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Other Supplementary Information for this manuscript include the following:

Supplementary Movie 1

Supplementary Appendix 1. The contribution of soil mosses to biogeochemistry

Using our global map (Fig. 2C), based on the cover of mosses, we estimated that mosses cover 9.4 M km² of our certainty area (excluding urban ecosystems). These numbers accord with those of an independent study of the cover of a range of different soil biocrusts worldwide³.

We then estimated the influence of soil mosses on soil organic C, N, P and Mg, which were all found to be positively significantly influenced by mosses (Fig. 3). To do this, we first determined the mean differences in soil organic C, N, P and Mg between moss and unvegetated bare soils. Given the importance of soil mosses in supporting multiple soil attributes in natural compared with urban greenspaces (Figs. 4A, Supplementary Figs. 13 and 14), we restrict these analyses to values from natural ecosystems. Then, we estimated the mean bulk density found in natural soils across the globe (average of 1.25g cm³ according to SoilGrids250m 2.0 [ref.⁵⁷]). Finally, we estimated the amount of C (Gt) in 9.4M km² covered by mosses in our certainty area. Using these figures, we found that soils covered by soil mosses (other than bare soils) support +6.43, 0.49, 0.10 and 0.06 Gt, respectively, of organic C, N, P and Mg in the global regions represented by our global survey (Fig. 2D) excluding outliers and regions with no data (top 5 cm of soil). This rough estimation aims to visualize the importance of soil mosses for key soil elements globally.

Supplementary Appendix 2. Meta-analysis #1:

Microcosm and field experiments aiming to investigate the effects of soil mosses on function.

We conducted a meta-analysis aiming to further investigate the effects of soil mosses on function from manipulative moss field and microcosm experiments. We hypothesized that soil mosses support function compared with procedure controls (e.g., moss removal). Peer-reviewed journal articles published before May 2022 were searched using Web of Science, Google Scholar and China Knowledge Resource Integrated Database (CNKI) with the following search term combinations: "mosses" AND "carbon" or "nitrogen" or "phosphorus" or "magnesium" or "soil respiration" or "glucose degradation" or "lignin degradation" or "phosphorus mineralization" or "pathogen control" or "diversity of invertebrates".

To avoid bias in publication selection, the following criteria were conducted to select the studies compiled in our database: (i) Experiments were conducted with at least one pair of data (moss treatment and control; e.g., moss removal or addition and control); (ii) At least one of the selected variables (i.e., carbon, nitrogen, phosphorous, Mg, soil respiration, glucose degradation, lignin degradation, P mineralization, pathogen control & soil biodiversity) was examined in all treatments and the control at the same temporal and spatial scales; (iii) Field or microcosms experiments with exclusion of observational data; (iv) The mean, standard deviations/errors, and sample sizes of these variables could be extracted from the figures, tables or context directly. See PRISMA diagram in Supplementary Fig. 16 for further details. Mean values were taken from tables or extracted from figures using Web PlotDigitizer (<https://apps.automeris.io/wpd/>).

We found data for soil carbon (total soil organic carbon, dissolved organic C and microbial biomass C), nitrogen (total N, available N, dissolved inorganic and organic N), phosphorus (available P, total P), Mg, soil respiration and glucose degradation from croplands, grasslands, shrublands and forest ecosystems. Data was analysed using the RII approach explained in the Methods section comparing values of moss and bare variables within each independent study site. We obtained an averaged RII index for soil C, N, P, Mg, soil respiration and glucose degradation, and then calculated moss fertility as done in the Methods section.

Supplementary Appendix 3. List of selected references in Supplementary Appendix 2.

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Supplementary Appendix 4. Meta-analysis #2:

Studies aiming to investigate the influence of soil mosses on function over time.

This meta-analysis aimed to investigate the influence of moss on function over time. We hypothesized that soil mosses accumulate soil function with time providing evidence that moss are not simply selecting locations with high nutrient content, but rather accumulate these nutrients over time. Peer-reviewed journal articles published before May 2022 were searched using Web of Science, Google Scholar and China Knowledge Resource Integrated Database (CNKI) with the following search term combinations: "mosses" AND "carbon" or "nitrogen" or "phosphorus" or "magnesium" or "soil respiration" or "glucose degradation" or "lignin degradation" or "phosphorus mineralization" or "pathogen control" or "diversity of invertebrates".

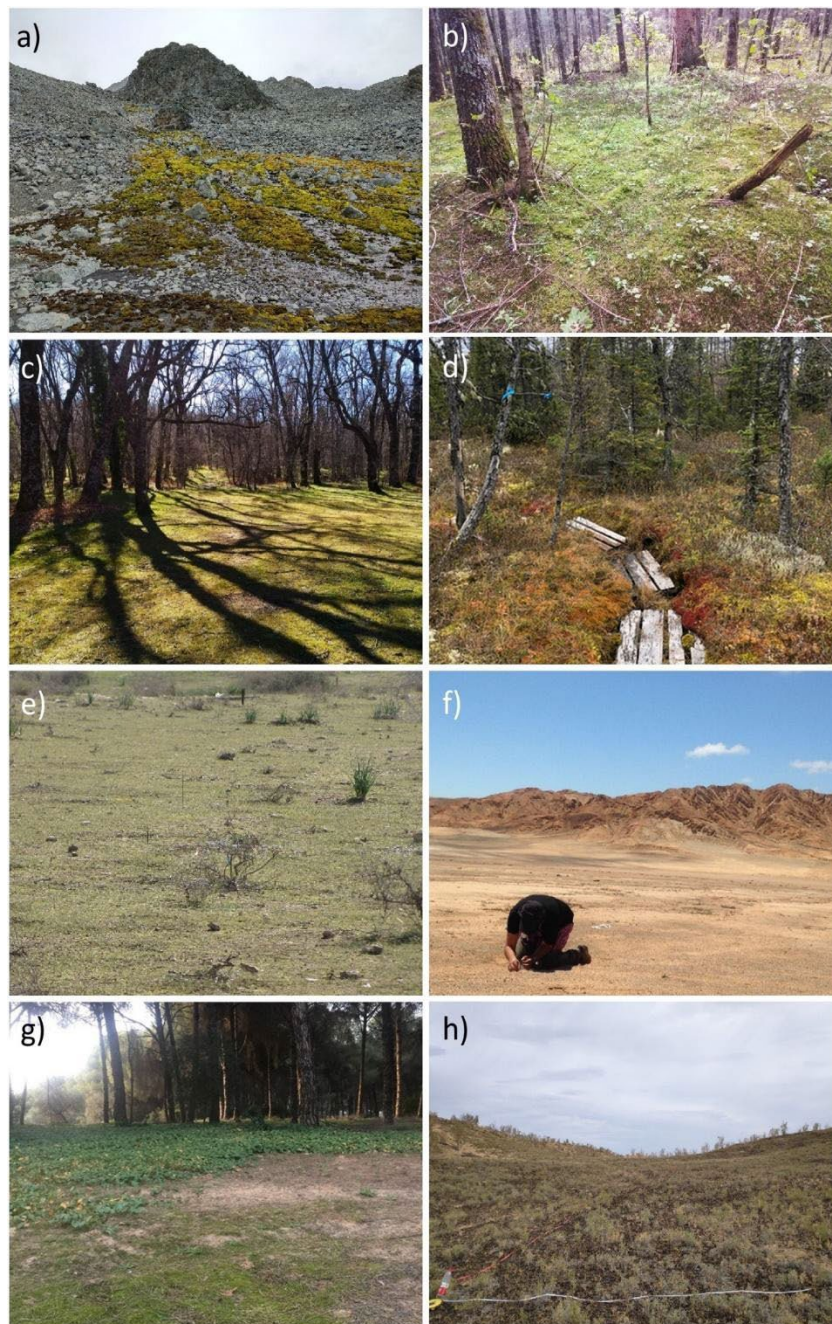
To avoid bias in publication selection, the following criteria were used to select the studies compiled in our database: (i) Studies focused on mosses; (ii) At least one of the selected variables (i.e., carbon, nitrogen, phosphorous, Mg, soil respiration, glucose degradation, lignin degradation, P mineralization, pathogen control and soil biodiversity) was examined in all treatments and the control at the same temporal and spatial scales; (iii) Field or microcosms experiments should include more than one sampling time, and worked on a fixed scale of time of temporal changes in soil attributed over months to avoid mixing temporal scales in our analyses; (iv) The mean, standard deviations/errors, and sample sizes of these variables could be extracted from the figures, tables or context directly. Mean values were taken from tables or extracted from figures using Web PlotDigitizer (<https://apps.automeris.io/wpd/>). See PRISMA diagram in Supplementary Fig. 17 for further details. Mean values were taken from tables or extracted from figures using Web PlotDigitizer (<https://apps.automeris.io/wpd/>).

We focused on data for soil carbon (total soil organic carbon, dissolved organic C and microbial biomass C) and soil respiration for which data was more available. Our dataset included data from croplands, grasslands, shrublands and forest ecosystems. The temporal changes in soil attributes were determined using the natural logarithm ($\ln$) of the response ratio (RR) as $\ln RR = \ln(t_x/t_0)$ as our effect size. In this equation, t_x is the mean value of a particular variable after time has passed and t_0 is the value for the original sampling time.

Supplementary Appendix 5. List of selected references in Supplementary Appendix 4.

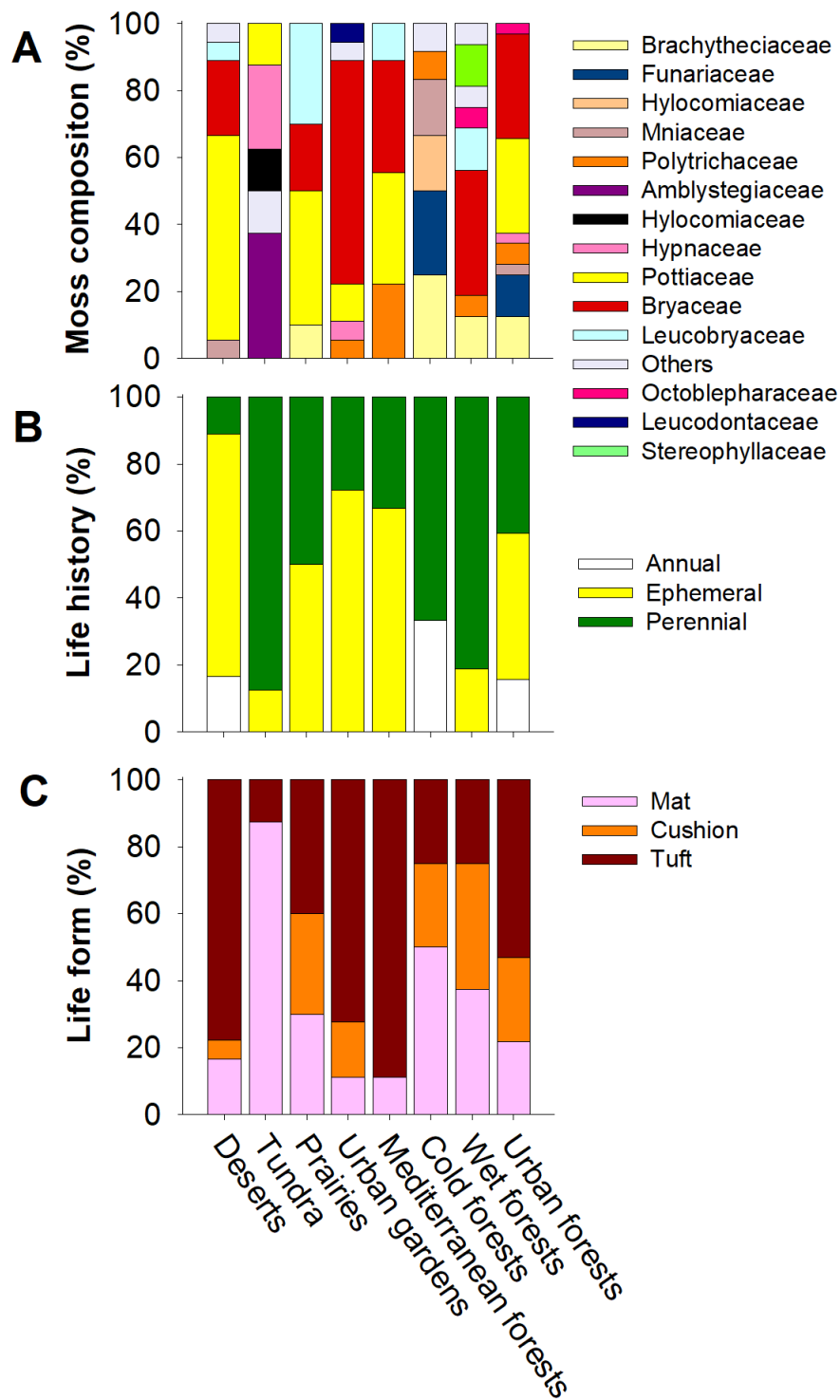
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Supplementary Figure 1. Example pictures of some of the studied ecosystems



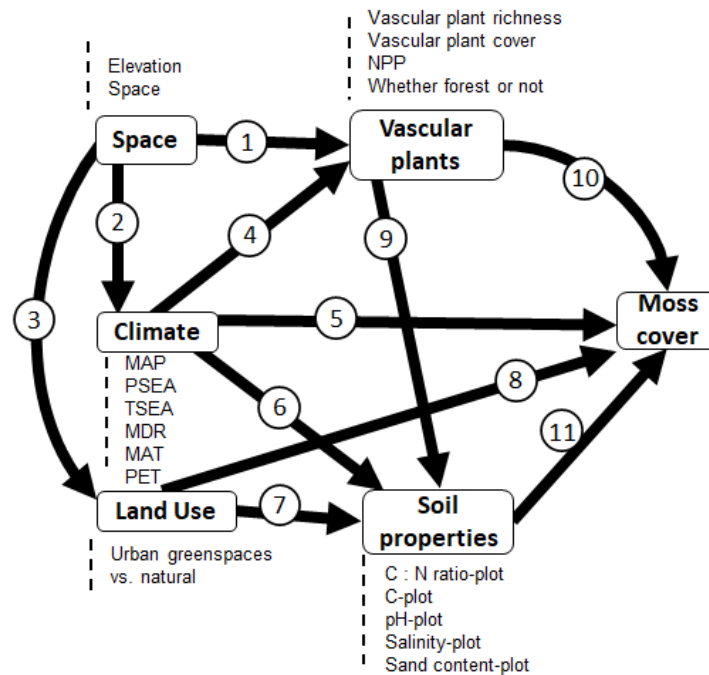
Supplementary Figure 1. Example pictures of some of the studied ecosystems. a) a moss heath in Antarctica; b) a subtropical forest in Mexico; c) a semi-arid forest in central Spain; d) a boreal forest in Northern Canada; e) a moss heath in a desert from Israel; f) a desert in Chile; g) a Mediterranean forest in Southern Spain; h) a desert in western China.

Supplementary Figure 2. Taxonomic and functional information on mosses



Supplementary Figure 2. Taxonomic and functional information associated with the mosses collected in our global field survey.

Supplementary Figure 3. A priori structural equation model

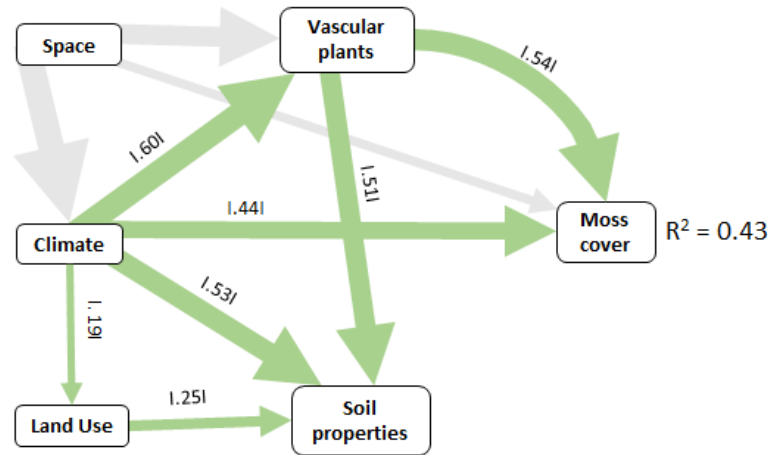


Path	Associations and reference	Rationale
1, 2, 3	Space → Vegetation, Climate, Land use type ⁵¹	Spatial location around the globe such as latitude and elevation can affect climatic conditions, plant growth and land use type.
4	Climate → Vegetation ⁵²⁻⁵³	Temperature and rainfall amount and seasonality affect plant cover and the biome type by, for example, regulating water availability. For instance, as rainfall declines, vegetation becomes shorter and sparser as water limitation constrains leaf growth. Similarly, as rainfall becomes more variable, plants with shallow roots (e.g., grasses) are more susceptible to mortality due to unstable water supply.
5	Climate cover ⁵⁴ → Moss	Changes in rainfall, climatic seasonality, diurnal range can affect water availability, thus influencing the coverage of mosses.

6	Climate → Soil ⁵¹	Changes in climate can affect soil properties directly by influencing ecological processes such as rock weathering, soil leaching, decomposition rate under different vegetation patches, or indirectly, by affecting soil microbial diversity.
7	Land use type → Soil ⁵⁵⁻⁵⁶	Urban greenspaces affect soil properties due to compaction (trampling) and fertilization.
8	Land use type → Moss cover ⁵⁷	Mosses in urban areas are more likely to be disturbed, affecting their composition and cover.
9	Vegetation → Soil ⁵⁸⁻⁵⁹	Plants can affect soil nutrients through plant-soil interactions and can affect pH and salinity by accumulating organic matter and salt.
10	Vegetation → Moss cover ⁶⁰	Plants can affect moss cover through resource competition such as light deprivation or litter burial.
11	Soil → Moss cover ⁶¹	Soil properties can affect moss growth and species composition by regulating soil stability and abiotic stress.

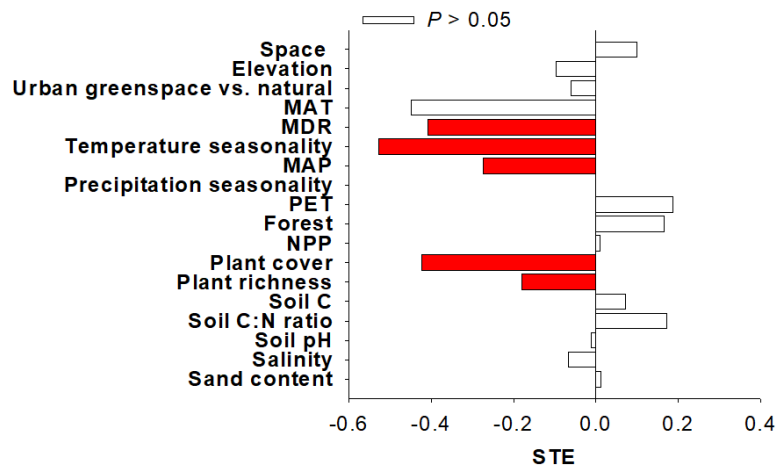
Supplementary Figure 3. *A priori* structural equation model assessing the direct and indirect effects of Climate (mean annual precipitation [MAP], precipitation seasonality [PSEA], temperature seasonality [TSEA], mean diurnal range [MDR], mean annual temperature [MAT], potential evapotranspiration [PET]), Vascular vegetation (vascular plant cover, NPP, whether forest or not, vascular plant richness), plot-level soil (C:N ratio, C, pH, salinity and sand content) and Land use type (urban greenspaces vs. natural) on moss cover after taking account of the Space effect (spatial and elevation) across the globe (Supplementary Table 3). Rectangles represent the response variables and circles represent the hypothesized pathways. We grouped the different categories of predictors (climate, soil, vegetation, land use and spatial influence) in the same box in the model for graphical simplicity, however these boxes do not represent latent variables. Numbers adjacent to arrows are indicative of the effect size of the relationship. R^2 denotes the proportion of variance explained. This model has five degrees of freedom coming from a lack of relationship between five climate attributes and urban greenspaces/natural ecosystems, as both natural and urban greenspaces are known to be present in all types of climates (Supplementary Table 3).

Supplementary Figure 4. Structural Equation Model – direct and indirect effects. Direct and indirect associations among space, climate, vascular vegetation, land use and soil properties



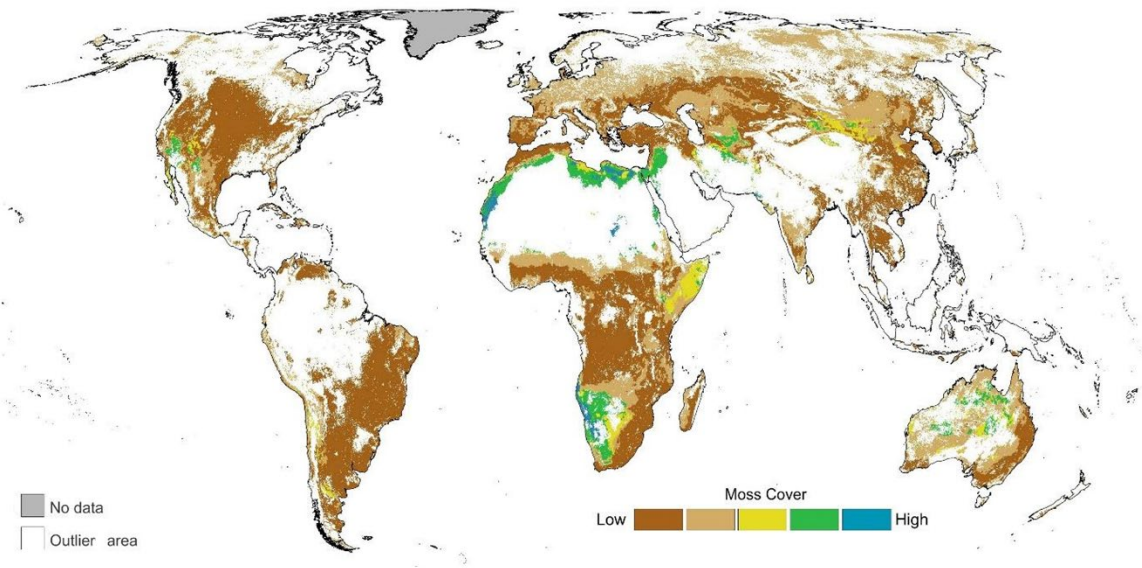
Supplementary Figure 4. Structural Equation Model of the direct and indirect associations among space (average distance among sites to control for spatial autocorrelation), climate, vascular vegetation, land use (urban greenspaces *cf.* natural) and soil properties in driving the proportion of moss cover (see Supplementary Table 3 for more details and Supplementary Fig. 4 for *a priori* model). We grouped the different categories of predictors (climate, soil, vegetation, land use and spatial influence) as composite variables. In this SEM, the effects of composite variables (in green) on moss cover are only interpretable in absolute terms ($|x|$). Numbers adjacent to arrows are indicative of the effect size of the relationship. R^2 denotes the proportion of variance explained.

Supplementary Figure 5. Total standardized effects from environmental conditions



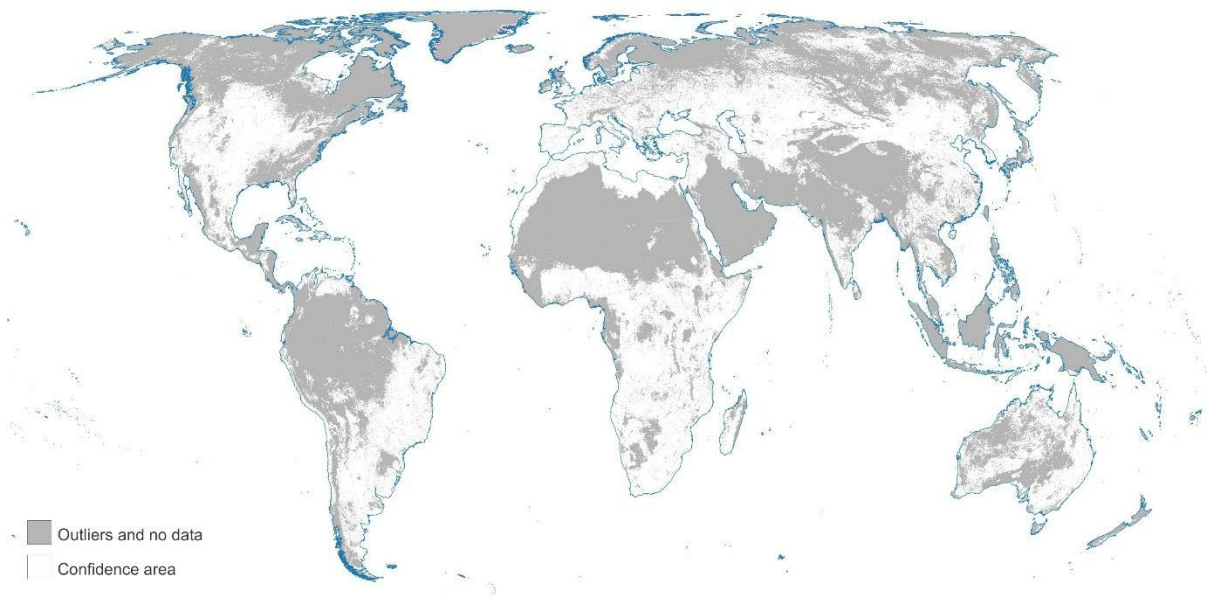
Supplementary Figure 5. Total standardized effects (STE) from environmental conditions on the cover of soil mosses ($n = 123$ sites). See Supplementary Table 3 for information on predictors. MAT = Mean annual temperature; MAP = Mean annual precipitation; PET = Potential evapotranspiration; MDR = Mean diurnal temperature range.

Supplementary Figure 6. Simplified version of the map in Fig. 2D



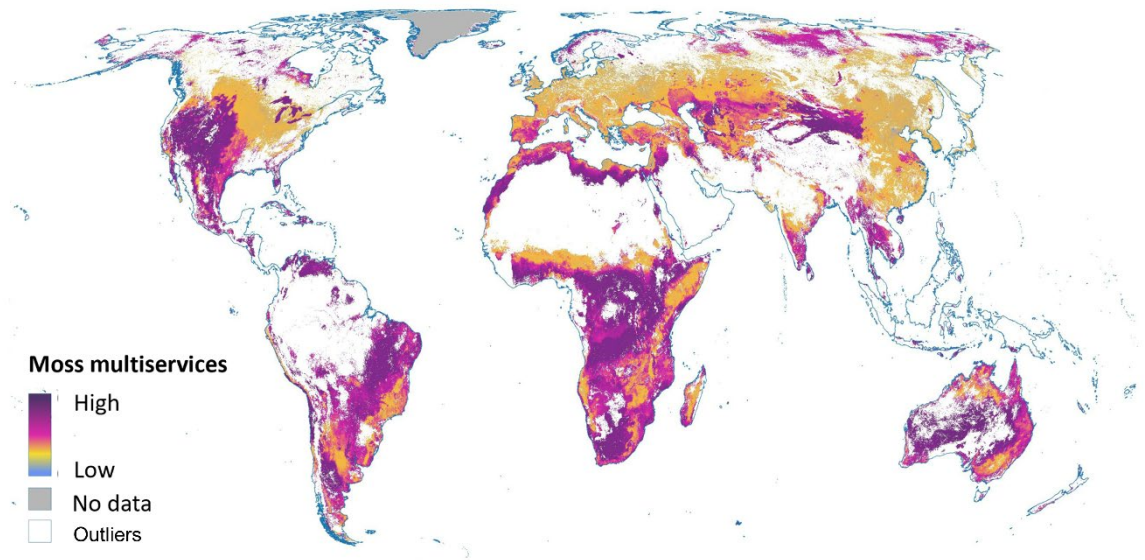
Supplementary Figure 6. Simplified version of the map in Fig. 2D. Predicted distribution of moss cover in ecosystems across the globe, based on machine learning modelling with a $R^2 = 0.86$ (determined as predicted vs. observed moss cover). Locations with high uncertainty, and areas not represented by environmental conditions in our study are masked in white. $n = 123$ sites in all cases.

Supplementary Figure 7. Global map of uncertainty regions



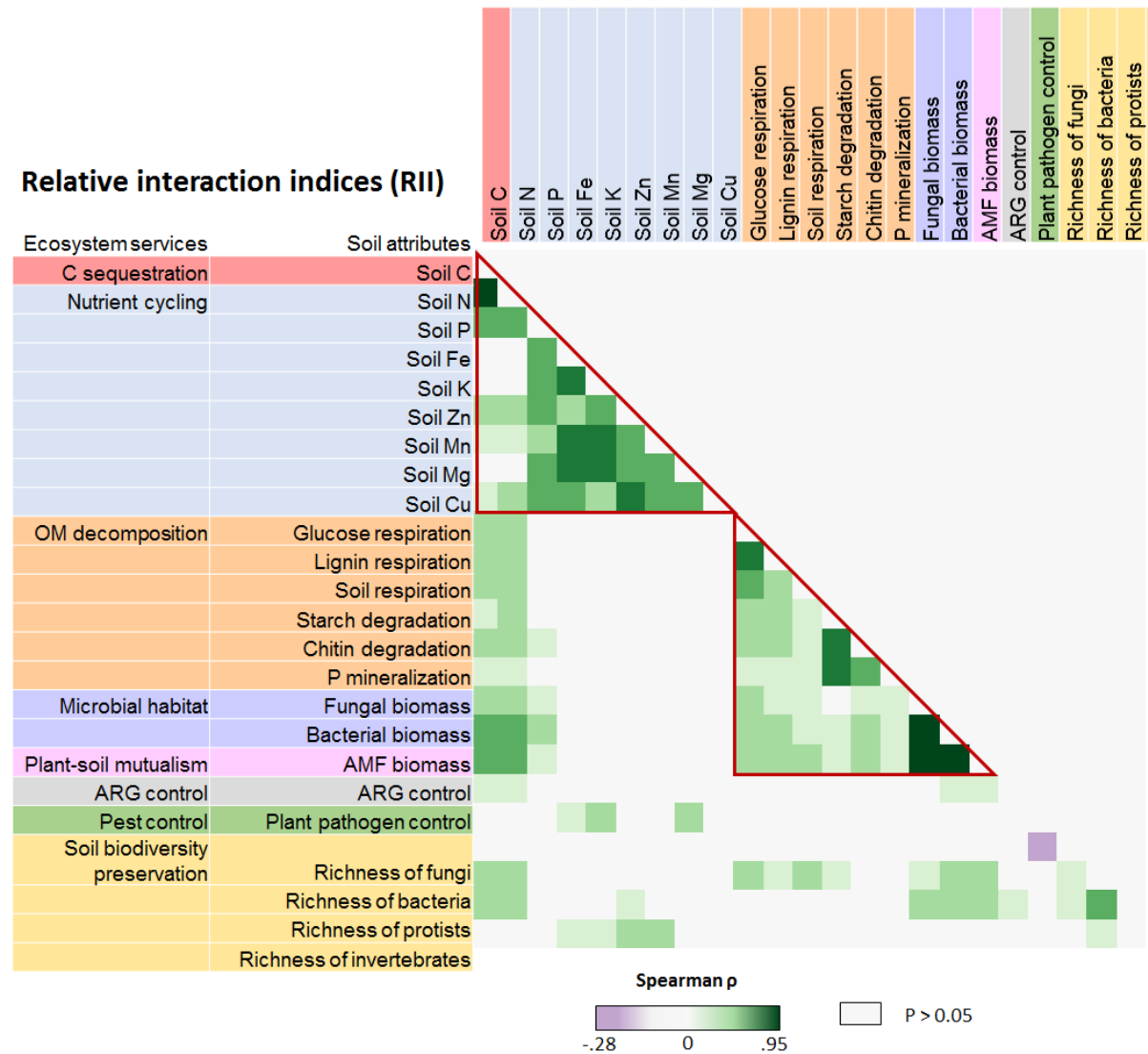
Supplementary Figure 7. Global map highlighting the uncertainty regions excluded from our analyses, based on the lack of environmental representativity of our survey for these regions.

Supplementary Figure 8. Moss contribution to multiple ecosystem services



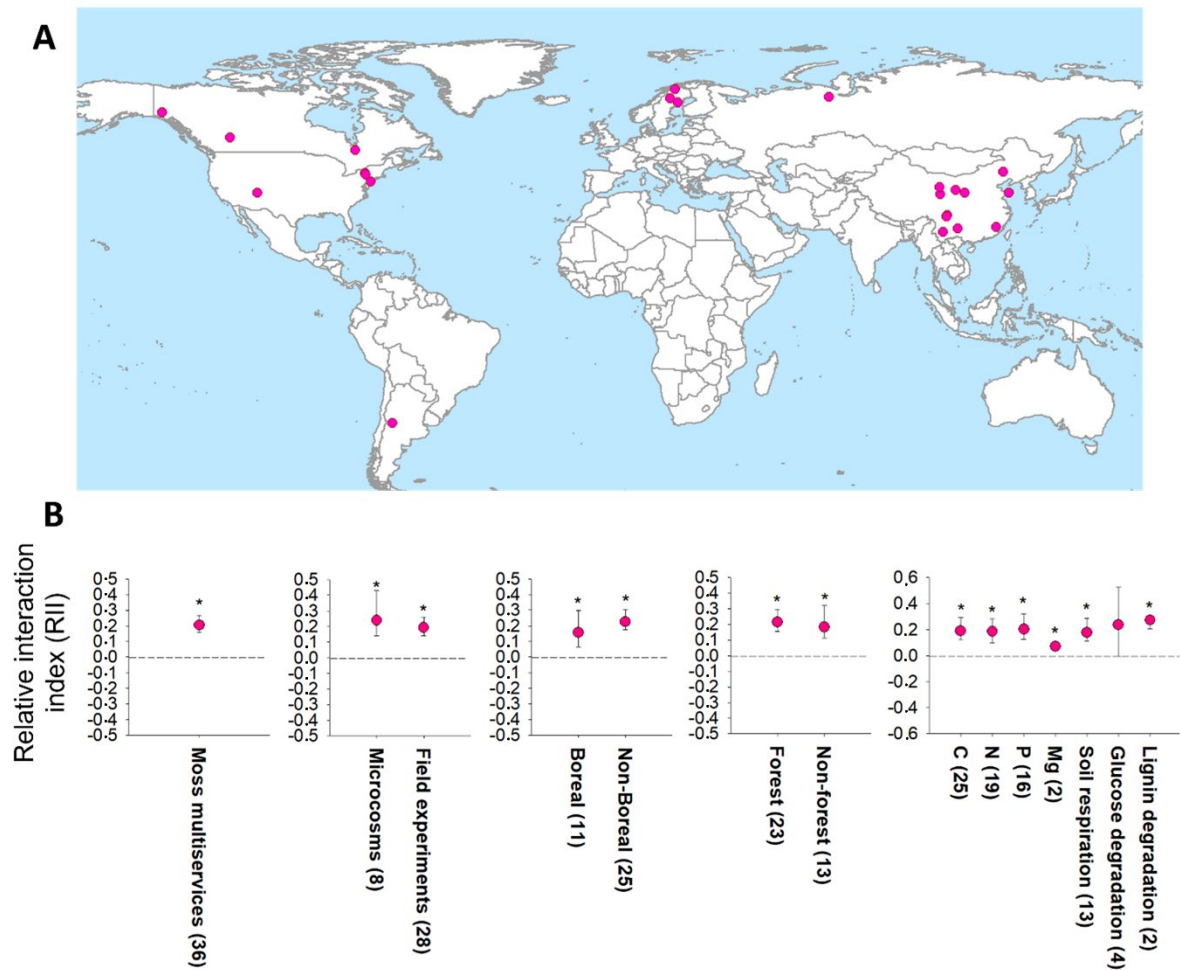
Supplementary Figure 8. Predicted contribution of soil mosses to support multiple ecosystem services simultaneously. This map was conducted using machine learning modeling with a $R^2 = 0.69$ (determined as predicted *cf.* observed moss contributions to ecosystem services). Locations with high uncertainty, and areas not represented by environmental conditions in our study are masked in white. $n = 123$ sites in all cases. Areas in white are those not represented by environmental conditions included in this study.

Supplementary Figure 9. Spearman correlations - RII and soil attributes



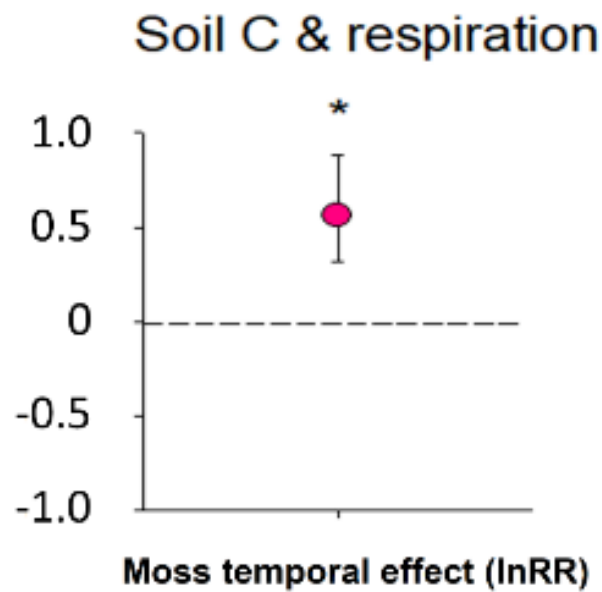
Supplementary Figure 9. Spearman correlations between the relative interaction indices (RII) of soil mosses on 24 individual soil attributes (Supplementary Table 6).

Supplementary Figure 10. Experimental effects of mosses on multiple services



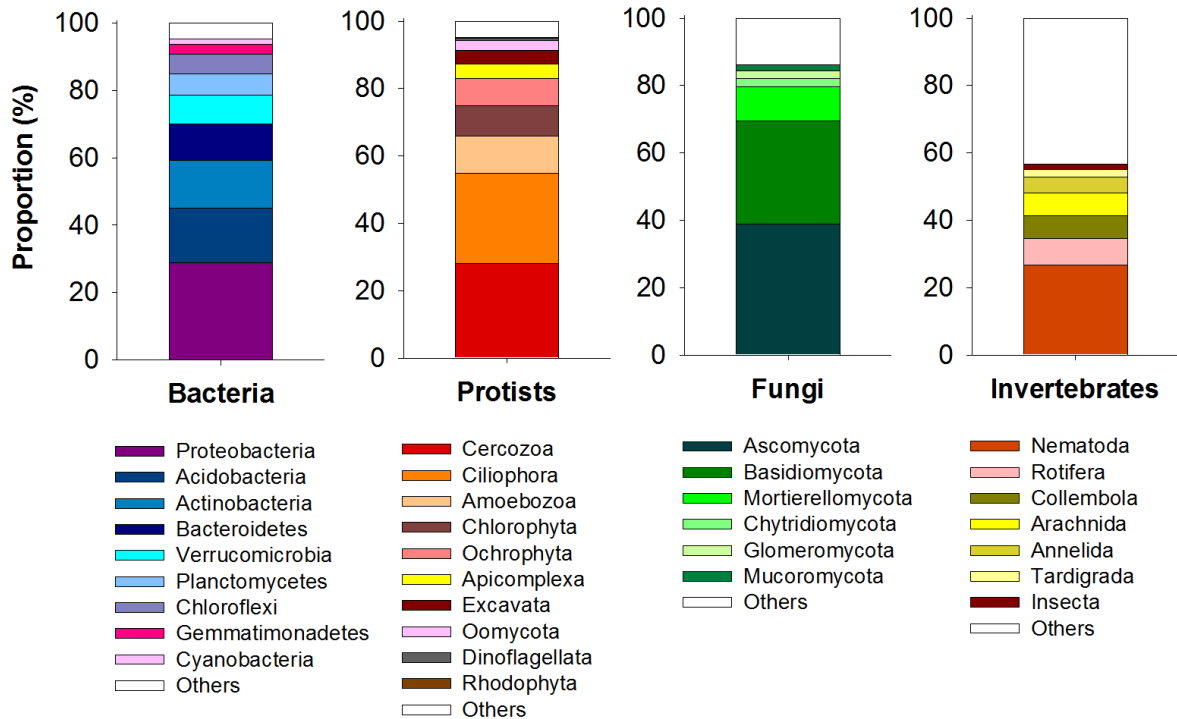
Supplementary Figure 9. Experimental effects of mosses on multiple services. Moss relative interaction indices (RII) for multiple ecosystem services retrieved from an independent meta-analytical literature search (Meta-analysis #1) for manipulative moss microcosm/field experiments adding/removing mosses to investigate their effect on soil function compared with a procedure control (bare soils) (Supplementary Appendices 2-3) (mean $\pm$ bootstrap CI 95%). * $P < 0.05$.

Supplementary Figure 11. Experimental effects of mosses - carbon and respiration



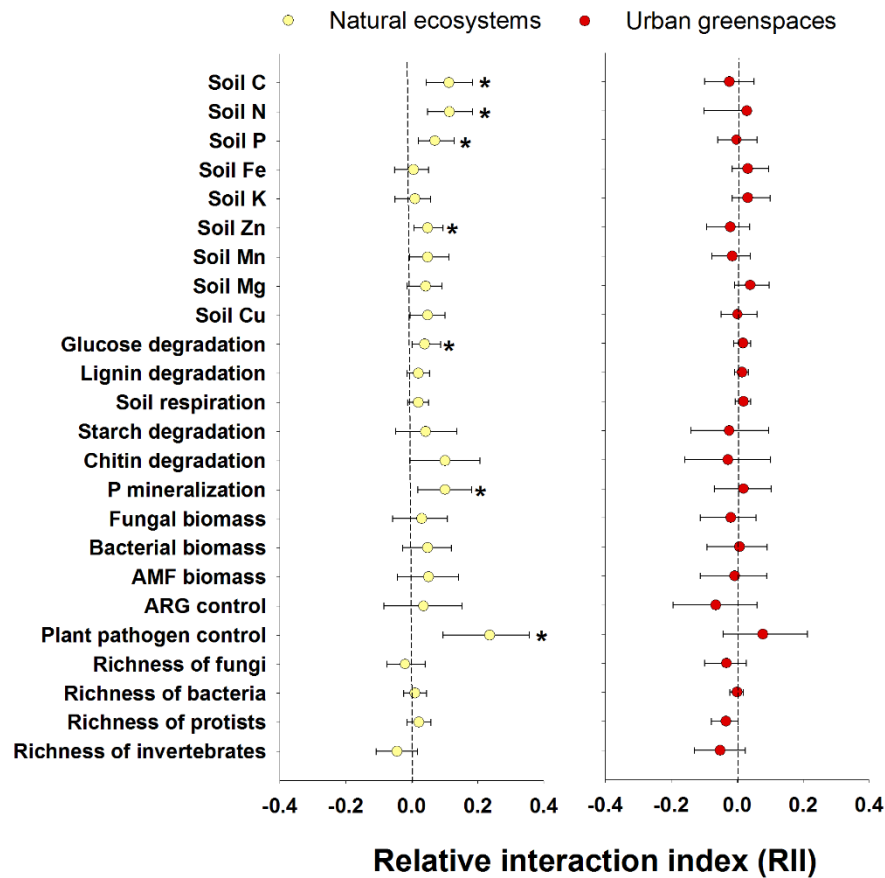
Supplementary Figure 10. Experimental temporal effects of mosses on carbon and soil respiration. Moss temporal effect on soil function from an independent meta-analytical literature search for studies monitoring soil function under moss over time (Meta-analysis #2; Supplementary Appendices 4-5) (mean $\pm$ bootstrap CI 95%, $n = 156$, $*P < 0.05$).

Supplementary Figure 12. Soil community composition - microbes and invertebrates



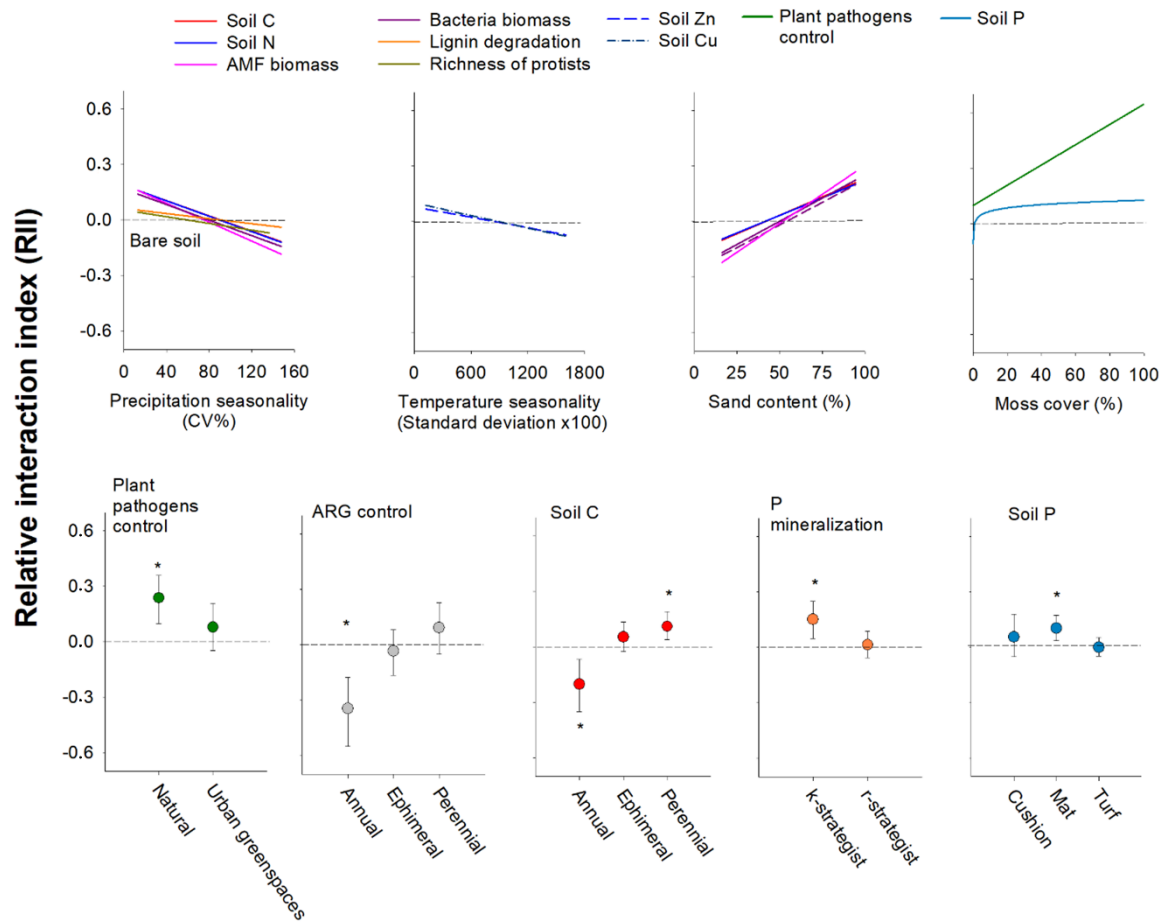
Supplementary Figure 11. Soil community composition of bacteria, protists, fungi and invertebrates found beneath soil mosses.

Supplementary Figure 13. Moss relative interaction indices and soil attributes



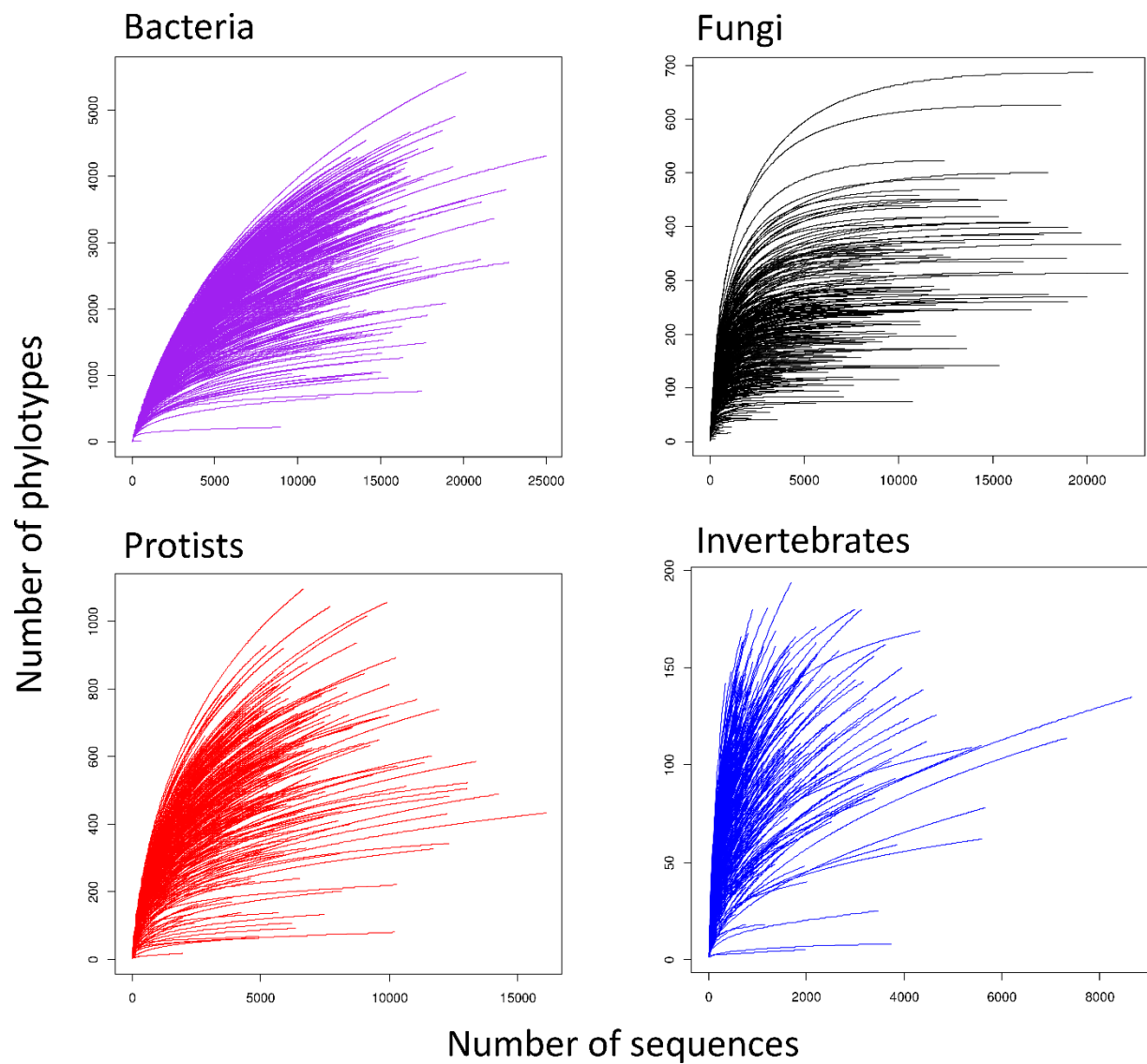
Supplementary Figure 13. Moss relative interaction indices (RII) for 24 individual soil attributes in natural ecosystems and urban greenspaces (Supplementary Table 5) (mean $\pm$ bootstrap CI 95%). * $P < 0.05$. Richness of invertebrates ($n = 102$), Richness of fungi (moss: 107, vegetation: 108), Richness of protists (moss: 114, vegetation: 110), fungal Natural ecosystems ($n = 62$), Richness of bacteria (moss: 121, vegetation: 117), ARG control (moss: 123, vegetation: 119). Vegetation: Cu, Fe, K, Mg, Mn, P, Zn, Bacterial biomass ($n = 122$). For the remaining moss and vegetation attributes ($n = 123$).

Supplementary Figure 14. Climate, soil, moss traits and RII



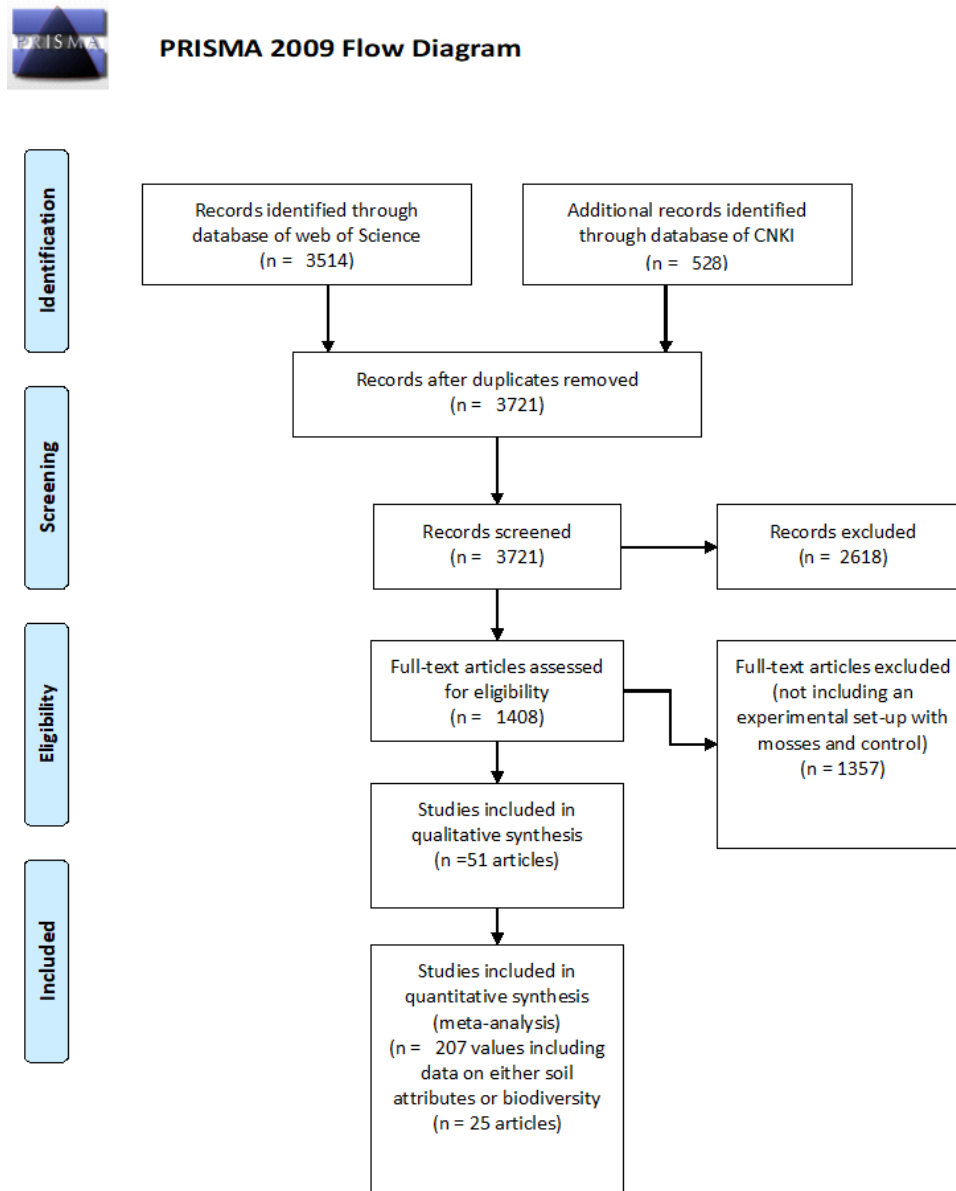
Supplementary Figure 14. Selected examples of the importance of climate, soil properties and moss traits in regulating the relative interaction indices (RII) of soil mosses on individual soil attributes (e.g., RII for soil C). Lines are fitted linear or logarithmic models. Only significant regressions are included ($P < 0.05$). Error bars are bootstrapped CI 95% ($n = 123$ sites).

Supplementary Figure 15. Rarefaction curves for soil biodiversity.



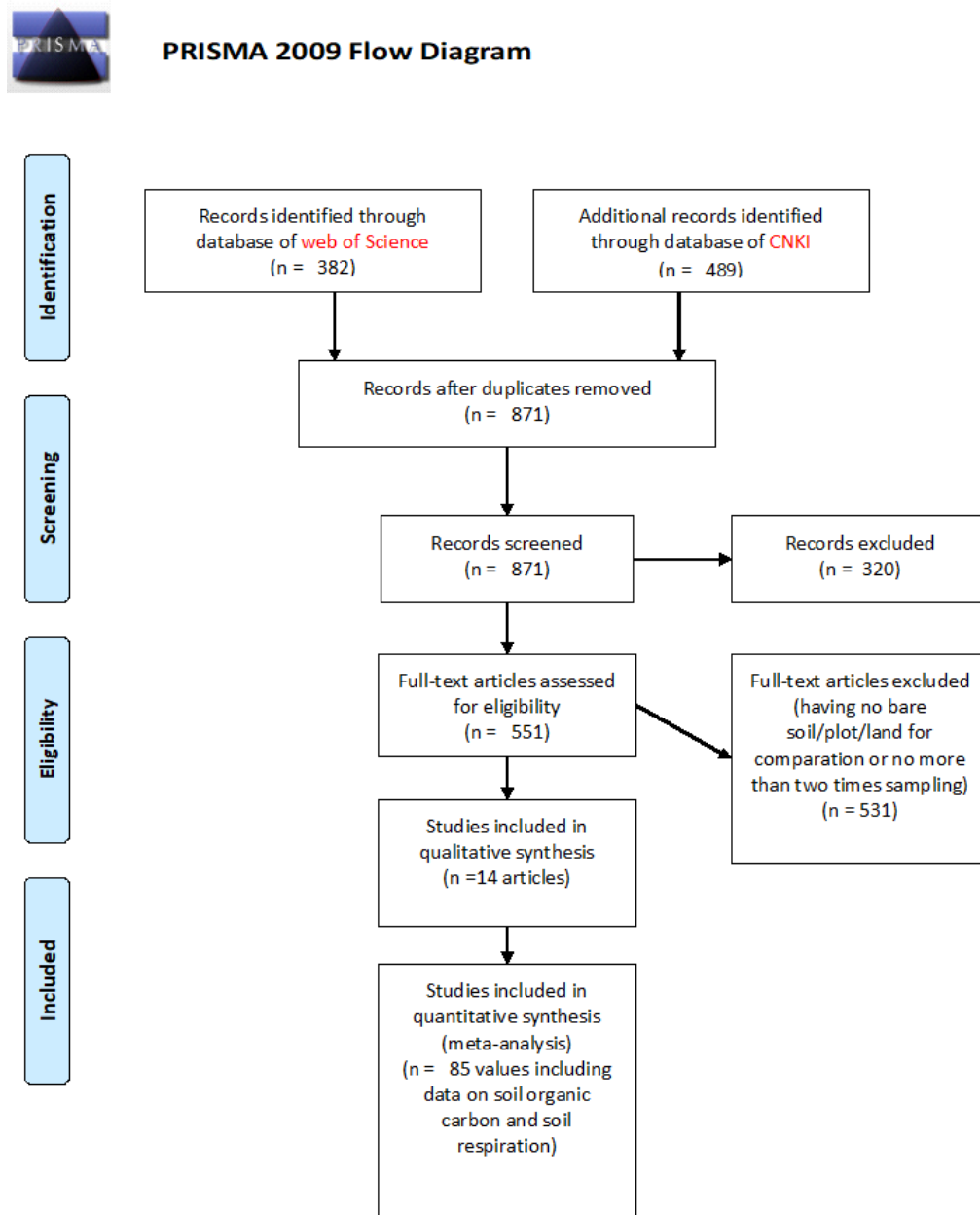
Supplementary Figure 15. Rarefaction curves for soil biodiversity.

Supplementary Figure 16. PRISMA diagram - meta-analysis #1



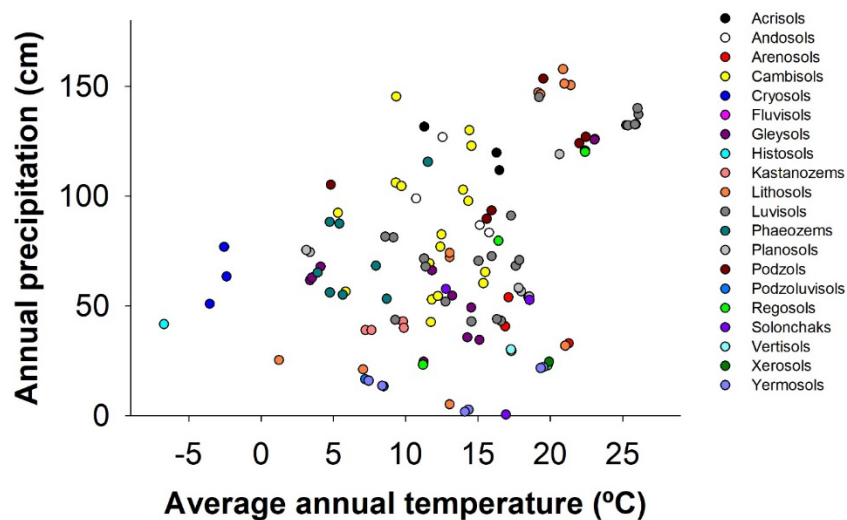
Supplementary Figure 16. PRISMA diagram including the workflow for Meta-analysis #1 in Supplementary Appendix 2.

Supplementary Figure 17. PRISMA diagram - meta-analysis #2



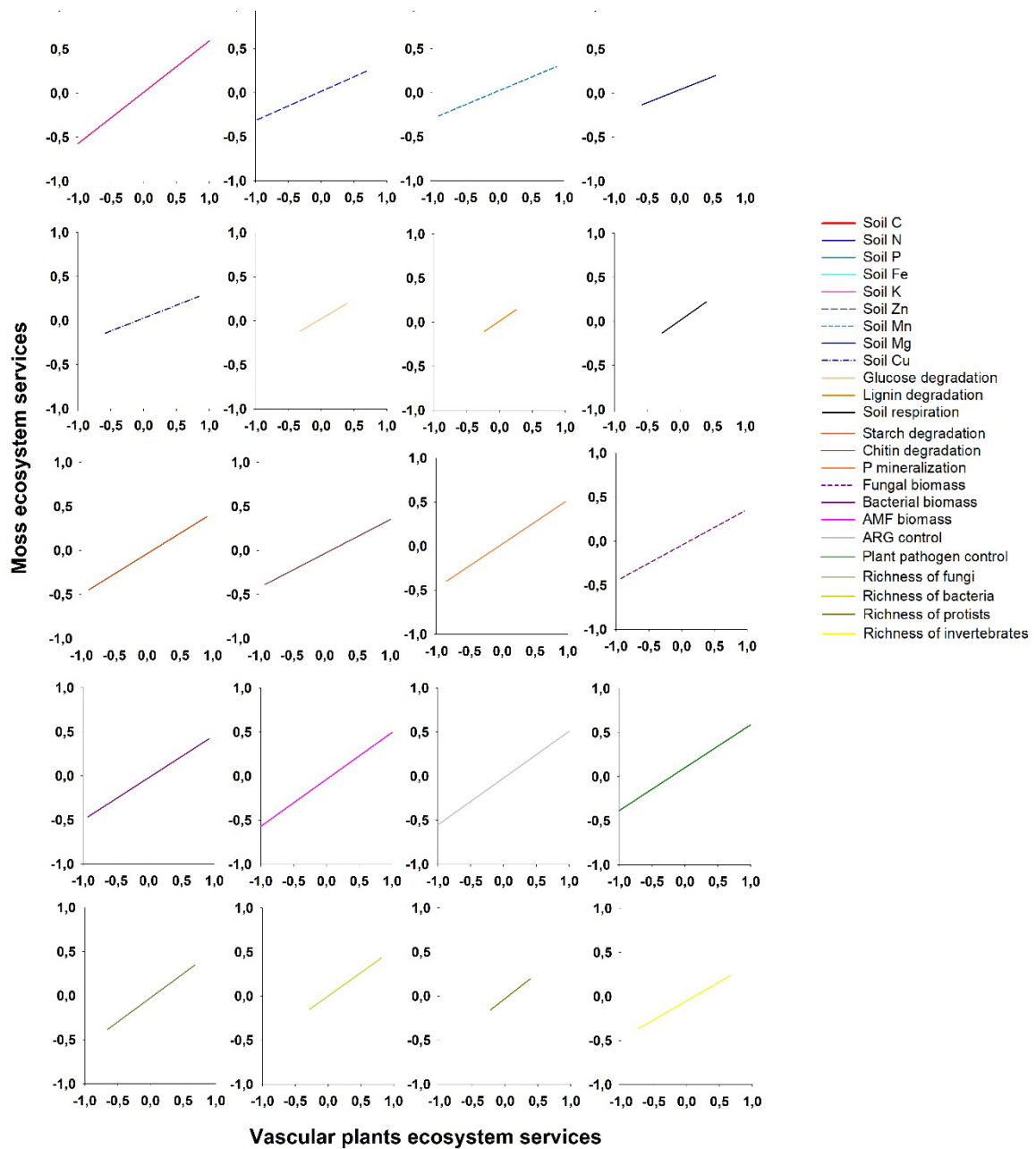
Supplementary Figure 17. PRISMA diagram including the workflow for Meta-analysis #2 in Supplementary Appendix 4.

Supplementary Figure 18. Study sites in relation to a temperature and rainfall



Supplementary Figure 18. Location of study sites in relation to a global temperature and precipitation highlighting the surveyed soil types⁶².

Supplementary Figure 19. Extended version of Fig. 3B



Supplementary Figure 19. Extended version of Fig. 3B aiming to provide a more detailed information on the relationship between vascular plant and moss contributions to ecosystem services.

Supplementary Table 1. Ecosystem type included in Figure S2

Note, *n* is given in parentheses.

Ecosystem type	Characteristics
Deserts (18 sites)	Arid ecosystems (Köppen climate classification)
Tundra (8 sites)	Cold and polar (Köppen climate classification) grasslands, moss heaths and shrublands
Prairies (10 sites)	Temperate (Köppen climate classification) grasslands and shrublands
Urban gardens (18 sites)	Urban lawns in city parks and multi-residential shared gardens
Mediterranean forests (9 sites)	Mediterranean (Köppen climate classification) forests
Cold forests (12 sites)	Cold and boreal forests (Köppen climate classification)
Wet forests (16 sites)	Tropical, subtropical and oceanic forests (Köppen climate classification)
Urban forests (32 sites)	Urban forests in city parks

Supplementary Table 2. Characteristics of the study sites

Supplementary Table 2. Information on the location, climatic zone and vegetation of all sites, and the family, genus/species and life form of the major moss species ($n = 123$). See Supplementary Table 1 for additional information on ecosystem types.

Site ID	Latitude	Longitude	Elevation	Country	Moss family	Moss species name	Life form	Ecosystem type	Vascular plant species
1	41.735278	126.04472	530	China	Mniaceae	<i>Mnium</i> sp.	Perennial	Cold Forest	<i>Quercus mongolica</i>
2	42.275278	127.4425	621	China	Brachytheciaceae	<i>Myuroclada Maximowiczii</i>	Perennial	Cold Forest	<i>Acer tegmentosum</i>
3	42.840556	129.46361	360	China	Brachytheciaceae	<i>Myuroclada Maximowiczii</i>	Perennial	Tundra	<i>Betula dahurica</i>
4	43.338889	128.2375	504	China	Mniaceae	<i>Mnium</i> sp.	Perennial	Cold Forest	<i>Quercus mongolica</i>
5	43.877778	126.60667	308	China	Hypnaceae	<i>Homomallium</i> sp.	Perennial	Tundra	<i>Tilia amurensis</i>
6	41.739444	125.94278	406	China	Hypnaceae	<i>Pylaisiella brotheri</i>	Perennial	Urban forest	<i>Pinus thunbergii</i>
7	42.175278	127.50028	733	China	Polytricaceae	<i>Polytrichum</i> sp.	Perennial	Urban garden	<i>Acer triflorum</i>
8	42.910833	129.49	209	China	Mniaceae	<i>Mnium</i> sp.	Perennial	Urban forest	<i>Pinus thunbergii</i>
9	43.380833	128.22417	513	China	Polytricaceae	<i>Polytrichum</i> sp.	Perennial	Urban forest	<i>Larix gmelinii</i>
10	43.8425	126.52306	216	China	Hypnaceae	<i>Pylaisiella brotheri</i>	Perennial	Urban garden	<i>Larix gmelinii</i>
11	-62.6616	-60.3822	1	Antarctica	Amblystegiaceae	<i>Sanionia uncinata</i>	Perennial	Tundra	-
12	-62.16514	-58.46962	0	Antarctica	Amblystegiaceae	<i>Sanionia uncinata</i>	Perennial	Tundra	-

13	-62.66851	-61.10233	0	Antarctica	Amblystegiaceae	<i>Sanionia uncinata</i>	Perennial	Tundra	-
14	-51.01681	-73.05431	351	Chile	Pottiaceae	<i>Ceratodon purpureus</i>	Ephemeral	Tundra	-
15	-18.4578	-69.79671	2252	Chile	Ptychomitriaceae	<i>Ptychomitrium</i> sp.	Ephemeral	Desert	<i>Browningia candelaris</i>
16	-28.38328	-70.6931	643	Chile	Pottiaceae	<i>Desmatodon</i> sp.	Ephemeral	Desert	<i>Atriplex clivicola</i>
17	-32.89728	-71.16476	523	Chile	Pottiaceae	<i>Desmatodon</i> sp.	Ephemeral	Prairie	<i>Stachys</i> sp.
18	-33.38221	-70.96345	1145	Chile	Pottiaceae	<i>Tortula</i> sp.	Ephemeral	Mediterranean forest	<i>Schinus latifolius</i>
19	-18.48735	-70.08175	1060	Chile	Pottiaceae	<i>Desmatodon</i> sp.	Ephemeral	Desert	<i>Tillandsia marconae</i>
20	-28.50475	-70.76084	589	Chile	Pottiaceae	<i>Desmatodon</i> sp.	Ephemeral	Desert	<i>Atriplex vallenarensis</i>
21	-32.87365	-71.18333	213	Chile	Pottiaceae	<i>Desmatodon</i> sp.	Ephemeral	Prairie	<i>Festuca</i> sp.
22	-33.3739	-70.60738	880	Chile	Pottiaceae	<i>Desmatodon</i> sp.	Ephemeral	Urban forest	<i>Acacia caven</i>
23	-19.26889	-43.585	1055	Brazil	Leucobryaceae	<i>Campylopus carolinae</i>	Perennial	Prairie	<i>Eragrostis</i> sp.
24	-19.26528	-43.58361	1055	Brazil	Leucobryaceae	<i>Campylopus pilifer</i>	Perennial	Prairie	<i>Eragrostis</i> sp.
25	-19.29444	-43.60583	1036	Brazil	Leucobryaceae	<i>Campylopus carolinae</i>	Perennial	Prairie	<i>Echinolaena inflexa</i>
26	-19.87365	-43.97256	836	Brazil	Bryaceae	<i>Leucobryum</i> sp.	Perennial	Urban garden	<i>Zoysia japonica</i>

27	-19.93988	-44.03903	919	Brazil	Bryaceae	<i>Bryum</i> sp.	Ephemeral	Urban forest	<i>Merostachys</i> spp.
28	-19.93922	-44.18447	824	Brazil	Bryaceae	<i>Leucobryum</i> sp.	Perennial	Urban garden	<i>Brachiaria brizantha</i>
29	40.242019	-105.2118	1737	USA	Pottiaceae	<i>Tortula ruralis</i>	Ephemeral	Desert	<i>Pinus ponderosa</i>
30	39.190366	-109.1152	1452	USA	Pottiaceae	<i>Syntrichia caninervis</i>	Ephemeral	Desert	<i>Junniper</i> sp.
31	41.315937	-104.8272	1874	USA	Bryaceae	<i>Bryum</i> sp.	Ephemeral	Desert	<i>Poa fendleriana</i>
32	40.161436	-105.1207	1519	USA	Bryaceae	<i>Bryum</i> sp.	Ephemeral	Urban garden	<i>Poa</i> sp.
33	39.112631	-108.6077	1397	USA	Bryaceae	<i>Bryum</i> sp.	Ephemeral	Urban garden	<i>Poa</i> sp.
34	41.155998	-104.8312	1874	USA	Bryaceae	<i>Rosulabryum capillare</i>	Ephemeral	Urban garden	<i>Poa</i> sp.
35	39.8291	-104.812	1603	USA	Bryaceae	<i>Bryum</i> sp.	Ephemeral	Desert	<i>Populus</i> sp.
36	42.44511	-83.44231	199	USA	Hylocomiaceae	<i>Rhytidium rugosum</i>	Perennial	Cold Forest	<i>Quercus</i> sp.
37	42.43936	-83.67509	280	USA	Bryaceae	<i>Bryum</i> sp.	Ephemeral	Urban garden	<i>Poa</i> sp.
38	67.301801	14.390105	4	Norway	Hypnaceae	<i>Hypnum revolvens</i>	Perennial	Tundra	<i>Sorbis aucuparia</i>
39	59.85207	17.597665	20	Sweden	Hylocomiaceae	<i>Hylocomnium splendens</i>	Perennial	Cold Forest	<i>Picea arbis</i>
40	46.575556	0.3352778	106	France	Brachytheciaceae	<i>Brachythecium rutabulum</i>	Perennial	Urban forest	<i>Celtis Australis</i>
41	46.506944	0.3716667	140	France	Polytrichaceae	<i>Polytrichum formosum</i>	Perennial	Wet forest	<i>Quercus robur</i>
42	46.325	-0.467222	18	France	Pottiaceae	<i>Ceratodon purpureus</i>	Ephemeral	Urban forest	<i>Alnus glutinosa</i>
43	46.303889	-0.684444	6	France	Brachytheciaceae	<i>Eurhynchium hians</i>	Perennial	Wet forest	<i>Fraxinus Angustifolia</i>
44	47.396389	0.6772222	56	France	Bryaceae	<i>Ptychostomum capilare</i>	Ephemeral	Urban forest	<i>Acer Pseudoplatanus</i>
45	47.335556	0.7513889	96	France	Brachytheciaceae	<i>Eurhynchium striatum</i>	Perennial	Wet forest	<i>Quercus Robur</i>

46	46.052184	14.478296	297	Slovenia	Polytrichaceae	<i>Atrichum undulatum</i>	Annual	Cold Forest	<i>Carpinus betulus</i>
47	45.526132	13.717189	78	Slovenia	Calliergonaceae	<i>Calliergonella cuspidata</i>	Perennial	Wet forest	<i>Quercus pubescens</i>
48	46.580933	15.636299	345	Slovenia	Brachytheciaceae	<i>Rhynchostegium confertum</i>	Perennial	Cold Forest	<i>Fagus sylvatica</i>
49	46.051899	14.479875	297	Slovenia	Brachytheciaceae	<i>Pseudoscleropodium purum</i>	Perennial	Urban forest	<i>Tilia cordata</i>
50	45.544423	13.73122	5	Slovenia	Brachytheciaceae	<i>Kindbergia praelonga</i>	Perennial	Urban forest	<i>Pinus pinea</i>
51	46.565195	15.648796	321	Slovenia	Brachytheciaceae	<i>Eurhynchium striatum</i>	Perennial	Urban forest	<i>Acer pseudoplatanus</i>
52	-25.78791	28.20304	1433	South Africa	Bryaceae	<i>Bryum argenteum</i>	Ephemeral	Prairie	<i>Senegalia caffra</i>
53	-26.48338	28.21157	1648	South Africa	Bryaceae	<i>Bryum argenteum</i>	Ephemeral	Prairie	<i>Poa</i> sp.
54	-33.33378	18.27285	117	South Africa	Pottiaceae	<i>Trichostomum brachydontium</i>	Perennial	Prairie	<i>Cynodon</i> sp.
55	-25.76184	28.22027	1368	South Africa	Bryaceae	<i>Rosulabryum</i> sp.	Ephemeral	Urban forest	<i>Cynodon</i> sp.
56	-26.16431	28.131	1627	South Africa	Fissidentaceae	<i>Fissidens</i> sp.	Ephemeral	Urban garden	<i>Rorippa</i> sp.
57	-33.90396	18.40195	9	South Africa	Pottiaceae	<i>Trichostomum brachydontium</i>	Perennial	Urban forest	Unknown
58	40.07264	116.18201	47	China	Funariaceae	<i>Funaria hygrometrica</i>	Annual	Cold Forest	<i>Adenanthera pavonina</i> L.
59	36.221806	117.01884	183	China	Funariaceae	<i>Funaria hygrometrica</i>	Annual	Urban forest	<i>Pinus</i> sp.
60	39.075328	117.1478	9	China	Funariaceae	<i>Funaria hygrometrica</i>	Annual	Cold Forest	<i>Ulmus pumila</i>
61	40.01034	116.38861	45	China	Funariaceae	<i>Funaria hygrometrica</i>	Annual	Urban forest	<i>Ginkgo biloba</i>

62	39.08455	117.68621	2	China	Funariaceae	<i>Funaria hygrometrica</i>	Annual	Urban forest	<i>Ulmus pumila</i>
63	36.20803	117.11024	355	China	Funariaceae	<i>Funaria hygrometrica</i>	Annual	Cold Forest	<i>Quercus gomeziana</i>
64	44.62965	88.268417	568	China	Pottiaceae	<i>Syntrichia caninervis</i>	Ephemeral	Desert	<i>Ephedra przewalskii</i>
65	45.117241	86.022085	334	China	Pottiaceae	<i>Syntrichia caninervis</i>	Ephemeral	Desert	<i>Haloxylon ammodendron</i>
66	43.834214	88.045233	1993	China	Mniaceae	<i>Mnium hornum</i>	Perennial	Desert	<i>Picea schrenkiana</i>
67	44.268534	88.150298	509	China	Pottiaceae	<i>Crossidium squamiferum</i>	Annual	Desert	<i>Tamarix</i> sp.
68	44.698902	86.236809	365	China	Bryaceae	<i>Bryum argenteum</i>	Ephemeral	Desert	<i>Tamarix</i> sp.
69	43.830834	87.657023	840	China	Bryaceae	<i>Bryum argenteum</i>	Ephemeral	Urban garden	<i>Ulmus pumila</i>
70	-23.82545	133.35473	695	Australia	Leucobryaceae	<i>Campylopus introflexus</i>	Perennial	Desert	<i>Triodia basedowii</i>
71	-27.4922	153.4294	83	Australia	Leucobryaceae	<i>Campylopus introflexus</i>	(Hedw.) Brid.	Wet forest	<i>Eucalyptus racemosa</i>
72	-34.1802	142.1729	43	Australia	Pottiaceae	<i>Didymodon torquatus</i>	(Hedw.) Brid.	Desert	<i>Chenopodium nitrariaceum</i>
73	-33.8812	150.8546	78	Australia	Bryaceae	<i>Gemmabryum pachytheca</i>	Ephemeral	Wet forest	<i>Eucalyptus piperita</i>
74	-34.0721	151.0012	120	Australia	Leucobryaceae	<i>Campylopus introflexus</i>	Perennial	Wet forest	<i>Angophora costata</i>
75	-23.70826	133.87457	580	Australia	Bryaceae	<i>Gemmabryum pachytheca</i>	Ephemeral	Urban forest	<i>Pennisetum clandestinum</i>
76	-27.4984	153.01603	25	Australia	Bryaceae	<i>Gemmabryum pachytheca</i>	Ephemeral	Urban garden	<i>Cynodon dactylon</i>

77	-34.1854	142.1696	54	Australia	Bryaceae	<i>Gemmabryum pachythea</i>	Ephemeral	Urban garden	<i>Pennisetum clandestinum</i>
78	-33.8814	150.8533	78	Australia	Bryaceae	<i>Bryum argenteum</i>	Ephemeral	Urban garden	<i>Pennisetum clandestinum</i>
79	-34.0822	151.0126	204	Australia	Bryaceae	<i>Gemmabryum pachythea</i>	Ephemeral	Urban garden	<i>Cynodon dactylon</i>
80	41.476763	2.147501	94	Spain	Pottiaceae	<i>Didymodon</i> sp.	Ephemeral	Mediterranean forest	<i>Quercus ilex</i>
81	41.415993	2.150663	144	Spain	Pottiaceae	<i>Didymodon</i> sp.	Ephemeral	Urban forest	<i>Pinus Halepensis</i>
82	46.725463	-116.9231	822	USA	Brachytheciaceae	<i>Eurhynchium praelongum</i>	Perennial	Cold Forest	<i>Pinus</i> sp.
83	46.74008	-117.1752	746	USA	Leucodontaceae	<i>Antitrichia</i> sp.	Perennial	Urban garden	<i>Acer spicatum</i>
84	44.496464	-123.3382	97	USA	Leucodontaceae	<i>Antitrichia californica</i>	Perennial	Mediterranean forest	<i>Ulmus</i> sp.
85	44.53041	-123.2599	75	USA	Pottiaceae	<i>Barbula vinealis</i>	Ephemeral	Urban garden	<i>Acer macrophyllum</i>
86	19.603005	-99.47802	3164	Mexico	Thuidiaceae	<i>Thuidium delicatulum</i>	Perennial	Wet forest	<i>Abies religiosa</i>
87	19.601338	-99.47592	3164	Mexico	Bryaceae	<i>Rosulabryum</i> sp.	Ephemeral	Wet forest	<i>Cupressus lusitanica</i>
88	19.081	-99.1701	3102	Mexico	Bryaceae	<i>Rosulabryum</i> sp.	Ephemeral	Wet forest	<i>Pinus montezumae</i>
89	19.31056	-99.18308	2318	Mexico	Bryaceae	<i>Rosulabryum</i> sp.	Ephemeral	Urban garden	<i>Buddleja cordata</i>
90	19.294317	-99.19391	2335	Mexico	Bryaceae	<i>Rosulabryum</i> sp.	Ephemeral	Urban forest	<i>Cupressus lusitanica</i>
91	19.418751	-99.18632	2257	Mexico	Funariaceae	<i>Funaria</i> sp.	Annual	Urban forest	<i>Ligustrum lucidum</i>

92	40.57222	-4.15333	974	Spain	Bryaceae	<i>Rosulabryum</i> sp.	Ephemeral	Desert	<i>Quercus pirenaica</i>
93	40.41056	-3.69028	642	Spain	Pottiaceae	<i>Tortula</i> sp.	Ephemeral	Urban forest	<i>Buxus sempervirens</i>
94	37.358066	-5.934926	13	Spain	Bryaceae	<i>Bryum</i> sp.	Ephemeral	Mediterranean forest	<i>Stenotaphrum secundatum</i>
95	37.358998	-5.952151	13	Spain	Bryaceae	<i>Bryum</i> sp.	Ephemeral	Mediterranean forest	<i>Eucalyptus</i> sp.
96	37.416482	-5.995864	11	Spain	Pottiaceae	<i>Tortula</i> sp.	Ephemeral	Prairie	<i>Fraxinus</i> sp.
97	58.61782	-93.80862	34	Canada	Hylocomiaceae	<i>Hylocomium</i> sp.	Perennial	Tundra	<i>Empetrum</i> sp.
98	58.62337	-93.81469	36	Canada	Sphagnaceae	<i>Sphagnum</i> sp.	Perennial	Cold Forest	<i>Picea mariana</i>
99	7.757	4.828	368	Nigeria	Octoblepharaceae	<i>Octoblepharum albidum</i>	Perennial	Wet forest	Unknown
100	7.756	4.811	357	Nigeria	Octoblepharaceae	<i>Octoblepharum</i> sp.	Perennial	Urban forest	<i>Maranthochloa purpurea</i>
101	7.517	4.528	265	Nigeria	Bryaceae	<i>Rosulabryum</i> sp.	Ephemeral	Urban forest	<i>Elaeis guineensis</i>
102	7.492	4.585	272	Nigeria	Pottiaceae	<i>Barbula</i> sp.	Ephemeral	Urban garden	<i>Musa</i> sp.
103	7.616	4.414	272	Nigeria	Stereophyllaceae	<i>Stereophyllum</i> sp.	Perennial	Wet forest	<i>Elaeis guineensis</i>
104	7.615	4.385	276	Nigeria	Stereophyllaceae	<i>Stereophyllum</i> sp.	Perennial	Wet forest	<i>Elaeis guineensis</i>
105	28.296	-81.0404	24	USA	Bryaceae	<i>Leucobryum</i> sp.	Perennial	Wet forest	<i>Pinus palustris</i>
106	28.040376	-81.96656	63	USA	Bryaceae	<i>Leucobryum</i> sp.	Perennial	Urban forest	<i>Ficus macrophylla</i>
107	27.4712	-81.5303	43	USA	Bryaceae	<i>Leucobryum</i> sp.	Perennial	Wet forest	<i>Quercus virginiana</i>
108	27.483416	-81.42115	39	USA	Bryaceae	<i>Leucobryum</i> sp.	Perennial	Urban forest	<i>Quercus virginiana</i>
109	26.9093	-82.0678	4	USA	Bryaceae	<i>Leucobryum</i> sp.	Perennial	Wet forest	<i>Pinus elliotii</i>

110	26.9335	-82.0562	5	USA	Bryaceae	<i>Leucobryum</i> sp.	Perennial	Urban forest	<i>Pinus pinea</i>
111	37.201074	-5.844497	41	Spain	Pottiaceae	<i>Didymodon</i> sp.	Ephemeral	Mediterranean forest	<i>Pinus pinea</i>
112	37.192943	-5.766639	60	Spain	Pottiaceae	<i>Tortula</i> sp.	Ephemeral	Urban forest	<i>Citrus</i> sp.
113	40.095551	-8.493462	176	Portugal	Polytrichaceae	<i>Polytrichum</i> sp.	Perennial	Mediterranean forest	<i>Pinus pinaster</i>
114	40.20521	-8.420558	74	Portugal	Pottiaceae	<i>Barbula</i> sp.	Ephemeral	Urban forest	<i>Tilia europaea</i>
115	41.15715	-8.48495	196	Portugal	Polytrichaceae	<i>Polytrichum commune</i>	Perennial	Mediterranean forest	<i>Quercus suber</i>
116	41.1672	-8.679033	22	Portugal	Polytrichaceae	<i>Polytrichum commune</i>	Perennial	Urban forest	<i>Arce</i> sp.
117	31.751981	35.129151	612	Israel	Brachytheciaceae	<i>Camptothecium aureum</i>	Perennial	Prairie	<i>Cistus creticus</i>
118	31.770055	35.223453	786	Israel	Bryaceae	<i>Bryum caespiticium</i>	Ephemeral	Urban forest	<i>Olea europaea</i>
119	31.24933	34.741503	234	Israel	Pottiaceae	<i>Crossidium crassinerve</i> var. <i>loevipilum</i>	Annual	Desert	<i>Noaea mucronata</i>
120	31.234653	34.792731	264	Israel	Pottiaceae	<i>Crossidium crassinerve</i> var. <i>loevipilum</i>	Annual	Urban forest	<i>Eucalyptus camandulensis</i>
121	31.27107	34.650329	183	Israel	Pottiaceae	<i>Crossidium crassinerve</i> var. <i>loevipilum</i>	Annual	Desert	<i>Noaea mucronata</i>
122	31.309503	34.63066	152	Israel	Pottiaceae	<i>Aloina bifrons</i>	Ephemeral	Urban forest	<i>Atriplex halimus</i>
123	37.185032	-5.756612	59	Spain	Bryaceae	<i>Bryum</i> sp.	Ephemeral	Mediterranean forest	<i>Olea europaea</i>

Supplementary Table 3. Predictors used in Structural Equation Modeling

Predictor group	Predictor	Units
Space	Average spatial dissimilarity	Average between-site Euclidean distance based on latitude, longitude (sine) and longitude (cosine; decimal degrees)
	Elevation	m
Vascular plants	Vascular plant cover	%
	Vascular plant richness	Number of perennial plant species
	NPP	Landsat NDVI (30m resolution)
	Forest	Forest = 1; Others = 0
	Mean annual temperature (MAT)	°C
Climate	Mean annual precipitation (MAP)	mm
	Temperature seasonality (TSEA)	Standard deviation ×100
	Precipitation seasonality (PSEA)	Coefficient of Variation
	Diurnal temperature range (MDR)	Mean of monthly (max temp - min temp)
	Potential evapotranspiration (PET)	mm day ⁻¹
	Plot-level soil organic carbon	%
	Plot-level soil C:N ratio	unitless
Soil	Plot-level soil sand content	%
	Plot-level soil pH	unitless
	Plot-level salinity	Electrical conductivity; µS/cm
	Urban greenspaces vs. natural ecosystems	Urban greenspaces =1; natural ecosystems = 0
	Land use type	

Supplementary Table 4. Rationale for selecting specific ecosystem services.

Ecosystem services	<i>Rationale</i>
C sequestration	The content of total soil organic carbon content is fundamental for supporting soil fertility, water and climate regulation, and organic matter decomposition. By supporting greater contents of carbon, soils provide a fundamental service to humankind in the fight against climate change.
Nutrient cycling	The content of multiple nutrients is critical for supporting the productivity of plants and microbes in terrestrial ecosystems, supporting the entire ecosystem food web and ecological network.
OM decomposition	OM decomposition is a fundamental soil process supporting the re-entrance of available nutrients and carbon to the soil system from plant, animal and microbial detritus.
Microbial habitat	Microbial biomass provides an indicator of soil biota biomass, and therefore of the capacity of soils to support microbial life and habitats. Soil microbial biomass is also indirectly associated and important for supporting other ecosystem services such as carbon sequestration and nutrient cycling.
Plant-soil mutualism	Plant-soil mutualistic relationships such as those supported by arbuscular mycorrhizal (AMF) fungi are essential for supporting the network of interactions in terrestrial ecosystems, and the multiple benefits for plants and microbes through carbon, nutrient and water exchange that keep terrestrial ecosystems running. AMF biomass is also indirectly associated with microbial habitat, and with other ecosystem services such as carbon and nutrient cycling.
ARG control	Antibiotic resistance genes (ARGs) are associated with the natural capacity of bacteria to override the attack of other soil microbes that use antimicrobial components to compete for resources (e.g., space, nutrients or water). Soil ARGs have also the potential to influence human health, and many natural ARGs are known to pass to human pathogens. Identifying the drivers of ARGs in the soil system is essential to better understand the distribution of these important microbial traits.
Pest control	Soil-borne potential plant pathogens can largely impact the productivity of terrestrial ecosystems by providing a reservoir of important pathogens that can potentially attack plants under certain environmental contexts (e.g., droughts). Identifying the drivers of soil-borne fungal plant pathogens is critical to forecast potential pests.
Soil biodiversity preservation	Soil biodiversity constitutes one of the largest portions of the biodiversity of the planet, and has been proven to deliver multiple ecosystem functions.

Supplementary Table 5. Soil attributes considered in this study.

Ecosystem services	Soil attribute	Specific soil variable
C sequestration	Soil C	Soil total organic carbon content
Nutrient cycling	Soil N	Soil total nitrogen content
	Soil P	Soil total phosphorus content
	Soil Fe	Soil iron content
	Soil K	Soil potassium content
	Soil Zn	Soil zinc content
	Soil Mn	Soil manganese content
	Soil Mg	Soil magnesium content
	Soil Cu	Soil copper content
OM decomposition	Glucose respiration	Soil respiration in response to glucose addition
	Lignin respiration	Soil respiration in response to lignin addition
	Soil respiration	Soil basal respiration
	Starch degradation	Activity of β -glucosidase
	Chitin degradation	Activity of N-acetylglucosaminidase
	P mineralization	Activity of phosphatase
Microbial habitat	Fungal biomass	Biomass of fungi
	Bacterial biomass	Biomass of bacteria
Plant-soil mutualism	AMF biomass	Biomass of arbuscular mycorrhizal fungi
ARG control	ARG control	Inverse of antibiotic resistance gene abundance
Pest control	Plant pathogen control	Inverse of the proportion of soil-borne potential fungal plant pathogens
Soil biodiversity preservation	Richness of fungi	Diversity of fungi
	Richness of bacteria	Diversity of bacteria
	Richness of protists	Diversity of protists
	Richness of invertebrates	Diversity of invertebrates

Supplementary Table 6. Correlations among moss, vascular plants and services.

Supplementary Table 6. Correlations between the contribution of moss and vascular plants to ecosystem services. This table includes Spearman correlations of the contribution of moss and vascular plants to nature (average of all moss and vascular plant RII), and also between the relative interaction indices (RII) of soil mosses and vascular plants on 24 individual soil attributes.

Ecosystem service	Soil attribute	Spearman ρ	P value
Multiservices	Multiservices	0.442	<0.001
C sequestration	Soil C	0.372	<0.001
Nutrient cycling	Soil N	0.445	<0.001
	Soil P	0.290	0.001
	Soil Fe	0.397	<0.001
	Soil K	0.469	<0.001
	Soil Zn	0.323	<0.001
	Soil Mn	0.342	<0.001
	Soil Mg	0.329	<0.001
	Soil Cu	0.393	<0.001
OM decomposition	Glucose respiration	0.407	<0.001
	Lignin respiration	0.426	<0.001
	Soil respiration	0.456	<0.001
	Starch degradation	0.451	<0.001
	Chitin degradation	0.383	<0.001
	P mineralization	0.509	<0.001
Microbial habitat	Fungal biomass	0.337	<0.001
	Bacterial biomass	0.435	<0.001
Plant-soil mutualism	AMF biomass	0.460	<0.001
ARG control	ARG control	0.439	<0.001
Pest control	Plant pathogen control	0.467	<0.001
Soil biodiversity preservation	Richness of fungi	0.518	<0.001
	Richness of bacteria	0.435	<0.001
	Richness of protists	0.368	<0.001
	Richness of invertebrates	0.339	0.001

Supplementary Table 7. Predictors in the Random Forest and Spearman correlations

Refers to Fig. 4 in the main text

Predictor group	Predictor	Units
Space	Average spatial dissimilarity	Average between-site Euclidean distance based on latitude, longitude (sine) and longitude (cosine; decimal degrees)
	Elevation	m
Vegetation	Vascular plant cover	%
	Vascular plant richness	Number of perennial plant species
	NPP	Landsat NDVI (30m resolution)
	Forest	Forest = 1; Others = 0
	Urban greenspaces vs. natural ecosystems	Urban greenspaces =1; natural ecosystems = 0
	Mean annual temperature (MAT)	°C
Climate	Mean annual precipitation (MAP)	mm
	Temperature seasonality (TSEA)	Standard deviation ×100
	Precipitation seasonality (PSEA)	Coefficient of Variation
	Diurnal temperature range (MDR)	Mean of monthly (max temp - min temp)
	Potential evapotranspiration (PET)	mm day ⁻¹
Soil	Plot-level soil organic carbon	%
	Plot-level soil C:N ratio	unitless
	Plot-level soil sand content	%
	Plot-level soil pH	unitless
	Plot-level salinity	Electrical conductivity; µS/cm
Moss	Moss cover	%
	Acrocarpus	Acrocarpus = 1; Pleurocarpus = 0
	Life history	Annual = 1; Ephemeral = 2; Perennial = 3
	Growth strategy	k-selected = 0; r-selected = 1
	Mat	Mat = 1; others = 0
	Turf	Turf = 1; others = 0
	Cushion	Cushion = 1; others = 0
	Funariaceae	Funariaceae = 1; others = 0
	Brachytheciaceae	Brachytheciaceae = 1; others = 0
	Pottiaceae	Pottiaceae = 1; others = 0
	Bryaceae	Bryaceae = 1; others = 0

Supplementary Table 8. SEM correlations within group categories. MAT: mean annual temperature, MAP: mean annual precipitation, PSEA: seasonal precipitation, TSEA: seasonal temperature, MDR: mean diurnal temperature range, NPP: net primary productivity, Prich: Vascular plant richness, Pcov: Vascular plant cover, C: soil carbon, C:N: soil C:N ratio.

Refers to Fig. 2B in the main text

Variables			Correlation	P-value
MDR	↔	PET	0.500	0.001
MAT	↔	PET	0.788	0.001
C	↔	C:N	0.517	0.001
MAT	↔	MAP	0.369	0.002
MAP	↔	TSEA	-0.481	0.002
MAT	↔	TSEA	-0.745	0.002
TSEA	↔	PET	-0.387	0.002
pH	↔	C	-0.369	0.002
C	↔	Salinity	0.353	0.002
Salinity	↔	Sand	-0.245	0.003
C	↔	Sand	-0.399	0.003
MAP	↔	MDR	-0.256	0.004
Forest	↔	NPP	0.360	0.006
Pcov	↔	NPP	0.280	0.010
pH	↔	C:N	-0.208	0.036

502 **Supplementary Table 9. List of antibiotic resistance genes.**

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Gene Name	Type	Gene Classification	Resistance Mechanism	Forward Primer	Reverse Primer
16S rRNA	16S rRNA	16S rRNA	Internal control	GGGTTGCGCTCGTTGC	ATGGYTGTCGTCAGCTCGTG
catB3	ARG	FCA	deactivate	GCACTCGATGCCTTCCAAAA	AGAGCCGATCCAAACGTCAT
catB8	ARG	FCA	deactivate	CACTCGACGCCTTCCAAAG	CCGAGCCTATCCAGACATCATT
cfr	ARG	FCA	deactivate	GCAAAATTCAGAGCAAGTTACGAA	AAAATGACTCCCAACCTGCTTTAT
floR	ARG	FCA	efflux	ATTGTCTTCACGGTGTCCGTTA	CCGCGATGTCGTCGAACT
cmlA1-01	ARG	FCA	efflux	TAGGAAGCATCGGAACGTTGAT	CAGACCGAGCACGACTGTTG
cmlA1-02	ARG	FCA	efflux	AGGAAGCATCGGAACGTTGA	ACAGACCGAGCACGACTGTTG
cmx(A)	ARG	FCA	efflux	GCGATCGCCATCCTCTGT	TCGACACGGAGCCTTGGT
catA1	ARG	FCA	deactivate	GGGTGAGTTTCACCAGTTTTGATT	CACCTTGTCGCCTTGCGTATA
qnrA	ARG	FCA	unknown	AGGATTTCTCACGCCAGGATT	CCGCTTTCATGAAACTGCAA
aac	ARG	Aminoglycoside	deactivate	CCCTGCGTTGTGGCTATGT	TTGGCCACGCCAATCC
aacC1	ARG	Aminoglycoside	deactivate	GGTCGTGAGTTCGGAGACGTA	GCAAGTTCCCGAGGTAATCG
aacC2	ARG	Aminoglycoside	deactivate	ACGGCATTCTCGATTGCTTT	CCGAGCTTCACGTAAGCATTT
aacC4	ARG	Aminoglycoside	deactivate	CGGCGTGCGGACACGAT	AGGGAACCTTTGCCATCAACT
aac(6')I1	ARG	Aminoglycoside	deactivate	GACCGGATTAAGGCCGATG	CTTGCCCTTGATATTCAGTTTTTATAAC CA
aacA/aphD	ARG	Aminoglycoside	deactivate	AGAGCCTTGGAAGATGAAGTTT	TTGATCCATACCATAGACTATCTCATC A
aac(6')-Iy	ARG	Aminoglycoside	deactivate	GCTTTGCGGATGCCTCAAT	GGAGAACAAAAATACCTTCAAGGAA A
aac(6')-II	ARG	Aminoglycoside	deactivate	CGACCCGACTCCGAACAA	GCACGAATCCTGCCTTCTCA
aacC	ARG	Aminoglycoside	deactivate	CGTCACTTATTCGATGCCCTTAC	GTCGGGCGCGGCATA
aac(6')-Ib-01	ARG	Aminoglycoside	deactivate	GTTTGAGAGGCAAGGTACCGTAA	GAATGCCTGGCGTGTTTGA

aac(6')-Ib-02	ARG	Aminoglycoside	deactivate	CGTCGCCGAGCAACTTG	CGGTACCTTGCCTCTCAAACC
aadA5-01	ARG	Aminoglycoside	deactivate	ATCACGATCTTGCGATTTTGCT	CTGCGGATGGGCCTAGAAG
aadA5-02	ARG	Aminoglycoside	deactivate	GTTCTTGCTCTTGCTCGCATT	GATGCTCGGCAGGCAAAC
aac(6')-Ib-03	ARG	Aminoglycoside	deactivate	AGAAGCACGCCCCGACACTT	GCTCTCCATTTCAGCATTGCA
aadA1	ARG	Aminoglycoside	deactivate	AGCTAAGCGCGAACTGCAAT	TGGCTCGAAGATACCTGCAA
aadA2-01	ARG	Aminoglycoside	deactivate	ACGGCTCCGCAGTGGAT	GGCCACAGTAACCAACAAATCA
aadA-01	ARG	Aminoglycoside	deactivate	GTTGTGCACGACGACATCATT	GGCTCGAAGATACCTGCAAGAA
aadA2-02	ARG	Aminoglycoside	deactivate	CTTGTCGTGCATGACGACATC	TCGAAGATACCCGCAAGAATG
aadD	ARG	Aminoglycoside	deactivate	CCGACAACATTTCTACCATCCTT	ACCGAAGCGCTCGTCGTATA
aadA2-03	ARG	Aminoglycoside	deactivate	CAATGACATTCTTGCGGGTATC	GACCTACCAAGGCAACGCTATG
aadA9-01	ARG	Aminoglycoside	deactivate	CGCGGCAAGCCTATCTTG	CAAATCAGCGACCGCAGACT
aadA-02	ARG	Aminoglycoside	deactivate	CGAGATTCTCCGCGCTGTA	GCTGCCATTCTCCAAATTGC
aadA9-02	ARG	Aminoglycoside	deactivate	GGATGCACGCTTGGATGAA	CCTCTAGCGGCCGGAGTATT
aadE	ARG	Aminoglycoside	deactivate	TACCTTATTGCCCTTGGAAGAGTTA	GGAACATGTCCCTTTTAATTCTACAA TCT
spcN-01	ARG	Aminoglycoside	deactivate	AAAAGTTTCGATGAAACACGCCTAT	TCCAGTGGTAGTCCCCGAATC
spcN-02	ARG	Aminoglycoside	deactivate	CAGAATCTTCCTGAAAAGTTTGATG AA	CGCAGACACGCCGAATC
aadA-1-01	ARG	Aminoglycoside	deactivate	AAAAGCCCCGAAGAGGAACTTG	CATCTTTCACAAAGATGTTGCTGTCT
aph6ia	ARG	Aminoglycoside	deactivate	CCCATCCCATGTGTAAGGAAA	GCCACCGCTTCTGCTGTAC
aph(2')-Id-02	ARG	Aminoglycoside	deactivate	TGAGCAGTATCATAAGTTGAGTGAA AAG	GACAGAACAATCAATCTCTATGGAAT G
aph(2')-Id-01	ARG	Aminoglycoside	deactivate	TAAGGATATACCGACAGTTTTGGAA A	TTTAATCCCTCTTCATACCAATCCATA
aph	ARG	Aminoglycoside	deactivate	TTTCAGCAAGTGGATCATGTAAAA T	CCAAGCTGTTTCCACTGTTTTTC
aphA1	ARG	Aminoglycoside	deactivate	TGAACAAGTCTGGAAAGAAATGCA	CCTATTAATTTCCCTCGTCAAAAA
aadA-1-02	ARG	Aminoglycoside	deactivate	CGGAATTGAAAAAACTGATCGAA	ATACCGGCTGTCCGTCATTT

str	ARG	Aminoglycoside	deactivate	AATGAGTTTTGGAGTGTCTCAACGT A	AATCAAAACCCCTATTAAAGCCAAT
strA	ARG	Aminoglycoside	deactivate	CCGGTGGCATTGAGAAAAA	GTGGCTCAACCTGCGAAAAG
strB	ARG	Aminoglycoside	deactivate	GCTCGGTCGTGAGAACAATCT	CAATTTTCGGTCGCCTGGTAGT
ampC-01	ARG	Beta Lactamase	deactivate	TGGCGTATCGGGTCAATGT	CTCCACGGGCCAGTTGAG
ampC-02	ARG	Beta Lactamase	deactivate	GCAGCACGCCCCGTAA	TGTACCCATGATGCGCGTACT
ampC-04	ARG	Beta Lactamase	deactivate	TCCGGTGACGCGACAGA CTGTTTCGAGCTGGGTTCTATAAGTA AA	CAGCACGCCGGTGAAAGT CAGTATCTGGTCACCGGATCGT
ampC-05	ARG	Beta Lactamase	deactivate	CCGCTCAAGCTGGACCATAC	CCATATCCTGCACGTTGGTTT
ampC-06	ARG	Beta Lactamase	deactivate	CCGCCAGAGCAAGGACTA	GCTCGACTTCACGCCGTAAG
ampC-07	ARG	Beta Lactamase	deactivate	CAGCCGCTGATGAAAAAATATG	CAGCGAGCCCACTTCGA
ampC-09	ARG	Beta Lactamase	deactivate	TGGCCGCAGCAGAAAGA	CCGTTTTATGCACCCAGGAA TACCAGTATCAATCGCATATACACCT AA
ampC/blaDHA	ARG	Beta Lactamase	deactivate	GCAAGTTGAAGCGAAAGAAAAGA	AATAAACGCGATGGGTTCCA
bla1	ARG	Beta Lactamase	deactivate	CACACAGCTGATGGCTTATCTAAAA	GCCACTGTTTGCCTGTCAGTT
bla-ACC-1	ARG	Beta Lactamase	deactivate	CCGCGGCGAAATTAAGC	ATAGCTTTTGTGGCCAGCATCA
blaCMY	ARG	Beta Lactamase	deactivate	AAAGCCTCAT GGGTGCATAAA	CGGATGGGCTTGTCTCTT
blaCMY2-01	ARG	Beta Lactamase	deactivate	GCGAGCAGCCTGAAGCA	TTCAGTGCATCCAGACGAA ATCGGATTATAGTTAACCAGGTCAGA TTT
blaCMY2-02	ARG	Beta Lactamase	deactivate	GGAGGCGTGACGGCTTTT	GCATTGCCCAACGTCAGATT
blaCTX-M-01	ARG	Beta Lactamase	deactivate	GCCGCGGTGCTGAAGA	CGTTCATCGGCACGGTAGA
blaCTX-M-02	ARG	Beta Lactamase	deactivate	CGATACCACCACGCCGTTA	GTCGAGACGGAACGTTTCGT
blaCTX-M-03	ARG	Beta Lactamase	deactivate	CTTGCGGTTGCGCTGAT	CTCCGCTGCCGGTTTTATC
blaCTX-M-04	ARG	Beta Lactamase	deactivate	GCGATAACGTGGCGATGAAT	GTGCCTGAGTCAATTCTTTCAAAG
blaCTX-M-05	ARG	Beta Lactamase	deactivate	CACAGTTGGTGACGTGGCTTAA	
blaCTX-M-06	ARG	Beta Lactamase	deactivate	GCAATGTGCTCAACGTTCAAG	
blaGES	ARG	Beta Lactamase	deactivate		

blaIMP-01	ARG	Beta Lactamase	deactivate	AACACGGTTTGGTGGTTCTTGTA	GCGCTCCACAAACCAATTG
blaIMP-02	ARG	Beta Lactamase	deactivate	AAGGCAGCATTTTCCTCTCATTTT	GGATAGATCGAGAATTAAGCCACTCT
bla-L1	ARG	Beta Lactamase	deactivate	CACCGGGTTACCAGCTGAAG	GCGAAGCTGCGCTTGTAAGTC
blaMOX/blaCMY	ARG	Beta Lactamase	deactivate	CTATGTCAATGTGCCGAAGCA	GGCTTGTCCTCTTTCGAATAGC
blaOCH	ARG	Beta Lactamase	deactivate	GGCGACTTGCGCCGTAT	TTTTCTGCTCGGCCATGAG
blaOKP	ARG	Beta Lactamase	deactivate	GCCGCCATCACCATGAG	GGTGACGTTGTCACCGATCTG
blaOXA1/blaOXA30	ARG	Beta Lactamase	deactivate	CGGATGGTTTGAAGGGTTTATTAT	TCTTGGCTTTTATGCTTGATGTTAA
blaOXA10-01	ARG	Beta Lactamase	deactivate	CGCAATTATCGGCCTAGAACT	TTGGCTTTCCGTCCCATT
blaOXA10-02	ARG	Beta Lactamase	deactivate	CGCAATTATCGGCCTAGAACT	TTGGCTTTCCGTCCCATT
blaOXY	ARG	Beta Lactamase	deactivate	CGTTCAGGCGGCAGGTT	GCCGCGATATAAGATTTGAGAATT
blaPAO	ARG	Beta Lactamase	deactivate	CGCCGTACAACCGGTGAT	GAAGTAATGCGGTTCTCCTTTCA
blaPER	ARG	Beta Lactamase	deactivate	TGCTGGTTGCTGTTTTTGTGA	CCTGCGCAATGATAGCTTCAT
blaPSE	ARG	Beta Lactamase	deactivate	TTGTGACCTATTCCCTGTAAATAGA A	TGCGAAGCACGCATCATC
blaROB	ARG	Beta Lactamase	deactivate	GCAAAGGCATGACGATTGC	CGCGCTGTTGTCGCTAAA
blaSFO	ARG	Beta Lactamase	deactivate	CCGCCGCCATCCAGTA	GGGCCGCCAAGATGCT
blaSHV-01	ARG	Beta Lactamase	deactivate	TCCCATGATGAGCACCTTTAAA	TTCGTCACCGGCATCCA
blaSHV-02	ARG	Beta Lactamase	deactivate	CTTTCCCATGATGAGCACCTTT	TCCTGCTGGCGATAGTGGAT
blaTEM	ARG	Beta Lactamase	deactivate	AGCATCTTACGGATGGCATGA	TCCTCCGATCGTTGTCAGAAGT
blaTLA	ARG	Beta Lactamase	deactivate	ACACTTTGCCATTGCTGTTTATGT	TGCAAATTTTCGGCAATAATCTTT GAAAGATTCCCTTTATCTATCTCAGAC AA
blaVEB	ARG	Beta Lactamase	deactivate	CCCGATGCAAAGCGTTATG	
blaVIM	ARG	Beta Lactamase	deactivate	GCACTTCTCGCGGAGATTG	CGACGGTGATGCGTACGTT
blaZ	ARG	Beta Lactamase	deactivate	GGAGATAAAGTAACAAATCCAGTTA GATATGA	TGCTTAATTTTCCATTTGCGATAAG
cepA	ARG	Beta Lactamase	deactivate	AGTTGCGCAGAACAGTCCTCTT	TCGTATCTTGCCCGTCGATAAT

cfiA	ARG	Beta Lactamase	deactivate	GCAGCGTTGCTGGACACA	GTTCCGGGATAAACGTGGTGACT
cfxA	ARG	Beta Lactamase	deactivate	TCATTCCTCGTTCAAGTTTTTCAGA	TGCAGCACCAAGAGGAGATGT
cphA-01	ARG	Beta Lactamase	deactivate	GCGAGCTGCACAAGCTGAT	CGGCCCAGTCGCTCTTC
cphA-02	ARG	Beta Lactamase	deactivate	GTGCTGATGGCGAGTTTCTG	GGTGTGGTAGTTGGTGTTGATCAC
fox5	ARG	Beta Lactamase	deactivate	GGTTTGCCGCTGCAGTTC	GCGGCCAGGTGACCAA
mecA	ARG	Beta Lactamase	protection	GGTTACGGACAAGGTGAAATACTGA T	TGTCTTTTAATAAGTGAGGTGCGTTA ATA
NDM1	ARG	Beta Lactamase	deactivate	ATTAGCCGCTGCATTGAT	CATGTCTGAGATAGGAAGTG
pbp	ARG	Beta Lactamase	protection	CCGGTGCCATTGGTTTAGA	AAAATAGCCGCCCAAGATT
pbp2x	ARG	Beta Lactamase	protection	TTTCATAAGTATCTGGACATGGAAG AA	CCAAAGGAACTTGCTTGAGATTAG
Pbp5	ARG	Beta Lactamase	protection	GGCGAACTTCTAATTAATCCTATCC A	CGCCGATGACATTCTTCTTATCTT
penA	ARG	Beta Lactamase	protection	AGACGGTAACGTATAACTTTTTTGAA AGA	GCGTGTAGCCGGCAATG
carB	ARG	MLSB	efflux	GGAGTGAGGCTGACCGTAGAAG	ATCGGCGAAACGCACAAA
ereA	ARG	MLSB	deactivate	CCTGTGGTACGGAGAATTCATGT	ACCGCATTGCTTTTGCTT
ereB	ARG	MLSB	deactivate	GCTTTATTTTCAGGAGGCGGAAT	TTTTAAATGCCACAGCACAGAATC
erm(34)	ARG	MLSB	protection	GCGCGTTGACGACGATTT	TGGTCATACTCGACGGCTAGAAC TCTATAATCACAATAACCACTTGAA CGT
erm(35)	ARG	MLSB	protection	TTGAAAACGATGTTGCATTAAGTCA	
erm(36)	ARG	MLSB	protection	GGCGGACCGACTTG CAT	TCTGCGTTGACGACGGTTAC ATATCCATCTCCACCATTAATAGTAA ACC
ermA	ARG	MLSB	protection	TTGAGAAGGGATTTGCGAAAAG	
ermA/ermTR	ARG	MLSB	protection	ACATTTTACCAAGGAAC TTGTGGAA	GTGGCATGACATAAACCTTCATCA TTTATACCTCTGTTTGTAGGGAATTG AA
ermB	ARG	MLSB	protection	TAAAGGGCATT TAACGACGAAACT	
ermC	ARG	MLSB	protection	TTTGAAATCGGCTCAGGAAAA	ATGGTCTATTTCAATGGCAGTTACG
ermF	ARG	MLSB	protection	CAGCTTTGGTTGAACATTTACGAA	AAATTCCTAAAATCACAACCGACAA

ermJ/ermD	ARG	MLSB	protection	GGA	CTCGGCAATGGTCAGAA	CCCCGAAACGCAATATAATGTT
ermK-01	ARG	MLSB	protection	GTTTGATATTGGCATTGT	CAGAGAA	ACCATTGCCGAGTCCACTTT
ermK-02	ARG	MLSB	protection	GAGCCGCAAGCCCCTTT		GTGTTTCATTGACGCGGAGTAA
ermT-01	ARG	MLSB	protection	GTTCACTAGCACTATTTT	AATGAC	GAAGGGTGTCTTTTAA
ermT-02	ARG	MLSB	protection	GTAAAATCCCTAGAGA	AATACTTTCA	TGAGTGATATTTTGAAGGGTGTCTT
ermX	ARG	MLSB	protection	GCTCAGTGGTCCCCATGGT		ATCCCCCGTCAACGTTT
ermY	ARG	MLSB	protection	TTGTCTTTGAAAGTGAAGCAACAGT		TAACGCTAGAGAACGATTTGTATTGA
lmrA-01	ARG	MLSB	efflux	TCGACGTGACCGTAGTGAACA		CGTGACTACCCAGGTGAGTTGA
lnuA-01	ARG	MLSB	deactivate	TGACGCTCAACACACTCAAAAA		TTCATGCTTAAGTTCCATACGTGAA
lnuB-01	ARG	MLSB	deactivate	TGAACATAATCCCCTCGTTTAAAGA		TAATTGCCCTGTTTCATCGTAAATAA
lnuB-02	ARG	MLSB	deactivate	AAAGGAGAAGGTGACCAATACTCT		GGAGCTACGTCAAACAACCAGTT
lnuC	ARG	MLSB	deactivate	TGGTCAATATAACAGATGTAAACCA		CACCCCAGCCACCATCAA
matA/mel	ARG	MLSB	efflux	TAGTAGGCAAGCTCGGTGTTGA		CCTGTGCTATTTTAAGCCTTGTTTCT
mdtA	ARG	MLSB	efflux	CCTAACGGGCGTGACTTCA		TTCACCTGTTTCAAGGGTCAAA
mefA	ARG	MLSB	efflux	CCGTAGCATTGGAACAGCTTTT		AAACGGAGTATAAGAGTGCTGCAA
mphA-01	ARG	MLSB	deactivate	CTGACGCGCTCCGTGTT		GGTGGTGCATGGCGATCT
mphA-02	ARG	MLSB	deactivate	TGATGACCCTGCCATCGA		TTCGCGAGCCCCTCTTC
mphB	ARG	MLSB	deactivate	CGCAGCGCTTGATCTTGTAG		TTACTGCATCCATACGCTGCTT
mphC	ARG	MLSB	deactivate	CGTTTGAAGTACCGAATTGGAAA		GCTGCGGGTTTGCCTGTA
msrA-01	ARG	MLSB	efflux	CTGCTAACACAAGTACGATTCCAAA		TCAAGTAAAGTTGTCTTACCTACACC
msrC-01	ARG	MLSB	efflux	TCAGACCGGATCGGTTGTC		CCTATTTTTTGGAGTCTTCTCTCTAAT

oleC	ARG	MLSB	efflux	CCCGGAGTCGATGTTCTGA	GCCGAAGACGTACACGAACAG
pikR1	ARG	MLSB	protection	TCGACATGCGTGACGAGATT	CCGCGAATTAGGCCAGAA
pikR2	ARG	MLSB	protection	TCGTGGGCCAGGTGAAGA	TTCCCCTTGCCGGTGAA
vatB-01	ARG	MLSB	deactivate	GGAAAAAGCAACTCCATCTCTTGA	TCCTGGCATAACAGTAACATTCTGA
vatB-02	ARG	MLSB	deactivate	TTGGGAAAAAGCAACTCCATCT	CAATCCACACATCATTTCCAACA
vatC-01	ARG	MLSB	deactivate	CGGAAATTGGGAACGATGTT	GCAATAATAGCCCCGTTTCCTA
vatC-02	ARG	MLSB	deactivate	CGATGTTTGGATTGGACGAGAT	GCTGCAATAATAGCCCCGTTT
vatE-01	ARG	MLSB	deactivate	GGTGCCATTATCGGAGCAAAT	TTGGATTGCCACCGACAAT
vatE-02	ARG	MLSB	deactivate	GACCGTCTACCAGGCGTAA	TTGGATTGCCACCGACAATT
vgaA-01	ARG	MLSB	efflux	CGAGTATTGTGGAAAGCAGCTAGTT	CCCGTACCGTTAGAGCCGATA
vgaA-02	ARG	MLSB	efflux	GACGGGTATTGTGGAAAGCAA	TTTCCTGTACCATTAGATCCGATAATT
vgb-01	ARG	MLSB	deactivate	AGGGAGGGTATCCATGCAGAT	ACCAAATGCGCCCGTTT
vgbB-01	ARG	MLSB	efflux	CAGCCGGATTCTGGTCCTT	TACGATCTCCATTCAATTGGGTAAA
vgbB-02	ARG	MLSB	deactivate	ATACGAGCTGCCTAATAAAGGATCT T	TGTGAACCACAGGGCATTATCA
sul2	ARG	Sulfonamide	protection	TCATCTGCCAAACTCGTCGTTA	GTCAAAGAACGCCGCAATGT
sul1	ARG	Sulfonamide	protection	CAGCGCTATGCGCTCAAG	ATCCCGCTGCGCTGAGT
sulA/foIP-01	ARG	Sulfonamide	protection	CAGGCTCGTAAATTGATAGCAGAAG	CTTTCCTTGCGAATCGCTTT
sulA/foIP-03	ARG	Sulfonamide	protection	CACGGCTTCGGCTCATGT	TGCCATCCTGTGACTAGCTACGT
dfrA1	ARG	Sulfonamide	deactivate	GGAATGGCCCTGATATTCCA	AGTCTTGCGTCCAACCAACAG
dfrA12	ARG	Sulfonamide	deactivate	CCTCTACCGAACCGTCACACA	GCGACAGCGTTGAAACAACACTAC
folA	ARG	Sulfonamide	deactivate	CGAGCAGTTCTGCCAAAG	CCCAGTCATCCGGTTCATAATC
tet(32)	ARG	Tetracycline	protection	CCATTACTTCGGACAACGGTAGA	CAATCTCTGTGAGGGCATTTAACA
tet(34)	ARG	Tetracycline	unknown	CTTAGCGCAAACAGCAATCAGT	CGGTGATACAGCGCGTAAACT
tet(35)	ARG	Tetracycline	unknown	ACCCCATGACGTACCTGTAGAGA	CAACCCACACTGGCTACCAAGTT

tet(36)-01	ARG	Tetracycline	protection	AGAATACTCAGCAGAGGTTCAGTTCC T	TGGTAGGTCGATAACCCGAAAAT
tet(36)-02	ARG	Tetracycline	protection	TGCAGGAAAGACCTCCATTACAG	CTTTGTCCACACTTCCACGTACTATG
tet(37)	ARG	Tetracycline	unknown	GAGAACGTTGAAAAGGTGGTGAA	AACCAAGCCTGGATCAGTCTCA
tetA-01	ARG	Tetracycline	efflux	GCTGTTTGTCTGCCGAAA	GGTTAAGTTCCTTGAACGCAAACT
tetA-02	ARG	Tetracycline	efflux	CTCACCAGCCTGACCTCGAT	CACGTTGTTATAGAAGCCGCATAG
tetB-01	ARG	Tetracycline	efflux	AGTGCGCTTTGGATGCTGTA	AGCCCCAGTAGCTCCTGTGA
tetB-02	ARG	Tetracycline	efflux	GCCCAGTGCTGTTGTTGTCAT	TGAAAGCAAACGGCCTAAATACA
tetC-01	ARG	Tetracycline	efflux	CATATCGCAATACATGCGAAAAA	AAAGCCGCGGTAAATAGCAA
tetC-02	ARG	Tetracycline	efflux	ACTGGTAAGGTAAACGCCATTGTC	ATGCATAAACCAGCCATTGAGTAAG
tetD-01	ARG	Tetracycline	efflux	TGCCGCGTTTGATTACACA	CACCAGTGATCCCGGAGATAA
tetD-02	ARG	Tetracycline	efflux	TGTCATCGCGCTGGTGATT	CATCCGCTTCCGGGAGAT
tetE	ARG	Tetracycline	efflux	TTGGCGCTGTATGCAATGAT	CGACGACCTATGCGATCTGA
tetG-01	ARG	Tetracycline	efflux	TCAACCATTGCCGATTCTGA	TGGCCCGCAATCATG
tetG-02	ARG	Tetracycline	efflux	CATCAGCGCCGGTCTTATG	CCCCATGTAGCCGAACCA
tetH	ARG	Tetracycline	efflux	TTTGGGTCATCTTACCAGCATTA	TTGCGCATTATCATCGACAGA
tetJ	ARG	Tetracycline	efflux	GGGTGCCGCATTAGATTACCT	TCGTCCAATGTAGAGCATCCATA
tetK	ARG	Tetracycline	efflux	CAGCAGTCATTGGAAAATTATCTGA TTATA	CCTTGTAATAACCTACCAAAAATCAA AATA
tetL-01	ARG	Tetracycline	efflux	AGCCCGATTTATTCAAGGAATTG	CAAATGCTTTCCCCCTGTTCT
tetL-02	ARG	Tetracycline	efflux	ATGGTTGTAGTTGCGCGCTATAT	ATCGCTGGACCGACTCCTT
tetM-01	ARG	Tetracycline	protection	CATCATAGACACGCCAGGACATAT	CGCCATCTTTTGCAGAAATCA
tetM-02	ARG	Tetracycline	protection	TAATATTGGAGTTTATAGCTCATGTTG ATG	CCTCTCTGACGTTCTAAAAGCGTATTA T
tetO-01	ARG	Tetracycline	protection	ATGTGGATACTACAACGCATGAGAT T	TGCCTCCACATGATATTTTTCCT
tetPA	ARG	Tetracycline	efflux	AGTTGCAGATGTGTATAGTCGTAAA CTATCTATT	TGCTACAAGTACGAAAACAAAACCTAG AA

tetPB-01	ARG	Tetracycline	protection	ACACCTGGACACGCTGATTTT	ACCGTCTAGAACGCGGAATG
tetPB-02	ARG	Tetracycline	protection	TGATACACCTGGACACGCTGAT	CGTCCAAAACGCGGAATG
tetPB-03	ARG	Tetracycline	protection	TGGGCGACAGTAGGCTTAGAA	TGACCCCTACTGAAACATTAGAAATAT ACCT
tetPB-05	ARG	Tetracycline	protection	CTGAAGTGGAGCGATCATTCC CGCCTCAGAAGTAAGTTCATACACT	CCCTCAACGGCAGAAATAACTAA
tetQ	ARG	Tetracycline	protection	AAG	TCGTTCATGCGGATATTATCAGAAT
tetR-02	ARG	Tetracycline	efflux	CGCGATAGACGCCTTCGA	TCCTGACAACGAGCCTCCTT
tetR-03	ARG	Tetracycline	efflux	CGCGATGGAGCAAAAGTACAT TTAAGGACAACTTTCTGACGACAT	AGTGAAAAACCTTGTTGGCATAAAA
tetS	ARG	Tetracycline	protection	C	TGTCTCCCATTGTTCTGGTTCA
tetT	ARG	Tetracycline	protection	CCATATAGAGGTTCCACCAAATCC	TGACCCCTATTGGTAGTGGTTCTATTG
tetU-01	ARG	Tetracycline	unknown	GTGGCAAAGCAACGGATTG	TGCGGGCTTGCAAAACTATC
tetV	ARG	Tetracycline	efflux	GCGGGAACGACGATGTATATC	CCGCTATCTCACGACCATGAT
tetW-01	ARG	Tetracycline	protection	ATGAACATTCCCACCGTTATCTTT	ATATCGGCGGAGAGCTTATCC
tetX	ARG	Tetracycline	unknown	AAATTTGTTACCGACACGGAAGTT	CATAGCTGAAAAAATCCAGGACAGTT
vanA	ARG	Vancomycin	protection	AAAAGGCTCTGAAAACGCAGTTAT	CGGCCGTTATCTTGTA AAAACAT
vanB-01	ARG	Vancomycin	protection	TTGTCGGCGAAGTGGATCA	AGCCTTTTTCCGGCTCGTT
vanC-01	ARG	Vancomycin	protection	ACAGGGATTGGCTATGAACCAT	TGACTGGCGATGATTTGACTATG
vanC-02	ARG	Vancomycin	protection	CCTGCCACAATCGATCGTT	CGGCTTCATTCCGGCTTGATA
vanC-03	ARG	Vancomycin	protection	AAATCAATACTATGCCGGGCTTT	CCGACCGCTGCCATCA
vanC1	ARG	Vancomycin	protection	AGGCGATAGCGGGTATTGAA	CAATCGTCAATTGCTCATTTC
vanC2/vanC3	ARG	Vancomycin	protection	TTTGA CTGTCGGTGCTTGTGA ATTTGAATTGGCAGGTATACAGGTT	TCAATCGTTTCAGGCAATGG
vanG	ARG	Vancomycin	protection	A	TGATTTGTCTTTGTCCATACATAATGC
vanHB	ARG	Vancomycin	protection	GAGGTTTCCGAGGCGACAA	CTCTCGGCGGCAGTCGTAT
vanHD	ARG	Vancomycin	protection	GTGGCCGATTATACCGTCATG	CGCAGGTCATT CAGGCAAT

vanRA-01	ARG	Vancomycin	protection	CCCTTACTCCCACCGAGTTTT	TTCGTCGCCCCATATCTCAT
vanRA-02	ARG	Vancomycin	protection	CCACTCCGGCCTTGTCATT	GCTAACCACATTCCCCTTGTTTT
vanRB	ARG	Vancomycin	protection	GCCCTGTTCGGATGACGAA	TTACATAGTCGTCTGCCTCTGCAT
vanRC	ARG	Vancomycin	protection	TGCGGGAAAACTGAACGA	CCCCCATAACGGTTTTGATTA
vanRC4	ARG	Vancomycin	protection	AGTGCTTTGGCTTATCTCGAAAA	TCCGGCAGCATCACATCTAA
vanRD	ARG	Vancomycin	protection	TTATAATGGCAAGGATGCACTAAAG T	CGTCTACATCCGGAAGCATGA
vanSA	ARG	Vancomycin	protection	CGCGTCATGCTTTCAAAATTC	TCCGCAGAAAGCTCAATTTGTT
vanSB	ARG	Vancomycin	protection	GCGCGGCAAATGACAAC	TTTGCCATTTTATTCGCACTGT
vanSC-01	ARG	Vancomycin	protection	ATCAACTGCGGGAGAAAAGTCT	TCCGCTGTTCCGCTTCTT
vanSC-02	ARG	Vancomycin	protection	GCCATCAGCGAGTCTGATGA	CAGCTGGGATCGTTTTTCCTT
vanTC-01	ARG	Vancomycin	protection	CACACGCATTTTTTCCCATCTAG	CAGCCAACAGATCATCAAAACAA
vanTC-02	ARG	Vancomycin	protection	ACAGTTGCCGCTGGTGAAG	CGTGGCTGGTCGATCAAAA
vanTE	ARG	Vancomycin	protection	GTGGTGCCAAGGAAGTTGCT	CGTAGCCACCGCAAAAAAAT
vanTG	ARG	Vancomycin	protection	CGTGTAGCCGTTCCGTTCTT	CGGCATTACAGGTATATCTGGAAA AAATAGTAAATTGCTCATCTGGCACA T
vanWB	ARG	Vancomycin	protection	CGGACAAAGATACCCCCTATAAAG	
vanWG	ARG	Vancomycin	protection	ACATTTTCATTTTGGCAGCTTGAC	CCGCCATAAGAGCCTACAATCT
vanXA	ARG	Vancomycin	protection	CGCTAAATATGCCACTTGGGATA	TCAAAAGCGATTCAGCCAACCT
vanXB	ARG	Vancomycin	protection	AGGCACAAAATCGAAGATGCTT	GGGTATGGCTCATCAATCAACTT
vanXD	ARG	Vancomycin	protection	TAAACCGTGTTATGGGAACGAA	GCGATAGCCGTCCCATAAGA
vanYB	ARG	Vancomycin	protection	GGCTAAAGCGGAAGCAGAAA	GATATCCACAGCAAGACCAAGCT
vanYD-01	ARG	Vancomycin	protection	AAGGCGATACCCTGACTGTCA	ATTGCCGGACGGAAGCA
vanYD-02	ARG	Vancomycin	protection	CAAACGGAAGAGAGGTCACTTACA	CGGACGGTAATAGGGACTGTTC
acrA-01	ARG	Multidrug	efflux	CAACGATCGGACGGGTTTC	TGGCGATGCCACCGTACT

acrA-02	ARG	Multidrug	efflux	GGTCTATCACCTACGCGCTATC	GCGCGCACGAACATACC
acrA-03	ARG	Multidrug	efflux	CAGACCCGCATCGCATATT	CGACAATTCGCGCTCATG
acrA-04	ARG	Multidrug	efflux	TACTTTGCGCGCCATCTTC	CGTGCGCGAACGAACAT
acrB-01	ARG	Multidrug	efflux	AGTCGGTGTTGCGCGTTAAC	CAAGGAAACGAACGCAATACC
acrR-01	ARG	Multidrug	efflux	GCGCTGGAGACACGACAAC	GCCTTGCTGCGAGAACAAA
acrR-02	ARG	Multidrug	efflux	GATGATACCCCCTGCTGTGAGA	ACCAAACAAGAAGCGCAAGAA
adeA	ARG	Multidrug	efflux	CAGTTCGAGCGCCTATTTCTG	CGCCCTGACCGACCAAT
acrA-05	ARG	Multidrug	efflux	CGTGCGCGAACGAACA	ACTTTGCGCGCCATCTTC
acrF	ARG	Multidrug	efflux	GCGGCCAGGCACAAAA	TACGCTCTTCCCACGGTTTC
ceoA	ARG	Multidrug	efflux	ATCAACACGGACCAGGACAAG	GGAAAGTCCGCTCACGATGA
cmeA	ARG	Multidrug	efflux	GCAGCAAAGAAGAAGCACCAA	AGCAGGGTAAGTAAACTAAGTGGTA AATCT
cmr	ARG	Multidrug	efflux	CGGCATCGTCAGTGGAAAT	CGGTTCCGAAAAAGATGGAA
emrD	ARG	Multidrug	efflux	CTCAGCAGTATGGTGGTAAGCATT	ACCAGGCGCCGAAGAAC
marR-01	ARG	Multidrug	efflux	GCGGCGTACTGGTGAAGCTA	TGCCCTGGTCGTTGATGA
mdet11	ARG	Multidrug	efflux	ATACAGCAGTGGATATTGGTTTAAT TGT	TGCATAAGGTGAATGTTCCATGA
mdtE/yhiU	ARG	Multidrug	efflux	CGTCGGCGCACTCGTT	TCCAGACGTTGTACGGTAACCA
mepA	ARG	Multidrug	efflux	ATCGGTCGCTCTTCGTTTAC	ATAAATAGGATCGAGCTGCTGGAT
mexA	ARG	Multidrug	efflux	AGGACAACGCTATGCAACGAA	CCGGAAAGGGCCGAAAT
mexD	ARG	Multidrug	efflux	TTGCCACTGGCTTTCATGAG	CACTGCGGAGAACTGTCTGTAGA
mexE	ARG	Multidrug	efflux	GGTCAGCACCGACAAGGTCTAC	AGCTCGACGTAATTGAGGAACAC
mexF	ARG	Multidrug	efflux	CCGCGAGAAGGCCAAGA	TTGAGTTCGGCGGTGATGA
mtrC-01	ARG	Multidrug	efflux	GGACGGGAAGATGGTCCAA	CGTAGCGTTCGGTTCGAT

mtrC-02	ARG	Multidrug	efflux	CGGAGTCCATCGACCATTG	ATCGTCGGCAAGGAGAATCA
mtrD-02	ARG	Multidrug	efflux	GGTCGGCACGCTCTTGTC	TGAAGAATTTGCGCACCCTAC
mtrD-03	ARG	Multidrug	efflux	CCGCCAAGCCGATATAGACA	GGCCGGGTTGCCAAA
oprD	ARG	Multidrug	efflux	ATGAAGTGGAGCGCCATTG	GGCCACGGCGAACTGA
oprJ	ARG	Multidrug	efflux	ACGAGAGTGGCGTCGACAA	AAGGCGATCTCGTTGAGGAA
pmrA	ARG	Multidrug	efflux	TTTGCAGGTTTTGTTCTAATGC	GCAGAGCCTGATTCTCTCTTTG
putative multidrug	ARG	Multidrug	efflux	AATTTTGCCGATTATTGCTGAAA	GATTGTCATCATTCGTTTATCACCAA
qac	ARG	Multidrug	efflux	CAATAATAACCGAAATAATAGGGA CAAGTT	AATAAGTGTTCTAGTGTTGGCCATA G
qacA	ARG	Multidrug	efflux	TGGCAATAGGAGCTATGGTGTTT	AAGGTAACACTATTTTCGGTCCAAAT C
qacA/qacB	ARG	Multidrug	efflux	TTTAGGCAGCCTCGCTTCA	CCGAATCCAAATAAAACCCAATAA
qacEdelta1-01	ARG	Multidrug	efflux	TCGCAACATCCGCATTAAAA	ATGGATTTCAGAACCAGAGAAAGAA A
qacEdelta1-02	ARG	Multidrug	efflux	CCCCTTCCGCCGTTGT	CGACCAGACTGCATAAGCAACA
qacH-01	ARG	Multidrug	efflux	GTGGCAGCTATCGCTTGGAT	CCAACGAACGCCCACAA
qacH-02	ARG	Multidrug	efflux	CATCGTGCTTGTGGCAGCTA	TGAACGCCCAGAAGTCTAGTTTT
rarD-02	ARG	Multidrug	efflux	TGACGCATCGCGTGATCT	AAATTTTCTGTGGCGTCTGAATC
sdeB	ARG	Multidrug	efflux	CACTACCGCTTCCGCACTTAA	TGAAAAAACGGGAAAAGTCCAT
tolC-01	ARG	Multidrug	efflux	GGCCGAGAACCTGATGCA	AGACTTACGCAATTCGGGGTTA
tolC-02	ARG	Multidrug	efflux	CAGGCAGAGAACCTGATGCA	CGCAATTCGGGGTTGCT
tolC-03	ARG	Multidrug	efflux	GCCAGGCAGAGAACCTGATG	CGCAATTCGGGGTTGCT
ttgA	ARG	Multidrug	efflux	ACGCCAATGCCAAACGATT	GTCACGGCGCAGCTTGA
ttgB	ARG	Multidrug	efflux	TCGCCCTGGATGTACACCTT	ACCATTGCCGACATCAACAAC
yceE/mdtG-01	ARG	Multidrug	efflux	TGGCACAAAATATCTGGCAGTT	TTGTGTGGCGATAAGAGCATTAG

yceE/mdtG-02	ARG	Multidrug	efflux	TTATCTGTTTTCTGCTCACCTTCTTTT	GCGTGGTGACAAACAGGCTTA
yceL/mdtH-01	ARG	Multidrug	efflux	TCGGGATGGTGGGCAAT	CGATAACCGAGCCGATGTAGA
yceL/mdtH-02	ARG	Multidrug	efflux	CGCGTGAAACCTTAAGTGCTT	AGACGGCTAAACCCCATATAGCT
yceL/mdtH-03	ARG	Multidrug	efflux	CTGCCGTAAATGGATGTATGC	ACTCCAGCGGGCGATAGG
yidY/mdtL-01	ARG	Multidrug	efflux	GCAGTTGCATATCGCCTTCTC	CTTCCCGGCAAACAGCAT
yidY/mdtL-02	ARG	Multidrug	efflux	TGCTGATCGGGATTCTGATTG	CAGGCGCGACGAACATAAT
fabK	ARG	other	deactivate	TTTCAGCTCAGCACTTTGGTCAT	AAGGCATCTTTTTCAGCCAGTTC
imiR	ARG	other	unknown	CCGGACTAGAGCTTCATGTAAGC	CCCACGCGGTACTCTTGTAAG
nisB	ARG	other	unknown	GGGAGAGTTGCCGATGTTGTA	AGCCACTCGTTAAAGGGCAAT
speA	ARG	other	unknown	GCAAGAGGTATTTGCTCAACAAGA	CAGGGTCACCTCATAAAGAAAA
bacA-01	ARG	other	deactivate	CGGCTTCGTGACCTCGTT	ACAATGCGATACCAGGCAAAT
bacA-02	ARG	other	deactivate	TTCCACGACACGATTAAGTCATTG	CGGCTCTTTCGGCTTCAG
fosB	ARG	other	deactivate	TCACTGTAACTAATGAAGCATTAGA CCAT	CCATCTGGATCTGTAAAGTAAAGAGA TC
fosX	ARG	other	deactivate	GATTAAGCCATATCACTTTAATTGT GAAAG	TCTCCTTCCATAATGCAAATCCA
nimE	ARG	other	unknown	TGCGCCAAGATAGGGCATA	GTCGTGAATTCGGCAGGTTTA
pncA	ARG	other	unknown	GCAATCGAGGCGGTGTTC	TTGCCGCAGCCAATTCA
sat4	ARG	other	deactivate	GAATGGGCAAAGCATAAAAACTTG	CCGATTTTGAAACCACAATTATGATA

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