

Supplementary information

<i>Supplementary tables</i>	2
Supplementary Table S1. Track table for 16S rRNA bacterial gene amplicons.	2
Supplementary Table S2. Track table for 18S rRNA eukaryotic gene amplicons.	3
Supplementary Table S3. Statistics on individual assemblies.	4
Supplementary Table S4. Statistics on contigs from the individual assemblies.....	5
Supplementary Table S5. Statistics on co-assembly.	6
Supplementary Table S6. Statistics on contigs from the co-assembly.	7
Supplementary Table S7. Statistics on bins from the co-assembly.....	7
<i>Supplementary figures</i>	8
Supplementary Figure S1. Map of Norway and Svalbard.....	8
Supplementary Figure S2. GAM partial effect splines.....	9
Supplementary Figure S3. NMDS plots.....	9
Supplementary Figure S4. Heatmaps of bacterial and eukaryotic ASVs.	10

Supplementary tables

Supplementary Table S1. Track table for 16S rRNA bacterial gene amplicons.

”Final” represents the number of reads per sample after removal of chimeras (non-chim) and taxonomic groups (non-bacterial, chloroplasts and mitochondrial reads) which were used for downstream analyses.

sample_id	input	filtered	denoisedF	denoisedR	merged	non-chim	final
FI001	154249	55850	54580	54639	54310	54057	34227
FI003	98353	36053	33164	33395	32366	32366	27033
FI007	109868	46366	43697	43802	42986	42975	15262
FI011	115356	46161	42201	42411	41180	41178	32109
FI016	87327	34701	32981	33147	32643	32634	25717
SV001	195573	72027	70501	70659	70033	69075	59961
SV002	155539	54555	53880	53909	53764	53691	40475
SV003	236801	84899	83062	83331	82338	77472	71224
SV004	120930	45290	44981	45000	44939	44900	26033
SV005	162410	61032	59072	59146	58544	58192	44770
SV006	118482	46523	45154	45243	44956	44940	29625
SV007	164783	69106	67719	67844	67409	66803	50162
SV008	170598	66039	63936	64175	63233	61067	35655
SV010	138077	55618	53387	53531	52897	52382	36896
SV011	13678	3715	3434	3427	3361	3361	2912
SV012	124804	41187	39504	39621	39065	38104	34337
SV013	135936	54141	51076	51260	50075	49481	23107
SV014	100253	40664	39612	39626	39318	39316	22662
SV015	108453	46315	45769	45836	45715	45574	12045
SV016	80471	32452	31528	31619	31425	31425	17881
SV017	74830	31633	30825	30879	30701	30605	9229
SV018	100263	38883	38531	38536	38470	38420	17145
SV020	102308	34041	32663	32761	32343	32338	26722
SV021	2729	753	685	685	683	683	443
SV022	122312	44796	44082	44090	43964	43887	34697
SV025	45929	17488	16893	16944	16785	16755	10322
SV026	79558	29043	27652	27703	27370	27370	22512
SV027	109650	43471	42957	42984	42834	42834	28745
SV028	97969	37947	37243	37303	37040	37027	26658
SV029	78873	29432	28567	28590	28405	28405	14923
SV030	109542	40425	40117	40119	40047	40044	13751

Supplementary Table S2. Track table for 18S rRNA eukaryotic gene amplicons.
 ”Final” represents the number of reads per sample after removal of chimeras (non-chim) and taxonomic groups (non-eukaryotic reads) which were used for downstream analyses.

sample_id	input	filtered	denoisedF	denoisedR	merged	nonchim	final
FI001	66174	28984	28611	28709	27350	27065	27065
FI003	86198	31361	30679	30997	29102	29078	29078
FI007	57704	24910	24534	24713	24027	24014	24014
FI011	119484	54035	53022	53580	51423	51352	51352
FI016	47780	22379	22047	22279	21557	21348	21348
SV001	160205	62193	61996	61997	61486	55192	55192
SV002	95154	39472	39189	39368	38533	38247	38247
SV003	181764	69830	69584	69597	68406	59117	59117
SV004	92115	41617	41505	41565	41051	40877	40877
SV005	99523	45544	45077	45215	42929	40909	40909
SV006	206679	100801	100459	100577	99648	96748	96748
SV007	146541	75362	75216	75259	74836	73679	73679
SV008	133478	58688	58177	58401	56977	51257	51257
SV010	104054	49764	49338	49463	48333	47854	47854
SV011	8513	2543	2448	2497	2280	2262	2262
SV012	88157	34856	34396	34576	33106	32903	32903
SV013	200353	88301	87914	88091	84393	76425	76425
SV014	80231	36100	35779	35880	34492	33145	33145
SV015	169445	81586	81337	81471	80084	76194	76194
SV016	166576	78796	78473	78585	77417	75676	75676
SV017	70532	33898	33736	33804	33414	32970	32970
SV018	51731	25060	24868	24966	23889	22156	22156
SV020	60053	22964	22737	22837	22398	22346	22346
SV021	1730	596	563	575	533	533	533
SV022	111753	49657	49286	49193	47348	44903	44903
SV025	82202	36077	35820	35862	35079	34840	34840
SV026	122414	54945	54550	54644	53222	53010	53010
SV027	176407	81558	81163	81255	79580	78580	78580
SV028	87619	39919	39527	39659	37898	36243	36243
SV029	61952	28247	27947	28068	27152	26747	26747
SV030	109331	50902	50663	50812	49698	48374	48374

Supplementary Table S3. Statistics on individual assemblies.

These represents the statistics of the assemblies on individual samples used for gene centric analyses.

sample_id	reads	bases	Contigs	ORFs	rRNAs	tRNAs/tmRNAs	orphans	KEGGs
FI001	76352015	11298812868	2150046	2667375	3419	12042	1598391	470785
FI003	204872670	30413584587	950412	1221795	5006	6081	678255	272330
FI007	193948616	28623298602	1570282	2148906	6489	11054	933443	464551
FI011	209291026	31127806831	1219269	1638738	7393	7464	797964	384800
SV001	191597030	28338597082	1712073	2123421	1755	9017	1405891	326300
SV002	206818460	30648775353	1471880	2139766	1844	8645	1511305	296765
SV003	167274998	24818473672	1101066	1575809	1854	7325	801573	333780
SV004	221887646	32995386440	821926	1034302	717	2516	841694	78071
SV005	286414908	42287187965	2901240	3210355	2832	8820	2361282	380079
SV006	297078804	43877484261	1426617	1948665	2235	6884	1232195	345242
SV007	226988110	33680205801	1330959	1809207	1843	7113	992115	348205
SV008	233337150	34675672954	1919810	2620613	3355	12854	1442064	487942
SV010	183932292	27306805471	1472374	1921297	3280	10033	1080928	394378
SV012	193326296	28841692630	1968537	2770905	4918	15158	1115526	700978
SV013	166131216	24397957305	2625123	2995121	4454	8934	2366422	275221
SV014	196016900	28928952640	2294479	2999685	2274	7958	2389962	256664
SV015	212528672	31376275079	842784	1273957	1153	3476	1084644	86697
SV016	168260984	24770973549	1715745	2113586	1991	7263	1622871	206969
SV017	229461798	33811886830	1324686	1680727	2240	5313	1142251	227367
SV018	172753032	25116269196	1944003	2262620	1193	6093	1969440	109555
SV020	214114304	31610359828	2379191	3218094	3573	13234	1580612	667458
SV021	259821972	38193426132	2513955	3169841	2259	9460	2414577	284448
SV022	188424994	27639514547	2346491	2653170	1605	6833	2094365	262708
SV025	172644254	25428742084	2187150	2723259	2013	8515	2078897	257005
SV026	189758494	28171842702	2558999	3423245	3887	12849	1548341	796246
SV027	242767068	35724616333	2975974	3480374	2291	10612	2757420	274442
SV028	190761616	28095270082	2336941	2746123	1924	8898	1932258	359992
SV029	274370272	40587111587	2650686	3406422	2684	11177	2614564	339451
SV030	158854134	23438173216	1647300	2076711	1438	7721	1452798	230976

Supplementary Table S4. Statistics on contigs from the individual assemblies.

sample_id	contigs	Total length	longest contig	N50	N90	Congruent	Disparity >0	Disparity >= 0.25
FI001	2150046	1679210594	557644	950	347	2147952 (99.9%)	2095 (0.1%)	1441 (0.1%)
FI003	950412	627719699	445152	706	327	949796 (99.9%)	617 (0.1%)	340 (0.0%)
FI007	1570282	1009805849	494339	664	332	1569539 (100.0%)	744 (0.0%)	593 (0.0%)
FI011	1219269	859448132	613874	782	329	1217906 (99.9%)	1364 (0.1%)	965 (0.1%)
SV001	1712073	1366111996	771697	942	361	1711245 (100.0%)	829 (0.0%)	545 (0.0%)
SV002	1471880	1312122718	933739	1237	361	1469967 (99.9%)	1914 (0.1%)	1057 (0.1%)
SV003	1101066	906601732	1653268	1001	359	1100082 (99.9%)	985 (0.1%)	639 (0.1%)
SV004	821926	560466971	716751	763	322	821512 (99.9%)	415 (0.1%)	134 (0.0%)
SV005	2901240	1942386688	1238945	750	327	2900176 (100.0%)	1065 (0.0%)	565 (0.0%)
SV006	1426617	1065500501	590453	995	316	1425221 (99.9%)	1397 (0.1%)	876 (0.1%)
SV007	1330959	960549695	785307	889	326	1329922 (99.9%)	1038 (0.1%)	629 (0.0%)
SV008	1919810	1427880997	701864	864	340	1918604 (99.9%)	1207 (0.1%)	834 (0.0%)
SV010	1472374	1070903407	596689	893	328	1471519 (99.9%)	856 (0.1%)	527 (0.0%)
SV012	1968537	1473576905	584294	878	347	1966789 (99.9%)	1749 (0.1%)	1345 (0.1%)
SV013	2625123	1411308551	454483	548	323	2624706 (100.0%)	418 (0.0%)	291 (0.0%)
SV014	2294479	1918843493	1026994	1091	361	2293289 (99.9%)	1191 (0.1%)	645 (0.0%)
SV015	842784	784787426	1084123	1860	339	842302 (99.9%)	483 (0.1%)	225 (0.0%)
SV016	1715745	1302666623	636583	901	347	1714544 (99.9%)	1202 (0.1%)	746 (0.0%)
SV017	1324686	899241632	677971	726	341	1323934 (99.9%)	753 (0.1%)	482 (0.0%)
SV018	1944003	1244267800	460295	682	324	1942790 (99.9%)	1214 (0.1%)	707 (0.0%)
SV020	2379191	1812753044	469761	888	352	2376829 (99.9%)	2363 (0.1%)	1622 (0.1%)
SV021	2513955	2003512665	1280353	1008	353	2512252 (99.9%)	1704 (0.1%)	1094 (0.0%)
SV022	2346491	1610239791	581059	788	323	2345235 (99.9%)	1257 (0.1%)	769 (0.0%)
SV025	2187150	1641257977	304361	902	345	2185852 (99.9%)	1299 (0.1%)	742 (0.0%)
SV026	2558999	1771709787	587263	750	341	2556833 (99.9%)	2167 (0.1%)	1667 (0.1%)
SV027	2975974	2103280956	520579	818	333	2974548 (100.0%)	1427 (0.0%)	894 (0.0%)
SV028	2336941	1637479561	871054	786	335	2335128 (99.9%)	1814 (0.1%)	1255 (0.1%)
SV029	2650686	2049311732	1026964	906	351	2649150 (99.9%)	1537 (0.1%)	988 (0.0%)
SV030	1647300	1231651914	481381	893	335	1645662 (99.9%)	1639 (0.1%)	1012 (0.1%)

Supplementary Table S5. Statistics on co-assembly.

These represents the reads and bases used for co-assembly as well as number of open reading frames (ORFs), rRNAs, tRNAs/tmRNAs, orphans and KEGG annotations (KEGGs) obtained from the co-assembled contigs.

sample_id	reads	bases	ORFs	rRNAs	tRNAs/tmRNAs	orphans	KEGGs
FI001	171515890	25386092937	5139299	5718	27440	2799429	1080167
FI003	204872670	30413584587	3468305	6432	33579	1174768	1267392
FI007	193948616	28623298602	3597916	5874	33163	929060	1347327
FI011	209291026	31127806831	5048504	6790	41519	1709515	1634123
SV001	191597030	28338597082	4018011	5415	25919	1589064	1133052
SV002	206818460	30648775353	4098826	5128	19485	2115554	1023364
SV003	167274998	24818473672	3997421	5179	23775	1268957	1298263
SV004	221887646	32995386440	1139820	4079	8897	497552	384792
SV005	286414908	42287187965	7556814	6698	33293	4279689	1485232
SV006	297078804	43877484261	4916916	6374	28307	2062780	1315082
SV007	226988110	33680205801	4166874	5501	25508	1433787	1265565
SV008	233337150	34675672954	5819780	6096	35850	2500024	1468464
SV010	183932292	27306805471	5803875	6590	36799	2531547	1464666
SV012	193326296	28841692630	4698437	6167	37765	1350918	1507127
SV013	166131216	24397957305	3777788	6439	28011	1406026	1176559
SV014	196016900	28928952640	6200855	5877	24458	3771317	1105635
SV015	212528672	31376275079	2839832	4988	12131	1754121	525027
SV016	168260984	24770973549	5386679	5718	22821	3189874	1008250
SV017	229461798	33811886830	3518842	5881	21298	1562766	970504
SV018	172753032	25116269196	3776197	4392	11587	2667429	493312
SV020	214114304	31610359828	5046158	5737	31285	1852852	1473853
SV021	259821972	38193426132	6702346	6262	27615	4044010	1190309
SV022	188424994	27639514547	5464814	5202	18208	3533572	897279
SV025	172644254	25428742084	5146048	5408	20096	3155457	901790
SV026	189758494	28171842702	5026961	6310	32852	1808721	1441068
SV027	242767068	35724616333	5999722	5560	21173	3925227	927698
SV028	190761616	28095270082	6372159	5687	23330	4000314	1049993
SV029	274370272	40587111587	7185810	6396	32234	4349354	1264616
SV030	158854134	23438173216	4568878	4395	15860	2880101	729123
Assembly	6024953606	890312435696	536734552	253721	2558264	324925193	81319509

Supplementary Table S6. Statistics on contigs from the co-assembly.

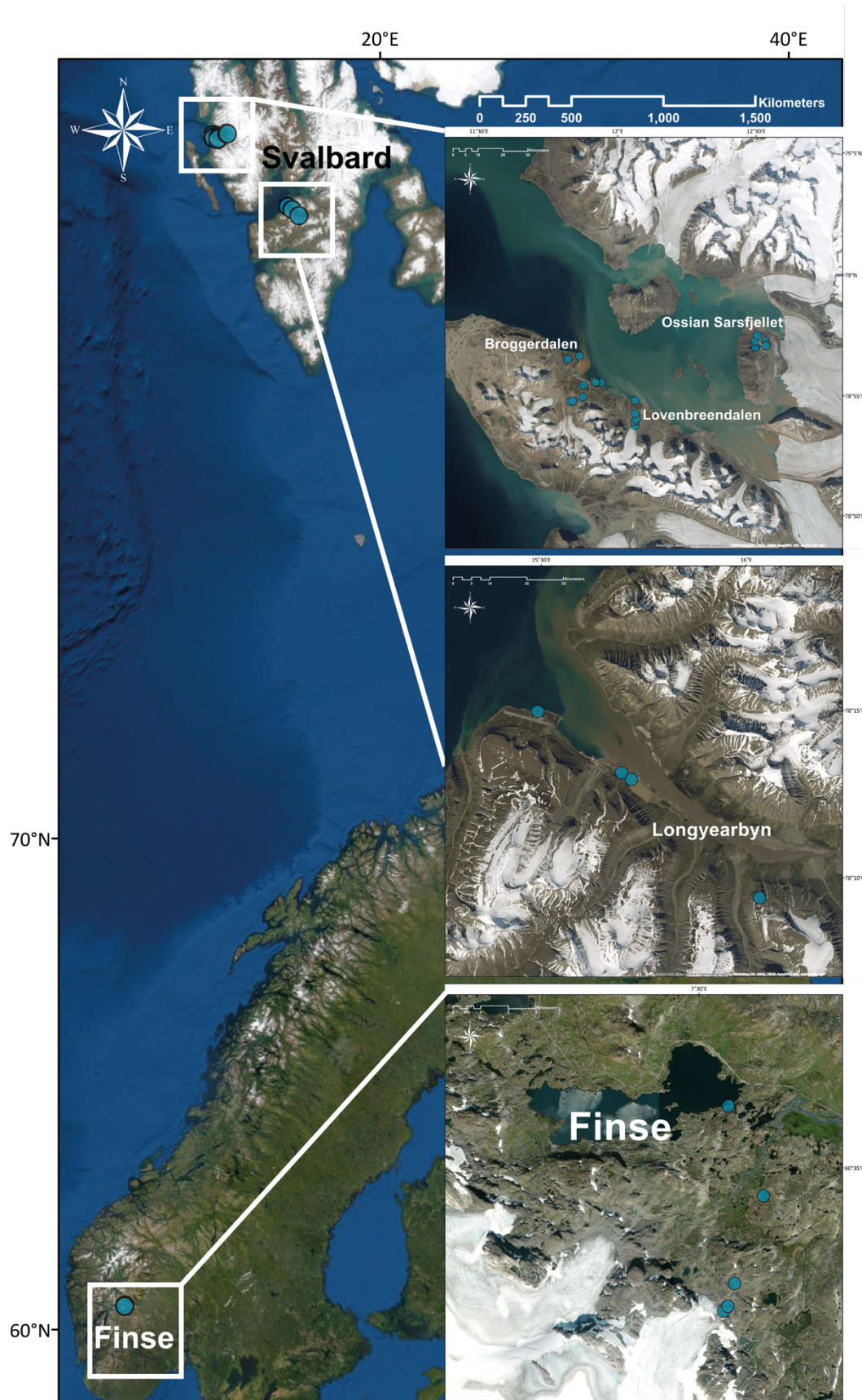
	Coassembly
Number of contigs	6704263
Total length	15900628689
Longest contig	676008
Shortest contig	1000
N50	2635
N90	1161
Contigs at superkingdom (k) rank	2997852 (44.7%) in 4 superkingdoms
Contigs at phylum (p) rank	2611829 (39.0%), in 219 phyla
Contigs at class (c) rank	2115438 (31.6%), in 280 classes
Contigs at order (o) rank	1725599 (25.7%), in 727 orders
Contigs at family (f) rank	1382099 (20.6%), in 1565 families
Contigs at genus (g) rank	937851 (14.0%), in 4914 genera
Contigs at species (s) rank	446916 (6.7%), in 2909 species
Congruent	6592740 (98.3%)
Disparity >0	111524 (1.7%)
Disparity >= 0.25	110136 (1.6%)

Supplementary Table S7. Statistics on bins from the co-assembly.

	Coassembly
Number of bins	1981
Complete >= 50%	200
Complete >= 75%	21
Complete >= 90%	1
Contamination < 10%	1955
Contamination >= 50%	2
Congruent bins	932
Disparity >0	1049
Disparity >= 0.25	471
Hi-qual bins (>90% complete,<10% contam)	0
Good-qual bins (>75% complete,<10% contam)	17

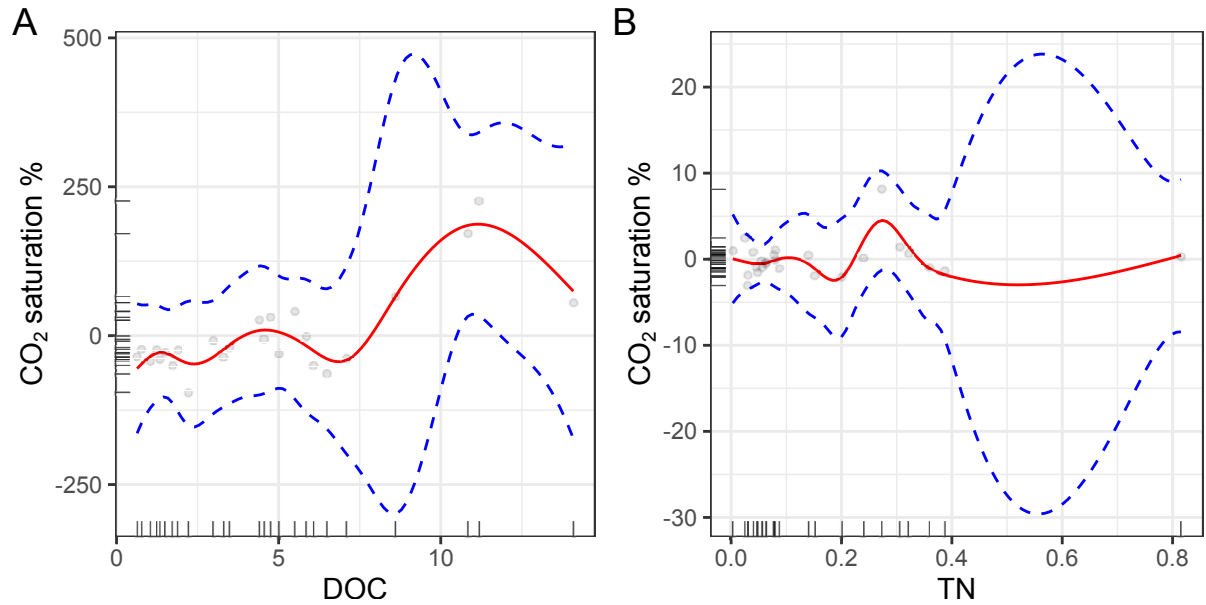
Supplementary figures

Supplementary Figure S1. Map of Norway and Svalbard.



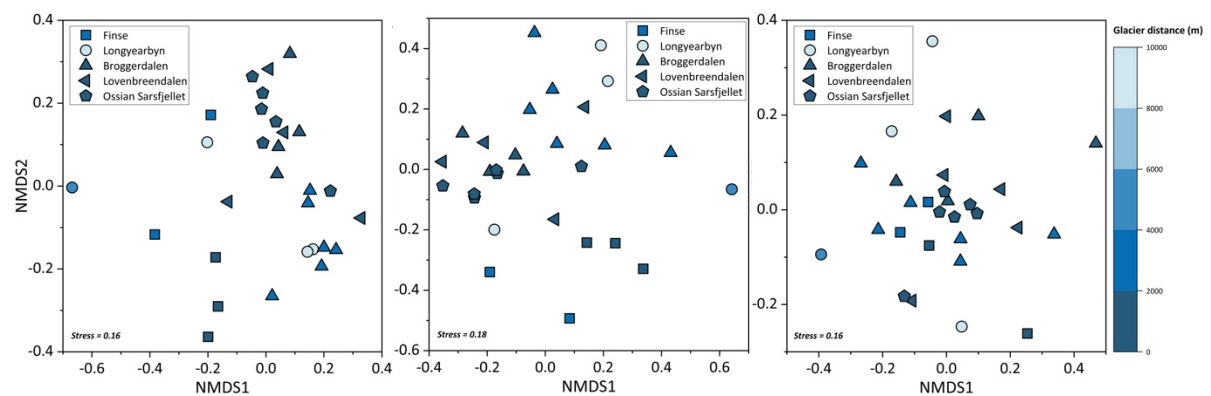
Supplementary Figure S2. GAM partial effect splines.

GAM partial effect splines. (as shown by red lines) for significant variables modeling CO₂ saturation including dissolved organic carbon (DOC; A) and total nitrogen concentrations (TN, B). Standard errors are indicated by dotted lines while data points are shown by open circles.



Supplementary Figure S3. NMDS plots.

NMDS plots based on bacterial (A) and eukaryotic (B) ASV tables as well as functional profiles as assessed by KEGG annotations (C). Symbols indicates the chronosequence and color distance from glacier. Stress values are given for each plot.



Supplementary Figure S4. Heatmaps of bacterial and eukaryotic ASVs.
Heatmaps of bacterial (A) and eukaryotic (B) ASV tables.

