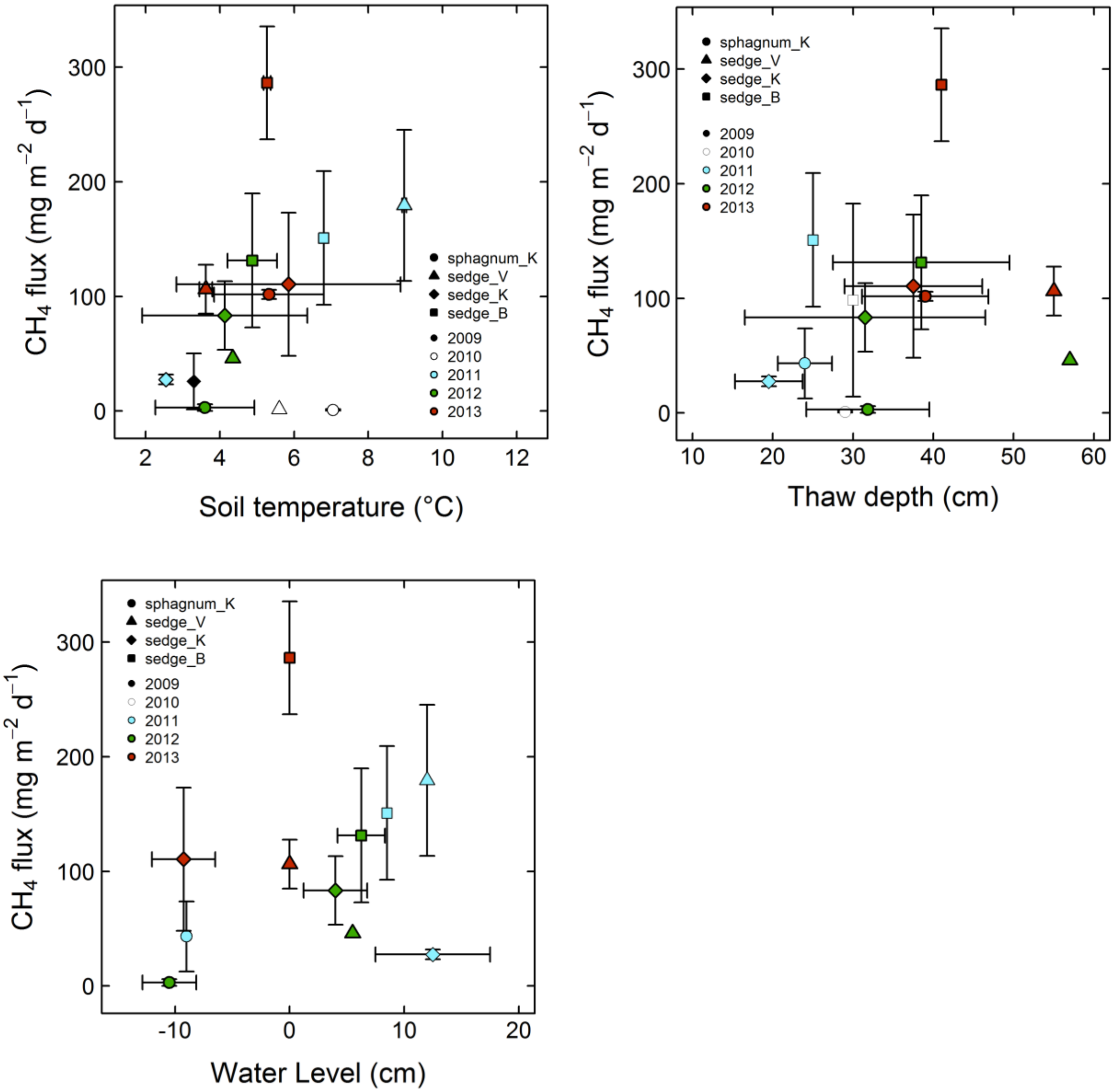

Figure S1. Averaged CH_4 flux over each wet area and each year plotted against (a) soil temperature (10 cm depth), (b) thaw depth, and (c) water level. Error bars represent standard deviations. Most observations for soil temperature and thaw depth were conducted at the same time of flux measurements, but not for all (Table S1).

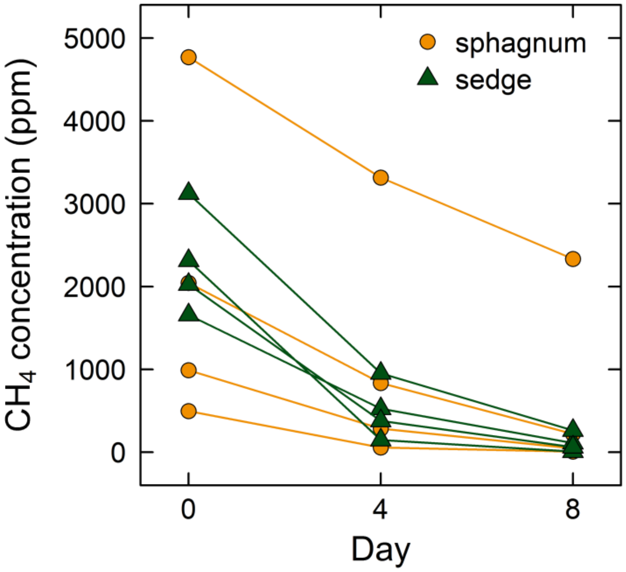

Figure S2. Declines in remaining CH_4 in headspace in the aerobic incubation experiment through CH_4 oxidation. Surface organic layers (0-13 cm) were incubated in quadruplicate at 8 °C.

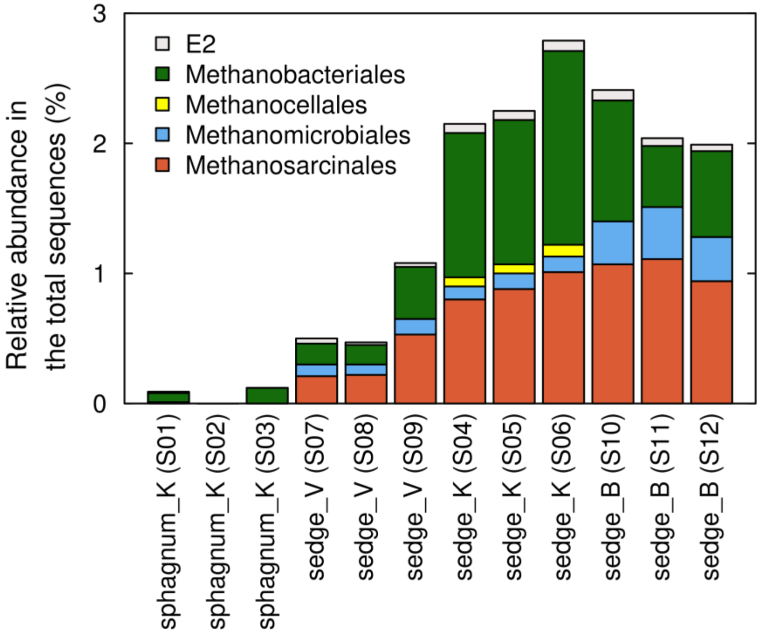

Figure S3. Phylogenetic compositions of methanogenic archaea by orders in wet areas. Soil samples (organic layers) were taken in triplicate from 10 cm depth in each wet area in July 2016. DNA was extracted from 3 g of the soil samples as described by Ikeda et al. (2004). Extracted DNA was purified using OneStep™ PCR Inhibitor Removal Kit (Zymo Research, Calif.) and quantified using the Quant-iT PicoGreen dsDNA assay Kit (Invitrogen, Carlsbad, Calif.). Amplicon sequencing was conducted targeting the V3/V4 regions of 16S rRNA genes (Caporaso et al. 2011). Sequences obtained were processed through the QIIME pipeline (Caporaso et al. 2010). A representative sequence was picked from each OTU and the Greengenes reference database (version 13.8) was used to assign taxonomic information and calculate the relative abundance of methanogenic archaea. See Table S3 for detailed results.

Table S1. Averaged CH_4 flux (in mg CH_4 m^{-2} day^{-1}) over each observation point and each year (2009–2013). Standard deviations are shown in case of $n \geq 3$. Dates of the flux observation are indicated in parenthesis. Superscripts represent observed environmental variables on each day: a) soil temperature (2009–2013), b) thaw depth (2010–2013), c) water level (2011–2013), and d) volumetric water content in surface soil (2011).

Observation points	Year				
	2009	2010	2011	2012	2013
tree mound_V	–	0 (Jul 16)	−1 ± 2 (Jul 23^{b}, 29^{abd})	0 (Aug 7^{ab})	0 (Aug 2^{ab})
sedge_V (wet area)	3 ± 3 (Jul 23)	2 (Jul 16^{a})	179 ± 66 (Jul 23^{c}, 29^{acd})	46 (Aug 7^{abc})	106 ± 21 (Aug 2^{abc})
tree mound_K	0 (Jul 22)	−1 ± 3 (Jul 21^{ab})	0 (Jul 15^{bd}, 18^{bd})	0 (Jul 3^{ab}, 8^{a}, 12^{ab}, 24^{ab}; Aug 2^{ab}, 6^{ab})	1 (Jul 15^{ab})
sphagnum_K (wet area)	–	1 ± 1 (Jul 21^{ab})	43 ± 31 (Jul 11^{bd}, 17^{b}, 18^{bcd}, 21^{bcd})	3 ± 3 (Jul 3^{abc}, 8^{abc},12^{abc}, 24^{abc}; Aug 2^{abc}, 6^{abc})	102 ± 4 (Jul 11^{ab}, 18^{ab}, 25^{ab}, 31^{ab})
sedge_K (wet area)	26 ± 24 (Jul 22^{a})	–	28 ± 4 (Jul 11^{bcd}, 17^{bc}, 18^{bcd}, 21^{abcd})	83 ± 30 (Jul 3^{abc}, 8^{abc}, 12^{abc},20^{abc}, 21^{a}, 24^{abc}; Aug 2^{abc}, 6^{abc})	111 ± 63 (Jul 11^{abc}, 18^{abc}, 25^{abc}, 31^{abc})
tree mound_B	–	0 (Jul 20^{b})	0 (Jul 9^{bd}, 30^{bd})	−1 ± 1 (Jul 13^{ab}, Aug 9^{ab})	0 (Jul 16^{ab})
sedge_B (wet area)	79 ± 80 (Jul 25)	98 ± 84 (Jul 20^{b})	151 ± 58 (Jul 9^{bcd}, 30^{acd})	131 ± 58 (Jul 13^{ab}, Aug 9^{abc})	286 ± 49 (Jul 16^{abc})

Table S2. Dissolved CH_4 concentration (in µmol L^{-1}) in surface water and soil pore water averaged over each wet area and each year. Standard deviations are shown in case of $n \geq 3$.

Wet area	Depth	Year		
		2011	2012	2013
sphagnum_K	surface water	–	–	–
	10 cm	6 ± 3	317	–
	20 cm	–	176 ± 125	399 ± 68
	30 cm	–	266	351
sedge_V	surface water	3 ± 2	6	105
	10 cm	30 ± 17	150	249
	20 cm	–	52	168
	30 cm	–	–	–
sedge_K	surface water	12 ± 14	8 ± 8	74 ± 27
	10 cm	53 ± 31	244 ± 143	88 ± 27
	20 cm	–	368 ± 59	431 ± 123
	30 cm	–	519	450 ± 55
sedge_B	surface water	14	8 ± 14	4
	10 cm	21	380	392
	20 cm	–	351	322
	30 cm	–	–	194

Table S3. Phylogenic composition of methanogenic archaea in wet areas. Soils (organic layers) were sampled in July 2016 from 10 cm depth in the same wet areas as the CH_4 production incubation experiment in triplicate. Then, microbial communities in the samples were analyzed by amplicon sequencing of 16S rRNA gene. See Fig. S4 for a plot by the level of orders.

Order	Family	Genus	Relative abundance in the total sequences (%)											
			sphagnum_K (S01)	sphagnum_K (S02)	sphagnum_K (S03)	sedge_V (S07)	sedge_V (S08)	sedge_V (S09)	sedge_K (S04)	sedge_K (S05)	sedge_K (S06)	sedge_B (S10)	sedge_B (S11)	sedge_B (S12)
Methanosarcinales	Methanosarcinaceae	*Methanosarcina*	0.01	0.00	0.00	0.21	0.09	0.47	0.06	0.08	0.08	0.25	0.20	0.16
	Methanosaetaceae	*Methanosaeta*	0.00	0.00	0.00	0.00	0.13	0.06	0.74	0.80	0.93	0.82	0.91	0.78
Methanomicrobiales	Methanoregulaceae	*Candidatus* Methanoregula	0.00	0.00	0.00	0.09	0.07	0.10	0.10	0.10	0.11	0.23	0.32	0.28
	Methanospirillaceae	*Methanospirillum*	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.00	0.01
	Methanoregulaceae	Other Methanoregulaceae	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.02	0.01	0.08	0.08	0.05
Methanocellales		Methanocellales	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.07	0.09	0.00	0.00	0.00
Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	0.07	0.00	0.12	0.16	0.15	0.40	1.11	1.11	1.49	0.93	0.47	0.66
E2	[Methanomassiliicoccaceae]	[Methanomassiliicoccaceae]	0.01	0.00	0.00	0.04	0.02	0.03	0.07	0.07	0.08	0.08	0.06	0.05