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# Taxon interactions control the biogeography of cryoconite colonizing a High Arctic ice cap

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## SUPPLEMENTARY METHODS:

### DNA extraction

In 2mL centrifuge tubes, 0.5mL of hexadecyltrimethylammonium bromide (CTAB) buffer was added to each sample prior to addition of 3-4 glass beads and 0.5mL of phenol-chloroform-isoamyl alcohol. Samples were vortexed and subjected to bead beating for 30 seconds at maximum speed before centrifugation at 13 000rpm for 10 minutes. 0.5mL of chloroform-isoamyl-alcohol was added to the aqueous phase which was then vortexed and centrifuged as before. The supernatant was treated with 1mL polyethylene glycol (PEG 6000) and allowed to precipitate at room temperature for 2 hours and centrifugation at 12 000×g for 20 minutes at 4°C. All the supernatant was removed and the precipitated DNA washed with 1mL 70% ethanol and centrifuged at 13 000rpm for 20 minutes. The ethanol wash was repeated and the resultant pellet was air-dried in a Speedy Vac dryer for 8 minutes before resuspension in 50µL of 1×Tris EDTA (TE) buffer and stored at -20°C for downstream processing.

### PCR and sequencing

Core primers were modified by addition of a PGM sequencing adapter, a GT spacer and error correcting Golay barcode, as described in [Supplementary Table 1](#) (Whiteley *et al.* 2012). Individual reactions consisted of: MilliQ water, 1×GoTaq reaction Buffer, dNTPs (0.2mM), MgCl<sub>2</sub> (2.5mM), BSA (0.003mM), B-27F + MID# (0.1pmol/μL), A1-R357 (0.1pmol/μL) (Supplementary table 1), GoTaq, 1μL template DNA at a final volume of 25μL. Amplification conditions were: 95 °C for 5 mins initial denaturation; 30 cycles: 95 °C for 30 secs (denaturation), 60 °C for 30 secs (annealing), 72 °C for 45 secs (extension); 72 °C for 7 mins (final extension). This generated amplicon fragments of ~400 bp that were verified on 1 % agarose, purified of short fragments by Agencourt AMPureXP bead clean-up (Beckman Coulter, Brea, CA) and E-Gel® size select electrophoretic separation (Invitrogen) before concentrations were adjusted to 4 ng.μL.

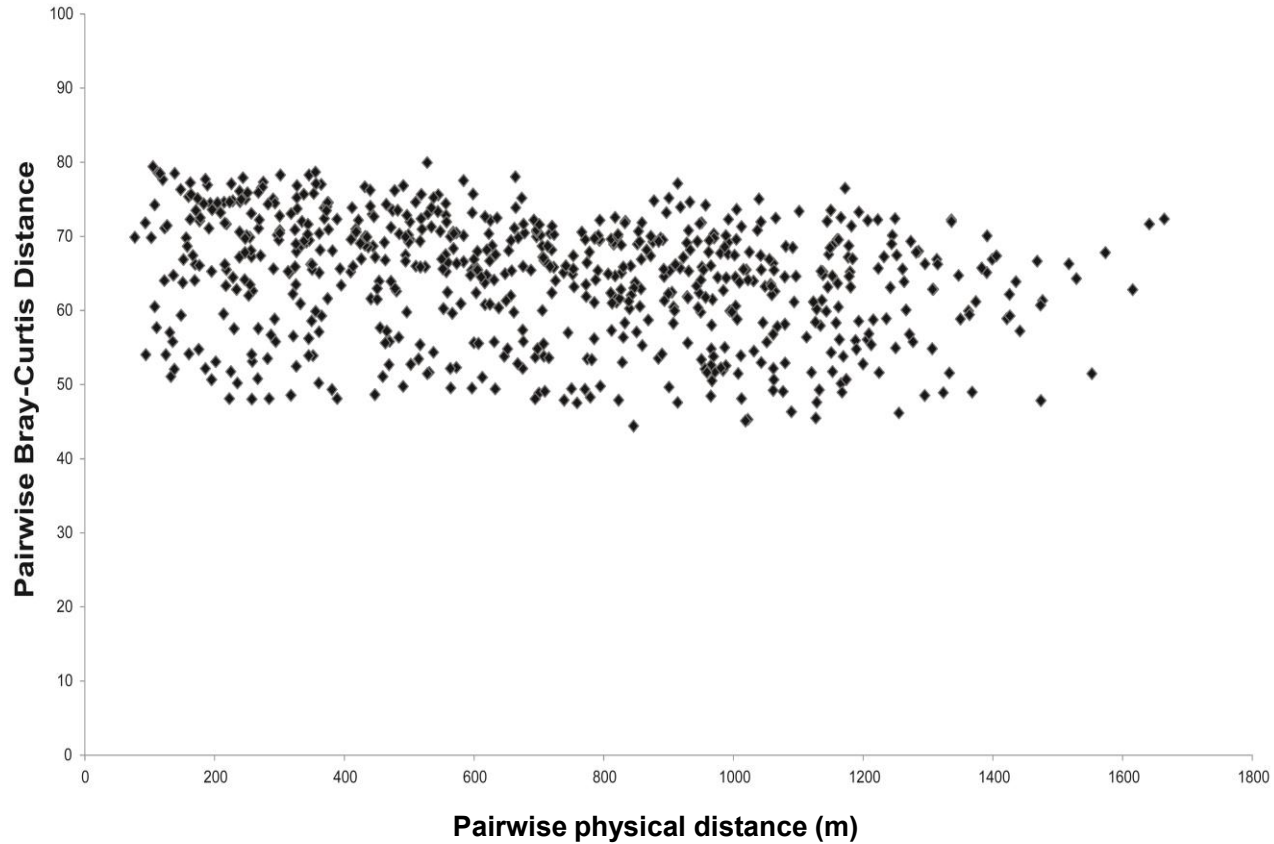
Fragment size distribution and DNA concentration was determined using a BioAnalyser 2100 (Agilent Technologies, USA) prior to sequencing. All samples were adjusted to an equimolar concentration (26 pM) for Emulsion PCR using Ion OneTouch (Life Technologies) and enriched for templated Ion Sphere particles (ISPs) using the Ion Xpress Template 400 kit (Life Technologies, USA) according to the manufacturer's instructions. Templated ISPs were loaded onto an Ion 316v2 chip and sequenced for 1200 flows, according to the Ion PGM 400 kit user guide.

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SUPPLEMENTARY DATA:

Supplementary Figure 1: distance decay relationship between pairwise Bray Curtis distance between 16S sequencing profiles and pairwise physical distance.



# Supplementary Table 1. Modified primers used for amplification of bacterial 16S rRNA gene regions (5'-3') V1-V3

Primer Name	Forward primer (Primer A-key) (30)	Ion Barcode (10)	Spacer	Template specific sequence-3' (19)	Notes
NGS_V1-V2_1	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CTAAGGTAAC	GT	AGAGTTTGATCMTGGCTCAG	27F
NGS_V1-V2_2	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TAAGGAGAAC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_3	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AAGAGGATTC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_4	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TACCAAGATC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_5	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CAGAAGGAAC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_6	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CTGCAAGTTC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_7	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TTCGTGATTC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_8	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TTCCGATAAC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_9	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TGAGCGGAAC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_10	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CTGACCGAAC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_11	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TCCTCGAATC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_12	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TAGTGGTTC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_13	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TCTAACGGAC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_14	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TTGGAGTGC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_15	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TCTAGAGGTC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_16	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TCTGGATGAC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_17	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TCTATTGTC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_18	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGGCAATTGC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_19	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TTAGTCGGAC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_20	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CAGATCCATC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_21	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TCGCAATTAC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_22	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TTCGAGACGC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_23	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TGCCACGAAC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_24	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AACCTCATTC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_25	CCATCTCATCCCTGCGTGTCTCCGACTCAG	GATCTGCGAT	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_26	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CAGCTCATCA	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_27	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CAAACAACAG	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_28	CCATCTCATCCCTGCGTGTCTCCGACTCAG	GCAACACCAT	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_29	CCATCTCATCCCTGCGTGTCTCCGACTCAG	GCGATATATC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_30	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGAGCAATCC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_31	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGTCGTGCAC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_32	CCATCTCATCCCTGCGTGTCTCCGACTCAG	GTATCTGCGC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_33	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGAGGGCCCG	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_34	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CAAATTCGGC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_35	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGATTGACCA	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_36	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGTTACGAGC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_37	CCATCTCATCCCTGCGTGTCTCCGACTCAG	GCATATGCAC	GT	AGAGTTTGATCMTGGCTCAG	
NGS_V1-V2_38	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CAACTCCCGT	GT	AGAGTTTGATCMTGGCTCAG	
	Reverse primer (Primer P1-key) (23)				
PGM_V1-V2_Rev	CCTCTCATGGGCAGTCGGTGAT			CTGCTGCCTYCCGTA	357R

# Supplementary Table 2: Diversity indices and environmental parameters measured

Sample	Number of OTUs	Pielou's evenness (J')	Shannon H'(loge)	Eastings (UTM)	Northings (UTM)	Chlorophyll a µg/g	Z (masl)	SLOPE (deg)	ASPECT (deg, 0=N clockwise)	FAA (m^2)	FLOWLENGTH (m)	CURVATURE	WETNESS	PDDs (in summer)	PositiveHrs	PDHrs	IR (W)	IRh (hrs)	IRkW	ACA (%)
1.1	476	0.64	3.97	526316	8672566	6.69	700.66	11.46	242.41	5075.00	1349.65	-8.69	0.002	77	1544	4379.4	525700	1659.4	525.7	3.41
1.2	512	0.74	4.61	526293	8672774	5.16	713.43	9.84	248.24	525.00	108.28	0.02	0.019	77	1507	4263.2	523400	1716.8	523.4	1.86
1.3	517	0.72	4.53	526380	8673063	4.04	738.02	7.64	265.13	4225.00	840.00	0.05	0.002	77	1438	4050.0	518100	1793.2	518.1	5.51
1.4	517	0.79	4.96	526472	8673272	5.96	746.95	5.91	292.91	75.00	12.07	-4.54	0.079	77	1416	3976.3	512000	1834.9	512	21.71
1.5	519	0.73	4.57	526630	8673519	9.09	736.29	7.40	6.65	2175.00	552.19	0.22	0.003	77	1443	4064.5	495000	1846.0	495	5.48
1.6	487	0.70	4.30	526789	8673341	5.90	761.18	7.60	344.10	175.00	32.07	-1.66	0.043	77	1380	3862.6	496300	1845.3	496.3	5.53
1.7	515	0.75	4.68	526670	8673046	5.97	769.58	4.80	270.38	2650.00	525.00	-4.88	0.002	77	1354	3797.4	520800	1821.7	520.8	5.01
2.1	474	0.70	4.33	526733	8672710	11.86	765.80	5.97	235.00	875.00	240.42	-3.31	0.007	77	1366	3826.6	529400	1756.2	529.4	10.63
2.2	526	0.76	4.77	526835	8672646	10.71	770.32	5.18	225.56	2425.00	678.82	0.02	0.002	77	1351	3791.8	530900	1771.8	530.9	5.00
2.3	412	0.65	3.91	526895	8672534	8.18	766.07	5.09	212.24	625.00	169.71	-1.54	0.008	77	1366	3824.5	532600	1761.9	532.6	9.53
2.4	492	0.74	4.61	526972	8672534	7.70	769.90	3.90	200.16	100.00	15.00	1.03	0.039	77	1352	3795.0	531600	1769.7	531.6	6.54
2.5	550	0.76	4.79	527013	8672440	5.83	763.33	5.37	190.19	850.00	165.00	0.07	0.006	77	1372	3845.7	535500	1751.2	535.5	9.02
2.6	508	0.73	4.55	526890	8672376	9.62	753.78	6.12	213.92	325.00	80.71	0.09	0.019	77	1392	3921.2	533500	1747.3	533.5	10.75
2.7	543	0.72	4.54	526777	8672378	10.56	745.87	7.01	225.11	900.00	245.42	0.01	0.008	77	1416	3985.1	532000	1734.6	532	9.69
2.8	519	0.73	4.58	526668	8672418	5.41	738.35	8.88	227.49	1400.00	388.91	0.04	0.006	77	1437	4047.3	533200	1696.3	533.2	7.15
2.9	487	0.70	4.31	526877	8672788	5.57	781.12	4.12	240.82	1400.00	378.55	-3.37	0.003	77	1311	3711.5	527400	1796.2	527.4	2.24
3.1	470	0.72	4.44	527537	8672831	7.82	775.99	8.45	142.28	725.00	197.99	0.30	0.012	77	1329	3749.2	539000	1691.4	539	4.95
3.2	508	0.70	4.36	527486	8672736	9.19	768.83	9.67	137.37	775.00	212.13	-3.00	0.012	77	1359	3803.2	538700	1659.6	538.7	4.42
3.5	498	0.67	4.16	527045	8672191	13.11	742.79	4.51	175.76	2475.00	490.00	0.12	0.002	77	1424	4010.5	532200	1767.2	532.2	5.36
3.6	472	0.59	3.65	527145	8672345	15.39	753.08	6.43	152.94	150.00	35.36	0.12	0.043	77	1394	3926.8	535700	1736.2	535.7	3.54
3.7	508	0.72	4.50	527187	8672514	6.20	767.40	6.89	152.90	75.00	14.14	0.04	0.092	77	1364	3814.2	537700	1719.3	537.7	5.76
3.8	508	0.71	4.39	527280	8672675	6.68	778.96	6.57	150.39	200.00	49.50	0.21	0.033	77	1315	3727.3	537300	1737.7	537.3	3.43
3.9	363	0.67	3.95	527335	8672826	5.55	790.62	4.96	153.38	1250.00	259.50	-1.72	0.004	76	1292	3643.4	534900	1751.2	534.9	3.42
3.1	525	0.75	4.69	527320	8672919	1.99	798.06	4.80	166.87	175.00	30.00	-3.86	0.027	76	1275	3591.1	536300	1763.3	536.3	4.05
3.11	524	0.77	4.80	527145	8672780	4.11	790.61	3.70	193.78	600.00	115.00	0.20	0.006	76	1292	3643.5	532900	1785.5	532.9	2.30
3.12	551	0.77	4.86	527077	8672700	4.93	784.68	3.57	187.34	525.00	100.00	0.25	0.007	76	1302	3685.8	532400	1787.1	532.4	2.43
4.1	503	0.64	3.99	527629	8672814	6.92	760.11	12.83	135.50	1200.00	332.34	-4.79	0.011	77	1384	3871.0	541000	1505.6	541	7.32
4.2	501	0.76	4.72	527674	8673000	3.53	778.42	11.06	128.27	1000.00	275.77	-2.05	0.011	77	1318	3731.2	537100	1646.3	537.1	2.68
4.3	447	0.76	4.65	527628	8673164	4.80	798.04	7.08	116.10	50.00	7.07	0.17	0.142	76	1275	3591.2	530300	1764.2	530.3	10.76
4.4	399	0.72	4.31	527729	8673119	5.90	782.33	10.84	117.11	525.00	141.42	-1.05	0.021	76	1308	3702.8	531400	1676.6	531.4	19.32
4.5	396	0.69	4.10	527845	8673224	5.20	769.05	11.63	107.42	1025.00	200.00	0.16	0.011	77	1356	3801.5	524900	1690.6	524.9	31.57
4.6	458	0.76	4.65	527755	8673356	1.98	789.52	8.95	104.60	700.00	135.00	-6.10	0.013	76	1293	3651.2	525200	1744.9	525.2	24.69
4.7	329	0.68	3.92	527634	8673387	3.05	802.25	3.63	58.27	200.00	49.50	-2.69	0.018	74	1263	3562.3	518800	1843.9	518.8	15.37
4.8	432	0.69	4.19	527533	8673301	3.04	805.80	0.47	67.50	375.00	70.00	-4.49	0.001	74	1259	3538.1	526300	1845.3	526.3	13.11
4.9	353	0.67	3.94	527439	8672989	9.89	799.16	5.03	147.00	225.00	56.57	0.23	0.022	74	1266	3583.5	534900	1773.9	534.9	6.90
4.1	515	0.78	4.85	527518	8673083	6.74	801.15	4.54	138.50	500.00	134.35	-1.00	0.009	74	1263	3569.8	532800	1776.9	532.8	5.32
4.11	489	0.78	4.81	527679	8673259	2.51	796.90	7.16	106.71	300.00	55.00	-1.02	0.024	76	1278	3599.2	526700	1768.8	526.7	2.92

Supplementary Table 3: Pairwise PERMANOVA comparison of bacterial community structure (at the OTU level) by sector of Foxfonna ice cap

Groups	t	P(perm)
G1, G4	1.6398	0.004
G1, G2	1.7124	0.001
G1, G3	1.5446	0.003
G4, G2	2.2761	0.001
G4, G3	1.5973	0.003
G2, G3	1.4803	0.007



# Supplementary Table 4: Marginal tests from distLM model of environmental predictors of bacterial community structure.

MARGINAL TESTS					
Variable	SS(trace)	Pseudo-F	P	Prop.	
E	2351.7	3.8009	0.001	9.80E-02	
N	2276.1	3.6659	0.001	9.48E-02	
Chl a ug/g	1380.4	2.1353	0.012	5.75E-02	
Z (masl)	1950.3	3.0947	0.002	8.12E-02	
SLOPE (deg)	2217.8	3.5625	0.002	9.24E-02	
ASPECT (deg, 0=N clockwise)	1861	2.9412	0.004	7.75E-02	
ACCUMAREA (m^2)	705.35	1.0595	0.355	2.94E-02	
FLOWLENGTH (m)	745.34	1.1214	0.283	3.10E-02	
CURVATURE	623.13	0.93268	0.474	2.60E-02	
WETNESS	538.76	0.80348	0.633	2.24E-02	
PDDs (in summer)	3549	6.0717	0.001	0.14783	
PositiveHrs	1915.8	3.0353	0.003	7.98E-02	
PDHrs	1826.8	2.8827	0.003	7.61E-02	
IR (W)	783.44	1.1807	0.238	3.26E-02	
IRh (hrs)	1579.3	2.4646	0.003	6.58E-02	
ACA (%)	1718.1	2.6979	0.012	7.16E-02	

Supplementary Table 5: Sequential tests from distLM model of environmental predictors of bacterial community structure. SS: sums of squares; Pseudo-F: test statistic

<b>Variable</b>	<b>Adj R<sup>2</sup></b>	<b>SS(trace)</b>	<b>Pseudo-F</b>	<b>P</b>	<b>Proportion explained</b>	<b>Cumulative variance</b>
<b>PDDs (in summer)</b>	<b>0.12</b>	<b>3549.0</b>	<b>6.1</b>	<b>0.001</b>	<b>0.15</b>	<b>0.15</b>
<b>SLOPE (deg)</b>	<b>0.21</b>	<b>2588.5</b>	<b>4.9</b>	<b>0.001</b>	<b>0.11</b>	<b>0.26</b>
<b>N</b>	<b>0.24</b>	<b>1248.6</b>	<b>2.5</b>	<b>0.001</b>	<b>0.05</b>	<b>0.31</b>
<b>ACA (%)</b>	<b>0.27</b>	<b>1005.9</b>	<b>2.1</b>	<b>0.011</b>	<b>0.04</b>	<b>0.35</b>
<b>E</b>	<b>0.31</b>	<b>1372.8</b>	<b>3.0</b>	<b>0.002</b>	<b>0.06</b>	<b>0.41</b>
<b>WETNESS</b>	<b>0.31</b>	<b>503.5</b>	<b>1.1</b>	<b>0.319</b>	<b>0.02</b>	<b>0.43</b>
<b>FAA (m<sup>2</sup>)</b>	<b>0.32</b>	<b>517.2</b>	<b>1.1</b>	<b>0.309</b>	<b>0.02</b>	<b>0.45</b>
<b>IRkW</b>	<b>0.32</b>	<b>459.1</b>	<b>1.0</b>	<b>0.399</b>	<b>0.02</b>	<b>0.47</b>
<b>PDHrs</b>	<b>0.33</b>	<b>661.2</b>	<b>1.5</b>	<b>0.106</b>	<b>0.03</b>	<b>0.50</b>
<b>Z (masl)</b>	<b>0.33</b>	<b>511.8</b>	<b>1.1</b>	<b>0.264</b>	<b>0.02</b>	<b>0.50</b>
<b>IR (W)</b>	<b>0.33</b>	<b>0.0</b>	<b>0.0</b>	<b>1.000</b>	<b>0.00</b>	<b>0.52</b>

## Supplementary Table 6: BLAST matches of core OTUs to closest environmental relatives (CER) and closest named relatives (CNR)

Core OTU	CER	CER #	CER %id	CER Habitat	CNR	CNR #	CNR %id	CER Habitat
Sphingobacteriaceae-61341	Uncultured actinobacterium clone IC4008	HQ622724.1	99	Svalbard ice	Pedobacter daechungensis	NR_041507	89	Korean lake sediment
Microbacteriaceae-32521	Frigoribacterium sp. MP117	KC256951	99	Tibetan glacier	Frigoribacterium sp. MP117	KC256951	99	Tibetan glacier
Intrasporangiaceae-46072	Uncultured bacterium clone ANTLV2_G12	DQ521529	98	Lake Vida ice, Antarctica	Oryzihumus sp. aerobe-19	KP185144	93	Korean grassland
Chloroflexi-37757	Uncultured bacterium clone gls106	KC286738	98	Chinese glacier	Azospirillum sp. YM 195	GU396257.1	89	Sugarcane rhizome
Intrasporangiaceae-27964	Uncultured bacterium clone gs34	JF420640	97	German glacier sediment	Humibacter albus	AM494541	91	sewage sludge
Gemmatimonadales-59904	Uncultured bacterium clone NC54g8_19617	JQ377159	97	FACE soil	Ellin5220	AY234571	92	soil
Phormidium-45763	Uncultured cyanobacterium clone LJ14_522	KM112145	98	Antarctic microbial mat	Phormidium autumnale Ant-Ph68	DQ493874.1	98	Signy island, Antarctica
Leptolyngbya-40205	Uncultured bacterium clone IC4002	HQ622720	98	Svalbard ice	Phormidesmis priestleyi ANT.L66.	AY493581	95	Antarctica
Xanthomonadaceae-51358	Uncultured gamma proteobacterium clone TSC52	EU359963	98	Taiwanese soil	Pseudoxanthomonas sacheonensis	HF585486	94	US soil
Betaproteobacteria-10679	Uncultured bacterium isolate LH2-01	EU440469.1	98	Stromatolite, Canadian Arctic	Telluria mixta	LN794206	92	Germany
Intrasporangiaceae-53638	Uncultured bacterium clone LD_RB_26	EU644104	97	Siberian tundra	Ornithinimicrobium tianjinense	JQ948045	92	China
Betaproteobacteria-5709	Uncultured bacterium clone KuyT-ice-10	EU263777.1	97	Tibetan glacier	Massilia sp. 4106	JX566591.1	90	Chinese soil
Comamonadaceae-22304	Uncultured bacterium clone F35	FJ230911.1	98	Chinese river	Curvibacter	FN543107	98	Putative symbiont
Intrasporangiaceae-1447	Uncultured bacterium clone KuyT-IWPB-17	EU263719.1	99	Tibetan glacier	Eubacterium sp. 4c	AY216882	93	French peat
Sphingomonadaceae-11564	Uncultured bacterium clone GB7N87003GM6UD	HM728220	98	Antarctic soil	Novosphingobium sp. R1-11	KP182170	96	Korean soil
Unassigned-53430	Uncultured bacterium clone GB7N87003FR93L	HM732819.1	98	Antarctic soil	Rhizobium sp. AC86c1	AY776225.1	90	Ethiopian soil

# Supplementary Table 7: Marginal tests from distLM model of core predictors of tail population structure

MARGINAL TESTS					
Variable	SS(trace)	Pseudo-F	P	Prop.	
Leptolyngbya-40205	2026	2.9744	0.005	7.83E-02	
Microbacteriaceae-32521	3167.9	4.8847	0.001	0.12247	
Betaproteobacteria-5709	4014	6.4291	0.001	0.15518	
Gemmatimonadales-59904	3912.4	6.2373	0.001	0.15125	
Chloroflexi-37757	4394.3	7.1628	0.001	0.16988	
Unassigned-53430	4359.6	7.0947	0.001	0.16854	
Sphingomonadaceae-11564	2592.8	3.8991	0.001	0.10024	
Intrasporangiaceae-1447	2633.1	3.9666	0.002	0.1018	
Intrasporangiaceae-46072	2889.7	4.4018	0.001	0.11172	
Intrasporangiaceae-53638	3597.1	5.6533	0.001	0.13906	
Intrasporangiaceae-27964	3161.2	4.873	0.001	0.12221	
Betaproteobacteria-10679	2801	4.2502	0.001	0.10829	
Phormidium-45763	1723.9	2.4991	0.007	6.66E-02	
Xanthomonadaceae-51358	2411.6	3.5986	0.001	9.32E-02	
Comamonadaceae-22304	2725	4.1213	0.001	0.10535	
Sphingobacteriaceae-61341	4527.6	7.4262	0.001	0.17504	

Supplementary Table 8: Sequential tests from distLM model of core predictors of tail population structure

Variable	Adj R <sup>2</sup>	SS(trace)	Pseudo- <i>F</i>	<i>P</i>	Proportion explained	Cumulative variance
<i>Sphingobacteriaceae-61341</i>	0.15147	4527.6	7.4262	0.001	0.175	0.17504
<i>Microbacteriaceae-32521</i>	0.26094	3284	6.1843	0.001	0.127	0.302
<i>Intrasporangiaceae-46072</i>	0.34344	2487.1	5.2721	0.001	0.096	0.39815
<i>Chloroflexi-37757</i>	0.40126	1801.3	4.187	0.001	0.070	0.46779
<i>Intrasporangiaceae-27964</i>	0.44508	1406.3	3.53	0.001	0.054	0.52215
<i>Gemmatimonadales-59904</i>	0.48589	1278.4	3.46	0.001	0.049	0.57158
<i>Phormidium-45763</i>	0.50599	788.11	2.22	0.001	0.030	0.60205
<i>Leptolyngbya-40205</i>	0.52088	654.59	1.90	0.002	0.025	0.62735
<i>Xanthomonadaceae-51358</i>	0.5314	548.33	1.63	0.005	0.021	0.64855
<i>Betaproteobacteria-10679</i>	0.53992	495.83	1.50	0.024	0.019	0.66772
<i>Intrasporangiaceae-53638</i>	0.54681	454.44	1.40	0.058	0.018	0.68529
<i>Betaproteobacteria-5709</i>	0.55312	434.32	1.35	0.074	0.017	0.70208
<i>Comamonadaceae-22304</i>	0.55863	412.16	1.30	0.112	0.016	0.71801
<i>Intrasporangiaceae-1447</i>	0.56352	394.48	1.26	0.139	0.015	0.73326
<i>Sphingomonadaceae-11564</i>	0.5677	376.68	1.21	0.187	0.015	0.74783
Unassigned-53430	0.5711	359.44	1.17	0.255	0.014	0.76172

# Supplementary Table 9: Marginal tests from distLM model of environmental and core OTU predictors of total population structure

Variable	SS(trace)	Pseudo-F	P	Prop.
E	2351.7	3.8009	0.001	9.80E-02
N	2276.1	3.6659	0.001	9.48E-02
Chl a ug/g	1380.4	2.1353	0.019	5.75E-02
Z (masl)	1950.3	3.0947	0.003	8.12E-02
SLOPE (deg)	2217.8	3.5625	0.001	9.24E-02
ASPECT (deg, 0=N clockwise)	1861	2.9412	0.005	7.75E-02
ACCUMAREA (m^2)	705.35	1.0595	0.329	2.94E-02
FLOWLENGTH (m)	745.34	1.1214	0.271	3.10E-02
CURVATURE	623.13	0.93268	0.47	2.60E-02
WETNESS	538.76	0.80348	0.633	2.24E-02
PDDs (in summer)	3549	6.0717	0.001	0.14783
PostitiveHrs	1915.8	3.0353	0.003	7.98E-02
PDHrs	1826.8	2.8827	0.004	7.61E-02
IR (W)	783.44	1.1807	0.226	3.26E-02
IRh (hrs)	1579.3	2.4646	0.013	6.58E-02
IRkW	783.44	1.1807	0.258	3.26E-02
ACA (%)	1718.1	2.6979	0.01	7.16E-02
Leptolyngbya-40205	1725.2	2.7099	0.006	7.19E-02
Microbacteriaceae-32521	3062.2	5.1172	0.001	0.12756
Betaproteobacteria-5709	3148.9	5.2839	0.001	0.13117
Gemmatimonadales-59904	2730	4.4907	0.001	0.11372
Chloroflexi-37757	3180	5.344	0.001	0.13246
Unassigned-53430	2955.8	4.9144	0.001	0.12312
Sphingomonadaceae-11564	2736.5	4.5028	0.001	0.11399
Intrasporangiaceae-1447	1600.1	2.4993	0.014	6.67E-02
Intrasporangiaceae-46072	2090.7	3.3388	0.003	8.71E-02
Intrasporangiaceae-53638	2078.3	3.3172	0.005	8.66E-02
Intrasporangiaceae-27964	2223.5	3.5725	0.001	9.26E-02
Betaproteobacteria-10679	1582.9	2.4707	0.011	6.59E-02
Phormidium-45763	1317.8	2.0328	0.043	5.49E-02
Xanthomonadaceae-51358	1456.3	2.2602	0.009	6.07E-02
Comamonadaceae-22304	1625.1	2.5412	0.01	6.77E-02
Sphingobacteriaceae-61341	4713.8	8.5514	0.001	0.19635

Supplementary Table 10 : Sequential tests of environmental and core OTU predictors of total community structure

Variable	Adj R <sup>2</sup>	SS(trace)	Pseudo- <i>F</i>	<i>P</i>	Proportion explained	Cumulative variance
<i>Sphingobacteriaceae-61341</i>	0.173	4713.8	8.55	0.001	0.2	0.2
<i>Microbacteriaceae-32521</i>	0.3	3431.6	7.36	0.001	0.14	0.34
<i>Intrasporangiaceae-46072</i>	0.377	2158.9	5.2	0.001	0.09	0.43
<i>Intrasporangiaceae-27964</i>	0.419	1298	3.35	0.001	0.05	0.48
<i>Leptolyngbya-40205</i>	0.454	1108.7	3.04	0.001	0.05	0.53
<i>Chloroflexi-37757</i>	0.476	815.45	2.33	0.001	0.03	0.56
<i>Phormidium-45763</i>	0.496	726.07	2.16	0.001	0.03	0.59
N	0.512	643.2	1.98	0.003	0.03	0.62
E	0.526	570.53	1.8	0.002	0.02	0.64
IRh (hrs)	0.535	473.19	1.53	0.018	0.02	0.66
<i>Intrasporangiaceae -1447</i>	0.543	447.6	1.47	0.05	0.02	0.68
Unassigned-53430	0.549	403.23	1.34	0.085	0.02	0.7
<i>Betaproteobacteria-5709</i>	0.555	384.11	1.29	0.137	0.02	0.72
PDHrs	0.563	426.21	1.46	0.045	0.02	0.73
<i>Gemmatimonadales-59904</i>	0.57	379.04	1.32	0.133	0.02	0.75
IR (W)	0.574	349.92	1.23	0.19	0.01	0.76
<i>Xanthomonadaceae-51358</i>	0.579	347.69	1.24	0.188	0.01	0.78
<i>Betaproteobacteria-10679</i>	0.585	344.71	1.24	0.227	0.01	0.79
PositiveHrs	0.588	319.18	1.16	0.308	0.01	0.81
<i>Sphingomonadaceae-11564</i>	0.59	291.21	1.07	0.405	0.01	0.82
PDDs (in summer)	0.599	306.95	1.15	0.296	0.01	0.86
Z (masl)	0.602	290.48	1.09	0.352	0.01	0.87
<i>Sphingomonadaceae-11564</i>	0.602	264.4	1	0.459	0.01	0.86

Supplementary Table 11: Sequential tests of environmental and core OTU predictors of tail community structure

Variable	Adj R <sup>2</sup>	SS(trace)	Pseudo- <i>F</i>	<i>P</i>	Proportion explained	Cumulative variance
<i>Sphingobacteriaceae-61341</i>	0.17	4985.8	8.36	0.001	0.19	0.19
<i>Microbacteriaceae-32521</i>	0.292	3584.5	7.05	0.001	0.14	0.33
<i>Intrasporangiaceae-46072</i>	0.367	2287.7	5.03	0.001	0.09	0.42
<i>Intrasporangiaceae-27964</i>	0.408	1389.6	3.27	0.001	0.05	0.47
<i>Leptolyngbya-40205</i>	0.441	1172.5	2.92	0.001	0.05	0.52
<i>Chloroflexi-37757</i>	0.464	884.78	2.3	0.001	0.03	0.55
<i>Phormidium-45763</i>	0.483	791.69	2.13	0.001	0.03	0.58
N	0.5	700.72	1.95	0.002	0.03	0.61
E	0.513	623.48	1.78	0.005	0.02	0.63
<i>Intrasporangiaceae-1447</i>	0.523	526.4	1.53	0.022	0.02	0.66
IRh (hrs)	0.531	496.06	1.47	0.036	0.02	0.67
<i>Unassigned-53430</i>	0.537	441.15	1.33	0.09	0.02	0.69
PDHrs	0.542	414.92	1.26	0.168	0.02	0.71
<i>Betaproteobacteria-5709</i>	0.551	466.38	1.45	0.05	0.02	0.73
<i>Gemmatimonadales-59904</i>	0.556	408.67	1.28	0.165	0.02	0.74
IRkW	0.561	383.75	1.22	0.202	0.01	0.76
<i>Xanthomonadaceae-51358</i>	0.566	379.77	1.22	0.208	0.01	0.77
Z (masl)	0.571	379.05	1.23	0.208	0.01	0.79
<i>Betaproteobacteria-10679</i>	0.574	346.03	1.13	0.328	0.01	0.8
WETNESS	0.576	334.33	1.1	0.344	0.01	0.81
<i>Sphingomonadaceae-11564</i>	0.577	313.92	1.03	0.421	0.01	0.82
<i>Intrasporangiaceae-53638</i>	0.581	341.19	1.13	0.342	0.01	0.84
ACA (%)	0.582	312.92	1.04	0.443	0.01	0.85
PDDs (in summer)	0.587	344.06	1.16	0.324	0.01	0.86
CURVATURE	0.592	328.7	1.12	0.36	0.01	0.88
Chlorophyll a $\mu\text{g g}^{-1}$	0.592	296.43	1.01	0.45	0.01	0.89
PositiveHrs	0.593	298.39	1.02	0.438	0.01	0.9
<i>Betaproteobacteria-5709</i>	0.593	291.84	1	0.474	0.01	0.89



Supplementary Table 12: Marginal tests from distLM model of environmental and core OTU predictors of tail population structure

Variable	SS(trace)	Pseudo-F	P	Prop.
E	2472.3	3.6988	0.001	0.10
N	2445.5	3.65E+00	0.001	0.09
Chl a ug/g	1499.8	2.15E+00	0.021	0.06
Z (masl)	2101.1	3.09E+00	0.002	0.08
SLOPE (deg)	2369	3.53E+00	0.001	0.09
ASPECT (deg, 0=N clockwise)	1969.2	2.88E+00	0.001	0.08
ACCUMAREA (m^2)	769.03	1.07E+00	0.318	0.03
FLOWLENGTH (m)	812.22	1.13E+00	0.289	0.03
CURVATURE	668.69	9.29E-01	0.477	0.03
WETNESS	599.19	8.30E-01	0.59	0.02
PDDs (in summer)	3771.8	5.97E+00	0.001	0.15
PostitiveHrs	2064.1	3.04E+00	0.002	0.08
PDHrs	1969.8	2.89E+00	0.003	0.08
IR (W)	825.09	1.15E+00	0.25	0.03
IRh (hrs)	1654.7	2.39E+00	0.008	0.06
IRkW	825.09	1.15E+00	0.275	0.03
Irhhrs	1653.8	2.39E+00	0.013	0.06
ACA (%)	1802.4	2.62E+00	0.007	0.07
Leptolyngbya-40205	1809	2.6319	0.008	0.07
Microbacteriaceae-32521	3228	4.99E+00	0.001	0.12479
Betaproteobacteria-5709	3288	5.10E+00	0.001	0.12712
Gemmatimonadales-59904	2803.4	4.25E+00	0.001	0.10838
Chloroflexi-37757	3354	5.21E+00	0.001	0.12967
Unassigned-53430	3136.9	4.83E+00	0.001	0.12127
Sphingomonadaceae-11564	2850.5	4.33E+00	0.001	0.1102
Intrasporangiaceae-1447	1672.1	2.42E+00	0.019	6.46E-02
Intrasporangiaceae-46072	2197.4	3.25E+00	0.005	8.50E-02
Intrasporangiaceae-53638	2191.5	3.24E+00	0.006	8.47E-02
Intrasporangiaceae-27964	2328.9	3.46E+00	0.004	9.00E-02
Betaproteobacteria-10679	1639.1	2.368	0.016	6.34E-02
Phormidium-45763	1390.3	1.99E+00	0.042	5.38E-02
Xanthomonadaceae-51358	1559.1	2.2449	0.006	6.03E-02
Comamonadaceae-22304	1729.1	2.51E+00	0.007	6.68E-02
Sphingobacteriaceae-61341	4985.8	8.36E+00	0.001	0.19275