Supplementary Information for

Measurement report: Soil reactive nitrogen gas emissions from the Tibetan Plateau

Lingling Deng[1,#], Yuhan Chen[1,#], Chunxiang Ye[2], Rui Wang[1], Ruhai Wang[3], Zehua Fu[3], Hongfang Zhao[1,*], Dianming Wu[1,*]

[1]Key Laboratory of Geographic Information Science (Ministry of Education), School of Geographic Sciences, East China Normal University, 200241 Shanghai, China
[2]State Key Joint Laboratory for Environmental Simulation and Pollution Control, Center for Environment and Health, College of Environmental Sciences and Engineering, Peking University, Beijing 100871, P. R. China
[3]State Key Laboratory of Soil and Sustainable Agriculture, Institute of soil Sciences, Chinese Academy of Sciences, 210008 Nanjing, China
[#]Lingling Deng and Yuhan Chen contributed equally to this work.

Correspondence to: Dianming Wu (dmwu@geo.ecnu.edu.cn), Hongfang Zhao (hfzhao@geo.ecnu.edu.cn)

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Table S1. Information on soil sampling sites in Linzhi, Tibet.

Sample ID	Longitude (°E)	Latitude (°N)	Elevation (m)	Land type
G1	94.74	29.76	3320.0	Grassland
G2	94.62	29.63	4333.3	Grassland
G3	94.72	29.70	3441.8	Grassland
G4	94.72	29.69	3436.4	Grassland
C1	94.73	29.76	3329.1	Cropland
C2	94.73	29.75	3346.4	Cropland
C3	94.42	29.56	2959.1	Cropland
C4	94.44	29.54	2954.1	Cropland
C5	94.44	29.41	2924.5	Cropland
C6	94.40	29.62	3031.7	Cropland
C7	94.43	29.59	2969.7	Cropland
C8	94.51	29.42	2940.4	Cropland
F1	94.73	29.76	3335.6	Forest
F2	94.72	29.73	3400.7	Forest
F3	94.73	29.67	3529.8	Forest
F4	94.40	29.62	3054.5	Forest
F5	94.43	29.44	2925.7	Forest
F6	94.82	29.47	2925.9	Forest
F7	94.82	29.47	2918.6	Forest
F8	94.46	29.45	2929.2	Forest
W1	94.62	29.63	4330.6	Wetland
W2	94.46	29.45	2924.7	Wetland
W3	94.46	29.45	2923.2	Wetland
BL1	94.43	29.44	2923.9	Bare land
BL2	94.82	29.47	2913.9	Bare land

Table S2. PCR reaction systems for soil bacteria, archaea and fungi.

Community	Primer	Reaction Component	Volume (μL)
Bacteria	338F/806R	5×FastPfu Buffer	4
		2.5 mM dNTPs	2
		Forward Primer(5 μM)	0.8
		Reverse Primer(5 μM)	0.8
		FastPfu Polymerase	0.4
		BSA	0.2
		Template DNA	10 ng
		Supplement ddH$_2$O to 20 μL	
Archaea	524F10extF/Arch958RmodR	2×Pro Taq	10
		Forward Primer(5 μM)	0.8
		Reverse Primer(5 μM)	0.8
		Template DNA	10 ng
		Supplement ddH$_2$O to 20 μL	
Fungi	ITS1F/ITS2R	10×Buffer	2
		2.5 mM dNTPs	2
		Forward Primer(5μM)	0.8
		Reverse Primer(5μM)	0.8
		rTaq Polymerase	0.2
		BSA	0.2
		Template DNA	10 ng
		Supplement ddH$_2$O to 20 μL	

Table S3. Primers and conditions used for real-time quantitative PCR.

Sample	Primer set	Target genes	Amplicon length (bp)	Thermal profile	Plasmid dilution	R^2	Efficiency (%)
Natural soil	Arch_*amo*AF (STAATGGTCTGGCTTAGACG) Arch_*amo*AR (GCGGCCATCCATCTGTATGT)	*amo*A	635	95°C, 3min; 40 cycles (95°C, 5s; 58°C, 30s; 72°C, 1min)	10^{-2}~10^{-8}	0.9998	102.71
	*nar*G 145F (ACSCAYGGSGTDAACTGYAC) *nar*G 773R (GGNACGTTNGADCCCCA)	*nar*G	626	95°C, 3min; 40 cycles (95°C, 5s; 58°C, 30s; 72°C, 1min)	10^{-1}~10^{-8}	0.9952	88.21
	*nir*K C2F (TGCACATCGCCAACGGNATGTWYGG) *nir*K C2R (GGCGCGGAAGATGSHRTGRTCNAC)	*nir*K	459	95°C, 3min; 40 cycles (95°C, 5s; 58°C, 30s; 72°C, 1min)	10^{-1}~10^{-8}	0.9982	100.00
	*nap*A 3F (CCCAATGCTCGCCACTG) *nap*A 3R (CATGTTKGAGCCCCACAG)	*nap*A	130	95°C, 3min; 40 cycles (95°C, 5s; 58°C, 30s; 72°C, 1min)	10^{-1}~10^{-6}	0.9995	104.93
	*nos*Z F (CGYTGTTCMTCGACAGCCAG) *nos*Z 1622R (CGSACCTTSTTGCCSTYGCG)	*nos*Z	454	95°C, 3min; 40 cycles (95°C, 5s; 58°C, 30s; 72°C, 1min)	10^{-1}~10^{-8}	0.9947	93.47
Fumigation soil	Arch_*amo*AF (STAATGGTCTGGCTTAGACG) Arch_*amo*AR (GCGGCCATCCATCTGTATGT)	*amo*A_AOA	635	50°C, 2min; 95°C, 30s; 40 cycles (95°C, 5s; 55°C, 30s; 72°C, 45s)	10^{-1}~10^{-7}	0.9986	101.86
	*amo*A 1F (GGGGTTTCTACTGGTGGT) *amo*A 2R (CCCCTCKGSAAAGCCTTCTTC)	*amo*A_AOB	491	50°C, 2min; 95°C, 30s; 40 cycles (95°C, 5s; 55°C, 30s; 72°C, 45s)	10^{-1}~10^{-7}	0.9971	86.77
	CA377f (GTGGTGGTGGTCBAAYTA) C576r (GAAGCCCATRTARTCNGCC)	comammox Clade A	198	50°C, 2min; 95°C, 30s; 40 cycles (95°C, 5s; 55°C, 30s; 72°C, 30s)	10^{-1}~10^{-7}	0.9980	103.25
	F1*nxr*A (CAGACCGACGTGTGCGAAAG) R2 *nxr*A (TCCACAAGGAACGGAAGGTC)	*nxr*A	324	50°C, 2min; 95°C, 30s; 40 cycles (95°C, 5s; 55°C, 30s; 72°C, 30s)	10^{-1}~10^{-7}	0.9980	104.46
	*nxr*B169f (TACATGTGGTGGAACA) *nxr*B638r (CGGTTCTGGTCRATCA)	*nxr*B	485	50°C, 2min; 95°C, 30s; 40 cycles (95°C, 5s; 56.2°C, 40s; 72°C, 45s)	10^{-1}~10^{-7}	0.9979	98.25
	*nap*A_F1 (CTGGACIATGGGYTTIAACCA) *nap*A_R1 (CCTTCYTTYTCIACCCACAT)	*nap*A	492	50°C, 2min; 95°C, 30s; 40 cycles (95°C, 5s; 58°C, 40s; 72°C, 30s)	10^{-1}~10^{-7}	0.9974	96.75
	F1aCu (ATCATGGTSCTGCCGCG)	*nir*K	473		10^{-1}~10^{-7}	0.9982	95.63

R3Cu (GCCTCGATCAGRTTGTGGTT)			50°C, 2min; 95°C, 30s; 40 cycles (95°C, 5s; 60°C, 30s; 72°C, 30s)			
cd3aF (GTSAACGTSAAGGARACSGG)	*nir*S	425	50°C, 2min; 95°C, 30s; 40 cycles	10^{-1}~10^{-7}	0.9979	102.94
R3cd (GASTTCGGRTGSGTCTTGA)			(95°C, 5s; 58°C, 40s; 72°C, 1min)			
*nos*Z F (CGYTGTTCMTCGACAGCCAG)	*nos*Z	454	50°C, 2min; 95°C, 30s; 40 cycles	10^{-1}~10^{-7}	0.9992	90.70
*nos*Z 1622R (CGSACCTTSTTGCCSTYGCG)			(95°C, 5s; 58°C, 30s; 72°C, 1min)			

Table S4. Emissions of soil Nr gas and soil properties in literature.

Latitude (°N)	Longitude (°E)	NO maximum flux (ng N m^{-2} s^{-1})	NO emission intensity (kg N ha^{-1} yr^{-1})	pH	Moisture (%)	NO_3^--N (mg kg^{-1})	NH_4^+-N (mg kg^{-1})	TN (%)	Land use type	Reference
34.03	102.73	3.33	0.021	6.7	60	4.4	10	0.57	Grassland	(Zhang et al., 2018)
34.06	102.73	21.67	0.094	7.1	40	1.7	18.4	0.52	Grassland	(Zhang et al., 2018)
34.05	102.6	52	0.29	NA	50	21.32	2.98	NA	Grassland	(Gao et al., 2016)
34.04	102.72	40	0.047	6.48	22	46.3	27.4	0.94	Forest	(Yao et al., 2019)
34.04	102.72	40	0.022	6.69	55	7.5	2.3	0.57	Grassland	(Yao et al., 2019)
37.61	101.31	95	0.056	8	49	1.7	5.1	0.48	Grassland	(Lin et al., 2019)
37.61	101.31	475	0.208	8.3	36	16.1	2.3	0.44	Cropland	(Lin et al., 2019)

NA: no data available.

Table S5. Physical and chemical properties of soil.

Physicochemical properties	Forest	Grassland	Cropland	Wetland	Bare land	*p* value
pH	6.47 ± 1.21 abcd	5.10 ± 0.19 b	6.36 ± 0.64 bd	7.84 ± 0.19 ac	8.14 ± 0.18 a	***0.009***
TN (%)	0.17 ± 0.13 b	0.52 ± 0.24 a	0.18 ± 0.07 b	0.10 ± 0.12 b	0.03 ± 0.01 b	***0.018***
TC (%)	2.98 ± 2.47 b	8.38 ± 4.99 a	2.18 ± 0.97 b	1.49 ± 2.04 b	0.33 ± 0.11 b	***0.021***
C/N ratio	15.78 ± 2.82 a	15.41 ± 2.09 ac	11.88 ± 1.33 b	12.35 ± 3.20 ab	12.92 ± 0.59 ab	***0.020***
NO_3^- (mg kg^{-1})	6.91 ± 8.45 a	11.16 ± 4.80 a	21.74 ± 19.13 a	1.01 ± 1.01 a	5.11 ± 0.68 a	0.059
NO_2^- (mg kg^{-1})	0.23 ± 0.47 a	0.00 ± 0.00 a	0.15 ± 0.29 a	0.01 ± 0.01 a	0.01 ± 0.00 a	0.064
NH_4^+ (mg kg^{-1})	2.01 ± 3.31 ac	1.98 ± 1.43 a	0.01 ± 0.50 b	0.29 ± 0.54 bc	0.21 ± 0.35 abc	***0.026***
Net nitrification rate (mg N kg^{-1} d^{-1})	0.28 ± 0.98 a	0.00 ± 4.50 a	1.52 ± 2.57 a	0.07 ± 0.05 a	0.02 ± 0.06 a	0.644
Net mineralization rate (mg N kg^{-1} d^{-1})	0.42 ± 1.52 a	-0.89 ± 4.20 a	1.22 ± 2.75 a	-0.02 ± 0.10 a	-0.05 ± 0.05 a	0.974
Clay content (%)	0.53 ± 0.20 abcd	1.00 ± 0.35 a	0.90 ± 0.33 ac	0.41 ± 0.36 bd	0.19 ± 0.24 b	***0.026***
Silt content (%)	46.51 ± 20.42 bc	74.74 ± 10.18 a	55.84 ± 8.61 ac	40.55 ± 32.60 bc	19.44 ± 4.71 b	***0.025***
Sand content (%)	52.57 ± 20.62 ac	24.26 ± 10.52 b	41.95 ± 7.52 bc	59.04 ± 32.95 ac	80.38 ± 4.95 a	***0.026***
Soil water content (%)	24.37 ± 22.99 b	72.74 ± 14.05 a	17.25 ± 10.44 b	38.97 ± 12.36 ab	19.66 ± 3.58 b	***0.028***

Notes: Values in the table are mean ± standard deviation (Forest: *N*=8; Grassland: *N*=4; Cropland: *N*=8; Wetland: *N*=3; Bare land: *N*=2). TN: total nitrogen; TC: total carbon; C/N ratio: TC/TN; Clay: particle size less than 0.002 mm; silt: particle size between 0.002 mm and 0.05 mm; sand: particle size more than 0.05 mm. Kruskal-Wallis test was used for one-way ANOVA between groups. Values in bold italics indicate significant differences ($p < 0.05$), and different lowercase letters show differences between groups.

Table S6. Statistics on the sequencing of bacterial, archaeal and fungal communities.

Community type	Bacteria	Archaea	Fungi
Raw Reads	1349099	1179084	1979324
Sequences	1202964	1079854	1589093
OTU	8355	531	5806
Phylum	50	12	17
Class	154	18	62
Order	381	29	167
Family	631	39	386
Genus	1297	57	926
Species	2757	111	1629

Table S7. Number of shared and unique species between groups based on OTU levels.

Group	Bacteria	Archaea	Fungi
Bare land × Cropland × Forest × Grassland × Wetland	878	46	75
Bare land × Cropland × Forest × Grassland	84	1	16
Bare land × Cropland × Forest × Wetland	387	15	40
Bare land × Cropland × Grassland × Wetland	33	1	4
Bare land × Forest × Grassland × Wetland	75	12	6
Cropland × Forest × Grassland × Wetland	723	6	116
Bare land × Cropland × Forest	268	7	27
Bare land × Cropland × Grassland	7	0	1
Bare land × Cropland × Wetland	69	3	6
Bare land × Forest × Grassland	11	0	5
Bare land × Forest × Wetland	215	11	24
Bare land × Grassland × Wetland	40	5	7
Cropland × Forest × Grassland	509	1	157
Cropland × Forest × Wetland	282	0	110
Cropland × Grassland × Wetland	82	1	44
Forest × Grassland × Wetland	148	5	49
Bare land × Cropland	38	0	18
Bare land × Forest	104	3	23
Bare land × Grassland	7	0	3
Bare land × Wetland	311	23	86
Cropland × Forest	1076	9	508
Cropland × Grassland	129	0	131
Cropland & Wetland	90	2	81
Forest × Grassland	228	13	124
Forest × Wetland	134	5	134
Grassland × Wetland	178	5	119
Bare land	136	23	170
Cropland	603	24	1178
Forest	610	146	1033
Grassland	313	107	676
Wetland	587	57	835

Table S8. Alpha diversity of soil microbial communities.

Community type	Index Type		Forest	Cropland	Grassland	Wetland	Bare land	*p* value
Bacteria	Richness	ACE	2376.33 ± 160.27 a	2814.21 ± 237.24 a	2169.85 ± 300.52 a	2863.85 ± 465.82 a	2770.96 ± 102.05 a	0.2976
		Chao1	2371.09 ± 152.26 a	2801.99 ± 233.73 a	2164.14 ± 295.01 a	2874.51 ± 467.83 a	2514.90 ± 150.15 a	0.2529
		Observed species	1829.36 ± 123.57 a	2173.84 ± 179.97 a	1736.19 ± 212.46 a	2256.83 ± 366.06 a	1808.70 ± 232.00 a	0.2747
	Evenness	Pielou	0.76 ± 0.02 a	0.81 ± 0.01 a	0.78 ± 0.02 a	0.82 ± 0.01 a	0.75 ± 0.05 a	0.2401
		equitability	0.04 ± 0.01 a	0.07 ± 0.01 a	0.06 ± 0.01 a	0.10 ± 0.01 a	0.06 ± 0.02 a	0.0799
	Diversity	Shannon	5.68 ± 0.17 a	6.17 ± 0.16 a	5.79 ± 0.26 a	6.33 ± 0.23 a	5.63 ± 0.49 a	0.2491
		Simpson	0.02 ± 0.00 a	0.01 ± 0.00 a	0.01 ± 0.00 a	0.01 ± 0.00 a	0.01 ± 0.01 a	0.2019
	Coverage	Good’s coverage	0.98 ± 0.00 a	0.98 ± 0.00 a	0.98 ± 0.00 a	0.98 ± 0.00 a	0.98 ± 0.00 a	0.3634
Archaea	Richness	ACE	76.61 ± 14.23 abc	56.15 ± 3.88 b	82.98 ± 13.63 abc	116.75 ± 26.54 ac	115.88 ± 2.48 a	***0.0398***
		Chao1	77.65 ± 14.28 abc	56.20 ± 4.10 b	82.09 ± 13.70 abc	117.49 ± 27.46 ac	116.10 ± 2.90 a	***0.0395***
		Observed species	73.66 ± 14.01 abc	49.61 ± 3.60 b	79.29 ± 14.30 abc	111.1 ± 25.83 ac	113.1 ± 1.50 a	***0.0287***
	Evenness	Pielou	0.52 ± 0.04 a	0.46 ± 0.05 a	0.43 ± 0.04 a	0.53 ± 0.06 a	0.57 ± 0.05 a	0.4487
		equitability	0.09 ± 0.03 a	0.10 ± 0.02 a	0.05 ± 0.01 a	0.07 ± 0.01 a	0.06 ± 0.02 a	0.4261
	Diversity	Shannon	2.16 ± 0.19 a	1.77 ± 0.20 a	1.86 ± 0.17 a	2.50 ± 0.41 a	2.69 ± 0.24 a	0.1355
		Simpson	0.21 ± 0.03 a	0.29 ± 0.08 a	0.29 ± 0.05 a	0.17 ± 0.05 a	0.16 ± 0.05 a	0.5013
	Coverage	Good’s coverage	1.00 ± 0.00 a	1.00 ± 0.00 a	1.00 ± 0.00 a	1.00 ± 0.00 a	1.00 ± 0.00 a	0.2714
Fungi	Richness	ACE	537.11 ± 79.02 a	774.96 ± 72.60 a	621.89 ± 115.18 a	752.57 ± 106.81 a	332.92 ± 9.11 a	0.0660
		Chao1	532.69 ± 78.48 a	769.93 ± 72.46 a	622.74 ± 112.82 a	763.89 ± 116.89 a	339.49 ± 5.10 a	0.0565
		Observed species	474.3 ± 71.56 abd	678.7 ± 60.33 ac	561.2 ± 96.09 abcd	733.5 ± 104.73 a	288.3 ± 48.50 b	***0.0396***
	Evenness	Pielou	0.53 ± 0.04 a	0.63 ± 0.02 a	0.61 ± 0.02 a	0.67 ± 0.07 a	0.37 ± 0.12 a	0.0733
		equitability	0.02 ± 0.00 abd	0.04 ± 0.01 ac	0.04 ± 0.00 a	0.05 ± 0.03 abcd	0.01 ± 0.00 b	***0.0465***
	Diversity	Shannon	3.24 ± 0.25 bd	4.06 ± 0.15 ac	3.83 ± 0.22 abcd	4.43 ± 0.55 a	2.09 ± 0.75 b	***0.0325***
		Simpson	0.14 ± 0.03 ab	0.05 ± 0.01 bc	0.05 ± 0.01 bc	0.05 ± 0.02 b	0.33 ± 0.13 a	***0.0171***
	Coverage	Good’s coverage	1.00 ± 0.00 a	1.00 ± 0.00 a	1.00 ± 0.00 a	1.00 ± 0.00 a	1.00 ± 0.00 a	0.0886

Notes: Values in the table are mean ± SE (Forest: *N*=8; Grassland: *N*=4; Cropland: *N*=8; Wetland: *N*=3; Bare land: *N*=2); Kruskal-Wallis test was used for one-way ANOVA between groups, values in bold italics indicate significant differences ($p < 0.05$), and different lowercase letters show differences between groups.

Table S9. Significance analysis of differences in soil microbial community structure.

Data sets	Group	Distance	ANOSIM		Adonis	
			R	*p* value	R^2	*Pr*(>F)
Bacteria	All groups	Bray-Curtis	0.3614	***0.001***	0.3321	***0.001***
	Forest × Grassland		0.0901	0.213	0.1578	0.057
	Forest × Cropland		0.0452	0.194	0.0962	0.102
	Forest × Wetland		0.2930	0.084	0.1708	***0.047***
	Forest × Bare land		0.5129	***0.028***	0.1950	0.060
	Cropland × Grassland		0.6801	***0.008***	0.3201	***0.002***
	Cropland × Wetland		0.6882	***0.016***	0.2827	***0.005***
	Cropland × Bare land		0.8060	0.054	0.3197	***0.030***
	Grassland × Wetland		0.6296	***0.023***	0.3398	***0.027***
	Grassland × Bare land		1.0000	0.063	0.4899	0.067
	Wetland × Bare land		0.1667	0.317	0.2908	0.200
Archaea	All groups	Bray-Curtis	0.3841	***0.001***	0.3528	***0.001***
	Forest × Grassland		0.3474	***0.036***	0.2168	***0.046***
	Forest × Cropland		0.0290	0.246	0.0805	0.257
	Forest × Wetland		0.5134	***0.019***	0.2514	***0.011***
	Forest × Bare land		0.0733	0.266	0.1513	0.160
	Cropland × Grassland		0.8033	***0.002***	0.3631	***0.002***
	Cropland × Wetland		0.8091	***0.007***	0.3286	***0.005***
	Cropland × Bare land		0.4698	0.096	0.2194	0.072
	Grassland × Wetland		0.5556	0.057	0.3169	0.084
	Grassland × Bare land		0.5357	0.063	0.3911	0.067
	Wetland × Bare land		0.3333	0.199	0.2885	0.300
Fungi	All groups	Bray-Curtis	0.3945	***0.001***	0.2505	***0.001***
	Forest × Grassland		0.0313	0.394	0.1104	0.061
	Forest × Cropland		0.1908	***0.007***	0.1202	***0.001***
	Forest × Wetland		0.0753	0.362	0.1244	***0.013***
	Forest × Bare land		0.6379	***0.028***	0.1283	***0.047***
	Cropland × Grassland		0.7022	***0.002***	0.1814	***0.002***
	Cropland × Wetland		0.9086	***0.004***	0.2153	***0.005***
	Cropland × Bare land		0.9914	***0.028***	0.2219	***0.030***
	Grassland × Wetland		0.5185	***0.023***	0.2267	***0.027***
	Grassland × Bare land		1.0000	0.063	0.2671	0.067
	Wetland × Bare land		0.1667	0.519	0.2746	0.400

Notes: the closer the R value to 1 in ANOSIM indicates that the difference between groups is greater than the difference within groups, and vice versa. The larger the R^2 in Adonis indicates that the subgroups have a higher degree of explanation of the differences. The *Pr* indicates the *p* value, which is less than 0.05, indicating that the test has a high degree of availability.

Table S10. Annual soil emissions of HONO, NO and NO_x from different land use types in Tibet in 2011.

Land use type	Annual soil emissions (Gg N yr^{-1})		
	HONO	NO	NO_x
Forest	1.5 ± 0.2	1.0 ± 0.7	1.3 ± 0.6
Grassland	2.0 ± 1.1	5.2 ± 2.8	5.2 ± 2.8
Cropland	0.5 ± 0.1	0.2 ± 0.1	0.3 ± 0.1
Wetland	< 0.1 ± 0.0	< 0.1 ± 0.0	< 0.1 ± 0.0
Bare land	3.0 ± 2.0	5.3 ± 4.2	13.6 ± 3.6
Total	7.0 ± 3.4	11.6 ± 7.8	20.3 ± 7.0

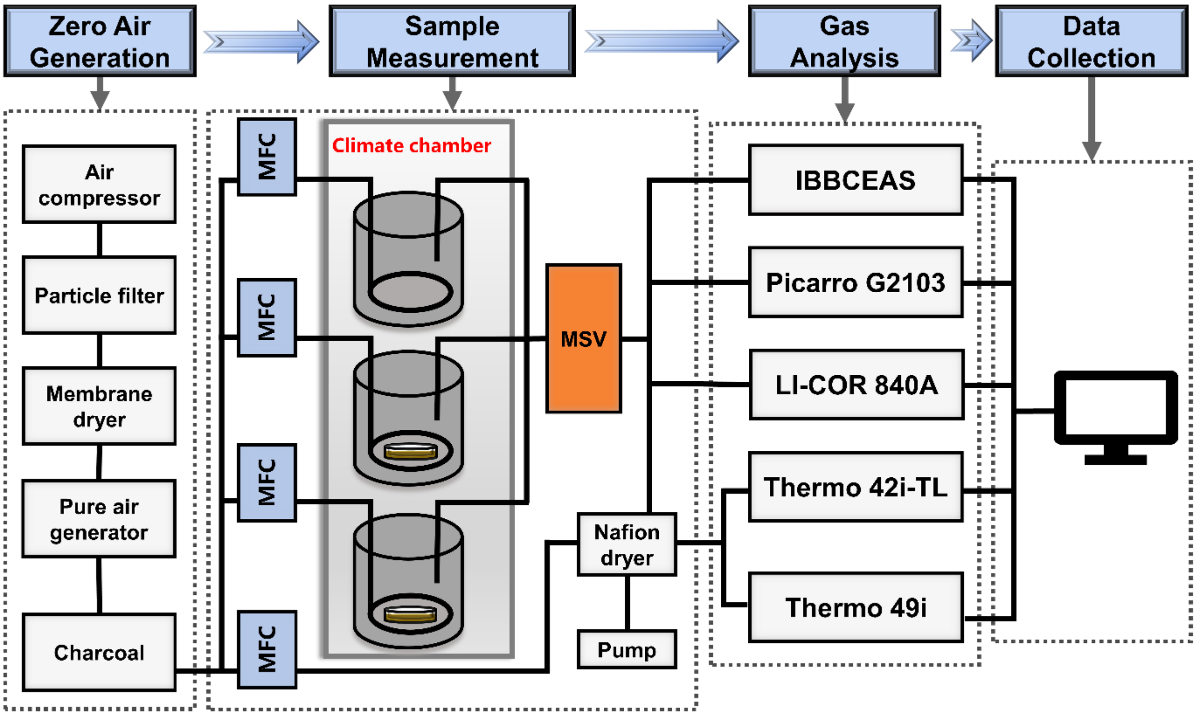

Fig. S1. Schematic overview of the MUlti-gaS dynamIC measurement system (MUSIC). Pure air generator (Thermo, model 1150-111); MFC: mass flow controller (0 ~ 10 L min^{-1} or 0 ~ 20 L min^{-1}, Bronckhorst, Germany); MSV: Multi-point switching valve; Nafion dryer (Model Perma Pure MD™110, Perma Pure LLC, USA); IBBCEAS: Incoherent Broadband Cavity Enhanced Absorption Spectroscopy (AIOFM-CEAS-TY19-1); Ammonia Analyzer (Picarro G2103, USA); Infrared CO_2/H_2O analyzer (LI-COR 840A, Lincoln, NE, USA); Chemiluminescent NO_x analyzer (Thermo 42i TL, Waltham, MA, USA); O_3 analyzer (Thermo 49i, USA).

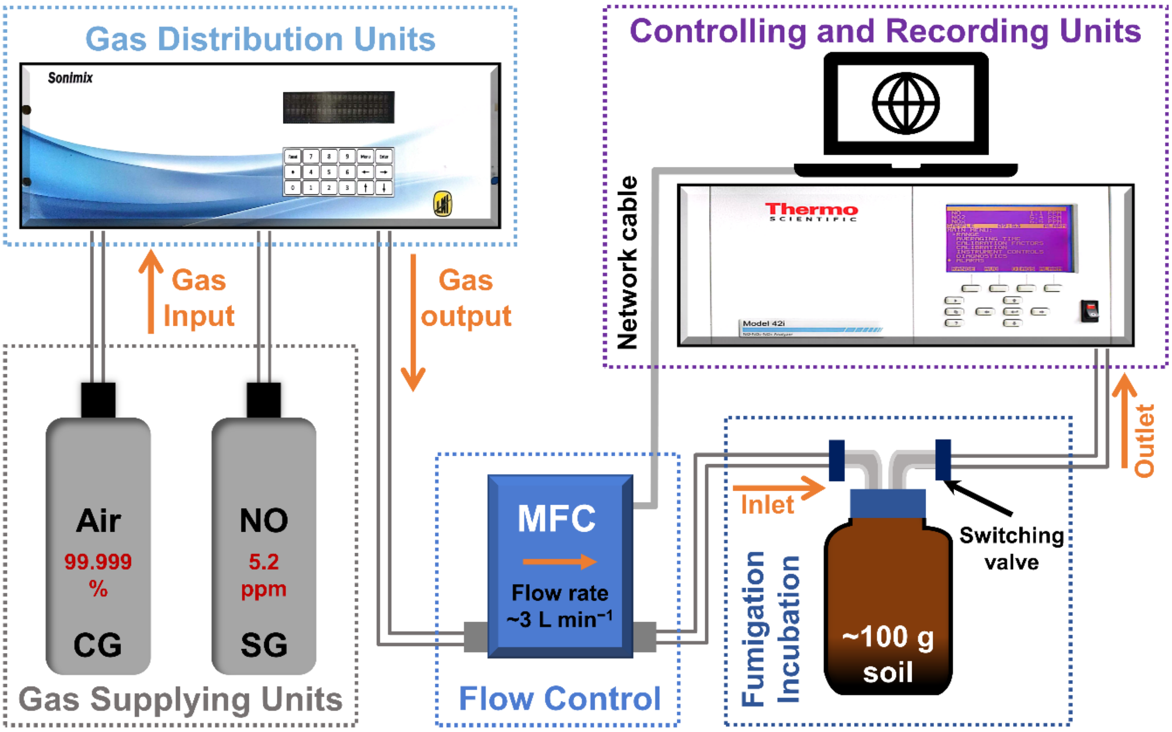

Fig. S2. Overview of the schematic diagram of the fumigated incubation unit. CG: carrier gas (dry oxygen 99.999%, Air Liquide, Shanghai); SG: NO standard gas (5.2 ppm, Air Liquide, Shanghai); Gas distribution units (SONIMIX 4001, LNI, Italy); MFC: mass flow controller (0 ~ 10 L min^{-1}; Bronckhorst, Germany); Controlling and recording units: Chemiluminescent NO_x analyser (Thermo 42i TL, Waltham, MA, USA).

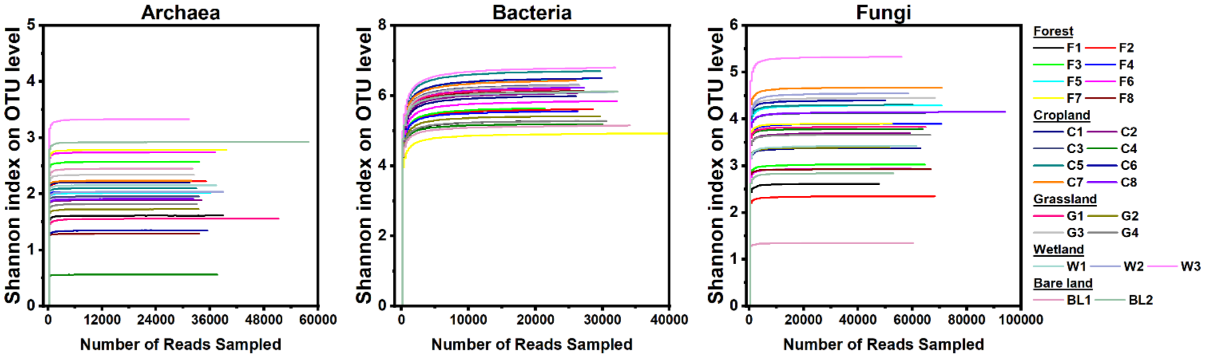

Fig. S3. Soil archaea, bacteria and fungi rarefaction curve.

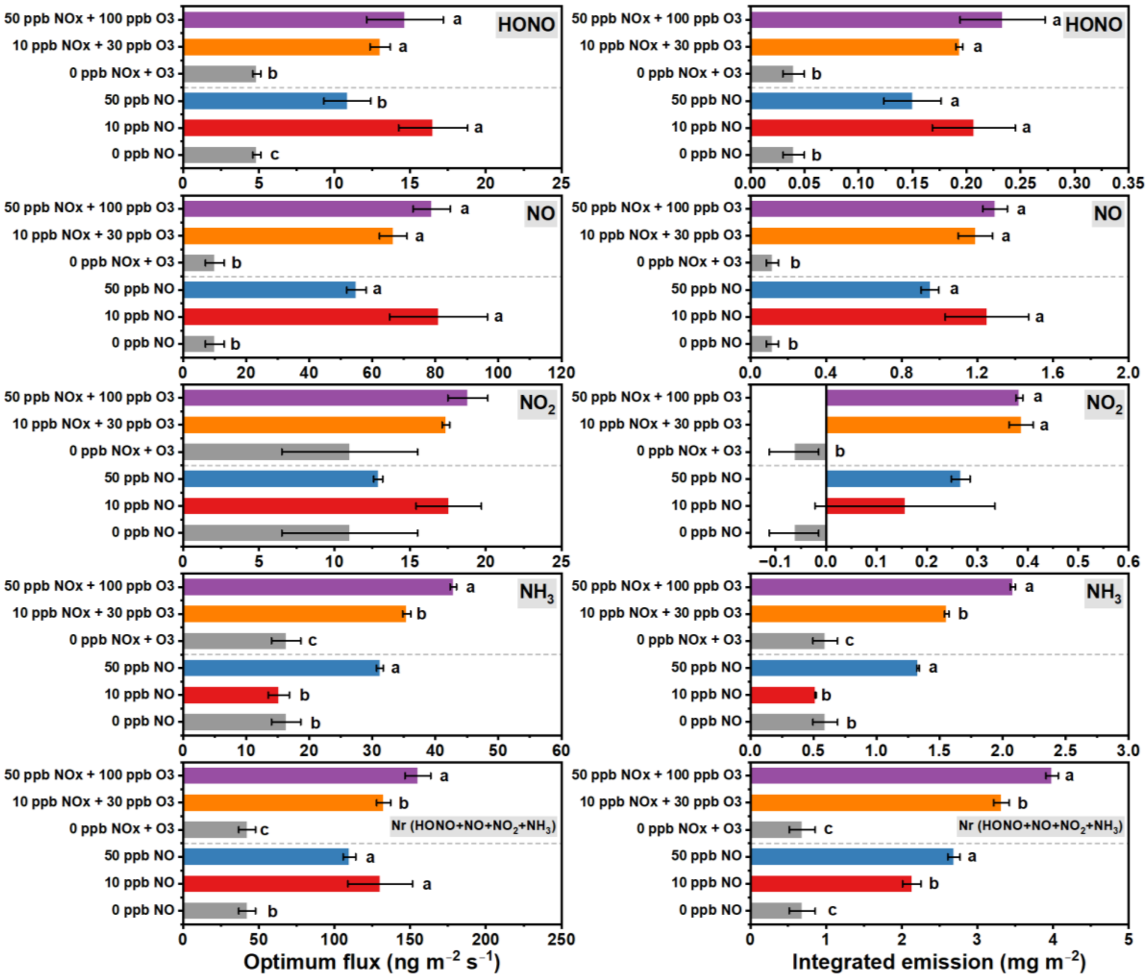

Fig. S4. Optimum fluxes and integrated emissions of reactive nitrogen gases (HONO, NO, NO_2, NH_3) from forest soils under NO and NO_x+O_3 fumigation treatments. The error bars show the standard error of three replicates. Multiple comparisons were based on Duncan's method, with different lowercase letters indicating differences between treatments.

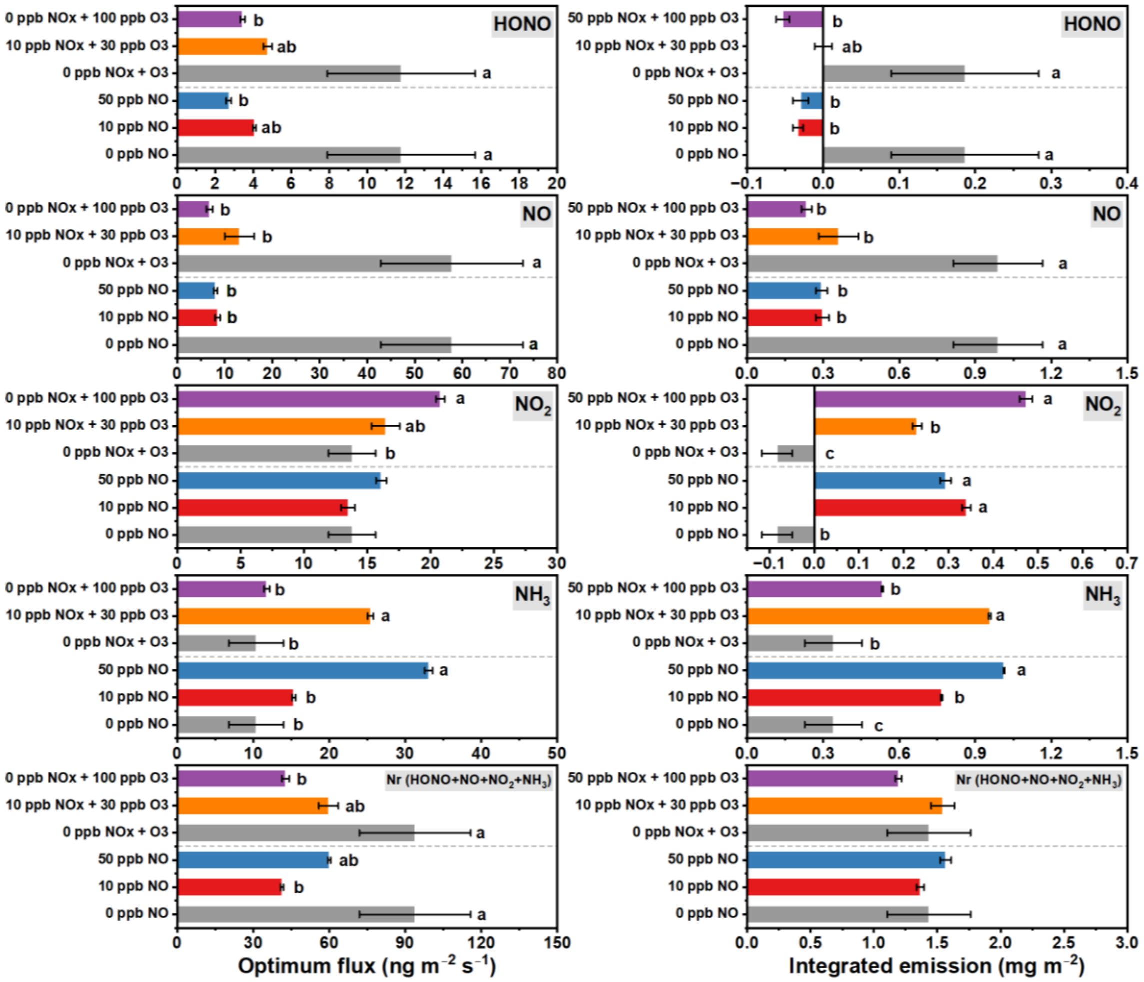

Fig. S5. Optimum fluxes and integrated emissions of reactive nitrogen gases (HONO, NO, NO_2, NH_3) from grassland soils under NO and NO_x+O_3 fumigation treatments. The error bars show the standard error of three replicates. Multiple comparisons were based on Duncan's method, with different lowercase letters indicating differences between treatments.

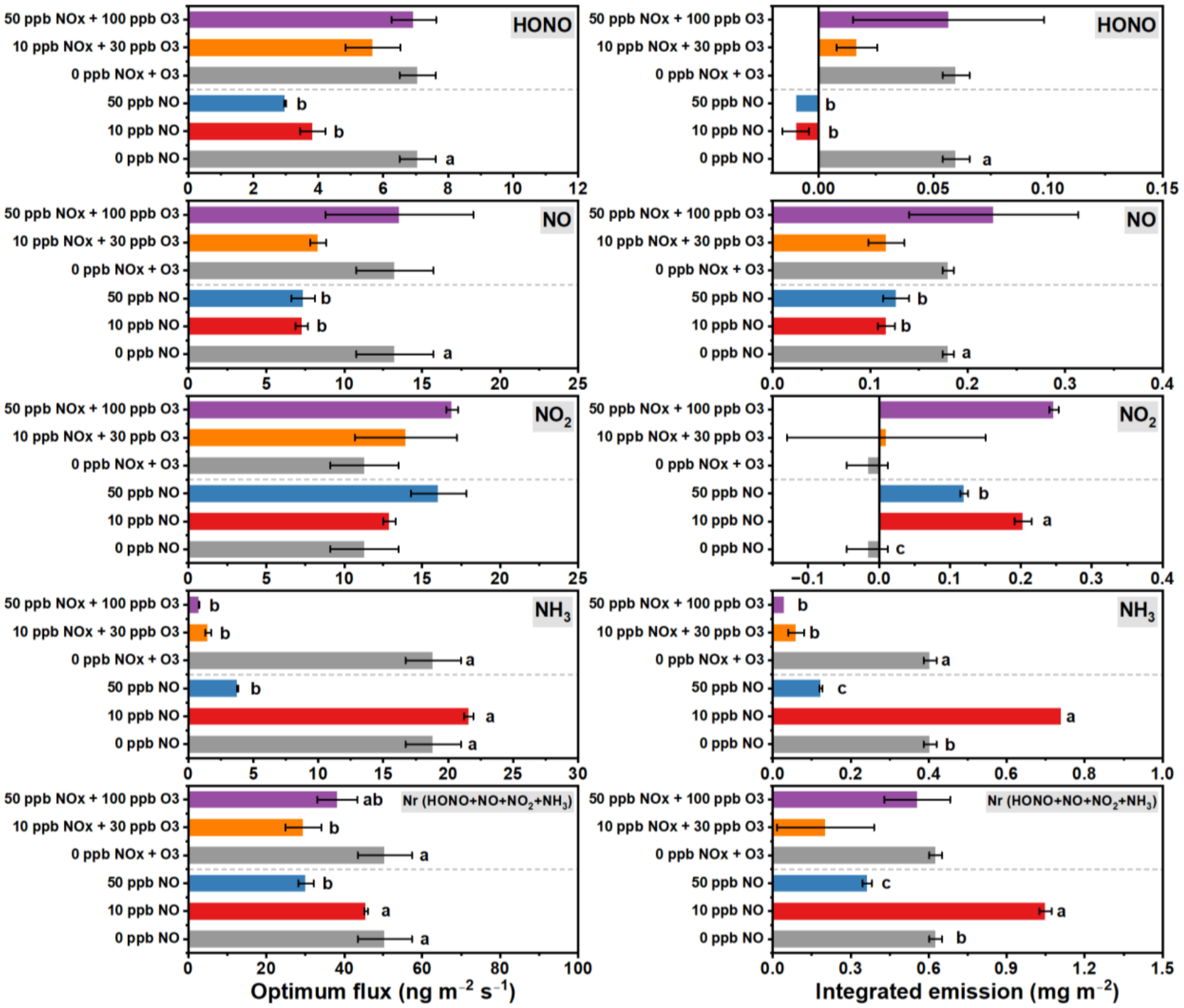

Fig. S6. Optimum fluxes and integrated emissions of reactive nitrogen gases (HONO, NO, NO_2, NH_3) from cropland soils under NO and NO_x+O_3 fumigation treatments. The error bars show the standard error of three replicates. Multiple comparisons were based on Duncan's method, with different lowercase letters indicating differences between treatments.

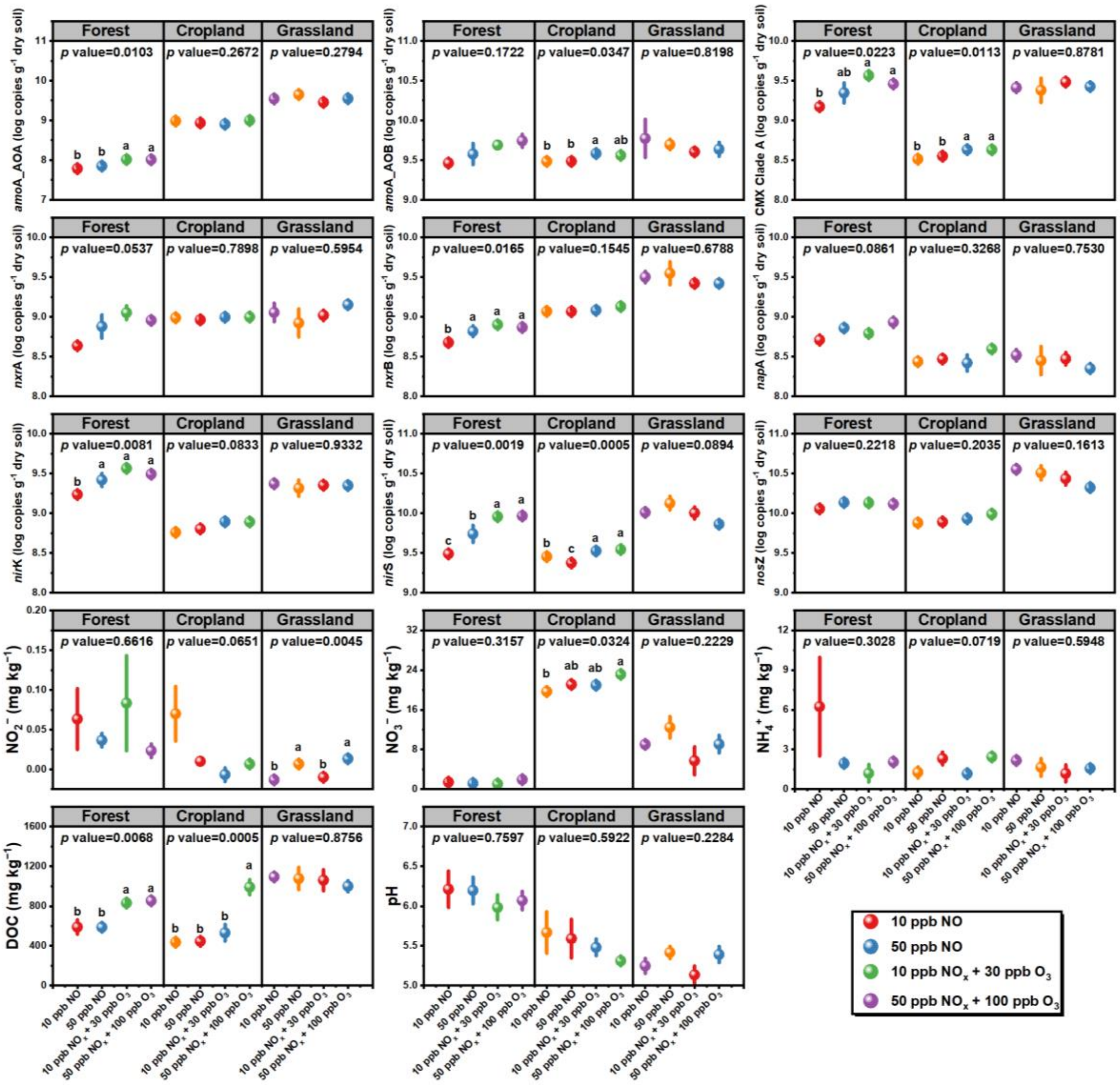

Fig. S7. Soil physicochemical and biological properties under different fumigation patterns and concentrations. The error bars show the standard error of three replicates. Multiple comparisons were based on Duncan's method, with different lowercase letters indicating differences between treatments.

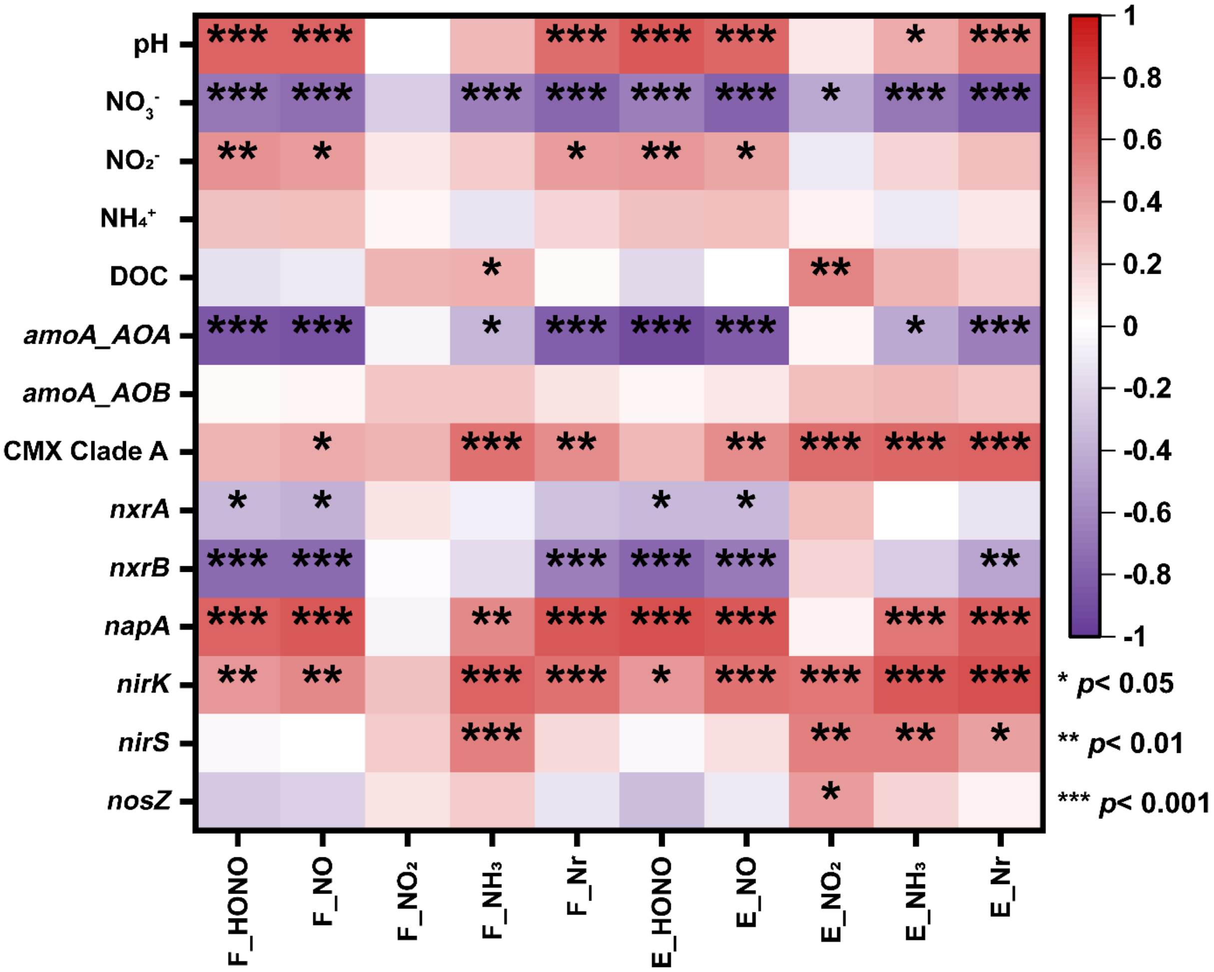

Fig. S8. Correlation matrix between fumigated soil physicochemical properties, functional genes and reactive nitrogen gas emission fluxes based on Pearson correlation analysis.

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