Table S1 Soil physiochemical properties in the pot experiment over the rice growth stages in 2016 (Wang et al., 2018b).

Soil and stages	Depth	Treatment	pH	DOC (mg/kg)	NH_4^+ (mg/kg)	NO_3^- (mg/kg)	N	C	C/N
BH seedling	0-5 cm	S0	7.9	46.1	39.21	9.73	0.11	2.15	19.43
		S1	7.8	87.48	39.96	0.65	0.14	2.59	17.99
		S2	7.68	102.53	41.75	0.36	0.13	2.45	18.8
	15-20 cm	S0	7.84	42.5	38.67	26.03	0.11	2.13	18.71
		S1	7.79	95.32	38.77	2.65	0.15	2.6	17.4
		S2	7.78	163.47	38.13	0.04	0.14	2.45	18.13
BH tillering	0-5 cm	S0	8.42	47.06	33.12	5.23	0.11	2.16	19.42
		S1	8.36	34.73	33.06	7.03	0.14	2.53	17.98
		S2	8.64	39.91	29.06	11.74	0.14	2.51	18.17
	15-20 cm	S0	8.76	38.53	29.32	4.73	0.11	2.22	19.49
		S1	8.73	41.65	28.65	9.29	0.15	2.63	18.02
		S2	8.79	47.8	28.58	9.64	0.14	2.39	17.56
BH heading	0-5 cm	S0	8.28	102.8	32.09	1.57	0.11	2.18	19.81
		S1	8.49	75.8	29.59	0.52	0.14	2.66	18.46
		S2	8.37	68.05	37.34	0.26	0.12	2.36	18.93
	15-20 cm	S0	8.66	76.75	35.93	0.18	0.11	2.18	19.8
		S1	8.48	62.48	28.77	0.91	0.14	2.49	18.18
		S2	8.46	92.27	33.78	0.58	0.13	2.37	18.65
TY seedling	0-5 cm	S0	6.37	61.98	48.33	0.13	0.21	2.04	9.53
		S1	6.13	66.19	50.63	-0.26	0.22	2.1	9.64
		S2	6.35	88.25	51.01	1.25	0.22	2.21	10.03
	15-20 cm	S0	6.05	50.27	50.98	1.46	0.22	1.98	8.94
		S1	6.03	67.54	53.31	-0.37	0.22	2.1	9.56
		S2	6.07	100.96	45.62	0.05	0.22	2.1	9.65
TY tillering	0-5 cm	CK	6.47	61.9	26.84	4.38	0.2	1.95	9.66
		S1	6.54	63.57	25.12	2.03	0.2	2.09	10.25
		S2	6.47	69	26.34	1.85	0.2	2.01	9.96
	15-20 cm	S0	6.25	86.22	25.19	2.2	0.19	1.87	9.64
		S1	6.18	68.65	26.76	2.95	0.2	2.01	9.81
		S2	6.39	71.28	25.39	1.99	0.2	2	10.09
TY heading	0-5 cm	S0	7.06	124.11	43.1	1.36	0.2	2.01	9.85
		S1	7.19	137.37	41.05	0.93	0.22	2.06	9.58
		S2	7.21	148.29	43.61	0.41	0.2	1.94	9.69
	15-20 cm	S0	6.88	152.26	41.65	0.01	0.21	1.96	9.51
		S1	6.51	176.59	44.76	0.14	0.2	2.02	9.9
		S2	6.56	192.54	49.22	2.74	0.2	2.02	10.19

Table S2 Spearman correlations of *nrfA* gene abundance versus soil physiochemical parameters across three sampling time points in the pot experiment in 2016

pH	NH_4^+ mg/kg	NO_3^- mg/kg	DOC mg/kg	N	C	S	C/N	*Eh* (mV)
-0.24*	0.55**	-0.32**	-0.02	0.24*	0.22*	0.02*	-0.12	-0.51*

Note: “*” and “**” labelled on r values denote $P<0.05$ and $P<0.01$, respectively).

Table S3 Coverage and diversity indices of *nrfA* gene transcript in different treatments of two soils

Soil	Treatment	coverage	ace	Shannon	Simpson	chao
BH	S0	99.35%	2421.66	5.42	0.017	1897.19
	S1	99.27%	2454.04	5.66	0.008	2075.07
	S2	99.27%	2550.98	5.64	0.008	2027.01
	N0	99.32%	2191.53	5.36	0.019	1988.76
TY	S0	99.43%	2433.83	4.20	0.027	1342.44
	S1	99.42%	2317.19	4.33	0.032	1449.96
	S2	99.46%	2017.00	4.63	0.024	1440.77
	N0	99.49%	2293.60	3.10	0.093	1322.96

Fig. S1 Richness and α-diversity indices of DNRA microbes based on *nrfA* gene transcript retrieved from the BH and TY soils.

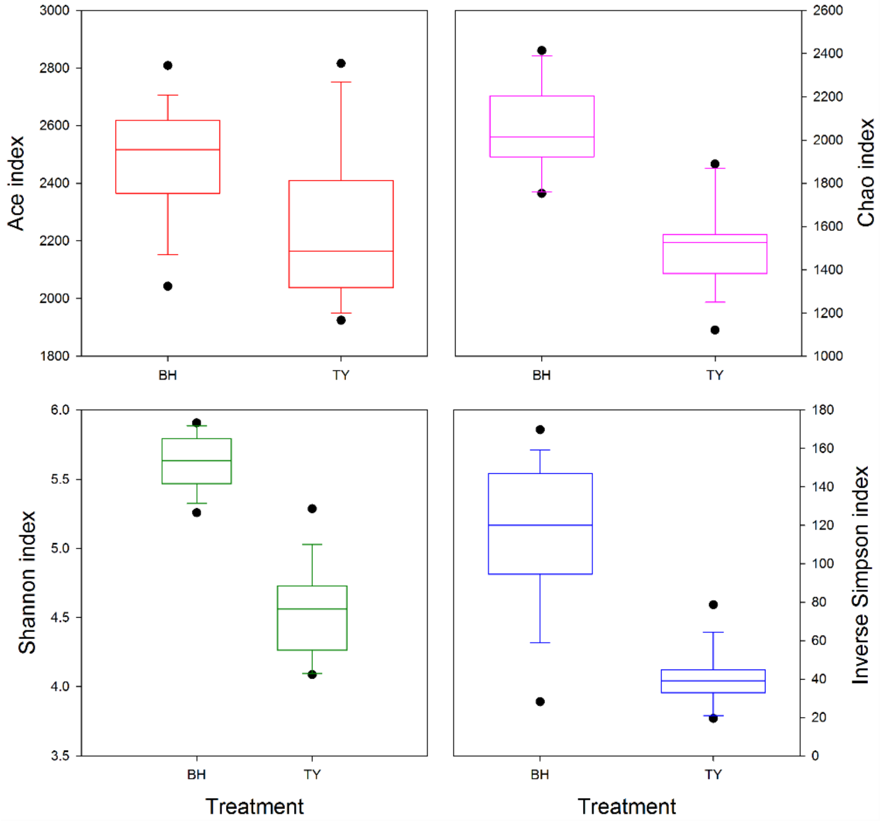
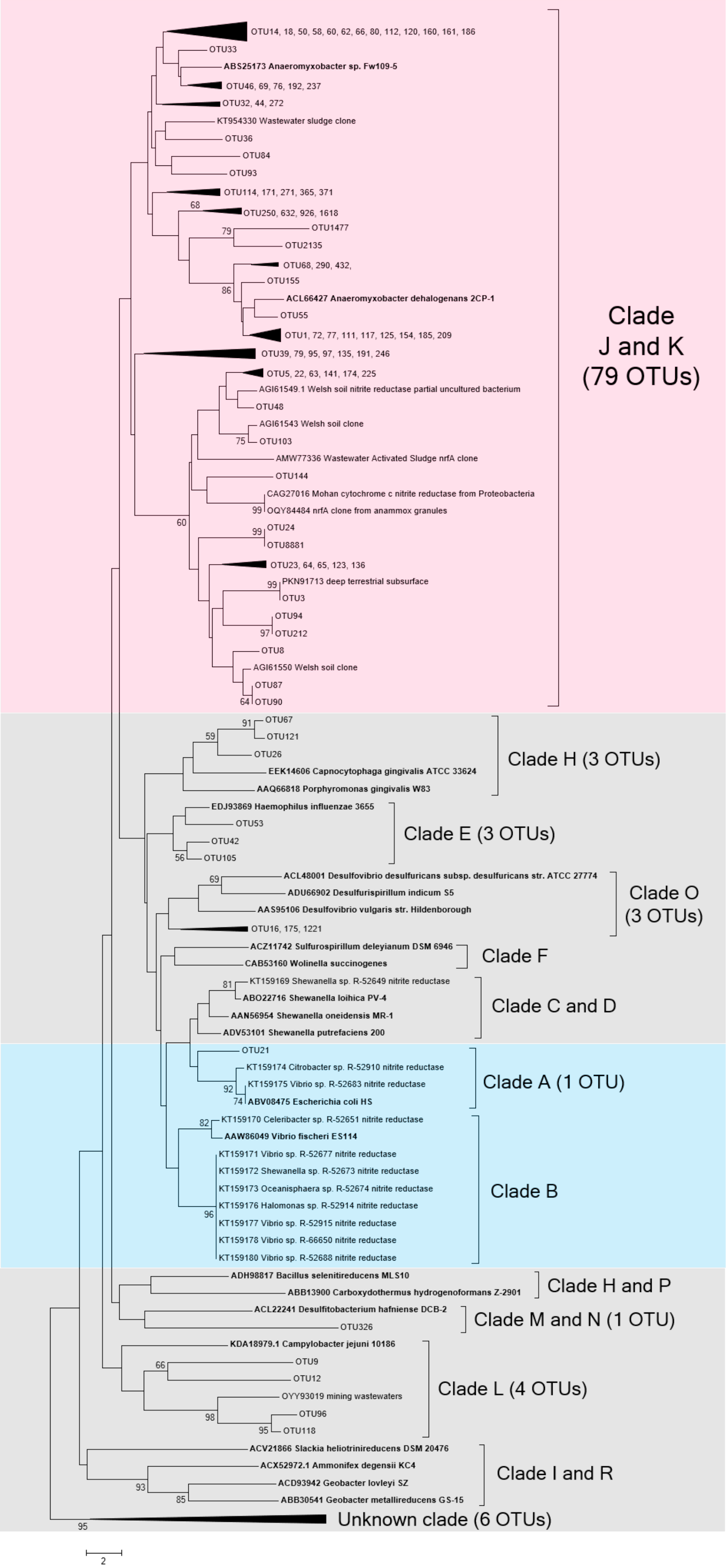


Fig. S2 Neighbor-joining phylogenetic tree of NrfA amino acid sequences based on *nrfA* gene transcripts retrieved from the BH and TY soils. Representative sequences of the most abundant 100 *nrfA* gene transcript OTUs were used for phylogenetic tree construction. The reference sequences with bold names were from the known DNRA bacterial strains and environmental samples, and used for the assignment of the NrfA clades according to Welsh and colleagues' classification (Welsh et al., 2014).


OTU14, 18, 50, 58, 60, 62, 66, 80, 112, 120, 160, 161, 186
OTU33
ABS25173 Anaeromyxobacter sp. Fw109-5
OTU46, 69, 76, 192, 237
OTU32, 44, 272
KT954330 Wastewater sludge clone
OTU36
OTU84
OTU93
OTU114, 171, 271, 365, 371
68
OTU250, 632, 926, 1618
79
OTU1477
OTU2135
OTU68, 290, 432,
OTU155
86
ACL66427 Anaeromyxobacter dehalogenans 2CP-1
OTU55
OTU1, 72, 77, 111, 117, 125, 154, 185, 209
OTU39, 79, 95, 97, 135, 191, 246
OTU5, 22, 63, 141, 174, 225
AGI61549.1 Welsh soil nitrite reductase partial uncultured bacterium
OTU48
AGI61543 Welsh soil clone
75
OTU103
AMW77336 Wastewater Activated Sludge nrfA clone
OTU144
CAG27016 Mohan cytochrome c nitrite reductase from Proteobacteria
99
OQY84484 nrfA clone from anammox granules
60
99
OTU24
OTU8881
OTU23, 64, 65, 123, 136
99
PKN91713 deep terrestrial subsurface
OTU3
OTU94
97
OTU212
OTU8
AGI61550 Welsh soil clone
OTU87
64
OTU90
Clade J and K (79 OTUs)
91
OTU67
59
OTU121
OTU26
EEK14606 Capnocytophaga gingivalis ATCC 33624
AAQ66818 Porphyromonas gingivalis W83
Clade H (3 OTUs)
EDJ93869 Haemophilus influenzae 3655
OTU53
OTU42
56
OTU105
Clade E (3 OTUs)
69
ACL48001 Desulfovibrio desulfuricans subsp. desulfuricans str. ATCC 27774
ADU66902 Desulfurispirillum indicum S5
AAS95106 Desulfovibrio vulgaris str. Hildenborough
OTU16, 175, 1221
Clade O (3 OTUs)
ACZ11742 Sulfurospirillum deleyianum DSM 6946
CAB53160 Wolinella succinogenes
Clade F
81
KT159169 Shewanella sp. R-52649 nitrite reductase
ABO22716 Shewanella loihica PV-4
AAN56954 Shewanella oneidensis MR-1
ADV53101 Shewanella putrefaciens 200
Clade C and D
OTU21
KT159174 Citrobacter sp. R-52910 nitrite reductase
92
KT159175 Vibrio sp. R-52683 nitrite reductase
74
ABV08475 Escherichia coli HS
Clade A (1 OTU)
82
KT159170 Celeribacter sp. R-52651 nitrite reductase
AAW86049 Vibrio fischeri ES114
KT159171 Vibrio sp. R-52677 nitrite reductase
KT159172 Shewanella sp. R-52673 nitrite reductase
KT159173 Oceanisphaera sp. R-52674 nitrite reductase
KT159176 Halomonas sp. R-52914 nitrite reductase
96
KT159177 Vibrio sp. R-52915 nitrite reductase
KT159178 Vibrio sp. R-66650 nitrite reductase
KT159180 Vibrio sp. R-52688 nitrite reductase
Clade B
ADH98817 Bacillus selenitireducens MLS10
ABB13900 Carboxydothermus hydrogenoformans Z-2901
Clade H and P
ACL22241 Desulfitobacterium hafniense DCB-2
OTU326
Clade M and N (1 OTU)
KDA18979.1 Campylobacter jejuni 10186
66
OTU9
OTU12
OYY93019 mining wastewaters
98
OTU96
95
OTU118
Clade L (4 OTUs)
ACV21866 Slackia heliotrinireducens DSM 20476
ACX52972.1 Ammonifex degensii KC4
93
ACD93942 Geobacter lovleyi SZ
85
ABB30541 Geobacter metallireducens GS-15
Clade I and R
95
Unknown clade (6 OTUs)
2