# Supplementary Online Material:

Contents:
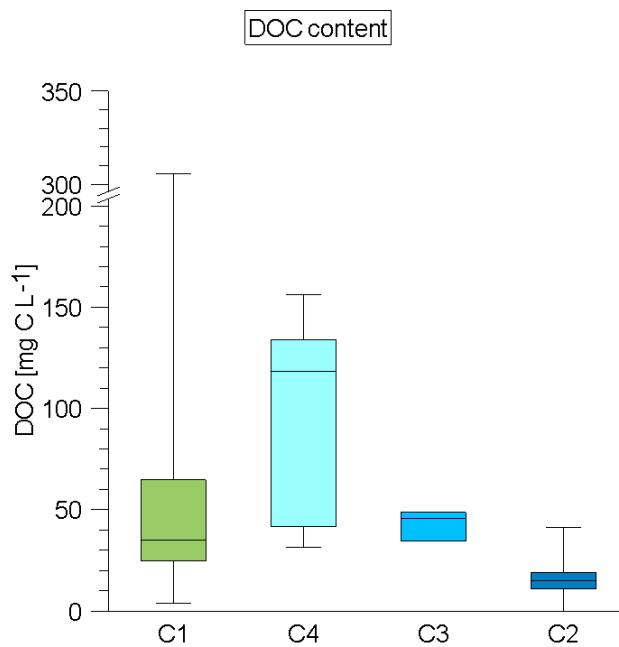
Figure S1: Boxplot of DOC concentrations of Unit II in mg C L^{-1}. Median lines are indicated within the boxes of which the size corresponds to±25% of the data, whereas the whiskers show the minimum and maximum of all data. C1: n=74, C4: n=5, C3: n=3, C2: n =12.
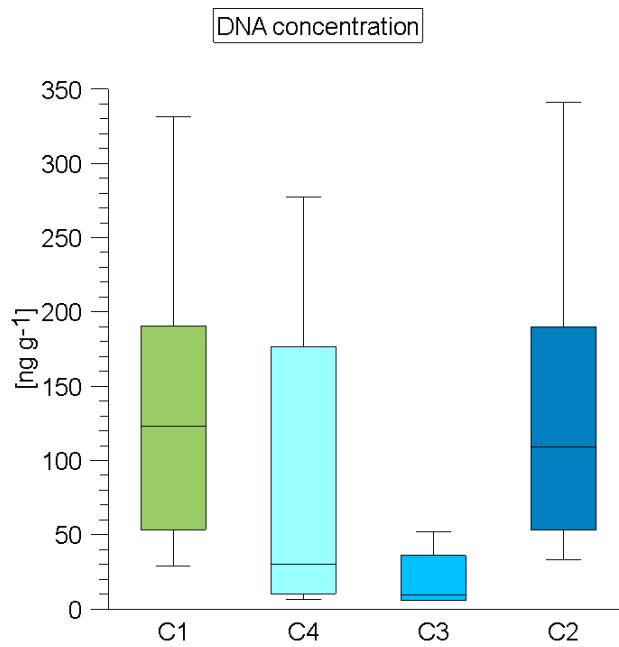
Figure S2: DNA concentrations in ng g^{-1} sediment wet weight of the cores C1, C4, C3 and C2. Box plots contain the mean values of all samples, obtained from two technical replicates each. Median lines are indicated within the boxes of which the size corresponds to ± 25% of the data, whereas the whiskers show the minimum and maximum of all data. C1, C4 and C3: n=6, C2: n=17.
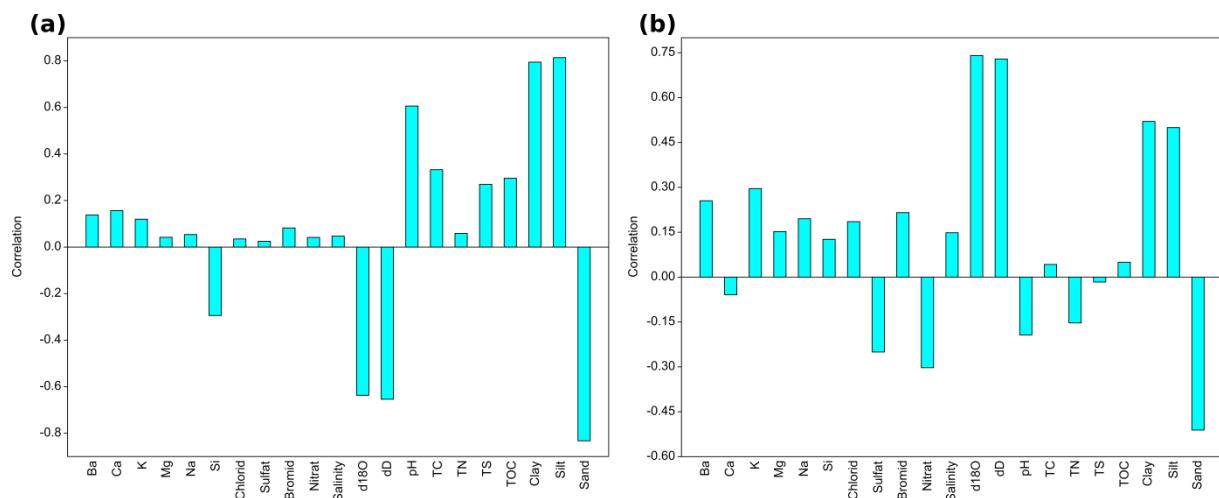
Figure S3: Loadings plots belonging to Figure 3: PCA of environmental, sedimentological and pore water data from Unit II. Shown are the correlations to a) PC1 and b) PC2 which were used to choose the physicochemical factors that are mainly responsible for the variance between samples in the PCA.
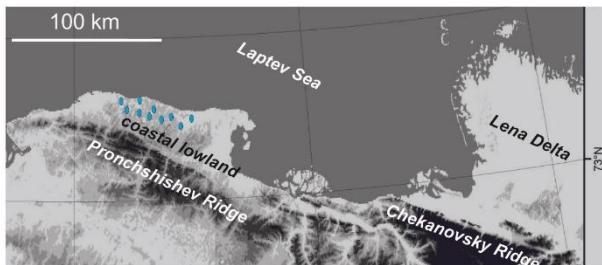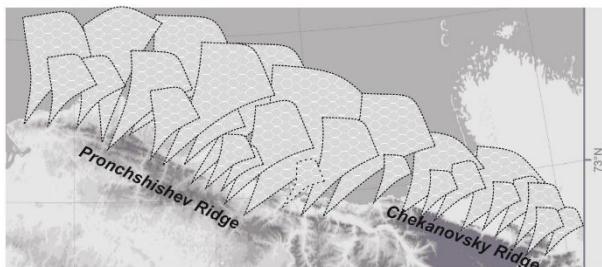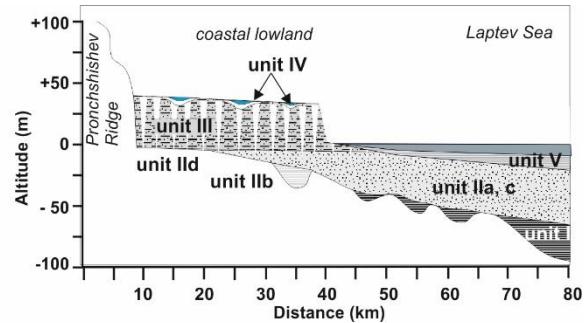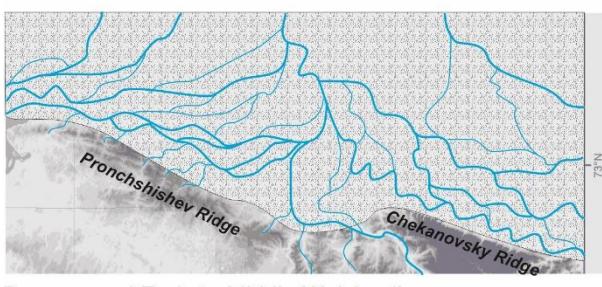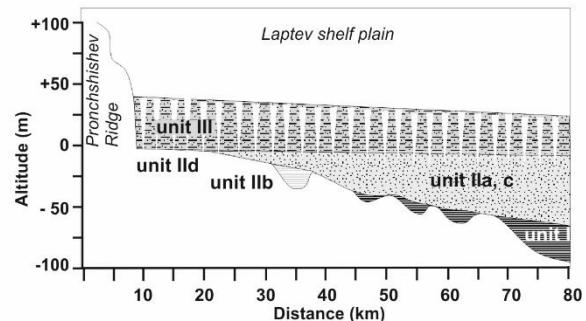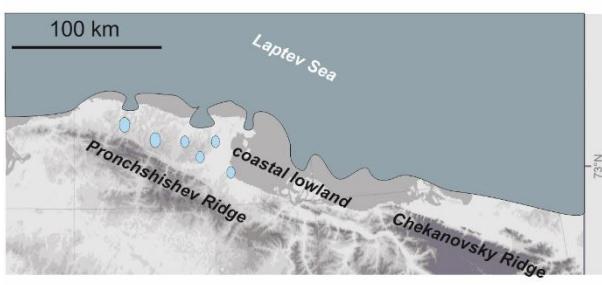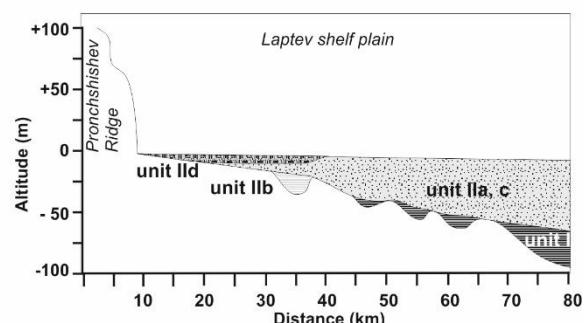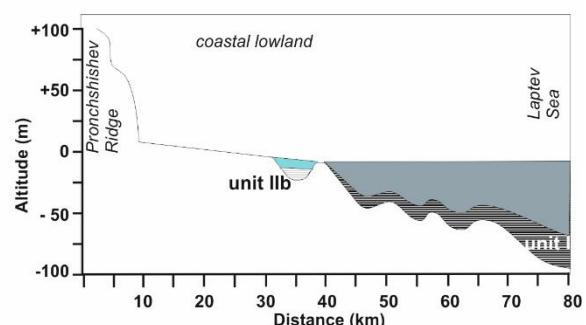
Figure S4: Schematic representation of the late Quaternary landscape dynamics in the western Laptev Sea coastal region and formation of the sediments units (modified after Winterfeld et al. (2011)).

Table S1: Site description of each borehole location. Mbsf stands for meters below sea floor and dedicates the depth in the submarine cores (C4, C3, C2), while mbs stands for meters below surface and is used for depth indication in the terrestrial core C1.

|	C1	C4	C3	C2
Distance to coast [km]	- 0.1	1.0	3.0	11.5
Water depth [m]	-	2.2	4.4	6.0
Frost table depth [mbsf]	0.0	1.7	7.6	29.0
Upper boundary of Unit II [mbs/mbsf]	22.0	13.3	8.6	35.0
Lower boundary of Unit II	61.0	29.8	27.1	58.5
Uppermost sample depth [mbs/mbsf]	27.3	13.3	8.6	38.5
Lowermost sample depth	44.3	29.8	24.9	58.4

Table S2: Minimum, maximum and mean values of environmental factors in Unit II significantly contributing to the bacterial community composition and microbial abundance.

	Core	Minimum	Maximum	Mean	Std.Dev.	n
Temperature [°C]	C1	-12.5	-12.4	-12.4	0.0	8
	C4	-7.1	-5.8	-6.4	0.5	4
	C3	-1.8	-1.2	-1.4	0.2	4
	C2	-1.6	-1.5	-1.5	0.0	4
Salinity [PSU]	C1	0.0	1.6	0.5	0.4	184
	C4	0.9	17.6	5.6	4.8	10
	C3	0.5	3.7	1.0	0.6	38
	C2	0.0	12.5	0.8	1.7	67
$\delta 18O$ [(‰) vs. SMOW]	C1	-30.8	-14.9	-22.3	4.0	184
	C4	-27.7	-18.8	-22.8	3.0	10
	C3	-20.6	-19.1	-20.1	0.3	38
	C2	-30.0	20.2	-27.6	1.5	67
δD [(‰) vs. SMOW]	C1	-241.8	-115.7	-177.2	32.9	184
	C4	-219.1	-144.0	-178.8	25.7	10
	C3	-162.9	-149.4	-158.4	2.9	38
	C2	-232.7	-156.8	-213.3	11.3	67

Table S3: Geochemical, pore water and environmental data of all samples at each drill site.

See "SuppInfo_Table_3"

Table S 4: Sample names of the molecular samples, their depth relative to sea level (meters below sea level, m bsl), relative to surface (meters below surface (m bs) in the terrestrial core and meters below sea floor (m bsf) in the submarine cores), and their corresponding lithology.

Sample Name	Depth [m bsl]	Depth [m bs/ m bsf]	Lithology
C1-1	1.3	27.3	sandy
C1-2	9.9	35.9	sandy
C1-3	12.1	38.1	sandy
C1-4	17.2	43.2	plant/wood detritus
C1-5	17.4	43.4	plant/wood detritus
C1-6	18.4	44.4	plant/wood detritus
C4-1	15.5	13.3	plant/wood detritus
C4-2	22.0	19.8	small peat inclusions
C4-3	25.0	22.8	small peat inclusions
C4-4	28.5	26.3	sandy with quartz gravel
C4-5	30.0	27.8	sandy with quartz gravel
C4-6	32.0	29.8	sandy with quartz gravel
C3-1	13.0	8.6	small peat inclusions
C3-2	16.0	11.6	small peat inclusions
C3-3	19.0	14.6	small peat inclusions
C3-4	21.5	17.1	sandy
C3-5	24.6	20.2	sandy
C3-6	29.2	24.8	sandy
CK1232	44.5	38.5	
C2-1	46.0	40.0	sandy
C2-2	48.1	42.1	sandy
CK1235	49.3	43.3	
CK1236	50.7	44.7	
CK1237	51.8	45.8	
C2-4	52.2	46.2	sandy
C2-5	54.6	48.6	plant/wood detritus
CK 1241	54.7	48.7	
C2-7	55.0	49.0	plant/wood detritus
C2-8/1244	56.1	50.1	plant/wood detritus
CK1245	57.8	51.8	
CK1246	58.2	52.2	
CK1247	58.7	52.7	
CK1248	61.6	55.6	
C2-9	62.9	56.9	plant/wood detritus
C2-10	64.4	58.4	sandy silt

Table S5: Oligonucleotide primers for Illumina MiSeq sequencing and quantitative PCR.

Target	Primer Sets	Primer Sequence 5'-3'	Size bp	T (°C)	No. of PCR Cycles	References
Illumina MiSeq sequencing						
Bacterial 16S rRNA	S-D-Bact-0341-b-S-17	CCT ACG GGA GGC AGC AG	464	55	35	(Muyzer et al., 1993)
	S-D-Bact-0785-a-A-21	GAC TAC HVG GGT ATC TAA TCC				(Herlemann et al., 2011)
Quantitative PCR						
Bacterial 16S rRNA	S-D-Bact-0341-b-S-17	CCT ACG GGA GGC AGC AG	193	55.7	40	(Muyzer et al., 1993)
	S-D-Bact-0517-a-A-18	ATT ACC GCG GCT GCT GG				(Muyzer et al., 1993)

Table S6: Barcode sequences for Illumina MiSeq sequencing.

Barcode ID Forward Primer	Barcode Sequence	Barcode ID Reverse Primer	Barcode Sequence
Bac-01-For	ACGAGTGCGT	Bac-01-Rev	ACGAGTGCGT
Bac-02-For	ACGCTCGACA	Bac-02-Rev	ACGCTCGACA
Bac-03-For	AGACGCACT	Bac-04-Rev	AGCACTGTAG
Bac-06-For	ATATCGCGAG	Bac-05-Rev	ATCAGACACG
Bac-07-For	CGTGTCTCTA	Bac-06-Rev	ATATCGCGAG
Bac-08-For	CTCGCGTGT	Bac-07-Rev	CGTGTCTCTA
Bac-11-For	TGATACGTCT	Bac-08-Rev	CTCGCGTGTC
Bac-13-For	CATAGTAGTG	Bac-11-Rev	TGATACGTCT
Bac-15-For	ATACGACGTA	Bac-13-Rev	CATAGTAGTG
Bac-16-For	TCACGTACTA	Bac-14-Rev	CGAGAGATAC
Bac-17-For	CGTCTAGTA	Bac-17-Rev	CGTCTAGTAC
Bac-19-For	TGTACTACT	Bac-18-Rev	TCTACGTAGC
Bac-23-For	TACTCTCGTG	Bac-19-Rev	TGTACTACTC
Bac-24-For	TAGAGACGAG	Bac-22-Rev	TACGAGTATG
Bac-25-For	TCGTCGCTCG	Bac-23-Rev	TACTCTCGTG
Bac-26-For	ACATACGCGT	Bac-24-Rev	TAGAGACGAG
Bac-27-For	ACGCGAGTAT	Bac-25-Rev	TCGTCGCTCG
Bac-28-For	ACTACTATGT	Bac-26-Rev	ACATACGCGT
Bac-31-For	AGCGTCGTCT	Bac-28-Rev	ACTACTATGT
Bac-33-For	ATAGAGTACT	Bac-30-Rev	AGACTATACT
Bac-34-For	CACGCTACGT	Bac-31-Rev	AGCGTCGTCT
Bac-35-For	CAGTAGACGT	Bac-33-Rev	ATAGAGTACT
Bac-36-For	CGACGTGACT	Bac-34-Rev	CACGCTACGT
Bac-38-For	TACACGTGAT	Bac-35-Rev	CAGTAGACGT
Bac-39-For	TACAGATCGT	Bac-36-Rev	CGACGTGACT
Bac-40-For	TACGCTGTCT	Bac-37-Rev	TACACACACT
Bac-41-For	TAGTGTAGAT	Bac-38-Rev	TACACGTGAT
Bac-42-For	TCGATCACGT	Bac-39-Rev	TACAGATCGT
Bac-44-For	TCTAGCGACT	Bac-40-Rev	TACGCTGTCT

Bac-45-For	TCTATACTAT	Bac-41-Rev	TAGTGTAGAT
Bac-49-For	ACGCGATCGA	Bac-44-Rev	TCTAGCGACT
Bac-50-For	ACTAGCAGTA	Bac-45-Rev	TCTATACTAT
		Bac-46-Rev	TGACGTATGT
		Bac-49-Rev	ACGCGATCGA
SfiA-MW00	ACACGT	SfiB-MW10	CAGTCA
SfiA-MW01	ACGTAC	SfiB-MW11	CATGAC
SfiA-MW02	ACTGCA	SfiB-MW12	GACTAG
SfiA-MW02	ACTGCA	SfiB-MW13	GAGATC
SfiA-MW03	AGAGTC	SfiB-MW14	GATCGA
SfiA-MW04	AGCTGA	SfiB-MW14	GATCGA
SfiA-MW05	AGTCAG	SfiB-MW15	GTACAC
SfiA-MW06	ATATCG	SfiB-MW15	GTACAC
SfiA-MW07	ATCGAT	SfiB-MW16	GTCACA
		SfiB-MW17	GTGTGT
		SfiB-MW18	TCAGAG
		SfiB-MW19	TCGAGA

Table S 7: Overview of sequencing reads: number of reads after the removal of singletons, number of reads that were removed when the background filter of 0.5% was applied, number of reads representing chloroplast, mitochondrial and archaeal taxa and finally the number of quality reads after the application of all filters. Critical samples with less than 15.000 raw reads are shaded red. Critical samples where the relative abundances within duplicates are comparable are colored light red. The dark red colored sample was not used for the calculation of the mean relative abundance as the relative abundances within duplicates differed.

	Raw reads	Background Reads (0.5%)	Chloroplast	Mitochondrial Taxa	Archaeal taxa	Quality reads
C1-1a	74760	20214	0	0	0	54546
C1-1b	89992	22879	0	0	0	67113
C1-2a	23789	15150	0	0	0	8639
C1-2b	25100	16330	0	0	0	8770
C1-3a	41727	24707	0	0	0	17020
C1-3b	8666	5185	0	0	0	3481
C1-4a	31071	22620	0	0	0	8451
C1-4b	5142	3761	0	0	0	1381
C1-5a	208578	100128	0	0	0	108450
C1-5b	147753	69180	0	0	0	78573
C1-6a	244866	100302	0	0	1790	142774
C1-6b	255535	113256	0	0	6331	135948
C4-1a	231425	70205	0	0	0	161220
C4-1b	103692	30996	0	0	0	72696
C4-2a	312930	64767	0	0	0	248163
C4-2b	18603	2840	0	0	0	15763
C4-3a	269853	99103	1765	0	0	168985
C4-3b	94463	33930	0	0	0	60533
C4-4a	170018	49851	0	0	1050	119117

C4-4b	180556	52147	0	0	0	128409
C4-5a	9823	4402	0	0	0	5421
C4-5b	17374	7566	0	0	0	9808
C4-6a	56201	23871	0	0	0	32330
C4-6b	20949	8951	0	0	0	11998
C3-1a	52885	27176	0	0	588	25121
C3-1b	180772	94154	1165	0	2402	83051
C3-2a	35528	13955	0	0	1511	20062
C3-2b	102122	39090	652	0	4780	57600
C3-3a	73935	22562	0	0	0	51373
C3-3b	25589	7940	0	0	0	17649
C3-4a	53553	16543	0	0	1899	35111
C3-4b	22552	6552	0	0	398	15602
C3-5a	128366	34045	1091	0	0	93230
C3-5b	16643	4179	152	0	0	12312
C3-6a	80004	20997	0	0	1349	57658
C3-6b	89902	21079	867	0	0	67956
CK1232-1	127284	59052	0	0	0	68232
CK1232-2	161752	70043	0	0	0	91709
C2-1a	53571	16678	0	0	0	36893
C2-1b	25615	7060	0	0	0	18555
C2-2a	55698	20602	0	0	0	35096
C2-2b	84301	25809	0	0	0	58492
CK1235-1	206215	122462	11152	0	0	72601
CK1235-2	74429	43777	4130	0	0	26522
CK1236-1	20564	11265	0	0	0	9299
CK1236-2	55725	30832	0	0	0	24893
CK1237-1	102376	62617	0	0	0	39759
CK1237-2	139700	86444	0	0	0	53256
C2-4a	136761	74460	0	0	0	62301
C2-4b	216318	118201	0	0	0	98117
C2-5a	48354	27604	0	0	0	20750
C2-5b	92506	55950	0	0	0	36556
CK1241-1	177526	115666	0	0	0	61860
CK1241-2	142667	88091	0	0	0	54576
C2-7a	63745	36419	0	0	0	27326
C2-7b	159960	88818	0	0	0	71142
C2-8a	22420	14376	0	0	0	8044
C2-8b	130842	85938	0	0	0	44904
CK1244-1	99934	54354	0	0	0	45580
CK1244-2	15808	9077	0	0	0	6731
CK1245-1	81822	42330	0	0	0	39492
CK1245-2	49130	24254	0	0	0	24876
CK1246-1	52169	30142	0	0	0	22027
CK1246-2	70027	43178	0	0	0	26849
CK1247-1	32592	14991	0	0	0	17601
CK1247-2	21821	9398	0	0	0	12423

CK1248-1	25455	16365	0	0	0	9090
CK1248-2	48980	32070	0	0	0	16910
C2-9a	37303	24313	0	0	0	12990
C2-9b	43272	26410	0	0	0	16862
C2-10a	1889	1288	0	0	0	601
C2-10b	213822	155149	1128	0	0	57545

Table S 8: Spearman correlation of DNA concentration, bacterial 16S rRNA gene abundance and total cell counts. P-values are shown above the diagonal and the correlation coefficient r_s below.

	DNA	16S rRNA gene copies	TCC
DNA		**>0.0001**	**>0.0001**
16S rRNA gene copies	0.87		**0.0001**
TCC	0.68	0.61	

Table S9: Minimum. maximum. mean values and standard deviation of microbial and bacterial abundance. n indicates the number of samples.

	Core	Min	Max	Mean	Std. dev.	n
DNA concentration	C1	28.6	331.3	141.6	105.6	6
[ng g^{-1}]	C4	6.2	277.5	88.5	102.6	6
	C3	5.6	51.9	19.8	17.8	6
	C2	8.7	341.5	106.9	94.0	17
16S rRNA gene copies	C1	2.4E+07	4.3E+08	1.6E+08	1.4E+08	6
[g^{-1} sediment]	C4	1.7E+06	1.6E+08	3.6E+07	5.8E+07	6
	C3	4.1E+06	6.2E+07	1.7E+07	2.1E+07	6
	C2	5.4E+06	1.5E+09	2.9E+08	4.0E+08	17
16S rRNA gene copies	C1	7.6E+05	1.4E+06	1.0E+06	2.6E+05	6
[ng^{-1} DNA]	C4	5.8E+04	5.8E+05	2.7E+05	1.6E+05	6
	C3	4.9E+05	1.2E+06	7.6E+05	2.2E+05	6
	C2	2.6E+05	1.7E+07	2.7E+06	4.2E+06	17
TCC	C1	6.8E+06	8.2E+07	5.0E+07	2.8E+07	6
[g^{-1} sediment]	C4	1.6E+06	4.4E+07	1.3E+07	1.5E+07	6
	C3	3.4E+05	3.4E+06	1.5E+06	1.0E+06	6
	C2	1.4E+06	4.9E+07	1.5E+07	1.3E+07	17

Table S10: Spearman correlation (non-linear) of DNA concentration, bacterial 16S rRNA gene abundance and total cell counts with environmental factors and pore water data. Values highlighted red are significant (< 0.05). R_s- values highlighted red show a negative correlation, whereas r_s-values highlighted green show a positive correlation.

	Temp	Salinity	Depth [mbsl]	Depth [mbs/mbsf]	Ba^{2+}	Ca^{2+}	K^+	Mg^{2+}	Na^+	Si_{aq}	Cl^-	SO_4^{2-}	Br^-	NO_3^-	δ18O	δD	pH	TC	TN	TS	TOC	Clay	Silt	Sand	Water Content
											p-value														
DNA	0.030	**0.039**	0.813	0.076	0.658	0.604	**0.020**	0.061	**0.021**	0.872	**0.011**	0.410	**0.015**	0.593	**0.027**	0.055	**0.008**	**0.017**	0.329	0.175	**0.045**	0.307	0.111	0.130	**0.006**
16S rRNA gene copies	0.173	**0.003**	0.164	**0.002**	0.860	0.248	**0.003**	**0.005**	**<0.001**	0.475	**<0.001**	0.128	**0.001**	0.587	**0.023**	0.054	**0.002**	**0.009**	0.175	0.056	**0.021**	0.821	0.886	0.926	**0.007**
16S / DNA	0.503	**<0.001**	0.216	**0.004**	0.799	**0.005**	**0.001**	**<0.001**	**<0.001**	0.268	**<0.001**	**0.016**	**<0.001**	0.425	0.369	0.528	**0.001**	0.218	0.171	0.135	0.284	0.055	0.102	0.084	0.153
TCC	**<0.001**	**0.008**	0.465	0.138	**0.024**	0.193	**0.012**	**0.029**	**0.002**	0.262	**0.001**	0.593	**0.002**	0.890	**0.028**	**0.027**	0.097	0.749	0.759	0.233	0.429	0.184	0.572	0.524	0.369
											correlation coefficient r_s														
DNA	-0.37	-0.35	0.04	0.30	-0.08	-0.09	-0.39	-0.32	-0.39	-0.03	-0.43	-0.14	-0.41	0.09	-0.37	-0.33	-0.44	0.40	0.17	-0.23	0.34	0.18	0.27	-0.26	0.47
16S rRNA gene copies	-0.24	-0.48	0.24	0.51	0.03	-0.20	-0.49	-0.46	-0.57	-0.12	-0.56	-0.26	-0.54	0.09	-0.38	-0.33	-0.52	0.44	0.23	-0.33	0.39	-0.04	0.03	-0.02	0.47
16S / DNA	-0.12	-0.63	0.21	0.47	0.04	-0.47	-0.55	-0.60	-0.71	-0.19	-0.67	-0.40	-0.66	-0.14	-0.16	-0.11	-0.54	0.21	0.24	-0.26	0.19	-0.33	-0.28	0.30	0.26
TCC	-0.64	-0.44	-0.13	0.26	-0.38	-0.23	-0.42	-0.37	-0.50	-0.19	-0.52	-0.09	-0.50	0.02	-0.37	-0.37	-0.28	0.06	0.05	-0.21	0.14	-0.23	-0.10	0.11	0.16

Table S11: Testing the correlation of the bacterial community with single pore water parameters and environmental factors with the Mantel Test.

	Correlation R	p-value
Temperature	**0.26**	**0.0001**
Depth [mbs/mbsf]	**0.37**	**0.0001**
Depth [mbsl]	**0.28**	**0.0002**
Salinity	0.10	0.0880
bulk material	-0.02	0.5886
Ba^{2+}	0.05	0.2507
Ca^{2+}	-0.04	0.6643
K^+	0.01	0.4582
Mg^{2+}	0.08	0.1385
Na^+	**0.15**	**0.0237**
Si_{aq}	0.12	0.0657
Cl^-	0.11	0.0864
SO_4^{2-}	0.10	0.0729
Br^-	0.10	0.0939
NO_3^-	-0.07	0.7884
Salinity	0.10	0.0883
$\delta^{18}O$	**0.40**	**0.0001**
δD	**0.40**	**0.0001**
pH	-0.09	0.8424
TOC	-0.03	0.6324
Water content	-0.03	0.6053

Table S12: One-way PerMANOVA of OTU data from each drill site. Summary presents the overall test statistics. Pairwise analysis shows Bonferroni corrected p-values above the diagonal and F-values below.

Summary		Pairwise				
			C1	C4	C3	C2
Permutation N:	9999					
Total sum of squares:	26.49	**C1**		0.0012	0.0006	0.0006
Within-group sum of squares:	19.41	**C4**	4.014		0.0006	0.0006
F:	8.276	**C3**	12.400	7.368		0.0006
p (same):	0.0001	**C2**	5.833	5.156	16.350	

Table S13: Analysis of variance (ANOVA) of DOC concentrations between all four cores and Dunn's post-hoc test with Bonferroni corrected p-values above and the z-statistic below the diagonal.

ANOVA

	Sum of squares	df	Mean square	F	p (same)
Between groups:	200.515	3	668.383	3.741	0.014
Within groups:	1554.47	87	178.675	**Permutation p (n=99999)**	
Total:	1754.99	90			0.04439

Dunn's test

	C1	C4	C3	C2
C1		0.212	1.000	**0.015**
C4	2.104		1.000	**0.002**
C3	0.706	0.762		0.156
C2	3.029	3.660	2.227	

Table S14: Fossil bioindicators according to Schirrmeister et al. (2008); Winterfeld et al. (2011); Müller et al. (2009) and their stratigraphical and paleoenvironmental interpretation.

Units	Bioindicator	Stratigraphy	Landscape, facies	Vegetation	Climate
IId	• Pollen*:* Cyperaceae, Poaceae*, Artemisia, Salix* • Spores: *Encalypta, Glomus* • Green algae: *Botryococcus, Pediastrum* • Ostracodes • Plant macro remains: Carex, *Salix* sp., *Saxifraga hirculus*, *Dryas Kobresia myosuroides, Thlaspitea rotundifolii* • Testacea: hygrophillic (Difflugia), sphagnobiotic (*Heleopera, Nebela, Argynnia* sp.) • Mammals: *Equus caballus, Mammuthus primigenius*	Middle Weichselian Interstadial	Floodplain, alluvial, boggy, periodically flooded	Grass-sedge tundra	Moderate, humid
IIc	No determinable fossil records found	Early Weichselian Stadial	fluvial		
IIb	Pollen: *Larix, Alnus fruticosa*, *Betula nana*, Ericales	Eemian Interglacial	Thermokarst lake	Shrub tundra	Temperate
IIa	No determinable fossil records found	Early Weichselian	fluvial		

		Stadial			
I	• Marine diatoms: *Hyalodiscus* sp.*, Paralia sulcata, Porosira glacialis, Thalassiosira* sp.*, Thalassiothrix longissima, Centralea* ind. • Fresh water diatoms: *Naicula radiosa, Eunotia praerupta, Pinnularia gibba, tetracyclus lacustris* • Sponge spicula • Pollen: *Larix, Alnus fruticosa*, *Betula nana*, Ericales • Spores: *Sphagnum*	Eemian Interglacial	Thermokarst lagoon	Shrub tundra	temperate

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