

Supplementary Information

***In-situ* sludge reduction in membrane-controlled anoxic-oxic-anoxic bioreactor: Performance and mechanism**

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Membranes

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Table S1. Chemical composition of synthetic wastewater.

Components	Concentration (mg/L)
Glucose	1000
NH ₄ Cl	140
KH ₂ PO ₄	25
NaNO ₃	40
MgSO ₄ ·7H ₂ O	5
FeCl ₃	2.33
NaHCO ₃	Appropriate to maintain pH = 7.0

Table S2. The average \pm standard deviation of basic quality parameters of effluent in three different bioreactors (n=25).

Items	Influent (mg/L)	Effluent (mg/L)			Removal (%)		
		MBR _{control}	AOA ₉₀	AOA ₈₀	MBR _{control}	AOA ₉₀	AOA ₈₀
DOC	399.44 \pm 2.36	2.32 \pm 0.81	3.38 \pm 1.21	3.14 \pm 1.71	>99.00	>99.00	>99.00
TP	6.08 \pm 0.17	0.07 \pm 0.14	0.62 \pm 0.46	0.65 \pm 0.25	98.72 \pm 2.25	89.82 \pm 7.51	89.28 \pm 4.16
TN	40.05 \pm 0.35	2.43 \pm 1.76	2.19 \pm 1.23	1.77 \pm 1.55	93.93 \pm 4.40	94.52 \pm 3.08	95.58 \pm 3.87

Table S3. The average of NH_4^+ and NO_3^- in the supernatant of different treatment units of MBRs (n=14).

Items	MBR _{control}			AOA ₉₀			AOA ₈₀		
	Anoxic	Oxic	M-tank	Anoxic	Oxic	M-tank	Anoxic	Oxic	M-tank
NH_4^+ (mg/L)	1.73±1.52	0.24±0.36	0.14±0.23	6.71±2.18	0.47±0.63	0.93±1.33	3.23±2.87	0.25±0.31	1.12±1.36
NO_3^- (mg/L)	0.18±0.32	1.62±1.43	1.60±1.57	0.14±0.16	1.05±0.77	0.20±0.61	0.21±0.21	1.57±1.08	0.62±0.75

Table S4. Sequencing of bacterial 16S rRNA gene along with alpha diversity of microbial taxa in three bioreactors.

Sample description	Sequencing results		Species richness	Species diversity	
	Effective tags	OTUs	Chao-1	Shannon	Simpson
MBR _{control} -A-0d	49148	1700	1700.3	6.78	0.033
MBR _{control} -O-0d	50916	1664	1664.5	6.65	0.0525
MBR _{control} -M-0d	50945	1652	1652.3	6.16	0.0837
AOA ₉₀ -A-0d	49437	1378	1378.4	6.38	0.0428
AOA ₉₀ -O-0d	53188	1285	1285.5	6.32	0.0428
AOA ₉₀ -M-0d	51434	1260	1260.5	5.82	0.0811
AOA ₈₀ -A-0d	47001	1803	1803.3	7.22	0.0289
AOA ₈₀ -O-0d	48234	1733	1733.3	7.3	0.0191
AOA ₈₀ -M-0d	45035	1745	1745.2	7.25	0.0246
MBR _{control} -A-45d	67700	1068	1068.5	6.18	0.072
MBR _{control} -O-45d	58027	984	984.6	5.78	0.102
MBR _{control} -M-45d	51426	1202	1202.2	5.56	0.133
AOA ₉₀ -A-45d	76204	1099	1099.2	6.67	0.0456
AOA ₉₀ -O-45d	67258	1155	1155.5	6.71	0.0439
AOA ₉₀ -M-45d	57062	1463	1463.1	7.13	0.0246
AOA ₈₀ -A-45d	65916	884	884.3	6.04	0.0639
AOA ₈₀ -O-45d	56788	1212	1212.1	5.83	0.0838
AOA ₈₀ -M-45d	56793	1115	1115.2	5.75	0.0695
MBR _{control} -A-90d	62360	988	988.9	5.26	0.129
MBR _{control} -O-90d	63004	959	959.7	6.14	0.0477
MBR _{control} -M-90d	47573	1088	1088.3	5.99	0.0606
AOA ₉₀ -A-90d	51723	952	953	5.74	0.0745
AOA ₉₀ -O-90d	66099	885	886.1	5.38	0.0602
AOA ₉₀ -M-90d	46637	1063	1063.2	5.78	0.0672
AOA ₈₀ -A-90d	54424	945	945.9	5.17	0.0961
AOA ₈₀ -O-90d	58247	971	972	5.3	0.117
AOA ₈₀ -M-90d	59330	756	756.7	3.91	0.213

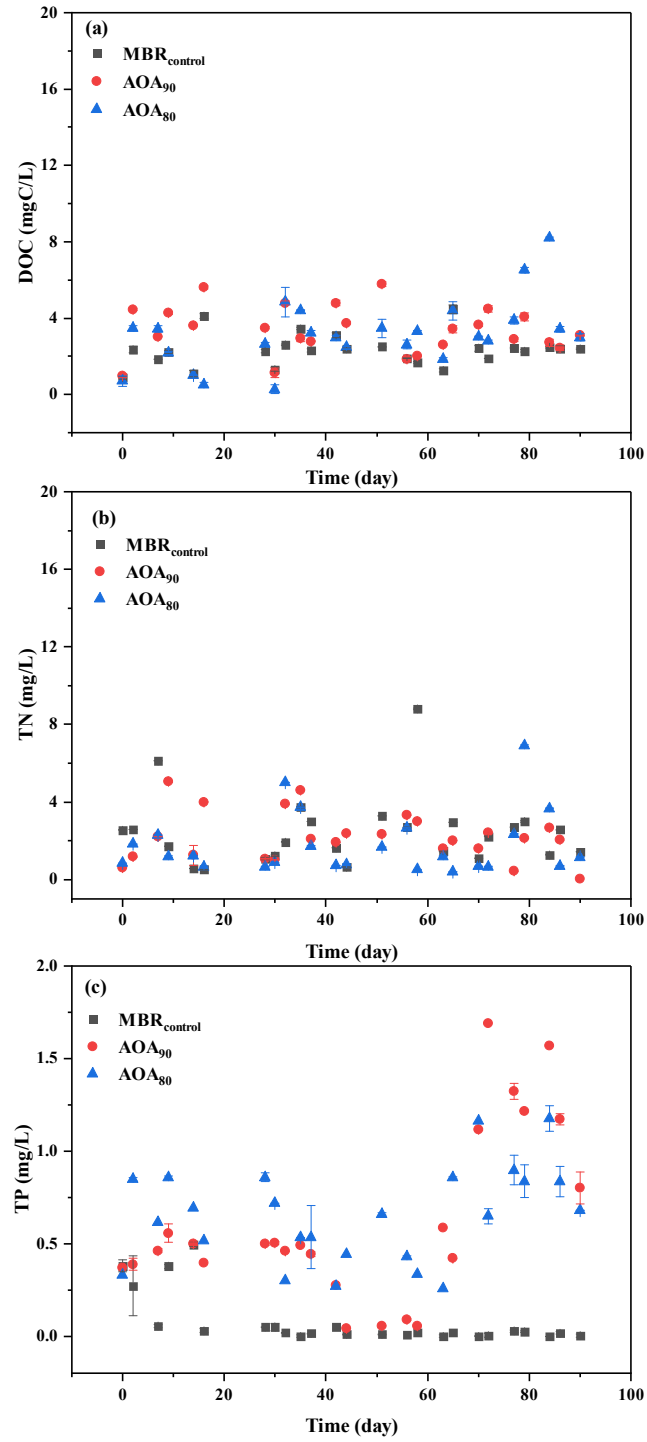


Figure S1. The temporal variations in basic quality parameters (DOC, TN, and TP) in effluents from MBRs (MBR_{control}, AOA₉₀, and AOA₈₀).

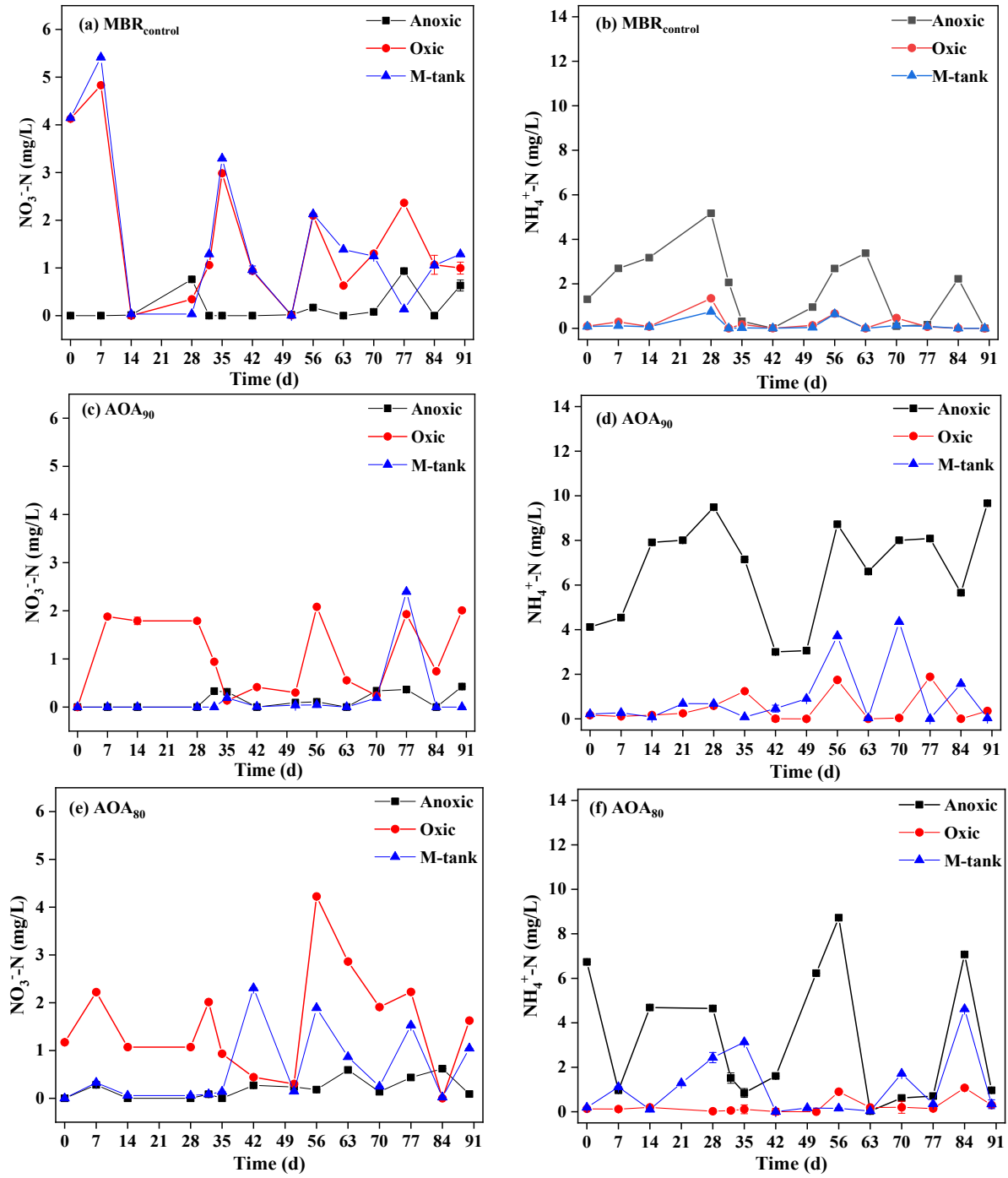


Figure S2. The temporal variations of NO_3^- -N and NH_4^+ -N in different tanks of $\text{MBR}_{\text{control}}$, AOA_{90} , and AOA_{80} .

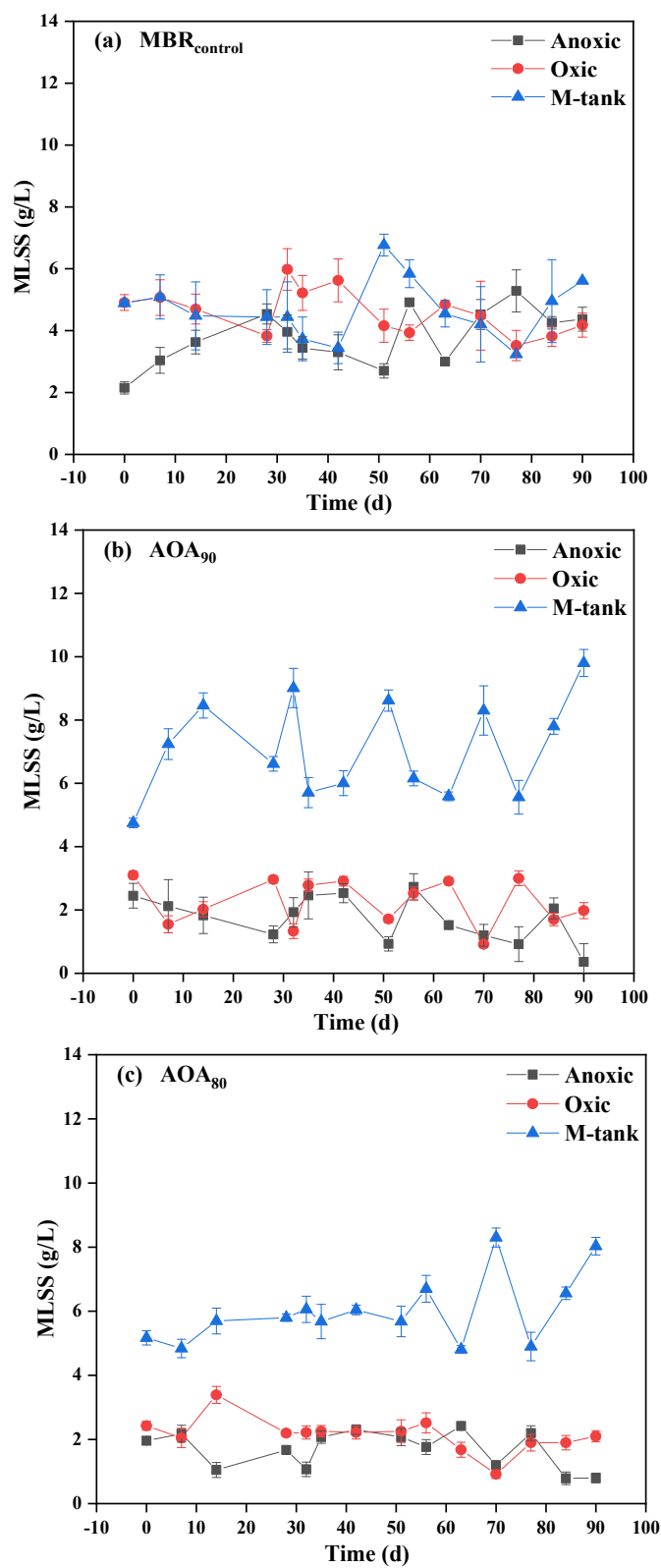


Figure S3. The MLSS concentration in different units of MBR_{control} (a), AOA₉₀ (b), and AOA₈₀ (c).

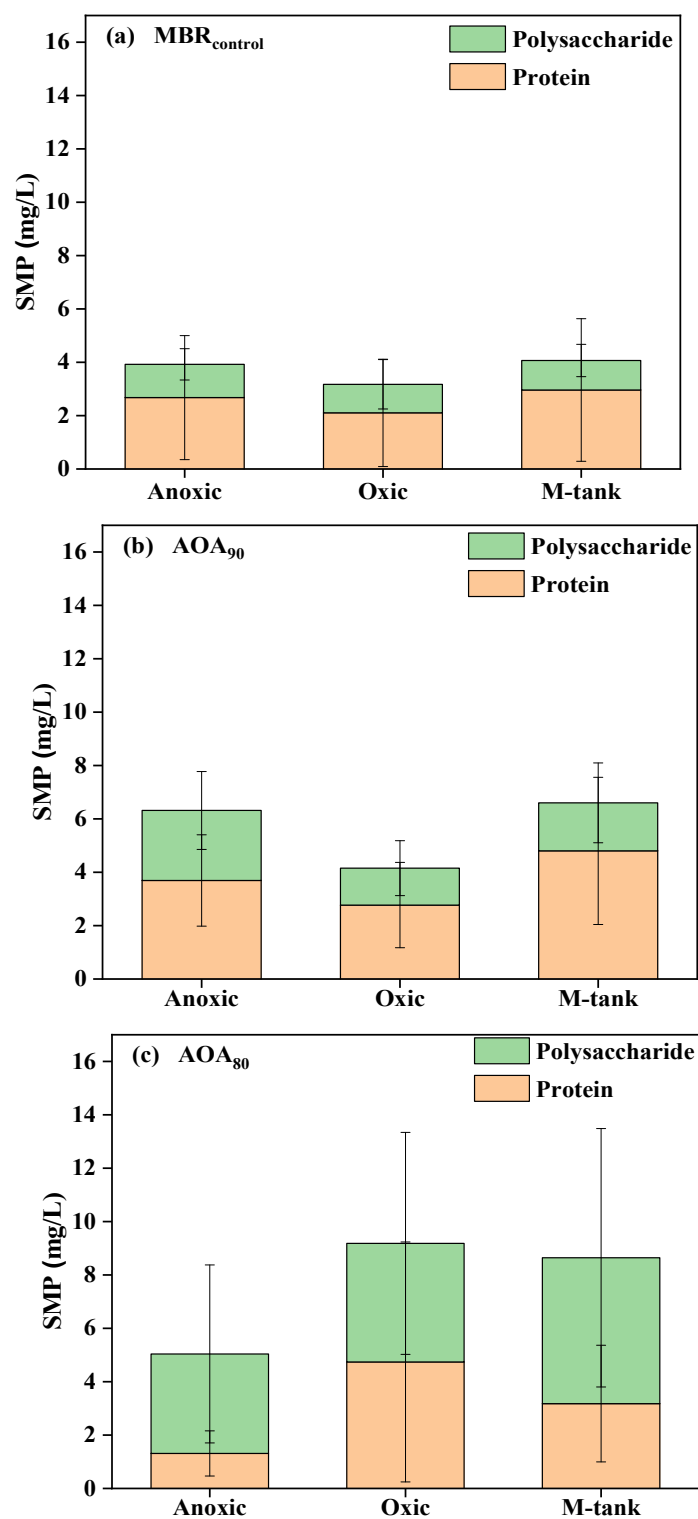


Figure S4. The average polysaccharide and protein in SMP in different units of MBR_{control} (a and b), AOA₉₀ (c and d), and AOA₈₀ (e and f).

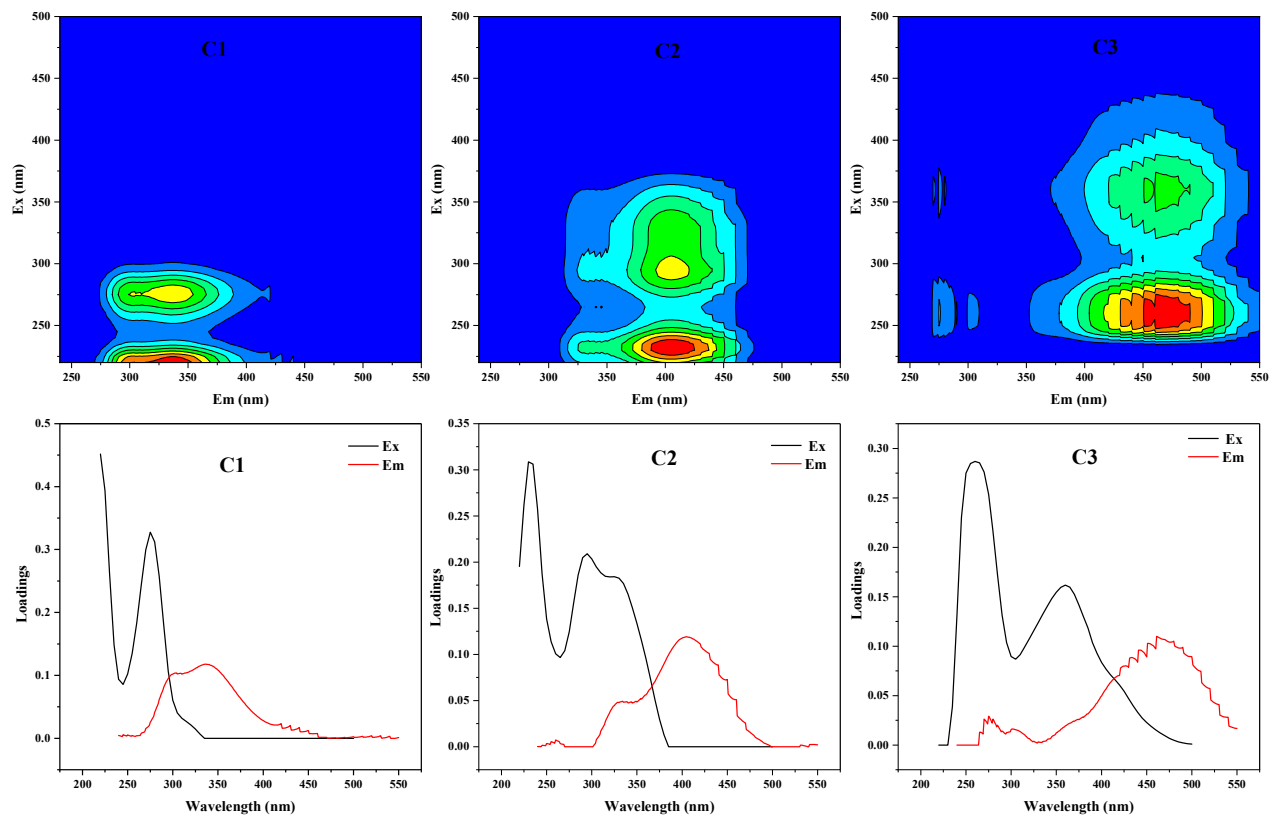


Figure S5. EEM-PARAFAC components, tryptophan-like (C1), fulvic-like (C2), and humic-like (C3).

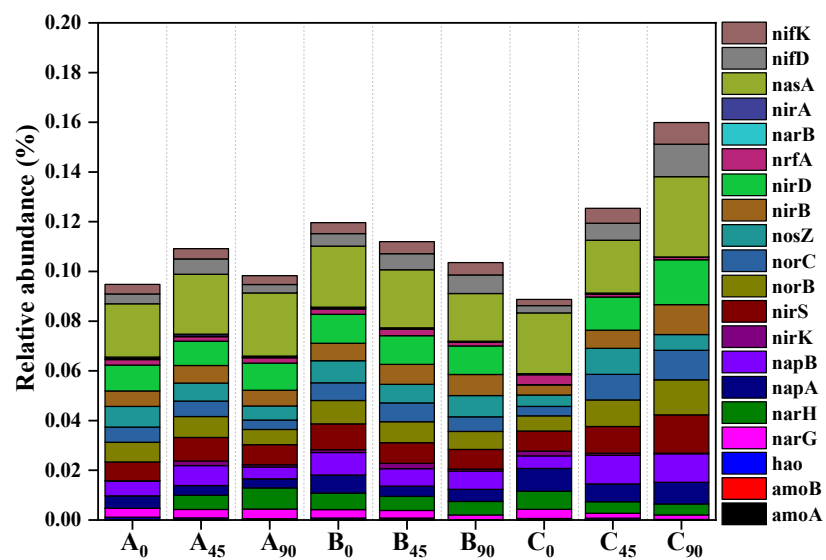


Figure S6. The relative abundance of functional genes responsible for nitrogen metabolism in MBR_{control} (A), AOA₉₀ (B), and AOA₈₀ (C). (The subscript of A, B, and C means the sampling time.)