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Table S1. Primers used in this study.

Genes	Primers	Sequences (5′-3′)	Product size	Reference
Bacterial 16S rRNA gene	341F	CCTACGGGAGGCAGCAG	193	[12]
	534R	ATTACCGCGGCTGCTGGCA		
Archaeal 16S rRNA gene	Arch 349F	GYGCASCAGKCGMGAAW	457	[10]
	Arch 806R	GGACTACVSGGGTATCTAAT		
Fungi ITS	ITS1F	CTTGGTCATTTAGAGGAAGTAA	420-825[a]	[9]
	ITS4	TCCTCCGCTTATTGATATGC		
Bacterial ammonium monooxygenase; *amoA*	amoA-1F	GGGGTTTCTACTGGTGGT	491	[9]
	amoA-2R	CCCCTCKGSAAAGCCTTCTTC		
Archaeal ammonium monooxygenase; *amoA*	amo196F	GGWGTKCCRGGRACWGCMAC	81	[11]
	amo277R	CRATGAAGTCRTAHGGRTADCC		
	Arch-amoAF	AATGGTCTGGSTTAGAMG	633	[4]
	Arch-amoAR	GCGGCCATCCATCTGTATGT		
Nitrogenase reductase; *nifH*	nifHF	AAAGGYGGWATCGGYAARTCCACCAC	400	[8]
	nifHRb	TGSGCYTTGTCYTCRCGGATBGGCAT		
Cu-containing nitrite reductase; *nirK*	nirK 1F	GGMATGGTKCCSTGGCA	514	[1]
	nirK 5R	GCCTCGATCAGRTTRTGGTT		
Nitrite reductase; *nirS*	nirS cd3AF	GTSAACGTSAAGGARACSGG	425	[7]
	nirS R3cd	GASTTCGGRTGSGTCTTGA		[11]
Nitrate reductase; *narG*	narG-f	TCGCCSATYCCGGCSATGTC	173	[3]
	narG-r	GAGTTGTACCAGTCRGCSGAYTCSG		
Nitrate reductase; *norB*	cnorB2F	GACAAGNNNTACTGGTGGT	389	[2]
	cnorB6R	GAANCCCCANACNCCNGC		
Nitrous oxide reductase; *nosZ*	nosZ-F	CGYTGTTCMTCGACAGCCAG	453	[6]
	nosZ-R	CGSACCTTSTTGCCSTYGCG		
	nosZqPCRF1[b]	TCGARCAGGAYTGGRACATYCT	162	[5]
	nosZqPCRF2[b]	ACAGGAYTATGATGTRCCGCACGGA	158	
	nosZqPCRF3[b]	TGACYGCCATYCGTTCWCACYTT	246	
	nosZGeoR	CTTGRTGCARCGCVGAACAGA		

[a]Products sizes varies.

[b]nosZGeoR was used as a reverse primer.

Table 2. Characteristics of soils.

Characteristics	Control	5C	8C
pH	6.95 ± 0.06	6.91 ± 0.05	6.87 ± 0.02
EC (μS/cm)	65.53 ± 4.44	56.67 ± 1.04	53.80 ± 6.24
TOC (mg/kg)	20,466.32 ± 478.68	18,679.25 ± 336.21	11,403.29 ± 199.29
Cumulative CO_2 (mg C/kg)	ND	2,259.81	9,412.82
TN (mg/kg)	1,995.26 ± 258.94	1,802.30 ± 522.59	2,021.99 ± 411.64
Inorganic N (mg/kg)	8.41 ± 1.17	16.14 ± 3.07	16.71 ± 0.79
NH_4^+ (mg/kg)	8.98 ± 0.78	17.07 ± 1.30	13.92 ± 1.73
NO_3^- (mg/kg)	1.35 ± 1.71	1.91 ± 1.10	1.07 ± 0.62
NO_2^- (mg/kg)	0.00	0.00	2.44 ± 1.46

ND: Not determined.

Table 3. ANOVA results for the genes tested in this study.

Genes	F	*p*-Value
Bacterial 16S rRNA gene	149.30	0.0010
Archaeal 16S rRNA gene	119.40	0.0014
Fungal ITS	20.33	0.0180
Bacterial *amoA*	223.76	0.0005
Archaeal *amoA*	360.77	0.0003
nifH	122.43	0.0013
narG	16.63	0.0238
nirS	1.70	0.3206
nirK	6.19	0.0348
norB	6.50	0.0812
nosZ	195.29	0.0007

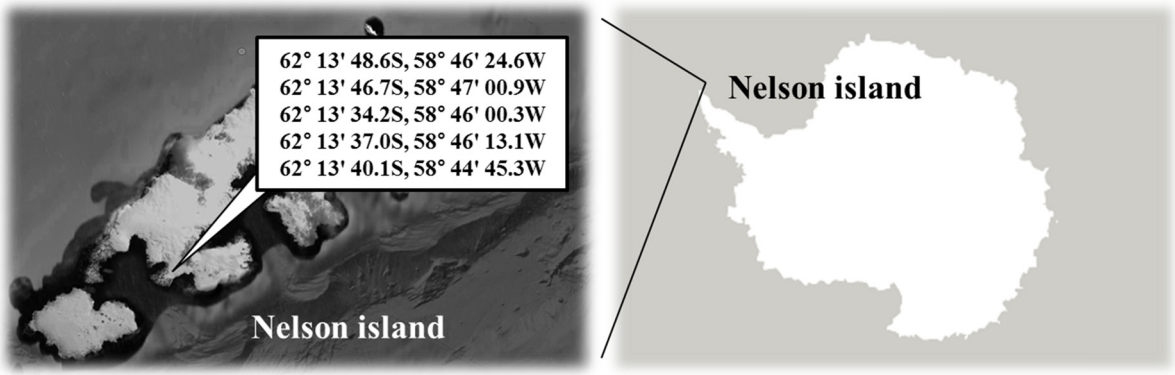

Fig. S1. Antarctic soil samples were collected from Nelson Island, Antarctica.
Five soil samples were taken within a 5 km radius. GPS coordinates of sampling points are shown in the picture.

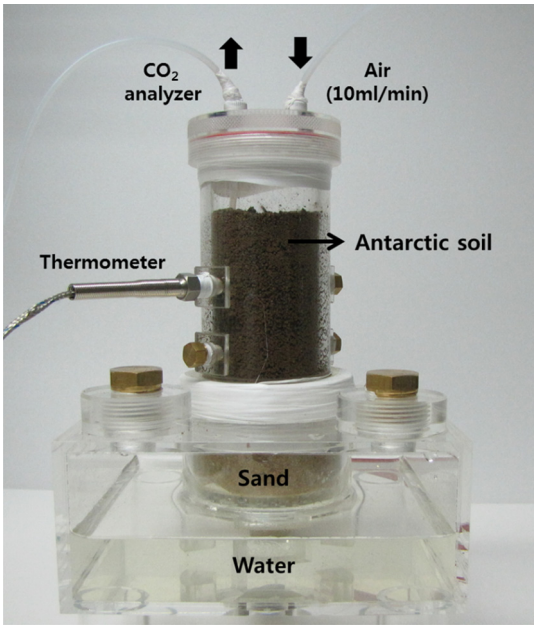

Fig. S2. Experimental design of the microcosms.
Sterile water was supplied from the bottom of the container through a sterile sand layer and the moisture level was kept at the constant level of Antarctic soils. Air was supplied to the headspace of the microcosms (10 ml/min). Soil respiration (CO_2) was taken from soil pores and analyzed by a CO_2 analyzer. The effect of warming was tested at 5ºC and 8ºC.

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