Soil variable	R^2	*p*-value
Total carbon	0.62	***
Total nitrogen	0.62	***
Gravimetric moisture	0.60	***
pH	0.59	***
Soil depth	0.51	***
Dissolved organic carbon	0.49	***
Total Dissolved Nitrogen (TDN)	0.49	***
Microbial biomass carbon (MBC)	0.42	***
Microbial biomass nitrogen (MBN)	0.42	***
Ammonium (NH_4)	0.35	***

Table S1. Goodness of fit (squared correlation coefficient, R^2; including *p*-values) statistics of the biogeochemical vectors that overlie the PCoA biplots in Figure 2. TDN is total dissolved nitrogen. Data used includes every sample across soil depth and time (n = 163, see Figure 1). *** indicates $p \leq 0.0001$.

Soil variable	ASV richness		Faith's diversity		Faith's diversity		Faith's diversity	
			All layers[a]		Organic layer[b]		Mineral layer[c]	
	r_S	*p*-value	r_S	*p*-value	r_S	*p*-value	r_S	*p*-value
pH	-0.408	***	0.642	***	0.275	*	0.045	NS
Soil depth	-0.408	***	0.638	***	0.394	***	-0.016	NS
PO_4	-0.256	***	0.059	NS	-0.425	***	-0.062	NS
MBP	0.274	***	-0.537	***	-0.553	***	0.178	NS
Total C	0.318	***	-0.694	***	-0.565	***	-0.148	NS
Total N	0.349	***	-0.542	***	0.311	**	-0.110	NS
Gravimetric moisture	0.354	***	-0.703	***	-0.230	*	-0.273	*
NH_4	0.364	***	-0.64	***	0.121	NS	-0.278	*
MBN	0.396	***	-0.678	***	-0.487	***	-0.048	NS
MBC	0.398	***	-0.675	***	-0.494	***	-0.030	NS

Table S2. Spearman correlations between either ASV richness or Faith's phylogenetic diversity index and the same soil variables used as bi-plot vectors in Figures 2 and Table S1 determined using *qiime diversity alpha-correlation* function. Faith's phylogenetic diversity was either calculated for the complete dataset (163 samples, a) or for organic (5-10 cm depth, b) and mineral (20-50 cm depth, c) soil layers separately. Soil edaphic variables are microbial biomass pools (carbon, MBC; nitrogen, MBN; and phosphorus, MBP), pH, total soil C and soluble nutrients (ammonium, NH_4; nitrate; NO_3; and phosphate, PO_4). Data used includes every sample across soil depth and time (n = 163, see Figure 1), and significance is shown as NS (not significant), $p > 0.05$; *, $p < 0.05$; **, $p < 0.01$; and ***, $p \leq 0.001$.

ASV#	Phylum	Class	Order	Family	Genus	Overall relative abundance
1	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae		2.24
2	Chloroflexi	AD3	AD3	AD3	AD3	1.14
3	Acidobacteriota	Acidobacteriae	Acidobacteriales			0.98
4	WPS-2	WPS-2	WPS-2	WPS-2	WPS-2	0.88
5	Proteobacteria	Gammaproteobacteria	WD260	WD260	WD260	0.87
6	Acidobacteriota	Acidobacteriae	Subgroup_2	Subgroup_2	Subgroup_2	0.85
7	Chloroflexi	AD3	AD3	AD3	AD3	0.76
8	Chloroflexi	AD3	AD3	AD3	AD3	0.73
9	Verrucomicrobiota	Verrucomicrobiae	Chthoniobacterales	Chthoniobacteraceae	Candidatus_Udaeobacter	0.69
10	Acidobacteriota	Acidobacteriae	Bryobacterales	Bryobacteraceae	Bryobacter	0.66
11	Acidobacteriota	Acidobacteriae	Acidobacteriales			0.60
12	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_Incertae_Sedis	Unknown_Family	Acidibacter	0.59
13	Acidobacteriota	Acidobacteriae	Subgroup_2	Subgroup_2	Subgroup_2	0.58
14	Acidobacteriota	Blastocatellia	Pyrinomonadales	Pyrinomonadaceae	RB41	0.56
15	Proteobacteria	Alphaproteobacteria	Elsterales			0.56
16	Acidobacteriota	Acidobacteriae	Subgroup_2	Subgroup_2	Subgroup_2	0.55
17	Acidobacteriota	Acidobacteriae	Acidobacteriales	Koribacteraceae	Candidatus_Koribacter	0.53
18	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae		0.52
19	Chloroflexi	Dehalococcoidia	S085	S085	S085	0.50
20	Acidobacteriota	Acidobacteriae	Acidobacteriales	Acidobacteriaceae	Acidipila	0.49

Table S3. Overall relative abundance of the 20 most abundant ASVs across all soil depths and time (n=163 soil samples, see Figure 1).

ASV_ID	Rel Abundance	Phylum	Class	Order	Family	Genus	r_S	*p*
1346	0.01	Bacteroidota	Bacteroidia	Sphingobacteriales	KD3-93	KD3-93	0.24	0.00
176	0.11	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_Incertae_Sedis	Unknown_Family	Candidatus_Ovatusbacter	0.24	0.00
4976	0.00	Bdellovibrionota	Bdellovibrionia	Bdellovibrionales	Bdellovibrionaceae	Bdellovibrio	0.23	0.00
6283	0.00	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae		0.23	0.00
2359	0.00	Acidobacteriota	Acidobacteriae	Solibacterales	Solibacteraceae	Candidatus_Solibacter	0.22	0.00
4664	0.00	Actinobacteriota	Acidimicrobiia	IMCC26256	IMCC26256	IMCC26256	0.22	0.00
661	0.03	Acidobacteriota	Acidobacteriae	Subgroup_2	Subgroup_2	Subgroup_2	0.22	0.01
8852	0.00	Verrucomicrobiota	Verrucomicrobiae	Methylacidiphilales	Methylacidiphilaceae		0.21	0.01
8583	0.00	Verrucomicrobiota	Chlamydiae	Chlamydiales	cvE6	cvE6	0.21	0.01
10767	0.00	Proteobacteria	Gammaproteobacteria	Diplorickettsiales	Diplorickettsiaceae		0.21	0.01
6386	0.00	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae		0.21	0.01
218	0.09	Proteobacteria	Alphaproteobacteria	Micropepsales	Micropepsaceae	uncultured_Alphaproteobacteria	0.21	0.01
6418	0.00	Actinobacteriota	Thermoleophilia	Solirubrobacterales	Solirubrobacteraceae	Conexibacter	0.20	0.01
10346	0.00	Bdellovibrionota	Oligoflexia	Oligoflexales			0.20	0.01
10367	0.00	Proteobacteria	Alphaproteobacteria	Paracaedibacterales	Paracaedibacteraceae	Candidatus_Finniella	0.20	0.01
1974	0.01	Myxococcota	Polyangia	Polyangiales	Polyangiaceae	Pajaroellobacter	-0.24	0.00
3704	0.00	Myxococcota	Polyangia	Polyangiales	Polyangiaceae	Pajaroellobacter	-0.24	0.00
1495	0.01	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Roseiarcus	-0.24	0.00
1804	0.01	Acidobacteriota	Acidobacteriae	Acidobacteriales			-0.24	0.00
1571	0.01	Acidobacteriota	Acidobacteriae	Bryobacterales	Bryobacteraceae	Bryobacter	-0.25	0.00
6005	0.00	Proteobacteria	Gammaproteobacteria	Diplorickettsiales	Diplorickettsiaceae	Aquicella	-0.25	0.00
7830	0.00	Proteobacteria	Gammaproteobacteria	Burkholderiales			-0.25	0.00
2451	0.00	Acidobacteriota	Acidobacteriae	Acidobacteriales			-0.26	0.00
10378	0.00	Bdellovibrionota	Bdellovibrionia	Bdellovibrionales	Bdellovibrionaceae	Bdellovibrio	-0.26	0.00
3272	0.00	Myxococcota	Myxococcia	Myxococcales	Myxococcaceae	Myxococcaceae	-0.27	0.00

4663	0.00	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae		-0.27	0.00
3525	0.00	Proteobacteria	Gammaproteobacteria	Diplorickettsiales	Diplorickettsiaceae		-0.28	0.00
3261	0.00	Proteobacteria	Gammaproteobacteria	Burkholderiales	A21b	A21b	-0.29	0.00
3095	0.00	Actinobacteriota	Actinobacteria	Frankiales	Acidothermaceae	Acidothermus	-0.29	0.00
2017	0.01	Acidobacteriota	Acidobacteriae	Bryobacterales	Bryobacteraceae	Bryobacter	-0.30	0.00

Table S4. Spearman correlations of the 15 most strongly positively (top) and negatively (bottom) correlated ASVs with soil depth. Values were determined using the Python script *observation_metadata_correlation.py*. Data are from all 163 samples, across seasonal time and soil depth (see Figure 1). Positive correlation coefficients (r_{S}) mean that ASV relative abundances increased with increasing soil depth and negative r_{S} values mean that taxa relative abundances decreased with increasing soil depth.

ASV_ID	Rel Abundance	Phylum	Class	Order	Family	Genus	r_S	p
1862	0.01	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae		0.24	0.00
1346	0.01	Bacteroidota	Bacteroidia	Sphingobacteriales	KD3-93	KD3-93	0.23	0.00
10767	0.00	Proteobacteria	Gammaproteobacteria	Diplorickettsiales	Diplorickettsiaceae		0.23	0.00
176	0.11	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_Incertae_Sedis	Unknown_Family	Candidatus_Ovatusbacter	0.23	0.00
3260	0.00	Verrucomicrobiota	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae		0.23	0.00
8583	0.00	Verrucomicrobiota	Chlamydiae	Chlamydiales	cvE6	cvE6	0.22	0.00
2359	0.00	Acidobacteriota	Acidobacteriae	Solibacterales	Solibacteraceae	Candidatus_Solibacter	0.21	0.01
2566	0.00	Bacteroidota	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter	0.21	0.01
9527	0.00	Cyanobacteria	Sericytochromatia	Sericytochromatia	Sericytochromatia	Sericytochromatia	0.21	0.01
5199	0.00	Chloroflexi	AD3	AD3	AD3	AD3	0.21	0.01
7509	0.00	Patescibacteria	Saccharimonadia	Saccharimonadales	Saccharimonadales	Saccharimonadales	0.21	0.01
10346	0.00	Bdellovibrionota	Oligoflexia	Oligoflexales	0	0	0.21	0.01
5184	0.00	Bdellovibrionota	Bdellovibrionia	Bdellovibrionales	Bdellovibrionaceae	Bdellovibrio	0.21	0.01
1620	0.01	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	0	0.21	0.01
3944	0.00	Proteobacteria	Gammaproteobacteria	Diplorickettsiales	Diplorickettsiaceae	Aquicella	0.21	0.01
4384	0.00	Proteobacteria	Gammaproteobacteria	Diplorickettsiales	Diplorickettsiaceae	Aquicella	-0.22	0.00
3525	0.00	Proteobacteria	Gammaproteobacteria	Diplorickettsiales	Diplorickettsiaceae	0	-0.23	0.00
3095	0.00	Actinobacteriota	Actinobacteria	Frankiales	Acidothermaceae	Acidothermus	-0.23	0.00
7900	0.00	Proteobacteria	Gammaproteobacteria	Diplorickettsiales	Diplorickettsiaceae	Aquicella	-0.23	0.00
3042	0.00	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Magnetospirillaceae	0	-0.23	0.00
10378	0.00	Bdellovibrionota	Bdellovibrionia	Bdellovibrionales	Bdellovibrionaceae	Bdellovibrio	-0.23	0.00
2461	0.00	Acidobacteriota	Blastocatellia	Pyrinomonadales	Pyrinomonadaceae	RB41	-0.24	0.00
5629	0.00	Dependentiae	Babeliae	Babeliales	Babeliaceae	Babeliaceae	-0.24	0.00
14308	0.00	Acidobacteriota	Acidobacteriae	Subgroup_13	Subgroup_13	Subgroup_13	-0.24	0.00
1906	0.01	Proteobacteria	Alphaproteobacteria	Elsterales	URHD0088	URHD0088	-0.24	0.00
2646	0.00	Acidobacteriota	Blastocatellia	Pyrinomonadales	Pyrinomonadaceae	RB41	-0.25	0.00
4663	0.00	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	0	-0.25	0.00
8322	0.00	Chloroflexi	OLB14	OLB14	OLB14	OLB14	-0.26	0.00

2017	0.01	Acidobacteriota	Acidobacteriae	Bryobacterales	Bryobacteraceae	Bryobacter	-0.26	0.00
3261	0.00	Proteobacteria	Gammaproteobacteria	Burkholderiales	A21b	A21b	-0.26	0.00

Table S5. Spearman correlations of the 15 most strongly positively (top) and negatively (bottom) correlated ASVs with soil pH. Values were determined using the Python script *observation_metadata_correlation.py*. Data used are from all 163 samples, across seasonal time and soil depth (see Figure 1). Positive correlation coefficient (r_S) means that taxon relative abundance increased with increasing pH and negative r_S means that taxon relative abundance decreased with increasing pH.

ASV#	Phylum	Class	Order	Family	Genus	Overall relative abundance (%)	Within SparCC component relative abundance (%)
Organic soil network component							
13	Acidobacteriota	Acidobacteriae	Subgroup_2	Subgroup_2	Subgroup_2	0.58	6.66
20	Acidobacteriota	Acidobacteriae	Acidobacteriales	Acidobacteriaceae	Acidipila	0.49	5.63
27	Acidobacteriota	Acidobacteriae	Acidobacteriales			0.42	4.89
29	Acidobacteriota	Acidobacteriae	Acidobacteriales			0.41	4.74
32	Acidobacteriota	Acidobacteriae	Subgroup_2	Subgroup_2	Subgroup_2	0.40	4.70
37	Actinobacteriota	Actinobacteria	Frankiales	Acidothermaceae	Acidothermus	0.35	4.21
43	Acidobacteriota	Acidobacteriae	Subgroup_2	Subgroup_2	Subgroup_2	0.31	3.63
45	Acidobacteriota	Acidobacteriae	Acidobacteriales	Acidobacteriaceae	Acidipila	0.31	3.60
53	Actinobacteriota	Actinobacteria	Frankiales	Acidothermaceae	Acidothermus	0.27	3.19
58	Proteobacteria	Gammaproteobacteria	WD260	WD260	WD260	0.25	2.95
59	Acidobacteriota	Acidobacteriae	Acidobacteriales	Acidobacteriaceae		0.25	2.83
60	Acidobacteriota	Acidobacteriae	Acidobacteriales	Acidobacteriaceae	Acidipila	0.25	2.88
65	Acidobacteriota	Acidobacteriae	Acidobacteriales			0.24	2.82
71	Acidobacteriota	Acidobacteriae	Acidobacteriales	Acidobacteriaceae	Granulicella	0.22	2.71
77	Acidobacteriota	Acidobacteriae	Acidobacteriales			0.22	2.51
Mineral soil network component							
2	Chloroflexi	AD3	AD3	AD3	AD3	1.14	6.95
4	WPS-2	WPS-2	WPS-2	WPS-2	WPS-2	0.88	5.00
7	Chloroflexi	AD3	AD3	AD3	AD3	0.76	4.14
8	Chloroflexi	AD3	AD3	AD3	AD3	0.73	5.01
9	Verrucomicrobiota	Verrucomicrobiae	Chthoniobacterales	Chthoniobacteraceae	Candidatus_Udaeobacter	0.69	4.66
12	Proteobacteria	Gammaproteobacteria	Gammaproteobacteria_Incertae_Sedis	Unknown_Family	Acidibacter	0.59	2.98
14	Acidobacteriota	Blastocatellia	Pyrinomonadales	Pyrinomonadaceae	RB41	0.56	3.52
19	Chloroflexi	Dehalococcoidia	S085	S085	S085	0.50	2.94
21	Actinobacteriota	Acidimicrobiia	IMCC26256	IMCC26256	IMCC26256	0.48	2.53
23	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae		0.46	3.67
26	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae		0.43	2.33
30	WPS-2	WPS-2	WPS-2	WPS-2	WPS-2	0.41	2.25
31	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Pseudolabrys	0.40	2.81
38	Proteobacteria	Alphaproteobacteria	Micropepsales	Micropepsaceae		0.34	2.05
44	Acidobacteriota	Acidobacteriae	Subgroup_2	Subgroup_2	Subgroup_2	0.31	1.81

Table S6. Relative abundance of the 15 most abundant ASVs within the organic and mineral soil network components, respectively, identified by SparCC analysis. Table shows ASV overall relative abundance across the entire dataset, and within the SparCC network component (n=163 soil samples for all, see Figure 1).

Group 1	Group 2	Sample size	Permutations	pseudo-F	p-value	
5 cm depth						
Autumn	Bud-break	15	999	1.331418	0.226	
Autumn	Early snow melt	12	999	3.185689	0.014	
Autumn	Frozen	19	999	2.950127	0.008	*
Autumn	Late snowmelt	11	999	1.241589	0.218	
Autumn	Peak summer	13	999	1.136819	0.264	
Bud-break	Early snow melt	13	999	5.230124	0.001	*
Bud-break	Frozen	20	999	6.249459	0.001	*
Bud-break	Late snowmelt	12	999	1.048186	0.365	
Bud-break	Peak summer	14	999	0.678305	0.717	
Early snow melt	Frozen	17	999	1.696945	0.053	
Early snow melt	Late snowmelt	9	999	4.009615	0.018	
Early snow melt	Peak summer	11	999	3.848512	0.005	*
Frozen	Late snowmelt	16	999	3.98834	0.003	*
Frozen	Peak summer	18	999	4.682041	0.001	*
Late snowmelt	Peak summer	10	999	0.919008	0.483	
10 cm depth						
Autumn	Bud-break	17	999	1.677024	0.075	
Autumn	Frozen	18	999	5.608545	0.001	*
Autumn	Late snowmelt	10	999	2.785497	0.004	*
Autumn	Peak summer	12	999	0.923899	0.508	
Bud-break	Frozen	23	999	3.7904	0.001	*
Bud-break	Late snowmelt	15	999	2.306229	0.032	
Bud-break	Peak summer	17	999	1.379574	0.196	
Frozen	Late snowmelt	16	999	1.388246	0.169	
Frozen	Peak summer	18	999	5.765646	0.001	*
Late snowmelt	Peak summer	10	999	2.933247	0.013	
20 cm depth						
Autumn	Bud-break	15	999	1.261305	0.150	
Autumn	Frozen	9	999	1.377752	0.157	
Autumn	Peak summer	12	999	1.13887	0.247	
Bud-break	Frozen	12	999	2.03096	0.016	
Bud-break	Peak summer	15	999	0.858988	0.673	
Frozen	Peak summer	9	999	2.189237	0.010	
30 cm depth						
Autumn	Bud-break	14	999	1.404761	0.135	
Autumn	Frozen	8	999	1.525712	0.239	
Autumn	Peak summer	12	999	1.276401	0.170	
Bud-break	Frozen	10	999	1.390644	0.152	
Bud-break	Peak summer	14	999	1.516393	0.092	
Frozen	Peak summer	8	999	1.038967	0.431	
40 cm depth						
Autumn	Frozen	12	999	2.048695	0.009	**
Autumn	Peak summer	12	999	1.34383	0.167	
Frozen	Peak summer	12	999	1.606587	0.083	
50 cm depth						
Autumn	Frozen	12	999	1.682336	0.07	

Table S7. Results of the pairwise PERMANOVA using the beta-group-significance function in QIIME2 generated for Figure 8. Significant probabilities are shown as in Table S2.

ASV#	Phylum	Class	Order	Family	Genus	Overall relative abundance (%)	Within soil layer relative abundance (%)
156	Caldisericota	Caldisericia	Caldisericales	Caldisericaceae	Caldisericum	0.13	4.82
292	Bacteroidota	Bacteroidia	Bacteroidales	Prolixibacteraceae	BSV13	0.07	2.55
321	Caldisericota	Caldisericia	Caldisericales	Caldisericaceae	Caldisericum	0.06	2.28
232	Actinobacteriota	Coriobacteriia	OPB41	OPB41	OPB41	0.08	1.96
372	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Rhodoferax	0.05	1.93
384	Bacteroidota	Bacteroidia	Bacteroidales	Paludibacteraceae	Paludibacter	0.05	1.83
395	Caldisericota	Caldisericia	Caldisericales	Caldisericaceae	Caldisericum	0.05	1.77
404	Caldisericota	Caldisericia	Caldisericales	Caldisericaceae	Caldisericum	0.05	1.74
406	Caldisericota	Caldisericia	Caldisericales	Caldisericaceae	Caldisericum	0.05	1.73
453	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Rhodoferax	0.04	1.60
273	Acidobacteriota	Holophagae	Subgroup_7	Subgroup_7	Subgroup_7	0.07	1.39
492	Proteobacteria	Gammaproteobacteria	Burkholderiales	Nitrosomonadaceae	GOUTA6	0.04	1.38
528	Bacteroidota	Bacteroidia	Bacteroidales	Paludibacteraceae	Paludibacter	0.04	1.34
569	Actinobacteriota	Thermoleophilia	Gaiellales	uncultured_Solirubrobacter		0.03	1.16
617	Desulfobacterota	Syntrophia	Syntrophales	Smithellaceae	Smithella	0.03	1.15

Table S8. Relative abundance of the 15 most abundant ASVs within the permafrost transition soil layer at 60 cm depth (n=6 soil samples, see Figure 1). Table shows ASV overall relative abundance across the entire dataset (n=163 soil samples), and within the 60 cm soil layer (n=6).

5 cm depth	Seasonal change	Winter (126-139)	Early snowmelt (146)	Late snowmelt (159)	Spring (173)	Bud-break (182-183)	Summer (203-209)	Autumn (229-234)
pH	$F_{6,35} = 2.8$, $p = 0.03$	3.4 ± 0.02	3.5 ± 0.02	3.4 ± 0.03	3.5 ± 0.06	3.4 ± 0.03	3.5 ± 0.05	3.4 ± 0.01
Total N	$F_{6,35} = 4.7$, $p = 0.001$	1.3 ± 0.07	1.2 ± 0.09	1.5 ± 0.14	1.9 ± 0.29	1.7 ± 0.02	1.8 ± 0.10	1.5 ± 0.06
Total C	$F_{6,35} = 2.2$, $p = 0.07$	44.4 ± 0.37	44.7 ± 0.3	43.7 ± 0.81	42.2 ± 0.34	44.1 ± 0.67	43.3 ± 0.80	44.4 ± 0.43
NO_3^--N	$F_{5,31} = 3.4$, $p = 0.02$	0.83 ± 0.11	N/A	1.26 ± 0.28	0.36 ± 0.19	0.30 ± 0.19	1.20 ± 0.40	0.60 ± 0.09
NH_4^+-N	$F_{6,35} = 2.2$, $p = 0.06$	3.1 ± 0.64	1.5 ± 0.11	1.9 ± 0.20	3.8 ± 0.20	2.7 ± 0.17	3.1 ± 0.50	2.7 ± 0.19
PO_4^{3-}-P	$F_{6,35} = 6.8$, $p < 0.0001$	15.1 ± 3.2	21.8 ± 4.14	8.1 ± 6.0	1.3 ± 0.48	2.2 ± 0.67	0.9 ± 0.44	1.6 ± 0.24
DOC	$F_{6,35} = 9.4$, $p < 0.0001$	1119 ± 76.4	889 ± 49.6	809 ± 52.2	671 ± 18.0	686 ± 20.6	635 ± 64.9	688 ± 25.4
DON	$F_{5,31} = 2.1$, $p = 0.09$	69.6 ± 7.4	46.9 ± 2.62	51.7 ± 5.9	58.3 ± 3.2	52.6 ± 2.3	51.3 ± 6.4	46.0 ± 2.1
MBC	$F_{6,35} = 15.5$, $p < 0.0001$	5845 ± 269	5899 ± 312	4059 ± 309	3013 ± 101	3689 ± 316	3157 ± 286	3778 ± 337
MBN	$F_{6,35} = 3.6$, $p < 0.01$	398 ± 33.9	413 ± 16.1	333 ± 20.3	280 ± 4.9	301 ± 25.4	281 ± 21.8	339 ± 28.0
MBP	$F_{6,35} = 14.1$, $p < 0.0001$	118 ± 14.5	147 ± 17.5	58.0 ± 31.1	14.9 ± 6.6	N/A	13.6 ± 7.1	13.2 ± 2.6

10 cm depth	Seasonal change	Winter (126-139)	Early snowmelt (146)	Late snowmelt (159)	Spring (173)	Bud-break (182-183)	Summer (203-209)	Autumn (229-234)
pH	$F_{6,34} = 8.4$, $p < 0.0001$	3.4 ± 0.08	3.4 ± 0.03	3.5 ± 0.10	3.7 ± 0.10	3.6 ± 0.06	3.6 ± 0.03	3.9 ± 0.01
Total N	$F_{6,34} = 2.6$, $p = 0.03$	1.6 ± 0.10	1.5 ± 0.13	1.5 ± 0.13	1.9 ± 0.09	1.7 ± 0.13	1.7 ± 0.12	2.0 ± 0.13
Total C		40.7 ± 3.0	42.1 ± 1.34	41.5 ± 1.03	39.9 ± 1.0	36.9 ± 3.5	39.2 ± 1.3	39.8 ± 1.30
NO_3^--N		0.53 ± 0.10	0.86 ± 0.86	0.59 ± 0.20	0.33 ± 0.12	0.20 ± 0.10	0.63 ± 0.14	0.35 ± 0.06
NH_4^+-N		3.0 ± 0.76	2.7 ± 0.38	1.6 ± 0.23	2.9 ± 0.16	2.4 ± 0.39	3.2 ± 0.90	2.2 ± 0.54
PO_4^{3-}-P	$F_{6,34} = 16.6$, $p < 0.0001$	3.9 ± 0.95	5.2 ± 1.8	3.0 ± 2.5	0.15 ± 0.10	0.44 ± 0.20	0.13 ± 0.07	0.20 ± 0.08
DOC	$F_{6,34} = 3.7$, $p < 0.01$	868 ± 95.5	1044 ± 182	758 ± 77.2	496 ± 71.0	596 ± 97.2	549 ± 51.8	467 ± 54.5
DON		66.7 ± 9.3	73.4 ± 12.6	51.5 ± 4.9	43.6 ± 4.8	48.7 ± 6.9	52.3 ± 6.6	44.2 ± 5.2
MBC	$F_{6,34} = 4.7$, $p < 0.01$	4005 ± 542	4647 ± 334	2724 ± 386	1360 ± 300	2146 ± 412	1433 ± 265	1546 ± 119
MBN	$F_{6,34} = 2.4$, $p < 0.05$	288 ± 43.6	361 ± 33.4	221 ± 38.2	127 ± 38.7	194 ± 38.7	137 ± 27.0	140 ± 19.2
MBP	$F_{6,34} = 6.5$, $p < 0.0001$	19.6 ± 9.6	25.2 ± 9.0	24.4 ± 21.4	0.2 ± 0.00	N/A	1.9 ± 0.57	2.5 ± 0.78

20 cm depth	Seasonal change	Winter (126-139)	Early snowmelt (146)	Late snowmelt (159)	Spring (173)	Bud-break (182-183)	Summer (203-209)	Autumn (229-234)
pH				4.8 ± 0.19	5.3 ± 0.30	5.0 ± 0.22	4.6 ± 0.08	5.2 ± 0.20
Total N				0.13 ± 0.01	0.11 ± 0.0	0.16 ± 0.03	0.21 ± 0.05	0.15 ± 0.00
Total C				2.8 ± 0.39	2.5 ± 1.0	3.3 ± 0.97	4.6 ± 0.93	3.4 ± 1.2
NO_3^--N	$F_{4,20} = 2.6$, $p = 0.07$			0.97 ± 0.30	0.62 ± 0.15	0.27 ± 0.08	0.32 ± 0.10	0.49 ± 0.11
NH_4^+-N				0.65 ± 0.09	0.30 ± 0.08	0.48 ± 0.07	0.45 ± 0.03	0.51 ± 0.20
PO_4^{3-}-P	$F_{4,20} = 2.3$, $p < 0.1$			0.82 ± 0.39	6.7 ± 4.7	1.5 ± 0.35	3.5 ± 0.36	2.4 ± 0.70
DOC	$F_{4,20} = 2.4$, $p = 0.08$			82.3 ± 14.7	47.2 ± 6.7	56.5 ± 5.7	67.4 ± 7.9	47.2 ± 9.0
DON				7.0 ± 1.4	4.4 ± 1.0	6.5 ± 0.78	7.6 ± 0.79	7.3 ± 2.4
MBC				53.3 ± 21.5	56.2 ± 26.4	73.8 ± 25.9	57.8 ± 23.0	60.6 ± 20.2
MBN				2.7 ± 0.82	4.5 ± 2.2	6.0 ± 1.3	5.4 ± 1.73	3.5 ± 0.69
MBP				1.1 ± 0.49	0.26 ± 0.10	N/A	1.4 ± 0.47	1.1 ± 0.24

30 cm depth	Seasonal change	Winter (126-139)	Early snowmelt (146)	Late snowmelt (159)	Spring (173)	Bud-break (182-183)	Summer (203-209)	Autumn (229-234)
pH					5.6 ± 0.39	5.5 ± 0.10	5.6 ± 0.11	5.8 ± 0.09
Total N					0.07 ± 0.05	0.07 ± 0.02	0.07 ± 0.01	0.08 ± 0.01
Total C					1.7 ± 1.0	1.2 ± 0.37	0.73 ± 0.28	1.2 ± 0.19
NO_3^--N					0.33 ± 0.03	0.26 ± 0.01	0.23 ± 0.10	0.30 ± 0.04
NH_4^+-N					0.24 ± 0.00	0.22 ± 0.01	0.14 ± 0.02	0.22 ± 0.07
PO_4^{3-}-P	$F_{3,18} = 12.7$, $p < 0.0001$				14.7 ± 13.2	1.6 ± 0.03	10.2 ± 0.70	8.9 ± 2.7
DOC	$F_{3,18} = 7.4$, $p < 0.01$				44.9 ± 4.4	34.9 ± 1.8	26.0 ± 2.0	29.8 ± 2.3
DON					3.8 ± 0.27	3.8 ± 0.22	2.6 ± 0.32	3.8 ± 0.85
MBC	$F_{3,18} = 6.8$, $p < 0.01$				31.6 ± 11.2	32.1 ± 4.2	8.3 ± 3.3	22.8 ± 6.3
MBN	$F_{3,18} = 4.0$, $p = 0.02$				1.2 ± 0.57	2.0 ± 0.18	0.64 ± 0.30	0.84 ± 0.22
MBP					0.35 ± 0.35	N/A	0.53 ± 0.28	0.86 ± 0.46

40 cm depth	Seasonal change	Winter (126-139)	Early snowmelt (146)	Late snowmelt (159)	Spring (173)	Bud-break (182-183)	Summer (203-209)	Autumn (229-234)
pH						5.9 ± 0.07	5.9 ± 0.07	6.0 ± 0.06
Total N						0.05 ± 0.01	0.06 ± 0.01	0.05 ± 0.01
Total C						0.57 ± 0.16	0.41 ± 0.09	0.41 ± 0.11
NO_3^--N						0.19 ± 0.08	0.24 ± 0.07	0.35 ± 0.07
NH_4^+-N						0.20 ± 0.02	0.13 ± 0.00	0.23 ± 0.11

PO_4^{3-}-P	$F_{2,15} = 25.6$, $p < 0.0001$					3.3 ± 0.66	13.2 ± 1.4	16.6 ± 2.2
DOC	$F_{2,15} = 2.8$, $p = 0.09$					24.0 ± 1.8	18.9 ± 1.6	20.3 ± 1.3
DON						1.8 ± 0.12	1.7 ± 0.20	3.1 ± 1.4
MBC	$F_{2,15} = 9.9$, $p = 0.02$					38.2 ± 17.7	4.5 ± 0.80	4.6 ± 1.5
MBN	$F_{2,15} = 14.2$, $p < 0.001$					4.0 ± 1.9	0.16 ± 0.04	0.33 ± 0.11
MBP						N/A	1.6 ± 1.1	0.67 ± 0.55

50 cm depth	Seasonal change	Winter (126-139)	Early snowmelt (146)	Late snowmelt (159)	Spring (173)	Bud-break (182-183)	Summer (203-209)	Autumn (229-234)
pH							5.9 ± 0.06	6.0 ± 0.05
Total N							0.04 ± 0.01	0.06 ± 0.01
Total C							0.20 ± 0.04	0.35 ± 0.08
NO_3^--N	$F_{1,10} = 3.8$, $p = 0.08$						0.13 ± 0.08	0.27 ± 0.06
NH_4^+-N							0.08 ±0.01	0.12 ± 0.02
PO_4^{3-}-P	$F_{1,10} = 11.6$, $p < 0.01$						8.8 ± 1.3	20.7 ± 3.9
DOC							13.2 ± 0.51	16.8 ± 2.3
DON							1.2 ± 0.08	1.5 ± 0.15
MBC	$F_{1,10} = 3.9$, $p = 0.08$						3.3 ± 0.77	5.3 ± 0.40
MBN							0.16 ± 0.06	0.33 ± 0.08
MBP							1.1 ± 0.46	1.4 ± 0.54

60 cm depth	Seasonal change	Winter (126-139)	Early snowmelt (146)	Late snowmelt (159)	Spring (173)	Bud-break (182-183)	Summer (203-209)	Autumn (229-234)
pH								6.1 ± 0.04
Total N								0.05 ± 0.01
Total C								0.33 ± 0.12
NO_3^--N								0.09 ± 0.02
NH_4^+-N								0.88 ± 0.06
PO_4^{3-}-P								27.4 ± 3.8
DOC								12.8 ± 0.73
DON								1.6 ± 0.57
MBC								6.5 ± 1.7
MBN								0.29 ± 0.1
MBP								N/A

Table S9. Biogeochemical properties within each soil layer down the thawing soil profile throughout the winter-spring-summer-autumn periods in low Arctic mesic birch hummock tundra near Daring Lake, Northwest Territories, Canada. The sampling times are divided into seven periods: Winter, two separate May-samplings before any thaw; Early snowmelt, sampled on the first day of mean diurnal air temperatures above 0 ˚C; Late snowmelt, sampled at complete snowmelt; Spring, two weeks into the snow-free season; Bud-break, the transitional period between spring and summer where new leaves emerge and most deciduous shrub productivity begins; Summer, mid-July sampling; and Autumn, late-August when senescence became apparent (Julian days shown in parentheses). Total soil N and C are % dry weight soil; and nitrate-N (NO_3^--N), ammonium-N (NH_4^+-N), phosphate-P (PO_4^{3-}-P), dissolved organic C (DOC) and N (DON), and microbial biomass C, N, and P (MBC, MBN, and MBP, respectively) are all μg g^{-1} dry weight soil. Values are means ± 1 S.E., and statistical results ($p \leq 0.1$) of linear mixed models with season as the fixed main effect are shown (n = 6-42 per depth interval, decreasing from the surface downwards, see Figure 1). Grey shading indicates soil samples that were frozen when sampled and N/A indicates values below detection limit (i.e. effectively zero but to be conservative, these values have been omitted).

Category of research-associated activity	Details of the research-associated activity necessary to complete the study	Environmental impacts of the activity that may be avoidable	Measure taken to reduce those environmental impacts
Travel	Travel from Queen's University in Kingston to Toronto airport (~250 km) for commercial flight to Yellowknife.	Greenhouse gas emissions associated with Kingston-Toronto flights.	Travelled from Kingston-Toronto airport by commercial passenger bus instead of flying.
Travel	Chartered air travel from Yellowknife to the remote tundra research field-site at Daring Lake each summer for various science research groups including multiple universities and government scientists.	Greenhouse-gas (GHG) emissions associated with each charter flight in and out of camp.	Maximized the number of passengers per flight, and minimized the total number of flights by careful, ongoing, scheduling coordination of travel plans among the different research groups.
Supplies use – chemicals	Acquisition of chemicals needed to make reagents.	GHG emissions associated with packaging and shipping.	Bought chemicals in bulk where possible and divided into aliquots each with a safety chemical identification label.
Supplies use – pipette tips and plastic containers and tubes for use in molecular biology research	Contamination is a large concern in molecular and microbiology research, and so lots of single-use new plastic products such as pipette tips, vials, centrifuge tubes and PCR tubes are used. Certain types of pipette tips are supplied pre-packaged in plastic sealed boxes, which creates further waste.	Resource use as well as waste associated with packaging and shipping of pipette tip and other plastic products. Energy use associated with autoclaving and incineration during processing this lab plastic waste.	Ordered pipette tips in bulk bags that were stacked into reused plastic boxes and autoclaved Decontamination washing and autoclave-sterilization of plastic (Falcon) tubes for re-use; substitution of single-use microbiology items with reusable ones; careful experiment planning that specifically includes the goal of

			reducing single-use items (Alves et al., 2020).
Supplies use – purified water	Deionized-distilled water required for stock solutions.	Fossil fuel energy required shipping and manufacture of the plastic involved in packaging deionized-distilled water, as well as in shipping pre-made solutions that would be required in place of lab-made stock solutions.	Used an in-lab still for pure water. Such stills can also be shared between labs, reducing overall costs as well as environmental impacts of acquiring commercially prepared pure water.
Supplies use – sample bags	Collecting soil samples for subsequent chemical analyses.	Clean plastic sealable heavy-duty freezer sample bags are an oil-product and their production entails GHG emissions.	Rinsed and washed and ethanol-sterilized emptied sample bags for re-use where possible.

Table S10. Specific measures deliberately taken by the authors to reduce the environmental impacts of the activities associated with completing the science reported in this study. For details on how to report such measures, see Grogan, P. (2021) Raising awareness of science's environmental footprint. *Frontiers in Ecology and the Environment* **19**:143-143.

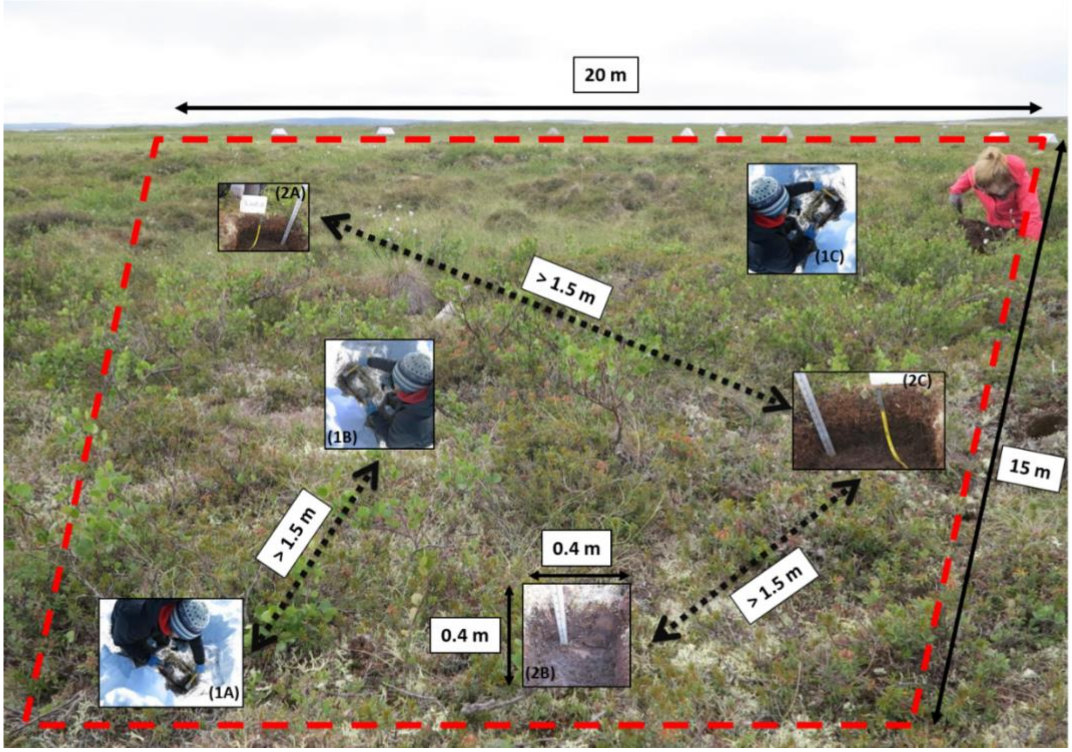

Figure S1. Illustration of the soil sampling methodology. The study area (20 x15 m) was staked out in low stature mesic birch hummock tundra, from which we sampled up to four frozen chunks when surface soils were frozen, or three replicate pits (0.4 x 0.4 m) when surface soils were thawed, per sampling time point. Separate pits over successive seasonal time points were dug at least 1.5 m apart, with replicate pits sampled within the same time point usually being further away. The inserts illustrate two different sampling times (with pits labelled 1A, 1B, and 1C and 2A, 2B, and 2C, respectively).

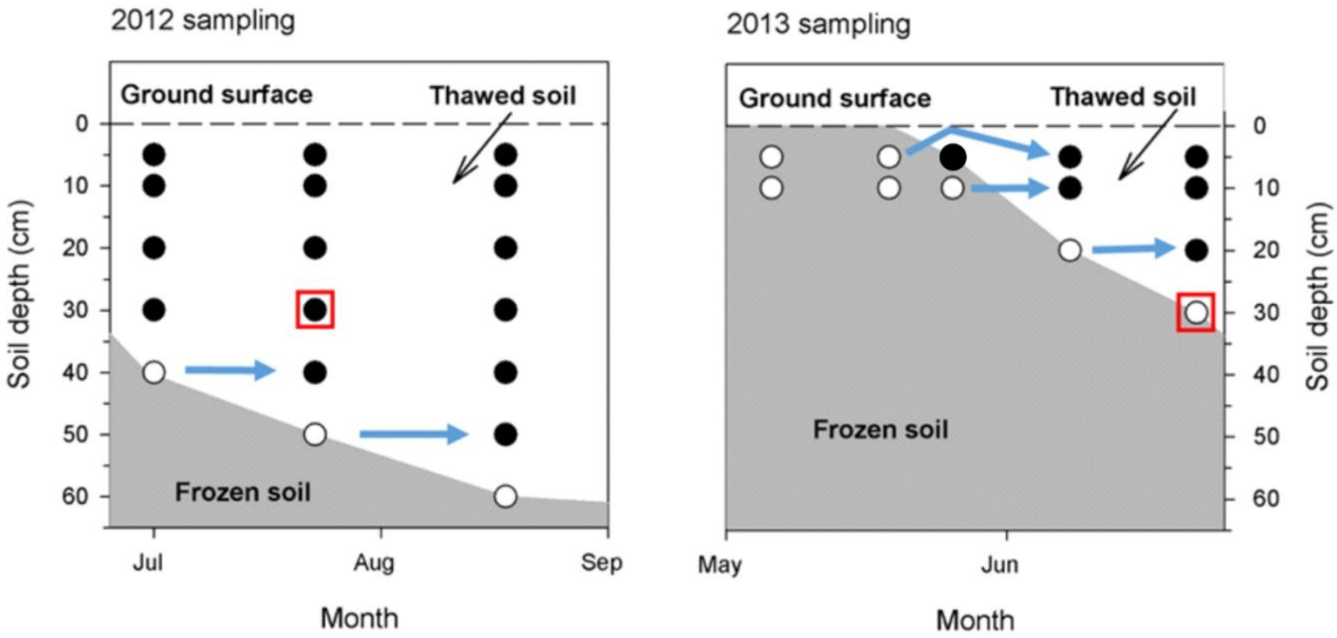

Figure S2. Illustration of the sampling design to collect samples vertically down the soil profile during sampling campaigns in 2012 (left; summer and autumn) and 2013 (right; winter through spring and bud-break). Grey shading represents the seasonal development of the thawing soil active layer, and white and black circles indicate sampling depths and corresponding soil thermal status (frozen and thawed, respectively) at each sampling time. Blue arrows indicate sample-pairs that were directly compared in our temporal analyses and which were sampled in succession within-year, while the red box show the only sample-pair where the comparison was performed “backwards” across sampling years (see Figures 7 and 8). All other analyses are concerned with frozen vs. thawed soil state, which are different from temporal change.

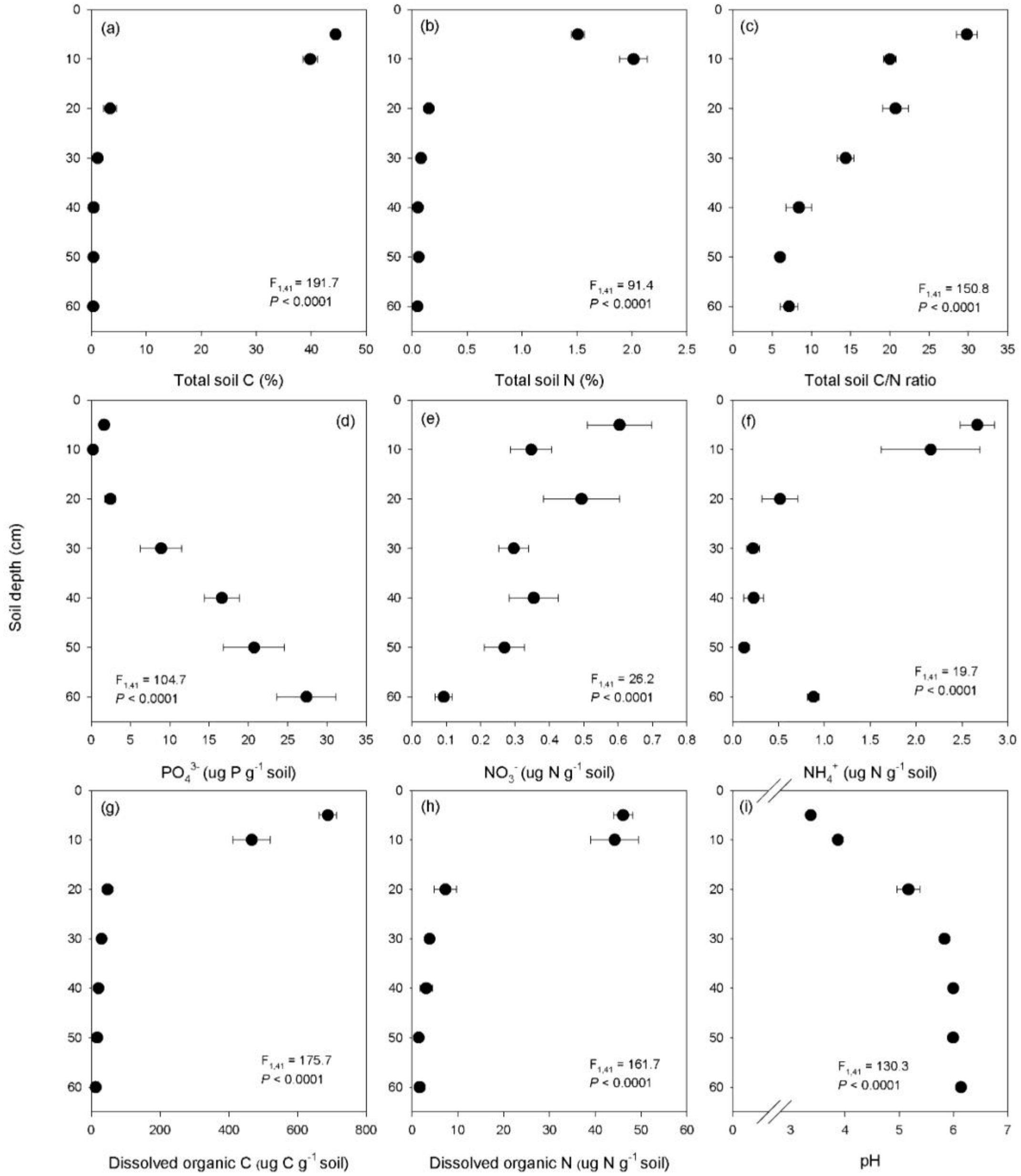

Figure S3. Soil biogeochemical properties down the thawed active layer and in the permafrost transition zone in late August (n = 6-7 for each of these soil depths, see Figure 1). Soil properties include total C (a), C/N ratio (b), pH (c), phosphate (PO_4^{3-}) (d), nitrate (NO_3^-) (e), ammonium (NH_4^+) (f), dissolved organic C (g), and N (h), and pH (i). Values are means ± 1 S.E. and although some values in the deeper soil intervals are too small to be visible in the figure, none of these were below detection limit. Results of linear mixed models with soil depth as fixed main effect are shown inside each panel.

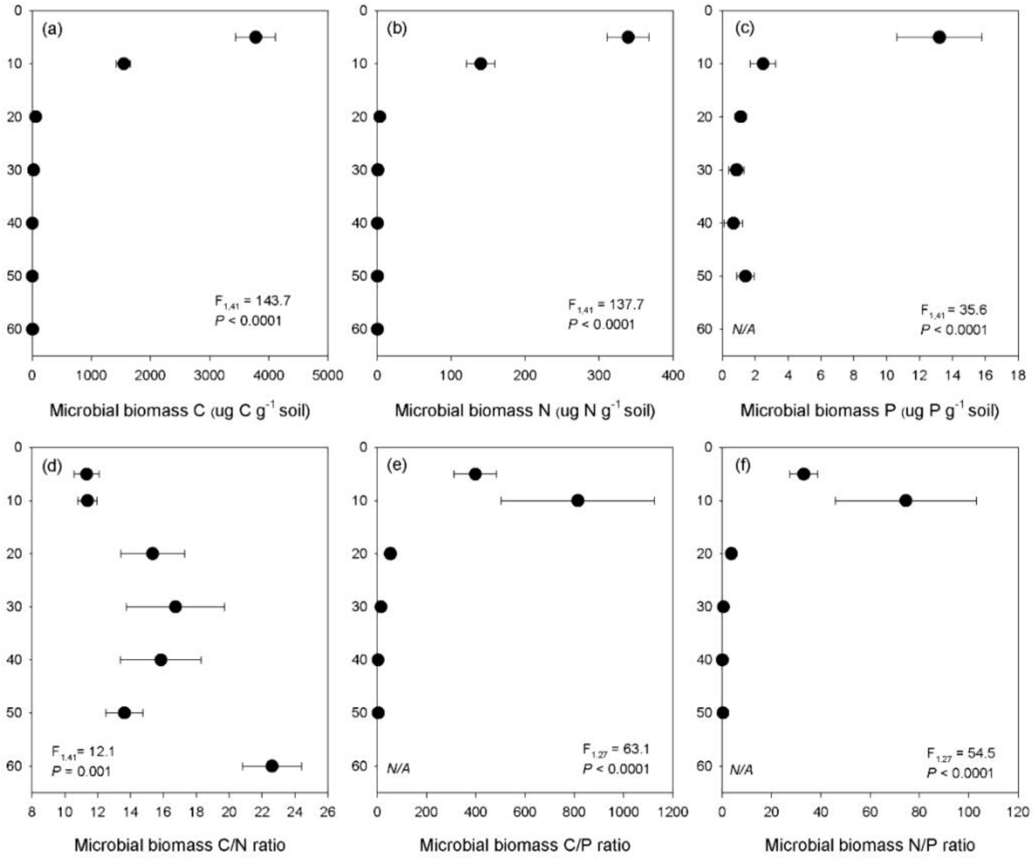

Figure S4. Changes in microbial biomass C, N, and P concentrations and ratios with soil depth as measured in the late August soil profile samples (n = 6-7 for each of these soil depths, see Figure 1). Soil properties are MBC (a), MBN (b), MBP (c), MBC/N (d), MBC/P (e), and MBN/P (f). Values are means ± 1 S.E. and although some values in the deeper soil intervals are too small to be visible in the figure, none of these were below detection limit except for MBP at 60 cm depth (i.e. effectively being zero but conservatively we omitted these data, including MBC/P and MBN/P at this depth). Results of linear mixed models with soil depth as fixed main effect are shown inside each panel.

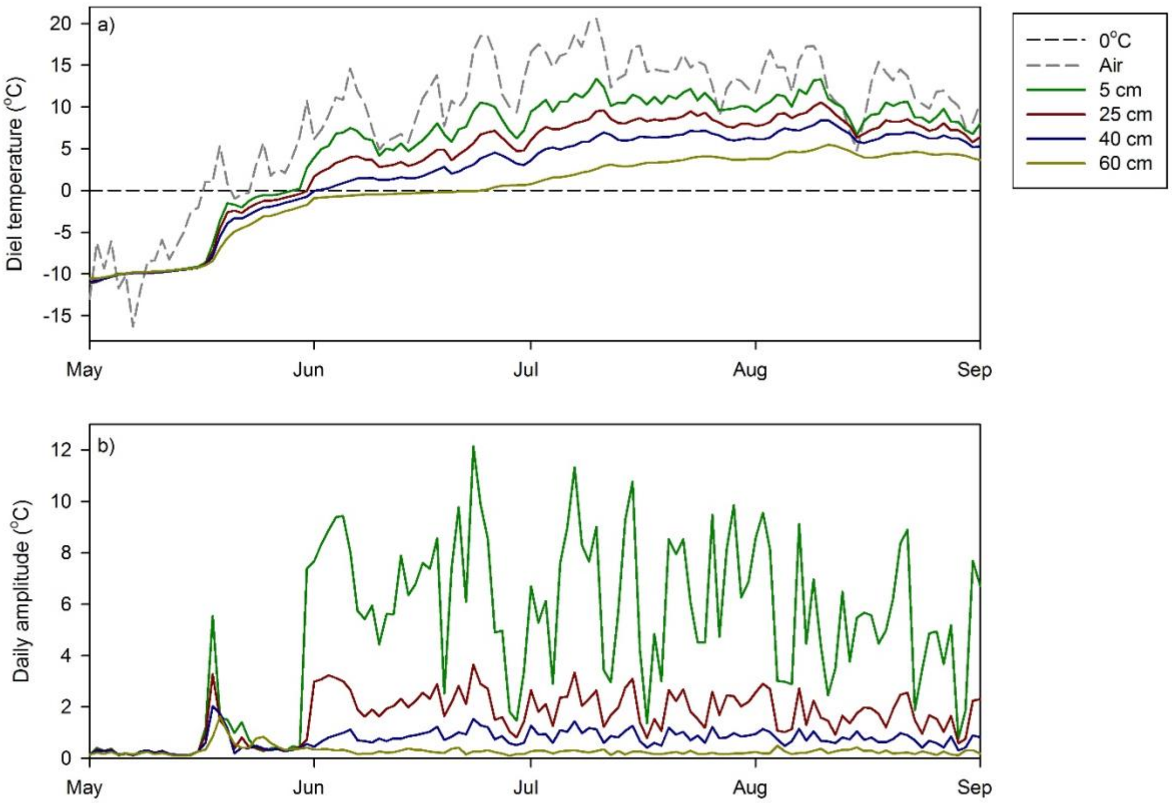

Figure S5. Daily mean air (150 cm aboveground) and soil temperatures (at 5, 25, 40, and 60 cm depths) (a) and diel soil temperature amplitudes (highest – lowest hourly temperature) (b) from May to September 2013 in low Arctic birch hummock tundra at Daring Lake, North West Territories, Canada. Data are from an eddy-covariance flux tower situated in broadly similar low shrub vegetation within 2 km of our study site.

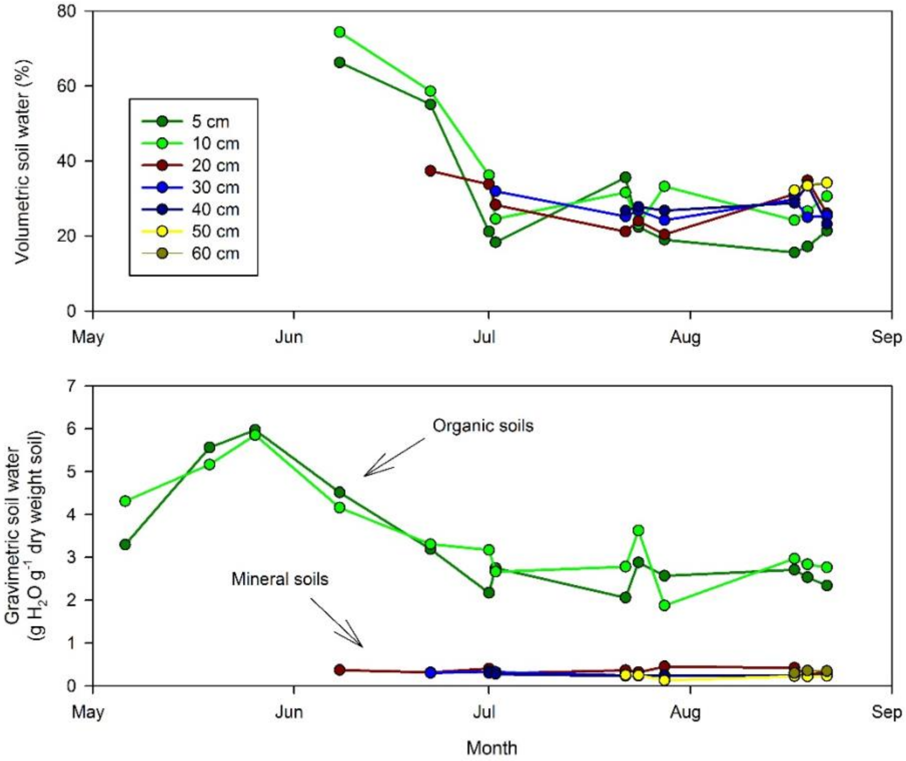

Figure S6. Soil volumetric (liquid water; %; top panel) and gravimetric (liquid plus frozen water; g H_2O g^{-1} dry weight soil; bottom panel) water content from May to September 2013 in low Arctic birch hummock tundra at Daring Lake, Northwest Territories, Canada. Volumetric water was measured by a handheld probe (see Methods) adjacent to each soil sample, and gravimetric water was determined for each soil sample by drying (n = 4-6 per soil depth at each sampling time).

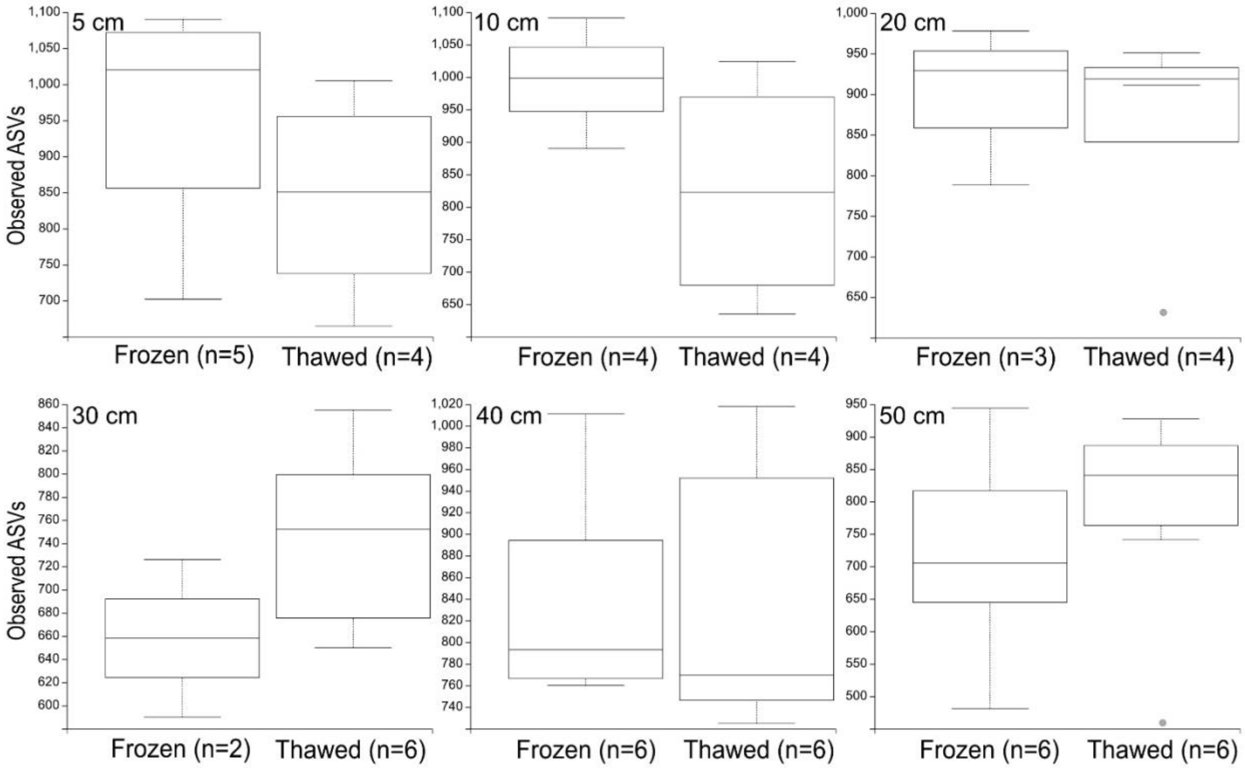

Figure S7. Bacterial phylotype richness (number of ASVs) in frozen and thawed soils (the latter were sampled approximately three weeks after thaw) of each sampling depth interval (n = 7-12 for each of these soil depths over the two sampling times, see Figure 1). Phylotype richness was calculated using rarefied samples (13,000 total sequences per sample).

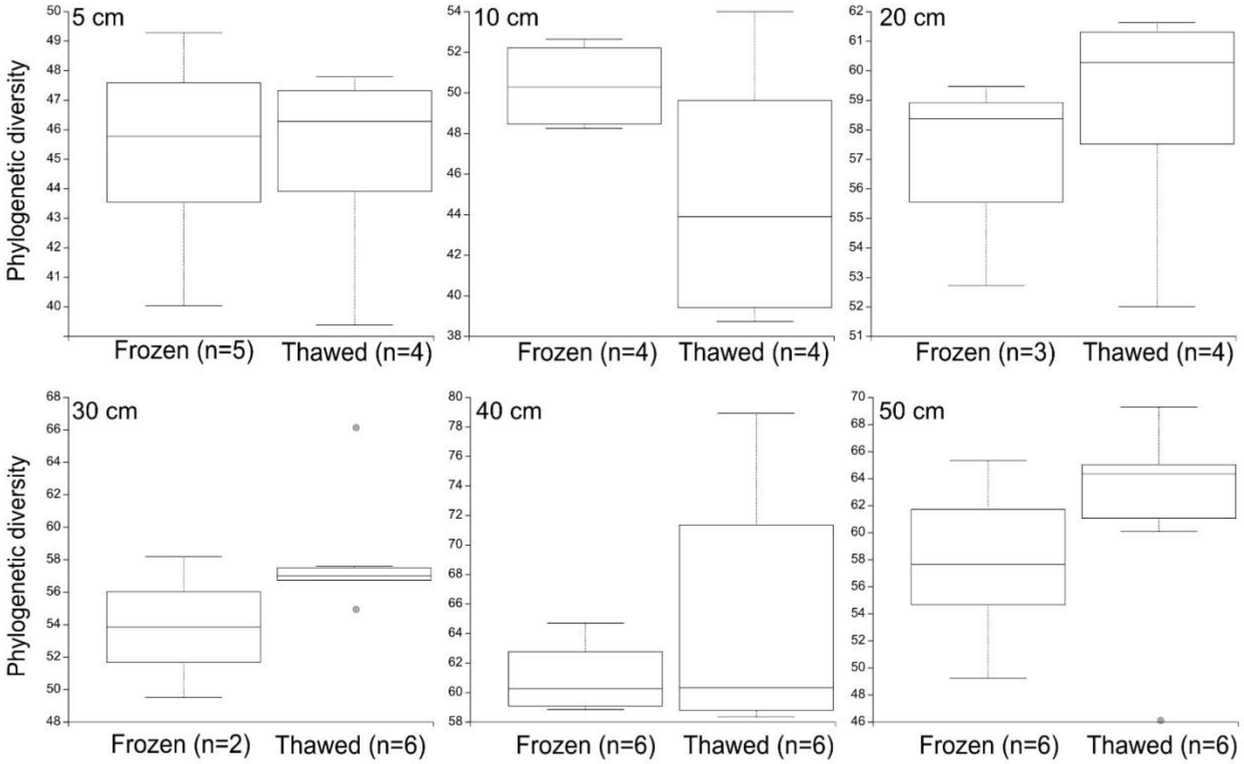

Figure S8. Bacterial phylogenetic (Faith's) diversity in frozen and thawed soils (the latter were sampled approximately three weeks after thaw) of each sampling depth interval (n = 7-12 for each of these soil depths over the two sampling times, see Figure 1). Phylogenetic diversity was calculated using rarefied samples (13,000 total sequences per sample).

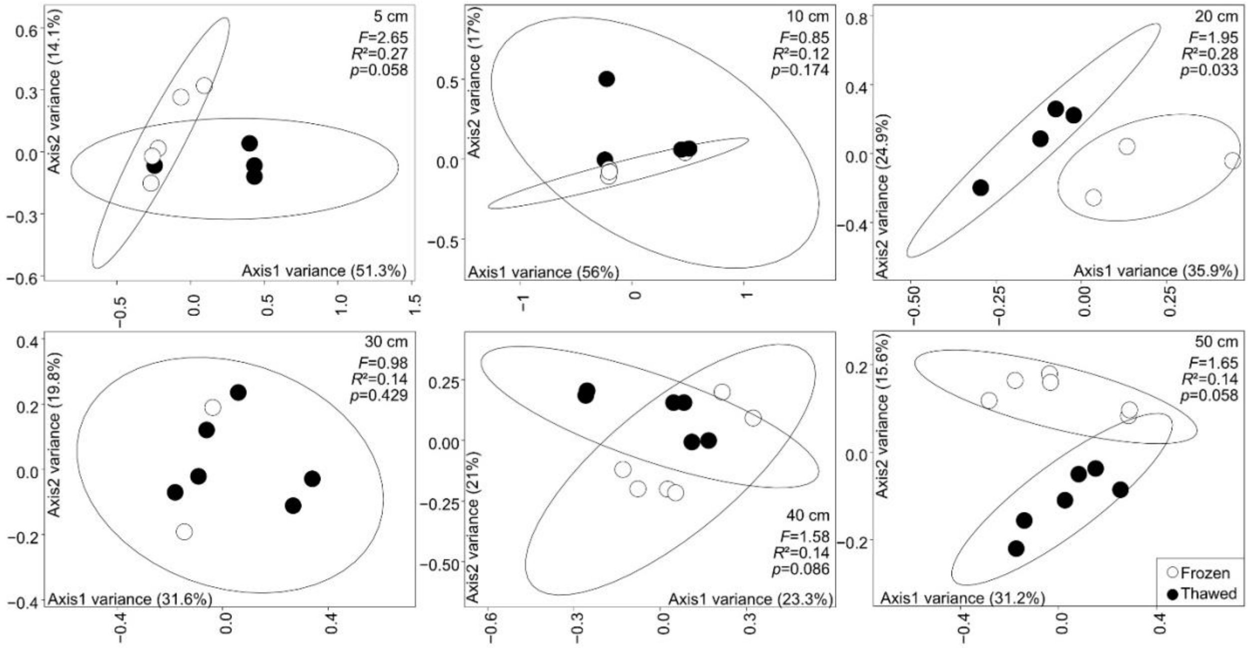

Figure S9. Principal coordinates analysis of Bray-Curtis compositional dissimilarity distances in bacterial community structure in frozen and thawed soils (the latter were sampled approximately three weeks after thaw) of each sampling depth interval (n = 7-12 for each of these soil depths over the two sampling times, see Figure S2). The *adonis* function in qiime2 was used to determine statistical significance between bacterial communities across soil thermal states.

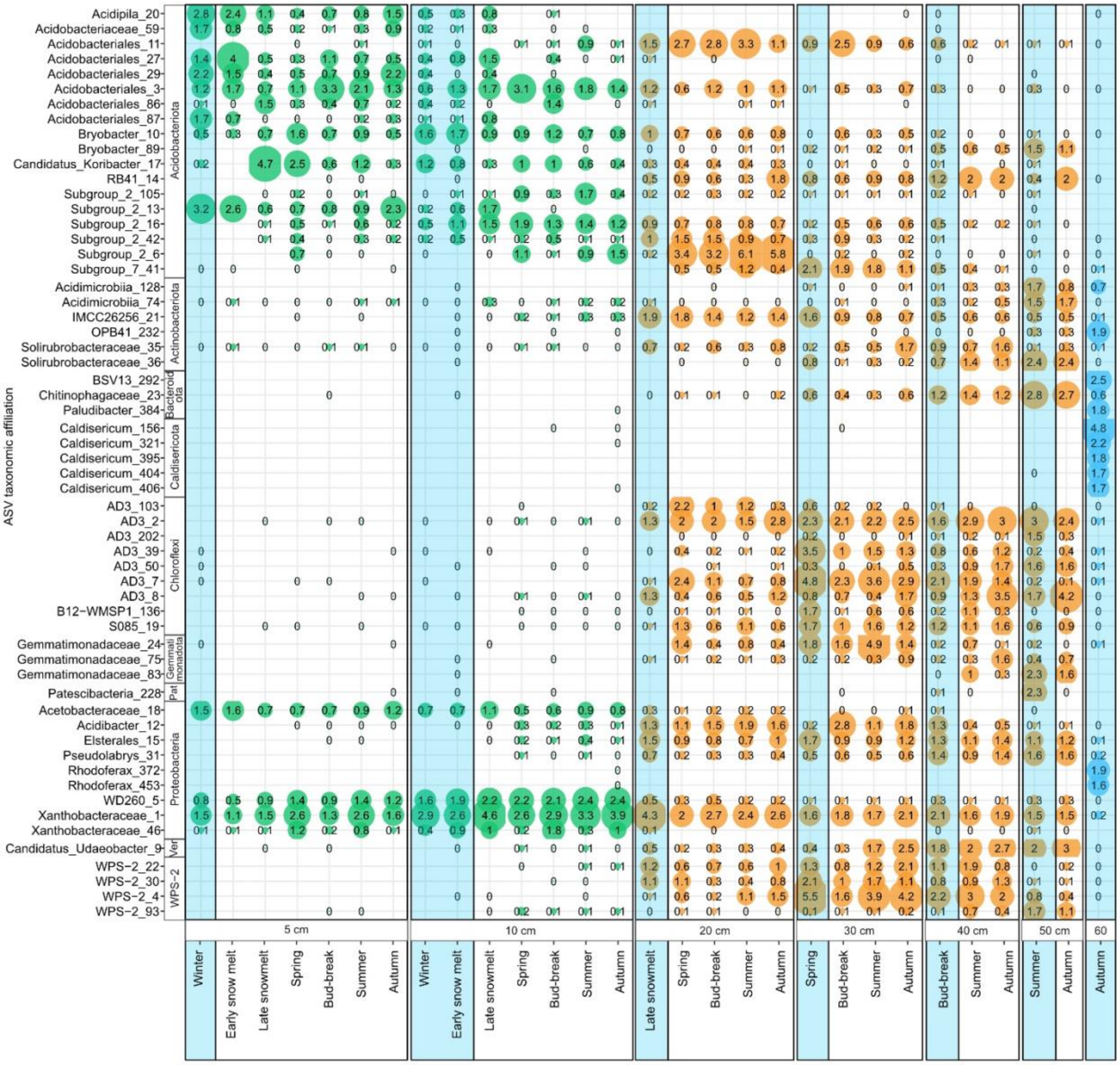

Figure S10. Temporal variation in the relative abundance of ASVs within each soil layer down the thawing soil. ASVs at or above 1.5% relative abundance are shown. Once an ASV reaches the threshold (1.5%) in at least one sample, the abundance in all samples is shown, even if below the threshold. ASVs are sorted on the y-axis by Phylum association (Patescibacteria (Pat), Verrucomicrobiota (Ver)) and each ASV taxonomic affiliation is followed by an ASV number. The sampling times are divided into seven periods; see Table S8 and Methods for details. Light blue shading indicates soil samples that were frozen when sampled.

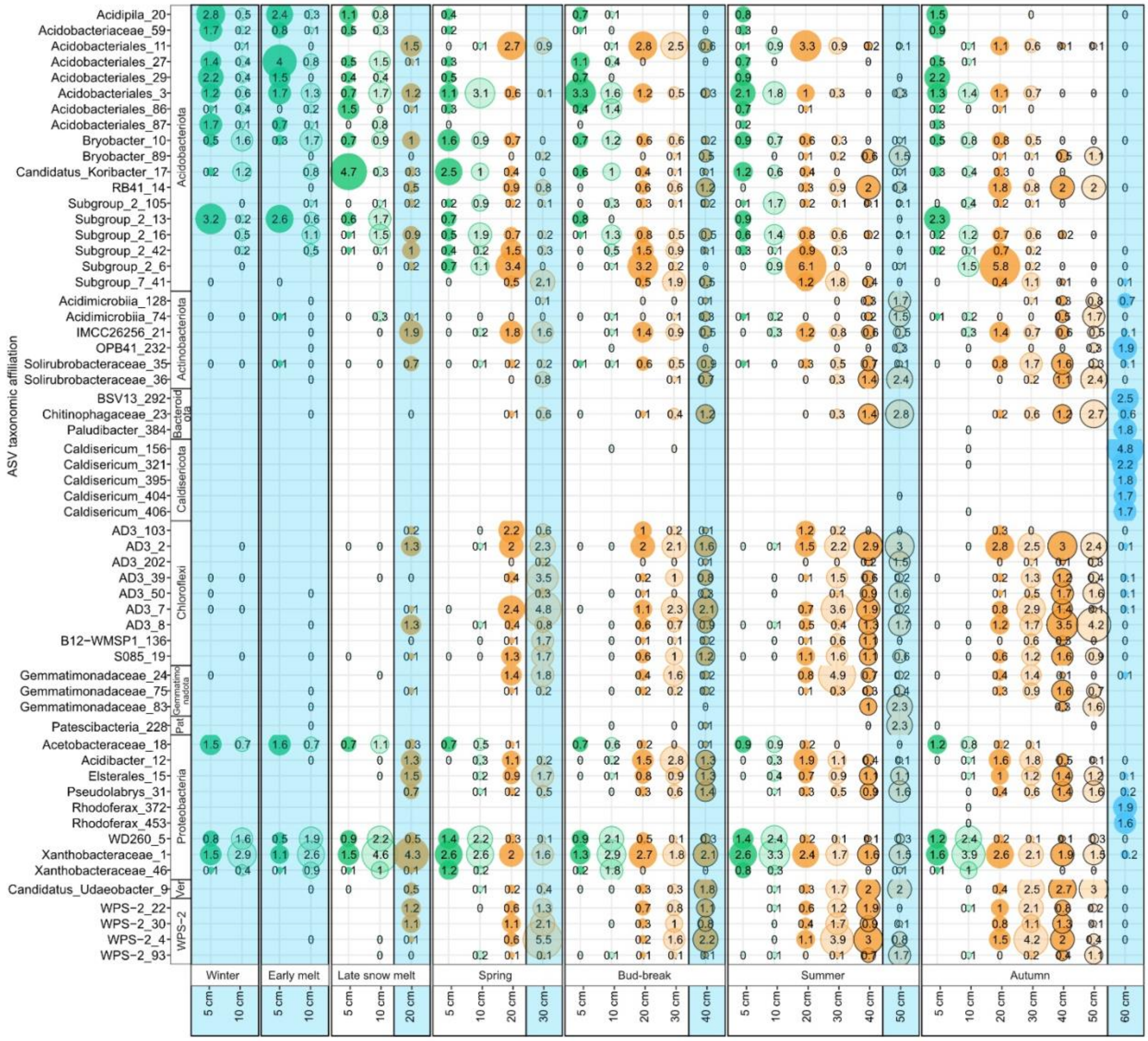

Figure S11. Depth-related variation in the relative abundance of ASVs within each season. ASVs at or above 1.5% relative abundance are shown. Once an ASV reaches the threshold (1.5%) in at least one sample, the abundance in all samples is shown, even if below the threshold. ASVs are sorted on the y-axis by Phylum association (Patescibacteria (Pat), Verrucomicrobiota (Ver)) and each ASV taxonomic affiliation is followed by an ASV number. The sampling times are divided into seven periods; see Table S8 and Methods for details. Light blue shading indicates soil samples that were frozen when sampled.