Table S1. Properties of tundra soil collected from CiPHER warming site in May 2010

Plot Soil Properties					
Depth	%C	%N	C:N	pH	bulk density
0- 15 cm	40.8 ± 0.5	1.2 ± 0.1	34.4 ± 2.2	4.69 ± 3.02	0.1 ± 0.5
15- 25 cm	34.3 ± 3.6	1.7 ± 0.2	20.7 ± 0.6	4.85 ± 0.08	0.3 ± 0.1
35- 58 cm	15.1 ± 2.7	0.6 ± 0.1	26.0 ± 1.5	5.1 ± 0.12	0.6 ± 0.1

Table S2. Cumulative CO_2-C respiration from the fast (CR1), slow (CR2), and passive (CR3) SOC pools and total (CRtot) the unit of g CO_2-C g^{-1} SOC. All values are the average of 6 replicates. Heat map, green to red, indicates highest to lowest values in each column.

Depth (cm)	Temp (°C)	Treatment	Time	CR1	CR2	CR3	CRtot
0- 15	15	control	2 weeks	0.009	0.008	0.002	0.019
15- 25	15	control	2 weeks	0.002	0.001	0.001	0.004
35- 58	15	control	2 weeks	0.001	0.000	0.000	0.002
0- 15	15	warming	2 weeks	0.009	0.005	0.002	0.017
15- 25	15	warming	2 weeks	0.001	0.001	0.000	0.002
35- 58	15	warming	2 weeks	0.001	0.001	0.000	0.001
0- 15	25	control	2 weeks	0.011	0.011	0.004	0.026
15- 25	25	control	2 weeks	0.003	0.002	0.002	0.007
35- 58	25	control	2 weeks	0.002	0.001	0.001	0.003
0- 15	25	warming	2 weeks	0.009	0.009	0.003	0.021
15- 25	25	warming	2 weeks	0.003	0.004	0.001	0.008
35- 58	25	warming	2 weeks	0.002	0.001	0.001	0.004
0- 15	15	control	3 months	0.010	0.039	0.013	0.062
15- 25	15	control	3 months	0.002	0.006	0.006	0.014
35- 58	15	control	3 months	0.002	0.002	0.003	0.007
0- 15	15	warming	3 months	0.010	0.024	0.014	0.049
15- 25	15	warming	3 months	0.001	0.004	0.003	0.008
35- 58	15	warming	3 months	0.001	0.003	0.001	0.005
0- 15	25	control	3 months	0.011	0.058	0.023	0.092
15- 25	25	control	3 months	0.004	0.012	0.010	0.025
35- 58	25	control	3 months	0.002	0.004	0.005	0.011
0- 15	25	warming	3 months	0.010	0.046	0.018	0.075
15- 25	25	warming	3 months	0.003	0.017	0.008	0.028
35- 58	25	warming	3 months	0.002	0.005	0.006	0.013
0- 15	15	control	9 months	0.010	0.069	0.038	0.117
15- 25	15	control	9 months	0.002	0.013	0.018	0.033
35- 58	15	control	9 months	0.002	0.006	0.008	0.016
0- 15	15	warming	9 months	0.010	0.040	0.041	0.092
15- 25	15	warming	9 months	0.001	0.010	0.009	0.020
35- 58	15	warming	9 months	0.001	0.008	0.004	0.013
0- 15	25	control	9 months	0.011	0.118	0.066	0.195
15- 25	25	control	9 months	0.004	0.028	0.029	0.061
35- 58	25	control	9 months	0.002	0.011	0.015	0.028
0- 15	25	warming	9 months	0.010	0.093	0.054	0.157
15- 25	25	warming	9 months	0.003	0.031	0.023	0.058
35- 58	25	warming	9 months	0.002	0.012	0.019	0.033
0- 15	15	control	years, 3	0.010	0.082	0.143	0.235
15- 25	15	control	years, 3	0.002	0.019	0.071	0.092
35- 58	15	control	years, 3	0.002	0.010	0.033	0.045
0- 15	15	warming	years, 3	0.010	0.045	0.155	0.210
15- 25	15	warming	years, 3	0.001	0.023	0.035	0.058
35- 58	15	warming	years, 3	0.001	0.020	0.017	0.038
0- 15	25	control	years, 3	0.011	0.165	0.234	0.411
15- 25	25	control	years, 3	0.004	0.050	0.111	0.165
35- 58	25	control	years, 3	0.002	0.030	0.060	0.092
0- 15	25	warming	years, 3	0.010	0.128	0.199	0.337
15- 25	25	warming	years, 3	0.003	0.049	0.090	0.142
35- 58	25	warming	years, 3	0.002	0.030	0.075	0.106

Table S3. Percentages of the cumulative CO_2 respiration from the decomposition of the fast (fCR1), slow (fCR2), and passive (fCR3) SOC pools out of the cumulative CO_2 respiration from the decomposition of total SOC and percentages of the respiration rate from the decomposition of the fast (fR1), slow (fR2), and passive (fR3) SOC pools out of the total respiration rate. All values are the average of 6 replicates. Heat map, green to red, indicates highest to lowest values in each column.

Depth (cm	Temp (°C)	Treatmen	Time	fCR1	fCR2	fCR3	fR1	fR2	fR3
0- 15	15	control	2 weeks	4.63E-01	4.16E-01	1.22E-01	1.75E-01	6.33E-01	1.92E-01
15- 25	15	control	2 weeks	4.42E-01	2.43E-01	3.16E-01	1.41E-01	3.69E-01	4.90E-01
35- 58	15	control	2 weeks	5.60E-01	2.05E-01	2.34E-01	4.28E-01	2.67E-01	3.06E-01
0- 15	15	warming	2 weeks	5.33E-01	3.19E-01	1.47E-01	2.26E-01	5.24E-01	2.50E-01
15- 25	15	warming	2 weeks	4.49E-01	3.66E-01	1.85E-01	6.34E-02	5.98E-01	3.39E-01
35- 58	15	warming	2 weeks	5.04E-01	3.39E-01	1.57E-01	1.67E-01	5.43E-01	2.90E-01
0- 15	25	control	2 weeks	4.24E-01	4.31E-01	1.45E-01	1.24E-01	6.43E-01	2.33E-01
15- 25	25	control	2 weeks	4.81E-01	3.02E-01	2.18E-01	1.40E-01	4.85E-01	3.75E-01
35- 58	25	control	2 weeks	5.65E-01	1.92E-01	2.43E-01	2.27E-01	3.39E-01	4.34E-01
0- 15	25	warming	2 weeks	4.45E-01	4.09E-01	1.46E-01	1.29E-01	6.33E-01	2.38E-01
15- 25	25	warming	2 weeks	4.34E-01	3.76E-01	1.90E-01	1.03E-01	5.67E-01	3.30E-01
35- 58	25	warming	2 weeks	5.05E-01	2.26E-01	2.69E-01	1.88E-01	3.63E-01	4.50E-01
0- 15	15	control	3 months	1.61E-01	6.10E-01	2.28E-01	6.07E-06	6.53E-01	3.47E-01
15- 25	15	control	3 months	1.28E-01	3.65E-01	5.07E-01	1.62E-06	3.94E-01	6.06E-01
35- 58	15	control	3 months	2.65E-01	3.28E-01	4.07E-01	9.95E-03	4.14E-01	5.76E-01
0- 15	15	warming	3 months	2.06E-01	4.95E-01	2.99E-01	3.78E-06	5.23E-01	4.77E-01
15- 25	15	warming	3 months	1.25E-01	5.53E-01	3.22E-01	8.07E-10	6.10E-01	3.90E-01
35- 58	15	warming	3 months	1.59E-01	5.43E-01	2.98E-01	5.37E-06	6.22E-01	3.78E-01
0- 15	25	control	3 months	1.33E-01	5.96E-01	2.71E-01	5.50E-07	6.06E-01	3.94E-01
15- 25	25	control	3 months	1.42E-01	4.68E-01	3.90E-01	1.17E-07	5.12E-01	4.88E-01
35- 58	25	control	3 months	1.90E-01	3.44E-01	4.66E-01	2.73E-05	4.08E-01	5.91E-01
0- 15	25	warming	3 months	1.38E-01	5.92E-01	2.70E-01	5.25E-06	6.17E-01	3.83E-01
15- 25	25	warming	3 months	1.32E-01	5.25E-01	3.43E-01	1.03E-06	5.33E-01	4.67E-01
35- 58	25	warming	3 months	1.58E-01	3.70E-01	4.72E-01	1.42E-04	4.22E-01	5.77E-01
0- 15	15	control	9 months	8.72E-02	5.65E-01	3.48E-01	1.13E-15	3.35E-01	6.65E-01
15- 25	15	control	9 months	5.49E-02	3.48E-01	5.97E-01	1.78E-17	2.68E-01	7.32E-01
35- 58	15	control	9 months	1.23E-01	3.48E-01	5.29E-01	6.91E-07	3.13E-01	6.87E-01
0- 15	15	warming	9 months	1.14E-01	4.34E-01	4.52E-01	7.68E-17	1.83E-01	8.17E-01
15- 25	15	warming	9 months	5.04E-02	5.69E-01	3.81E-01	2.80E-27	5.44E-01	4.56E-01
35- 58	15	warming	9 months	6.42E-02	5.76E-01	3.60E-01	1.15E-15	5.72E-01	4.28E-01
0- 15	25	control	9 months	6.35E-02	5.58E-01	3.78E-01	3.90E-19	4.39E-01	5.61E-01
15- 25	25	control	9 months	5.90E-02	4.62E-01	4.79E-01	2.63E-21	3.98E-01	6.02E-01
35- 58	25	control	9 months	7.59E-02	3.71E-01	5.53E-01	4.39E-14	3.68E-01	6.32E-01
0- 15	25	warming	9 months	6.60E-02	5.52E-01	3.82E-01	5.47E-16	4.00E-01	6.00E-01
15- 25	25	warming	9 months	5.98E-02	4.88E-01	4.52E-01	1.01E-17	3.45E-01	6.55E-01
35- 58	25	warming	9 months	6.24E-02	3.84E-01	5.53E-01	1.35E-11	3.65E-01	6.35E-01
0- 15	15	control	years, 3	4.36E-02	3.31E-01	6.26E-01	8.02E-61	6.61E-03	9.93E-01
15- 25	15	control	years, 3	2.09E-02	2.11E-01	7.68E-01	2.23E-68	3.50E-02	9.65E-01
35- 58	15	control	years, 3	4.45E-02	2.33E-01	7.23E-01	6.01E-26	5.85E-02	9.41E-01
0- 15	15	warming	years, 3	5.21E-02	2.15E-01	7.33E-01	3.78E-66	9.46E-04	9.99E-01
15- 25	15	warming	years, 3	1.79E-02	4.71E-01	5.11E-01	5.48E-107	2.61E-01	7.39E-01
35- 58	15	warming	years, 3	2.16E-02	5.02E-01	4.77E-01	4.62E-60	3.18E-01	6.82E-01
0- 15	25	control	years, 3	2.90E-02	3.94E-01	5.77E-01	8.83E-75	4.97E-02	9.50E-01
15- 25	25	control	years, 3	2.15E-02	3.11E-01	6.67E-01	2.67E-83	7.28E-02	9.27E-01
35- 58	25	control	years, 3	2.31E-02	3.15E-01	6.62E-01	3.28E-54	2.11E-01	7.89E-01
0- 15	25	warming	years, 3	3.00E-02	3.56E-01	6.14E-01	1.57E-61	3.37E-02	9.66E-01
15- 25	25	warming	years, 3	2.33E-02	3.13E-01	6.64E-01	1.51E-69	7.18E-02	9.28E-01
35- 58	25	warming	years, 3	1.97E-02	3.00E-01	6.80E-01	2.43E-43	1.64E-01	8.36E-01

Table S4. CO_2 respiration rates from the decomposition of fast (R1), slow (R2), and passive (R3) SOC pools with the unit of g CO_2-C g^{-1}SOC day^{-1}; the relative pool size of the fast (f1), slow (f2), and passive (f3) SOC pools; and the decomposition rate constant of the fast (k1), slow (k2), and passive (k3) SOC pools. All values are the average of 6 replicates. Heat map, green to red, indicates highest to lowest values in each column.

Depth (cm)	Temp (°C)	Treatmen	Time	R1	R2	R3	f1	f2	f3	k1	k2	k3
0- 15	15	control	2 weeks	1.52E-04	5.44E-04	1.42E-04	0.0050	0.0281	0.9669	0.1467	0.0131	0.0007
15- 25	15	control	2 weeks	3.03E-05	7.97E-05	6.71E-05	0.0009	0.0098	0.9893	0.0632	0.0054	0.0001
35- 58	15	control	2 weeks	4.76E-05	2.87E-05	3.06E-05	0.0006	0.0072	0.9922	0.0901	0.0031	0.0001
0- 15	15	warming	2 weeks	1.65E-04	3.54E-04	1.57E-04	0.0085	0.0406	0.9509	0.0900	0.0077	0.0005
15- 25	15	warming	2 weeks	6.31E-06	4.92E-05	3.28E-05	0.0011	0.0051	0.9938	0.1332	0.0092	0.0000
35- 58	15	warming	2 weeks	9.68E-06	3.73E-05	1.59E-05	0.0004	0.0036	0.9960	0.0771	0.0049	0.0000
0- 15	25	control	2 weeks	1.28E-04	7.76E-04	2.56E-04	0.0081	0.0344	0.9574	0.1353	0.0112	0.0007
15- 25	25	control	2 weeks	4.15E-05	1.47E-04	1.08E-04	0.0019	0.0107	0.9874	0.2455	0.0075	0.0002
35- 58	25	control	2 weeks	2.83E-05	4.75E-05	5.63E-05	0.0007	0.0062	0.9930	0.1168	0.0060	0.0001
0- 15	25	warming	2 weeks	1.43E-04	6.08E-04	2.07E-04	0.0052	0.0287	0.9661	0.1677	0.0135	0.0006
15- 25	25	warming	2 weeks	3.84E-05	2.45E-04	8.73E-05	0.0017	0.0187	0.9796	0.0862	0.0050	0.0003
35- 58	25	warming	2 weeks	3.11E-05	5.28E-05	7.16E-05	0.0011	0.0121	0.9868	0.0530	0.0030	0.0001
0- 15	15	control	3 months	2.17E-09	2.97E-04	1.41E-04	0.0057	0.0214	0.9729	0.1111	0.0378	0.0004
15- 25	15	control	3 months	2.85E-10	5.44E-05	6.67E-05	0.0008	0.0070	0.9922	0.1695	0.0123	0.0001
35- 58	15	control	3 months	4.50E-07	2.30E-05	3.05E-05	0.0003	0.0041	0.9956	0.1835	0.0131	0.0000
0- 15	15	warming	3 months	2.05E-09	1.69E-04	1.55E-04	0.0071	0.0154	0.9775	0.0926	0.0582	0.0003
15- 25	15	warming	3 months	3.48E-14	4.13E-05	3.26E-05	0.0006	0.0026	0.9967	0.1917	0.0132	0.0001
35- 58	15	warming	3 months	2.22E-10	3.30E-05	1.58E-05	0.0003	0.0025	0.9972	0.2792	0.0080	0.0000
0- 15	25	control	3 months	2.58E-10	4.94E-04	2.50E-04	0.0060	0.0203	0.9737	0.2362	0.0332	0.0008
15- 25	25	control	3 months	2.83E-11	1.17E-04	1.07E-04	0.0016	0.0063	0.9920	0.2990	0.0119	0.0002
35- 58	25	control	3 months	1.36E-09	4.35E-05	5.60E-05	0.0008	0.0059	0.9933	0.1693	0.0058	0.0001
0- 15	25	warming	3 months	4.61E-09	3.95E-04	2.03E-04	0.0062	0.0381	0.9557	0.1630	0.0169	0.0004
15- 25	25	warming	3 months	3.29E-10	1.22E-04	8.66E-05	0.0024	0.0142	0.9834	0.0978	0.0102	0.0002
35- 58	25	warming	3 months	1.82E-08	4.71E-05	7.11E-05	0.0010	0.0104	0.9886	0.0884	0.0039	0.0001
0- 15	15	control	9 months	2.17E-19	8.12E-05	1.37E-04	0.0064	0.0294	0.9642	0.1082	0.0302	0.0003
15- 25	15	control	9 months	1.57E-21	2.37E-05	6.58E-05	0.0009	0.0068	0.9923	0.2053	0.0099	0.0001
35- 58	15	control	9 months	2.38E-11	1.39E-05	3.04E-05	0.0004	0.0039	0.9957	0.1444	0.0144	0.0000
0- 15	15	warming	9 months	2.82E-20	3.83E-05	1.49E-04	0.0084	0.0195	0.9721	0.0944	0.0521	0.0003
15- 25	15	warming	9 months	6.83E-32	2.82E-05	3.22E-05	0.0008	0.0108	0.9884	0.2996	0.0017	0.0001
35- 58	15	warming	9 months	4.07E-20	2.47E-05	1.58E-05	0.0006	0.0109	0.9885	0.1628	0.0016	0.0000
0- 15	25	control	9 months	1.40E-22	2.11E-04	2.34E-04	0.0081	0.0288	0.9632	0.2390	0.0224	0.0007
15- 25	25	control	9 months	4.79E-25	6.88E-05	1.05E-04	0.0020	0.0048	0.9932	0.3023	0.0152	0.0003
35- 58	25	control	9 months	1.92E-18	3.54E-05	5.54E-05	0.0010	0.0048	0.9942	0.2067	0.0049	0.0001
0- 15	25	warming	9 months	3.26E-19	1.60E-04	1.94E-04	0.0087	0.0263	0.9649	0.1706	0.0155	0.0006
15- 25	25	warming	9 months	1.56E-21	5.54E-05	8.49E-05	0.0020	0.0137	0.9843	0.1817	0.0105	0.0002
35- 58	25	warming	9 months	1.72E-15	3.61E-05	7.00E-05	0.0010	0.0050	0.9940	0.2009	0.0047	0.0001
0- 15	15	control	years, 3	1.05E-64	7.98E-07	1.20E-04	0.0102	0.0818	0.9079	0.1826	0.0079	0.0002
15- 25	15	control	years, 3	1.02E-72	1.94E-06	6.19E-05	0.0020	0.0201	0.9780	0.1977	0.0037	0.0001
35- 58	15	control	years, 3	1.41E-30	1.94E-06	2.95E-05	0.0019	0.0114	0.9867	0.0764	0.0028	0.0000
0- 15	15	warming	years, 3	8.02E-70	1.30E-07	1.26E-04	0.0104	0.0450	0.9447	0.1729	0.0095	0.0002
15- 25	15	warming	years, 3	7.53E-112	7.28E-06	3.07E-05	0.0011	0.0280	0.9709	0.2926	0.0018	0.0000
35- 58	15	warming	years, 3	9.92E-65	6.82E-06	1.56E-05	0.0008	0.0247	0.9745	0.2079	0.0014	0.0000
0- 15	25	control	years, 3	2.25E-78	7.12E-06	1.76E-04	0.0120	0.1338	0.8542	0.2047	0.0096	0.0003
15- 25	25	control	years, 3	2.50E-87	6.95E-06	9.48E-05	0.0035	0.0531	0.9433	0.2089	0.0028	0.0001
35- 58	25	control	years, 3	1.34E-58	1.41E-05	5.25E-05	0.0020	0.0438	0.9541	0.1914	0.0011	0.0001
0- 15	25	warming	years, 3	2.45E-65	4.88E-06	1.57E-04	0.0104	0.1290	0.8606	0.2200	0.0068	0.0002
15- 25	25	warming	years, 3	1.98E-73	5.71E-06	7.78E-05	0.0034	0.0509	0.9457	0.2282	0.0061	0.0001
35- 58	25	warming	years, 3	2.48E-47	1.14E-05	6.51E-05	0.0021	0.0388	0.9591	0.1860	0.0015	0.0001

Table S5. One-way ANOVA P values comparing variations in estimated SOC parameters across depths for soils from each incubation temperature. Variables included cumulative CO_2 respiration from the fast (CR1), slow (CR2), and passive (CR2), SOC pools and total (CRtot), with the unit of g CO_2-C g^{-1} SOC; percentages of the cumulative CO_2 respiration from the decomposition of the fast (fCR1), slow (fCR2), and passive (fCR3) SOC pools out of the cumulative CO2 respiration from the decomposition of total SOC; the percentages of the respiration rate from the decomposition of the fast (fR1), slow (fR2), passive (fR3) SOC pools out of the total respiration rate; the CO2 respiration rate from the decomposition of the fast (R1), slow (R2), and passive (R3) SOC pools with the unit of g CO_2-C g^{-1}SOC day^{-1}; the relative pool size of the fast (f1), slow (f2), and passive (f3) SOC pools; and the decomposition rate constant of the fast (k1), slow (k2), and passive (k3) SOC pools.

Table S4 ANOVAs across depths		
Parameter	Inc. temp (°C)	P value
CR1	25	**5.08E-46**
CR1	15	**7.81E-31**
CR2	25	**8.18E-10**
CR2	15	**2.74E-13**
CR3	25	**0.00013**
CR3	15	**1.62E-06**
CRtot	25	**7.57E-10**
CRtot	15	**3.79E-12**
fCR1	25	0.61446
fCR1	15	0.31186
fCR2	25	**9.91E-06**
fCR2	15	0.56435
fCR3	25	**0.00624**
fCR3	15	0.23611
R1	25	**0.0142**
R1	15	**0.00163**
R2	25	**5.30E-10**
R2	15	**1.19E-09**
R3	25	**1.50E-28**
R3	15	**3.89E-37**
fR1	25	0.33273
fR1	15	0.08862
fR2	25	0.14677
fR2	15	0.80679
fR3	25	0.34147
fR3	15	0.54674
f1	25	**6.53E-34**
f1	15	**5.73E-28**
f2	25	**1.17E-05**
f2	15	**6.26E-12**
f3	25	**4.90E-07**
f3	15	**2.74E-15**
k1	25	**0.00152**
k1	15	**0.00042**
k2	25	**3.96E-15**
k2	15	**7.23E-11**
k3	25	**8.33E-22**
k3	15	**6.27E-18**

Table S6. One-way ANOVA P values; comparing variations in Estimated SOC parameters between incubation temperatures for soils from each depth including cumulative CO_2 respiration from the fast (CR1), slow (CR2), and passive (CR2), SOC pools and total (CRtot), with the unit of g CO_2-C g^{-1} SOC; percentages of the cumulative CO_2 respiration from the decomposition of the fast (fCR1), slow (fCR2), and passive (fCR3) SOC pools out of the cumulative CO2 respiration from the decomposition of total SOC; the percentages of the respiration rate from the decomposition of the fast (fR1), slow (fR2), passive (fR3) SOC pools out of the total respiration rate; the CO2 respiration rate from the decomposition of the fast (R1), slow (R2), and passive (R3) SOC pools with the unit of g CO_2-C g^{-1}SOC day^{-1}; the relative pool size of the fast (f1), slow (f2), and passive (f3) SOC pools; and the decomposition rate constant of the fast (k1), slow (k2), and passive (k3) SOC pools.

Table S5 ANOVAS between incubation temperatures		
Parameter	Depth	P value
CR1	0- 15 cm	0.572445
CR1	15- 25 cm	**1.90E-11**
CR1	35- 58 cm	**1.11E-06**
CR2	0- 15 cm	**0.002525**
CR2	15- 25 cm	**0.000331**
CR2	35- 58 cm	**0.018934**
CR3	0- 15 cm	0.143498
CR3	15- 25 cm	**0.027268**
CR3	35- 58 cm	**0.002766**
CRtot	0- 15 cm	**0.011098**
CRtot	15- 25 cm	**0.001468**
CRtot	35- 58 cm	**0.001808**
fCR1	0- 15 cm	0.256705
fCR1	15- 25 cm	0.829379
fCR1	35- 58 cm	0.677779
fCR2	0- 15 cm	0.070414
fCR2	15- 25 cm	0.704582
fCR2	35- 58 cm	0.053353
fCR3	0- 15 cm	0.643158
fCR3	15- 25 cm	0.622798
fCR3	35- 58 cm	**0.037357**
R1	0- 15 cm	0.732469
R1	15- 25 cm	0.162449
R1	35- 58 cm	0.954102
R2	0- 15 cm	**0.016961**
R2	15- 25 cm	**0.001741**
R2	35- 58 cm	**0.000349**
R3	0- 15 cm	**2.94E-06**
R3	15- 25 cm	**6.97E-11**
R3	35- 58 cm	**4.40E-16**
fR1	0- 15 cm	0.273328
fR1	15- 25 cm	0.67845
fR1	35- 58 cm	0.386358
fR2	0- 15 cm	0.229839
fR2	15- 25 cm	0.818163
fR2	35- 58 cm	0.16807
fR3	0- 15 cm	0.432429
fR3	15- 25 cm	0.898921
fR3	35- 58 cm	0.084902
f1	0- 15 cm	0.6489
f1	15- 25 cm	**4.49E-08**
f1	35- 58 cm	**3.83E-05**
f2	0- 15 cm	0.056827
f2	15- 25 cm	**0.010153**
f2	35- 58 cm	**0.013315**
f3	0- 15 cm	0.061339

f3	15- 25 cm	**0.005111**
f3	35- 58 cm	**0.009353**
k1	0- 15 cm	**1.17E-07**
k1	15- 25 cm	0.536001
k1	35- 58 cm	0.947167
k2	0- 15 cm	**0.005434**
k2	15- 25 cm	0.289877
k2	35- 58 cm	**0.027997**
k3	0- 15 cm	**0.001347**
k3	15- 25 cm	**6.96E-07**
k3	35- 58 cm	**3.38E-12**

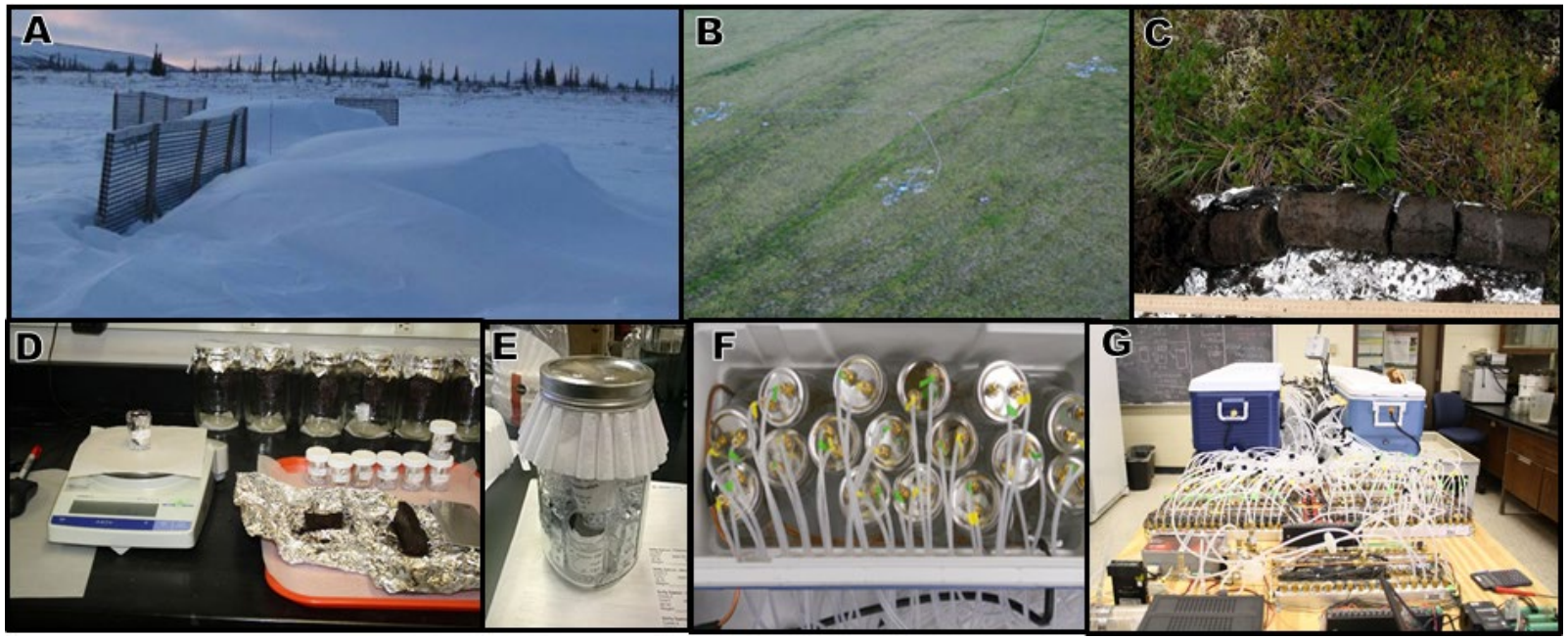

Figure S1. Photographs depict set up of winter warming field treatment and lab soil incubation. The Winter warming treatment was derived using snow fences to accumulate snow, providing an igloo effect over soils, followed by early Spring snow removal (A). Aerial photo shows six paired warmed and control plots, established in 3 blocks at the Carbon in Permafrost Experimental Heating Project (CIPEHR) site (B). Soil cores were collected across the ~60 cm depth profile and partitioned by depth (C). Subsamples (~10 g soil) of depth fractions were aliquoted into vials (D) and 8 vials were placed into incubation jars (E) allowing for easy retrieval of subsamples for DNA extraction throughout the incubation period. Jars were placed in incubators set to 25 °C or 15 °C (F) and respiration from each jar was monitored (G). Photo credits; Susan Natali (A &B), Edward Schuur (C), and Rosvel Bracho (D-G). Additional photos of the CIPEHR site are available at https://www2.nau.edu/schuurlab-p/CiPEHR.html.

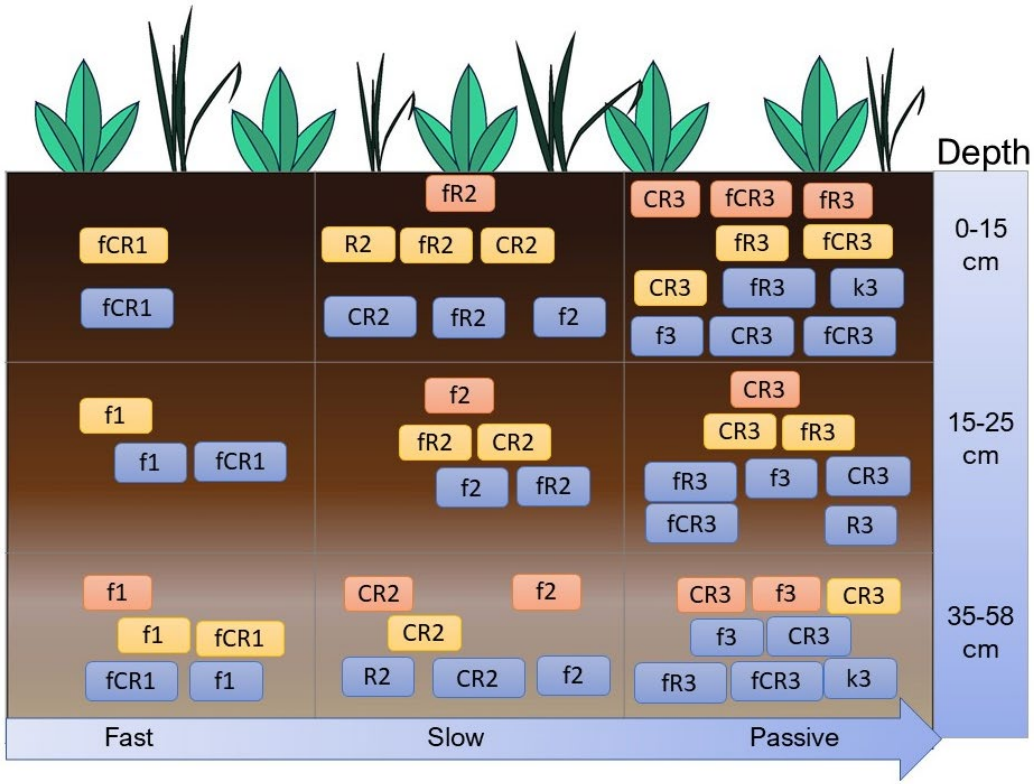

Figure S2. Estimated SOC parameters that were significantly associated with 16S (pink), ITS (yellow), or GeoChip (blue) community profiles, using Random forest (more than 30% variance explained). Parameters included cumulative CO_2 respiration from the fast SOC pool (CR1), slow SOC pool (CR2), passive SOC pool (CR2), and total (CRtot), with the unit of g CO_2-C g^{-1}SOC, percentages of the cumulative CO_2 respiration from the decomposition of the fast SOC (fCR1), slow SOC (fCR2), and passive SOC (fCR3) pools out of the cumulative CO_2 respiration from the decomposition of total SOC and the percentage of the respiration rate from the decomposition of the fast SOC (fR1), slow SOC (fR2), passive SOC (fR3) pools out of the total respiration rate, the CO_2 respiration rate from the decomposition of the fast SOC (R1), slow SOC (R2), and passive SOC (R3) pools with the unit of g CO_2-C g^{-1}SOC day^{-1}, the relative pool size of the fast SOC (f1), slow SOC (f2), passive SOC (f3) pools, and the decomposition rate constant of the fast SOC (k1), slow SOC (k2), passive SOC (k3) pools.

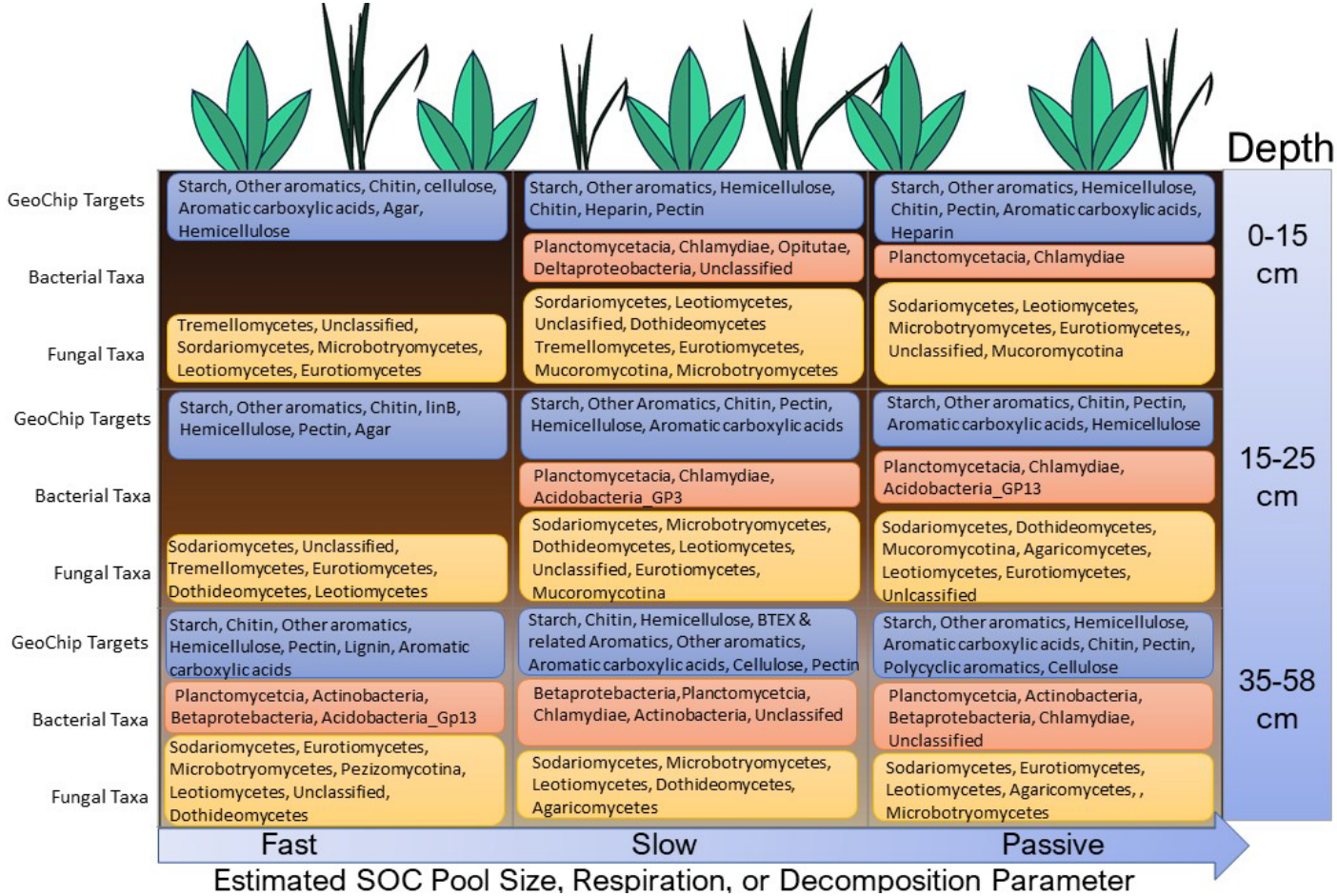

Figure S3. Classes and GeoChip probe categories that were identified using a Random Forest method. Bacterial/archaeal classes are in pink boxes, fungal classes are in yellow boxes, and GeoChip probe categories are in blue. To identify important classes and probe- categories estimated SOC parameters, shown in Figures S1, were investigated further. The %IncMSE value for all classes or probes were determined for each community profile at each depth. These values were used to generate heatmaps which highlight the classes or probes that could predict estimated SOC parameters relating to the fast, slow, or passive SOC pools (Figures S2, S5, & S6). All important classes (having values above the mean of 4 output by the heatmaps) were included into this figure. Unique classes or probe categories (corresponding with either fast SOC estimated parameters or slow and/or passive SOC estimated parameters) are presented in Figure 4.

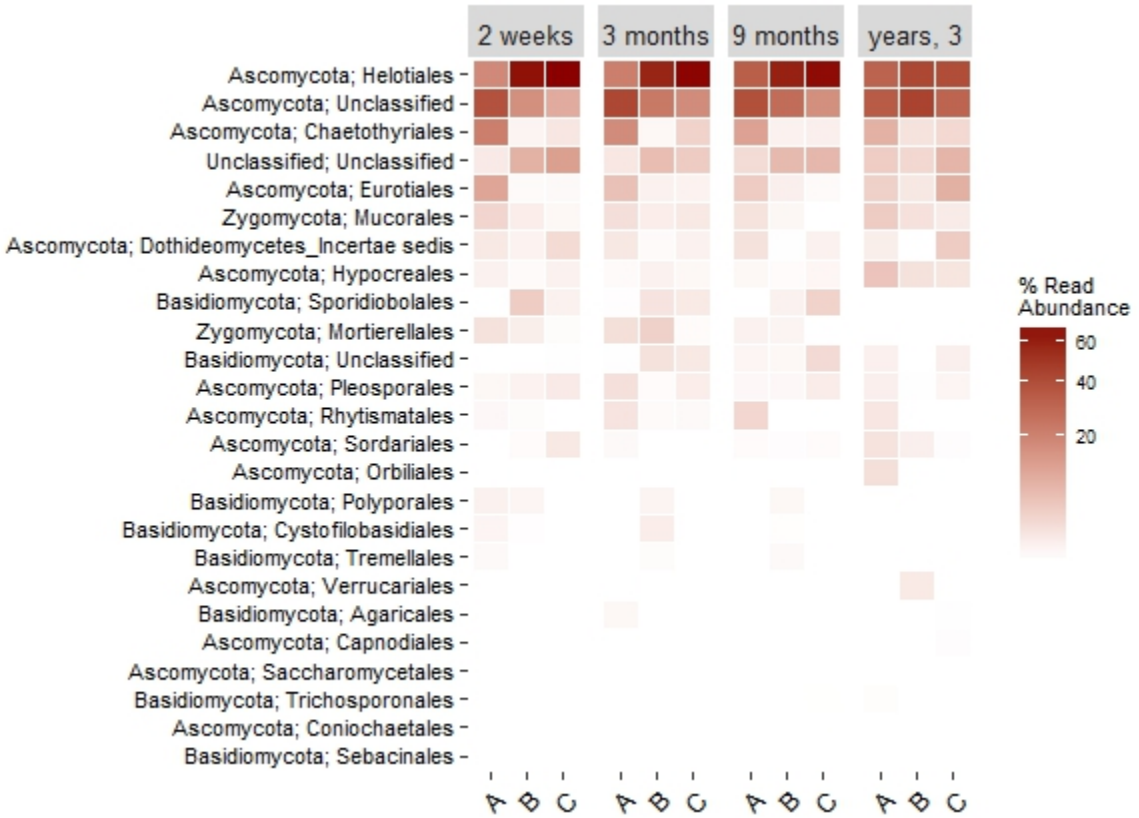

Figure S4. Heatmap of abundances of Fungal classes and genera based on ITS sequencing determined for soil from each time point and each depth (A = 0-15 cm, B = 15-25 cm, C = 35-58 cm).

Supplemental Methods

Field Site and Experimental Warming Design

The Carbon in Permafrost Experimental Heating Research (CiPEHR) project was established in September of 2008 in the Eight Mile Lake watershed (63°52'59''N, 149°13'32"W) (Mauritz et al 2017, Natali et al 2012, Natali et al 2014). At this site, snow fences were used to elicit a soil warming treatment by increasing snow cover behind the fences during the winter, coupled with early-spring snow removal to keep water input and snow melt timing similar to control plots (Natali et al 2011, Natali et al 2014). This enabled an average soil temperature increase of 2.3 ºC in warmed over the control plots. Detailed descriptions pertaining to the plant ecology and climate conditions of this region and the CiPEHR site design and maintenance can be found in previous reports (Natali et al 2011, Natali et al 2014, Schuur et al 2007, Schuur et al 2009). Samples were collected in May 2010, after two winter warming seasons. The soil of this moist acidic subarctic tundra is classified as a Gelisol (USA 1975) with a thick organic horizon (0.45 – 0.65 m) and an organic matter (OM) content of approximately 50 kg OM m^{-2} down to 1 m above a cryoturbated mineral horizon (Pries et al 2012, Schuur et al 2009). The active layer, induced by seasonal thaw, reaches a maximum depth in the control plots of approximately 60 cm, below which a permafrost layer is maintained (Natali et al 2014).

Three-Pool Carbon Modeling

To model and partition the SOC into fast (f1), slow (f2), and passive (f3) SOC pools we used a three-pool SOC decomposition model, described in detail previously (Feng et al 2017). This provided estimates of the proportion and decomposition rate constant of different SOC fractions using the following equation:

$$R = C_0 \times (f_1 \times k_1 \times e^{k_1 \times t} + f_2 \times k_2 \times e^{k_2 \times t} + f_3 \times k_3 \times e^{k_3 \times t}) \quad \text{Eq (1)}$$

where R is CO_2 respiration rate (mg CO_2-C g^{-1} soil day^{-1}) at time *t*, C_0 is initial SOC content (mg SOC g^{-1} soil), f_1, f_2, f_3, k_1, k_2, and k_3 are the relative pool sizes and decomposition rate constants of the fast, slow, and passive SOC components, and the sum of f_1, f_2, and f_3 is 1. The parameters in this model were estimated using Bayesian probabilistic inversion and the Metropolis-Hastings (M-H) algorithm (Xu et al 2006) and the inversion method details can be found in published literature (Li et al 2013, Liang et al 2015, Xu et al 2006).

Amplicon sequencing

Library construction and sequencing were processed using methods similar to those described in previous reports (Wu et al 2015). Here, universal primer sets, 515F (5′-GTGCCAGCMGCCGCGGTAA-3′) and 806R (5′-GGACTACHVGGGTWTCTAAT-3′) targeting the V3-V4 hypervariable region of the bacterial and archaeal 16S rRNA gene (Peiffer et al 2013), and gITS7F (5′-GTGARTCATCGARTCTTTG-3′) and ITS4R (5′-TCCTCCGCTTATTGATATGC-3′) for the fungal internal transcribed spacer (ITS) between 5.8S and 28S rRNA genes (Zhou et al 2016), were used in this study.

Library preparation was performed using a two-step PCR to avoid extra PCR bias that could be introduced by the added components in the long primers (Wu et al 2015). Phasing primers, which contained different-length spacers (0-7 bases) between the sequencing primer and the target gene to randomize base position during sequencing (Wu et al 2015), were designed and used in the second step of the two-step PCR.. The forward and reverse primers were used in a complementary manner to ensure that the total length of the amplified sequences remained constant. Both forward and reverse phasing primers have the Illumina adaptor, the Illumina sequencing primer, a spacer, and the target gene primer and a barcode of 12 bases in the reverse

primer between the sequencing primer and the adaptor. In the two-step PCR, soil DNA was firstly diluted to 2.5 ng/ μL with water to be used as template in the PCR reaction. The first round PCR was performed in a 25 μL reaction containing 2.5 μL 10 × PCR buffer II (including dNTPs), 0.25 U DNA polymerase, 0.4 μM of both forward and reverse target only primers and 4 μL diluted soil DNA. Reactions of 16S rRNA gene amplification were performed in triplicate and thermal cycling conditions were as follows: initial denaturation at 94 ºC for 3 min, followed by 10 cycles of 94 ºC for 25 s, 53 ºC for 25 s, and 68 ºC for 45 s, with a final extension at 68 ºC for 10 min. The amplification program described above was also used for the amplification of ITS except that 12 cycles were performed, and the annealing temperature was 52 ºC. The triplicate products from the first-round PCR were combined, purified with Agencourt® Ampure® XP beads (Beckman Coulter, Inc., CA, USA) according to the manufacturer's protocol, eluted by 50 μL water and aliquoted into three new PCR reactions. The second PCR was carried out in triplicate in a 25 μL reaction containing 2.5 μL 10 × PCR buffer II (including dNTPs), 0.25 U DNA polymerase, 0.4 μM of both forward and reverse phasing primers and 15 μL aliquot of the first round purified PCR product. The amplifications were cycled 20 times following the above program. PCR products from triplicate reactions were combined, visualized by 1% agarose gel electrophoresis and quantified by PicoGreen using a FLUOstar Optima fluorescence plant reader (BMG Labtech, Jena, Germany).

PCR products from different samples were pooled at equal molality (generally 300 samples) to be sequenced in the same MiSeq run. The pooled mixture was purified with a QIAquick gel extraction kit (Qiangen Sciences, Germantown, MD, USA) and re-quantified with PicoGreen. Sample libraries for sequencing were prepared according to the MiSeq Reagent Kit Preparation Guide (Illumina, SanDiego, CA, USA) as described previously (Caporaso et al 2012,

Wu et al 2015). Firstly, the combined sample library was diluted to 2 nM. Then, the sample library was denatured by mixing 10 µl of the diluted library and 10 µl of 0.2N fresh NaOH and incubated for 5 min at room temperature. A measure of 980 µl of chilled Illumina HT1 buffer was added to the denatured DNA and mixed to make a 20 pM library. Finally, the library was further adjusted to the desired concentration (~12 pM) for sequencing using chilled HT1 buffer. The library to be sequenced was mixed with a 12 pM PhiX library to achieve a 10% PhiX spike. A 500-cycle v2 MiSeq reagent cartridge (Illumina) was thawed for 1 hour in a water bath, inverted 10 times to mix the thawed reagents and stored at 4 ^{o}C for a short time until use. The 16S rRNA gene and ITS sequencing was performed for 251, 12 and 251 cycles for forward, index and reverse reads, respectively.

Sequence preprocessing

The raw reads of the 16S rRNA gene and ITS were collected by the MiSeq in FASTQ format, and then submitted to our website (http://zhoulab5.rccc.ou.edu:8080) for analyses using a sequence analysis pipeline built on the Galaxy platform (Giardine et al., 2005). First, the reads were assigned into different sample libraries based on the barcodes. Before combining forward and reverse reads, primer sequences at the end of each read was trimmed using the Btrim program (Kong 2011) with a threshold of QC > 25 over a 5-bp window size was used to filter the reads. For 16S and ITS, forward and reverse reads of same sequence with at least 20 bp overlap and < 5% mismatches were combined using FLASH (Magoč and Salzberg 2011). Any joined sequences with an ambiguous base or a length of < 245 bp for 16S rRNA gene or < 220 bp for ITS were discarded. Thereafter, OTUs were clustered by UPARSE (Edgar 2013) at 97% identity and singletons were removed from the remaining sequences for both 16S rRNA and ITS genes. In UPARSE, the greengenes

reference data set (DeSantis et al 2006)(16S) and the UNITE/QIIME released ITS reference data set (https://unite.ut.ee/repository.php) were used as reference databases to remove chimeras. To normalize samples to the same total read abundance, 14,665 sequences for 16S rRNA gene and 4,951 sequences for ITS were randomly selected (re-sampled) for each sample. Based on rarefaction analyses, these reads numbers sufficiently portrayed community diversity, as the same trends among samples as were observed with deeper sequencing. OTU taxonomic classification of ITS and 16S rRNA gene sequences was performed using representative sequences from each OTU through the Ribosomal Database Project (RDP) Classifier with 50% confidence estimates (Wang et al 2007).

GeoChip Analyses

For this, 500 ng of soil community DNA was labeled with the fluorescent dye Cy-3, hybridized to GeoChip 5.0 60K microarrays, and scanned with a NimbleGen MS200 Microarray Scanner using techniques described previously (Cong et al 2015). The image data were processed using the Agilent Feature Extraction program that designates values for probe signal intensities and background noise based on the scanned images. Extracted data were then loaded onto an in-house GeoChip data analysis pipeline (ieg.ou.edu/microarray/). Data normalization and quality filtering were performed with multiple standard steps (Liang et al 2010, Van Nostrand et al 2016) including removal of poor quality spots, spots with signal-to-noise (SNR) ratios less than 2 set to 0 signal intensity (i.e. below reliable detection limit), and transformation of signal intensities into relative abundances. Probes with positive signal in only 2 or fewer samples were removed. Probes with high signal intensities reflect a greater amount of hybridization and targeted genes more abundant in the sample.

Statistical Analyses

Probes or OTU's that showed significant correlation with at least one estimated SOC parameter within at least one depth and incubation temperature based on either Pearson or Spearman correlations with False Discovery Rate (FDR) corrections were retained based on the following cutoffs: 16S and ITS OTUs: $R2 > 0.1$, p-value < 0.2; GeoChip probes: $R2 > 0.3$, p-value < 0.05 (R package ieggr, available from http://ccl.oucreate.com/). Pearson and Spearman correlation analyses with FDR correction indicated that of the 16S OTU's a total of 10,075 of 14,665 (69%) showed significant correlations above the cutoff values and 3,129 of the 4,951 (63%) ITS OTU's passed. For GeoChip data only probes targeting genes involved in SOC decomposition were analyzed with 22,991 of 24,886 (92%) passing. Only probes and OTU's that passed these criteria were utilized for additional analyses.

To determine significance variation between community profiles across soil depths and incubation temperatures non-parametric multivariate dissimilarity tests were employed. These were based on distance matrices calculated with Bray-Curtis and Sørenson indices an included multi-response permutation procedures (MRPP), Adonis, and analysis of similarity (ANOSIM), which were performed using R package, vegan. Non-metric multidimensional scaling (NMDS) plots based on Bray-Curtis distance matrices of community data were generated using R package ampvis2 based functions in vegan and ggplot2 packages.

To determine significant correlations of the microbial communities to the estimated SOC decomposition parameters, Mantel tests with Pearson correlations were performed on Bray-Curtis distance matrices prepared from Wisconsin Square Root transformed community data and Euclidian distance matrix of the estimated SOC decomposition parameters (R package ecodist). Multiple Regression on distance Matrices (MRM) analyses were preformed to examine statistical correlations with community and estimated SOC decomposition parameters using Euclidian

distance matrices for SOC estimated parameters and Bray Curtis community distance matrices for (i) each depth and incubation temperature subset, (ii) each depth subset (incubation temperatures combined), and (iii) all community data (R package ecodist).

Random Forest analyses were employed to identify whether estimated SOC decomposition parameters could be predicted by the 16S, ITS, or GeoChip community profiles using R package, randomForest (Liaw and Wiener 2002). These models were output separately for all community data and community data subset by (i) depth + incubation temperature and (ii) depth only using both OTU level and class level community data. Estimated SOC decomposition parameters for which 30% or more variance could be explained by a give community data set, were investigated further with the goal of finding predictors (i.e., OTUs, probes, or classes). Predictor importance was quantified based on %IncMSE (the increase in mean squared error of prediction resulting from that OTU, probe, or class being permuted) and was determined for all OTUs, probes, and taxonomic classes in relation to each estimated SOC parameter passing the 30% threshold. These outputs were combined yielding, for example, a matrix of 16S OTU importance values for all passed estimated SOC parameters. For this purpose, OTU's not assigned importance by random forest were attributed a value of 0. The estimated SOC decomposition parameters were then classified as relating to fast, slow, or passive SOC and the probes (grouped by SOC substrate target) and bacterial and fungal classes that showed the greatest sum of importance values in association with estimated parameters in those pools were deemed as significant for predicting that SOC type. To reduce the effect of consistently abundant (i.e. ubiquitous) classes and probes from dominating these results, most of the discussion is focused on the identified probe categories and taxonomic classes that were significant to either the fast SOC parameters and not slow and/or passive pools or vice versa.

References

Caporaso JG, Lauber CL, Walters WA, Berg-Lyons D, Huntley J, Fierer N *et al* (2012). Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms. *The ISME journal* **6:** 1621-1624.

Cong J, Liu X, Lu H, Xu H, Li Y, Deng Y *et al* (2015). Analyses of the influencing factors of soil microbial functional gene diversity in tropical rainforest based on GeoChip 5.0. *Genomics data* **5:** 397-398.

DeSantis TZ, Hugenholtz P, Larsen N, Rojas M, Brodie EL, Keller K *et al* (2006). Greengenes, a chimera-checked 16S rRNA gene database and workbench compatible with ARB. *Applied and environmental microbiology* **72:** 5069-5072.

Edgar RC (2013). UPARSE: highly accurate OTU sequences from microbial amplicon reads. *Nature Methods* **10:** 996-998.

Feng W, Liang J, Hale LE, Jung CG, Chen J, Zhou J *et al* (2017). Enhanced decomposition of stable soil organic carbon and microbial catabolic potentials by long-term field warming. *Global change biology* **23:** 4765-4776.

Kong Y (2011). Btrim: A fast, lightweight adapter and quality trimming program for next-generation sequencing technologies. *Genomics* **98:** 152-153.

Li D, Zhou X, Wu L, Zhou J, Luo Y (2013). Contrasting responses of heterotrophic and autotrophic respiration to experimental warming in a winter annual-dominated prairie. *Global Change Biology* **19:** 3553-3564.

Liang J, Li D, Shi Z, Tiedje JM, Zhou J, Schuur EA *et al* (2015). Methods for estimating temperature sensitivity of soil organic matter based on incubation data: a comparative evaluation. *Soil Biology and Biochemistry* **80:** 127-135.

Liang Y, He Z, Wu L, Deng Y, Li G, Zhou J (2010). Development of a common oligonucleotide reference standard for microarray data normalization and comparison across different microbial communities. *Applied and environmental microbiology* **76:** 1088-1094.

Liaw A, Wiener M (2002). Classification and Regression by randomForest. *R news* **2:** 18-22.

198 Magoč T, Salzberg SL (2011). FLASH: Fast Length Adjustment of Short Reads to Improve
199 Genome Assemblies. *Bioinformatics*.

200
201 Mauritz M, Bracho R, Celis G, Hutchings J, Natali SM, Pegoraro E *et al* (2017). Nonlinear CO 2
202 flux response to 7 years of experimentally induced permafrost thaw. *Global change biology* **23:**
203 3646-3666.

204
205 Natali SM, Schuur EA, Trucco C, Hicks Pries CE, Crummer KG, Baron Lopez AF (2011).
206 Effects of experimental warming of air, soil and permafrost on carbon balance in Alaskan tundra.
207 *Global Change Biology* **17:** 1394-1407.

208
209 Natali SM, Schuur EA, Rubin RL (2012). Increased plant productivity in Alaskan tundra as a
210 result of experimental warming of soil and permafrost. *Journal of Ecology* **100:** 488-498.

211
212 Natali SM, Schuur EA, Webb EE, Pries CEH, Crummer KG (2014). Permafrost degradation
213 stimulates carbon loss from experimentally warmed tundra. *Ecology* **95:** 602-608.

214
215 Peiffer JA, Spor A, Koren O, Jin Z, Tringe SG, Dangl JL *et al* (2013). Diversity and heritability
216 of the maize rhizosphere microbiome under field conditions. *Proceedings of the National*
217 *Academy of Sciences* **110:** 6548-6553.

218
219 Pries CEH, Schuur EA, Crummer KG (2012). Holocene carbon stocks and carbon accumulation
220 rates altered in soils undergoing permafrost thaw. *Ecosystems* **15:** 162-173.

221
222 Schuur EA, Crummer KG, Vogel JG, Mack MC (2007). Plant species composition and
223 productivity following permafrost thaw and thermokarst in Alaskan tundra. *Ecosystems* **10:** 280-
224 292.

225
226 Schuur EA, Vogel JG, Crummer KG, Lee H, Sickman JO, Osterkamp T (2009). The effect of
227 permafrost thaw on old carbon release and net carbon exchange from tundra. *Nature* **459:** 556-
228 559.

229
230 USA SSS (1975). *Soil taxonomy: a basic system of soil classification for making and*
231 *interpreting soil surveys*. US Government Printing Office.

232
233 Van Nostrand JD, Yin H, Wu L, Yuan T, Zhou J (2016). Hybridization of environmental
234 microbial community nucleic acids by GeoChip. *Microbial Environmental Genomics (MEG)*.
235 Springer. pp 183-196.

Wang Q, Garrity GM, Tiedje JM, Cole JR (2007). Naïve Bayesian Classifier for Rapid Assignment of rRNA Sequences into the New Bacterial Taxonomy. *Applied and Environmental Microbiology* **73:** 5261-5267.

Wu L, Wen C, Qin Y, Yin H, Tu Q, Van Nostrand JD *et al* (2015). Phasing amplicon sequencing on Illumina Miseq for robust environmental microbial community analysis. *BMC microbiology* **15:** 125.

Xu T, White L, Hui D, Luo Y (2006). Probabilistic inversion of a terrestrial ecosystem model: Analysis of uncertainty in parameter estimation and model prediction. *Global Biogeochemical Cycles* **20**.

Zhou J, Deng Y, Shen L, Wen C, Yan Q, Ning D *et al* (2016). Temperature mediates continental-scale diversity of microbes in forest soils. *Nature Communications* **7**.