

TableS1. Enzymes

Enzyme	Acronym	General function	Substrate	EC no.
α -Glucosidase	AG	Hydrolysis of α -glucosyl residues, releases α -D-glucose	4-Methylumbelliferyl α -D-glucopyranoside	3.2.1.20
β -Glucosidase	BG	Hydrolysis of β -glucosyl residues, releases β -D-glucose; involved in the final step of cellulose hydrolysis	4-Methylumbelliferyl β -D-glucopyranoside	3.2.1.21
1,4- β -cellobiosidase	CBH	Hydrolysis of cellulose	4-Methylumbelliferyl β -D-cellobiopyranoside	3.2.1.91
β -N-acetylhexosaminidase	NAG	Hydrolysis of glycosidic bonds in chitin	4-Methylumbelliferyl N-acetyl- β -D-glucosaminide	3.2.1.52
β -Xylanase	XYL	Hydrolysis of hemicellulose	4-Methylumbelliferyl β -D-xylopyranoside	3.2.1.37
Phosphomonoesterase	P	Release of inorganic phosphate from simple phosphomonoesters, including organic and condensed inorganic phosphates	4-Methylumbelliferyl phosphate	3.1.3.2 (acid)
L-Alanine	ALA	Peptidase	L-Alanine 7-amido-4-methylcoumarin trifluoroacetate	3.5.1.28
L-Leucine	LEU	Peptidase	L-Leucine-7-amido-4-methylcoumarin hydrochloride	3.4.11.1
Phenol oxidase	PO	Lignin	l-dihydroxyphenylalanine (l-DOPA)	1.10.3.2
Peroxidase	POX	Lignin	l-dihydroxyphenylalanine (l-DOPA) and 0.3% H ₂ O ₂	1.11.1.7

TableS2. Changes in the extracellular enzyme activities between control and burned locations (nmol/gr soil C /hr). Values represent the averages between the sampling locations with standard deviations; AG, α -glucosidase, BG, β -glucosidase; CBH, β -cellobiohydrolase; XYL, β -xylosidase; NAG, N-acetyl glucosaminidase; P, phosphatase; LEU, leucine; ALA, alanine; ns, Not significant.

Control-15°C

<i>Depth (cm)</i>	<i>AG</i>	<i>BG</i>	<i>CBH</i>	<i>XYL</i>	<i>NAG</i>	<i>P</i>	<i>LEU</i>	<i>ALA</i>
0-10	7.3 ± 5.8	55.2 ± 23.4	13.3 ± 1.7	8.9 ± 2.7	50.0 ± 31.1	1725.5 ± 776.1	1.9 ± 1.8	1.9 ± 1.7
10-20	12.9 ± 7.8	112.5 ± 49.4	36.6 ± 13.0	29.6 ± 5.4	56.0 ± 8.2	1612.5 ± 915.0	2.3 ± 0.5	3.1 ± 1.7
20-30	5.2 ± 5.5	38.4 ± 22.2	16.0 ± 3.2	17.9 ± 5.7	32.9 ± 33.8	550.9 ± 376.8	0.5 ± 0.8	0.6 ± 0.6
30-40	7.3 ± 6.9	52.9 ± 33.8	17.3 ± 14.1	17.3 ± 6.2	20.4 ± 18.7	314.5 ± 99.2	2.6 ± 2.0	3.7 ± 4.0
40-50	4.7 ± 2.1	38.3 ± 6.4	7.5 ± 3.0	8.6 ± 2.8	22.7 ± 6.2	283.6 ± 45.5	1.1 ± 1.0	1.5 ± 1.5
50-60	29.8 ± 15.5	45.4 ± 3.5	37.7 ± 15.2	24.4 ± 5.0	45.1 ± 14.1	318.5 ± 152.4	2.6 ± 4.3	5.1 ± 8.7
60-70	29.4 ± 30.4	52.3 ± 33.5	36.3 ± 41.3	28.9 ± 34.8	51.3 ± 33.8	267.3 ± 124.5	1.8 ± 2.9	2.3 ± 3.6
70-80	78.9 ± 53.8	97.0 ± 52.1	98.3 ± 67.7	104.3 ± 71.2	173.6 ± 103.8	980.9 ± 438.7	6.8 ± 3.7	6.9 ± 2.7
80-90	20.5 ± 16.2	29.3 ± 14.8	12.4 ± 9.5	6.8 ± 9.2	38.6 ± 4.5	842.9 ± 795.1	0.9 ± 1.2	3.6 ± 5.6
90-100	27.5 ± 36.8	38.8 ± 17.5	28.0 ± 21.0	31.6 ± 30.5	69.0 ± 33.7	668.5 ± 686.5	2.4 ± 4.1	2.2 ± 2.6

Control-4°C

<i>Depth (cm)</i>	<i>AG</i>	<i>BG</i>	<i>CBH</i>	<i>XYL</i>	<i>NAG</i>	<i>P</i>	<i>LEU</i>	<i>ALA</i>
0-10	9.2 ± 8.6	32.9 ± 17.2	18.3 ± 20.3	8.2 ± 6.9	41.0 ± 43.0	1240.3 ± 645.8	1.7 ± 1.5	2.0 ± 1.3
10-20	3.8 ± 6.5	66.7 ± 17.1	13.2 ± 10.7	12.5 ± 3.3	39.6 ± 11.8	1378.2 ± 421.4	0.8 ± 1.4	1.8 ± 3.1
20-30	1.5 ± 2.1	34.6 ± 33.4	3.8 ± 5.5	5.1 ± 4.2	10.0 ± 7.1	609.7 ± 617.9	0.5 ± 0.6	0.5 ± 0.5
30-40	9.0 ± 9.3	37.8 ± 25.5	15.4 ± 11.2	12.9 ± 4.3	16.6 ± 8.5	229.5 ± 98.1	2.0 ± 2.0	2.9 ± 3.8
40-50	7.4 ± 1.1	23.1 ± 6.6	8.4 ± 3.5	9.9 ± 4.4	16.5 ± 4.5	210.5 ± 27.2	1.0 ± 1.0	1.3 ± 1.4
50-60	12.1 ± 20.9	15.2 ± 26.3	11.5 ± 19.9	12.5 ± 21.6	19.3 ± 33.5	341.0 ± 167.7	2.6 ± 2.8	4.9 ± 7.1
60-70	20.7 ± 26.7	27.9 ± 18.9	25.6 ± 27.3	24.5 ± 31.2	37.4 ± 35.7	232.9 ± 104.9	2.1 ± 2.4	2.6 ± 3.0
70-80	21.1 ± 0.0	22.4 ± 19.2	15.5 ± 18.9	20.1 ± 21.0	49.1 ± 48.4	1118.7 ± 987.1	9.4 ± 8.5	8.4 ± 7.1
80-90	0.0 ± 0.0	6.7 ± 6.7	2.2 ± 3.8	22.1 ± 35.1	25.3 ± 22.8	811.7 ± 718.4	0.1 ± 0.2	2.7 ± 4.2
90-100	30.2 ± 51.0	35.0 ± 53.6	41.1 ± 69.9	23.6 ± 40.9	38.3 ± 50.4	616.5 ± 620.0	2.0 ± 3.4	3.4 ± 3.1

Burn-15°C

<i>Depth (cm)</i>	<i>AG</i>		<i>BG</i>		<i>CBH</i>		<i>XYL</i>		<i>NAG</i>		<i>P</i>	<i>LEU</i>		<i>ALA</i>										
0-10	9.6	±	47.9	160.2	±	62.1	60.8	±	58.9	48.1	±	57.0	68.8	±	79.2	3482.9	±	697.3	3.1	±	1.6	4.6	±	4.4
10-20	22.5	±	6.5	198.2	±	19.5	75.2	±	18.3	106.7	±	9.9	97.1	±	14.1	3930.3	±	212.9	9.7	±	0.5	9.8	±	0.5
20-30	22.7	±	37.6	129.6	±	39.3	36.2	±	58.5	35.2	±	43.6	67.1	±	45.2	1187.9	±	126.6	3.4	±	0.4	6.7	±	0.1
30-40	6.0	±	3.1	52.2	±	40.3	37.9	±	10.6	34.9	±	3.2	42.9	±	5.0	416.3	±	335.3	0.0	±	0.8	0.4	±	3.7
40-50	105.3	±	0.3	155.5	±	9.3	134.0	±	1.6	120.7	±	0.9	152.4	±	0.2	1378.0	±	157.5	2.5	±	0.4	6.4	±	3.0
50-60	53.9	±	33.1	121.3	±	52.7	91.8	±	40.9	65.4	±	31.1	70.3	±	43.4	747.6	±	681.1	0.7	±	2.6	0.3	±	2.4
60-70	12.0	±	6.3	64.7	±	7.5	27.4	±	35.5	15.5	±	9.9	22.8	±	31.4	632.6	±	159.5	1.3	±	1.4	3.2	±	0.6
70-80	38.0	±	28.5	60.3	±	49.5	51.1	±	16.1	34.0	±	23.8	49.7	±	7.2	654.3	±	499.4	3.2	±	3.4	3.3	±	0.4
80-90	32.4	±	360.1	52.0	±	44.6	18.4	±	73.1	25.1	±	63.6	30.9	±	124.3	557.3	±	586.1	4.5	±	8.5	3.9	±	4.6
90-100	282.9	±	337.6	43.0	±	52.4	59.4	±	72.3	52.8	±	64.2	115.7	±	121.5	4732.7	±	531.7	9.1	±	9.1	9.3	±	9.6

Burn-4°C

<i>Depth (cm)</i>	<i>AG</i>		<i>BG</i>		<i>CBH</i>		<i>XYL</i>		<i>NAG</i>		<i>P</i>	<i>LEU</i>		<i>ALA</i>										
0-10	42.9	±	27.2	160.8	±	98.5	88.7	±	54.5	84.5	±	51.8	101.2	±	62.6	2180.6	±	932.1	3.2	±	2.1	4.7	±	3.0
10-20	40.2	±	23.7	140.9	±	80.8	70.4	±	40.9	94.7	±	54.4	96.7	±	56.7	2626.6	±	916.5	9.4	±	6.6	9.3	±	4.4
20-30	42.0	±	19.0	110.7	±	52.9	76.9	±	34.0	77.3	±	34.7	97.0	±	39.2	1076.4	±	440.1	6.7	±	0.6	7.4	±	0.6
30-40	1.2	±	1.7	32.7	±	10.4	15.3	±	0.7	16.4	±	0.6	32.2	±	7.6	538.3	±	22.9	2.6	±	1.2	3.3	±	1.5
40-50	34.9	±	34.1	76.3	±	75.6	63.8	±	58.4	41.2	±	38.4	34.1	±	34.2	1224.6	±	330.7	2.2	±	2.7	6.3	±	8.7
50-60	11.6	±	0.9	47.8	±	10.2	18.2	±	1.5	26.4	±	2.1	32.2	±	4.0	777.4	±	487.2	0.0	±	0.0	0.0	±	0.0
60-70	2.0	±	2.9	2.9	±	4.2	2.3	±	3.2	2.1	±	3.0	4.1	±	5.7	546.9	±	295.8	0.4	±	0.6	1.5	±	2.1
70-80	15.2	±	21.5	14.9	±	21.0	7.4	±	10.4	20.8	±	22.2	26.1	±	25.8	613.1	±	648.0	0.2	±	0.4	0.3	±	0.2
80-90	4.2	±	6.0	7.6	±	10.8	4.3	±	6.1	16.7	±	8.1	32.4	±	13.3	446.2	±	406.3	4.6	±	4.6	3.8	±	2.1
90-100	60.4	±	67.3	19.2	±	9.2	84.6	±	92.0	44.4	±	54.1	51.9	±	37.7	4518.8	±	510.3	0.0	±	0.0	0.4	±	0.5

p values of Tukey's HSD analysis comparing Control vs Burn

Soil layer	AG	BG	CBH	XYL	NAG	P	ALA	LEU
Surface	ns	0.001	0.021	0.001	ns	ns	0.002	0.005
Middle	ns	ns	ns	ns	ns	ns	ns	ns
Permafrost	ns	ns	ns	ns	ns	ns	ns	ns
Surface (mineral)	ns	0.001	0.016	0.001	0.015	0.002	0.026	0.017

TableS3. Overview of the Nome Creek metagenome sequencing and annotation

Sample Name	# reads (101bp) per sample	# of reads quality checks (bp)	Average Length after quality checks (bp)	Average GC content	# of genes with KO annotation*	% reads assembled to contigs	# of contigs	Average contig length (bp)
Active Layer-Burn-01	5.8E+07	5.7E+07	93.9	61.77	424,830	36.3%	488,007	436
Active Layer-Burn-02	3.5E+07	3.5E+07	91.7	60.29	179,523	20.4%	230,496	396
Active Layer-Control-01	6.6E+07	6.5E+07	90.6	60.45	349,466	29.6%	525,293	433
Active Layer-Control-02	6.6E+07	6.6E+07	92.7	59.95	376,504	23.5%	551,635	404
Intermediate Layer-Burn-01	7.0E+07	6.9E+07	93.4	63.20	498,216	50.0%	548,719	480
Intermediate Layer-Burn-02	9.0E+07	8.9E+07	91.9	60.50	527,132	44.6%	683,306	466
Intermediate Layer-Control-01	7.1E+07	7.0E+07	90.3	60.95	465,853	53.1%	602,260	479
Intermediate Layer-Control-02	6.6E+07	6.5E+07	92.7	61.64	474,106	47.8%	562,022	453
Permafrost Layer-Burn-01	6.4E+07	6.3E+07	93.3	63.05	474,062	62.6%	576,274	503
Permafrost Layer-Burn-02	7.7E+07	7.6E+07	92.3	62.30	516,012	40.8%	558,899	457
Permafrost Layer-Control-01	6.6E+07	6.4E+07	90.4	61.00	436,175	50.0%	373,132	483
Permafrost Layer-Control-02	6.1E+07	6.0E+07	92.1	62.60	467,116	59.4%	400,325	500

* for selected genes in the database

Table.S4 Pearson correlation coefficients of soil geochemical parameters and potential total enzyme activity to changes in the relative abundance of different phylogenetic groups in the Nome Creek samples. Significant correlations are highlighted as bold.

	pH	p	Water	p	C	p	N	p	Total enzyme activity	p
Acidobacteria	-0.030	0.900	-0.153	0.518	-0.101	0.669	0.071	0.765	-0.219	0.353
Actinobacteria	-0.173	0.465	0.421	0.063	0.338	0.144	0.445	0.049	0.143	0.545
AD3	0.512	0.021	-0.746	0.000	-0.661	0.001	-0.690	0.001	-0.450	0.046
Archaea	-0.044	0.852	0.370	0.107	0.058	0.807	-0.082	0.731	0.116	0.623
Euryarchaeota	-0.026	0.910	0.298	0.200	-0.035	0.883	-0.076	0.748	-0.047	0.843
Bacteroidetes	-0.455	0.043	0.742	0.000	0.500	0.025	0.349	0.130	0.456	0.043
Chloroflexi	0.169	0.474	0.156	0.511	-0.101	0.669	-0.324	0.163	0.076	0.747
Firmicutes	0.121	0.608	0.160	0.500	-0.158	0.504	-0.311	0.182	-0.042	0.857
Gemmatimonadetes	0.517	0.019	-0.610	0.004	-0.548	0.012	-0.656	0.002	-0.326	0.160
Proteobacteria	-0.601	0.005	0.511	0.021	0.748	0.000	0.804	0.000	0.543	0.013
Alphaproteobacteria	-0.358	0.120	0.179	0.448	0.321	0.167	0.599	0.005	0.040	0.864
Betaproteobacteria	0.490	0.028	-0.225	0.340	-0.401	0.079	-0.553	0.011	-0.195	0.408
Gammaproteobacteria	-0.579	0.007	0.482	0.031	0.652	0.001	0.736	0.000	0.442	0.050
Verrucomicrobia	-0.472	0.035	0.355	0.123	0.563	0.010	0.671	0.001	0.332	0.152