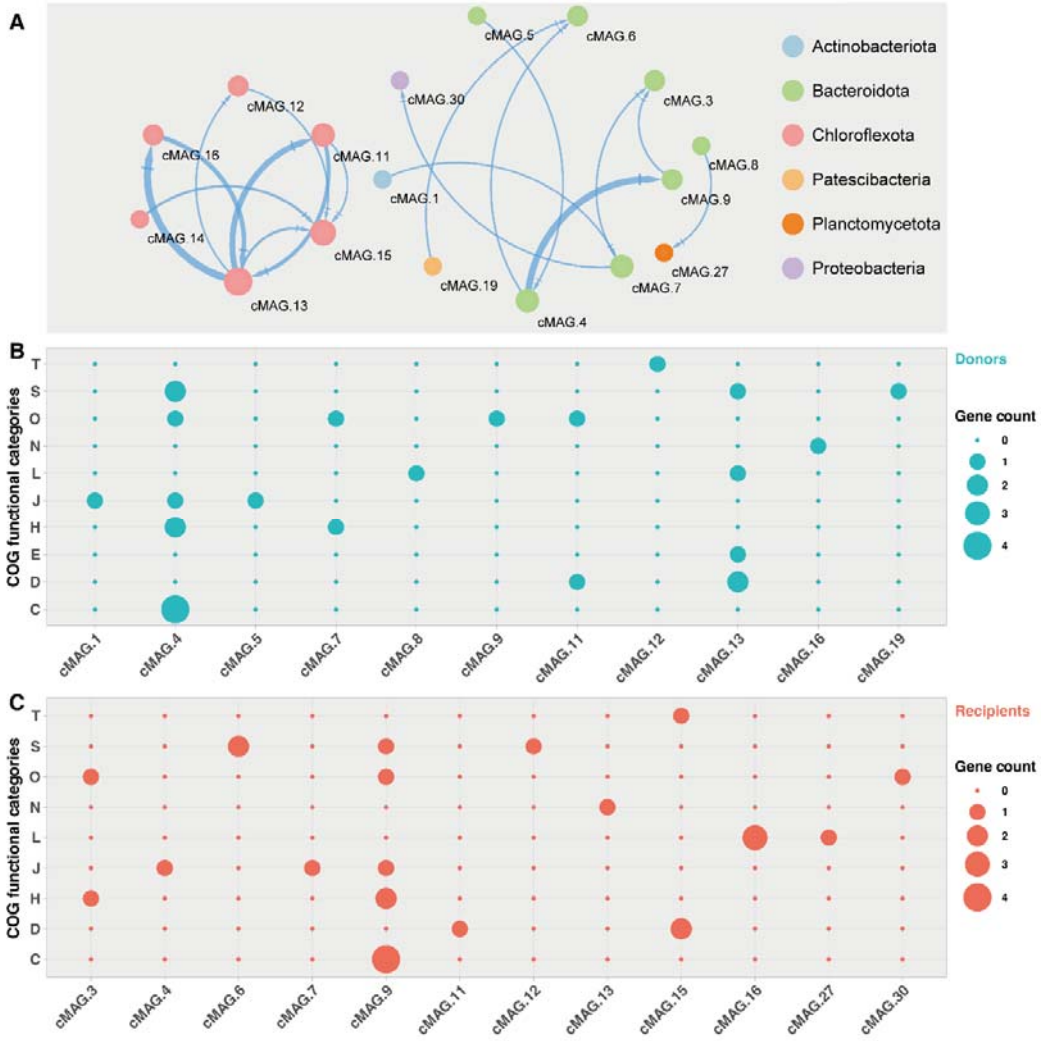
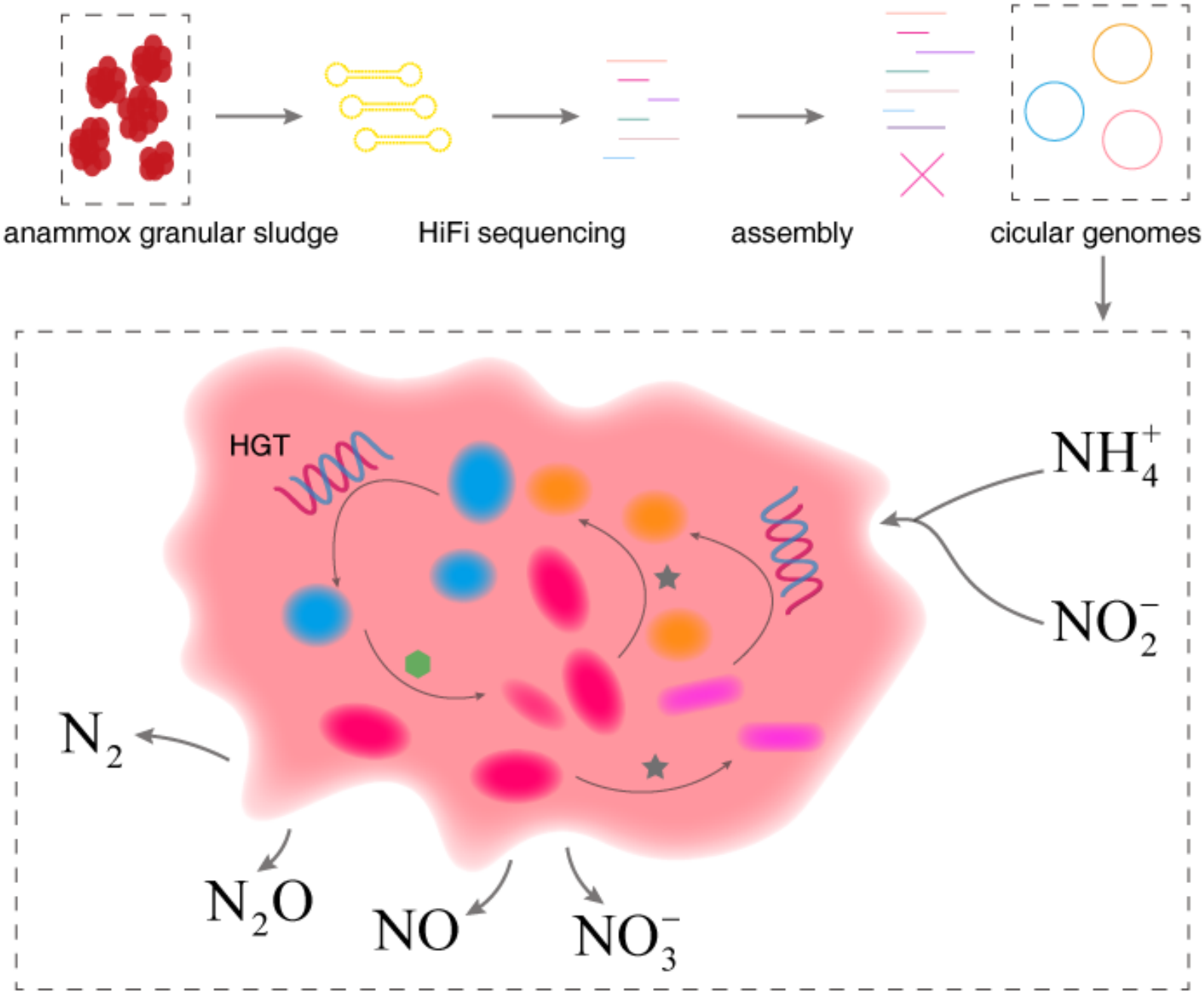

A
cMAG.5
cMAG.6
cMAG.12
cMAG.30
cMAG.3
cMAG.16
cMAG.11
cMAG.8
cMAG.1
cMAG.9
cMAG.14
cMAG.15
cMAG.27
cMAG.19
cMAG.7
cMAG.13
cMAG.4
Actinobacteriota
Bacteroidota
Chloroflexota
Patescibacteria
Planctomycetota
Proteobacteria
B
Donors
Gene count
0
1
2
3
4
COG functional categories
T
S
O
N
L
J
H
E
D
C
cMAG.1
cMAG.4
cMAG.5
cMAG.7
cMAG.8
cMAG.9
cMAG.11
cMAG.12
cMAG.13
cMAG.16
cMAG.19
C
Recipients
Gene count
0
1
2
3
4
COG functional categories
T
S
O
N
L
J
H
D
C
cMAG.3
cMAG.4
cMAG.6
cMAG.7
cMAG.9
cMAG.11
cMAG.12
cMAG.13
cMAG.15
cMAG.16
cMAG.27
cMAG.30

Fig. 7


anammox granular sludge
HiFi sequencing
assembly
cicular genomes
HGT
NH_4^+
NO_2^-
N_2
N_2O
NO
NO_3^-