

Supporting information for:

**Mercury methylating microbial community structure in boreal wetlands  
explained by local physicochemical conditions**

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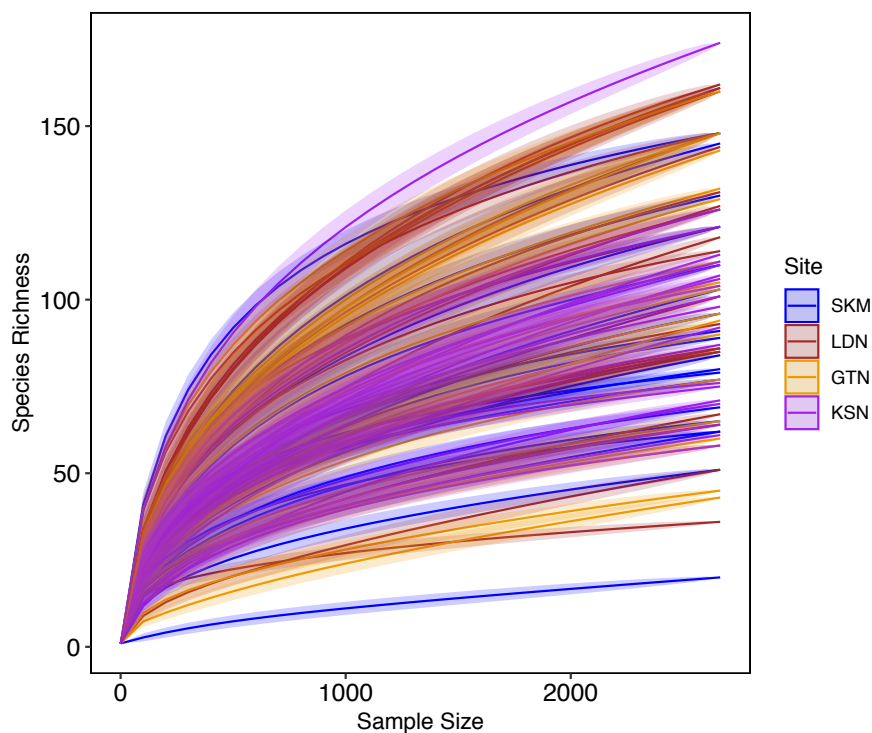
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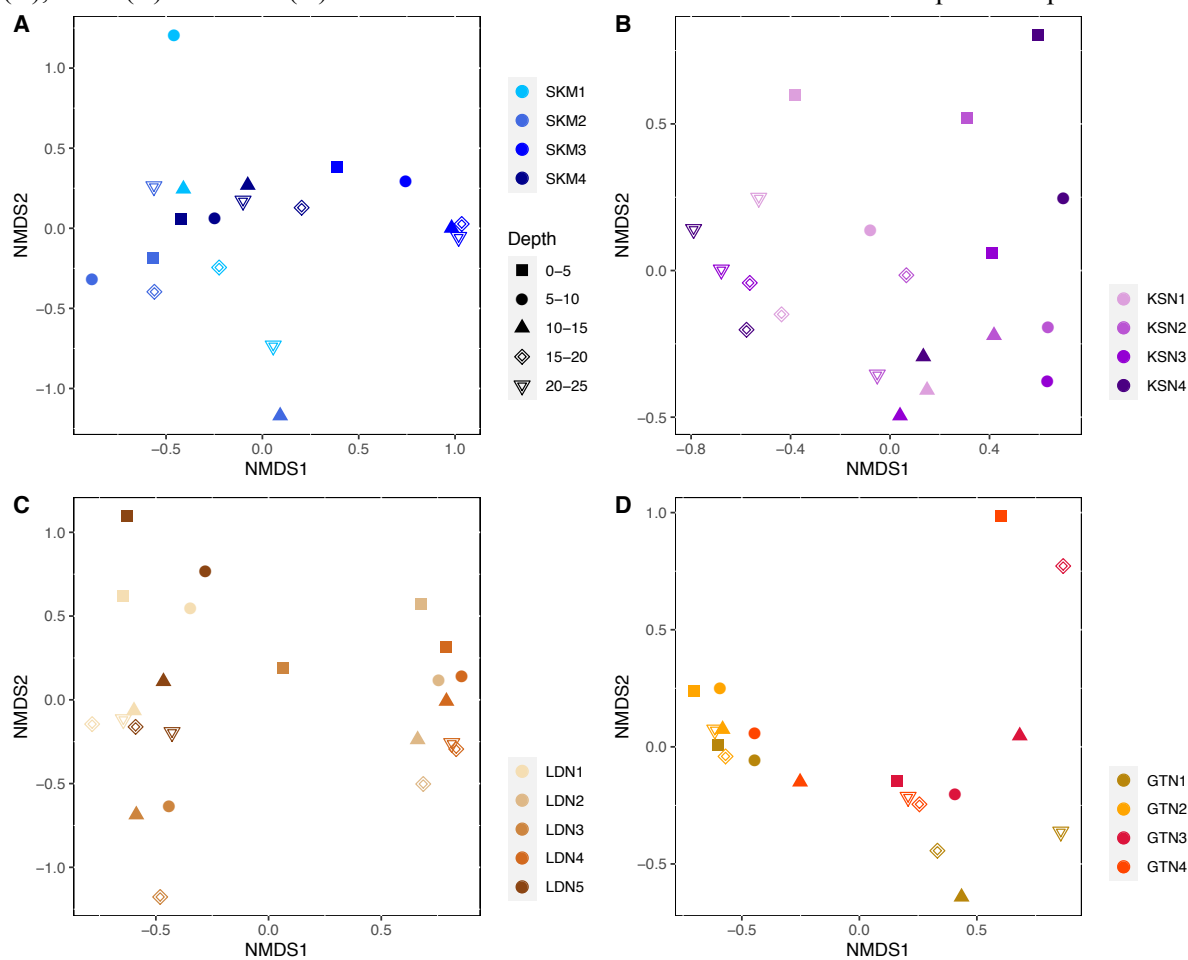
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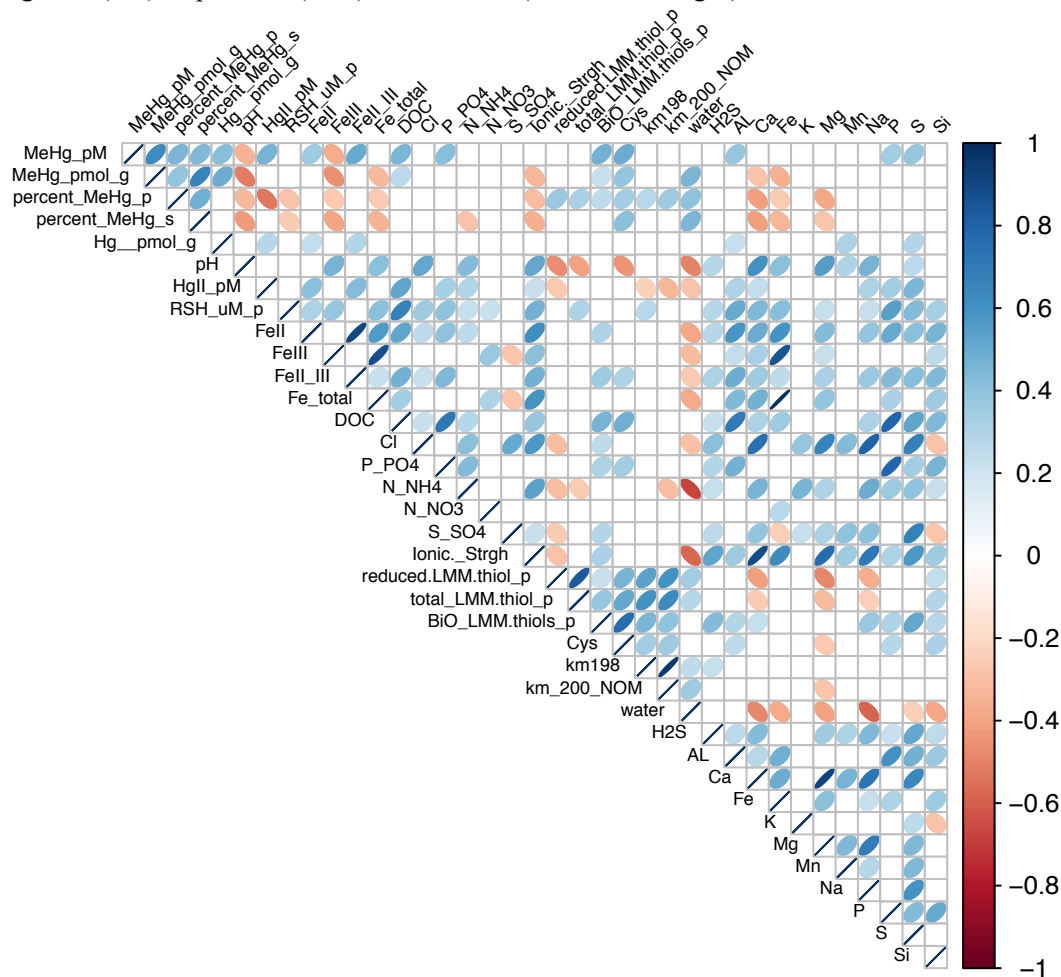
**Figure S1.** Rarefaction curve of the *hgcA* gene. Each line represents a wetland soil sample and is coloured by the site it was collected (blue: SKM; dark brown: LDN, orange: GTN; purple: KSN).



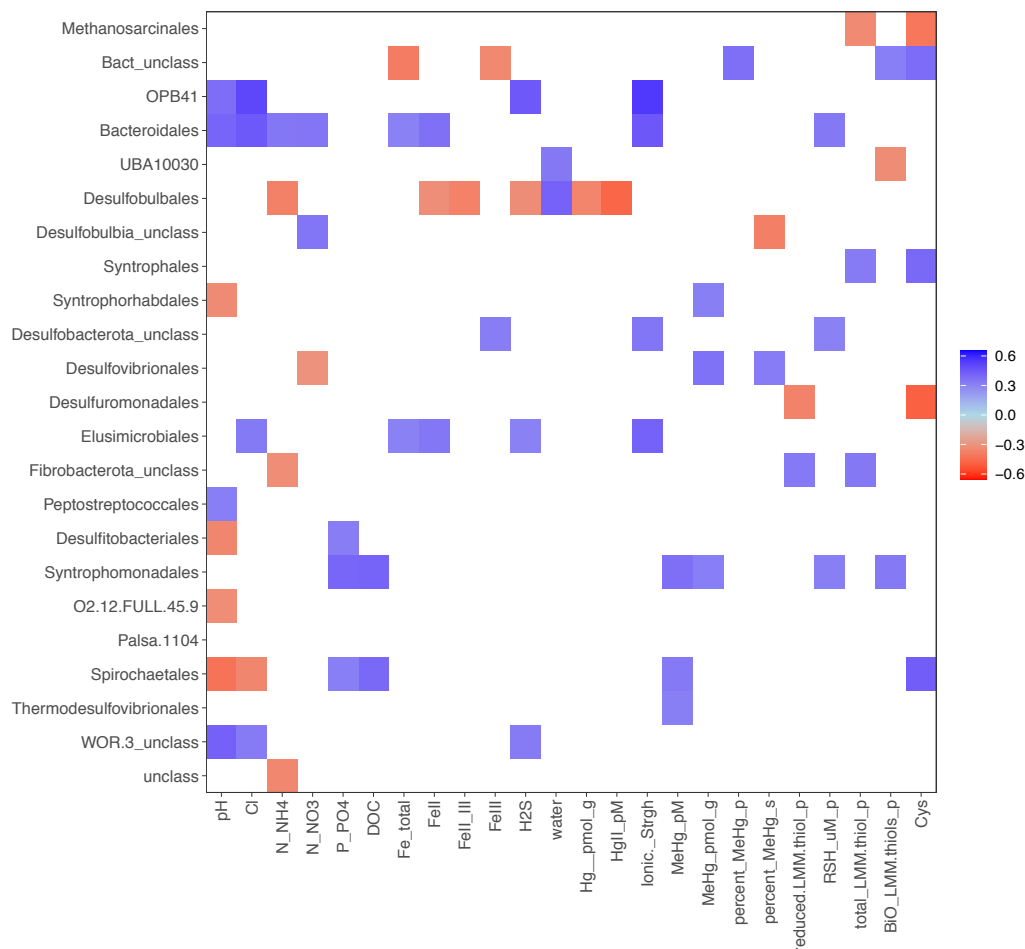
**Figure S2.** Nonmetric multidimensional scaling (NMDS) ordination of Hg<sup>II</sup> methylating microbial communities based on the Bray–Curtis dissimilarity of community composition at SKM (A), KSN (B), LDN (C) and GTN (D). Sites within a wetland are color coded and core-depth is shaped-coded.



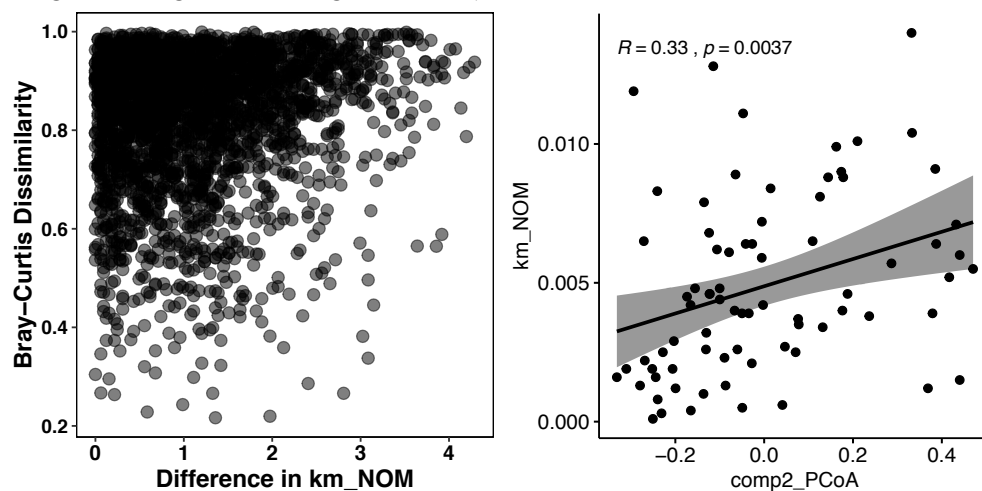
**Figure S3.** Significant ( $p < 0.05$ ) spearman correlations between different physicochemical parameters. The ellipses have their eccentricity parametrically scaled to the Pearson correlation value (narrower ellipses represents higher correlation values). The orientation of the ellipse indicates negative (red) or positive (blue) correlations (scale on the right).



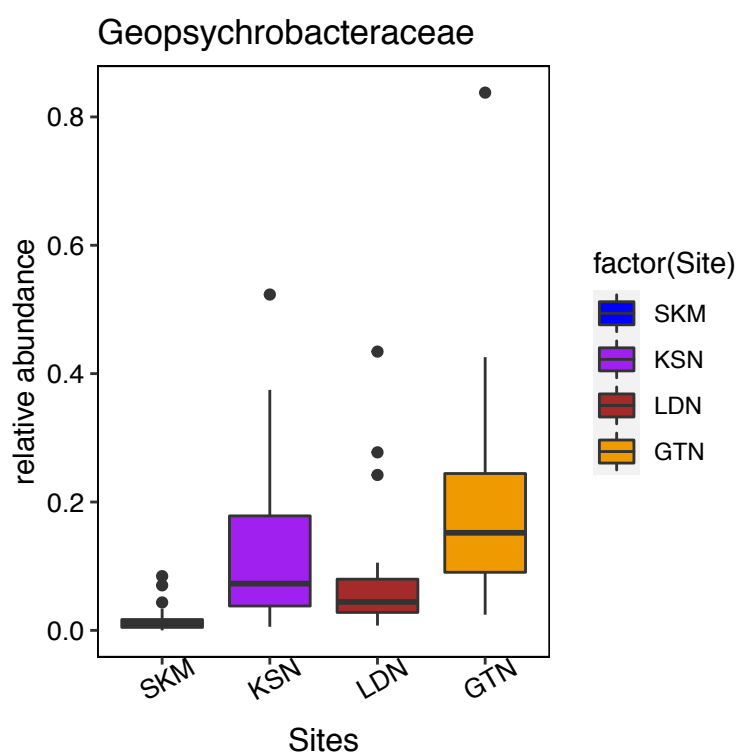
**Figure S4.** Heat map of *Spearman* significant ( $p < 0.05$ ) correlations between environmental variables and *hgcA*+ taxa at order level detected in the studied wetland soils. Colors represent the significant p-values of *Spearman* correlations. Red stands for negative significant correlations and blue for positive and significant correlations (scale on the right).



**Figure S5.** Left panel: Correlation plot (Mantel  $R = 0.13$ ,  $p$ -value = 0.003) between *hgcA*+ microbial community (Bray Curtis) dissimilarity and the Euclidean distance of  $k_m$  ( $k_m$  of spiked inorganic- $^{200}\text{Hg}$  bound to organic matter). Right panel: Regression analyses between the second component of the Principal coordinate analysis performed with the *hgcA*+ microbial community and  $k_m$  ( $k_m$  of spiked inorganic- $^{200}\text{Hg}$  bound to organic matter).



**Figure S6.** Relative abundance (%) of *hgcA*+ Geopsychrobacteraceae family at the different studied wetlands.



**Table S1.** Characterisation of the boreal wetlands. SKM: Storkälsmyran, KSN: Kroksjön, LDN: Långedalen and GTN: Gästern. All data presented in this table were extracted from Liem et al., (2020).

Location	Depth	Hg <sup>II</sup>	MeHg	$k_{\text{meth}}^{(198\text{Hg}^{\text{II}})}$	$k_{\text{meth}}^{(200\text{Hg}^{\text{II}}-\text{NOM})}$	Dry weight	DOC	P-PO <sub>4</sub>	N-NH <sub>4</sub>
		pmol g <sup>-1</sup>	pmol g <sup>-1</sup>	d <sup>-1</sup>	d <sup>-1</sup>	%	mg/L	µg L <sup>-1</sup>	µg L <sup>-1</sup>
SKM-1	0-5	600	41.4	0.0204	0.006	10.7	60.6	6.6	100
SKM-1	5-10	695	45.7	0.0442	0.0119	9.26	63.41	1.2	10.1
SKM-1	10-15	491	39	0.0384	0.0083	13.1	68.43	2.1	15.5
SKM-1	15-20	405	41	0.0096	0.0019	15.3	66.87	10	19.3
SKM-1	20-25	452	41.8	0.0062	0.0019	14.4	68.03	18	41.2
SKM-2	0-5	1010	93.9	0.0293	0.0065	11.9	66.85	51	597
SKM-2	5-10	752	97.4	0.012	0.0022	13.7	68.22	145	1490
SKM-2	10-15	607	48.5	0.0091	0.0016	14.5	66.61	111	1080
SKM-2	15-20	499	30	0.0083	0.0016	15.8	73.97	194	1550
SKM-2	20-25	552	47.2	0.014	0.0029	12.2	72.56	131	1190
SKM-3	0-5	501	53.3	0.0201	0.0057	18.1	68.82	12	58.6
SKM-3	5-10	619	87.5	0.0209	0.0037	17.2	70.07	2.8	40.3
SKM-3	10-15	608	24.4	0.0379	0.0062	17.5	52.04	2.6	33.1
SKM-3	15-20	584	13.7	0.0374	0.0068	17.7	53.49	6	37.3
SKM-4	0-5	652	39.2	0.0202	0.0046	15.9	71.02	5.4	27.3
SKM-4	5-10	659	50.2	0.0367	0.0088	15.6	68.3	2.5	12.9
SKM-4	10-15	424	44.4	0.0486	0.0088	18.6	88.81	17	110
SKM-4	15-20	360	40.7	0.0329	0.0059	16.8	85.41	26	137
SKM-4	20-25	349	15.5	0.0303	0.0065	18.9	84.72	39	397
LDN-1	0-5	945	92	0.0182	0.0046	6.11	67.4	1.2	22.9
LDN-1	5-10	1290	133	0.0327	0.0048	6.41	71.38	5.3	9.06
LDN-1	10-15	818	135	0.0568	0.0101	4.31	77.55	9.7	7.92
LDN-1	15-20	1260	163	0.0351	0.0064	5.97	62.17	13	22.4
LDN-1	20-25	1500	132	0.0169	0.0042	6.62	55.88	14	57.6
LDN-2	0-5	88.8	13.4	0.001	0.0001	19.7	44.93	1	90.6
LDN-2	5-10	353	13.7	0.0019	0.0003	27.8	39.45	2	121
LDN-2	10-15	225	6.11	0.0062	0.001	44	38.92	1.8	150
LDN-2	15-20	115	2.79	0.0038	0.0004	61.4	39.59	3.1	432

LDN-3	10-15	638	50.6	0.0212	0.0038	8.12	35.88	1.8	3.6
LDN-3	15-20	969	17.5	0.0043	0.0006	6.88	33.88	3.4	14.7
LDN-4	0-5	822	45.9	0.0087	0.0012	19.1	19.3	0.6	144
LDN-4	5-10	876	54.7	0.0138	0.0019	20.5	18	0.8	167
LDN-4	10-15	731	28	0.0079	0.0013	23.6	17.77	1	629
LDN-4	15-20	497	12.5	0.0129	0.0025	33.9	28.09	1	4490
LDN-4	20-25	687	68.8	0.0044	0.0008	42.2	26.44	1.1	4120
LDN-5	0-5	998	70.7	0.002	0.0005	3.11	80.75	5.4	32.7
LDN-5	5-10	1120	94.2	0.0106	0.0021	2.7	89.46	4.9	10.9
LDN-5	10-15	1200	72.8	0.005	0.0012	5.47	93.86	7.3	50.1
LDN-5	15-20	1020	55.2	0.0271	0.0039	12.9	145	18	47.5
LDN-5	20-25	567	24	0.0105	0.0015	13.5	235.6	23	64.2
GTN-1	0-5	422	11.1	0.0338	0.0045	11.6	49.12	6.2	1070
GTN-1	5-10	453	6.44	0.0189	0.004	23.7	57.5	3.7	1770
GTN-1	10-15	371	2.96	0.0404	0.0071	25.4	61.84	8.2	1970
GTN-1	15-20	381	3.97	0.0378	0.0052	22.6	83.75	73	4730
GTN-1	20-25	543	7.16	0.0446	0.0055	22.9	87.7	90	4740
GTN-2	0-5	461	8.75	0.0364	0.0079	8.2	31.36	1.1	45.7
GTN-2	5-10	457	3.64	0.0257	0.0048	18.1	32.44	2.4	66.4
GTN-2	10-15	428	4.81	0.0271	0.0044	22	46.96	2	79.4
GTN-2	15-20	456	6.8	0.0251	0.0039	24.7	62.6	2.2	152
GTN-2	20-25	535	79.6	0.0221	0.004	19.4	71.37	2.5	111
GTN-3	0-5	525	39.3	0.0376	0.009	8.8	131.3	2.8	1030
GTN-3	5-10	705	11.5	0.022	0.0046	10.5	139.6	3	1110
GTN-3	10-15	402	2.68	0.0163	0.0034	27	440.5	61	2050
GTN-4	0-5	725	85.3	0.05	0.0089	7.03	67.68	8.5	3610
GTN-4	5-10	1210	43.7	0.0879	0.0128	14	80.99	16	3850
GTN-4	10-15	643	4.67	0.0168	0.0026	26.7	116.1	20	4280
GTN-4	15-20	534	2.21	0.0167	0.0027	28.7	222.3	67	12500
GTN-4	20-25	565	4.52	0.0131	0.0023	25.9	294.6	29	13500
KSN-1	0-5	406	19.4	0.0063	0.0013	4.6	31.63	12	84.5
KSN-1	5-10	559	38.2	0.0137	0.0035	7.44	24.27	5.2	58.3
KSN-1	10-15	933	11.6	0.0339	0.0064	10	28.12	1.4	25.9
KSN-1	15-20	534		0.0323	0.0072	11	21.84	1.3	27.2
KSN-2	0-5	253	17.8	0.0111	0.0025	4.85	48.74	27	13.4
KSN-2	5-10	385	23.4	0.0312	0.006	4.71	57.55	1.5	9.9
KSN-2	10-15	308	31.5	0.0335	0.0091	6.15	53.96	2.3	12.1
KSN-2	15-20	464	24.3	0.0487	0.0099	4.53	39.21	1	12.5
KSN-2	20-25	182	37.3	0.0243	0.0064	7.03	38.22	1.3	20.2
KSN-3	0-5	202	20.9	0.0356	0.0084	4.18	34.11	2.2	20.6
KSN-3	5-10	244	15.1	0.0373	0.0081	4.71	38.89	1.7	11.5
KSN-3	10-15	296	21.3	0.0541	0.0111	4.97	45.96	2.7	11.4
KSN-3	15-20	710	10.8	0.0125	0.0032	5.83	41.76	1.4	10
KSN-3	20-25	823	1.92	0.0194	0.0042	10.6	39.12	1	9.5
KSN-4	0-5	144	18.8	0.0166	0.0039	4.04	41.91	3.2	20
KSN-4	5-10	259	19.7	0.0468	0.0104	4.39	43.46	2.1	18.3
KSN-4	10-15	283	21.2	0.0708	0.014	5.97	38.98	1.7	16.2
KSN-4	15-20	649	17	0.026	0.0061	11.3	39.59	1.2	12.3
KSN-4	20-25	406	3.06	0.0111	0.0026	30.4	36.49	1.3	17.1

**Table S2.** Characterisation of the boreal wetlands. SKM: Storkålsmyran, KSN: Kroksjön, LDN: Långedalen and GTN: Gästern. All data presented in this table were extracted from Liem et al., (2020).

No	pH	H <sub>2</sub> S μM	Hg <sup>II</sup> pM	BiO Total		RSH (ads) μmol g <sup>-1</sup>	SO <sub>4</sub> <sup>2-</sup> Total		Cl <sup>-</sup> mg L <sup>-1</sup>	Fe <sup>II</sup> μM	Fe <sup>III</sup> μM	DOC mg L <sup>-1</sup>	K mg L <sup>-1</sup>	Al mg L <sup>-1</sup>	Mn μg L <sup>-1</sup>	P μg L <sup>-1</sup>	N-NO <sub>3</sub> μg/L	
				MeHg pM	LMMLM nM		S mg L <sup>-1</sup>	S mg L <sup>-1</sup>										
SKM-1	4.2	<0.3	482	4.9	5	48		1.6	2.2	2.3	6.2	31	61	0.2	0.5	13	45	60.32
SKM-1	4.17	7.5	155	6.1	15	62	13	0.5	1.1	2.1	18	16	63	0.1	0.6	14	50	13.96
SKM-1	4.16	0.4	61	8.8	13	58		0.4	1.1	1.9	18	25	68	0.1	0.7	14	38	15.92
SKM-1	4.21	<0.3	126	9	3.5	20		0.2	1	1.8	24	19	67	0.3	0.7	15	94	16.87
SKM-1	4.25	<0.3	159	8.7	4.3	22		0.2	0.9	1.8	36	9	68	0.1	0.7	15	82	17.63
SKM-2	4.46	<0.3	40	17	8.1	40		<0.1	0.8	2.9	12	26	67	0.4	0.6	11	157	19.7
SKM-2	4.61	4.9	129	14	3.9	26	15	<0.1	0.8	2.2	21	15	68	0.6	0.6	10	316	20.21
SKM-2	4.66	14	48	16	3.2	29		0.2	0.8	2.3	18	20	67	0.5	0.6	10	261	23.91
SKM-2	4.58	9.6	58	13	2.6	21		<0.1	0.9	1.6	36	9.4	74	0.7	0.8	11	426	20.91
SKM-2	4.72	11	109	26	3.9	22		<0.1	0.8	2	38	9.5	73	0.7	0.9	13	316	41.29
SKM-3	4.56	<0.3	57	8.5	7.5	27	13	<0.1	0.7	2.9	11	46	69	1	0.7	18	76	11.69
SKM-3	4.8	2.5	38	18	5.1	34	6.9	0.5	1.3	2.3	14	62	70	0.1	0.9	22	33	17.66
SKM-3	4.91	0.7	108	9.1	9	54	12	0.4	1	1.2	13	73	52	<0.06	0.6	22	30	9.45
SKM-3	4.97	7.8	75	2.4	6.9	47	11	<0.1	0.8	0.5	16	100	53	<0.06	0.5	27	48	33.13
SKM-4	4.6	<0.3	67	15	5.6	29		<0.1	0.7	2.8	10	49	71	0.3	0.7	10	38	40.04
SKM-4	4.67	<0.3	70	11	6.5	29	9.5	<0.1	0.7	2.9	11	53	68	0.5	0.6	7	40	17.51
SKM-4	4.69	<0.3	70	13	9.9	44		<0.1	0.8	2.8	14	78	89	0.4	0.8	10	83	22.32
SKM-4	5.62	5.1	76	9.1	7.8	25		<0.1	0.8	2.8	15	90	85	0.4	0.9	12	100	22.65
SKM-4	4.7	3	52	8.8	7.7	25		<0.1	0.8	2.7	17	77	85	0.4	1	15	108	22.36
LDN-1	4.2	<0.3	82	23	6.9	35	3.9	4.1	4.6	8.2	18	18	67	2.4	1.1	179	34	13.08
LDN-1	4.5	44	44	72	21	61	6.4	3.6	4.3	8.4	47	15	71	1.7	1.2	167	51	10.38
LDN-1	4.4	19	59	92	37	102	9.9	0.6	1.7	9.8	56	7.5	78	0.7	1.4	142	70	10.72
LDN-1	4.54	51	41	19	11	71	13	0.1	1.2	9.6	43	7.1	62	0.2	1.1	110	47	16.61
LDN-1	4.78	34	23	7.4	8.5	47	20	<0.1	1.2	9.1	40	8.3	56	0.1	0.9	97	45	13.23
LDN-2	5.64	<0.3	77	6.8	3.2	13		0.3	0.8	9.7	2.7	25	45	0.6	0.5	99	<20	17.93
LDN-2	5.87	<0.3	41	3.9	3.5	13	2.8	0.1	0.7	8.8	8	70	39	0.6	0.5	197	<20	36.86
LDN-2	5.9	<0.3	38	3.2	2.9	20		0.1	0.6	8.8	6.4	51	39	0.6	0.4	183	<20	26.3
LDN-2	5.89	<0.3	30	2.7	3	16		0.1	0.6	8.3	90	60	40	0.6	0.5	<1	<20	13.09
LDN-3	5.17	1.1	68	21	4.5	11		0.4	0.9	7.7	30	28	36	0.3	0.9	<1	25	29.36
LDN-3	5.16	10	138	8.6	0.9	4.6		0.3	0.9	8.4	40	13	34	<0.06	1	170	21	35.75
LDN-4	5.64	<0.3	101	5.1	3.1	12		1	1.2	7.2	0.1	13	19	1	0.2	219	<20	16.5
LDN-4	6.06	0.4	221	4.8	2.4	8.5	6.3	1	1.2	7	0.1	16	18	0.9	0.2	208	<20	13.98
LDN-4	5.6	<0.3	35	5.8	2.5	9.8		0.9	1.1	7	0.1	26	18	1	0.1	<1	<20	15.68
LDN-4	5.84	<0.3	145	5.3	2.5	1.5		<0.1	0.3	5.9	352	58	28	1	0.1	<1	<20	22.7
LDN-4	5.8	1.7	45	4.3	1.1	5.5		<0.1	0.3	7.1	10	220	26	1.4	0.2	<1	<20	36.92
LDN-5	4.74	<0.3	74	8.7	3.1	14	4	<0.1	0.6	5.9	4.5	32	81	0.2	0.4	98	53	13.99
LDN-5	4.73	<0.3	246	12	5.4	21	5.8	0.1	0.9	7.6	5.5	59	89	0.7	0.9	119	52	17.17
LDN-5	5.02	0.4	216	3.3	2.6	15	6.1	0.1	0.9	7	4.9	61	94	0.3	0.7	132	60	43.88
LDN-5	4.9	1	179	9.5	6.9	22	9.1	<0.1	1.2	6.2	23	82	145	0.1	0.8	90	89	42.77
LDN-5	4.99	0.7	159	5.5	3.6	15	9.1	<0.1	1.9	5.9	60	42	236	0.1	1.3	55	123	55.45
GTN-1	5.61	21	59	3.9	3.1	20	17	1.3	2.3	12	4.1	52	49	1.6	0.3	57	51	42.06
GTN-1	5.61	11	50	4.4	4	17	7.9	1	2.2	12	4	32	58	1.8	0.7	71	53	11.68
GTN-1	5.5	23	30	3.6	7.1	28	6.3	1	2.3	12	5.8	57	62	1.8	0.8	82	86	10.78
GTN-1	5.62	13	52	3.8	4.2	26	7.6	0.2	2	11	17	114	84	3.2	1.1	50	327	13.61
GTN-1	5.54	13	261	2.8	4.3	24	7.7	<0.1	2	11	25	123	88	3.2	1.1	21	374	12.07
GTN-2	6.1	270	23	4.1	3.9	26		3.9	4.6	14	1.5	11	31	0.4	0.3	71	<20	7.95
GTN-2	5.86	190	58	2.9	3.4	15		2.6	3.4	14	2.4	17	32	0.5	0.3	77	24	44.23
GTN-2	5.93	49	37	1.8	2.3	7.8		0.3	1.7	15	26	62	47	0.1	0.4	98	32	31.32
GTN-2	6.06	180	31	3.1	5.3	22		0.2	2.2	13	90	124	63	0.1	0.5	116	54	31.37
GTN-2	5.86	120	31	4.2	5.1	29		0.1	2.6	13	165	112	71	0.1	0.9	120	106	33.91
GTN-3	4.79	<0.3	47	6.9	4.5	23		1.2	4.9	7.1	18	60	131	6.3	2.1	139	130	65.23
GTN-3	4.5	<0.3	164	4.5	4.6	28		1.2	5	7.5	22	68	140	5.8	2.1	145	132	63.75
GTN-3	4.88	<0.3	556	7.6	4.1	45		0.3	11	13	375	269	440	1.3	3.8	<1	458	52.52
GTN-4	6.16	13	31	11	5.5	32		0.9	3.6	9.9	5	159	68	0.9	0.6	59	69	46.41
GTN-4	6.08	17	31	16	14	38		0.6	4.1	9.4	47	150	81	0.7	0.9	79	106	54.96
GTN-4	6.09	10	140	16	3.5	13		0.3	4.9	9	164	138	116	0.6	1.2	91	171	36.95
GTN-4	5.97	10	442	16	2.1	33		<0.1	7.9	7.2	172	183	222	1.6	2.9	53	300	34.8

GTN-4	5.93	27	217	6.7	1.7	23		<0.1	12	9	317	109	295	2.1	4.5	68	305	68.6
KSN-1	4.64	<0.3	23	3.2	4.1	27		0.2	0.5	1.2	1.1	24	32	1.5	0.2	2	65	44.12
KSN-1	4.45	<0.3	17	3.5	3.3	21	9.4	<0.1	0.3	0.9	0.7	36	24	0.5	0.3	4	32	39.36
KSN-1	4.73	<0.3	4.4	4.2	0.2	36		<0.1	0.4	0.6	1.7	78	28	0.2	0.5	24	38	40.83
KSN-1	4.81	<0.3	2.2	3.6	4.7	63		<0.1	0.3	0.5	0.2	63	22	0.2	0.4	21	29	45.7
KSN-2	4.65	<0.3	34	5.2	3.6	8.8		0.3	0.8	3	3.6	44	49	0.9	0.6	3	113	25.46
KSN-2	4.81	<0.3	30	6.7	3.9	8.4	6.6	0.1	0.8	2.6	7.4	81	58	0.2	0.9	6	56	23.48
KSN-2	4.85	<0.3	22	4	0.5	18		0.1	0.7	2.5	6.6	102	54	0.3	0.8	10	54	28.43
KSN-2	5.36	<0.3	30	2.8	1.9	24		<0.1	0.5	2.1	4.5	247	39	0.1	0.6	30	45	34.23
KSN-2	5.82	<0.3	17	1.8	1.6	7.1		<0.1	0.5	2.3	129	178	38	0.6	0.7	59	53	35.16
KSN-3	4.62	0.4	10	3.2	3.3	48	5.3	<0.1	0.4	2.2	0.1	24	34	0.5	0.5	8	<20	42.02
KSN-3	5.54	1.4	40	3.2	3.3	64	9.9	<0.1	0.5	2.2	0.1	28	39	0.6	0.5	8	23	31.37
KSN-3	4.77	4	25	2.7	2.7	49	22	<0.1	0.6	1.4	1.1	71	46	0.3	0.9	14	38	27.77
KSN-3	5.04	6.8	19	1.9	1.8	29	22	<0.1	0.6	1.2	2.2	135	42	0.2	1.1	27	26	22.56
KSN-3	5.42	4.8	19	1.8	2	22	11	<0.1	0.5	1.3	1.5	145	39	0.3	1.1	30	27	22.76
KSN-4	4.6	<0.3	19	3.2	3.6	45		<0.1	0.5	3.5	0.1	22	42	1.6	0.3	4	38	46.27
KSN-4	4.7	<0.3	31	3.9	3.5	119	10	<0.1	0.5	3.2	0.7	33	43	0.9	0.4	6	35	30.37
KSN-4	4.96	<0.3	13	2.9	2.4	126		<0.1	0.7	3	1.7	93	39	0.4	0.4	26	33	30.59
KSN-4	5.3	<0.3	41	1.4	2.3	44		<0.1	0.7	3	17	140	40	0.3	0.5	37	40	29.21
KSN-4	5.32	<0.3	29	0.7	0.6	47		<0.1	0.6	2.8	136	122	36	0.6	0.8	64	48	37.8



**Table S3.** Relative hgcA sequence abundances (%) at levels of phyla, class, order and family for the combined 81-sample dataset that included all four wetlands. Taxonomic levels are indicated with stepwise indents. Mean  $\pm$  SD: standard deviation.

phylum	class	order	Northern		Southern	
			SKM	KSN	GTN	LDN
			mean std	mean std	mean std	mean std
<b>Archaea</b>			<b>0.30<math>\pm</math>0.54</b>	<b>3.38<math>\pm</math>3.67</b>	<b>3.63<math>\pm</math>4.65</b>	<b>3.26<math>\pm</math>3.91</b>
<b>Halobacterota</b>	Methanosarcinia	Methanosarcinales	0.28 $\pm$ 0.48	3.33 $\pm$ 3.47	3.22 $\pm$ 3.05	3.24 $\pm$ 3.85
<b>Thermoplasmatota</b>	Thermoplasmata	Methanomassiliicoccales	0.02 $\pm$ 0.05	0.01 $\pm$ 0.04	0.01 $\pm$ 0.01	0.02 $\pm$ 0.05
	unclass	unclass	0.00 $\pm$ 0.00	0.04 $\pm$ 0.17	0.40 $\pm$ 1.59	0.00 $\pm$ 0.00
<b>Bacteria</b>						
<b>Unclass</b>	unclass	Bact_unclass	<b>51.78<math>\pm</math>22.05</b>	<b>32 <math>\pm</math>18.5</b>	<b>21.2<math>\pm</math>17.86</b>	<b>34.1<math>\pm</math>20.7</b>
<b>Acidobacteriota</b>			<b>0.84<math>\pm</math>1.61</b>	<b>0.32<math>\pm</math>0.31</b>	<b>0.19<math>\pm</math>0.20</b>	<b>0.79<math>\pm</math>1.17</b>
	Acidobacteriae	Bryobacteriales	0.05 $\pm$ 0.08	0.01 $\pm$ 0.02	0.00 $\pm$ 0.00	0.00 $\pm$ 0.00
	UBA6911	unclass	0.79 $\pm$ 1.54	0.31 $\pm$ 0.30	0.19 $\pm$ 0.20	0.79 $\pm$ 1.17
<b>Actinobacteriota</b>			<b>5.29<math>\pm</math>14</b>	<b>21.9<math>\pm</math>33</b>	<b>9.43<math>\pm</math>13</b>	<b>1.99<math>\pm</math>4</b>
	Coriobacteriia	OPB41	4.43 $\pm$ 11.16	18.08 $\pm$ 18.17	8.78 $\pm$ 11.47	0.40 $\pm$ 0.37
	unclass	unclass	0.86 $\pm$ 2.84	3.86 $\pm$ 14.50	0.65 $\pm$ 1.32	1.59 $\pm$ 3.15
<b>Bacteroidota</b>			<b>1.12<math>\pm</math>2</b>	<b>0.94<math>\pm</math>1</b>	<b>2.16<math>\pm</math>2</b>	<b>3.57<math>\pm</math>6</b>
	Bacteroidia	Bacteroidales	0.01 $\pm$ 0.02	0.32 $\pm$ 0.52	0.04 $\pm$ 0.12	0.10 $\pm$ 0.49
	UBA10030	UBA10030	1.12 $\pm$ 2.01	0.63 $\pm$ 0.78	2.11 $\pm$ 2.06	3.46 $\pm$ 5.02
<b>Chloroflexota</b>			<b>0.01<math>\pm</math>0.05</b>	<b>0.00<math>\pm</math>0.01</b>	<b>0.00<math>\pm</math>0.00</b>	<b>0.00<math>\pm</math>0.01</b>
	Anaerolineae	Anaerolineales	0.00 $\pm$ 0.00	0.00 $\pm$ 0.01	0.00 $\pm$ 0.00	0.00 $\pm$ 0.01
	Dehalococcoidia	Dehalococcoidales	0.01 $\pm$ 0.05	0.00 $\pm$ 0.00	0.00 $\pm$ 0.00	0.00 $\pm$ 0.00
<b>Desulfobacterota</b>			<b>1.97<math>\pm</math>3.19</b>	<b>0.98<math>\pm</math>1.63</b>	<b>0.23<math>\pm</math>0.49</b>	<b>1.57<math>\pm</math>3.96</b>
	BSN033	SM23-61	0.01 $\pm$ 0.04	0.00 $\pm$ 0.00	0.00 $\pm$ 0.00	0.00 $\pm$ 0.00
	Desulfobacteria	Desulfobacteriales	0.00 $\pm$ 0.00	0.00 $\pm$ 0.00	0.00 $\pm$ 0.01	0.00 $\pm$ 0.01
	Desulfobulbia	Desulfobulbales	0.00 $\pm$ 0.00	0.00 $\pm$ 0.00	0.00 $\pm$ 0.01	0.66 $\pm$ 2.04
	Desulfobulbia	unclass	0.01 $\pm$ 0.03	0.20 $\pm$ 0.42	0.04 $\pm$ 0.07	0.24 $\pm$ 0.80
	Desulfomonilia	UBA1062	0.00 $\pm$ 0.00	0.00 $\pm$ 0.00	0.01 $\pm$ 0.02	0.01 $\pm$ 0.03
	Syntrophia	Syntrophales	1.39 $\pm$ 1.99	0.26 $\pm$ 0.35	0.05 $\pm$ 0.05	0.45 $\pm$ 0.70
	Syntrophorhabdia	Syntrophorhabdales	0.42 $\pm$ 0.83	0.05 $\pm$ 0.15	0.12 $\pm$ 0.32	0.03 $\pm$ 0.05
	unclass	unclass	0.13 $\pm$ 0.29	0.47 $\pm$ 0.71	0.01 $\pm$ 0.03	0.18 $\pm$ 0.34
<b>Desulfobacterota_A</b>			<b>8.91<math>\pm</math>11.55</b>	<b>3.19<math>\pm</math>5.65</b>	<b>6.85<math>\pm</math>12.46</b>	<b>0.99<math>\pm</math>1.17</b>
	Desulfovibronia	Desulfovibrionales	8.91 $\pm$ 11.55	3.19 $\pm$ 5.65	6.85 $\pm$ 12.46	0.99 $\pm$ 1.17
<b>Desulfuromonadota</b>			<b>3.86<math>\pm</math>2.72</b>	<b>15.44<math>\pm</math>14.12</b>	<b>23.31<math>\pm</math>18.74</b>	<b>12.9<math>\pm</math>11.82</b>
	Desulfuromonadia	Desulfuromonadales	3.84 $\pm$ 2.67	15.43 $\pm$ 14.10	23.31 $\pm$ 18.74	12.89 $\pm$ 11.81
		unclass	0.02 $\pm$ 0.05	0.00 $\pm$ 0.00	0.00 $\pm$ 0.00	0.00 $\pm$ 0.00
<b>Elusimicrobiota</b>			<b>0.58<math>\pm</math>1.53</b>	<b>1.22<math>\pm</math>2.03</b>	<b>0.64<math>\pm</math>1.61</b>	<b>0.03<math>\pm</math>0.06</b>
	Elusimicrobia	Elusimicrobiales	0.58 $\pm$ 1.53	1.22 $\pm$ 2.03	0.64 $\pm$ 1.61	0.03 $\pm$ 0.05
	Endomicrobia	unclass	0.00 $\pm$ 0.00	0.00 $\pm$ 0.00	0.00 $\pm$ 0.00	0.00 $\pm$ 0.01
<b>Fibrobacterota</b>			<b>0.79<math>\pm</math>1.69</b>	<b>0.19<math>\pm</math>0.49</b>	<b>0.17<math>\pm</math>0.30</b>	<b>0.40<math>\pm</math>0.63</b>
	OXYB2-FULL-49-7	OXYB2-FULL-49-7	0.13 $\pm$ 0.24	0.13 $\pm$ 0.38	0.05 $\pm$ 0.09	0.13 $\pm$ 0.37

	unclass	unclass	0.65±1.46	0.06±0.11	0.12±0.21	0.27±0.27
<b>Firmicutes_A</b>			<b>0.02±0.09</b>	<b>0.02±0.04</b>	<b>0.00±0.01</b>	<b>0.01±0.03</b>
	Clostridia	Clostridiales	0.00±0.00	0.00±0.00	0.00±0.00	0.00±0.01
	Clostridia	Peptostreptococcales	0.02±0.09	0.02±0.04	0.00±0.01	0.00±0.02
<b>Firmicutes_B</b>			<b>2.11±4.56</b>	<b>1.09±1.71</b>	<b>1.16±2.79</b>	<b>0.63±1.60</b>
	Desulfitobacteriia	Desulfitobacteriales	0.88±2.87	0.00±0.01	0.00±0.00	0.01±0.03
	Desulfotomaculia	Desulfotomaculales	0.02±0.07	0.01±0.04	0.00±0.00	0.10±0.49
	Syntrophomonadia	Syntrophomonadales	1.21±1.62	1.08±1.66	1.16±2.79	0.52±1.08
<b>Firmicutes_C</b>	Negativicutes	unclass	<b>0.00±0.01</b>	<b>0.00±0.00</b>	<b>0.00±0.00</b>	<b>0.00±0.00</b>
<b>Goldbacteria</b>	PGYV01	unclass	<b>0.00±0.00</b>	<b>0.00±0.00</b>	<b>0.02±0.04</b>	<b>0.00±0.00</b>
<b>Margulisbacteria</b>	WOR-1	O2-12-FULL-45-9	<b>0.09±0.19</b>	<b>0.00±0.01</b>	<b>0.00±0.00</b>	<b>0.00±0.00</b>
<b>Myxococcota</b>	Polyangia	Palsa-1104	<b>0.06±0.19</b>	<b>0.08±0.19</b>	<b>0.00±0.00</b>	<b>0.01±0.02</b>
<b>Nitrospirota</b>	Thermodesulfovibrionia	Thermodesulfovibrionales	<b>0.68±0.48</b>	<b>0.36±0.45</b>	<b>0.55±0.85</b>	<b>0.31±0.45</b>
<b>Spirochaetota</b>			<b>1.50±1.79</b>	<b>0.14±0.18</b>	<b>0.06±0.14</b>	<b>0.18±0.20</b>
	Spirochaetia	Spirochaetales	1.50±1.79	0.14±0.18	0.05±0.13	0.18±0.19
	UBA6919	GWB1-36-13	0.00±0.00	0.00±0.00	0.00±0.01	0.00±0.01
<b>Synergistota</b>	Synergistia	Synergistales	<b>0.00±0.00</b>	<b>0.00±0.02</b>	<b>0.00±0.00</b>	<b>0.00±0.00</b>
<b>Verrucomicrobiota</b>			<b>0.07±0.12</b>	<b>0.00±0.02</b>	<b>0.00±0.01</b>	<b>0.04±0.13</b>
	Kiritimatiellae	LD1-PB3	0.00±0.00	0.00±0.01	0.00±0.00	0.00±0.01
	Lentisphaeria	unclass	0.07±0.12	0.00±0.01	0.00±0.01	0.04±0.12
<b>WOR-3</b>	WOR-3	unclass	<b>1.00±2.88</b>	<b>0.42±0.60</b>	<b>0.11±0.15</b>	<b>0.45±1.64</b>
<b>Unclass</b>	unclass	unclass	<b>19.01±13.71</b>	<b>18.27±11.42</b>	<b>30.25±13.78</b>	<b>38.8±15.51</b>