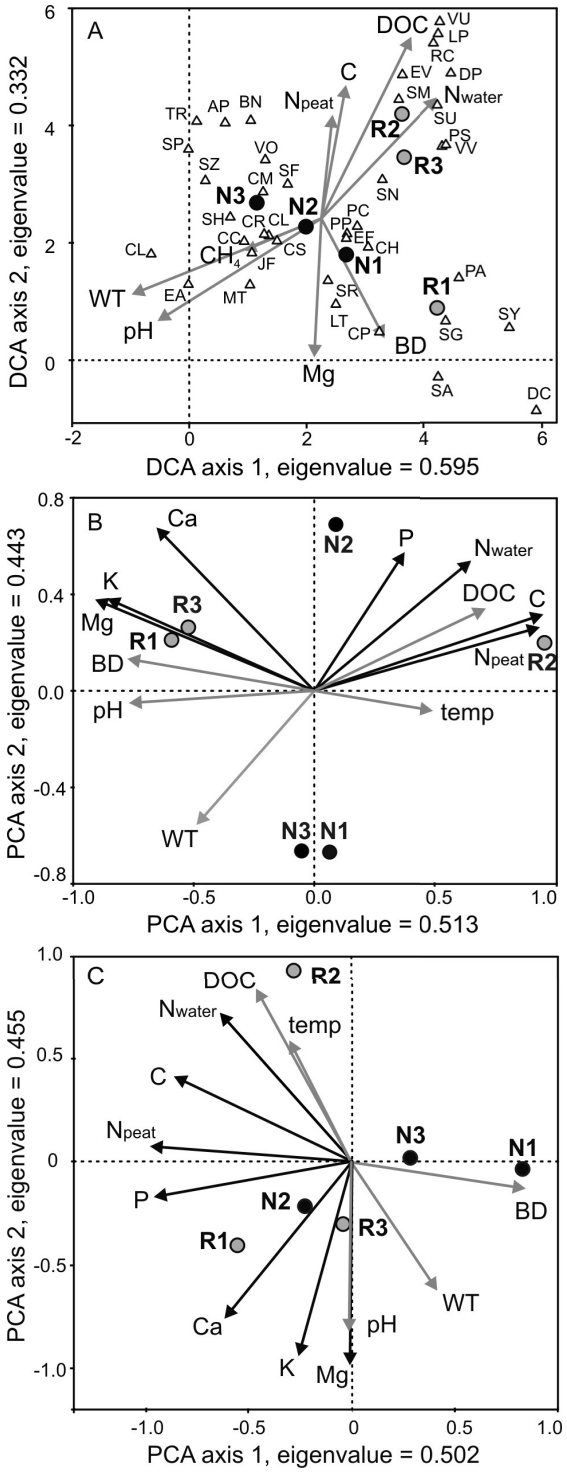

Figure S1. (A) Detrended correspondence analysis (DCA) of vegetation and principal component analysis (PCA) of peat chemistry at the depths of (B) 0-7.5 cm and (C) 7.5-15 cm of natural (N1-N3) and restored (R1-R3) peatlands. Environmental variables with >0.5 correlation

with the axes are included (grey arrows) but do not affect the placement of the study sites. WT, water table level; BD, bulk density; DOC, dissolved organic carbon; temp, peat temperature at the depth of 5 cm; CH_4, mean emission rate for the growing season . AP *Andromeda polifolia*; BN *Betula nana*; CP *Calamagrostis purpurea*; CS *Calliergon stramineum*; CC *Carex canescens*; CH *C. chordorrhiza*; CL *C. lasiocarpa*; CI *C. limosa*; CM *Carex magellanica*; CR *C. rostrata*; DC *Deschampsia cespitosa*; DP *Dicranum polysetum*; EF *Equisetum fluviatile*; EA *Eriophorum angustifolium*; EV *Eriophorum vaginatum*; JF *Juncus filiformis*; LP *Ledum palustre*; LT *Lysimachia thyrsiflora*; MT *Menyanthes trifoliata*; PA *Picea abies*; PS *Pleurozium schreberi*; PC *Polytrichum commune*; PP *Potentilla palustris*; RC *Rubus chamaemorus*; Salix SA *Salix aurita*; SH *Salix phylicifolia*; SZ *Scheuchzeria palustris*; SY *Sciuro-hypnum* spp.; SN *Sphagnum angustifolium*; SF *S. fallax*; SG *S. girgensonii*; SM *S. magellanicum*; SP *S. papillosum*; SR *S. riparium*; SU *S. russowii*; TR *Trichophorum cespitosa*; VO *Vaccinium oxycoccus*; VU *V. uliginosum*; VV*V. vitis-idaea*.

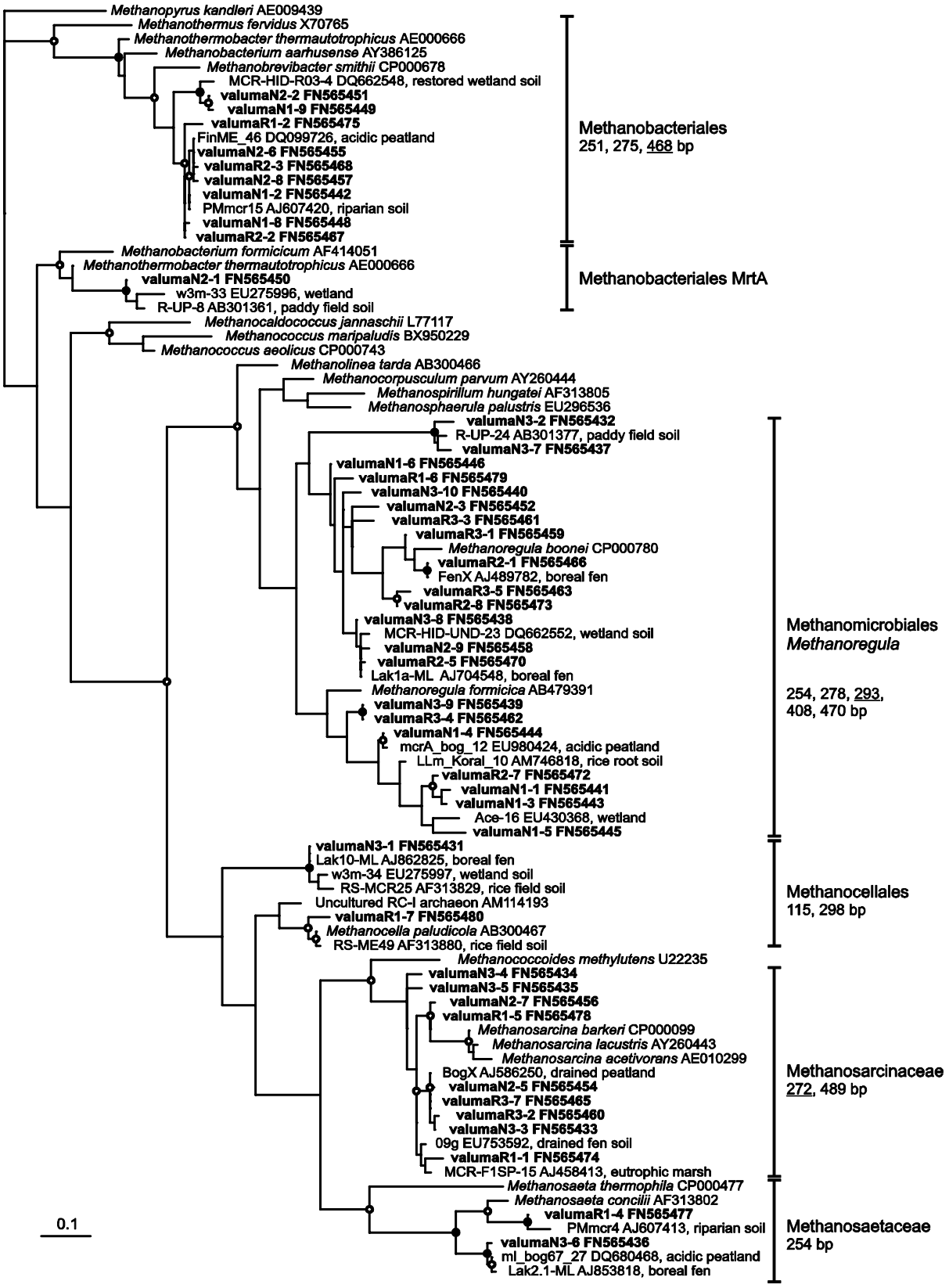
Methanopyrus kandleri AE009439
Methanothermus fervidus X70765
Methanothermobacter thermautotrophicus AE000666
Methanobacterium aarhusense AY386125
Methanobrevibacter smithii CP000678
MCR-HID-R03-4 DQ662548, restored wetland soil
valumaN2-2 FN565451
valumaN1-9 FN565449
valumaR1-2 FN565475
FinME_46 DQ099726, acidic peatland
valumaN2-6 FN565455
valumaR2-3 FN565468
valumaN2-8 FN565457
valumaN1-2 FN565442
PMmcr15 AJ607420, riparian soil
valumaN1-8 FN565448
valumaR2-2 FN565467
Methanobacterium formicicum AF414051
Methanothermobacter thermautotrophicus AE000666
valumaN2-1 FN565450
w3m-33 EU275996, wetland
R-UP-8 AB301361, paddy field soil
Methanocaldococcus jannaschii L77117
Methanococcus maripaludis BX950229
Methanococcus aeolicus CP000743
Methanolinea tarda AB300466
Methanocorpusculum parvum AY260444
Methanospirillum hungatei AF313805
Methanosphaerula palustris EU296536
valumaN3-2 FN565432
R-UP-24 AB301377, paddy field soil
valumaN3-7 FN565437
valumaN1-6 FN565446
valumaR1-6 FN565479
valumaN3-10 FN565440
valumaN2-3 FN565452
valumaR3-3 FN565461
valumaR3-1 FN565459
Methanoregula boonei CP000780
valumaR2-1 FN565466
FenX AJ489782, boreal fen
valumaR3-5 FN565463
valumaR2-8 FN565473
valumaN3-8 FN565438
MCR-HID-UND-23 DQ662552, wetland soil
valumaN2-9 FN565458
valumaR2-5 FN565470
Lak1a-ML AJ704548, boreal fen
Methanoregula formicica AB479391
valumaN3-9 FN565439
valumaR3-4 FN565462
valumaN1-4 FN565444
mcrA_bog_12 EU980424, acidic peatland
LLm_Koral_10 AM746818, rice root soil
valumaR2-7 FN565472
valumaN1-1 FN565441
valumaN1-3 FN565443
Ace-16 EU430368, wetland
valumaN1-5 FN565445
valumaN3-1 FN565431
Lak10-ML AJ862825, boreal fen
w3m-34 EU275997, wetland soil
RS-MCR25 AF313829, rice field soil
Uncultured RC-I archaeon AM114193
valumaR1-7 FN565480
Methanocella paludicola AB300467
RS-ME49 AF313880, rice field soil
Methanococcoides methylutens U22235
valumaN3-4 FN565434
valumaN3-5 FN565435
valumaN2-7 FN565456
valumaR1-5 FN565478
Methanosarcina barkeri CP000099
Methanosarcina lacustris AY260443
Methanosarcina acetivorans AE010299
BogX AJ586250, drained peatland
valumaN2-5 FN565454
valumaR3-7 FN565465
valumaR3-2 FN565460
valumaN3-3 FN565433
09g EU753592, drained fen soil
valumaR1-1 FN565474
MCR-F1SP-15 AJ458413, eutrophic marsh
Methanosaeta thermophila CP000477
Methanosaeta concilii AF313802
valumaR1-4 FN565477
PMmcr4 AJ607413, riparian soil
valumaN3-6 FN565436
ml_bog67_27 DQ680468, acidic peatland
Lak2.1-ML AJ853818, boreal fen
0.1
Methanobacteriales
251, 275, 468 bp
Methanobacteriales MrtA
Methanomicrobiales
Methanoregula
254, 278, 293,
408, 470 bp
Methanocellales
115, 298 bp
Methanosarcinaceae
272, 489 bp
Methanosaetaceae
254 bp

Figure S2.

Figure S2. Phylogenetic tree of partial McrA sequences (133 aa) from peatland clones (in bold) and reference sequences. In bold sequence names, R refers to restored sites (R1-R3) and N to natural sites (N1-N3). Size of terminal restriction fragments is indicated for each group, and the most abundant T-RFs are underlined. No T-RFs were detected corresponding to Methanobacteriales MrtA for the isoenzyme methyl-coenzyme M reductase II. Scale indicates 10% sequence divergence. Nodes with bootstrap values ≥95% are marked with filled circles and ≥75% with open circles. The maximum likelihood tree was rooted with *Methanopyrus kandleri*.

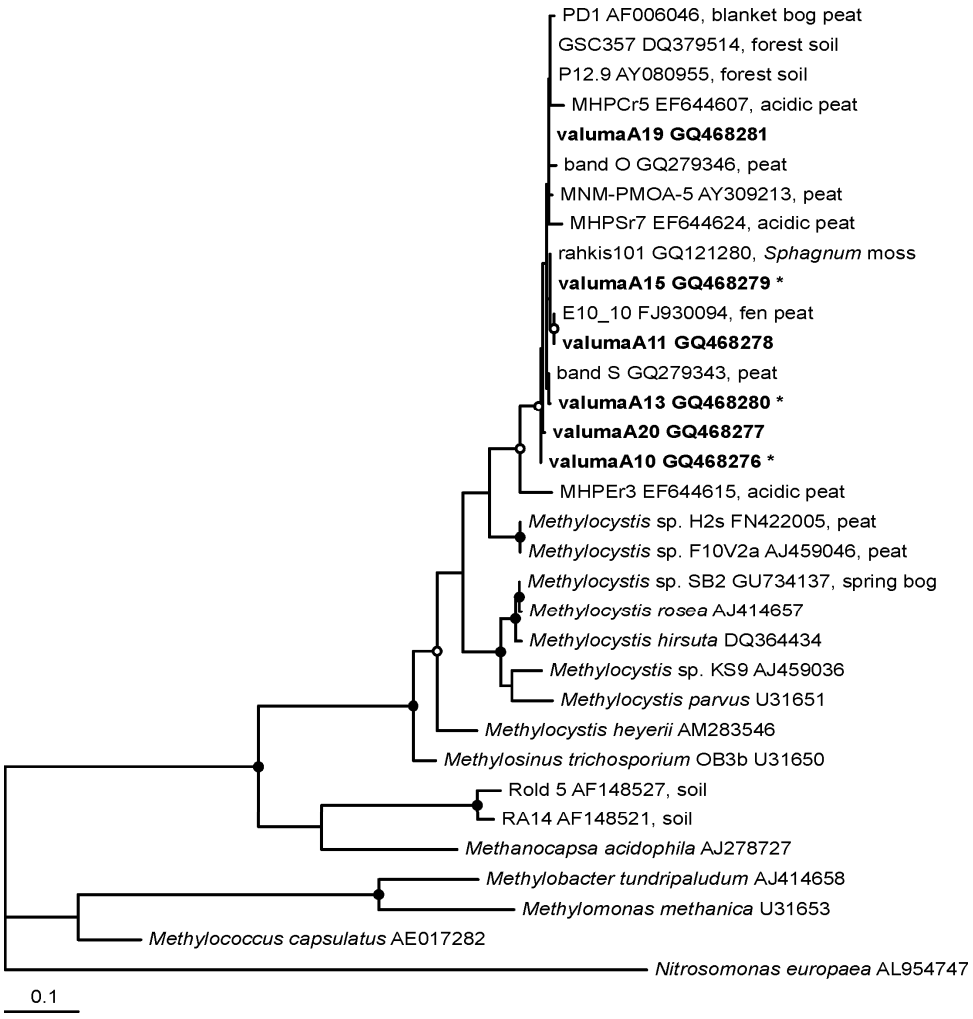

Figure S3. Phylogenetic tree of partial *pmoA* sequences (435 bp) from peatland DGGE bands (in bold) and reference methanotroph sequences. Scale indicates 10% sequence divergence. Nodes with bootstrap values ≥95% are marked with filled circles and ≥75% with open circles. The maximum likelihood tree was rooted with *Nitrosomonas europea amoA*. Bands common to samples with identical banding patterns are marked with an asterisk.

Supplementary materials and methods

Vegetation and peat chemistry. The vegetation of the sites was inventoried from 12 to 69 plots (2 m × 2 m) in 2009, the number of plots depending on the size of the site. The field and bottom layer vegetation was determined visually as a percentage cover of each species (scale 0; 0.1, 0.2, 0.3, 0.5; 1, 2, 3...98, 99, 100%). Tree and shrub saplings less than 50 cm in height were included. The peat profiles in the upstream parts of sites N1, N3, R1, and R3 were mixed with mineral soil. The layers had probably been formed by sedimented suspended solid material that had eroded from the ditches of the upstream drained peatlands and had been deposited in the buffer area. Water table levels were measured from plastic tubes inserted next to the gas sampling points, but redox conditions and oxygen concentrations were not determined. Peat chemistry is presented as an average of eight replicate samples of the 0-7.5-cm and the 7.5-15-cm layer of each site. Total carbon and total nitrogen content of peat (%) were determined by LECO CHN-1000 analyzer (ISO 10694:1995). P, Ca, Mg, and K content of peat (mg kg^{-1}) was analyzed by inductively coupled plasma atomic emission spectrometer (ICP-AES) after microwave wet digestion in HNO_3/HCl. Peat pH was measured in water (ISO 10390: 1994). Dissolved organic carbon (DOC) content of water (mg l^{-1}) was determined with Shimadzu TOC-5000 analyzer (SFS-EN 1484:1997), total nitrogen of water with Lachat Quickchem 8000 FIA analyzer (SFS-EN ISO 11905-1:1998), and pH of water with Denver 20 pH-meter (SFS 3021:1979).

Quantitative PCR. The abundance of methanogens and methanotrophs was compared by quantitative PCR (qPCR) of *mcrA* and *pmoA*. Reactions (20 µl) were run in duplicate in Rotor-Gene 6000 (Corbett Research, Australia) and contained 1 × qPCR master mix (Maxima qPCR kit, Fermentas, Lithuania), 0.375 µM of primers and 1 µl of template DNA. The primers for

pmoA were A189f (6) and A621r (10) and for *mcrA* mlas and mcra-rev (7, 9). The *mcrA* primers amplify the same region as the primers used in T-RFLP analysis. The program for *mcrA* qPCR was 95 °C for 10 min, 40 cycles of 95 °C for 30 s, 55 °C for 45 s and 72 °C for 30 s, followed by 72 °C for 7 min. The program for *pmoA* qPCR was the touchdown program used in end point PCR (10), but with initial denaturation of 10 min and 42 cycles. Fluorescence was measured at the end of extension step. Standards were 10^2, 10^3, 10^4, and 10^5 copies of *mcrA* fragment in plasmid DNA or purified *pmoA* PCR fragment. Standards were quantified with Qubit fluorometer (Invitrogen, Carlsbad, CA, USA). Primer dimers were not observed based on melting curves. Efficiency, calculated from the slope of standard curves, was 86.5% for *mcrA* and 94.3% for *pmoA* assays. Linear regression coefficients of the standard curves were r^2= 0.998 for both *mcrA* and *pmoA*. Presence of inhibitors was tested by spiking peat DNA samples with 10^6 copies of *mcrA* or 10^5 copies of *pmoA* standard DNA and comparing amplification results with unspiked samples. Inhibition percentage was calculated with formula $1-[(Ct_{sample} - Ct_{standard})/Ct_{standard})]\times100$ (3). Three field replicates from sites N3 and R2 were tested with both *mcrA* and *pmoA* qPCR. Two samples from R2 showed minor inhibition in *mcrA* qPCR (-2.3% and -0.5%), and the third one together with all samples of N3 and *pmoA* qPCR for both sites showed no inhibition. Results are given as gene copies per peat volume (cm^3) instead of dry weight of soil because of the variation in mineral soil content of the samples (Table 1).

Statistical analyses. Methane emissions rates and numbers of methanogens and methanotrophs of natural and restored sites were compared by nested analysis of variance (ANOVA) in SPSS (v. 15.0, SPSS Inc.). Emission rates were log-transformed. Methanogen and methanotroph community composition was compared by analysis of similarity (ANOSIM) with Past package

(5) with significance assessment by 10000 permutations. Within-site community variation of methanogens and methanotrophs was measured as multivariate dispersion by calculating distances from a centroid for replicates of each site with PERMDISP2 program (2). The distances of natural and restored sites were then compared using nested ANOVA. Methanogen and methanotroph data were analyzed in ANOSIM and multivariate dispersion as binary matrices based on presence or absence of T-RFs or sequenced DGGE bands using Dice distance measure. In addition, ANOSIM was carried out with relative abundances of *mcrA* T-RFs based on peak areas and Bray-Curtis distances. Level of statistical significance in all analyses was $P<0.05$.

Multivariate analyses were carried out with Canoco 4.52 (9) to explore variation of microbial communities, vegetation, and buffer area chemistry and to link the variation to environmental variables. The soil chemistry was explored using principal component analysis (PCA) with chemical characteristics as response variables. Initial detrended correspondence analyses (DCA) where detrending was conducted by segments showed high compositional variation in vegetation and methanogen communities. In both analyses, the length of first gradient was over 4, suggesting unimodal response to describe species distribution better than linear model, and DCA was therefore used to analyze vegetation and methanogen data. Methanogen data included the relative abundances of T-RFs based on peak areas. DCA of methanotroph communities showed a short first gradient (3.1), suggesting linear response to be sufficient to describe variation. We therefore applied PCA to analyze methanotroph communities. The environmental variables included in the analyses were CH_4 emission rate (growing season average), peat bulk density, peat carbon content, peat nitrogen content, peat Ca, Mg, and K content, water table level, dissolved organic carbon (DOC), total nitrogen and total

phosphorus of water, and pH of peat and water. In the analyses of microbial communities, chemical variables were introduced as the first two PCA axes of peat chemistry, and vegetation as the first two DCA axes of vegetation.

Analysis of T-RFLP data. The *mcrA* T-RFLP electropherograms were analysed with Peakscanner software (v. 1.0, Applied Biosystems). If close T-RFs could not be consistently aligned among samples, they were combined for further analyses to avoid misinterpretation (T-RFs 251+254 bp, 468+470 bp). Terminal restriction fragments (T-RFs) were assigned to phylogenetic groups by determining *in silico* terminal fragments of clone sequences in GeneDoc software (http://www.nrbsc.org/gfx/genedoc/) and by T-RFLP analysis of clones.

Phylogenetic analysis. Deduced McrA amino acid sequences and *pmoA* nucleotide sequences were screened with NCBI BLAST (http://www.ncbi.nlm.nih.gov/BLAST) and aligned with ClustalW (http://www.ebi.ac.uk/clustalw). Evolutionary models were selected with ProtTest (1) and FindModel (http://www.hiv.lanl.gov/content/sequence/findmodel/findmodel.html). Maximum likelihood trees were constructed with PhyML (4) with model LG+I+G+F for McrA and GTR+G for *pmoA*. The *pmoA* tree was constructed with nucleic acid sequences to better illustrate the differences between closely related sequences. Bootstrap values were generated from 100 replicates in PhyML.

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Table S1. Distribution of *mcrA* terminal fragments (T-RFs) in analysis of methanogen communities in natural (N1-3) and restored (R1-3) peatlands. Samples are field replicates of peat samples (n=7-8).

	T-RF (bp), % of total peak area													
site, sample	105	115	193	254	258	272	275	278	293	298	408	419	470	489
N1 A1	1.1	0	0	10.5	0	12.5	0	15.2	18.1	1.3	0	0	40	1.3
B1	0	0	0	7.9	0	0	0	30.1	7.4	0	3.1	0	46.9	4.5
B2	1	0	0	7.6	0	6.1	0	7.7	4.9	0	0	0	68.3	4.5
C5	0	0	0	9	0	11.3	0	0	25	0	0	0	43.4	11.3
C4	0	0	0	11.5	0	5.4	0	3.6	28.8	0	0	0	44.2	6.6
D4	1	0	0	8.4	0	1.1	0	30	8.2	1.4	3.8	0	46.1	0
D3	2.8	0	0	7.1	0	0	0	5.2	47.3	0	0	0	37.6	0
E2	0	0	0	8.4	0	7.8	0	3.3	32.3	0	0	0	40.2	7.9
N2 A1	0	0	0	6	0	10.6	0	0	12.1	0	8.9	0	53.9	8.5
B2	0	0	0	7.1	0	10.9	0	0	18.7	0	9	0	50.7	3.7
C2	0	0	0	6.8	0	8.9	0	0	38.2	0	5.5	0	38.4	2.1
C3	0	0	0	4.8	0	12.8	0	0	25.7	0	0	0	51.3	5.3
D1	0	0	0	4.7	0	10.9	0	0	29.2	0	4.6	0	47.1	3.6
D2	0	0	0	0	0	8.3	0	5.5	30.1	0	7.8	0	45.9	2.4
E3	0	0	0	3.9	0	7.8	0	0	32.5	0	17	0	35.7	3
N3 A1	0	0	0	13.2	0	6.5	0	13.7	10.5	1	0	0	52.9	2
B1	0	0	0	14.2	0	9.6	0	2.2	15	0	19.2	0	23.3	16.4
B2	0	0	0	8.6	0	19.1	0	8.8	13.7	0	3	0	45	1.9
C3	0	0	0	13.5	0	5.9	0	7.4	18.2	0	2.3	0	36.8	15.9
C4	0	0	0	15.4	0	16.1	0	9	6.8	3	2.3	0	39.9	7.6
D2	0	0	0	17.7	0	9	0	8.5	6.4	3.7	3.5	0	36.7	14.6
D3	0	0	0	11	0	11.7	0	7.5	11.1	1.3	2.8	0	38.1	16.5
E2	0	0	0	12.2	0	13.4	0	12.2	14.9	1.5	1.6	0	37.1	7.1
R1 A1	0	0	0	3.6	0	39.6	0	0	24.2	0	0	0	31.3	1.3
A2	0	0	0	5.6	0	48.8	2.3	0	16.6	0	0	0	26.7	0
B1	0	0	0	8.2	0	28.2	6.4	0	16.8	0	3	0	37.4	0
B2	0	0	0	0	0	10	0	7.5	71.7	0	0	0	10.8	0
C1	0	0	0	3.7	0	41.8	0	0	1.8	0	8.2	0	44.6	0
C2	0	0	0	2	0	22.1	0	2.4	54.6	0	0	0	19	0
D1	0	3.1	0	45.4	0	49.2	0	0	2.4	0	0	0	0	0
D2	0	0	0	0	0	14.6	0	0	0	0	0	0	0	85.4
R2 A2	0	0	0	2	0	0	0	3.5	2.1	0	33.8	0	53	5.6
B1	0	0	0	58.9	0	0	0	0	0	10.2	0	11.4	19.5	0
B3	0	0	0	18.5	0	0	0	0	0	2.2	29.7	0	42.2	7.4
B5	0	0	0	0	0	0	0	0	0	0	0	0	91.6	8.4
C3	0	0	0	1.9	2.4	0	0	0	0	71.8	0	7.7	0	16.2
C5	0	0	0	0	0	0	0	100	0	0	0	0	0	0
D1	0	0	0	2.2	0	0	0	0	0	0	0	0	61.3	36.5
R3 A1	0	0	0	14.1	0	18.6	0	3.4	16.2	0	0	0	47.8	0
B1	0	0	0	4.5	0	12.6	0	4.7	23	0	5.4	0	46.2	3.7
B2	0	0	0	3.4	0	9.7	0	3	40.5	0	1.4	0	26.1	15.8
C4	0	0	0	0	0	15.6	0	4.8	15.7	1	0	0	59.7	3.3
C3	0	0	2.9	0	0	3	0	2.2	63.6	0	0	0	26	2.1
D2	0	0	0	0	0	0	0	0	51.7	1.7	0	0	18.9	27.6
D3	0	0	1.1	12.1	0	0	0	0	22.4	2.3	2	0	5.5	54.6
E3	0	0	0	0	0	0	0	10.7	59.9	0	0	0	20.2	9.2

Table S2. Distribution of *pmoA* DGGE bands in analysis of methanotroph communities in natural (N1-3) and restored (R1-3) peatlands. Samples are biological replicates of peat samples (n=7-8).

		DGGE band					
site	sample	A10	A20	A19	A11	A15	A13
N1	A1	1	0	0	0	1	1
	B1	1	0	0	0	1	1
	B2	1	0	0	0	1	1
	C4	1	0	0	0	1	1
	C5	1	0	0	0	1	1
	D3	1	0	0	0	1	1
	D4	1	0	0	0	1	1
	E2	1	0	0	0	1	1
N2	A1	1	0	0	0	1	1
	B1	1	0	0	0	1	1
	B2	1	0	0	0	1	1
	C2	1	0	0	0	1	1
	C3	1	0	0	0	1	1
	D1	1	0	0	0	1	1
	D2	1	0	0	0	1	1
	E2	1	0	0	0	1	1
N3	A1	1	0	0	0	0	0
	B1	1	0	0	0	0	0
	B2	1	0	0	0	0	1
	C3	1	0	0	0	0	1
	C4	1	0	0	0	0	1
	D2	1	0	0	0	0	0
	D3	1	0	0	0	0	1
	E2	1	0	0	0	0	1
R1	A1	1	0	0	0	1	1
	A2	1	0	0	0	1	1
	B1	1	0	0	0	1	1
	B2	1	0	0	0	1	1
	C1	1	0	0	0	1	1
	C2	1	0	0	0	1	1
	D1	1	0	0	0	1	1
	D2	1	0	0	0	1	1
R2	A2	0	1	1	1	1	0
	B1	0	1	1	1	1	0
	B3	0	0	1	1	1	0
	B5	0	1	1	1	1	1
	C3	0	1	1	1	1	1
	C5	0	1	1	1	0	1
	D1	0	1	1	1	1	1
R3	A1	1	0	0	0	1	1
	B1	1	0	0	0	1	1
	B2	1	0	0	0	1	1
	C3	1	0	0	0	1	1
	C4	1	0	0	0	1	1
	D2	1	0	0	0	1	1
	D3	1	0	0	0	1	1