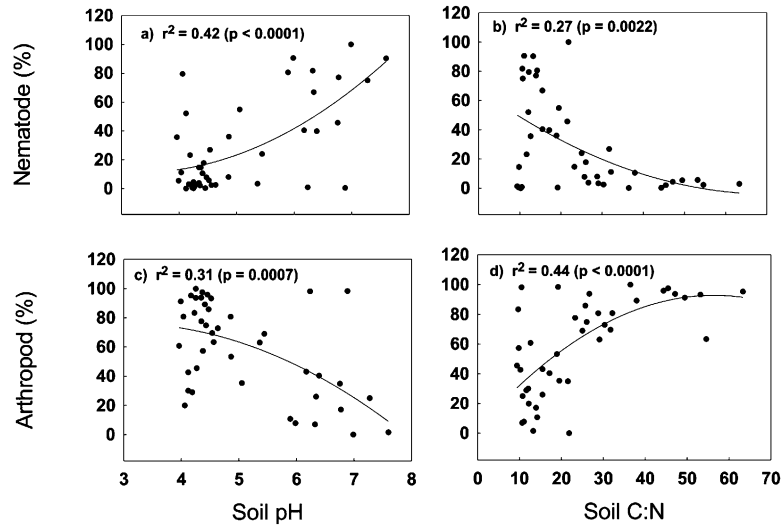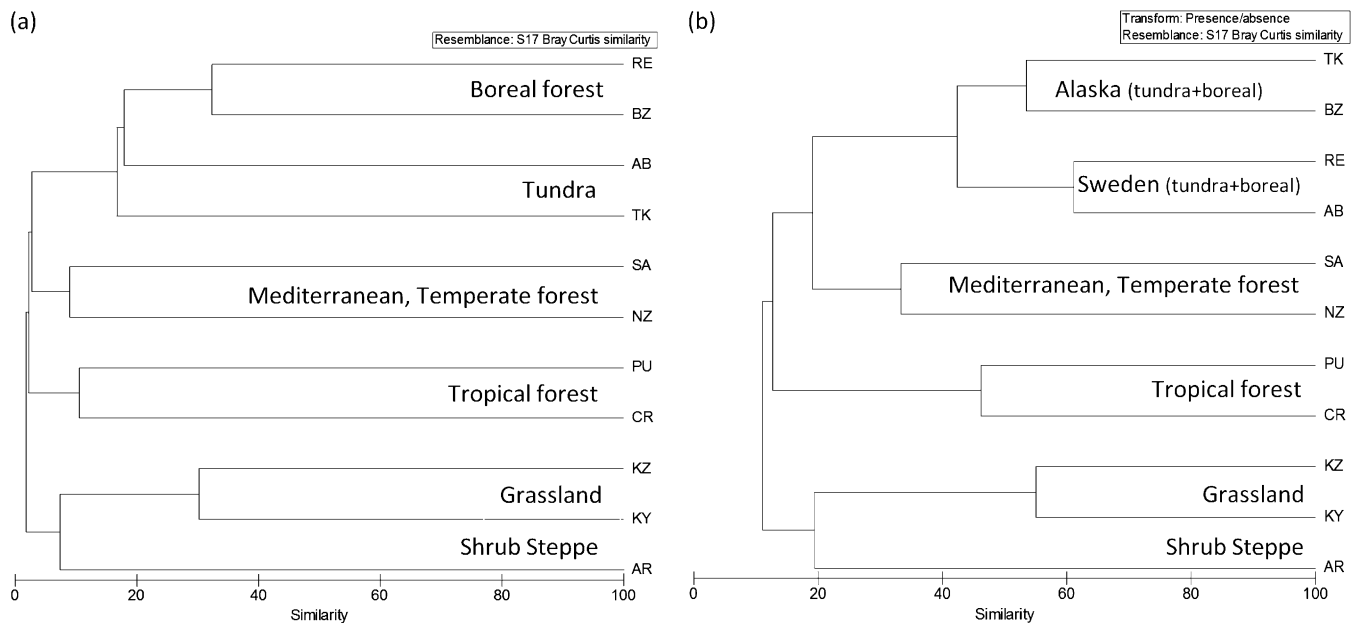# Supporting Information

Wu et al. 10.1073/pnas.1103824108
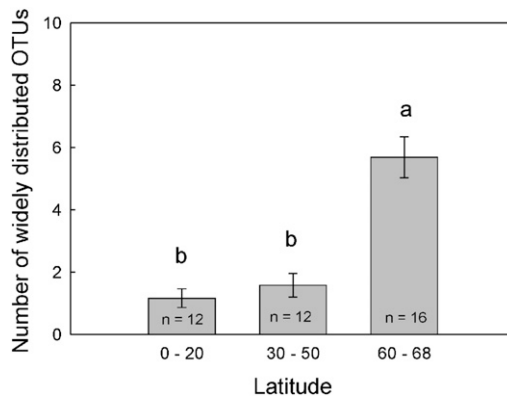

Fig. S1. Correlation between (*A*) nematode proportion at each plot and soil pH, (*B*) nematode proportion and soil C:N ratio, (*C*) arthropod proportion and soil pH, and (*D*) arthropod proportion and soil C:N ratio ($n = 42$).

Fig. S2. Cluster analysis of OTUs observed at 2 or more of 11 locations on the basis of (*A*) abundance of OTUs and (*B*) presence/absence of OTUs.

Fig. S3. OTUs observed at four or more locations from three different latitude ranges. Vertical bars represent ± SE. Letters above each bar (*A* and *B*) indicate that means are significantly different (*P* < 0.05) from each other.
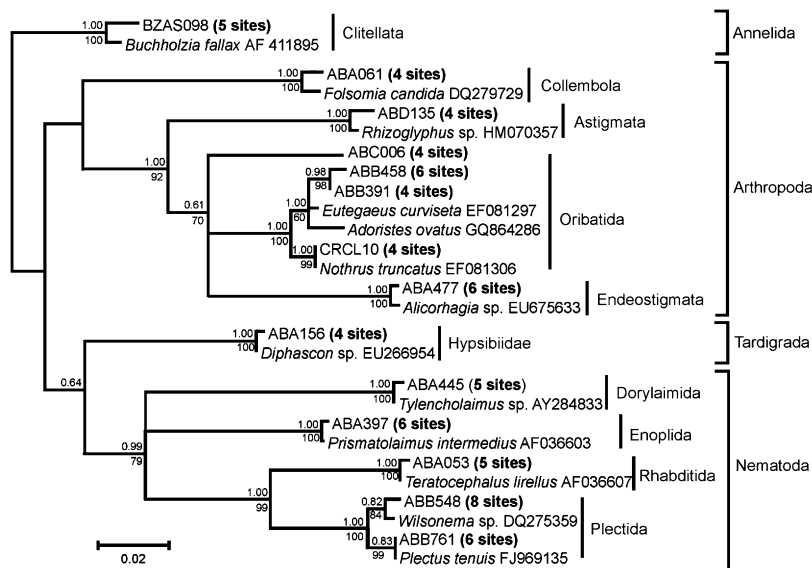
Fig. S4. Phylogenetic tree of the 14 most widely distributed OTUs demonstrating GenBank identification of small soil animals. The number above each node represents posterior probabilities from a Bayesian analysis (1). The number below each node represents bootstrap values from a distance analysis using maximum composite likelihood (2). GenBank entries are identified by the species name and GenBank identifier. Locations from the present study are identified by a unique number and the number of locations at which they were found. (Scale, the number of substitutions per site from the distance analysis.)

1. Ronquist F, Huelsenbeck JP (2003) MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* 19:1572—1574.
2. Tamura K, Dudley J, Nei M, Kumar S (2007) MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. *Mol Biol Evol* 24:1596—1599.

Fig. S5. 3D MDS ordination plot (3D stress: 0.10) summarizing the community structure as measured by the sequence analysis of 17,516 environmental rRNA gene sequences from 11 global locations. The vertical dotted line partitions the locations identified (11 in total) as above-ground biodiversity hotspots. Plots from CR, NZ, PU, and SA are all to the *Right* of the dotted line and represent locations identified as above-ground biodiversity hotspots. The plots representing the 7 other locations not identified as above-ground biodiversity hotspots fall to the *Left* of the dotted line.

Table S1. Composition of the number of OTUs generated for 17,516 sequences assembled using sequence similarity criteria ranging from 95 to 99% and phylogenetic distance ranging from 0.01 to 0.05

Sequencher similarity, %	Total OTUs	Singleton	≥4 locations	≥6 locations
99	2,259	1,773	14	5
98	1,520	1,155	23	7
97	1,247	949	32	12
95	870	642	34	15
ESPRIT distance				
0.01	3,536	2,421	5	1
0.02	1,989	1,377	10	3
0.03	1,551	1,052	16	6
0.05	996	701	34	10

The total number of OTUs, the number of sequences found only once (singletons) and the number of total OTUs found at at least four or six locations are shown.

Table S2. *T*-test comparisons of each environmental parameter (mean $\pm$ SE) between arthropod- and nematode-dominated locations

Environmental parameters	Locations dominated by arthropods (six locations, 24 plots)	Locations dominated by nematodes (four locations, 14 plots)*	*P* value	Site dominated by both (TK plots)
Latitude	48 $\pm$ 21	21 $\pm$ 19	**<0.01**	68 $\pm$ 0
Mean annual temperature (°C)	9.5 $\pm$ 11.4	18.5 $\pm$ 6.8	**0.01**	−6.9 $\pm$ 0.0
Mean annual precipitation (mm)	1031 $\pm$ 924	1781 $\pm$ 1716	0.09	322 $\pm$ 0
Soil temperature (°C) average	12.7 $\pm$ 6.9	23.7 $\pm$ 3.5	**<0.01**	5.1 $\pm$ 1.0
Respiration average (g CO_2/m^2/h)	0.62 $\pm$ 0.5	0.67 $\pm$ 0.4	0.74	0.38 $\pm$ 0.08
Litter average (g/m^2)	405 $\pm$ 217	202 $\pm$ 236	**0.01**	229 $\pm$ 14
Root biomass (mg/g soil)	120 $\pm$ 193	6 $\pm$ 7	**0.03**	59 $\pm$ 80
Soil bulk density (g/cm^3)	0.67 $\pm$ 0.40	1.39 $\pm$ 0.20	**0.00**	0.63 $\pm$ 0.40
Soil moisture (%)	85 $\pm$ 62	41 $\pm$ 27	**0.02**	102 $\pm$ 38
Soil pH	4.5 $\pm$ 0.6	5.9 $\pm$ 1.3	**<0.01**	5.6 $\pm$ 0.8
Soil EC (microsiemen)	60 $\pm$ 40	62 $\pm$ 41	0.92	25 $\pm$ 14
Soil C%	11 $\pm$ 11	3 $\pm$ 2	**0.01**	6 $\pm$ 4
Soil N%	0.42 $\pm$ 0.42	0.29 $\pm$ 0.19	0.28	0.4 $\pm$ 0.2
Soil C:N	32 $\pm$ 15	14 $\pm$ 3	**<0.01**	18 $\pm$ 2
Microbial C (μg/g)	951 $\pm$ 1324	350 $\pm$ 221	0.10	255 $\pm$ 120
Microbial N (μg/g)	132 $\pm$ 186	58 $\pm$ 41	0.15	43 $\pm$ 19
Soil NO_3 (μg/g)	4.8 $\pm$ 6.5	23.6 $\pm$ 33.1	**0.01**	6.1 $\pm$ 1.9
Soil NH_4 (μg/g)	5.0 $\pm$ 4.9	12.1 $\pm$ 16.6	0.06	0.9 $\pm$ 0.3
Soil inorganic N (μg/g)	9.8 $\pm$ 9.7	35.7 $\pm$ 47.9	**0.01**	7.0 $\pm$ 2.2

*There were four replicate plots at each location except one, which had only two plots.
  Bold values are statistically significant.

Table S3. Comparison of the average number of OTUs common to 4 or more locations, OTUs observed at only one site, and singletons within the 42 plots representing all 11 locations (*n* = 4 if not otherwise indicated)

Location	Number of OTUs common to 4 or more locations	Number of OTUs found at a single location or found only once	
		OTUs at 1 location	Singleton
AB	4.0 $\pm$ 1.5[a,b]	59.8 $\pm$ 7.8	51.5 $\pm$ 7.3
TK	5.5 $\pm$ 1.0[a]	65.8 $\pm$ 11.7	52.3 $\pm$ 10.5
RE	6.8 $\pm$ 1.8[a]	51.3 $\pm$ 3.2	38.5 $\pm$ 2.9
BZ	6.5 $\pm$ 0.9[a]	62.8 $\pm$ 4.8	51.3 $\pm$ 5.6
KZ	1.5 $\pm$ 0.3[b,c]	59.5 $\pm$ 22.2	47.0 $\pm$ 20.1
CR	0.8 $\pm$ 0.5[c]	57.5 $\pm$ 27.8	47.3 $\pm$ 24.4
KY	1.8 $\pm$ 0.5[b,c]	82.0 $\pm$ 6.8	59.8 $\pm$ 5.9
PU	1.0 $\pm$ 0.6[c]	34.8 $\pm$ 8.5	23.8 $\pm$ 7.9
SA	1.0 $\pm$ 0.7[c]	45.3 $\pm$ 7.2	39.3 $\pm$ 7.2
NZ	2.3 $\pm$ 0.9[b,c]	37.3 $\pm$ 12.8	24.3 $\pm$ 9.9
AR	1.0 $\pm$ 0.0*,[c]	20.5 $\pm$ 12.5*	17.0 $\pm$ 12.0*
P value	<0.01	0.26	0.37

  Values with different superscript letters (a, b, and c) are statistically different from each other.
*Sequences were only obtained from two plots.

Table S4. *T*-test comparisons of each environmental parameter (mean $\pm$ SE) between locations identified as above-ground biodiversity hotspots and locations not identified as above-ground biodiversity hotspots

Environmental parameters	Locations identified (1) as above-ground diversity hotspots (4 locations, 16 plots)	Locations not identified (1) as above-ground diversity hotspots (7 locations, 26 plots)*	P value
Latitude	25 ± 4	51 ± 5	**<0.01**
Mean annual temperature (°C)	21.1 ± 1.4	4.7 ± 2.0	**<0.01**
Mean annual precipitation (mm)	2370 ± 353	502 ± 56	**<0.01**
Soil temperature (°C) average	20.2 ± 1.0	12.8 ± 1.8	**<0.01**
Respiration average (g CO_2/m^2/h)	0.77 ± 0.12	0.52 ± 0.08	0.06
Litter average (g/m^2)	435 ± 67	251 ± 35	**0.01**
Root biomass (mg/g soil)	18 ± 9	113 ± 37	0.06
Soil bulk density (g/cm^3)	1.02 ± 0.09	0.84 ± 0.10	0.22
Soil moisture (%)	37 ± 10	75 ± 12	0.67
Soil pH	4.3 ± 0.04	5.6 ± 0.22	**<0.01**
Soil EC (microsiemen)	79 ± 8	45 ± 8	**<0.01**
Soil C%	6 ± 1	9 ± 2	0.29
Soil N%	0.32 ± 0.05	0.39 ± 0.08	0.50
Soil C:N	23 ± 4	25 ± 3	0.65
Microbial C (μg/g)	381 ± 63	871 ± 253	0.14
Microbial N (μg/g)	77 ± 18	112 ± 35	0.47
Soil NO_3 (μg/g)	22.8 ± 7.8	4.1 ± 0.8	**<0.01**
Soil NH_4 (μg/g)	14.8 ± 3.6	2.2 ± 0.4	**<0.01**
Soil inorganic N (μg/g)	37.6 ± 10.9	6.3 ± 0.8	**<0.01**

*There were 4 replicate plots at each location except 1 that had only two plots.
  Bold values are statistically significant.