



Bacterial community shift in depth profiles of Alaskan permafrost soil ecosystem

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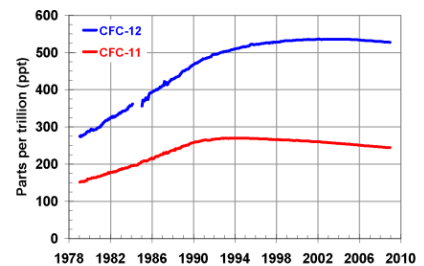
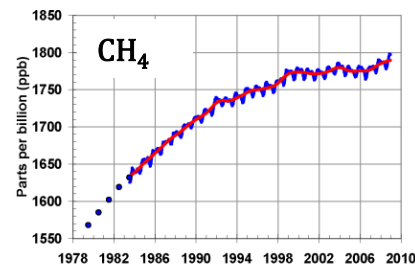
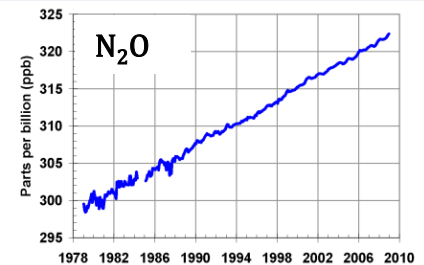
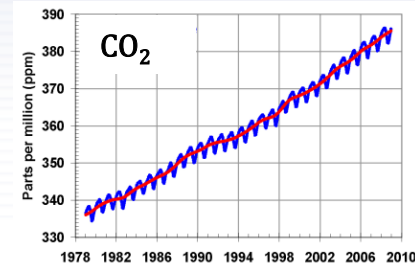


Permafrost distribution

- Circum-Arctic map of permafrost and ground ice conditions







http://www.lter.uaf.edu/bnz_permafrost.cfm



<http://www.esrl.noaa.gov/gmd/aggi/>

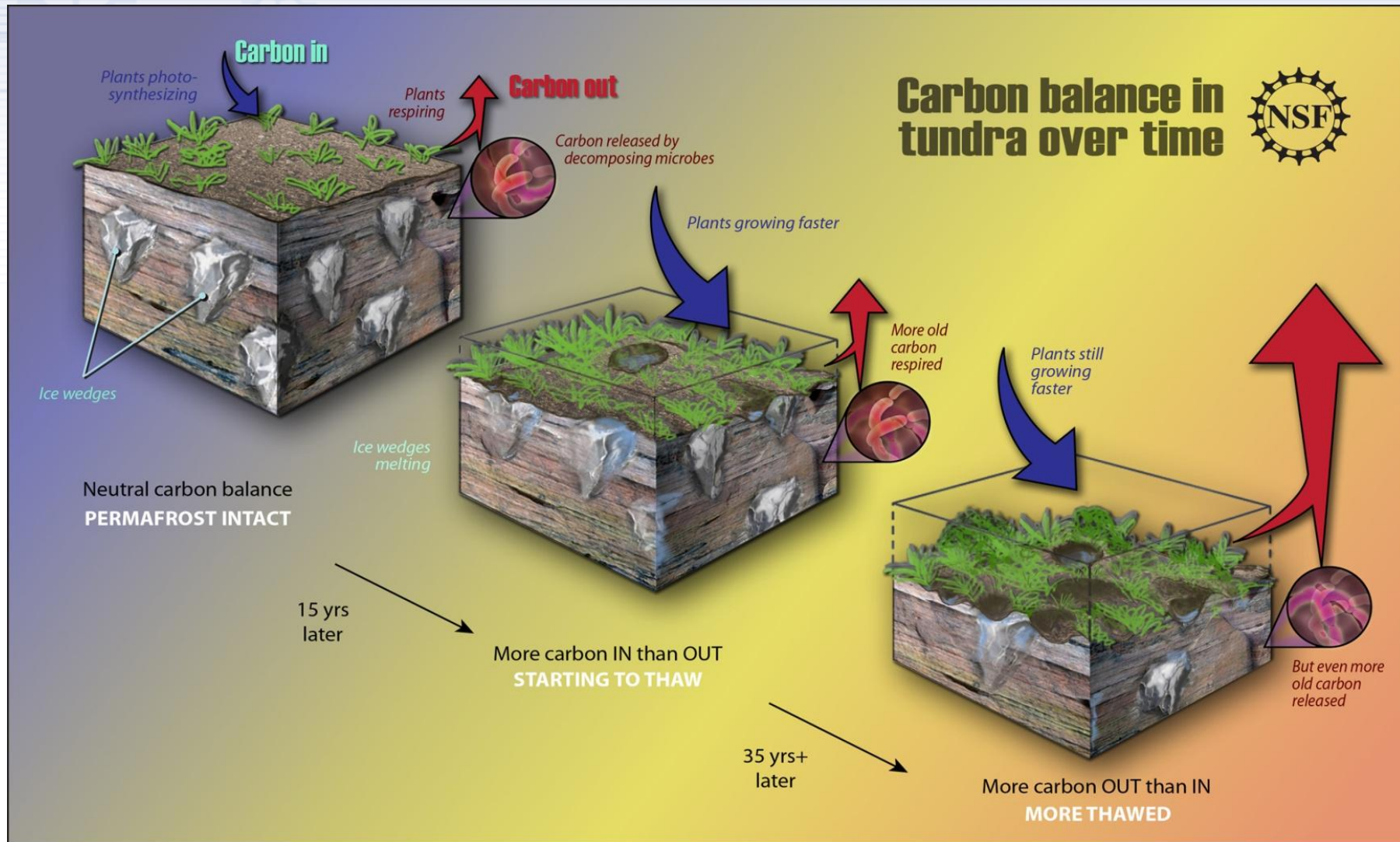
Permafrost

-  Isolated
-  Sporadic
-  Discontinuous
-  Continuous





Carbon balance in tundra soils



Study area

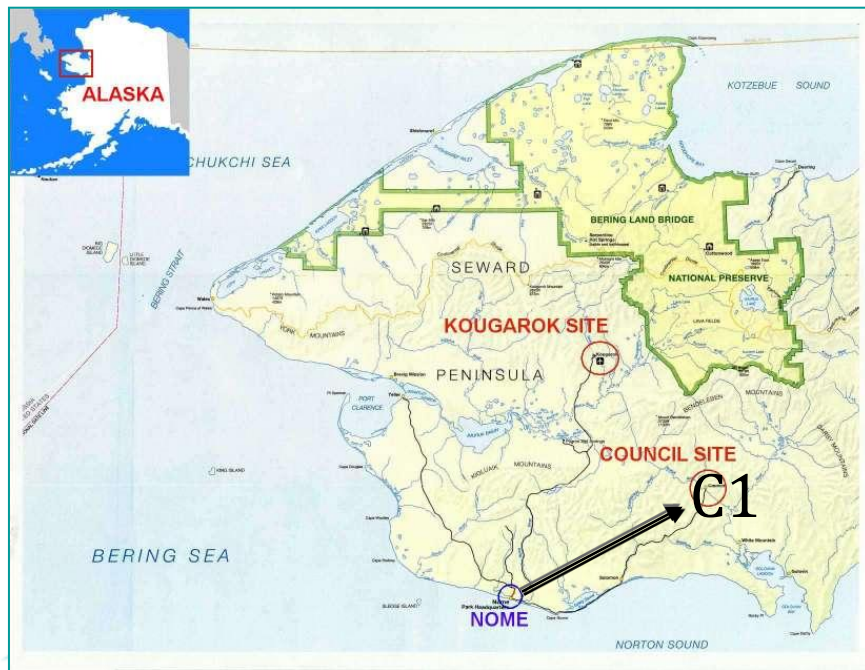
Council in Seward Peninsular, Alaska ($64^{\circ} 50.593' \text{ N}$, $163^{\circ} 42.484' \text{ W}$)

North wind or Northwest, $2\text{-}6 \text{ ms}^{-1}$ (max. 12 ms^{-1})

Air temp, $-30 - 20^{\circ}\text{C}$; soil temp, $-15 - 10^{\circ}\text{C}$

Maximum snow depth; 70 cm in May and November

Sampling date: 15~19 July, 2010





Plants community




❖ Characterization

- The border line of the Boreal Coniferous Forest
- Representative plants in Tundra area
- The root of plant reaches until 30 cm of litter layer and does not until to permafrost layer
- Significant distribution of plants depends on the moisture content

Scientific name	Common name	Importance Value
<i>Vaccinium uliginosum</i>	blueberry	47.9
<i>Ledum palustre</i>	labrador tea	31.0
<i>Betula nana</i>	dwarf birch	27.9
<i>Carex aquatilis</i>	water sedge	22.8
<i>Rubus chamaemorus</i>	cloud berry	22.2
<i>Erophorum scheuchzeri</i>	cotton grass	19.9
<i>Empetrum nigrum</i>	crowberry	14.5
<i>Vaccinium vitis-idaea</i>	cowberry	13.8



Sample information

Depth(cm)	Soil Character		C1	C2	C3
			64° 50' 36" 163°42' 29"	64°50' 34" 163°42' 34"	64° 50' 38" 163° 42' 39"
0-5 cm		undecomposed litter layer, yellow brown	C1-0	C2-0	C3-0
5-10 cm			C1-5	C2-5	C3-5
10-15 cm			C1-10	C2-10	C3-10
15-20 cm		decomposed layer, reddish brown	C1-15	C2-15	C3-15
20-25 cm			C1-20	C2-20	C3-20
25-30 cm			C1-25	C2-25	C3-25
30-30 cm		soil with ice, grey color	C1-30	C2-30	C3-30



Soil physical properties (C1)

	Depth (cm)	pH (1:5)	EC (dS m ⁻¹)	Total Organic Carbon (%)	Total Nitrogen (%)	Total Phosphorus (%)
Organic layer	0-5	4.65 (0.24)	0.05 (0.01)	35.37 (1.97)	1.13 (0.02)	0.10 (0.01)
	5-10	4.96 (0.05)	0.04 (0.01)	36.10 (0.26)	1.09 (0.22)	0.10 (0.03)
	10-15	4.98 (0.19)	0.03 (0.01)	36.76 (0.34)	1.67 (0.32)	0.12 (0.02)
	15-20	4.97 (0.14)	0.03 (0.01)	36.43 (0.50)	1.96 (0.20)	0.12 (0.01)
	20-25	5.01 (0.13)	0.03 (0.01)	34.88 (2.60)	1.45 (0.40)	0.11 (0.03)
Mineral layer	25-30	5.37 (0.18)	0.03 (0.01)	21.69 (12.07)	0.68 (0.29)	0.05 (0.01)
	30-35	5.36 (0.06)	0.03 (0.01)	17.15 (0.68)	0.60 (0.08)	0.05 (0.01)

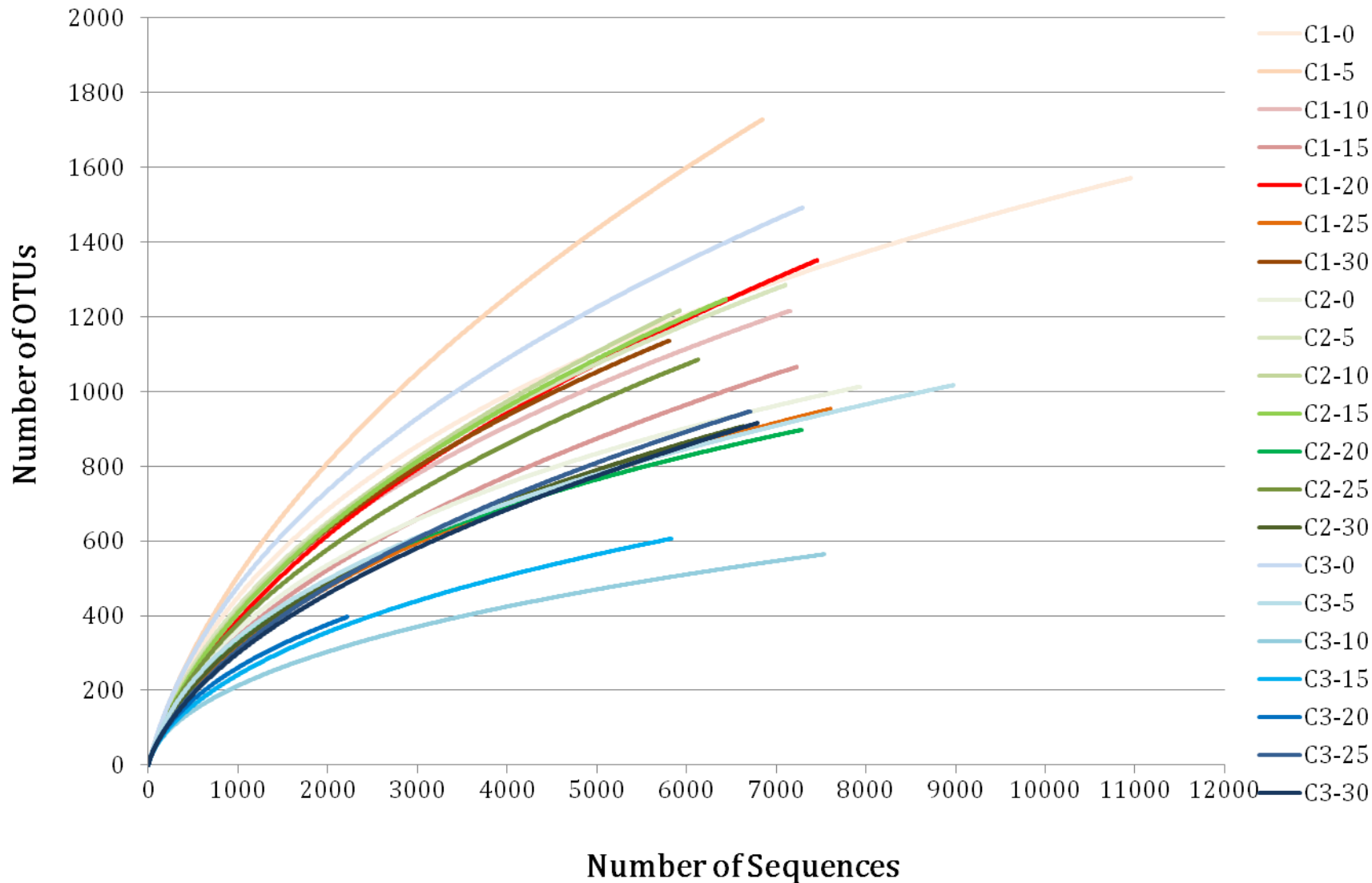


Diversity indices

Sample	Total read	No. of Bact	No of Euk	OTUs	ACE	Chao1	Shannon	Simpson
C1-0	10955	10922	33	1569	2870.5	2392.9	6.06	0.010
C1-5	6845	6839	6	1725	5483.4	3884.1	6.32	0.007
C1-10	7154	7154	0	1216	2811.5	2207.7	5.87	0.010
C1-15	7230	7220	10	1059	3057.6	2221.8	5.41	0.019
C1-20	7454	7447	7	1346	3955.1	2868.1	5.51	0.024
C1-25	7601	7600	1	952	2140.3	1646.8	5.22	0.019
C1-30	5805	5795	10	1133	2682.3	1959.1	5.82	0.009
C2-0	7941	7930	11	1012	1783.4	1533.5	5.57	0.012
C2-5	7104	7097	7	1282	3039.8	2374.1	5.86	0.011
C2-10	5924	5924	0	1217	3524.6	2532.3	5.83	0.009
C2-15	6438	6434	4	1246	3217.1	2431.0	5.65	0.020
C2-20	7280	7280	0	897	1572.5	1326.0	5.26	0.021
C2-25	6127	6125	2	1083	3008.7	2210.4	5.65	0.011
C2-30	6637	6636	1	906	1981.7	1518.5	5.39	0.013
C3-0	7292	7290	2	1490	3696.7	2780.0	6.28	0.005
C3-5	8979	8975	4	1014	2167.8	1815.5	5.54	0.011
C3-10	7538	7534	4	561	1137.3	906.9	4.63	0.024
C3-15	5832	5831	1	605	1273.8	1042.1	4.77	0.022
C3-20	2222	2222	0	397	909.6	762.5	4.80	0.020
C3-25	6713	6709	4	945	2416.9	1858.6	5.13	0.019
C3-30	6798	6798	0	916	2628.2	1853.1	5.08	0.019

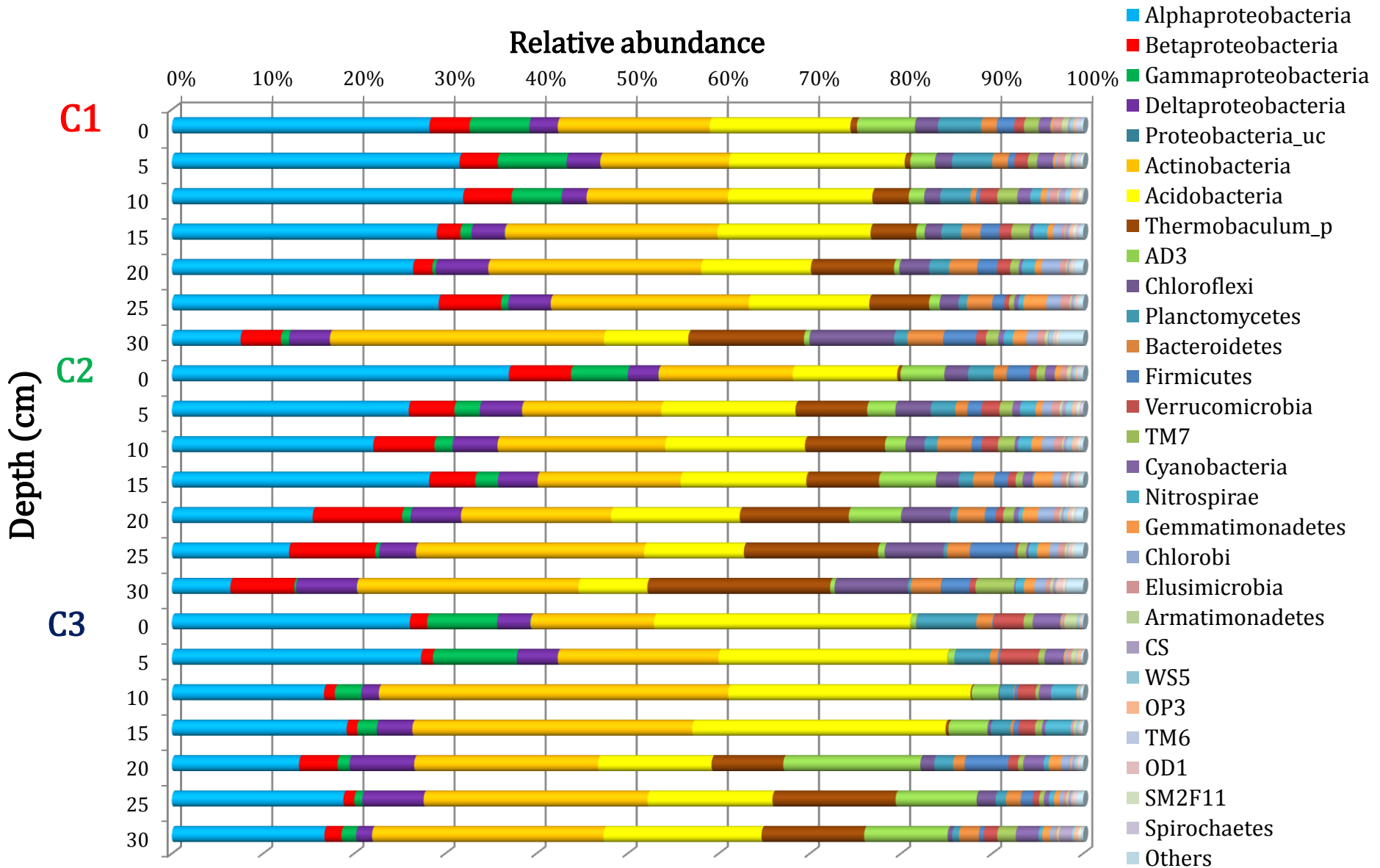


Rarefaction analysis





Microbial community (Phylum level)



Name	Assignment	C1							C2							C3						
		0	5	10	15	20	25	30	0	5	10	15	20	25	30	0	5	10	15	20	25	30
Cluster_001	Proteobacteria;;Alphaproteobacteria;;Rhizobiales;;Bradyrhizobiaceae;;Pseudolabrys;EU937836_s	1.6	2.9	7.6	14.7	17.1	17.6	2.1	6.8	8.0	10.0	12.1	9.6	4.8	2.3	0.0	1.0	1.6	5.7	8.2	9.6	8.8
Cluster_002	Thermobaculum_p;;Thermobaculum_c;;AY221067_o;;AY221067_f;;AY221067_g;AY221067_g_uc	0.1	0.1	2.8	4.0	7.3	5.2	11.2	0.2	6.6	6.8	5.7	10.2	12.5	17.7	0.0	0.0	0.1	0.2	6.5	11.6	9.3
Cluster_003	Proteobacteria;;Alphaproteobacteria;;Rhizobiales;;Bradyrhizobiaceae;;Afipia_g1;Afipia birgiae	6.3	5.7	6.5	2.4	1.5	3.5	0.9	5.6	2.6	2.2	3.3	1.7	1.1	0.3	2.9	2.9	3.6	2.8	1.2	2.8	2.8
Cluster_004	Actinobacteria;;Actinobacteria_c;;Micrococcales;;Intrasporangiaceae;;Oryzihumus;Oryzihumus_uc	2.0	2.8	1.3	3.2	4.8	6.4	4.7	6.1	1.0	2.4	3.0	4.3	5.7	3.7	0.0	0.1	0.1	0.7	5.7	4.7	5.7
Cluster_005	Actinobacteria;;Thermoleophilia;;Solirubrobacteriales;;Solirubrobacteraceae;;Solirubrobacter;EU861899_s	2.1	1.2	3.5	6.3	1.5	0.9	1.0	1.0	3.7	4.8	2.2	1.8	1.7	1.6	0.8	1.1	4.1	4.4	2.4	1.5	3.0
Cluster_006	Actinobacteria;;Actinobacteria_c;;Streptosporangiales;;Thermomonosporaceae;;EU861937_g;FJ625358_s	1.3	0.6	1.3	0.3	0.0	0.1	0.5	1.0	1.6	0.7	0.2	0.1	0.1	0.1	0.9	4.4	17.7	9.7	0.1	0.4	0.0
Cluster_007	Actinobacteria;;Acidimicrobiia;;Acidimicrobiales;;Aciditerrimonas_f;;Aciditerrimonas;Aciditerrimonas_uc	1.5	1.0	1.1	3.5	2.6	2.9	0.7	0.7	1.0	1.5	1.1	1.2	1.0	0.5	1.3	1.3	5.3	4.7	3.1	3.7	4.2
Cluster_008	Proteobacteria;;Gammaproteobacteria;;Xanthomonadales;;Sinobacteraceae;;EU150278_g;EU150278_s	2.8	3.3	2.3	0.4	0.1	0.4	0.2	3.3	0.9	0.8	0.8	0.1	0.0	0.0	3.6	5.9	1.6	0.7	0.5	0.3	0.2
Cluster_009	Proteobacteria;;Alphaproteobacteria;;Rhizobiales;;Bradyrhizobiaceae;;Pseudolabrys;DQ404659_s	0.6	0.3	0.8	1.6	1.4	2.8	1.0	1.8	1.1	1.0	1.6	1.2	3.3	1.9	1.5	1.3	0.2	0.2	1.2	1.2	0.5
Cluster_010	Acidobacteria;;Acidobacteria_c;;Acidobacteriales;;Koribacter_f;;EU881356_g;AB238768_s	0.0	0.1	1.2	0.8	0.2	0.7	0.2	0.2	0.5	0.7	0.6	0.4	0.0	0.0	0.1	0.3	8.4	10.2	0.9	0.9	0.0



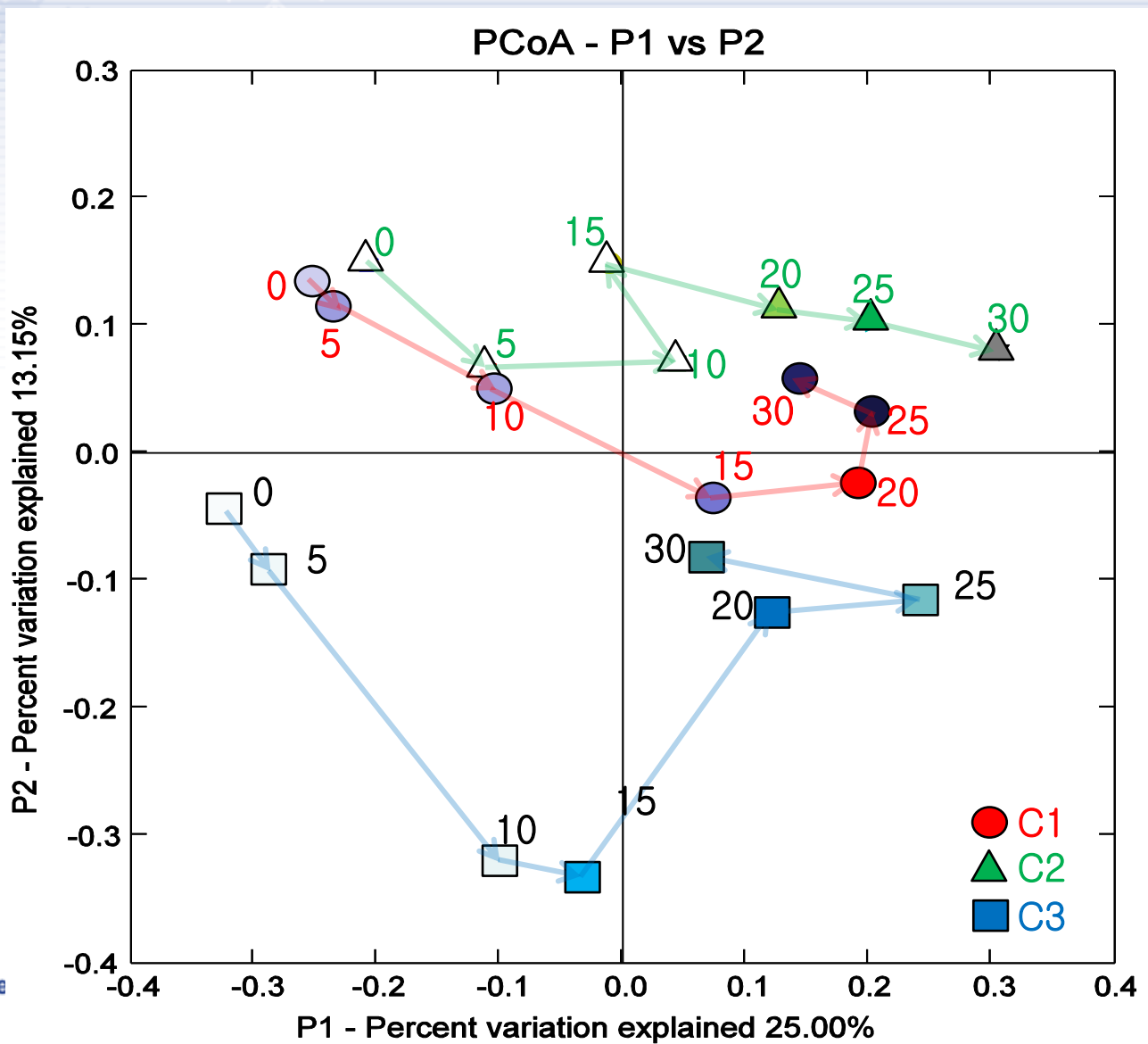
Abundant species

>10.1
5.1~10.0
1.1~5.0
0.6~1.0
0.1~0.5
0

Name	Taxonomy	C1							C2							C3						
		0	5	10	15	20	25	30	0	5	10	15	20	25	30	0	5	10	15	20	25	30
Cluster_011	Actinobacteria;;Actinobacteria_c;;Micrococcales;;Intrasporangiaceae;;Oryzihumus;GQ397075_s	0.6	0.8	0.3	1.1	2.5	2.2	1.4	0.7	0.3	0.6	1.2	1.3	1.5	1.0	0.0	0.0	0.0	0.1	2.5	1.9	5.6
Cluster_012	Acidobacteria;;Holophagae;;EU937852_o;;EU937852_f;;EU937852_g;EU937852_s	0.0	0.1	0.8	3.0	2.1	2.3	1.1	0.1	1.4	2.0	1.4	2.8	2.6	1.4	0.0	0.0	0.0	0.0	1.2	1.1	0.3
Cluster_013	Acidobacteria;;Acidobacteria_c;;Acidobacteriales;;Koribacter_f;;EU881356_g;EF600559_s	0.1	0.4	1.3	3.1	1.1	0.9	0.2	1.0	1.9	2.8	1.1	1.1	1.0	0.6	0.2	0.3	3.1	1.2	0.2	0.4	0.1
Cluster_014	Proteobacteria;;Betaproteobacteria;;DQ009366_o;;EF516600_f;;DQ404630_g;DQ404630_s	0.1	0.5	1.1	0.5	0.4	2.9	1.2	0.6	0.9	2.2	1.6	3.8	2.4	1.7	0.0	0.1	0.3	0.1	1.1	0.2	0.7
Cluster_015	Acidobacteria;;Acidobacteria_c;;Acidobacteriales;;Acidobacteriaceae;;Acidobacterium;DQ906073_s	0.4	0.4	0.3	0.6	0.8	0.1	0.2	0.4	0.5	0.3	0.4	0.1	0.1	0.0	2.6	2.4	2.1	2.6	0.7	2.4	2.7
Cluster_016	Proteobacteria;;Alphaproteobacteria;;Rhizobiales;;Bradyrhizobiaceae;;Pseudolabrys;EU801228_s	0.6	1.6	2.3	1.0	0.5	0.2	0.1	2.0	1.6	0.7	0.3	0.1	0.0	0.0	0.1	3.0	2.3	1.5	0.0	0.1	0.1
Cluster_017	AD3;;AD3_c;;AD3_o;;EF018548_f;;EF018548_g;EF018646_s	0.3	0.2	0.0	0.1	0.0	0.5	0.0	2.4	0.6	0.7	3.3	3.8	0.4	0.1	0.0	0.0	0.0	0.0	10.0	3.4	0.1
Cluster_018	Actinobacteria;;Thermoleophilia;;Solirubrobacteriales;;Conexibacteraceae;;Conexibacter;Conexibacter_uc	0.8	0.8	1.2	1.5	0.3	0.2	0.4	0.3	1.0	0.6	0.9	0.1	0.0	0.0	0.4	0.3	2.4	3.5	0.8	1.3	0.5
Cluster_019	Proteobacteria;;Alphaproteobacteria;;Rhizobiales;;Beijerinckiaceae;;DQ984545_g;DQ984545_g_uc	2.1	2.0	1.3	0.1	0.2	0.2	0.2	2.1	0.5	0.1	0.6	0.0	0.0	0.0	1.5	2.2	0.1	0.5	0.2	0.0	0.1
Cluster_020	Proteobacteria;;Deltaproteobacteria;;DQ906906_o;;EU335336_f;;EU335336_g;EU335383_s	0.0	0.0	0.1	0.4	0.6	0.9	0.2	0.0	0.3	0.8	1.4	1.4	0.6	0.4	0.1	0.5	0.6	2.2	4.3	3.8	0.4



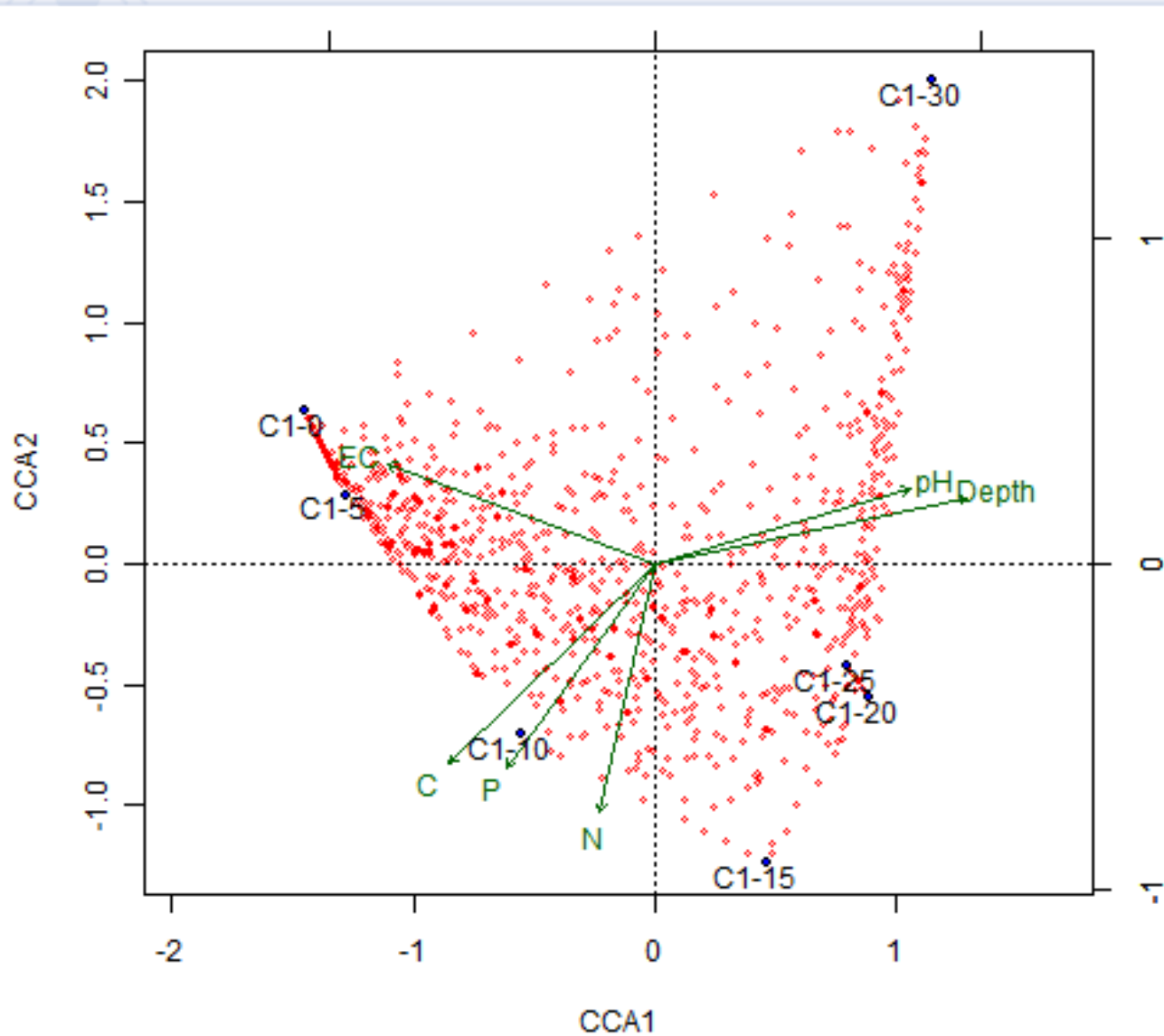
Com-com analysis



FastUniFrac
3% cutoff



Correlation with environmental factors





Conclusions

1. Unexpected diverse microbes and some indigenous bacterial division such as *Thermobaculum* were observed.
2. Bacterial community shifts were recognized along the soil depth profiles in all sites based on the analysis of Bacterial communities and community clustering.
3. Different bacterial community patterns below 30 cm were notable for further study.
4. Significant correlation between bacterial communities along depths and environmental factors was detected.
5. The study presented here may extend new perspectives for the research regarding the correlation between bacterial communities and environmental factors in the high Arctic permafrost soil of Alaska.

