Supplementary Materials

Table S1. Detailed soil properties, gross and net N turnover rates, abundance of functional N genes, and production rates of greenhouse gases (GHG: N_2O, CO_2, CH_4) and NO, HONO measured mainly in laboratory incubations of soil surface samples and in situ gas fluxes at two types of N availability hotspots: exemplified by a best described site of bare surfaces on permafrost peatland and thermokarst disturbed and revegetated retrogressive thaw slump (RTS), and undisturbed sites associated with the hotspots: vegetated surfaces on permafrost peatland and intact, fully vegetated soil adjacent to thaw slump, respectively. For RTS sites, a distinction was made between two subsites: slump floor (SF) and thaw mound (TM).

	Permafrost Peatland		**Mineral Upland Soils in Thermokarst Landscapes**		
			Disturbed, Revegetated RTS **		
Soil and Microbial Properties	**Bare Surfaces ***	**Vegetated Surfaces ***	**Slump Floor (SF)**	**Thaw Mound (TM)**	**Undisturbed Fully Vegetated Site Next to RTS ****
pH	3.3 [86] 4.0 ± 0.2 [248]	3.4 [86] 3.8 ± 0.0 [248]	8.2 ± 0.3 [87] 6.1 ± 0.2 [257]	7.9 ± 0.0 [257]	5.7 ± 0.3 [87]
C/N	24 ± 2 [86] 19 ± 0 [248]	62 ± 16 [86] 40 ± 4 [248]	14.1 ± 1.1 [87] 15.3 ± 1.7 [257]	12.8 ± 0.1 [257]	38.0 ± 3.7 [87]
WFPS (%)	70 ± 3 [86] 35 ± 3 [248]	27 ± 16 [86] 17 ± 2 [248]	52 ± 9 [87] 67 ± 3 [257]	60 ± 3 [257]	13 ± 6 [87]
SOM (%)	95 ± 1 [86] 94 ± 1 [248]	98 ± 0 [86] 98 ± 0 [248]	8 ± 0 [87] 13 ± 2 [257]	8 ± 0 [257]	27 ± 3 [87]
DOC (μg g dw^{-1}) (μg C g dw^{-1})	849 ± 234 [217] 1340 ± 107 [248]	613 ± 152 [217] 1350 ± 61 [248]	75 ± 18 [382]	226 ± 7 [382]	n.d.
TN (%)	2.2 ± 0.3 [86] 2.6 ± 0.1 [248]	0.8± 0.2 [86] 1.2 ± 0.1 [248]	0.24 ± 0.03 [87] 0.43 ± 0.11 [257]	0.34 ± 0.01 [257]	0.29 ± 0.03 [87]
δ^{15}N in bulk soil (‰)	n.d.	n.d.	1.02 ± 0.13 [87] 1.76 ± 0.07 [257]	1.95 ± 0.08 [257]	1.24 ± 0.25 [87]
Ammonium (μg N g dw^{-1})	4.6 ± 3.3 [217] 25.0 ± 15.0 [86] 116.0 ± 39.0 [203] 94.0 ± 37.0 [248] 5.4 ± 0.6 [206] 62.6 ± 5.3 [256]	0.9 ± 3.0 [217] 9.0 ± 3.0 [86] 35.0 ± 6.0 [203] 36.0 ± 8.0 [248] 0.0 ± 0.0 [206] 36.4 ± 7.1 [256]	2.6 ± 0.8 [87] 0.1 ± 0.1 [257]	0.0 ± 0.0 [257]	9.0 ± 11.7 [87]
Nitrat (μg N g dw^{-1})	15.9 ± 11.9 [217] 12.0 ± 6.0 [86] 60.0 ± 11.0 [203] 419.0 ± 54.0 [248] 15.0 ± 3.0 [206] 178.9 ± 7.3 [256]	0.08 ± 0.13 [217] 4.0 ± 2.0 [86] 11.0 ± 4.0 [203] 3.2 ± 1.1 [248] 0.0 ± 0.0 [206] 7.9 ± 0.6 [256]	0.7 ± 0.3 [87] 0.6 ± 0.1 [257]	81.6 ± 24.3 [257]	0.0 ± 0.0 [87]
DOC/DIN (mol mol^{-1}) (μg C g dw^{-1}) (μg N g dw^{-1})$^{-1}$	42 [217] 3 [248]	636 [217] 34 [248]	123 [382]	3 [382]	
DIN/TN (%)	0.2 [86] 2.0 [248]	0.2 [86] 0.3 [248]	0.1 [87] 0.02 [257]	2.4 [257]	0.3 [87]
Gross N mineralization (mg N m^{-2} d^{-1})	600 ± 400 [86] 270 ± 90 [203]	100 ± 30 [86] 10 ± 10 [203]	n.d.	n.d.	n.d.
Gross N mineralization (μg N g dw^{-1} d^{-1})	23.7 ± 6.2 [86] 9.9 ± 3.5 [203]	16.6 ± 1.7 [86] 1.3 ± 1.0 [203]	15.1 ± 10.1 [87]	n.d.	b.d.
Net N mineralization (mg N m^{-2} d^{-1})	18.5 ± 6 [217] 90 ± 50 [203]	0.1 ± 0.1 [217] 1 ± 3 [203]	n.d.	n.d.	n.d.
Net N mineralization	n.d.	n.d.	7.4 ± 1.4 [87]	1.4 ± 0.5 [257]	−20.9 ± 16.6 [87]

(µg N g dw^{-1} d^{-1}) mean of p.a.s. 0.8°			0.5 ± 0.3 [257]		
Gross nitrification (µg N g dw^{-1} d^{-1}) mean of p.a.s. 6.6	3.2 ± 1.9 [203] 13.5 ± 1.1 [120]	0.2 ± 0.1 [203] n.d.	b.d.	n.d.	b.d.
Net nitrification (aerobic nitrate production) (µg N g dw^{-1} d^{-1}) mean of p.a.s. −0.4	n.d.	n.d.	2.6 ± 0.2 [87] [k] 0.5 ± 0.3 [257]	1.4 ± 0.5 [257]	−6.0 ± 2.9 [87]
Net aerobic N_2O production (ng N g dw^{-1} d^{-1})	n.d.	n.d.	0.14 ± 0.01 [87] 0.42 ± 0.57 [382]	0.06 ± 0.01 [382]	0.12 ± 0.05 [87]
Net denitrification (anaerobic N_2O production with, (without acetylene)) (µg N g dw^{-1} d^{-1})	0.56 (0.37) [206]	<0.004 (b.d.) [206]	2.8 ± 1.8 (0.6 ± 0.4) [87] n.d. (0 ± 0) [257]	n.d. (0.2 ± 0.02) [257]	0.01 ± 0.00 [87] (0.01 ± 0.00) [87]
Functional nitrification gene AOA *amoA* (copies gdw^{-1})	6.4 × 10^{8} [120]	8.0 × 10^{6} [120]	2.0 × 10^{7} [87]	n.d.	5.4 × 10^{7} [87]
AOB *amoA* (copies gdw^{-1})	b.d.	b.d.	3.3 × 10^{7} [87]	n.d.	4.2 × 10^{6} [87]
Functional nitrification gene *amoA* (% of *16S rRNA*)	n.d.	n.d.	7 [87]	n.d.	1 [87]
amoA (% of N genes)	n.d.	n.d.	3.4 ± 1.0 [87]	n.d.	0.5 ± 1.0 [87]
Functional denitrification gene (% and %/% of *16S rRNA*) [206] and (% and %/% of N genes) [87]					
narG	7.6 ± 2.8 [206]	0.04 ± 0.01 [206]	42 ± 0.9 [87]	n.d.	45 ± 9.3 [87]
nirS + *nirK*	034 ± 0.08 [206]	0.88 ± 0.13 [206]	29 ± 0.1 [87]	n.d.	15 ± 0.6 [87]
(*nirS* + *nirK*)/*nosZ*	0.20 × 10^{3} [206]	0.88 × 10^{3} [206]	2.4 ± 0.2 [87]	n.d.	0.5 ± 0.1 [87]
N_2O fluxes (mg N m^{-2} d^{-1})	6.55 ± 2.83 [86] 2.04 ± 1.15 [203] 0.29 ± 0.07 [248] 1.01 ± 0.43 [120] 0.01 ± 0.00 [256]	0.03 ± 0.04 [86] -0.01 ± 0.00 [203] <0.08 ± 0.03 [248] 0.03 ± 0.03 [120] −0.06 ± 0.01 [256]	1.64 ± 2.61 [87]	n.d.	−0.001 ± 0.018 [87]
NO fluxes (mg N m^{-2} d^{-1})	1.42 ± 0.13 [256]	0.006 ± 0.002 [256]	n.d.	n.d.	n.d.
HONO fluxes (mg N m^{-2} d^{-1})	0.06 ± 0.02 [256]	b.d. [256]	n.d.	n.d.	n.d.
CO_2 fluxes (soil respiration) (g C m^{-2} d^{-1})	1.51 ± 0.66 [245] 0.99 ± 0.09 [248]	1.18 ± 0.07 [245] 2.16 ± 0.27 [248]	2.28 ± 0.78 [258]	n.d.	0.34 ± 0.18 [258]
Aerobic CO_2 production (µg C g dw^{-1} d^{-1})	27.0 [245]	91.6 [245]	0.8 ± 0.5 [383] 6.1 ± 0.6 [257] 2.3 ± 1.5 [258]	1.8 ± 0.9 [257]	6.3 ± 2.4 [383] 7.5 ± 1.7 [258]
CH_4 fluxes (mg C m^{-2} d^{-1})	160 ± 5 [248] 1.36 ± 2.19 [252]	<90 ± 3 [248] 0.37 ± 0.35 [252]	−0.05 ± 0.05 [87]	n.d.	−0.19 ± 0.05 [87]
Anaerobic CH_4 production (ng C g dw^{-1} d^{-1})	n.d.	n.d.	0.02 ± 0.06 [383] 14.9 ± 13.8 [257]	7.8 ± 11.0 [257]	0.00 ± 0.00 [383]

* Peat plateau in Seida, Komi Republic, Russia N 67°03′, E 62°57′ (Figures 1 and 2), bare peat surfaces covered by a thin layer of moss but without vascular plants, vegetated site with typical bog vegetation [86]. ** Retrogressive thaw slump, Kurungnakh Island, Lena Delta, Russia, N 72°20, E 126°17′ (Figures 1 and 2), undisturbed site: Holocene cover deposits vegetated with moss, sedge and dwarf shrub communities on the top of the RTS, disturbed thermokarst site: Yedoma revegetated with grasses (*Arctagrostis arundinacea*) subdivided slump floor (SF, SF3V in [257]; SF3 in [257,258], Yedoma mixed with younger Holocene and thaw mounds (TM, TM1V in [257] dominating by late Pleistocene Yedoma as described in Marushchak et al. [87]. Ref. [86] soil samples from 0–10 cm depth were collected once per month in June-August 2008 and N mineralization rates were measured in oxic incubations at 15 °C for 24 h, N_2O fluxes were measured weekly in situ between May/June until October. Ref. [87] soil samples were collected in July 2016 at a depth of 0–

10 cm, CH_4 and N_2O fluxes were measured in situ twice in July 2016, N turnover rates were estimated in soil incubations using the ^{15}N dilution technique at 5 °C for 24 h. N_2O production due to nitrification were measured under oxic and due to denitrification under anoxic conditions with or without addition of acetylene at 10 °C for 6 days. Ref. [120] soil samples were collected from June to August 2011 from a depth of up to 10 cm; N_2O fluxes were measured on one day, and nitrification was measured in incubations at 13 °C for 30 days. Ref. [217] soil samples collected from 0–5 cm depth in July 2011, N mineralization rates measured in situ using buried bag technique at field temperature for 25 days. Ref. [206] soil parameters were measured in September 2010 from a depth of 0–5 cm, denitrification rates were measured in anoxic incubation at 20 °C for 160 days. Ref. [203] N_2O fluxes, N mineralization and nitrification rates measured by ^{15}DIN labeling experiments in situ from July to August in 2010 at field temperature for 24 days, with N_2O fluxes measured before labeling. Ref. [245] soil samples for incubations were collected in August 2007 from a depth of 0–10 cm, CO_2 fluxes are soil respiration rates measured in situ, and CO_2 production was measured in soil incubations at 15 °C for one month. Ref. [248] soil parameters were measured from a depth of 0–5 cm in July 2012 and 2013, CO_2 fluxes were measured as average soil microbial respiration in situ in summer 2013, N_2O fluxes during the growing season from June to September in 2012 and 2013, for vegetated sites only data for warmed sites were available, but they showed that not warmed N_2O fluxes are smaller. Ref. [252] CH_4 fluxes measured in situ in the period July-October 2007 and May-October 2008. Ref. [256] N fluxes were measured in the laboratory at 21 °C on soil cores taken to a depth of 10 cm in August 2016. Ref. [257] soil samples were collected in July, 2019 at a depth of 0–20 cm, aerobic CO_2; N_2O and anaerobic CH_4 and N_2O production rates were measured in incubations at temperature of 4 °C for 28 days, N turnover rates in slurry incubations at 4 °C for 40 days, SOM calculated from TC. Ref. [383] Unpublished data from M. E. Marushchak et al. measured in the same oxic and anoxic incubations as described for N_2O [87]. Ref. [258] CO_2-fluxes measured as soil respiration in situ in July 2017, CO_2 production was measured in incubations of soil samples from 0–10 cm at 4 °C for 175 days. Ref. [382] Unpublished data from R. Wegner et al. measured oxic incubations for as described in [257] data are means ± standard division from cited publications, therefore mainly site variations, all gas fluxes were measured with static chamber technique. *amoA* = gene of subunit A of ammonia monooxygenase, AOA = ammonia-oxidizing archaea, AOB = ammonia-oxidizing bacteria, b.d. = below detection limit, DIN = dissolved inorganic nitrogen, DOC = dissolved organic carbon, dw = dry weight, *narG* = gene of nitrate reductase, n.d. = not determined, *nirS*, *nirK* = genes of nitrite reductases, *nosZ* = gene of N_2O reductase, p.a.s. = mean rates of permafrost-affected soils from Ramm et al. [59], SOM = soil organic matter, TN = total nitrogen, WFPS = water-filled pore space.

Table S2. Biochemical traits of hotspots with high N availability and adjacent control sites with N limitation using the example of a study site: water-filled pore space (WFPS), C/N ratio, dissolved inorganic nitrogen (DIN, ammonium + nitrate) and nitrate, microbial net N turnover: N mineralization, nitrification, denitrification, and abundance of genes of key functional enzymes of nitrification (*amo*, ammonia monooxygenase), denitrification (*nirS* + *nir K*, nitrite reductases) and (*nirS* + *nirK*)/*nosz* ratio (nitrite reductase/N_2O reductase) in subarctic bare (BP) and vegetated peatland (VP), Arctic retrogressive thaw slump (RTS) and undisturbed site (URTS), thermoerosion-gully (TEG) and undisturbed site (UTRG) on the Tibet Plateau, Arctic bare alluvial soils (AS) and vegetated floodplain (VP) and animal-influenced permafrost affected soils of the Arctic (AIA) and Antarctic (AIAA) and non-influenced soils of Arctic (NIA) and Antarctic (NIAA).

Soil and Microbial Properties	**Subarctic Bare Peat (BP)** *Vegetated Peat (VP)*	**Arctic Retrogressive Thaw Slump (RTS)** *Undisturbed Site (URTS)*	**Thermo-Erosion Gully (TEG) of Tibet Plateau** *Undisturbed Site (UTEG)*	**Arctic Alluvial Soil (AS)** *Vegetated Floodplain (VP)*	**Arctic Animal Influenced Soil (AIA)** *Non-Influencend (NAIA)*	**Antarctic Animal Influenced Soil (AIAA)** *Non-Influencend (NAIAA)*
	N Hotspot Site					
	N Limitation Site					
WFPS (%)	53 ± 25 *22 ± 7*	60 ± 8 *13 ± 6*	n.d. *n.d.*	n.d. *n.d.*	n.d. *n.d.*	85 ± 2 *25 ± 1*
C/N	22 ± 4 *51 ± 16*	14 ± 1 *38 ± 4*	n.d. *n.d.*	15 *14*	n.d. *n.d.*	7 ± 1 *12 ± 2*
DIN (µg N g dw^{-1})	177 ± 14 *24 ± 8*	29 ± 46 *9 ± 12*	n.d. *n.d.*	91 ± 57 *0.3 ± 0.4*	2276 ± 1380 *0.6 ± 0.3*	146 ± 49 *1.7 ± 0.1*
DIN/TN (%)	1.1 ± 1.3 *0.3 ± 0.1*	0.9 ± 1.4 *0.3*	n.d. *n.d.*	4.6 ± 2.9 *0.0 ± 0.0*	8.2 *0.0*	0.7 ± 0.3 *0.2 ± 0.0*
Nitrat (µg N g dw^{-1})	116.8 ± 2.8 *4.4 ± 7.7*	27.6 ± 46.7 *0.0 ± 0.0*	4.5 ± 0.4 *1.8 ± 0.0*	89.0 ± 56.7 *0.0 ± 0.0*	2270.0 ± 1380.0 *0.3 ± 0.3*	90.2 ± 49.2 *0.5 ± 0.0*
Net N-mineralization (µg N g dw^{-1} d^{-1})	n.d. *n.d.*	3.10 ± 3.75 *−20.90 ± 16.60*	n.d. *n.d.*	1.70 *0.10*	n.d. *n.d.*	n.d. *n.d.*
Net nitrification (µg N g dw^{-1} d^{-1})	n.d. *n.d.*	1.47 ± 1.10 *−6.00 ± 2.90*	n.d. *n.d.*	13.00 ± 0.31 *4.99 ± 0.07*	n.d. *n.d.*	1.28 ± 0.26 *0.33 ± 0.04*
Net denitrification (anoxic N_2O production with acetylene) (µg N g dw^{-1} d^{-1})	0.56 *0.00*	2.80 ± 1.80 *0.01 ± 0.00*	n.d. *n.d.*	n.d. *n.d.*	96.0 ± 24.0 *0.0 ± 0.0*	3.70 ± 2.80 *0.21 ± 0.04*
Functional nitrification gene *amoA* (% of *16S rRNA*)	n.d. *n.d.*	7.00 *1.00*	n.d. *n.d.*	4.77 *0.66*	n.d. *n.d.*	8.68 ± 7.85 *7.33 ± 6.70*
Functional denitrification gene *nirS+nirK* (% of *16S rRNA*, *of N genes or **log10 g dw^{-1})	0.34 ± 0.08 *0.88 ± 0.13*	29.0 ± 0.1 * *15.0 ± 0.6 **	4.14 ± 0.04 ** *3.94 ± 0.04 ***	n.d. *n.d.*	9.29 ± 8.90 ** 0.00 ± 0.00 **	7.08 ± 7.00 ** *3.82 ± 3.69 ***
(nirS+nirK)/nosZ (%/% of *16S rRNA*, *N genes)	0.20 × 10^3 *0.88 × 10^3*	2.4 ± 0.2 * *0.5 ± 0.1 **	6.05 ± 1.11 *3.00 ± 1.05*	n.d. *n.d.*	3.09 *0.00*	n.d. *n.d.*
N_2O fluxes (mg N m^{-2} d^{-1})	1.98 ± 3.19 *0.01 ± 0.03*	1.64 ± 2.61 *0.00 ± 0.02*	1.97 ± 0.32 *0.02 ± 0.00*	n.d. *n.d.*	0.40 ± 0.24 *0.00 ± 0.00*	0.38 ± 1.15 *0.02 ± 0.00*
References	See Table 1	See Table A1	[219]	[119,303,305]	[235]	[189,190,237]

Description of sites and measurements: subarctic peatland site in Table 1; Arctic retrogressive thaw slump in Table A1; thermo-erosion-gully on northeastern Tibetan Plateau, China, N 37°28′, E 100°17′ at ~3900 m a.s.l. in the discontinuous permafrost zone, soil samples collected from a depth of 0–15 cm in summer 2015, data are from the early stage, 3 years after collapse and control site. N_2O was measured in situ in summer 2015/2016; Arctic non-vegetated alluvial and vegetated floodplain soils from Samoylov Island, Lena Delta Russia, N 72°22′, E 126°28′, collected in late August 2008 from a depth of 0–5 cm for DIN, net N mineralization and net nitrification were measured in incubations with Lena River water from samples in July 2019 from a depth of 25–35 cm for 14 days at 20–25 °C and in July 2008 from a depth of 0–5 cm for 6 weeks at ~5 °C; Arctic animal-influenced soils from Ny-Ålesund, Svalbard, Norway collected below seabird colonies (*Rissa tridactyla*, *Fulmarus glacialis*), data from sites BL-T-M and BL-C (N 78°59′, E 12°06′) from a depth of 0–5 cm were collected in July 2015, denitrification rates were measured in incubations at 10 °C for 6 h, and in situ N_2O measurements; Antarctic animal-influenced soils from on Ardley Island on the Fildes Peninsula (S 61°51′–62°15′, W 57°30′–59°00′) collected from penguin colonies (*Pygoscelis adeliae*, *P. papua*, *P. antarcticus*) from a depth of 0–15 cm in summer 2014/2015, potential nitrification rates were estimated in incubations with 1 mM ammonium at 15 °C for 24 h, denitrification rates were measured in slurries labeled with ^{15}N-nitrate labeling at 10 °C for 8 h, and in situ N_2O measurements. data are means ± standard division from cited publications, therefore mainly site variations, all gas fluxes were measured with static chamber technique. *amoA* = gene of subunit A of ammonia monooxygenase, DIN = dissolved inorganic nitrogen, dw = dry weight, n.d. = not determined, *nirS*, *nirK* = genes of nitrite reductases, *nosZ* = gene of N_2O reductase, WFPS = water-filled pore space.