

Supplementary Materials

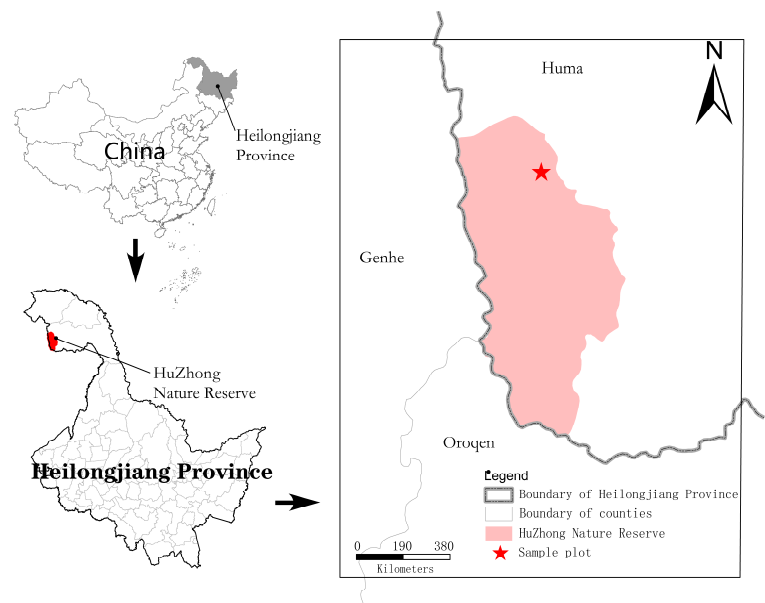


Figure S1. Map of the field sampling sites on the Greater Khingan Mountains.

Table S1. Soil physicochemical properties under different temperature treatments.

Treatments	TN (g/kg)	SOC (g/kg)	MBC (mg/kg)	AN (mg/kg)	AK (mg/kg)	AP (mg/kg)	pH
CK	2.60 ± 0.00 a	61.72 ± 0.82 a	50.77 ± 0.22 d	82.72 ± 1.35a	129.15 ± 0.65 a	80.13 ± 0.63 a	4.58 ± 0.00a
T ₁	2.51 ± 0.00 c	60.06 ± 0.41 a	73.00 ± 0.00 b	77.99 ± 0.91b	116.35 ± 1.20 c	79.83 ± 0.56 a	4.52 ± 0.01b
T ₂	2.58 ± 0.00 a	60.92 ± 0.00 a	75.60 ± 0.00 a	79.80 ± 1.65ab	121.82 ± 1.18 b	82.12 ± 0.43 a	4.50 ± 0.00c
T ₃	2.54 ± 0.01 b	59.78 ± 0.87 a	68.40 ± 0.15 c	76.83 ± 0.71b	123.44 ± 0.81 b	81.52 ± 1.21 a	4.46 ± 0.00d

Data were mean ± standard error (*n* = 3); different lowercase letters in the same column indicate significant differences (*p* < 0.05).

Table S2. Relative abundance (>1%) of potential functional pathways at level 2 in different treatments.

Pathway Level 1	Pathway Level 2	CK	T ₁	T ₂	T ₃
Metabolism	Carbohydrate metabolism	12.22 ± 0.48 b	13.24 ± 0.62 ab	13.66 ± 0.09 a	13.53 ± 0.03 ab
	Lipid metabolism	3.98 ± 0.09 a	3.80 ± 0.15 ab	3.67 ± 0.03 b	3.72 ± 0.01 ab
	Metabolism of cofactors and vitamins	7.90 ± 0.42 a	7.26 ± 0.52 a	6.92 ± 0.07 a	7.14 ± 0.04 a
	Energy metabolism	8.40 ± 0.72 a	7.42 ± 0.76 a	6.76 ± 0.07 a	6.76 ± 0.06 a
	Nucleotide metabolism	5.14 ± 0.07 a	4.98 ± 0.10 ab	4.91 ± 0.03 b	4.91 ± 0.01 b
	Amino acid metabolism	11.94 ± 0.51 b	11.68 ± 0.23 b	12.43 ± 0.18 ab	12.94 ± 0.03 a
	Metabolism of terpenoids and polyketides	3.03 ± 0.15 a	2.90 ± 0.15 a	2.76 ± 0.04 a	2.70 ± 0.02 a
	Xenobiotics biodegradation and metabolism	3.97 ± 0.31 b	3.83 ± 0.25 b	4.47 ± 0.17 ab	4.93 ± 0.04 a
	Metabolism of other amino acids	2.72 ± 0.09 c	2.81 ± 0.09 bc	2.98 ± 0.08 b	3.24 ± 0.00 a
	Glycan biosynthesis and metabolism	2.45 ± 0.04 b	2.51 ± 0.01 ab	2.42 ± 0.05 b	2.60 ± 0.00 a
Genetic Information Processing	Translation	4.47 ± 0.17 a	3.99 ± 0.28 a	3.93 ± 0.11 a	4.17 ± 0.02 a
	Folding, sorting and degradation	2.38 ± 0.12 a	2.22 ± 0.14 a	2.10 ± 0.02 a	2.15 ± 0.01 a
Environmental Information Processing	Replication and repair	4.09 ± 0.13 a	3.86 ± 0.16 a	3.74 ± 0.04 a	3.80 ± 0.02 a
	Membrane transport	9.66 ± 0.94 a	10.28 ± 0.76 a	10.88 ± 0.97 a	8.23 ± 0.18 a
	Signal transduction	8.55 ± 0.52 a	9.15 ± 0.24 a	8.29 ± 0.21 a	8.49 ± 0.01 a
Cellular Processes	Cell motility	2.56 ± 0.20 b	2.82 ± 0.05 ab	2.72 ± 0.11 ab	3.01 ± 0.01 a
	Cell growth and death	2.03 ± 0.14 ab	1.82 ± 0.11 b	1.84 ± 0.10 b	2.20 ± 0.00 a
Human Diseases	Infectious disease: bacterial	1.34 ± 0.15 b	1.98 ± 0.27 a	1.66 ± 0.17 ab	1.08 ± 0.01 b

Data were mean ± standard error (*n* = 3), different lowercase letters in the same row indicate significant differences (*p* < 0.05).

Table S3. Network diagram data.

Source: Bacterial Phyla	Target: Functional Pathways at Level 2	Correction	<i>p</i>
others	Cell motility	-0.90	<0.01
others	Glycan biosynthesis and metabolism	-0.76	<0.01
Patescibacteria	Amino acid metabolism	-0.73	0.01
Patescibacteria	Glycan biosynthesis and metabolism	-0.73	0.01
Firmicutes	Membrane transport	-0.73	0.01
Patescibacteria	Metabolism of other amino acids	-0.71	0.01
Patescibacteria	Xenobiotics biodegradation and metabolism	-0.69	0.01
Acidobacteriota	Signal transduction	-0.68	0.01
Actinobacteriota	Metabolism of other amino acids	-0.65	0.02
Verrucomicrobiota	Signal transduction	-0.63	0.03
Proteobacteria	Energy metabolism	-0.62	0.03
Proteobacteria	Nucleotide metabolism	-0.62	0.03
Firmicutes	Infectious disease bacterial	-0.62	0.03
Firmicutes	Glycan biosynthesis and metabolism	0.62	0.03
Actinobacteriota	Lipid metabolism	0.63	0.03
Desulfobacterota	Cell motility	0.65	0.02
Acidobacteriota	Amino acid metabolism	0.67	0.02
Proteobacteria	Cell motility	0.67	0.02

Source represents the bacterial phyla, which is the starting point of the line of connection. Target represents functional pathways at level 2, which is the endpoint of the line of connection. The absolute values of correlation were used as a measure for the thickness of the lines in Figure 6. Correction represents the positive or negative correlation, -1 represents the negative correlation, and 1 represents the positive correlation.