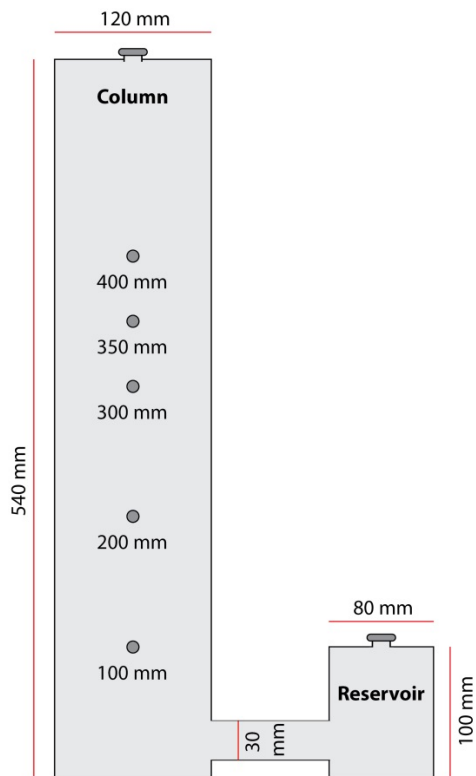


1 **Supplementary material**



2
3 **Fig. S1** Dimensions of mesocosm columns.

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5 **Table S1** Change in read count during data processing.

Step	Moss Field		Moss Washed		Moss incubated	
	Read count (average)	SEM	Read count (average)	SEM	Read count (average)	SEM
1 Unprocessed reads	31 301	± 2 569	32 001	± 2 117	45 380	± 13 738
2 Screen sequences	28 443	± 2 351	29 082	± 1 958	41 585	± 12 791
3 Unique sequences	27 912	± 2 311	28 488	± 1 923	40 541	± 12 439
4 Aligned sequences	27 912	± 2 311	28 488	± 1 923	40 541	± 12 439
5 Screened alignment	27 912	± 2 311	28 488	± 1 923	40 541	± 12 439
6 Filter positions in alignment	27 912	± 2 311	28 488	± 1 923	40 541	± 12 439
7 Pre-clustering	27 912	± 2 311	28 488	± 1 923	40 541	± 12 439
8 Chimera removal	23 924	± 2 032	24 129	± 1 667	31 278	± 9 097
9 Non-target lineage removal	7 847	± 578	9 028	± 669	18 003	± 5 700
<i>Total read count per group</i>	<i>23 542</i>		<i>27 083</i>		<i>54 009</i>	
10 Random subsample	6 500	± 0	6 500	± 0	6 500	± 0

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10 **Table S2** Change in read quality during data processing.

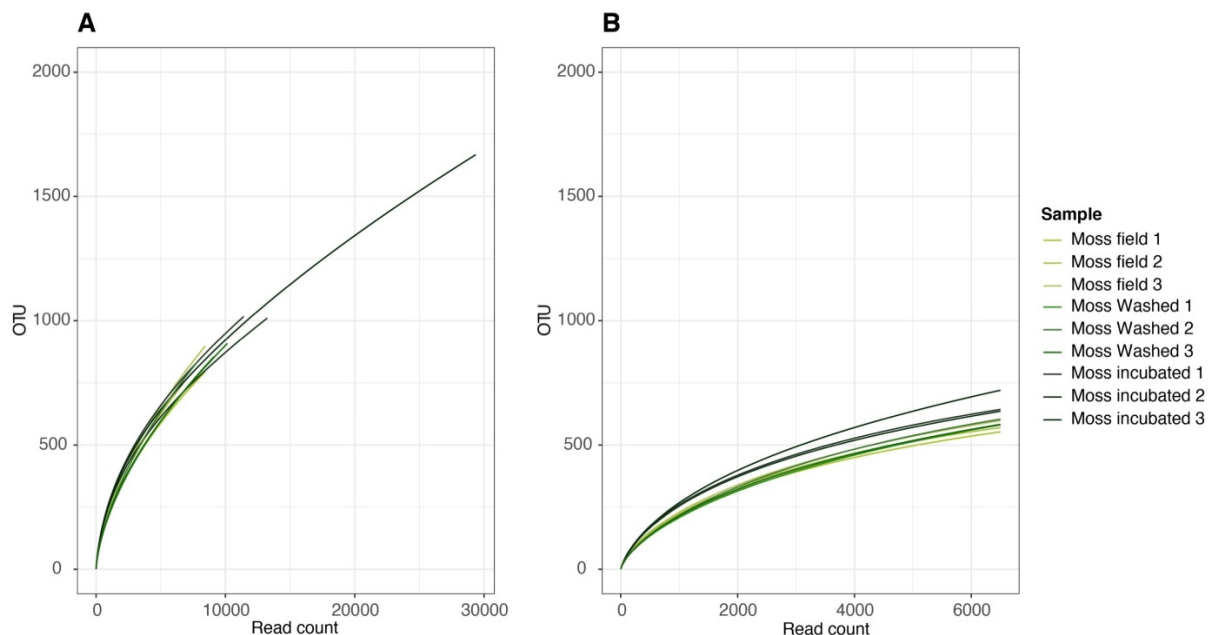
Step		Total read count	# Unique reads	Mean read length (bp)	Max. ambiguous positions	Max. polymers
1	Unprocessed reads	326 045		444	308	297
2	Screen sequences	297 333		445	0	45
3	Unique sequences	297 333	154 224	445	0	45
4	Align sequences	297 333	154 224	407	0	28
5	Screen alignment	290 823	148 011	407	0	8
6	Filter positions in alignment	290 823	82 822	407	0	8
7	Pre-clustering	290 823	50 548	407	0	8
8	Chimera removal	237 994	12 021	407	0	8
9	Non-target lineage removal	104 634	10 068	411	0	8

11

12 **Table S3** Primer sequences used in this study.

Target gene	Primer name	Sequence	Reference
<i>pmoA</i>	A189f	5'-GGNGACTGGGACTTCTGG-3'	(Holmes et al. 1995)
	A682r	5'-GAASGCNGAGAAGAASGC-3'	(Holmes et al. 1995)
<i>mmoX</i>	mmoX1	5'-CGGTCCGCTGTGGAAGGGCATGAAGCGCGT-3'	(Miquez et al. 1997)
	mmoX2	5'-GGCTCGACCTTGAAGTTGGAGCCATACTCG-3'	(Miquez et al. 1997)
<i>16S rRNA</i> <i>Bacteria</i>	Bact 341f	5'-CCTACGGGNGGCWGCAG-3'	(Klindworth et al. 2013)
	Bact 785r	5'-GACTACHVGGGTATCTAATCC-3	(Klindworth et al. 2013)

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15 **Fig. S2** Rarefaction curves before (A) and after (B) subsampling, singletons were removed.

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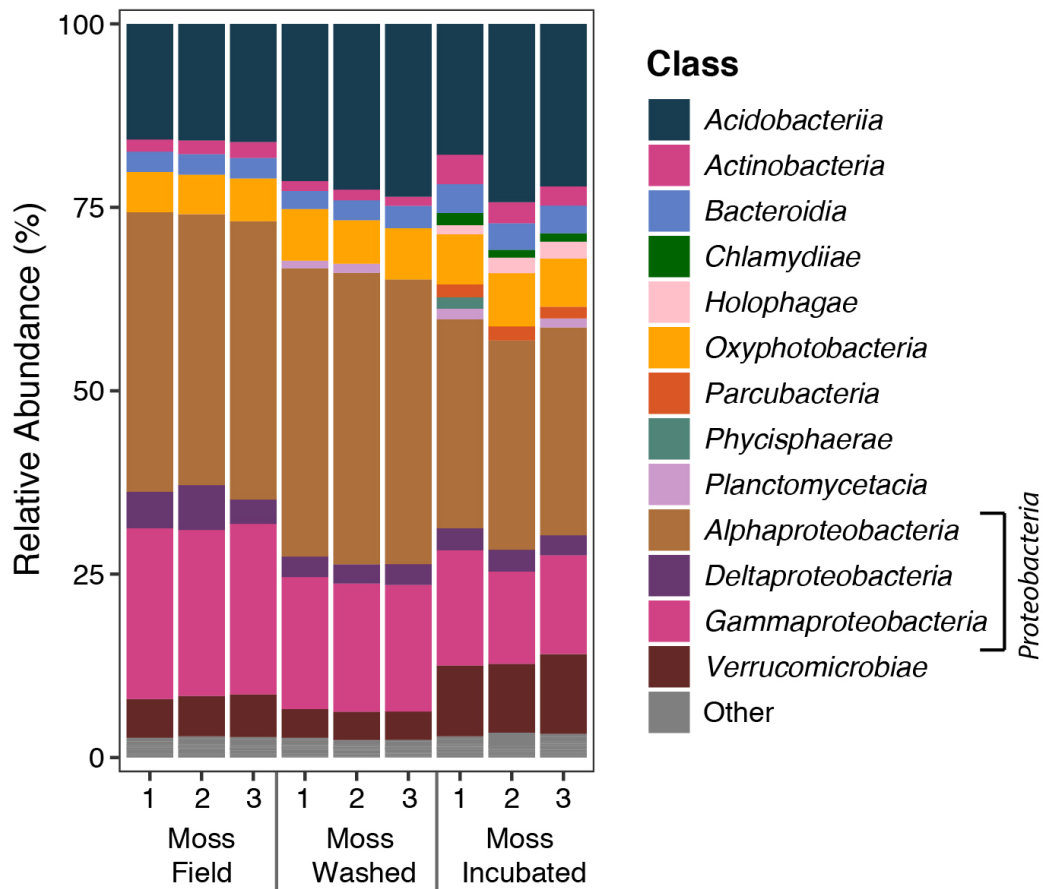
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18 **Table S4** Alpha diversity index for the different samples.

Sample	Observed species number (S)	Richness			Evenness Pielou (J)
		Shannon (H)	Fisher's alpha	Chao1 ACE	
Moss Field	1136	4.53	263.0	1607.3 1729.4	0.64
Moss Washed	1215	4.23	287.0	1762.1 2001.5	0.60
Moss Incubated	1213	4.77	286.4	2046.3 2061.7	0.67

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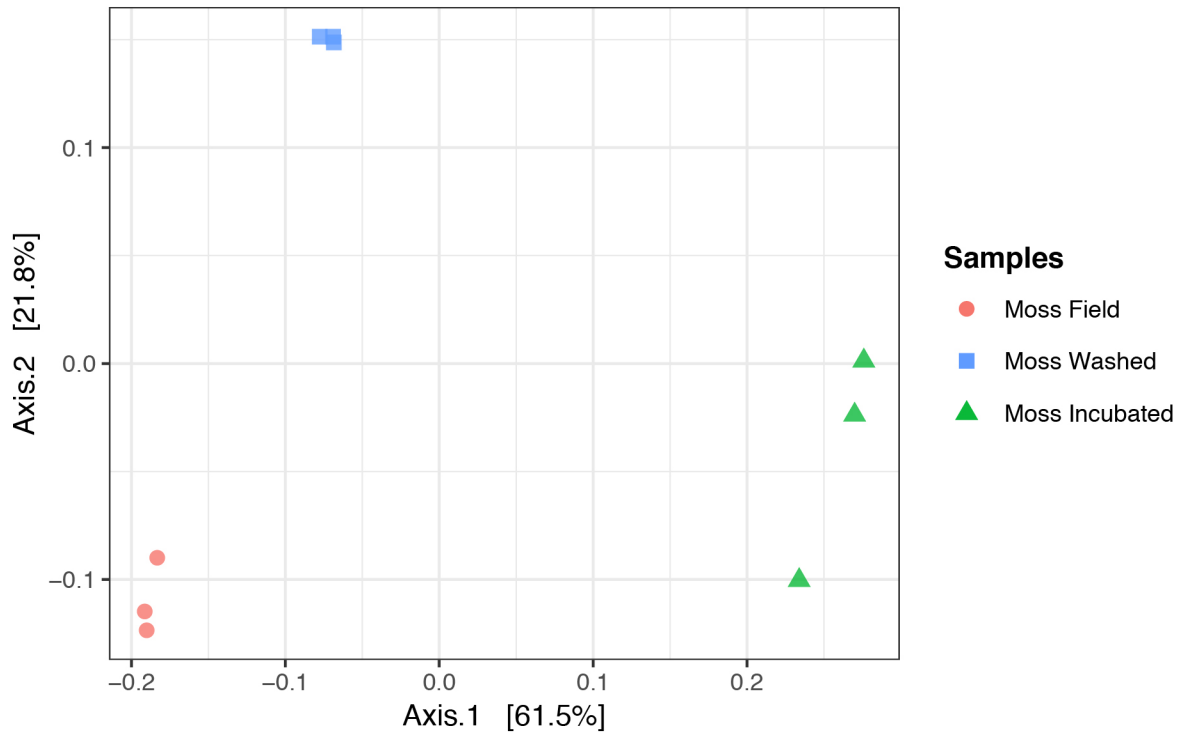
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22 **Fig. S3** Phylogenetic classification of the bacterial community per sample based on 16s rRNA gene amplification
 23 and sequencing. Taxonomic groups with a relative abundance <1% are depicted as "Other".

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26 **Fig. S4** Principal Coordinate Analysis (PCoA) of the microbial diversity using Bray-Curtis dissimilarity. The different
 27 samples are coded according to colour.

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29 **Tables S5** Relative abundances (RA in %) of Verrucomicrobial microorganisms in the bacterial 16s rRNA
 30 community profile.

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	Relative abundance (%)			RA (%)
	Moss Field	Moss Washed	Moss incubated	
<i>Verrucomicrobia; Verrucomicrobiae;</i>				
<i>Chthoniobacterales</i>	6.60	3.11	3.15	15
<i>Methylacidiphilales</i>	0.75	0.29	1.62	10
<i>Opitutales</i>	2.06	2.78	7.75	5
<i>Pedosphaerales</i>	6.54	4.23	14.85	2
<i>S-BQ2-57_soil_group</i>	0.02	0	0	1
<i>unclassified</i>	0.02	0.15	0.08	0
<i>Verrucomicrobiales</i>	0.09	0.06	0.94	

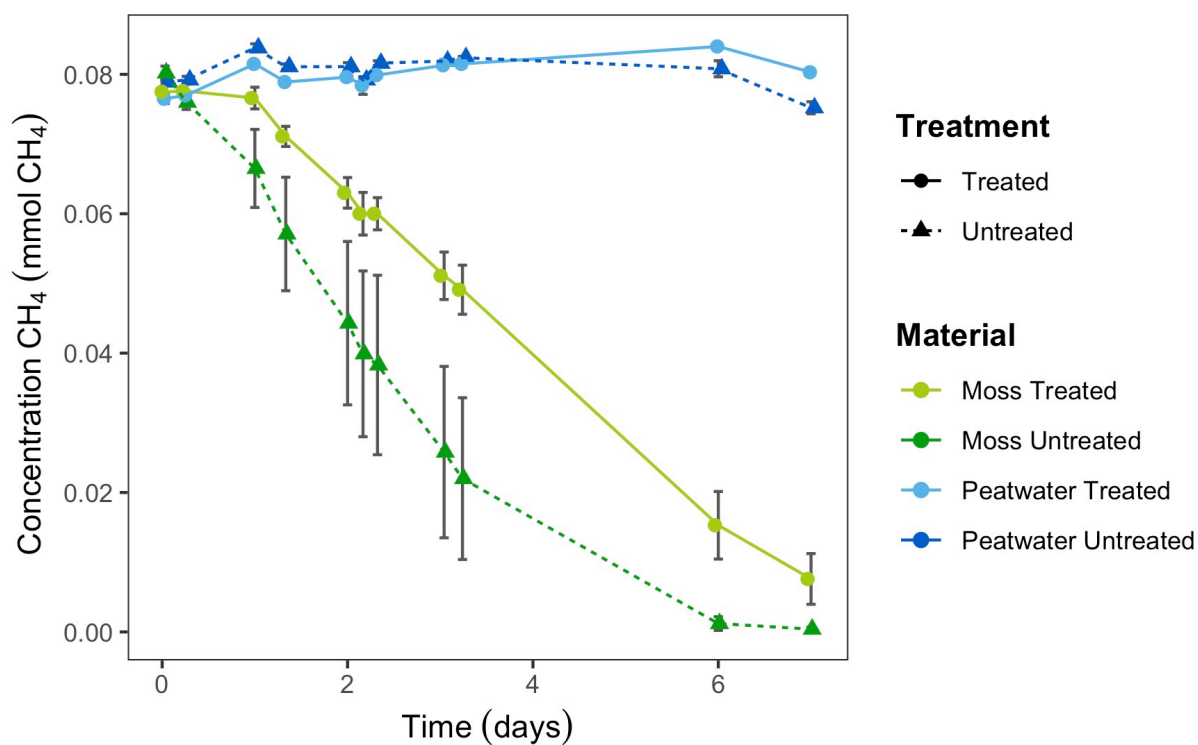


Fig. S5 Potential CH_4 oxidation rate in batch assays, prior to mesocosm incubation round 1. CH_4 concentration (mmol) in the headspace is displayed over time (days) for incubations with: mosses (unwashed (dark green, $n=3$) and washed (light green, $n=3$)) and peat water (unfiltered (dark blue, $n=3$) and filtered (light blue, $n=3$)). Error bars indicate the standard error of the mean.

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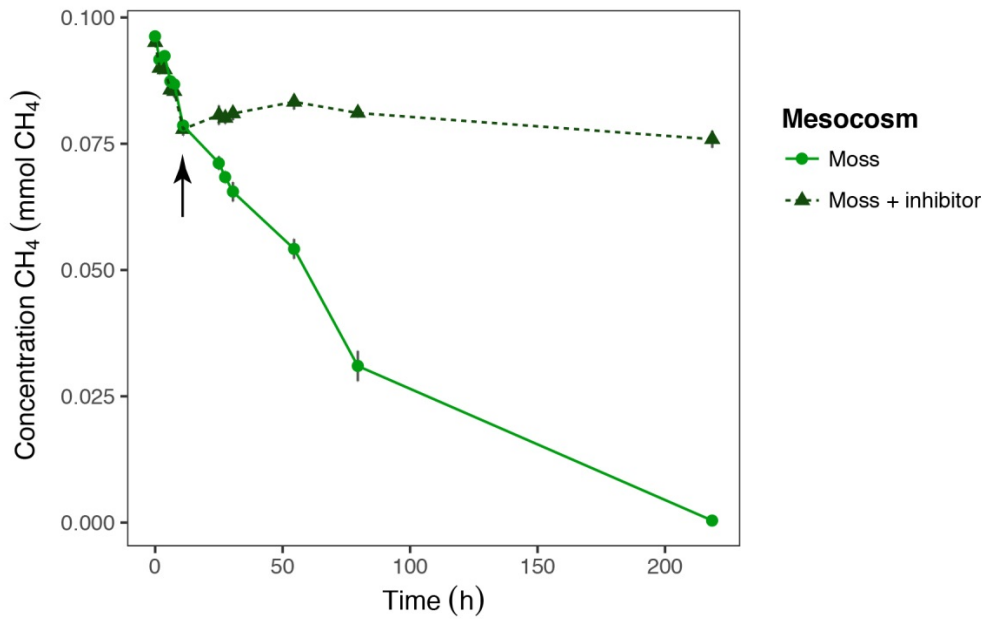
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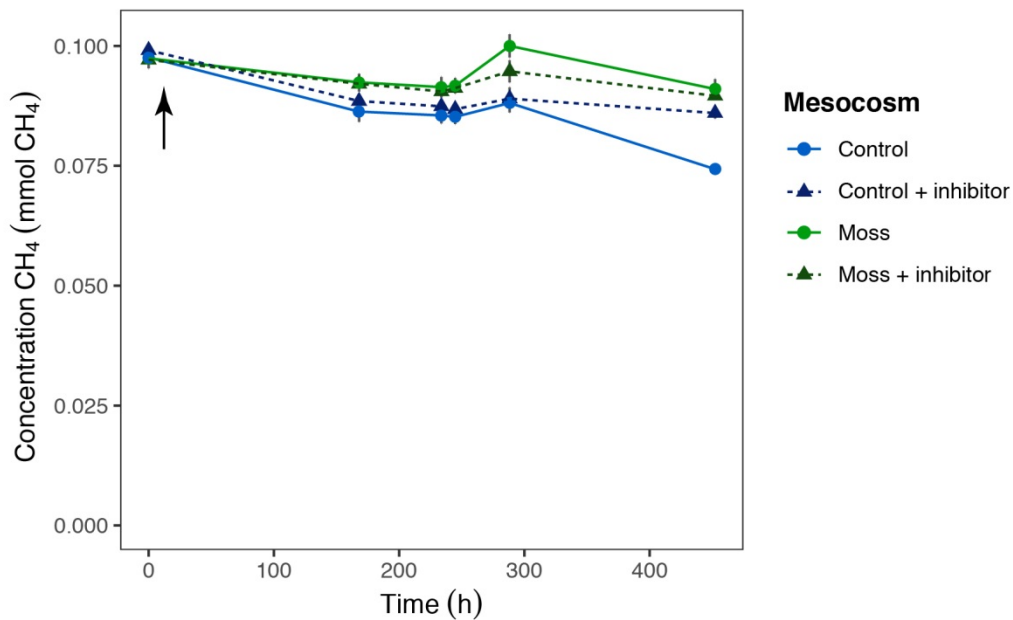
Table S6 Mean potential CH_4 oxidation rate in mosses ($\mu\text{mol CH}_4 \text{ g}^{-1} \text{ DW day}^{-1}$) and peat water ($\mu\text{mol CH}_4 \text{ ml}^{-1} \text{ day}^{-1}$) prior to mesocosm incubation round 1.

Round 1					
Material	Treatment	Methane oxidation rate			
		$(\mu\text{mol CH}_4 \text{ g}^{-1} \text{ DW day}^{-1})$	SE	R2	n
Moss	Washed	121	4.1	0.98	3
Moss	Field	165	29	0.99	3
Water	Treatment	Methane oxidation rate			
		$(\mu\text{mol CH}_4 \text{ ml}^{-1} \text{ day}^{-1})$	SE	R2	n
Water	Filtered	0.01	0.003	0.40	3
Water	Field	0.08	0.02	0.48	3



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 49 **Fig. S6** Potential CH₄ oxidation rate of the mosses in batch assays, after mesocosm incubation round 1. CH₄
 50 concentration (mmol) in the headspace is displayed over time (h) for incubations with mosses, either with PMO
 51 inhibitor acetylene (light green, n=3) or without PMO inhibitor (dark green, n=3). Arrow indicates addition of
 52 acetylene gas. Error bars indicate the standard error of the mean.

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 57 **Fig. S7** Potential CH₄ oxidation rate of peat water in batch assays, after mesocosm incubation round 1. CH₄
 58 concentration (mmol) in the headspace is displayed over time (h) for incubations with peat water from the moss
 59 mesocosm (green) or peat water from the control mesocosm (blue). Incubations are either with PMO inhibitor
 60 (lighter colors, dashed line, n=3) or without PMO inhibitor (darker colors, dashed line, n=3). Arrow indicates
 61 addition of acetylene gas. Error bars indicate the standard error of the mean.

62 **Table S7** Mean potential CH₄ oxidation rate in mosses ($\mu\text{mol CH}_4 \text{ g}^{-1} \text{ DW day}^{-1}$) and peat water ($\mu\text{mol CH}_4 \text{ ml}^{-1}$
 63 day^{-1}) prior to mesocosm incubation round 2.

Round 2					
Material	Treatment	Methane oxidation rate			
		$(\mu\text{mol CH}_4 \text{ g}^{-1} \text{ DW day}^{-1})$	SE	R2	n
Moss	Washed	215	7.6	0.99	3
Moss	Field	281	14	0.99	3
Methane oxidation rate					
Material	Treatment	Methane oxidation rate			
		$(\mu\text{mol CH}_4 \text{ ml}^{-1} \text{ day}^{-1})$	SE	R2	n
Water	Filtered	-0.04	0.03	0.35	3

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66 **Table S8** Mean potential CH₄ oxidation rate in mosses ($\mu\text{mol CH}_4 \text{ g}^{-1} \text{ DW day}^{-1}$) and peat water ($\mu\text{mol CH}_4 \text{ ml}^{-1}$
 67 day^{-1}) after mesocosm incubation round 2.

Round 2						
Material	Mesocosm	Treatment	Methane oxidation rate			
			$(\mu\text{mol CH}_4 \text{ g}^{-1} \text{ DW day}^{-1})$	SE	R2	n
Moss	Moss		121	12	0.97	3
Moss	Moss	+ inhibitor	-2.0	0.6	0.33	3
Material	Mesocosm	Treatment	Methane oxidation rate			
			$(\mu\text{mol CH}_4 \text{ ml}^{-1} \text{ day}^{-1})$	SE	R2	n
Water	Moss		0.10	0.02	0.94	3
Water	Moss	+ inhibitor	-0.02	0.00	0.71	3
Water	Control		-0.01	0.01	0.39	3
Water	Control	+ inhibitor	-0.02	0.00	0.91	3

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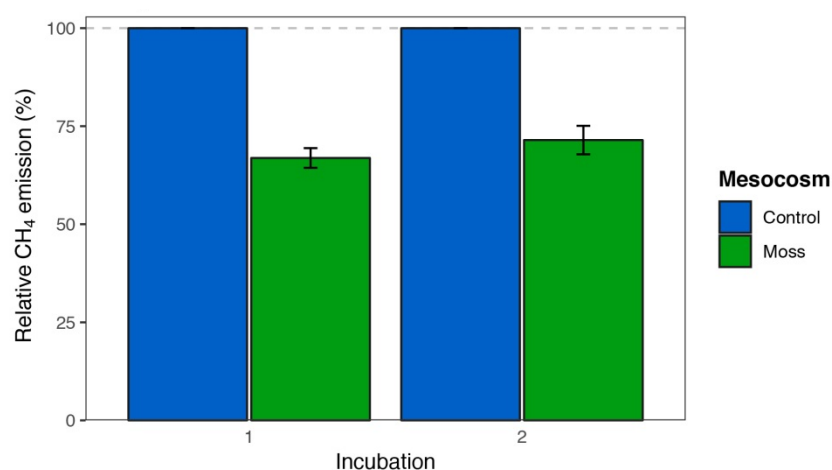
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Fig. S8 Relative CH₄ emission (as % of emission in control mesocosm) from the control mesocosm (blue) and the moss mesocosms (green), shown for incubation round 1 and incubation round 2. Each bar represents the average relative CH₄ emission of days 8-32 and error bars indicate the standard error.

Table S9 Composition of the unfiltered and filtered porewater.

	NO₃⁻		NH₄⁺		PO₄³⁻		Al		Ca		Fe		K	
porewater	($\mu\text{mol L}^{-1}$)		($\mu\text{mol L}^{-1}$)		($\mu\text{mol L}^{-1}$)		($\mu\text{mol L}^{-1}$)		($\mu\text{mol L}^{-1}$)		($\mu\text{mol L}^{-1}$)		($\mu\text{mol L}^{-1}$)	
unfiltered	1.22	± 0.07	12.58	± 2.83	0.68	± 0.05	9.27	± 2.21	30.51	± 1.06	14.69	± 2.45	9.03	±
filtered	2.17	± 0.54	3.55	± 0.27	0.31	± 0.06	4.52	± 0.36	33.25	± 2.06	4.12	± 0.17	5.18	±
	Mg		Mn		Na		P		S		Si		Zn	
porewater	($\mu\text{mol L}^{-1}$)		($\mu\text{mol L}^{-1}$)		($\mu\text{mol L}^{-1}$)		($\mu\text{mol L}^{-1}$)		($\mu\text{mol L}^{-1}$)		($\mu\text{mol L}^{-1}$)		($\mu\text{mol L}^{-1}$)	
filtered	26.62	± 0.67	0.44	± 0.02	172.44	± 3.32	2.04	± 0.21	24.08	± 0.58	9.45	± 0.40	0.58	±
unfiltered	21.70	± 0.04	0.46	± 0.02	170.04	± 3.28	0.48	± 0.12	20.61	± 0.67	9.85	± 0.21	0.43	±