Supplementary Material for

Temperature dependence of denitrification microbial communities and functional genes in an expanded granular sludge bed reactor treating nitrate-rich wastewater

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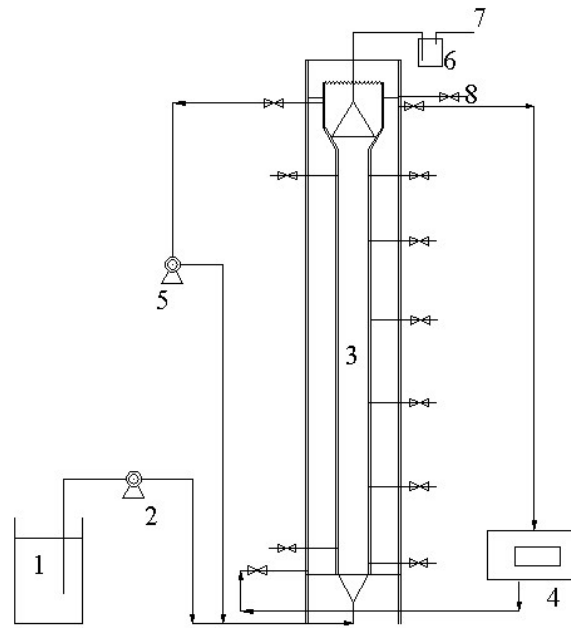Tel.: +86 025 89680377.

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Fig. S1. Experimental apparatus and process flow chart of the EGSB reactor operated at 35±1℃, in which: (1) Influent tank; (2) Influent pump; (3) EGSB reactor (4) Water bath temperature control system;(5) Recycling pump; (6) gas sampler; (7) wet gas meter; (8) effluent water;
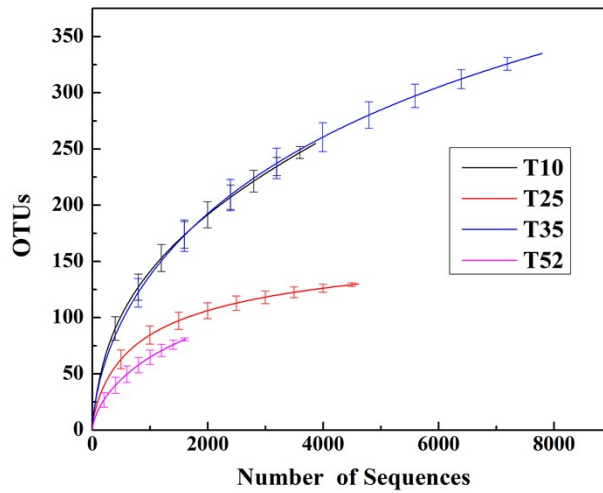
Fig. S2. Rarefaction curves for the T10, T25, T35, and T52 samples at a similarity of 97%. The rarefaction curves, which plot the number of observed OTUs as a function of the number of sequences, were computed using the RDP Pyrosequencing Pipeline Rarefaction tool. The error bars show 95% confidence intervals. The samples were arranged in descending order of their OTUs.

Table S1 Sample T10, T25, T35 and T52 in the genus level of the classification

genus(T35)	sequences	%	genus(T10)	sequences	%
Halomonas	3243	41.62	Halomonas	3159	81.59
Azoarcus	2270	29.13	Pseudomonas	178	4.60
Pseudomonas	201	2.58	Marinobacter	112	2.89
Wandonia	190	2.44	Azoarcus	101	2.61
Marinobacter	67	0.86	Wandonia	73	1.89
Acetoanaerobium	62	0.80	Proteiniclasticum	33	0.85
Desulfonatronum	51	0.65	Psychrobacter	28	0.72
Methyloversatilis	50	0.64	Idiomarina	26	0.67
Paracoccus	48	0.62	Pseudidiomarina	12	0.31
Castellaniella	47	0.60	Corynebacterium	8	0.21
Proteiniclasticum	47	0.60	Alkaliphilus	8	0.21
Alkaliphilus	42	0.54	Natronincola	5	0.13
Zymobacter	37	0.47	Alkalibacterium	5	0.13
Idiomarina	33	0.42	Anoxynatronum	4	0.10
Clostridium IV	26	0.33	Acetoanaerobium	4	0.10
Thauera	23	0.30	Paracoccus	3	0.08
Anoxynatronum	21	0.27	Stappia	3	0.08
Garciella	19	0.24	Selenihalanaerobacter	2	0.05
Labrenzia	16	0.21	Erysipelothrix	2	0.05
Tindallia	16	0.21	Nitriliruptor	1	0.03
Natronincola	15	0.19	Dietzia	1	0.03
Alishewanella	14	0.18	Alkaliflexus	1	0.03
Anaerovorax	14	0.18	Petrimonas	1	0.03
Acinetobacter	12	0.15	Phyllobacterium	1	0.03
Gordonia	11	0.14	Pseudaminobacter	1	0.03
Alkaliflexus	9	0.12	Chelativorans	1	0.03
Erysipelothrix	9	0.12	Devosia	1	0.03
Corynebacterium	7	0.09	Rhodobaca	1	0.03
Desulfitispora	7	0.09	Alkalilimnicola	1	0.03
Brucella	6	0.08	Legionella	1	0.03
Truepera	6	0.08	Alishewanella	1	0.03
Acholeplasma	6	0.08	Methylophaga	1	0.03
Exiguobacterium	5	0.06	Anaerovorax	1	0.03
Desulfuromonas	4	0.05	Anaerobranca	1	0.03
Azomonas	4	0.05	Clostridium IV	1	0.03
Pelospora	4	0.05	Saccharofermentans	1	0.03
Pannonibacter	3	0.04	Sporolactobacillaceae_incert	1	0.03
Pseudidiomarina	3	0.04	Haloplasma	1	0.03
Saccharofermentans	3	0.04	unclassified genus	87	2.25
Haloactinobacterium	2	0.03	**genus(T25)**	**sequences**	**%**
Devosia	2	0.03	Halomonas	2106	45.68
Aidingimonas	2	0.03	Azoarcus	1128	24.47
Desulfitibacter	2	0.03	Pseudomonas	424	9.20
Clostridium III	2	0.03	Wandonia	96	2.08
Rhodococcus	1	0.01	Marinobacter	50	1.08
Dietzia	1	0.01	Proteiniclasticum	40	0.87
Proteiniphilum	1	0.01	Paracoccus	39	0.85
Flavobacterium	1	0.01	Alkaliphilus	36	0.78
Variovorax	1	0.01	Acetoanaerobium	30	0.65
Ochrobactrum	1	0.01	Desulfonatronum	25	0.54
Albidovulum	1	0.01	Acinetobacter	24	0.52
Rhodobaca	1	0.01	Idiomarina	24	0.52
Serpens	1	0.01	Alkaliflexus	18	0.39
Azorhizophilus	1	0.01	Gordonia	16	0.35
Aeromonas	1	0.01	Anoxynatronum	15	0.33
Dethiobacter	1	0.01	Clostridium IV	15	0.33
Anaerotruncus	1	0.01	Corynebacterium	14	0.30
Clostridium XI	1	0.01	Labrenzia	14	0.30
Bacillus	1	0.01	Alishewanella	14	0.30

genus(T52)	sequences	%	genus	sequences	%
unclassified genus	1116	14.32	Aminobacterium	14	0.30
genus(T52)	*sequences*	*%*	Natronincola	13	0.28
Halomonas	1244	76.89	Castellaniella	12	0.26
Azoarcus	135	8.34	Desulfuromonas	11	0.24
Pseudomonas	43	2.66	Thauera	11	0.24
Wandonia	29	1.79	Tindallia	9	0.20
Idiomarina	27	1.67	Erysipelothrix	8	0.17
Psychrobacter	12	0.74	Rhodococcus	7	0.15
Marinobacter	11	0.68	Azomonas	7	0.15
Anoxynatronum	11	0.68	Desulfitispora	7	0.15
Natronincola	10	0.62	Zymobacter	6	0.13
Alkaliphilus	10	0.62	Flavobacterium	4	0.09
Acetoanaerobium	6	0.37	Anaerovorax	4	0.09
Proteiniclasticum	5	0.31	Exiguobacterium	4	0.09
Corynebacterium	4	0.25	Acholeplasma	4	0.09
Pseudidiomarina	4	0.25	Brucella	3	0.07
Alishewanella	4	0.25	Ochrobactrum	3	0.07
Desulfonatronum	2	0.12	Desulfitibacter	3	0.07
Pseudaminobacter	2	0.12	Garciella	3	0.07
Paracoccus	2	0.12	Dendrosporobacter	3	0.07
Desulfitispora	2	0.12	Indibacter	2	0.04
Haloplasma	2	0.12	Rhodobaca	2	0.04
Dietzia	1	0.06	Pseudidiomarina	2	0.04
Alkaliflexus	1	0.06	Clostridium XI	2	0.04
Nitratireductor	1	0.06	Truepera	2	0.04
Rhodobaca	1	0.06	Haloactinobacterium	1	0.02
Clostridium XI	1	0.06	Chelativorans	1	0.02
Selenihalanaerobacter	1	0.06	Devosia	1	0.02
Alkalibacterium	1	0.06	Roseibium	1	0.02
Truepera	1	0.06	Anaerobranca	1	0.02
Aminobacterium	1	0.06	Pelospora	1	0.02
unclassified genus	44	2.72	Acetanaerobacterium	1	0.02
			Ethanoligenens	1	0.02
			Sporolactobacillaceae_incert	1	0.02
			Halolactibacillus	1	0.02
			Planomicrobium	1	0.02
			Aminomonas	1	0.02
			unclassified genus	324	7.03

Table S2 P values of nitrate removal of T10, T25, T35 and T52

Samples	P
T35-T52	0.287399
T35-T15	6.49E-06
T35-T10	5.96E-08
T35-T25	8.91E-07
T25-T10	5.3E-08
T25-T52	0.015201
T25-T15	0.7643
T15-T10	5.28E-08
T15-T52	0.014387
T10-T52	6.63E-08