Juottonen H, Kieman M, Fritze H, Hamberg L, Laine AM, Merilä P, Peltoniemi K, Putkinen A, Tuittila ES: **Integrating decomposers, methane-cycling microbes and ecosystem carbon fluxes along a peatland successional gradient in a land uplift region**

Supplementary materials

Contents:

Supplementary methods

Methane and carbon dioxide fluxes

The gas flux measurements were conducted as described in Alm and others (2007), with some modifications. In brief, CH_4 flux was measured with a closed opaque chamber (60 × 60 × 30 cm) equipped with a fan to ensure circulation of air inside the chamber. Four 60-ml air samples were taken from the chamber into plastic syringes at 5-min intervals and transferred into glass vials (Labco Exetainer, UK) via injection with over pressure. The vials were stored at 4 ºC until gas chromatographic (GC) analyses (HP-5890A). CH_4 flux rates were calculated as the linear rate of change in gas concentration over time (mg CH_4 m^{-2} h^{-1}). CO_2 efflux, i.e., ecosystem respiration (RE), was measured with a transparent plastic chamber (chamber size 60 × 60 × 30 cm), covered with an opaque lid, connected to a portable infrared gas analyser (EGM-4, PP Systems, UK). CO_2 concentration in the chamber was recorded at 15-s intervals for a period of 120 to 240 s following placement of the chamber on the sample plot. During the RE measurements, air temperature was

measured inside the chamber. RE was calculated from the linear change in chamber gas concentration as a function of time (g CO_2 m^2 h^{-1}) in relation to chamber volume and temperature.

Analyses of potential CO_2 production, CH_4 production, and CH_4 oxidation

From each peat section (uppermost, middle, deepest), 15 ml of peat was transferred to 120-ml glass flasks sealed with rubber septa. Samples for CO_2 production and CH_4 oxidation were stored at 4°C until GC analyses. Flasks for CH_4 production contained 30 ml of distilled water and were flushed with nitrogen gas (N_2) for 1 min before and after sample addition and stored at 4°C until analysed. GC analyses were carried out as described in Perkiömäki and Fritze (2002), Jaatinen and others (2005) and Merilä and others (2006). Prior to the GC measurements, the flasks were flushed for 1 min with N_2 (CH_4 production) or air (aerobic CO_2 production and CH_4 oxidation) to remove residual gases. The flasks were incubated at 15°C in the dark for 4 days (CH_4 production) or 1-2 days (CO_2 production and CH_4 oxidation). The flasks for CH_4 oxidation received 100 µl of CH_4 as substrate. After GC monitoring, the samples were measured for dry weight (60 °C, 7 d), and the volumes of the analyzed samples were determined by the quotient of dry weight and bulk density. Rates of gas production (aerobic CO_2 and CH_4) or consumption (CH_4) were calculated from the slope of the linear regression given by the gas concentration change over time. The rates were determined in relation to the sample volume (mg or µg dm^{-3} h^{-1}).

Molecular analyses of microbial groups

Polymerase chain reaction (PCR)

For denaturing gradient gel electrophoresis (DGGE), a 40 base pair (bp) long GC-rich DNA sequence (a GC-clamp) was attached either to the forward or the reverse primer to promote efficient

separation of DNA sequences even with minor differences. Fungi were amplified with primers ITS1F-[GC] and ITS2 that amplify the internal transcribed spacer region (Gardes and Bruns 1993). Actinobacterial primers were S-C-Act-0235-a-S-20-[GC] and S-C-Act-0878-a-A-19 that amplify actinobacterial 16S ribosomal RNA genes (Stach and others 2003). Type II methanotrophs (tII-MOB) were detected with the primer pair A189f and A621r-[GC] (Holmes and others 1995; Tuomivirta and others 2009) for methanotroph-specific *pmoA* gene for particulate methane monooxygenase. Methanogens were detected with the primer pair of Luton and others (2002) that amplifies methanogen-specific *mcrA* gene for methyl-coenzyme M reductase. The forward *mcrA* primer was fluorescently labelled with 5´6-carboxyfluorescein (6-FAM) for terminal restriction fragment length polymorphism (T-RFLP) analysis. PCR reactions contained 0.5 mM (fungi, actinobacteria and tII-MOB) or 0.3 mM (methanogens) of each primer, 200 µM of dNTPs, and 0.5-1 U of DNA polymerase (Biotools B & M Labs S.A., Madrid, Spain) in 1 × polymerase buffer. Programs for thermal cycling were as follows: Fungi: initial denaturation 95 °C for 8 min, followed by 39 cycles 95 °C for 35 s, 58 °C for 55 s and 72 °C for 45s - 3 min (extension time was prolonged from 45 s to 2 min after 13 cycles and to 3 min after 26 cycles). Actinobacteria: 95 °C for 5 min, followed by 30-35 cycles 95 °C for 45 s, 65 °C for 45 s and 72 °C for 1 min, final extension 72 °C 10 min. MOB: 95 °C for 3 min, 42 cycles 95 °C for 30s; 1 °C touchdown from 70 °C to 59 °C (in 12 cycles) for 45 s and 72 °C for 30 s, final extension 72 °C for 10 min. Methanogens: 94 ºC for 3 min, 40 cycles 94 ºC for 45 s, 52 ºC for 1 min, and 72 ºC for 1 min, final extension 72 °C for 7 min. When re-amplifying the excised DGGE bands (see below), the number of cycles was reduced to 20 for actinobacteria and to 15 for tII-MOB (with constant annealing temperature of 59°C). Fungal DGGE band PCR was performed with 25 cycles, constant extension time of 1.5 min and a final extension at 72°C for 7 min.

DGGE of fungi, actinobacteria and tII-MOB

All DGGE gels were prepared and run in 1 × TAE, but other parameters varied according to the microbial group. For fungi the urea gradient was 18-58%, acrylamide-bisacrylamide (37.5:1) (Biorad, Hercules, CA, USA) concentration was 7.5% (wt/vol), and running conditions were at 60 °C, with a constant voltage of 75 V for 16 h (D-Code, Biorad) (Korkama-Rajala and others 2008). For actinobacteria the corresponding values were 48-62%, 6%, 60 °C, 70 V, and 16 h, respectively (Jaatinen and others 2008) and for tII-MOB 35-70%, 6.5%, 61 °C, 180 V, 5 h, respectively. Control ladders with bands of known mobility were included in each gel to compare the mobility of sample bands between individual runs. The banding patterns were visualized and individual bands were excised from the gels as described in Korkama-Rajala and others (2008). The excised bands were re-amplified by PCR and run in DGGE to verify differences in band mobility. Sequence similarity of the bands with similar mobility in DGGE was verified by sequencing at least one representative band in each site. Re-amplified bands were used as templates for PCR with primers without GC clamp and Sanger sequenced by Macrogen Sequencing Service (Europe). The number of sequenced bands was 329 for fungi, 192 for actinobacteria, and 91 for tII-MOB. Phylogenetic trees of fungal, actinobacterial and tIIMOB sequences were constructed as maximum likelihood trees in MEGA7 (Kumar and others 2016).

T-RFLP of methanogens

The *mcrA* PCR products were excised from agarose gel, purified with Wizard® SV Gel and PCR Clean-Up System (Promega, Madison, WI, USA), and digested with *Msp*I (Fermentas, Vilnius, Lithuania) at 37 ºC overnight. T-RFLP analysis of the digested PCR products was performed as described in Juottonen and others (2008). The peak areas of individual terminal restriction fragments (T-RFs) from 50 to 500 bp were proportioned to the total peak area of each sample. The

T-RFs that represented >1% of the total area of all T-RFs in each sample were included in the community composition data. T-RFs of different lengths were considered as different OTUs. Methanogens were identified by sequencing of *mcrA* clones. PCR products from sites SJm1, SJ2, SJ3, and SJ5 were cloned with TOPO TA cloning kit (Invitrogen), 48-56 clone PCR products per library were screened by RFLP with MspI, and 13-18 clones per library (in total 62) were Sanger sequenced with vector primer T7 (Macrogen Sequencing Service Europe). A maximum likelihood tree of the derived amino acid sequences of the clone sequences and reference sequences identified by Blast (https://blast.ncbi.nlm.nih.gov) was constructed with PhyML (v. 3.1, Guindon and others 2010) after model selection with ProtTest3 (LG+I+F+G; Darriba and others 2011). Bootstrap values were generated from 100 replicates.

Statistical analyses in Tables S3 and S4

Differences in soil microbial biomasses, microbial activity potentials and soil properties (bulk density, OM, C, N, C/N and pH) between soil layers were investigated using linear models in R (v. 3.1.1, R Core Team 2014). Only differences between the uppermost vs. middle and uppermost vs. deepest layer were investigated. Response variables were log-transformed to achieve normality.

Differences in RE, CH_4 emission, WL (expressed as the distance of the mean water table from the peatland surface in cm, negative values indicating below the surface), microbial biomasses, activities and soil properties between the first successional stage (SJ0) and the other successional stages (SJ1-SJ6 and SJm1) were investigated using linear models in R. Mean values for the three soil layers were used as responses in microbial biomass, microbial activity potentials and soil property data. Response variables were log-transformed when needed to achieve normality. Differences in the cover of plant groups (grasses, herbs, sedges, shrubs, *Sphagnum* mosses, other mosses and hepatics) along successional stages (SJ0 vs. other stages) were investigated using

generalized linear models assuming quasi-binomial distribution (with logit link) in R (Pinheiro and others 2014).

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Supplementary figures

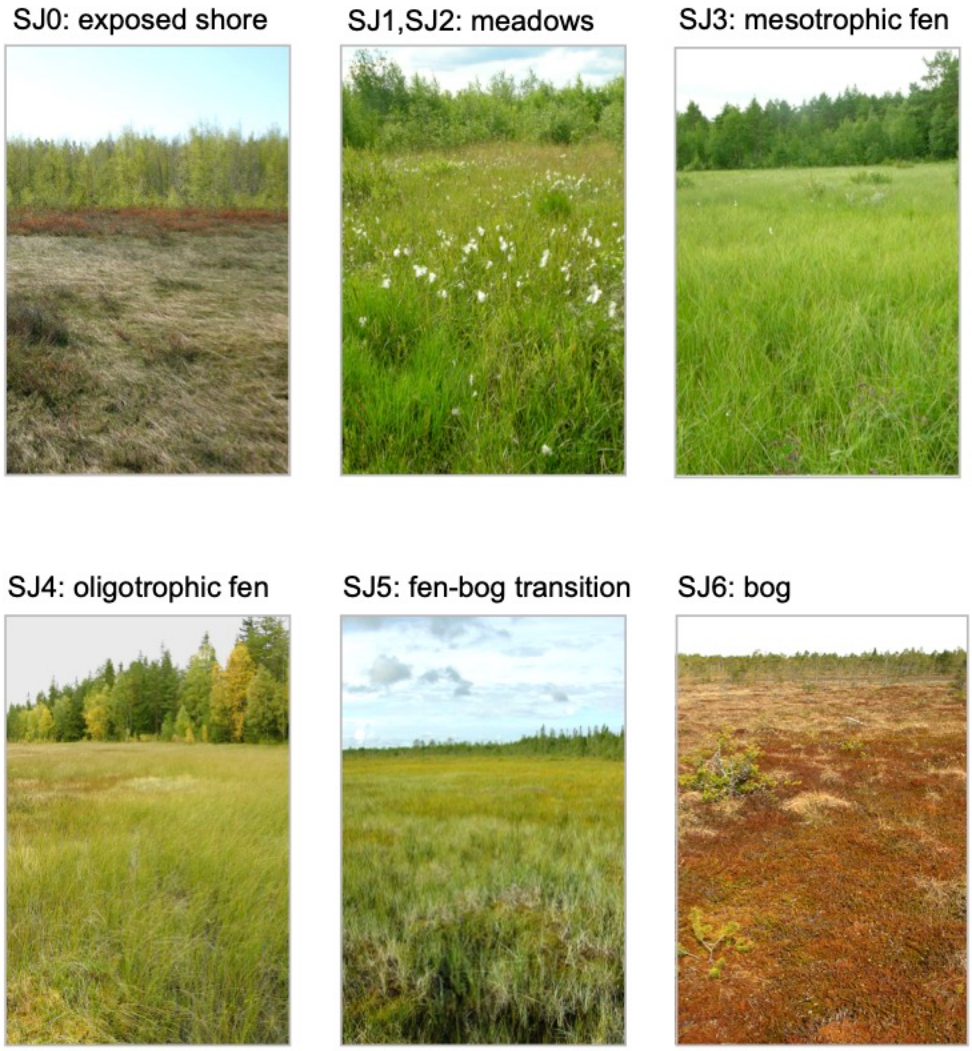

Figure S1. Study sites representing different successional stages on boreal land uplift coast.

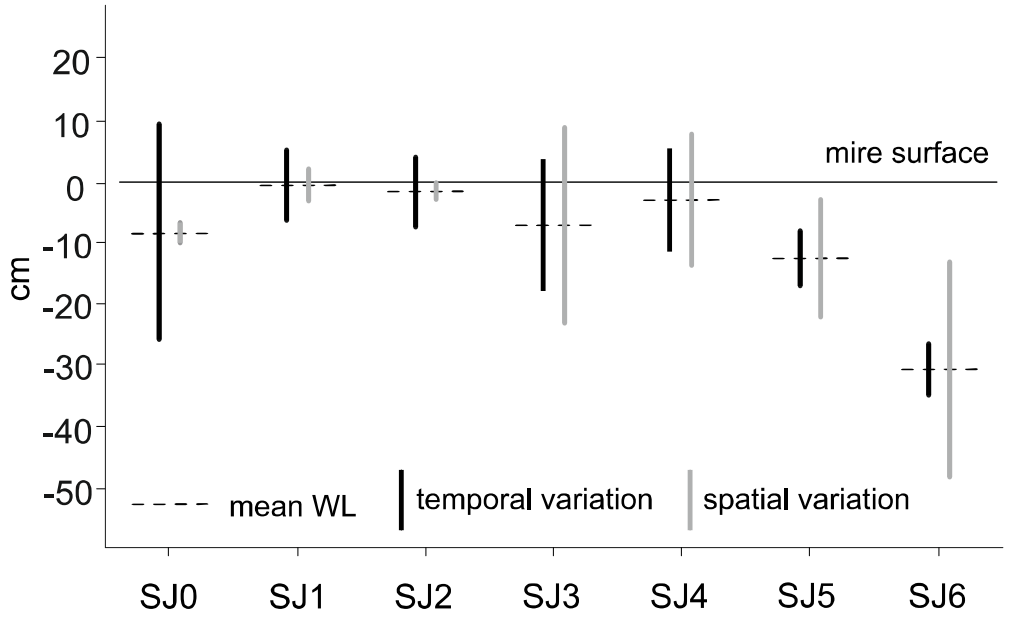

Figure S2. Spatial (microform-related) and temporal variation of water level (WL) in peatland sites SJ0-SJ6.

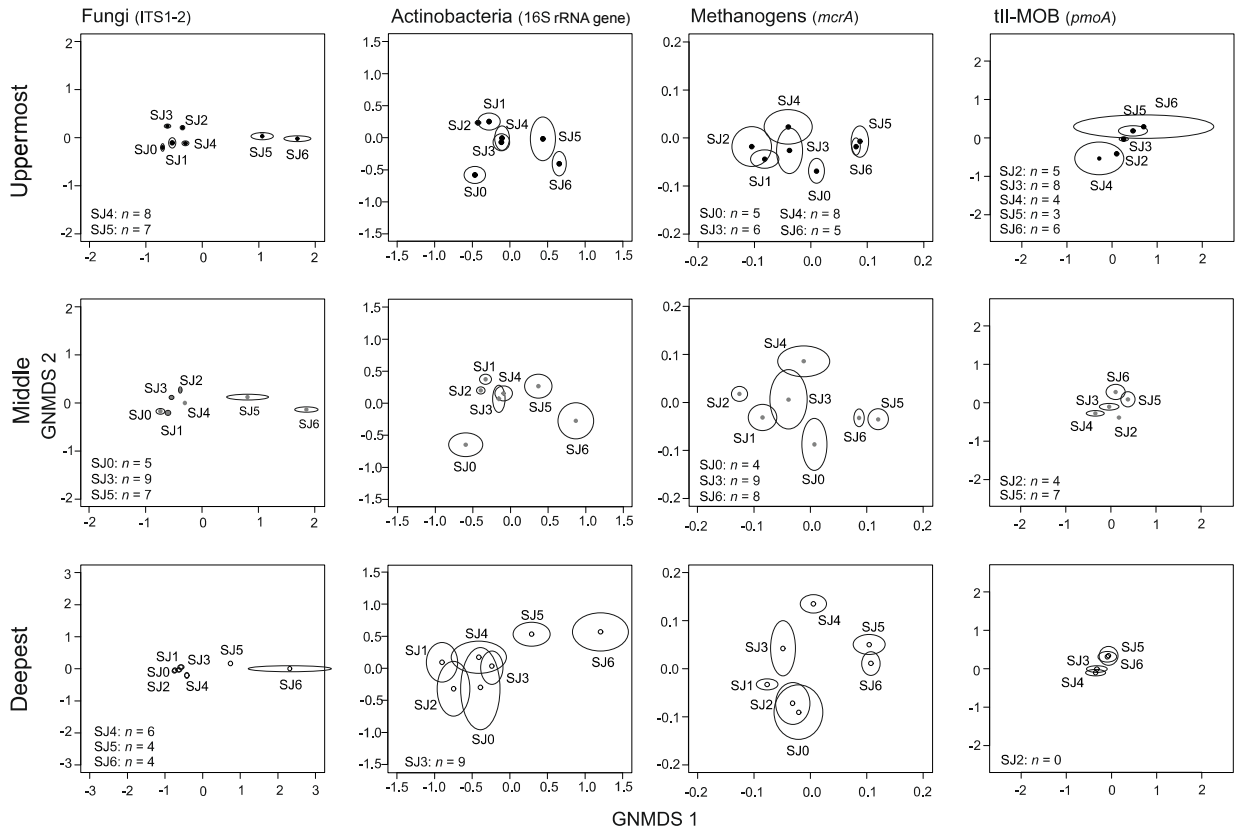

Figure S3. Global non-metric multidimensional scaling (GNMDS) ordinations of fungi, actinobacteria, methanogens, and tII-MOB in sites SJ0–SJ6, separately for uppermost, middle and deepest layer. Ovals represent 95% confidence intervals. The number of peat profiles analysed by PCR: SJ0 $n = 6$, SJ1 $n = 6$, SJ2 $n = 6$, SJ3 $n = 10$, SJ4 $n = 9$, SJ5 $n = 8$, SJ6 $n = 9$. When the number of samples in the ordination deviates from these numbers, it is marked in the subfigures.

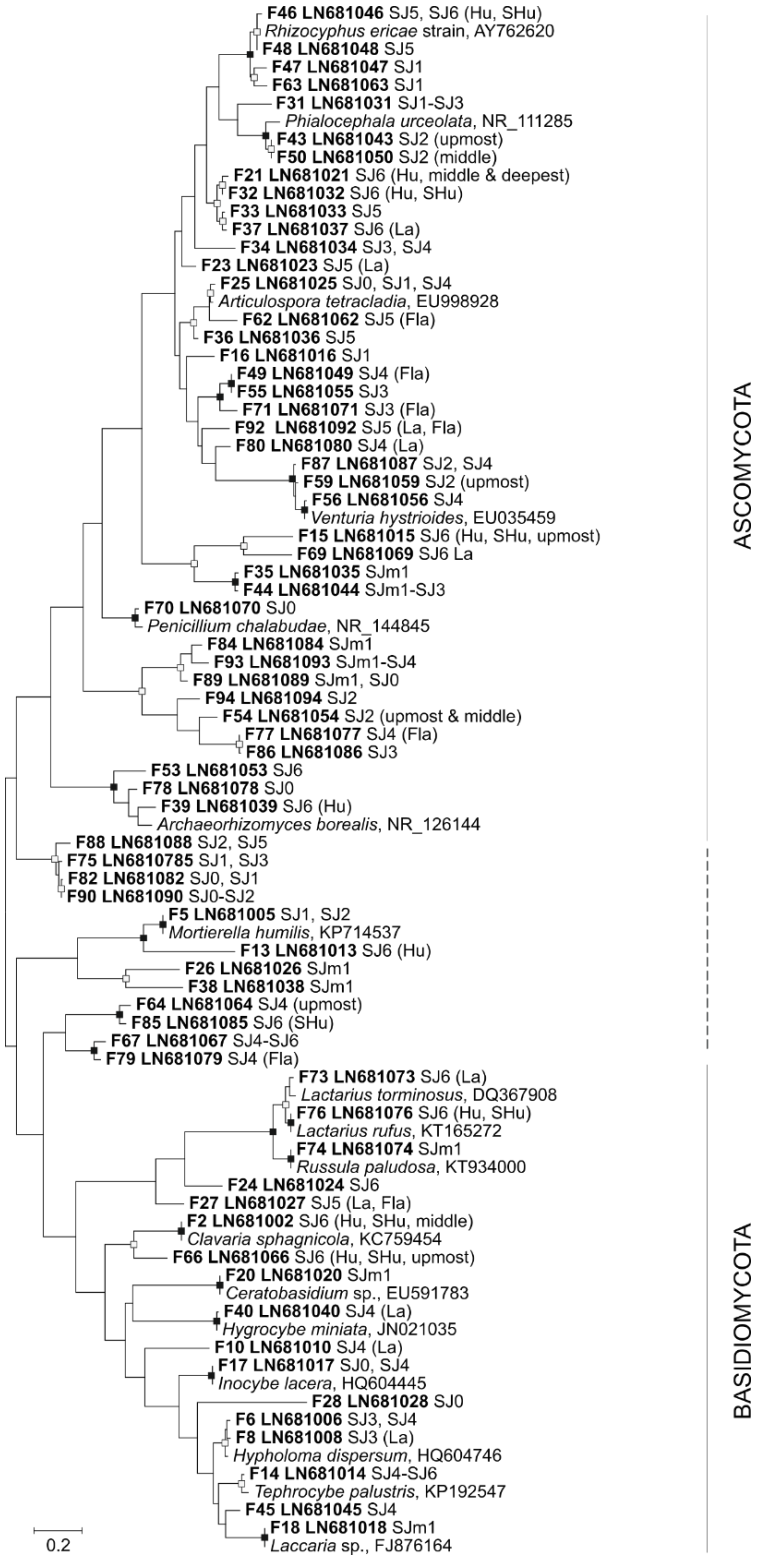

Figure S4. Maximum likelihood tree of the 69 fungal ITS1-2 sequences (**in bold**) found in sites SJm1–SJ6, and reference fungal sequences. Site information of each sequence is defined by microform and/or layer when accurate. Microform abbreviations: Hu = hummock, SHu = shrubby hummock, La = lawn, Fla = flark. Nodes with bootstrap values ≥ 95% are marked with filled squares and ≥ 75% with open squares. Scale bar represents 20 % sequence divergence.

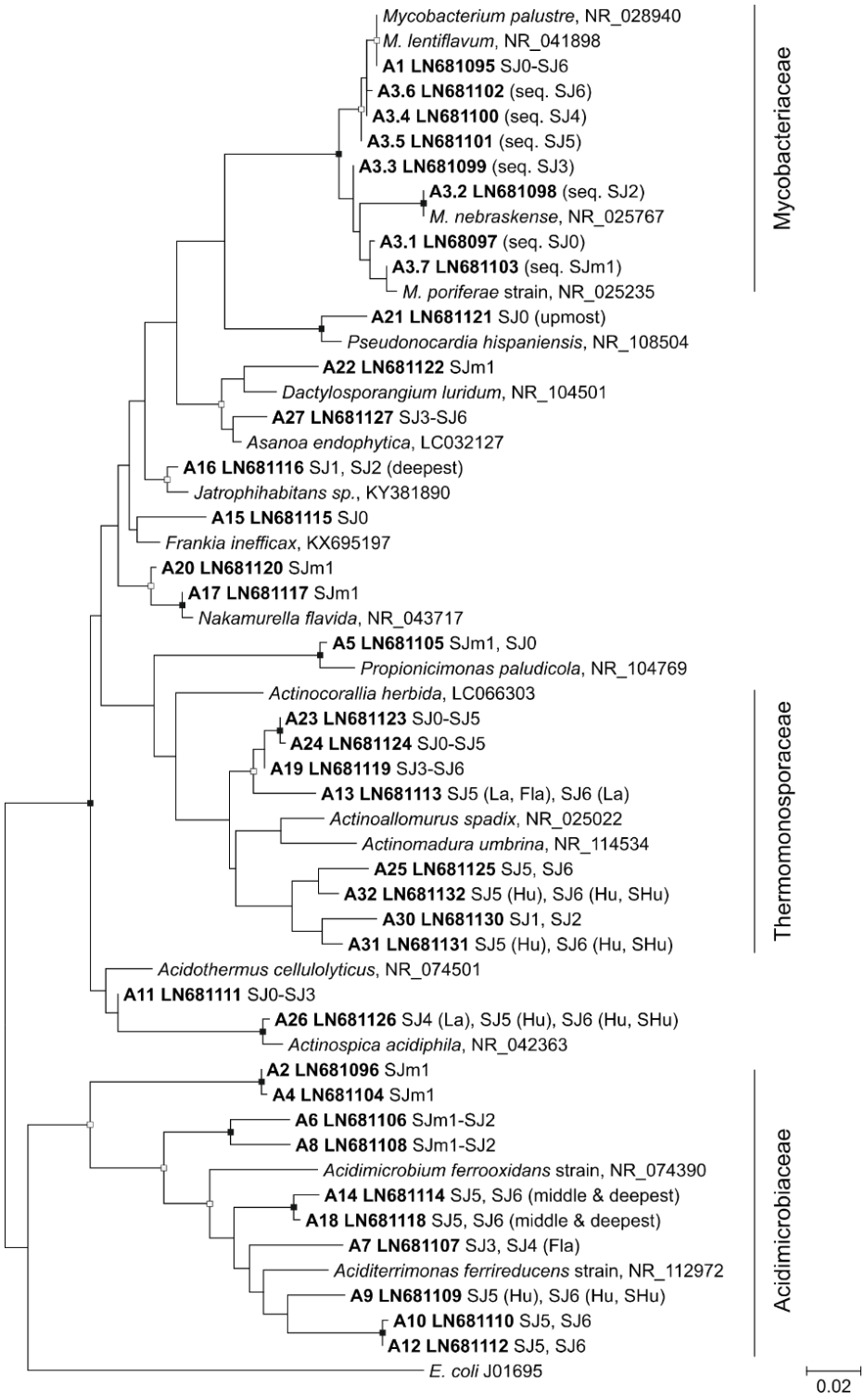

Figure S5. Maximum likelihood tree of 30 actinobacterial partial 16S rDNA sequences (**in bold**) detected in sites SJm1–SJ6, and reference actinobacterial sequences. Site information of each sequence is defined by microform and/or layer when accurate. Microform abbreviations: Hu = hummock, SHu = shrubby hummock, La = lawn, Fla = flark. Nodes with bootstrap values ≥ 95% are marked with filled squares and ≥ 75% with open squares. The tree was rooted with *E. coli* 16S rDNA. Scale bar indicates 2 % sequence divergence.

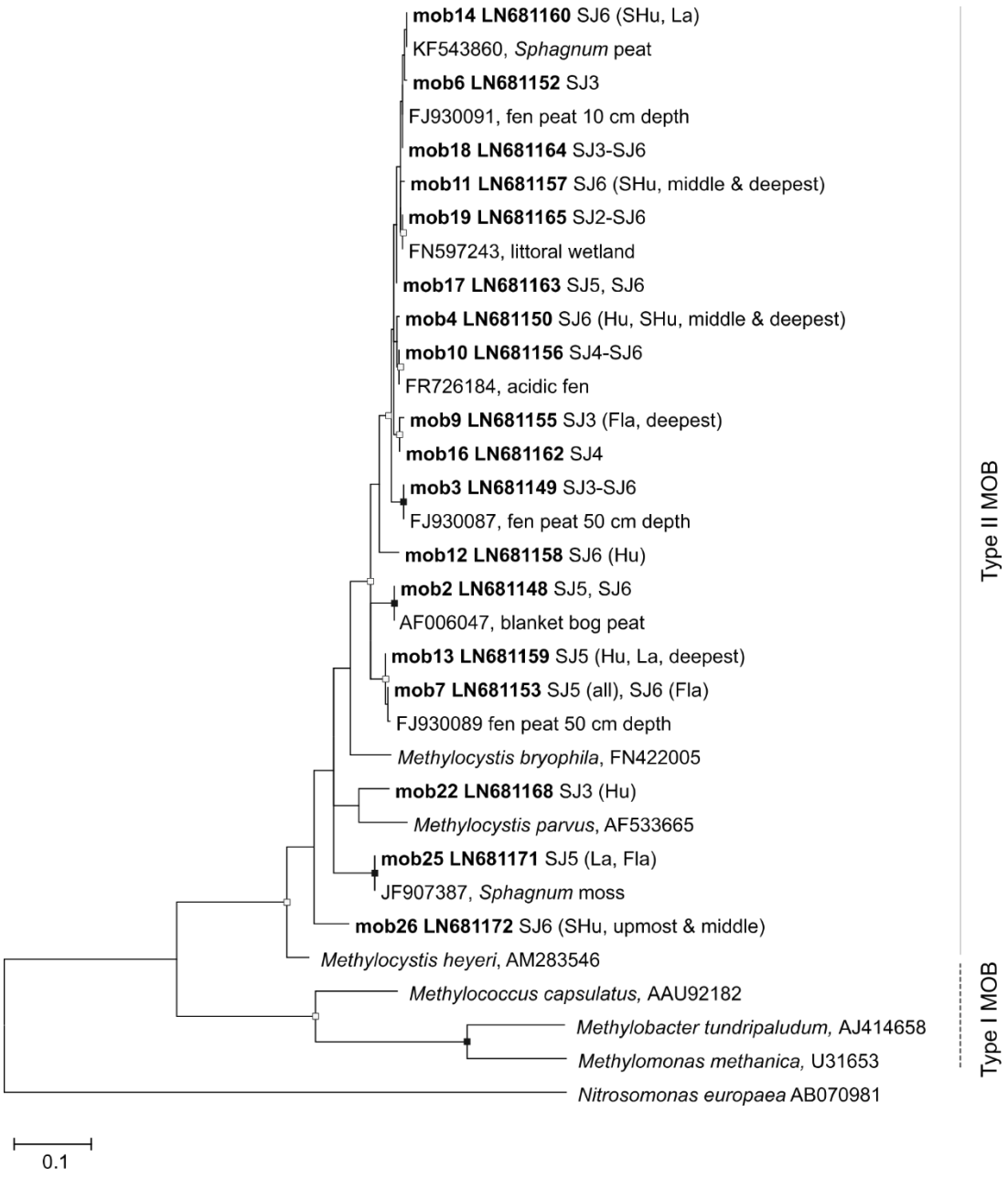

Figure S6. Maximum likelihood tree of 18 tII-MOB partial *pmoA* sequences (**in bold**) found in sites SJm1–SJ6, and reference methanotroph sequences. Nodes with bootstrap values ≥ 95% are marked with filled squares and ≥ 75% with open squares. The tree was rooted with *Nitrosomonas europea amoA*. Scale bar indicates 10% sequence divergence.

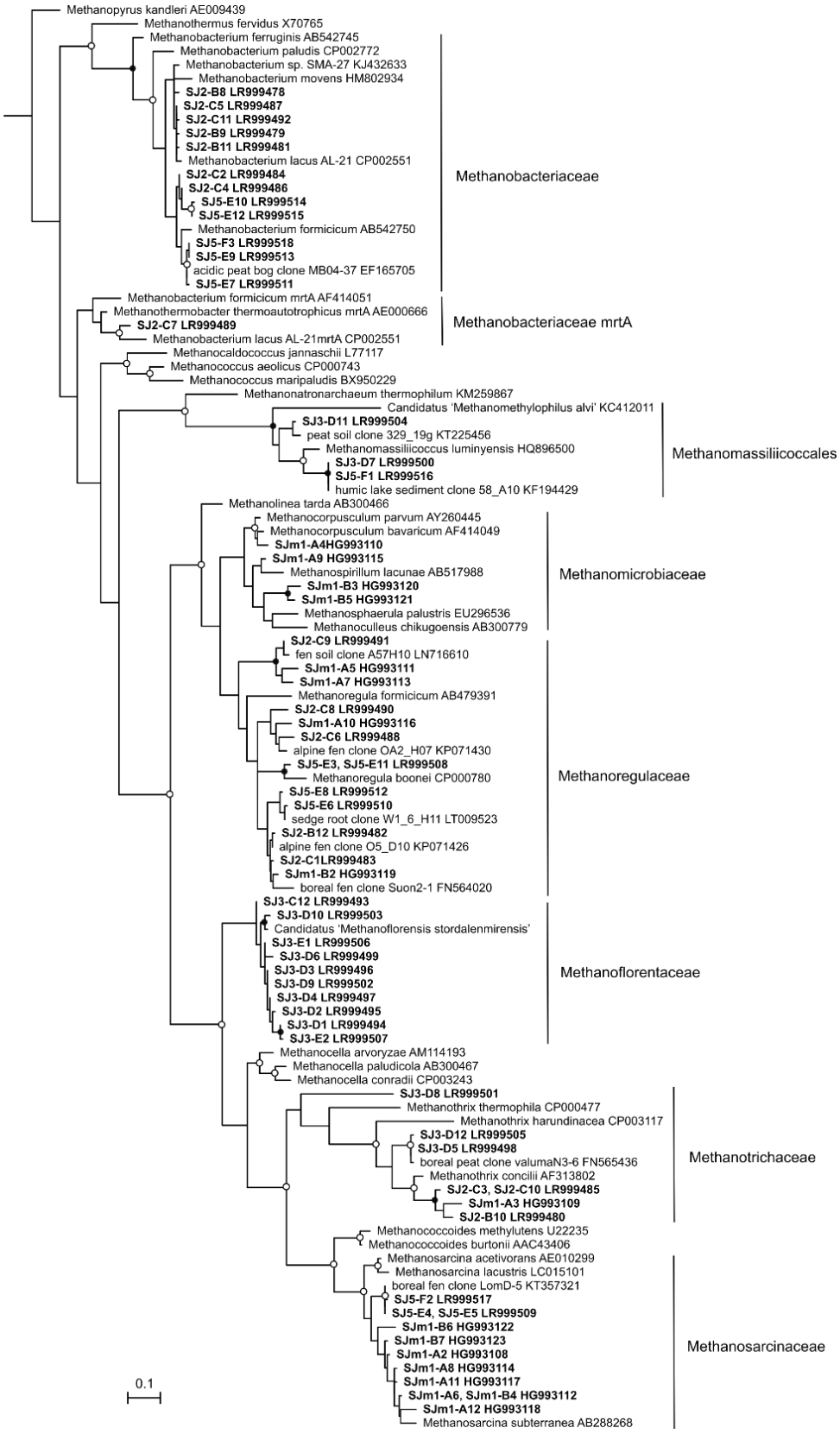

Figure S7. Maximum likelihood tree of 61 methanogen partial *mcrA* sequences (**in bold**; derived amino acid sequences) in sites SJ1, SJ2, SJ3, and SJ5, and reference methanogen sequences. Nodes with bootstrap values ≥ 95% are marked with filled squares and ≥ 75% with open squares. The tree was rooted with *Methanopyrus kandleri mcrA*. Scale bar indicates 10% sequence divergence.

Supplementary tables

Supplementary Table S1. List of plant species observed in the sample plots of the study sites SJ0–SJ6, sorted in functional groups and by the occurrence in the sites. For sites SJ3–SJ6 the microform-specific occurrence is marked in parenthesis, no marking means occurrence in all site-specific microforms. SHu = Shrubby hummock, Hu = Hummock, La = Lawn, Fla = Flark.

Functional group	Plant species	Site[a]
Vascular plants		
Grasses	*Agrostis stolonifera, Festuca rubra*	SJ0
	A. canina, Calamagrostis stricta	SJ1, SJ2
Herbs	*Odontites litoralis, Parnassia palustris, Triglochin maritima*	SJ0
	Galium palustre, Lysimachia thyrsiflora, Peucedanum palustre, Potentilla palustris	SJ1-SJ3
	Equisetum fluviatile	SJ2, SJ3 (Fla), SJ4
	Menyanthes trifoliata	SJ3 (La), SJ4, SJ5 (La)
	Utricularia intermedia	SJ4, SJ5
	Drosera rotundifolia	SJ4 (La), SJ5 (Hu, La), SJ6
	Scheuzeria palustris	SJ5
Sedges	*Carex glareosa, Juncus gerardii*	SJ0
	C. nigra	SJ1, SJ2
	C. canescens	SJ1-SJ3
	Eriophorum angustifolium	SJ1-SJ4, SJ5 (Fla)
	C. chordorrhiza, C. limosa, C. rostrata	SJ3, SJ4, SJ5 (La, Fla)
	E. vaginatum	SJ3 (La), SJ5 (Hu, La), SJ6
	C. dioica, C. lasiocarpa, C. magellanica	SJ4 (*C. d.* & *C. m.* La, *C. l.* Fla)
	C. livida	SJ4, SJ5 (Fla)
	C. pauciflora	SJ5, SJ6
Shrubs	*Alnus incana, Salix myrtilloides*	SJ1
	Pinus sylvestris	SJ1, SJ2, SJ4 (Fla), SJ5 (Hu), SJ6
	Betula pubescens	SJ2, SJ4 (La)
	Andromeda polifolia	SJ3 (La), SJ4, SJ5, SJ6 (SHu)
	Vaccinium oxycoccos	SJ3-SJ6
	S. lapponum	SJ4
	B. nana, Empetrum nigrum, Rubus chamaemorus	SJ5 (Hu, La), SJ6
	Chamaedaphne calyculata	SJ6
	Ledum palustre, V. uliginosum	SJ6 (SHu)
Mosses		
Sphagnum sp.	*Sphagnum subsecundum*	SJ2-SJ4
	S. fimbriatum, S. obtusum, S. squarrosum	SJ3
	S. papillosum	SJ3 (Fla), SJ4, SJ5 (Fla, La), SJ6 (La)
	S. platyphyllum	SJ4 (Fla), SJ5 (La)
	S. angustifolium, S. majus	SJ5 (*S. a.* La, *S. m.* Fla)
	S. balticum	SJ5 (La), SJ6 (La)
	S. fuscum	SJ5 (Hu, La), SJ6
	S. magellanicum	SJ5 (Hu), SJ6 (La)

Brown mosses	*Drephanocladus sp.*	SJ0
	Warnstorfia exannulata	SJ0-SJ2
	Brachythecium sp.	SJ1, SJ3 (Fla)
	Calliergon cordifolia	SJ1, SJ4
	W. fluitans	SJ3, SJ4, SJ5 (La, Fla)
Feather mosses	*Polytrichum strictum*	SJ3 (La), SJ5 (Hu)
	Pleurozium schreberii	SJ6 (SHu)
Hepatics	*Scapania sp.*	SJ2
	Cladopodiella fluitans	SJ5 (La, Fla)
	Mylia anomala	SJ6 (SHu, Hu)

[a] SJ0 = Exposed shore; SJ1 = Epilobium meadow; SJ2 = Equisetum meadow; SJ3 = Mesotrophic fen; SJ4 = Oligotrophic fen; SJ5 = Fen-bog transition; SJ6 = Bog

Table S2. Correlations between plant functional type cover and soil properties (all layers have been included as mean values). Statistically significant correlations ($p < 0.05$) are in bold and indicative ($0.05 \leq p < 0.10$) have been underlined.

Variable	OM	C	N	C:N	pH	Shrubs	Sedges	Grasses	Herbs	*Sphag-num* sp.	Other mosses	Hepatics
Bulk density	**-0.61**	**-0.63**	**-0.31**	**-0.74**	**0.73**	**-0.46**	0.02	**0.64**	-0.09	**-0.77**	**0.41**	0.19
OM		**1.00**	**0.88**	0.20	**-0.29**	0.17	**0.33**	**-0.42**	**0.44**	0.16	**-0.30**	-0.16
C			**0.89**	0.19	**-0.28**	0.16	**0.33**	**-0.42**	**0.46**	0.17	**-0.31**	-0.18
N				-0.26	0.10	-0.20	**0.47**	-0.20	**0.61**	-0.20	-0.16	-0.15
C:N					**-0.80**	**0.76**	**-0.36**	**-0.45**	**-0.32**	**0.86**	**-0.36**	-0.13
pH						**-0.53**	0.02	**0.38**	0.09	**-0.71**	0.12	0.04
Shrubs							**-0.46**	**-0.28**	**-0.28**	**0.57**	**-0.30**	-0.11
Sedges								-0.01	**0.28**	**-0.39**	0.12	-0.05
Grasses									-0.11	**-0.48**	0.13	0.03
Herbs										-0.25	0.16	-0.11
Sphagnum sp.											**-0.50**	-0.12
Other mosses												0.19

Supplementary Table S3. Differences in plant functional type cover and field measurements (ecosystem respiration (RE), CH_4 emissions and water level (WL)) between the first successional stage (SJ0) and the other successional stages (SJ1–SJ6), and differences in soil properties and microbial variables between the first successional stage (SJ0), and the other stages (SJ1–SJ6) and the unexposed sea bottom (SJm1) in a peatland successional gradient. Generalized linear models were used for plant cover, linear models were used for other variables. Mean values ± SE for each site are presented, and the highest value in the gradient is underlined. Statistically significant *p* values after multiple comparisons are **in bold**. Different sample numbers (*n*) comprise the stable sample plots (plant functional type cover and field measurements, the former *n*) and the three layers of the soil sample points (soil properties, microbial activity potential and microbial PLFAs, the latter *n*). na = not applicable.

Variable	$R^2_{adj.}$	SJm1[a] (*n* = 0 or 12)	SJ0[a] (*n* = 6 or 18)	SJ1[a] (*n* = 6 or 18)	SJ2[a] (*n* = 6 or 18)	SJ3[a] (*n* = 10 or 30)	SJ4[a] (*n* = 9 or 27)	SJ5[a] (*n* = 8 or 24)	SJ6[a] (*n* = 9 or 27)
Vegetation cover[b]									
Grasses	-	na	5.37± 1.28	8.33 ± 4.38	5.25 ± 1.28	**0.00 ± 0.00**	**0.00 ± 0.00**	**0.00 ± 0.00**	**0.00 ± 0.00**
Herbs	-	na	1.17 ± 0.78	3.85 ± 1.55	6.10 ± 1.53	7.13 ± 1.63	9.24 ± 2.74	2.75 ± 0.94	0.00 ± 0.00
Sedges	-	na	7.95 ± 1.08	**26.42 ± 4.97**	21.93 ± 2.22	**36.48 ± 5.16**	18.98 ± 3.62	12.00 ± 2.67	6.56 ± 3.00
Shrubs	-	na	0.00 ± 0.00	0.60 ± 0.41	0.15 ± 0.06	6.41 ± 3.94	**14.08 ± 2.25**	**12.36± 5.10**	**45.38 ± 9.66**
Sphagnum sp.	-	na	0.00 ± 0.00	0.00 ± 0.00	7.33 ± 3.38	**48.90 ± 10.97**	**52.47 ± 12.99**	**75.56 ± 10.25**	**92.94 ± 2.40**
Other mosses[c]	-	na	2.20 ± 1.10	32.35 ± 8.62	**37.50 ± 6.02**	2.26 ± 0.70	5.59 ± 3.75	18.39 ± 9.06	0.22 ± 0.22
Hepatics	-	na	0.00 ± 0.00	0.00 ± 0.00	6.50 ± 4.73	0.00 ± 0.00	0.00 ± 0.00	1.01 ± 0.68	0.29 ± 0.14
Total cover	-	na	16.68± 1.86	**71.55± 6.09**	**84.77 ± 4.87**	**101.18 ± 10.58**	**100.36± 8.51**	**122.08 ± 4.01**	**145.39± 6.10**
Vascular plants	-	na	14.48 ± 0.86	**39.20 ± 5.47**	33.43 ± 3.35	**50.02 ± 5.79**	**42.30 ± 4.12**	27.11 ± 3.76	**51.93 ± 7.29**
Mosses & Hepatics	-	na	2.20 ± 1.10	**32.35 ± 8.62**	**51.33 ± 5.89**	**51.16 ± 10.61**	**58.06 ± 11.39**	**94.96 ± 1.76**	**93.46 ± 2.26**
Field measurements[d]									
RE	0.55	na	0.29 ± 0.01	**0.46 ± 0.03**	0.42 ± 0.02	**0.61 ± 0.04**	0.40 ± 0.02	0.32 ± 0.04	0.39 ± 0.03
CH_4 emission	0.63	na	0.08 ± 0.05	**2.55 ± 0.38**	**2.82 ± 0.28**	**2.95 ± 0.44**	**3.18 ± 0.33**	**3.03 ± 0.53**	**1.69 ± 0.63**
WL	0.39	na	-8.43 ± 0.72	-0.65 ± 1.09	-1.90 ± 0.56	-6.66 ± 5.18	-2.89 ± 3.67	-12.60 ± 3.47	**-31.40 ± 6.02**
Soil properties[e]									
pH	0.93	**6.51 ± 0.11**	6.10 ± 0.18	**5.23 ± 0.02**	**5.14 ± 0.02**	**4.71 ± 0.06**	**5.16 ± 0.03**	**4.43 ± 0.05**	**4.24 ± 0.03**
Bulk density	0.98	1529.07 ± 55.93	1525.51 ± 72.00	1457.87 ± 21.92	**1373.58 ± 57.39**	**131.08 ± 31.54**	**79.89 ± 8.58**	**35.90 ± 5.52**	**42.49 ± 4.04**
OM	0.80	6.89 ± 1.69	7.97 ± 0.30	**21.00 ± 1.70**	**20.75 ± 1.50**	**59.23 ± 7.69**	**69.03 ± 7.30**	**33.41 ± 5.44**	**41.45 ± 4.04**
C	0.83	2.22 ± 0.61	3.22 ± 0.20	**9.79 ± 0.81**	**9.80 ± 1.13**	**32.06 ± 3.97**	**38.41 ± 4.14**	**17.47 ± 2.93**	**21.47 ± 2.08**
N	0.57	0.62 ± 0.04	0.58 ± 0.03	0.95 ± 0.03	0.64 ± 0.04	**1.82 ± 0.30**	**2.45 ± 0.30**	0.81 ± 0.16	0.47 ± 0.05
C:N	0.89	3.48 ± 0.85	4.58 ± 0.20	7.22 ± 0.48	**10.63 ± 1.03**	**23.95 ± 2.77**	**22.10 ± 2.33**	**30.66 ± 3.59**	**49.75 ± 2.63**
Microbial activity potential[e]									
CO_2 production	0.39	0.35 ± 0.15	0.49 ± 0.16	3.21 ± 1.71	**5.61 ± 1.93**	1.74 ± 0.24	1.08 ± 0.10	0.87± 0.08	1.16 ± 0.13
CH_4 production	0.56	3.19 ± 1.29	8.03 ± 3.45	**128.54 ± 48.40**	**195.88 ± 75.41**	30.38 ± 8.21	22.33 ± 5.97	9.76 ± 1.88	1.95 ± 0.78
CH_4 oxidation	0.72	7.64 ± 2.31	5.78 ± 1.19	**58.75 ± 29.44**	**164.24 ± 61.52**	**141.87 ± 24.42**	**88.60 ± 12.05**	**111.04 ± 27.22**	**130.37 ± 20.94**
Microbial PLFAs[e]									
F-PLFA	0.54	1.22 ± 0.33	1.58 ± 0.25	**24.96 ± 14.04**	**33.49 ± 11.24**	2.98 ± 0.48	2.01 ± 0.41	2.24 ± 0.27	3.09 ± 0.75
B-PLFA	0.54	8.07 ± 2.20	10.32 ± 1.41	**54.93 ± 10.14**	**117.43 ± 36.76**	**36.75 ± 8.38**	20.00 ± 3.87	13.78 ± 1.59	12.96 ± 2.04
Act-PLFA	0.68	0.30 ± 0.18	0.59 ± 0.52	**6.08 ± 5.19**	**8.19 ± 7.49**	1.83 ± 0.64	0.93 ± 0.27	0.32 ± 0.11	0.34 ± 0.03
F:B	0.16	0.15 ± 0.02	0.16 ± 0.03	0.19 ± 0.05	0.19 ± 0.02	0.14 ± 0.04	0.12 ± 0.03	0.24 ± 0.03	0.29 ± 0.06

[a] SJm1= Under the sea level; SJ0 = Exposed shore; SJ1 = Epilobium meadow; SJ2 = Equisetum meadow; SJ3 = Mesotrophic fen; SJ4 = Oligotrophic fen; SJ5 = Fen-bog transition; SJ6 = Bog

[b] Mean values of cover percentage determined from the stable sample plots in July 2007. Quasi binomial distribution with logit link was used to estimate generalized linear models. Note: For total cover no model was estimated due to values >100. For total cover and other vegetation variables differences from SJ0 were estimated using SE-values (2 × SE = 95%'s confidence interval) in case cover was zero for SJ0.

[c] Other mosses include brown and feather mosses.

[d] Mean values measured from the stable sample plots during the growing season June-September 2007. Standard error was calculated from sample plot specific means, and thus it represents the spatial variation within a site. WL is the distance of the mean water level from the mire surface in centimeters, negative values indicate below the surface. Units of the variables: RE (g CO_2 m^{-2} h^{-1}); CH_4 emission (mg CH_4 m^{-2} h^{-1}). Log transformation was performed for CH_4 emission before the linear model was estimated.

[e] Mean values determined from the soil profiles cored from the sample points in August 2007. The mean values were first calculated for each of the three layers (uppermost, middle and deepest), and then the site mean and SE were calculated from the layer means. Log transformation was performed before the linear model was estimated except for bulk density and pH. Units of the variables: Bulk density, organic matter (OM), carbon (C) and nitrogen (N) (g dm^{-3}); CO_2 production (mg CO_2 dm^{-3} h^{-1}); CH_4 production and CH_4 oxidation (µg CH_4 dm^{-3} h^{-1}); PLFAs (µmol PLFA dm^{-3}): F = fungal, B = bacterial, Act = actinobacterial. F:B = the ratio of F-PLFA to B-PLFA.

Supplementary Table S4. Differences in soil properties, microbial activity potentials and abundance of microbial PLFAs between the uppermost and the two lower layers (middle and deepest) in sites SJm1–SJ6, in respective vertical order. Mean values ± SE, are presented for each layer. Linear models were used to analyse differences between the layers. Statistically significant differences ($p < 0.05$) are in **bold** (p values were corrected due to multiple comparisons between the uppermost and lower layers). Prefixes in PLFAs: F = fungal, B = bacterial, Act = actinobacterial. F:B = the ratio of F-PLFA to B-PLFA.

Variable (sample plots)	SJm1[a] (n = 4)	SJ0[a] (n = 6)	SJ1[a] (n = 6)	SJ2[a] (n = 6)	SJ3[a] (n = 10)	SJ4[a] (n = 9)	SJ5[a] (n = 8)	SJ6[a] (n = 9)
Soil properties								
Bulk density	1431.9 ± 176.0[b]	1288.2 ± 110.6	824.7 ± 80.1	649.8 ± 122.6	30.9 ± 9.8[b]	31.0 ± 7.9	13.7 ± 2.6[b]	25.1 ± 5.2
($g\ dm^{-3}$)	1711.0 ± 28.8	**1667.9 ± 75.8**	**1785.8 ± 13.6**	**1701.7 ± 44.9**	**121.6 ± 32.9**	**76.9 ± 17.7**	**32.2 ± 7.0**	41.3 ± 5.0
	1444.2 ± 245.1	**1620.4 ± 60.8**	**1763.1 ± 14.0**	**1769.2 ± 10.7**	**240.8 ± 57.0**	**131.8 ± 2.0**	**61.8 ± 8.4**	**61.1 ± 5.9**
OM	13.1 ± 4.1[b]	17.9 ± 0.9[b]	53.4 ± 4.9[b]	50.7 ± 3.7[b]	23.9 ± 6.2	26.8 ± 6.5	13.2 ± 2.5[b]	24.6 ± 5.2
($g\ dm^{-3}$)	4.7 ± 0.8	**3.6 ± 0.2**	**5.7 ± 0.3**	**7.5 ± 1.3**	**62.0 ± 10.3**	**65.1 ± 14.5**	**30.8 ± 6.8**	40.5 ± 5.0
	2.8 ± 0.7	**2.5 ± 0.1**	**3.8 ± 0.2**	**4.0 ± 0.4**	**91.7 ± 9.0**	**115.2 ± 2.0**	**56.2 ± 8.1**	**59.3 ± 5.7**
C	3.6 ± 1.4[b]	8.5 ± 0.6[b]	26.3 ± 2.3[b]	25.3 ± 2.7[b]	12.3 ± 3.1[b]	14.3 ± 3.5	6.7 ± 1.3[b]	12.7 ± 2.7
($g\ dm^{-3}$)	2.3 ± 1.2	**0.7 ± 0.1**	**1.9 ± 0.2**	**3.0 ± 1.4**	**31.9 ± 5.0**	**36.1 ± 8.3**	**15.7 ± 3.6**	20.4 ± 2.5
	0.7 ± 0.1	**0.5 ± 0.1**	**1.1 ± 0.2**	**1.1 ± 0.2**	**51.9 ± 5.5**	**64.9 ± 1.3**	**30.0 ± 4.6**	**31.4 ± 3.3**
N	0.7 ± <0.1	0.8 ± 0.1[b]	1.6 ± 0.1	1.3 ± 0.1	0.5 ± 0.2[b]	0.7 ± 0.2[b]	0.2 ± 0.0[b]	0.2 ± <0.1[b]
($g\ dm^{-3}$)	0.7 ± 0.1	**0.4 ± <0.1**	**0.6 ± <0.1**	**0.4 ± 0.1**	**1.8 ± 0.4**	**2.3 ± 0.6**	**0.5 ± 0.1**	**0.4 ± <0.1**
	0.4 ± 0.1	**0.5 ± <0.1**	**0.6 ± 0.1**	**0.2 ± <0.1**	**3.2 ± 0.5**	**4.3 ± 0.1**	**1.8 ± 0.4**	**0.8 ± 0.1**
C:N	5.2 ± 2.2[b]	11.3 ± 0.6[b]	16.4 ± 1.1	19.3 ± 1.5	27.7 ± 2.2	29.1 ± 4.0[b]	36.6 ± 3.1[b]	55.4 ± 3.0
	2.9 ± 1.3	**1.6 ± 0.0**	**3.1 ± 0.4**	**7.5 ± 2.2**	25.0 ± 4.1	22.1 ± 3.2	34.9 ± 4.2	52.0 ± 2.3
	2.4 ± 0.9	**0.9 ± 0.1**	**2.1 ± 0.8**	**5.2 ± 0.7**	19.2 ± 2.3	**15.1 ± 0.2**	**20.5 ± 3.9**	**41.9 ± 3.8**
pH	6.4 ± 0.2	6.3 ± 0.1	5.3 ± <0.1	5.1 ± <0.1	4.7 ± 0.1	5.1 ± <0.1	4.5 ± <0.1	4.3 ± 0.1
	6.5 ± 0.2	6.1 ± 0.3	5.1 ± <0.1	5.2 ± <0.1	4.7 ± 0.1	5.2 ± <0.1	4.4 ± 0.1	4.2 ± <0.1
	6.7 ± 0.1	5.9 ± 0.2	5.3 ± <0.1	5.1 ± 0.1	4.8 ± 0.1	5.2 ± <0.1	4.4 ± 0.1	4.3 ± 0.1
CO_2 production	1.0 ± 0.4[b]	1.4 ± 0.5[b]	9.2 ± 4.9[b]	15.9 ± 5.5[b]	1.7 ± 0.3[b]	1.1 ± 0.2	0.7 ± 0.1[b]	0.9 ± 0.1[b]
($mg\ dm^{-3}\ h^{-1}$)	0.1 ± 0.1	**<0.1 ± <0.1**	**0.4 ± 0.2**	**0.9 ± 0.3**	1.8 ± 0.5	0.9 ± 0.1	1.0 ± 0.1	0.9 ± 0.1
	<0.1 ± <0.1	**<0.1 ± <0.1**	**<0.1 ± <0.1**	**<0.1 ± <0.1**	1.7 ± 0.2	1.3 ± 0.1	0.8 ± 0.1	1.6 ± 0.3
CH_4 production	6.5 ± 2.0[b]	23.7 ± 10.4[b]	360.3 ± 128.5[b]	572.8 ± 225.2[b]	26.5 ± 11.2[b]	33.9 ± 14.7[b]	4.2 ± 1.7[b]	1.1 ± 0.7[b]
($\mu g\ dm^{-3}\ h^{-1}$)	2.8 ± 2.1	**0.4 ± 0.4**	**25.2 ± 21.3**	**14.7 ± 4.8**	45.4 ± 26.4	6.0 ± 1.1	12.2 ± 4.7	0.9 ± 0.5
	0.3 ± 0.2	**<0.1 ± <0.1**	**0.1 ± <0.1**	**0.1 ± 0.1**	19.2 ± 12.1	27.1 ± 10.1	12.9 ± 3.4	3.8 ± 2.1
CH_4 oxidation	19.9 ± 8.8[b]	9.4 ± 2.7	154.3 ± 88.7[b]	444.0 ± 178.0[b]	63.4 ± 31.2	54.1 ± 11.1	41.7 ± 17.9[b]	28.2 ± 17.0[b]
($\mu g\ dm^{-3}\ h^{-1}$)	2.9 ± 2.4	5.3 ± 1.0	**15.3 ± 2.9**	**23.5 ± 3.5**	189.4 ± 55.9	119.5 ± 18.3	**213.6 ± 57.5**	**185.5 ± 33.2**
	0.2 ± 0.2	**2.6 ± 0.9**	**6.7 ± 0.3**	**34.3 ± 21.5**	172.8 ± 39.4	92.2 ± 40.6	77.8 ± 23.1	**177.4 ± 59.2**

F-PLFA	2.7 ± 0.7[b]	4.0 ± 0.6[b]	73.5 ± 42.0[b]	98.6 ± 33.6[b]	4.2 ± 0.8[b]	3.5 ± 0.9[b]	4.1 ± 0.8[b]	5.9 ± 1.7[b]
(µmol dm^{-3})	0.8 ± 0.4	**0.4 ± 0.1**	**1.2 ± 0.3**	**1.4 ± 0.3**	4.1 ± 1.1	2.0 ± 0.8	**2.0 ± 0.3**	2.7 ± 0.8
	0.3 ± 0.1	**0.3 ± 0.1**	**0.2 ± <0.1**	**0.5 ± 0.1**	**0.7 ± 0.1**	**0.5 ± 0.1**	**0.7 ± 0.1**	**0.6 ± 0.2**
B-PLFA	16.6 ± 3.7[b]	25.2 ± 4.0[b]	149.8 ± 29.5[b]	338.1 ± 109.6[b]	32.7 ± 13.2[b]	22.0 ± 6.9	8.6 ± 2.3	9.5 ± 1.5
(µmol dm^{-3})	6.2 ± 3.9	**3.5 ± 0.5**	**12.2 ± 2.3**	**11.3 ± 1.6**	55.9 ± 12.5	25.2 ± 3.2	**21.3 ± 3.1**	12.4 ± 2.1
	1.4 ± 0.7	**2.2 ± 0.3**	**2.7 ± 0.3**	**2.9 ± 0.4**	21.6 ± 4.1	12.8 ± 3.2	11.4 ± 1.3	17.0 ± 7.1
Act-PLFA	0.7 ± 0.2[b]	1.6 ± 0.2[b]	16.4 ± 2.1[b]	23.2 ± 7.3[b]	1.7 ± 0.9[b]	1.0 ± 0.4[b]	0.1 ± <0.1[b]	0.3 ± 0.1[b]
(µmol dm^{-3})	0.22 ± 0.18	**0.1 ± <0.1**	**1.7 ± 0.1**	**1.3 ± 0.2**	3.0 ± 1.0	1.3 ± 0.3	**0.4 ± 0.1**	0.4 ± 0.1
	<0.1 ± <0.1	**<0.1 ± <0.1**	**0.2 ± <0.1**	**0.1 ± <0.1**	0.8 ± 0.2	0.4 ± 0.1	**0.5 ± 0.1**	0.4 ± 0.2
F:B	0.2 ± <0.1	0.2 ± <0.1[b]	0.4 ± 0.1[b]	0.3 ± <0.1	0.3 ± 0.1[b]	0.2 ± <0.1[b]	0.6 ± 0.1[b]	0.6 ± 0.1[b]
	0.1 ± <0.1	0.1 ± <0.1	**0.1 ± <0.1**	**0.1 ± <0.1**	**0.1 ± <0.1**	**0.1 ± <0.1**	**0.1 ± <0.1**	**0.3 ± 0.1**
	0.2 ± <0.1	0.2 ± <0.1	**0.1 ± <0.1**	0.2 ± 0.1	**<0.1± <0.1**	**0.0 ± <0.1**	**0.1 ± <0.1**	**<0.1 ± <0.1**

[a] SJm1= Under the sea level; SJ0 = Exposed shore; SJ1 = Epilobium meadow; SJ2 = Equisetum meadow; SJ3; Mesotrophic fen; SJ4 = Oligotrophic fen; SJ5 = Fen-bog transition; SJ6 = Bog

[b] Log transformation was performed before the models were estimated to achieve normality (applies for all layers although marked only for the uppermost layer)

Supplementary Table S5. Mean values ± SE for microform specific cover of functional plant types, ecosystem respiration (RE), CH_4 emission, water level (WL), soil properties, microbial activity potentials and abundance of microbial PLFAs in sites SJ3-SJ6. Different sample numbers (*n*) comprise the stable sample plots (plant cover and field measurements, the former *n*) and the three layers of the soil sample points (soil properties, microbial activity potential and microbial PLFAs, the latter *n*).

Variable	SJ3[a]		SJ4[a]		SJ5[a]			SJ6[a]		
	Lawn	Flark	Lawn	Flark	Hummock	Lawn	Flark	Shrubby Hummock	Hummock	Lawn
	(*n* = 5 or 15)	(*n* = 5 or 15)	(*n* = 4 or 12)	(*n* = 5 or 15)	(*n* = 2 or 6)	(*n* = 3 or 9)	(*n* = 3 or 9)	(*n* = 3 or 9)	(*n* = 3 or 9)	(*n* = 3 or 9)
Vegetation cover[b]										
Total cover	127.9 ± 10.6	74.5 ± 6.2	123.1 ± 5.1	82.2 ± 7.7	135.6 ± 4.5	122.1 ± 5.5	113.1 ± 3.3	162.1 ± 10.6	147.6 ± 3.3	126.5 ± 1.8
Vascular plants	51.9 ± 11.4	48.1 ± 5.0	31.7 ± 3.5	50.8 ± 3.6	40.1 ± 1.0	26.0 ± 6.4	19.6 ± 2.2	76.9 ± 7.9	49.1 ± 3.6	29.8 ± 1.4
Mosses & Hepatics	76.0 ± 9.3	26.3 ± 10.6	91.4 ± 7.6	31.4 ± 5.6	95.5 ± 3.5	96.1 ± 1.6	93.5 ± 4.5	85.2 ± 2.9	98.5 ± 0.5	96.7 ± 0.7
Grasses	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0
Herbs	8.2 ± 3.1	6.1 ± 1.3	4.5 ± 2.1	13.0 ± 4.1	0.0 ± 0.0	2.5 ± 0.9	4.8 ± 1.6	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0
Sedges	31.1 ± 8.8	41.8 ± 5.3	10.7 ± 2.7	25.6 ± 4.3	6.0 ± 4.0	14.0 ± 5.6	14.0 ± 3.8	1.2 ± 0.9	0.2 ± 0.2	18.3 ± 1.7
Shrubs	12.6 ± 7.1	0.2 ± 0.2	16.5 ± 2.9	12.1 ± 3.3	34.1 ± 5.0	9.5 ± 2.3	0.7 ± 0.6	75.7 ± 8.2	48.9 ± 3.5	11.5 ± 0.3
Sphagnum mosses	74.6 ± 9.1	23.2 ± 11.3	90.3 ± 8.4	22.2 ± 7.2	80.5 ± 3.5	96.0 ± 1.5	51.8 ± 21.8	84.2 ± 3.2	98.0 ± 0.6	96.7 ± 0.7
Other mosses[c]	1.4 ± 0.9	3.1 ± 1.0	1.2 ± 0.8	9.1 ± 6.6	15.0 ± <0.1	<0.1 ± <0.1	39.0 ± 19.5	0.7 ± 0.7	0.0 ± 0.0	0.0 ± 0.0
Hepatics	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	<0.1 ± <0.1	2.7 ± 1.5	0.3 ± 0.3	0.5 ± 0.3	0.0 ± 0.0
Field measurements[d]										
RE	0.6 ± <0.1	0.6 ± <0.1	0.4 ± <0.1	0.5 ± <0.1	0.5 ± <0.1	0.3 ± <0.1	0.2 ± <0.1	0.5 ± <0.1	0.4 ± 0.1	0.4 ± <0.1
CH_4 emission	2.1 ± 0.6	3.8 ± 0.4	2.3 ± 0.3	3.9 ± 0.2	1.5 ± 0.3	2.6 ± 0.3	4.5 ± 0.7	0.7 ± 0.2	0.3 ± <0.1	4.1 ± 0.5
WL	-20.3 ± 5.2	6.9 ± 1.0	-13.5 ± 5.9	5.6 ± 2.3	-24.4 ± 2.0	-15.5 ± 1.7	-1.9 ± 1.3	-47.9 ± 3.0	-38.0 ± 1.1	-8.3 ± 0.5
Soil Properties[e]										
Bulk density	60.0 ± 31.4	202.2 ± 90.5	54.4 ± 37.1	100.3 ± 26.8	42.9 ± 12.4	39.1 ± 15.3	28.0 ± 14.3	45.4 ± 14.0	51.9 ± 4.8	30.2 ± 12.7
OM	40.6 ± 17.9	77.9 ± 21.8	47.6 ± 31.5	86.2 ± 23.7	41.4 ± 11.8	36.5 ± 13.6	25.0 ± 12.1	44.2 ± 13.5	50.9 ± 4.7	29.2 ± 12.2
C	22.5 ± 10.4	41.6 ± 12.6	26.2 ± 17.8	48.2 ± 13.8	21.6 ± 6.4	19.2 ± 7.5	13.0 ± 6.6	23.6 ± 7.6	25.8 ± 2.3	15.0 ± 6.5
N	1.1 ± 0.6	2.5 ± 0.9	1.5 ± 1.3	3.2 ± 1.0	0.9 ± 0.4	0.9 ± 0.6	0.7 ± 0.5	0.6 ± 0.3	0.4 ± 0.1	0.4 ± 0.2
C:N	29.4 ± 3.4	18.5 ± 2.0	29.3 ± 7.7	16.3 ± 1.6	40.6 ± 4.6	30.2 ± 6.3	24.5 ± 4.3	46.5 ± 6.9	59.3 ± 2.6	43.4 ± 2.8
pH	4.6 ± 0.1	4.8 ± <0.1	5.2 ± 0.02	5.1 ± <0.1	4.3 ± 0.1	4.4 ± <0.1	4.5 ± <0.1	4.3 ± <0.1	4.2 ± <0.1	4.3 ± 0.1
Microbial activity potential[e]										
CO_2 production	1.9 ± 0.2	1.6 ± 0.1	0.9 ± 0.2	1.2 ± 0.1	0.8 ± 0.1	1.0 ± <0.1	0.8 ± 0.1	1.6 ± 0.4	0.8 ± 0.1	1.1 ± 0.3
CH_4 production	40.3 ± 23.6	20.4 ± 15.9	9.2 ± 6.0	32.8 ± 15.9	7.7 ± 5.2	8.3 ± 3.2	12.7 ± 5.0	3.4 ± 3.2	0.1 ± <0.1	2.4 ± 0.5
CH_4 oxidation	147.1 ± 73.9	136.7 ± 32.7	112.1 ± 43.3	69.8 ± 22.1	130.1 ± 65.7	179.7 ± 88.6	29.7 ± 14.2	212.8 ± 108.5	84.6 ± 55.4	93.7 ± 9.1
Microbial PLFAs[e]										
F-PLFA	3.7 ± 1.6	2.3 ± 1.1	1.7 ± 0.7	2.3 ± 1.3	1.9 ± 0.8	2.4 ± 1.0	2.3 ± 1.1	5.7 ± 3.0	2.7 ± 1.6	0.9 ± 0.1
B-PLFA	28.1 ± 10.5	45.4 ± 13.8	10.5 ± 2.9	27.6 ± 6.4	13.1 ± 5.0	13.6 ± 3.4	14.4 ± 4.4	10.6 ± 1.0	9.9 ± 1.4	18.4 ± 8.1
Act-PLFA	2.4 ± 0.9	6.9 ± 2.6	1.0 ± 0.4	3.5 ± 1.0	1.4 ± 0.5	1.2 ± 0.3	0.6 ± 0.1	1.2 ± 0.3	1.3 ± 0.5	1.7 ± 0.6
F:B	0.2 ± 0.1	0.1 ± <0.1	0.2 ± 0.1	0.1 ± <0.1	0.3 ± 0.2	0.3 ± 0.2	0.2 ± 0.1	0.5 ± 0.2	0.3 ± 0.2	0.1 ± 0.1

[a]SJ3 = Mesotrophic fen; SJ4 = Oligotrophic fen; SJ5 = Fen-bog transition; SJ6 = Bog

[b] Vegetation cover as percentage of area estimated from the sample plots in July 2007.

[c] Other mosses include brown and feather mosses.

[d] Mean values of the measurements from stable sample plots during the growing season June-September 2007. Water level is the distance of the mean water table from the mire surface in centimeters, and negative values indicate distance below the surface. Units of the variables: RE (g CO_2 m^{-2} h^{-1}); CH_4 emission (mg CH_4 m^{-2} h^{-1}).

[e] Mean values determined from the soil profiles cored from the sample points in August 2007. The mean values were first calculated for each of the three layers (uppermost, middle and deepest), and then the microform mean and SE were calculated from the layer means, and thus SE represents vertical variation within a microform. Units of the variables: Bulk density, organic matter (OM), carbon (C) and nitrogen N (g dm^{-3}); *in vitro* CO_2 production (mg CO_2 dm^{-3} h^{-1}); *in vitro* CH_4 production and CH_4 oxidation (µg CH_4 dm^{-3} h^{-1}); PLFAs (µmol PLFA dm^{-3}): F = fungal, B = bacterial, Act = actinobacterial. F/B = the ratio of F-PLFA to B-PLFA.

Supplementary Table S6. Mean values ± SE for layer specific (uppermost, middle and deepest layer) soil properties, microbial activity potentials and microbial biomasses in the different microforms in sites SJ3-SJ6 presented in respective vertical order.

Variable	SJ3[a]		SJ4[a]		SJ5[a]			SJ6[a]		
	Lawn	Flark	Lawn	Flark	Hummock	Lawn	Flark	Shrubby hummock	Hummock	Lawn
	(*n* = 5)	(*n*= 5)	(*n*= 4)	(*n*= 5)	(*n*= 2)	(*n*= 3)	(*n*= 3)	(*n*= 3)	(*n*= 3)	(*n*= 3)
Soil Properties										
Bulk density	13.4 ± 0.5	48.4 ± 16.7	10.5 ± 1.6	47.4 ± 8.4	19.6 ± 4.0	16.6 ± 3.7	6.8 ± 1.4	21.8 ± 0.7	42.6 ± 7.9	10.8 ± 2.0
(g dm^{-3})	46.8 ± 15.3	196.3 ± 42.9	24.7 ± 3.0	118.7 ± 12.1	47.2 ± 21.0	32.3 ± 13.2	22.1 ± 2.4	44.1 ± 5.2	54.2 ± 3.0	25.8 ± 7.7
	119.8 ± 33.7	361.8 ± 78.5	128.1 ± 2.9	134.7 ± 2.0	61.9 ± 22.8	68.3 ± 16.0	55.2 ± 13.8	70.3 ± 12.5	58.9 ± 9.6	54.0 ± 9.7
OM	11.5 ± 1.4	36.4 ± 9.5	9.9 ± 1.5	40.3 ± 6.9	19.1 ± 3.9	16.1 ± 3.7	6.5 ± 1.4	21.4 ± 0.6	41.9 ± 7.8	10.5 ± 2.0
(g dm^{-3})	37.1 ± 9.6	87.0 ± 8.4	22.7 ± 2.8	99.0 ± 10.4	45.7 ± 20.0	31.1 ± 12.7	20.6 ± 2.7	43.1 ± 5.1	53.3 ± 3.0	25.0 ± 7.5
	73.2 ± 12.0	110.2 ± 7.0	110.1 ± 2.4	119.3 ± 1.3	59.4 ± 21.6	62.4 ± 15.4	47.9 ± 12.8	68.2 ± 12.0	57.5 ± 9.6	52.1 ± 9.3
C	5.9 ± 0.7	18.7 ± 4.8	5.2 ± 0.8	21.5 ± 3.7	9.7 ± 1.9	8.2 ± 1.8	3.3 ± 0.7	11.3 ± 0.3	21.5 ± 4.0	5.3 ± 1.0
(g dm^{-3})	19.8 ± 5.6	44.1 ± 2.5	11.9 ± 1.5	55.4 ± 5.8	23.5 ± 10.7	15.9 ± 6.6	10.3 ± 1.3	22.0 ± 2.7	26.6 ± 1.6	12.5 ± 3.7
	41.8 ± 8.2	62.1 ± 4.2	61.5 ± 1.3	67.6 ± 0.8	31.5 ± 13.2	33.5 ± 8.5	25.5 ± 6.9	37.6 ± 7.2	29.2 ± 4.8	27.3 ± 5.1
N	0.2 ± <0.1	0.9 ± 0.3	0.1 ± <0.1	1.2 ± 0.3	0.2 ± 0.1	0.2 ± <0.1	0.2 ± 0.0	0.2 ± <0.1	0.3 ± 0.1	0.1 ± <0.1
(g dm^{-3})	0.9 ± 0.4	2.6 ± 0.2	0.4 ± 0.1	3.9 ± 0.4	0.7 ± 0.5	0.5 ± 0.2	0.5 ± 0.2	0.4 ± 0.1	0.4 ± <0.1	0.3 ± 0.1
	2.4 ± 0.7	3.9 ± 0.4	4.1 ± 0.1	4.5 ± 0.1	1.6 ± 1.2	2.0 ± 0.7	2.0 ± 0.7	1.2 ± 0.3	0.5 ± 0.1	0.7 ± 0.2
C:N	32.9 ± 2.5	22.5 ± 1.6	41.1 ± 1.3	19.5 ± 1.9	45.9 ± 8.4	38.2 ± 1.3	28.9 ± 2.0	55.5 ± 3.6	63.8 ± 1.5	46.8 ± 4.1
	32.9 ± 6.5	17.1 ± 1.1	31.8 ± 2.4	14.3 ± 0.1	44.5 ± 17.0	34.7 ± 1.8	28.6 ± 3.4	50.9 ± 2.9	59.4 ± 2.1	45.6 ± 1.7
	22.6 ± 4.3	15.9 ± 0.4	15.0 ± 2.4	15.2 ± 0.2	31.5 ± 15.7	17.7 ± 2.4	15.9 ± 0.6	33.0 ± 2.4	54.8 ± 5.5	38.0 ± 3.2
pH	4.4 ± 0.1	4.9 ± <0.1	5.2 ± <0.1	5.1 ± <0.1	4.4 ± <0.1	4.5 ± 0.1	4.6 ± 0.1	4.4 ± 0.1	4.1 ± 0.1	4.3 ± 0.1
	4.6 ± 0.2	4.8 ± <0.1	5.2 ± <0.1	5.2 ± 0.1	4.2 ± 0.1	4.4 ± 0.1	4.5 ± 0.2	4.3 ± 0.1	4.2 ± <0.1	4.2 ± <0.1
	4.7 ± 0.1	4.8 ± 0.1	5.2 ± <0.1	5.1 ± 0.1	4.3 ± 0.1	4.4 ± 0.1	4.6 ± 0.1	4.2 ± <0.1	4.2 ± 0.1	4.3 ± 0.1
Microbial activity potential										
CO_2 prod.	1.7 ± 0.2	1.7 ± 0.7	0.8 ± 0.2	1.3 ± 0.4	0.5 ± 0.2	0.9 ±0.1	0.6 ± 0.1	1.2 ± 0.3	1.0 ± 0.2	0.7 ± 0.1
(mg dm^{-3} h^{-1})	2.2 ± 1.0	1.5 ± 0.3	0.7 ± 0.1	1.1 ± 0.1	1.0 ± 0.4	1.0 ± 0.1	1.1 ± 0.2	1.2 ± 0.1	0.7 ± 0.1	0.8 ± 0.3
	1.8 ± 0.3	1.6 ± 0.2	1.3 ± 0.1	1.2 ± <0.1	0.8 ± 0.2	1.1 ± 0.4	0.6 ± <0.1	2.3 ± 0.4	0.7 ± 0.1	1.8 ± 0.5
CH_4 prod.	1.1 ± 0.8	52.0 ± 15.6	0.6 ± 0.4	60.6 ± 19.5	0.2 ± 0.2	3.8 ±3.0	7.3 ± 2.7	<0.1 ± <0.1	<0.1 ± <0.1	3.4 ± 1.6
(µg dm^{-3} h^{-1})	82.7 ± 49.2	8.0 ± 4.3	6.4 ± 2.4	5.7 ± 1.1	5.2 ± 2.3	6.5 ± 4.4	22.6 ± 9.8	0.4 ± 0.4	0.1 ± 0.1	2.3 ± 1.3
	37.1 ± 22.4	1.3 ± 1.1	20.7 ± 14.4	32.2 ± 15.0	17.6 ± 8.2	14.5 ± 6.9	8.1 ± 4.2	9.7 ± 4.7	0.1 ± 0.1	1.5 ± 1.3

CH_4 oxid.	6.0 ± 4.0	120.8 ± 52.0	27.7 ± 8.2	75.2 ± 12.3	8.6 ± 1.9	81.8 ± 40.6	23.7 ± 4.1	4.0 ± 3.0	4.6 ± 3.1	75.9 ± 41.7
(µg dm^{-3} h^{-1})	179.3 ± 111.5	199.5 ± 39.9	137.4 ± 36.4	105.2 ± 17.0	234.4 ± 78.0	356.6 ± 77.8	56.7 ± 10.7	265.9 ± 64.8	191.1 ± 22.2	99.7 ± 40.5
	255.9 ± 45.7	89.7 ± 38.2	171.0 ± 77.8	29.1 ± 7.9	147.3 ± 2.2	100.7 ± 27.0	8.6 ± 0.7	368.6 ± 92.0	58.0 ± 20.1	105.6 ± 72.1
Microbial PLFAs										
F-PLFA	4.1 ± 0.7	4.3 ± 1.4	2.0 ± 0.7	4.8 ± 1.4	3.4 ± 1.5	4.2 ± 1.6	4.3 ± 1.3	11.0 ± 2.9	5.7 ± 1.7	1.1 ± <0.1
(µmol dm^{-3})	6.1 ± 1.8	2.0 ± 0.7	2.7 ± 1.8	1.3 ± 0.2	1.5 ± 0.0	2.3 ± 0.9	2.0 ± 0.4	5.5 ± 1.0	2.0 ± 0.8	0.7 ± 0.2
	0.8 ± 0.3	0.6 ± 0.1	0.4 ± 0.2	0.6 ± 0.2	0.7 ± 0.3	0.7 ± 0.1	0.7 ± 0.1	0.5 ± 0.1	0.3 ± 0.1	1.1 ± 0.6
B-PLFA	11.7 ± 3.0	53.7 ± 23.5	5.7 ± 1.2	35.1 ± 8.5	4.2 ± 0.5	8.1 ± 3.9	12.1 ± 4.6	12.6 ± 3.4	9.3 ± 1.8	6.7 ± 2.1
(µmol dm^{-3})	47.7 ± 20.1	64.0 ± 16.4	15.8 ± 1.6	32.8 ± 1.8	21.5 ± 8.0	19.7 ± 6.8	22.8 ± 4.7	9.8 ± 1.4	12.6 ± 0.2	14.7 ± 6.6
	24.9 ± 6.9	18.4 ± 4.8	10.2 ± 4.7	14.8 ± 4.5	13.5 ± 2.0	13.2 ± 2.5	8.2 ± 0.9	9.2 ± 1.3	7.8 ± 1.3	34.0 ± 19.6
Act-PLFA	0.7 ± 0.1	7.9 ± 3.6	0.3 ± 0.1	4.1 ± 0.8	0.3 ± <0.1	0.6 ± 0.4	0.4 ± 0.2	1.5 ± 0.4	2.0 ± 0.6	0.7 ± 0.3
(µmol dm^{-3})	3.7 ± 1.4	10.7 ± 3.9	1.7 ± 0.2	5.0 ± 0.6	2.1 ± 1.0	1.6 ± 0.4	0.8 ± 0.1	1.5 ± 0.3	1.4 ± 0.3	1.8 ± 1.0
	2.8 ± 0.9	2.0 ± 0.5	1.0 ± 0.4	1.5 ± 0.5	1.9 ± 0.9	1.4 ± 0.4	0.8 ± 0.2	0.7 ± 0.2	0.4 ± 0.1	2.7 ± 1.4
F:B	0.5 ± 0.2	0.1 ± <0.1	0.3 ± 0.1	0.1 ± <0.1	0.8 ± 0.3	0.6 ± 0.1	0.4 ± 0.1	0.9 ± <0.1	0.6 ± 0.2	0.2 ± 0.1
	0.2 ± <0.1	<0.1 ± <0.1	0.2 ± 0.1	<0.1 ± <0.1	0.1 ± <0.1	0.2 ± 0.1	0.1 ± <0.1	0.6 ± 0.1	0.2 ± 0.1	0.1 ± <0.1
	<0.1 ± <0.1	0.1 ± <0.1	<0.1 ± <0.1	<0.1 ± <0.1	<0.1 ± <0.1	0.1 ± <0.1	0.1 ± <0.1	0.1 ± <0.1	<0.1 ± <0.1	<0.1 ± <0.1

[a] SJ3 = Mesotrophic fen; SJ4 = Oligotrophic fen; SJ5 = Fen-bog transition; SJ6 = Bog

Supplementary Table S7. Maximum correlations (*r*) of vector variables in the GNMDS ordination of plant communities in the peatland successional gradient (sites SJ0-SJ6) and their statistical significance (*p*).

Variable	*r*	*p*
Plant cover[a]		
Grasses	0.50	0.002
Herbs	0.47	0.002
Sedges	0.58	0.002
Shrubs	0.74	0.001
Sphagnum sp.	0.80	0.001
Other mosses	0.18	0.477
Hepatics	0.09	0.859
Field measurements[b]		
WL	0.68	0.001
CH_4 emission	0.64	0.001
RE	0.29	0.111
Soil properties[c]		
Bulk density	0.87	0.001
OM	0.55	0.001
C	0.56	0.001
N	0.52	0.001
C:N	0.86	0.001
pH	0.87	0.001
Potential microbial activity[c]		
CO_2 production	0.15	0.576
CH_4 production	0.24	0.264
CH_4 oxidation	0.37	0.018
Microbial PLFAs[c]		
F-PLFA	0.25	0.210
B-PLFA	0.19	0.406
Act-PLFA	0.25	0.205
F:B	0.50	0.001
Microbial OTUs[d]		
Fungi	0.36	0.034
Actinobacteria	0.26	0.175
Methanogens	0.51	0.002
MOB-tII	0.76	0.001

[a] Cover percentage of each plant functional type determined from the stable sample plots in July 2007.

[b] Water level (WL), the distance of the mean water table from the mire surface in centimeters, RE (ecosystem respiration and CH_4 emission are the mean values of the sample plot-specific measurements in June-September 2007.

[c] Variables were determined from the three layers (uppermost, middle and deepest) of each soil profile. OM, organic matter; C, carbon; N, nitrogen; PLFA, phospholipid fatty acid; F, fungal; B, bacterial; Act, actinobacterial; F:B, the ratio of F-PLFA to B-PLFA. Microbial OTUs is the number of OTUs obtained by molecular fingerprinting methods DGGE + sequencing (fungi, actinobacteria and tII-MOB) and T-RPLP (methanogens).

Supplementary Table S8. Maximum correlations (*r*) of vector variables in the GNMDS ordination configurations of microbial communities in the peatland successional gradient (sites SJ0-SJ6, Fig. 5) and their statistical significance (*p*).

	Fungi		Actinobacteria		Methanogens		tII-MOB	
Variable	*r*	*p*	*r*	*p*	*r*	*p*	*r*	*p*
Plant cover[a]								
Shrubs	0.74	0.001	0.67	0.001	0.47	0.001	0.43	0.001
Sedges	0.54	0.001	0.43	0.001	0.45	0.001	0.37	0.002
Grasses	0.35	0.001	0.37	0.001	0.49	0.001	0.34	0.016
Herbs	0.40	0.001	0.42	0.001	0.46	0.001	0.42	0.001
Sphagnum sp.	0.67	0.001	0.69	0.001	0.63	0.001	0.50	0.001
Other mosses	0.26	0.004	0.40	0.001	0.32	0.001	0.22	0.132
Hepatics	0.16	0.179	0.09	0.503	0.17	0.113	0.19	0.101
Field measurements[b]								
Above WL	0.45	0.001	0.57	0.001	0.48	0.001	0.41	0.001
CH_4 emission	0.23	0.037	0.50	0.001	0.42	0.001	0.28	0.016
RE	0.41	0.001	0.14	0.219	0.38	0.001	0.22	0.092
Soil properties[c]								
Bulk density	0.54	0.001	0.60	0.001	0.62	0.001	0.38	0.011
OM	0.03	0.925	0.27	0.002	0.69	0.001	0.35	0.001
C	0.02	0.963	0.25	0.005	0.70	0.001	0.36	0.001
N	0.27	0.006	0.28	0.001	0.70	0.001	0.45	0.001
C:N	0.78	0.001	0.82	0.001	0.57	0.001	0.54	0.001
pH	0.71	0.001	0.70	0.001	0.51	0.001	0.72	0.001
Potential microbial activity[c]								
CO_2 production	0.19	0.076	0.20	0.045	0.19	0.071	0.26	0.046
CH_4 production	0.22	0.025	0.25	0.016	0.30	0.001	0.26	0.044
CH_4 oxidation	0.24	0.017	0.18	0.062	0.04	0.918	0.08	0.695
Microbial PLFAs[c]								
F-PLFA	0.13	0.273	0.18	0.077	0.22	0.032	0.25	0.058
B-PLFA	0.25	0.009	0.25	0.009	0.29	0.002	0.28	0.046
Act-PLFA	0.24	0.019	0.27	0.008	0.31	0.001	0.28	0.048
F:B	0.32	0.001	0.40	0.001	0.27	0.005	0.26	0.042
Microbial OTUs[c]	0.13	0.272	0.11	0.366	0.78	0.001	0.55	0.001

[a] Cover percentage of each plant functional type determined from the stable sample plots in July 2007.

[b] Water level (WL), the distance of the mean water table from the mire surface in centimeters, RE (ecosystem respiration and CH_4 emission are the mean values of the sample plot-specific measurements in June-September 2007.

[c] Variables were determined from the three layers (uppermost, middle and deepest) of each soil profile. OM, organic matter; C, carbon; N, nitrogen; PLFA, phospholipid fatty acid; F, fungal; B, bacterial; Act, actinobacterial; F:B, the ratio of F-PLFA to B-PLFA. Microbial OTUs is the number of OTUs obtained by molecular fingerprinting methods DGGE + sequencing (fungi, actinobacteria and tII-MOB) and T-RPLP (methanogens).