

Enhanced nitrite accumulation at mainstream conditions by a combination of free ammonia-based sludge treatment and low dissolved oxygen: reactor performance and microbiome analysis

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Table S1. Primers description used in this study

Target	primer	Sequence (5'-3')	reference
qPCR			
Bacteria	1055F	5'-ATGGCTGTCGTCAGCT-3'	1
	1392R	5'-ACGGGCGGTGTGTAC-3'	
AOB	CTO189f A/B	5'-GGAGRAAAGCAGGGGATCG-3'	2
	CTO189fC	5'-GGAGGAAAGTAGGGGATCG-3'	
<i>Nitrobacter</i>	RT1r	5'-CGTCCTCTCAGACCARCT-3'	3
	Nitro-1198f	5'-CCCCTAGCAAATCTCAAAAAACCG-3'	
<i>Nitrospira</i>	Nitro-1423R	5'-CTTCACCCCAGTCGCTGACC-3'	4
	NSR-1113f	5'-CCTGCTTTCAGTTGCTACCG-3'	
	NSR-1264R	5'-GTTTGCAGCGCTTGTACCG-3'	
High throughput sequencing			
Bacteria	341F	5'-CCTACGGGNGGCWGCAG-3'	5
	805R	5'-GACTACHVGGGTATCTAATCC-3'	

Table 2S. α -diversity index of bacterial communities among all biomass samples from the experimental reactor and the control reactor for clustering at 97% identity

Sample ID	OTUs	Shannon	ACE	Chao1	Coverage	Simpson
Seed sludge	316	2.974923	381.758273	393	0.998591	0.107252
C1	441	3.134701	557.816206	545.590909	0.99752	0.105
E1	519	3.722303	675.26718	724.909091	0.997029	0.051988
C2	595	4.065057	750.081716	750.012658	0.996969	0.037005
E2	626	3.985393	844.629792	855.4	0.99695	0.048427
C3	706	4.226328	848.782354	860.011111	0.997177	0.037181
E3	559	4.102786	732.909647	737.888889	0.995169	0.034825
C4	563	3.78523	751.542229	746.825	0.996286	0.051295
E4	599	3.745925	839.328063	827.735632	0.995784	0.051911
C5	509	3.445929	664.670992	664.208333	0.997481	0.069149
E5	542	3.342467	725.636759	684.738636	0.997218	0.095371

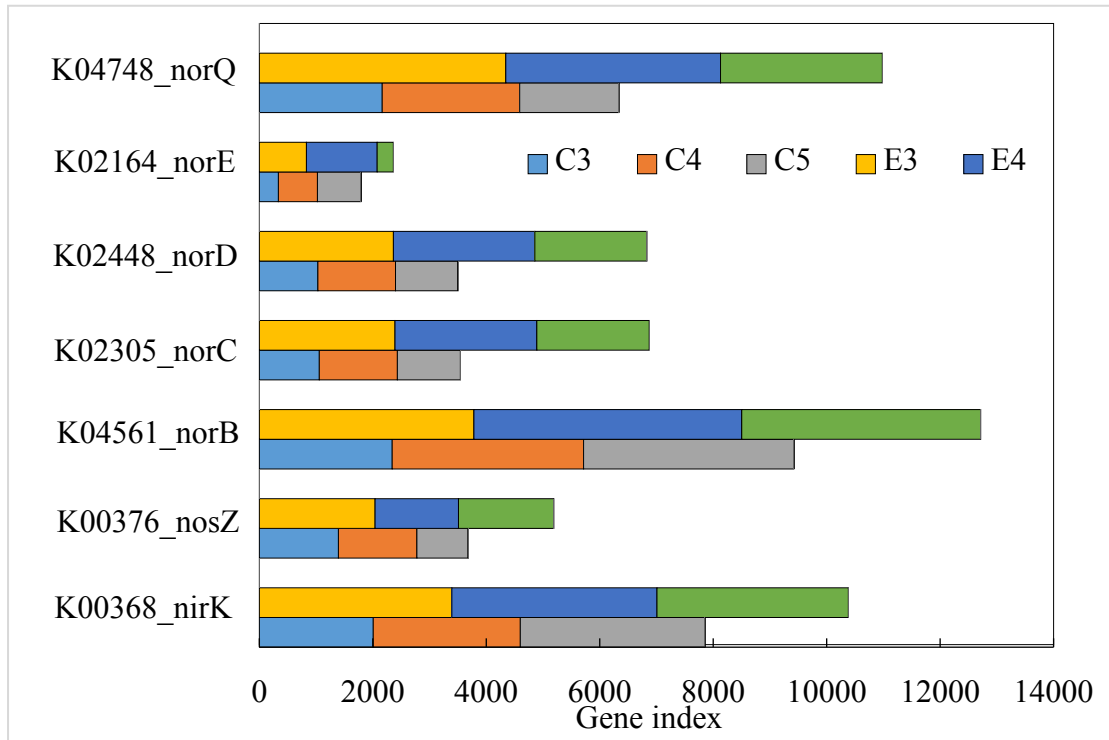


Fig. S1. Key genes involved in denitrification by PICRUSt prediction.

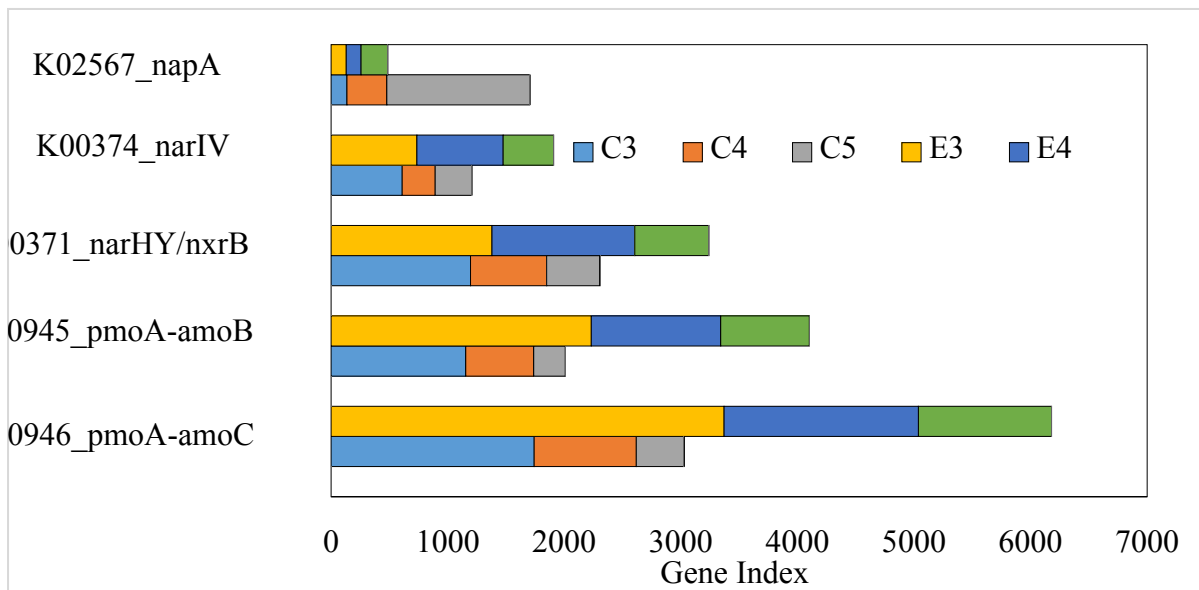


Fig. S2. Similar functional genes involved in nitrification by PICRUSt prediction.

Reference

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