Electronic Supplementary Material (ESI) for Environmental Science: Water Research & Technology.

Supplementary Information

Characterization of the nitrogen-transforming microbial community in the biofilms of a full-scale rotating biological contactor system treating wastewater from a fresh market building

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Table S1. Primers used in this study.

Microorganism, target gene	**Primer set**	**Annealing temp (°C)**		**Reference**
		PCR*	**qPCR**	
AOA, *amoA*	Arch-*amoA*F Arch-*amoA*R	53	53	(1)
AOB, *amoA*	*amoA*-1F *amoA*-2R	56	53	(2)
Anammox, 16S rRNA	A438f A684r	55	55	(3)
Comammox, *amoA*	*comamoA* AF *comamoA* SR	58	58	(4)
Nitrospira, nxrB	nxrB169f nxrB638r	56.2	56	(5)
Nitrobactor, nxrA	F1norA R2norA	60	55	(6)
Nitrotoga, 16S rRNA	Ntoga124F Ntoga1462R	63	-	(7)
DNRA, *nrfA*	nrfA2aw nrfAR1	53	-	(8)
	F1nrfA R1nrfA	45	-	(9)

*Primers were added with overhang adapters for sequencing analysis
forward overhang sequences: 5'TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG-[locus-specific sequence]
reverse overhang sequences: 5'GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG-[locus-specific sequence]

References

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Table S2. Diversity indices of T1 and T2 samples

	T1	**T2**
Ace	1,319	1,477
Chao1	1,325	1,480
Shannon	8.69	8.88

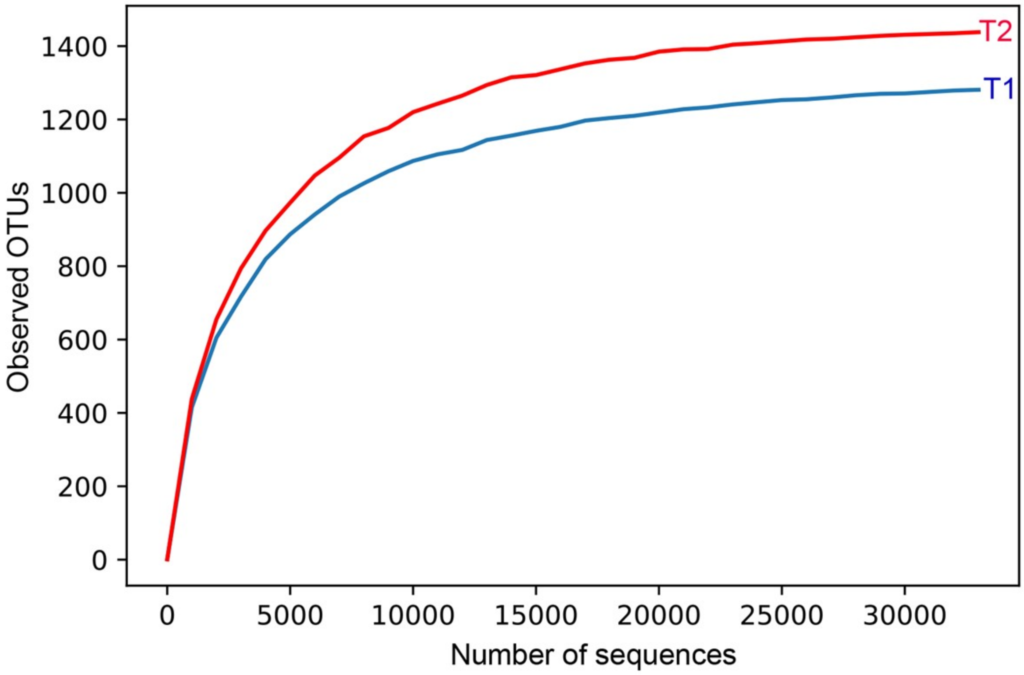

Figure S1. Rarefaction curves of T1 and T2 samples

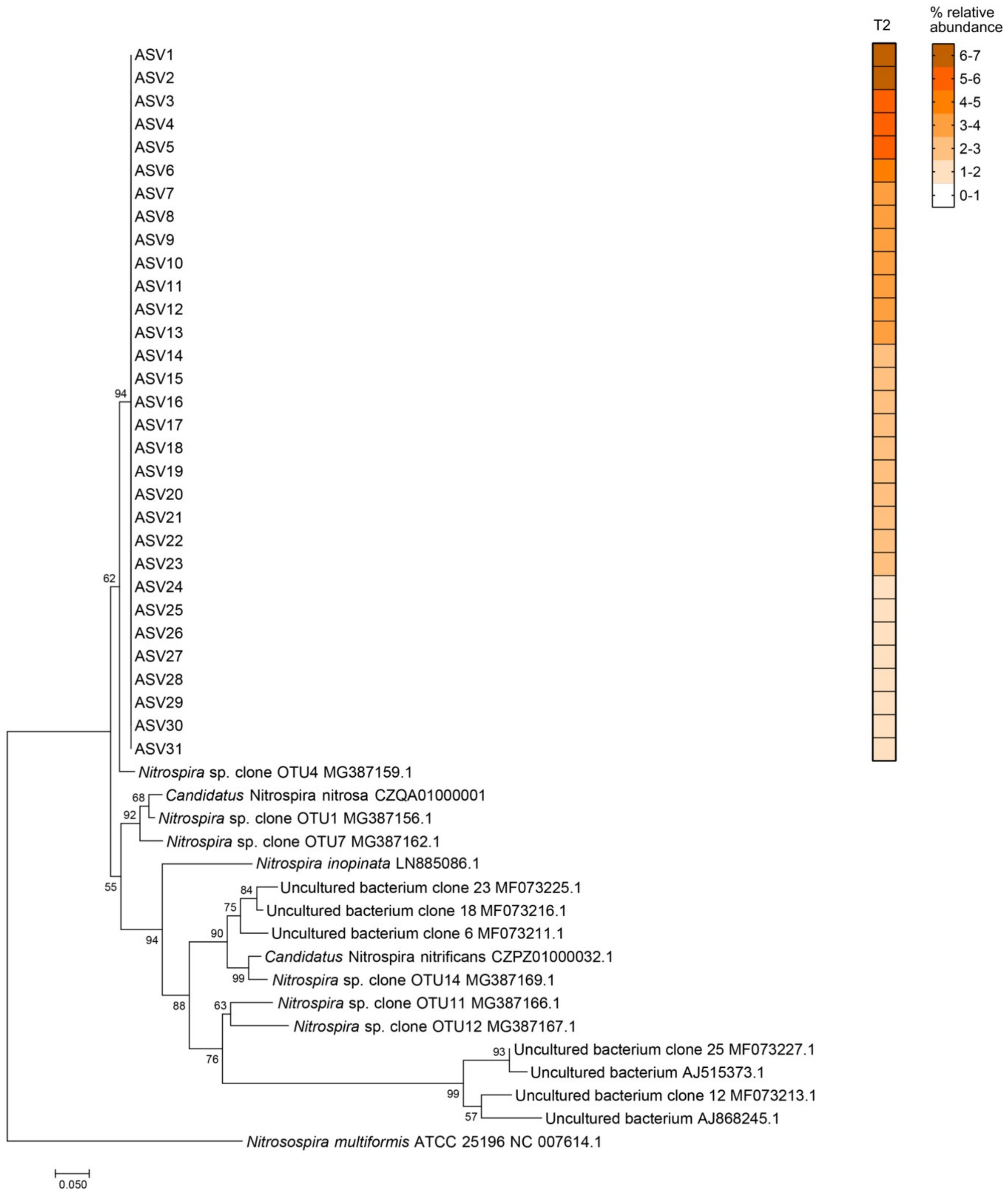

Figure S2. Neighbor-joining tree calculated based on sequences of comammox *amoA* gene fragments. The heat map on the right was generated based on the ASVs that show ≥1% relative abundance of sequences in the sample. In total, >94% of the total sequences was included in the analysis.

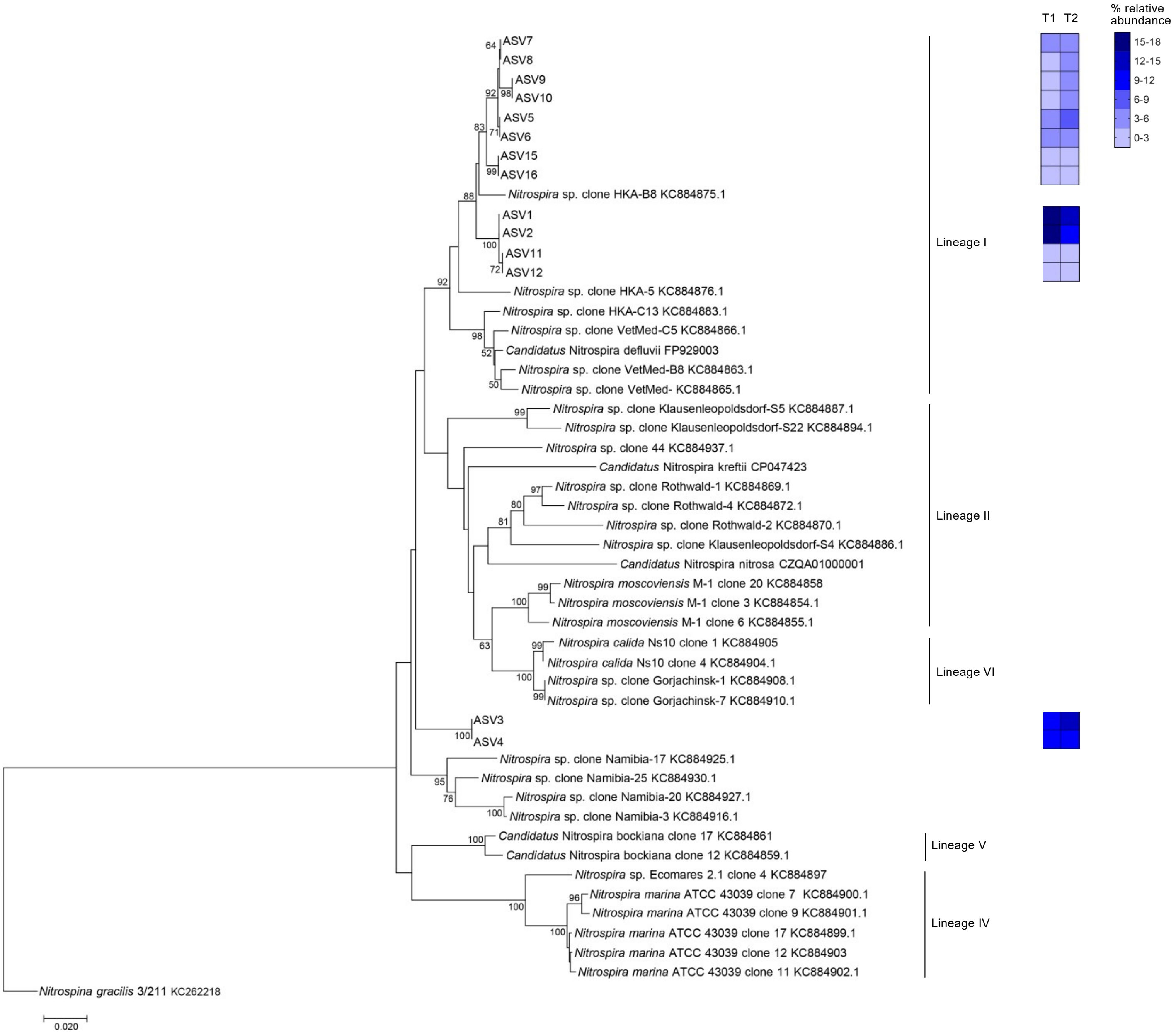

Figure S3. Neighbor-joining tree calculated based on sequences of *Nitrospira nxrB* gene fragments. The heat map on the right was generated based on the ASVs that show ≥1% relative abundance of sequences in each sample. In total, >80% of the total sequences were included in the anlysis.