

Cometabolism of the superphylum *Patescibacteria* with anammox bacteria in a long-term freshwater anammox column reactor

Suguru Hosokawa ¹, Kyohei Kuroda ², Takashi Narihiro ², Yoshiteru Aoi ³, Noriatsu Ozaki ¹, Akiyoshi Ohashi ¹, Tomonori Kindaichi ^{1,*}

Table 1. Summary of metagenomic data used in this study.

Platform	Sample	Total read bases (bp)	Total reads	GC (%)	Q20 (%)
HiSeq X	Day 4989	38,065,344,474	252,088,374	57.4	93.08
HiSeq X	Day 5054	40,701,966,044	269,549,444	54.8	93.98
HiSeq X	Day 5073	35,841,411,642	237,360,342	50.1	94.33
PacBio	Day 5054	504,195,732	80,740 ¹	56.3	100

¹as circular consensus reads > Q20.

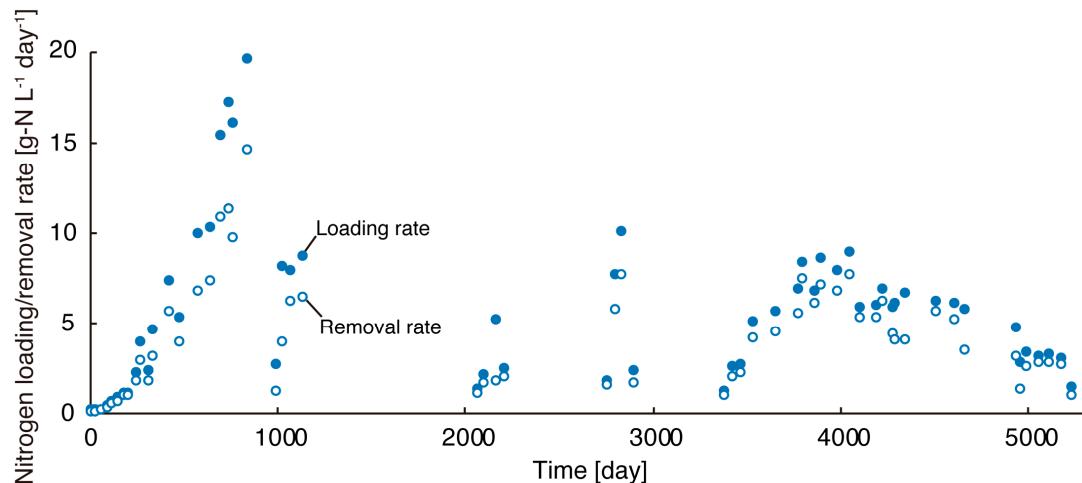


Figure S1. Nitrogen loading and removal rates of the up-flow column anammox bioreactor enriched using activated sludge. The filled and open circles represent the nitrogen loading and nitrogen removal rates, respectively.

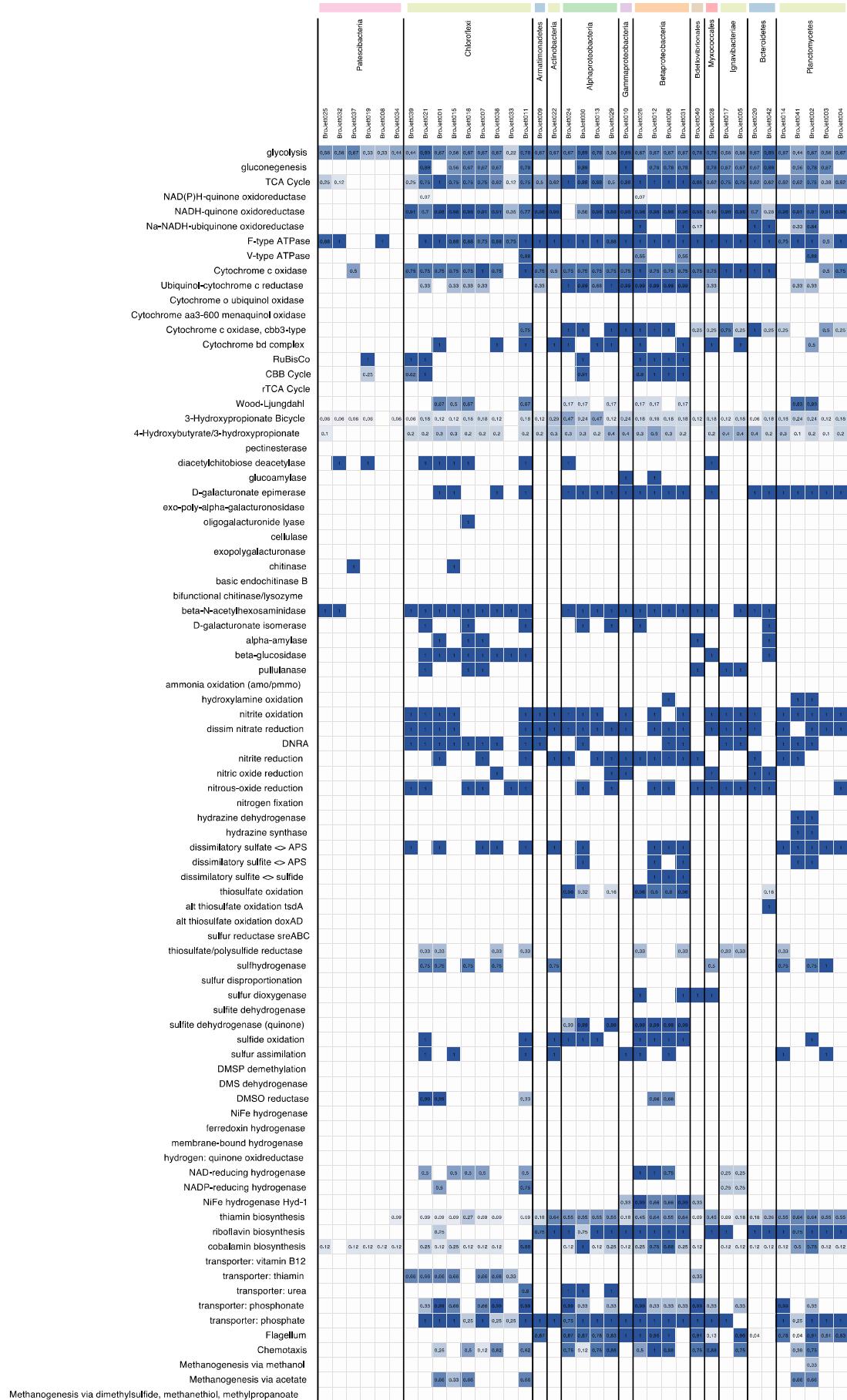


Figure S2. Heat map showing the metabolic function of each bin based on KEGG and Blastp.



Figure S2. Continued.

Table S2. Summary of genes related to the Poly-beta-1,6-N-acetyl-D-glucosamine synthase production in bins.

Bin ID	Taxonomy	Gene ID	Annotation based on KEGG	BLAST best hit			
				Sequence ID	Definition	Organism	Identity (%)
BroJett002	Brocadia	JLIMDFLJ_00876	Poly-beta-1,6-N-acetyl-D-glucosamine synthase (PgaC)	WP_052565201.1	Glycosyltransferase	Candidatus Brocadia sinica JPN1	100
BroJett002	Brocadia	JLIMDFLJ_01665	Poly-beta-1,6-N-acetyl-D-glucosamine N-deacetylase (PgaB)	WP_082059105.1	Polysaccharide deacetylase family protein	Candidatus Brocadia sinica JPN1	100
BroJett002	Brocadia	JLIMDFLJ_01715	Putative poly-beta-1,6 N-acetyl-D-glucosamine export porin (PgaA)	WP_052563194.1	Hypothetical protein	Candidatus Brocadia sinica JPN1	100
BroJett041	Jettenia	PMPPPIBB_01341	Poly-beta-1,6-N-acetyl-D-glucosamine synthase (PgaC)	NUN23464.1	Glycosyltransferase	Candidatus Jettenia caeni KSU-1	100
BroJett041	Jettenia	PMPPPIBB_01485	Poly-beta-1,6-N-acetyl-D-glucosamine synthase (PgaC)	KAA0247410.1	Glycosyltransferase family 2 protein	Candidatus Jettenia sp. AMX1	100
BroJett041	Jettenia	PMPPPIBB_00884	Putative poly-beta-1,6-N-acetyl-D-glucosamine synthase (PgaC)	KAA0249591.1	Glycosyltransferase	Candidatus Jettenia sp. AMX1	100
BroJett005	Ignavibacteriia	PDPPONAM_01618	Poly-beta-1,6-N-acetyl-D-glucosamine synthase (PgaC)	KAB2850933.1	Glycosyltransferase family 2 protein	Ignavibacterium sp. SB31	100
BroJett005	Ignavibacteriia	PDPPONAM_00653	Poly-beta-1,6-N-acetyl-D-glucosamine synthase (PgaC)	HCY77909.1	Glycosyltransferase family 2 protein	Ignavibacteriales bacterium UBA8501	59
BroJett005	Ignavibacteriia	PDPPONAM_02674	Poly-beta-1,6-N-acetyl-D-glucosamine synthase (PgaC)	QKJ99320.1	Glycosyltransferase	Ignavibacteriae bacterium IGN3	98
BroJett005	Ignavibacteriia	PDPPONAM_02814	Poly-beta-1,6-N-acetyl-D-glucosamine synthase (PgaC)	QKJ98219.1	Glycosyltransferase family 2 protein	Ignavibacteriae bacterium IGN3	95