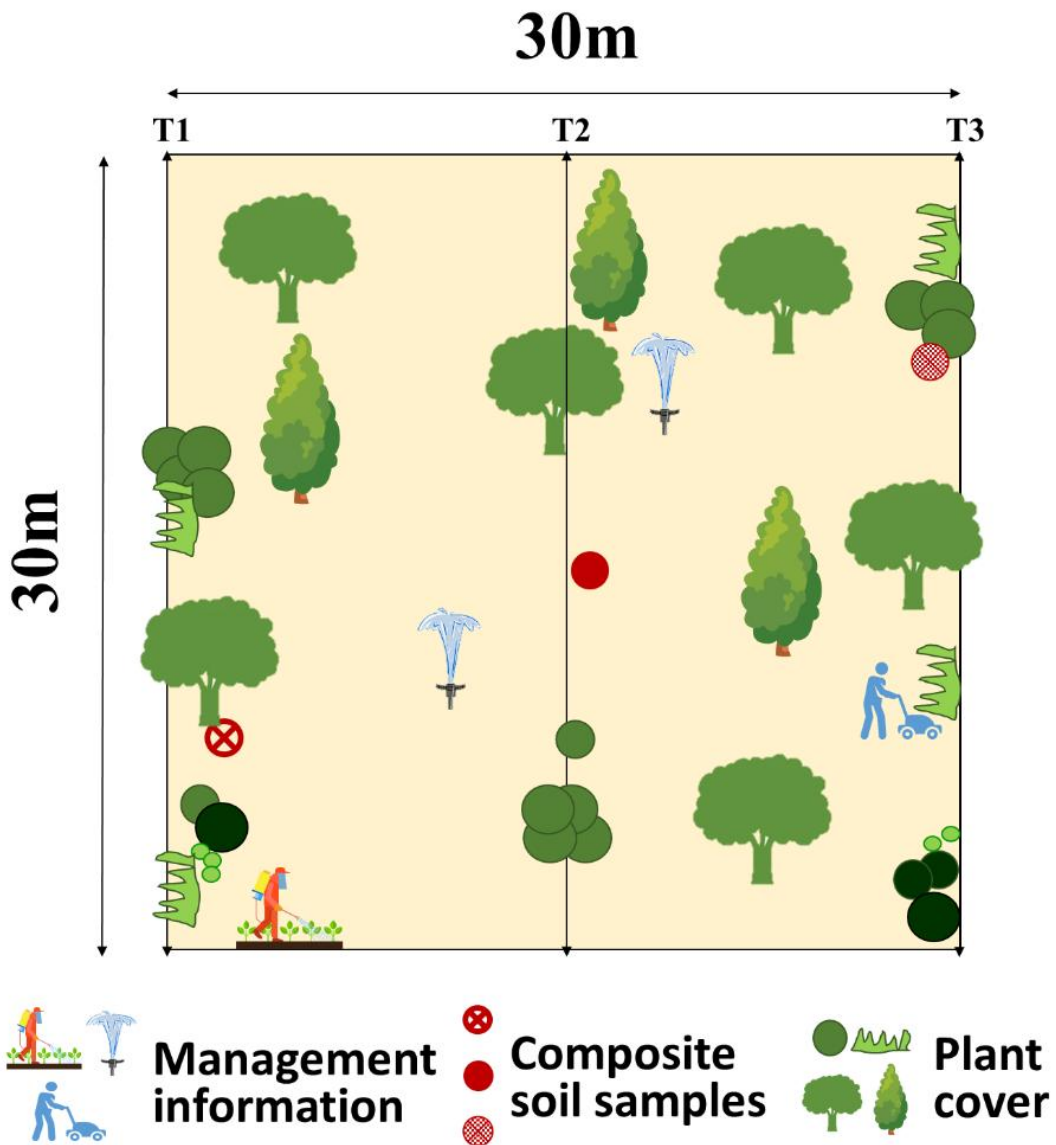


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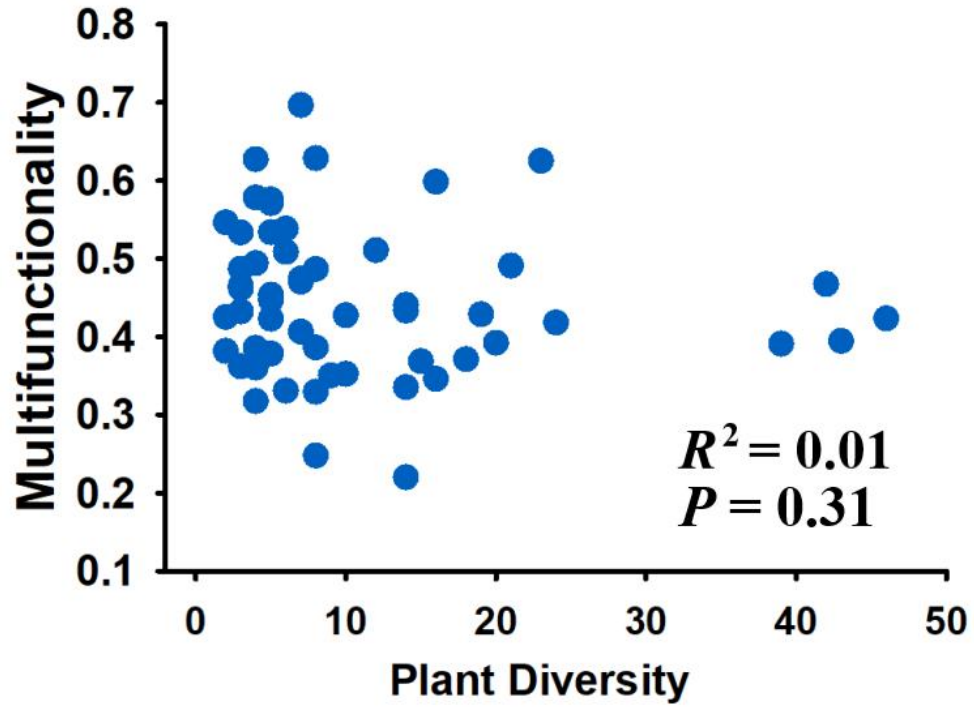
Supplementary Fig. 1 to 5

Supplementary Table 1 to 11

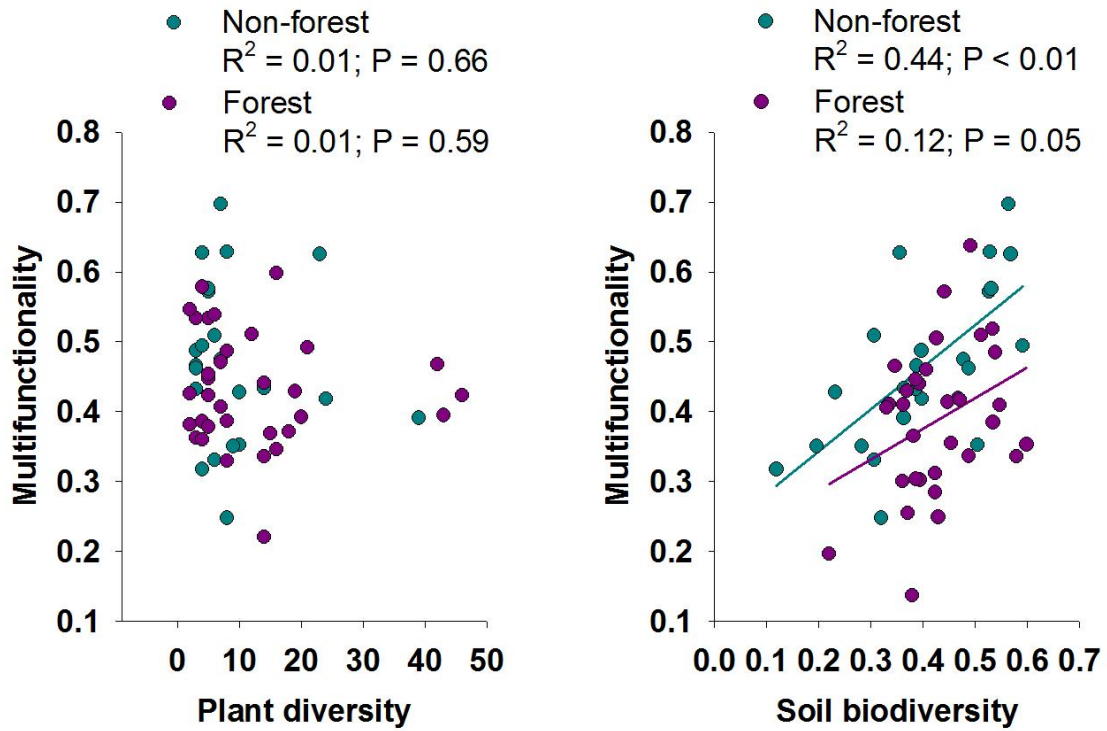
Supplementary References



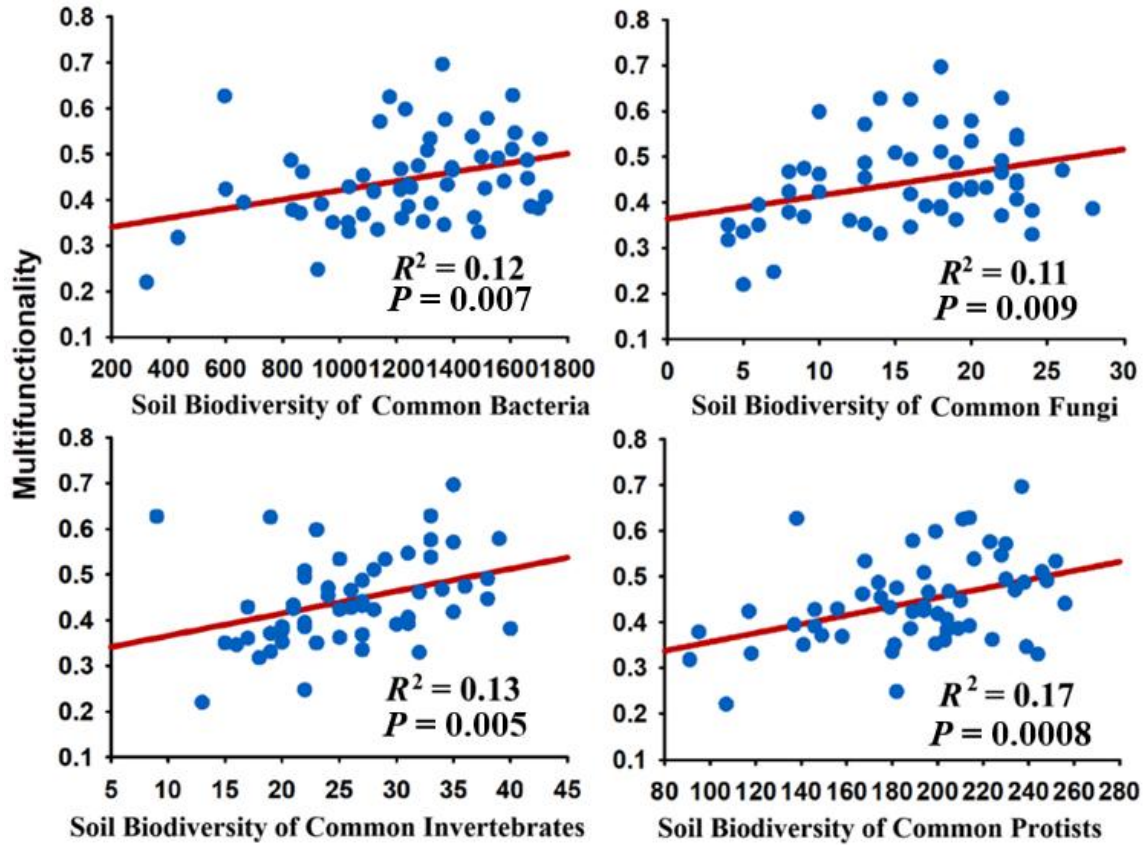
Supplementary Fig. 1. Summary of the sampling design in one of the 56 urban greenspaces included in this study. T1, T2, and T3 are the transects.



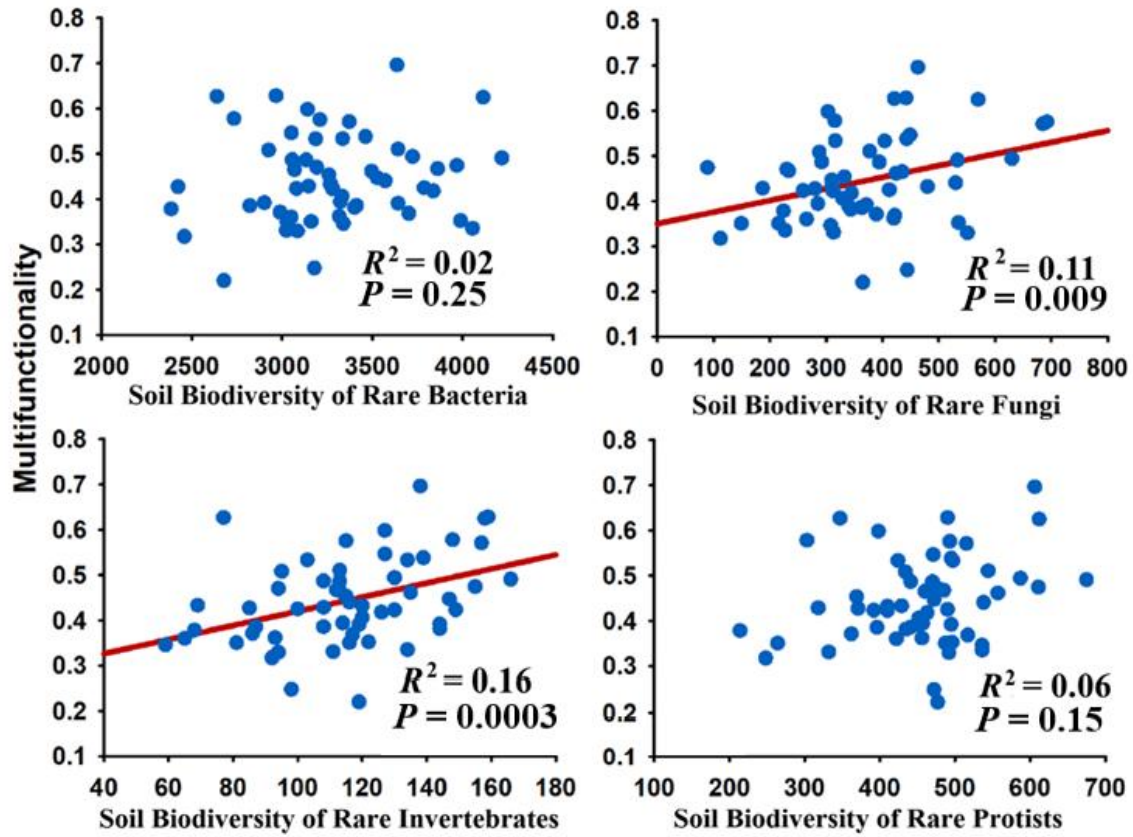
Supplementary Fig. 2. Ordinary least squares linear regression between perennial plant diversity (richness; number of perennial plant species) and ecosystem multifunctionality in urban greenspaces, $n = 56$ study sites.



Supplementary Fig. 3. Ordinary least squares linear regression between plant diversity (richness; number of perennial plant species) and soil biodiversity with ecosystem multifunctionality in urban greenspaces in urban forest ($n = 33$) and non-forest ($n = 23$) ecosystems. Non-forests include grass lawns and gardens.



Supplementary Fig. 4. Ordinary least squares linear regression between the soil biodiversity of the common taxa (bacteria, fungi, invertebrates, and protists) and multifunctionality, $n = 56$ study sites.



Supplementary Fig. 5. Ordinary least squares linear regression between the soil biodiversity of the rare taxa (bacteria, fungi, invertebrates, and protists) and multifunctionality, $n = 56$ study sites.

Supplementary Table 1. Detailed information for the 56 study sites.

Plot ID	Distance from Equator (Decimal Degree)	Climatic Zones	Vegetation Structure	Mycorrhizal Plants (ECM: Ectomycorrhizal AM: Endophytic mycorrhizal)
1	41.73944444	Continental	Forest	EcM
2	42.17527778	Continental	Grasslands	AM
3	42.91083333	Continental	Forest	EcM
4	43.38083333	Continental	Forest	EcM
5	43.8425	Continental	Shrublands	EcM
6	33.3739	Temperate	Forest	EcM-AM
7	19.87365187	Tropical	Grasslands	AM
8	19.93988	Tropical	Forest	AM
9	19.939216	Tropical	Grasslands	AM
10	40.161436	Arid	Grasslands	AM
11	39.112631	Arid	Grasslands	AM
12	41.155998	Arid	Grasslands	AM
13	42.43936	Continental	Grasslands	AM
14	59.85237	Continental	Grasslands	AM
15	51.752507	Temperate	Grasslands	AM
16	67.282663	Continental	Grasslands	AM
17	46.57555556	Temperate	Forest	AM
18	46.325	Temperate	Forest	EcM
19	47.39638889	Temperate	Forest	AM
20	46.051899	Continental	Forest	EcM
21	45.544423	Temperate	Forest	EcM
22	46.565195	Continental	Forest	AM
23	25.76184	Temperate	Forest	AM
24	26.16431	Temperate	Grasslands	NM
25	33.90396	Temperate	Forest	EcM-AM
26	23.56219444	Tropical	Forest	AM
27	25.14310278	Temperate	Grasslands	AM
28	27.20263889	Arid	Grasslands	AM
29	36.221806	Continental	Forest	EcM
30	40.01034	Continental	Forest	AM
31	39.08455	Continental	Forest	AM
32	43.830834	Arid	Grasslands	AM
33	23.708257	Arid	Forest	AM
34	27.4984	Temperate	Grasslands	AM
35	34.1854	Arid	Grasslands	AM
36	33.8814	Temperate	Grasslands	AM
37	34.0822	Temperate	Grasslands	AM
38	41.415993	Temperate	Forest	EcM

39	46.74008	Continental	Shrublands	AM
40	44.53041	Temperate	Grasslands	AM
41	19.31056	Temperate	Shrublands	AM
42	19.294317	Temperate	Forest	AM
43	19.418751	Temperate	Forest	AM
44	40.41056	Arid	Forest	AM
45	7.756	Tropical	Forest	AM
46	7.517	Tropical	Forest	AM
47	7.492	Tropical	Shrublands	AM
48	28.040376	Temperate	Forest	AM
49	27.483416	Temperate	Forest	EcM
50	26.9335	Temperate	Forest	EcM
51	37.192943	Temperate	Forest	AM
52	40.20521	Temperate	Forest	EcM
53	41.1672	Temperate	Forest	AM
54	31.770055	Temperate	Forest	AM
55	31.234653	Arid	Forest	EcM-AM
56	31.309503	Arid	Forest	NM-AM

Supplementary Table 2. Rationales on the selected ecosystem services and surrogates of functions.

Ecosystem Services	Ecological Functions	Rationale and hypotheses
Microbial-driven C pools	Labile carbon content	Microbial-driven C pools in the ecosystems is a key response for soil fertility, and includes the forms of carbon which are highly associated with microbially processed carbon (e.g., via organic matter depolymerization and mineralization processes) ¹ . In this study, we focused on carbon fractions associated with microbial activity such as the amount of carbon associated with minerals, and labile carbon content. We posit that soil biodiversity is positively associated with microbial-driven carbon pools in city parks.
	Mineral-associated carbon	
Water regulation	Infiltration potential	Water regulation is one of the critical functions and services of terrestrial ecosystem for indirect or direct human utilization. Water regulation is hydrological responses of terrestrial ecosystem to climate events and artificial irrigation ² . Soil biodiversity might influence water regulation (e.g., infiltration potential and water holding capacity) by helping to develop soil structure.
	Water holding capacity	
Nutrient cycling	Available phosphorus	Soil available macronutrients (e.g., nitrogen and phosphorus) are essential for supporting plant, microfauna, and microbial growth. Soil organisms, including nematodes, collembola, fungi, and bacteria, are responsible for a cascade of intricate soil nutrient conversion and cycling ³ , the changes of the biodiversity of plant and soil microbial organisms might be closely related to the variations of nutrient pools.
	Available nitrate	
	Available ammonium	
Plant-soil mutualism	Arbuscular mycorrhizal fungi biomass	Arbuscular mycorrhizal fungi (AMF) is a major factor contributing to the maintenance of ecosystem functioning (carbon cycling, plant productivity) ⁴ . Soil biodiversity might contribute to create habitats for symbiotic organisms by displacing other soil-borne organisms such as parasites and pathogens.
OM decomposition	Soil respiration	Soil basal respiration, labile carbon decomposition and refractory organic carbon decomposition are main ecological processes in terrestrial ecosystems. Soils harbor a rich diversity of invertebrate and microbial life, which drives biochemical processing such as litter and organic matter decomposition from local to global scales ⁵ . Soils with a higher biodiversity contain a larger number of metabolic tools to break down organic matter supporting larger respiration and enzymatic activity rates and low diversity soils.
	Glucose-induced respiration	
	Lignin-induced respiration	
	Starch degradation	
	Chitin degradation	
	Hemicellulose degradation P mineralization	
Plant productivity	Net plant productivity	Plant productivity is the fundamental driver of ecosystem function by providing the energy and fuel necessary for microbes to conduct multiple functions such as nutrient cycling and OM decomposition. At the same time, larger soil biodiversity and OM depolymerization can result in greater plant productivity supporting a myriad of processes from nutrient availability, pathogen and ARG control, and supporting water regulation ⁶ .
Pathogen control	Soil-borne plant pathogen control	Fungal plant pathogens are the key safety hazards for plant health and production. Soil biodiversity maintains productivity by suppressing plant disease. Soils with more biodiversity can create a barrier against microbial invasions ⁷ , protecting soils from soil-borne plant pathogens.

ARG control	ARG control	Large abundance of antibiotic resistance genes has the potential to influence human, plant and animal health ⁸ . Soil biodiversity regulates microbial structure and interactions, and have been recently found to regulate ARG control in natural ecosystems worldwide ⁹ .
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Supplementary Table 3. The microbial composition of common taxa.

Common Taxa	Class Level	Relative Abundance (%)	ASVs Number
Invertebrates	Chelicerata	0.45	1
	Chromadorea	2.080952381	8
	Enoplea	3.261904762	4
	Rotifera	3.445238095	5
Protists	Amoebzoa	6.523809524	73
	Apicomplexa	0.038095238	1
	Cercozoa	12.15178571	114
	Chlorophyta_Green_algae	2.842559524	20
	Ciliophora	13.91309524	103
	Dinoflagellata	0.220238095	4
	Excavata	2.14672619	30
	Ochrophyta	4.235119048	27
	Oomycota	2.728869048	13
	Red_algae_Rhodophyta	0.083928571	2
Bacteria	Acidobacteria	7.874285714	428
	Actinobacteria	7.943095238	506
	Alphaproteobacteria	8.490119048	458
	Armatimonadetes	0.03702381	7
	Bacteroidetes	4.790238095	305
	BRC1	0.016666667	3
	Chloroflexi	1.433095238	113
	Cyanobacteria	0.127380952	3
	Deltaproteobacteria	1.999404762	183
	Elusimicrobia	0.031071429	6
	Entotheonellaeota	0.144642857	10
	Fibrobacteres	0.011071429	2
	Firmicutes	0.324880952	18
	Gammaproteobacteria	6.09202381	317
	Gemmatimonadetes	0.6925	55
	Latescibacteria	0.054642857	5
	Nitrospirae	0.268214286	9
	Planctomycetes	1.518928571	174
	Rokubacteria	0.215714286	14
	Verrucomicrobia	4.102380952	211

	WS2	0.007261905	1
Fungi	Leotiomycetes	0.412797619	3
	Sordariomycetes	15.98125	36

Supplementary Table 4. The microbial composition of rare taxa.

Rare Taxa	Class Level	Relative Abundance (%)	ASVs Number
Invertebrates	Annelida	3.454761905	26
	Arthropoda	14.86904762	266
	Gastrotricha	0.307142857	7
	Mollusca	0.242857143	3
	Chromadorea	12.79761905	365
	Enoplea	9.057142857	114
	Platyhelminthes	0.578571429	23
	Rotifera	3.214285714	90
	Tardigrada	1.785714286	31
Protists	Amoebozoa	7.132142857	1190
	Apicomplexa	6.80297619	318
	Cercozoa	11.1702381	1816
	Chlorophyta Green algae	3.86875	399
	Ciliophora	12.98720238	1172
	Dinoflagellata	0.410714286	92
	Excavata	2.19672619	358
	Ochrophyta	4.38422619	528
	Oomycota	1.346130952	149
	Others	3.206547619	749
	Red algae Rhodophyta	0.348214286	54
Bacteria	Acetothermia	0.000238095	1
	Acidobacteria	7.464642857	5250
	Actinobacteria	6.431666667	5476
	Alphaproteobacteria	5.809404762	4342
	Armatimonadetes	0.32797619	426
	Bacteroidetes	6.694404762	4861
	BRC1	0.03952381	55
	Calditrichaeota	0.002619048	1
	Chlamydiae	0.055357143	108
	Chloroflexi	3.274166667	3160
	Cloacimonetes	0.000357143	1
	Cyanobacteria	0.782619048	539

	Dadabacteria	0.006904762	9
	Deinococcus-Thermus	0.01202381	21
	Deltaproteobacteria	3.68452381	3227
	Dependentiae	0.041071429	79
	Elusimicrobia	0.276785714	300
	Entotheonellaeota	0.233095238	163
	Epsilonbacteraeota	0.000238095	2
	FBP	0.088095238	110
	FCPU426	0.052380952	38
	Fibrobacteres	0.107261905	67
	Firmicutes	0.3625	353
	GAL15	0.001785714	3
	Gammaproteobacteria	5.045	2771
	Gemmatimonadetes	2.284642857	1794
	Halanaerobiaeota	0.000119048	1
	Hydrogenedentes	0.006190476	11
	Kiritimatiellaeota	0.005952381	10
	Latescibacteria	0.309047619	209
	Lentisphaerae	0.000119048	1
	Margulisbacteria	0.000357143	1
	Nitrospirae	0.13547619	93
	Omnitrophicaeota	0.05702381	79
	Others	0.577547619	823
	Patescibacteria	0.246428571	485
	PAUC34f	0.000595238	1
	Planctomycetes	5.144047619	5220
	Rokubacteria	0.105119048	69
	Spirochaetes	0.033571429	30
	Tenericutes	0.003452381	10
	Verrucomicrobia	3.651904762	2928
	WPS-2	0.123333333	99
	WS2	0.006309524	8
	WS4	0.000119048	1
	Zixibacteria	0.005833333	6
	Agaricomycetes	20.47708333	2644
Fungi	Agaricostilbomycetes	0.079166667	36
	Aphelidiomycetes	0.022619048	18

Archaeorhizomycetes	0.0625	25
Archaeosporomycetes	0.073809524	43
Atractiellomycetes	0.090178571	8
Basidiobolomycetes	0.01547619	11
Blastocladiomycetes	0.091666667	41
Calcarisporiellomycetes	0.010416667	5
Chytridiomycetes	0.147916667	55
Cladochytriomycetes	0.0125	5
Classiculomycetes	0.005357143	3
Cystobasidiomycetes	0.227678571	87
Dacrymycetes	0.004761905	1
Dothideomycetes	11.74285714	1821
Endogonomycetes	0.513392857	151
Entomophthoromycetes	0.007738095	3
Entorrhizomycetes	0.01547619	6
Eurotiomycetes	4.810416667	1062
Exobasidiomycetes	0.032440476	19
Geminibasidiomycetes	0.091964286	22
Geoglossomycetes	0.060714286	22
Glomeromycetes	1.394047619	382
GS01	0.007738095	7
GS14	0.013095238	9
GS17	0.027083333	16
GS18	0.019642857	7
GS19	0.002380952	4
GS25	0.007738095	3
GS27	0.010119048	4
GS37	0.025	6
Hyaloraphidiomycetes	0.005952381	4
Kickxellomycetes	0.038690476	14
Laboulbeniomycetes	0.055654762	24
Lecanoromycetes	0.230357143	88
Leotiomycetes	2.594345238	555
Lobulomycetes	0.085119048	49
Malasseziomycetes	0.041964286	14
Microbotryomycetes	0.754166667	145
Monoblepharidomycetes	0.11547619	46

Mortierellomycetes	7.76875	660
Mucoromycetes	0.608630952	129
Neocallimastigomycetes	0.001190476	1
Olpidiomycetes	0.065178571	28
Orbiliomycetes	0.267261905	115
Paraglomeromycetes	0.016071429	11
Pezizomycetes	2.543452381	370
Pezizomycotina_cls_Incertae_sedis	0.075297619	30
Polychytriomycetes	0.007142857	1
Pucciniomycetes	0.094047619	21
Rhizophlyctidomycetes	0.650595238	187
Rhizophydiomycetes	1.183035714	295
Rozellomycotina_cls_Incertae_sedis	0.951190476	345
Saccharomycetes	1.442857143	240
Schizosaccharomycetes	0.011011905	11
Sordariomycetes	9.630654762	1846
Spiculogloeomycetes	0.016666667	9
Spizellomycetes	0.836607143	259
Taphrinomycetes	0.020833333	14
Tremellomycetes	2.360119048	307
Tritirachiomycetes	0.053571429	27
Umbelopsidomycetes	0.055952381	15
Ascomycota_unidentified	7.369345238	2370
Ustilaginomycetes	0.095833333	23
Wallemiomycetes	0.006547619	3
Zoopagomycetes	0.093154762	49

Supplementary Table 5. Variation partitioning modeling of *P* values associated with the unique portions explained by different groups of predictors [soil biodiversity of the selected groups (bacteria, fungi, protists, and invertebrates), plant richness, environment (soil variables and climate), and space].

<i>Adjusted-P Value</i>	Plant Richness	Soil Biodiversity	Environment	Space
Multifunctionality	0.19	0.001	0.001	0.002
Dimension #1 of ecological functions	0.46	0.05	0.001	0.018
Dimension #2 of ecological functions	0.007	0.023	0.001	0.004
Dimension #3 of ecological functions	0.19	0.001	0.001	0.003
Labile carbon content	0.16	0.002	0.041	0.013
Mineral-associated carbon	0.322	0.142	0.002	0.002
Infiltration potential	0.39	0.047	0.041	0.005
Water holding capacity	0.111	0.003	0.001	0.01
Available phosphorus	0.16	0.02	0.018	0.005
Available nitrate	0.179	0.007	0.001	0.039
Available ammonium	0.268	0.007	0.007	0.0001
Arbuscular mycorrhizal fungi biomass	0.142	0.322	0.002	0.002
Soil respiration	0.126	0.012	0.002	0.008
Glucose-induced respiration	0.021	0.001	0.001	0.005
Lignin-induced respiration	0.0104	0.003	0.001	0.016
Starch degradation	0.049	0.021	0.002	0.001
Chitin degradation	0.222	0.072	0.001	0.005
Hemicellulose degradation	0.136	0.014	0.005	0.005
P mineralization	0.35	0.004	0.001	0.03
Net plant productivity	0.41	0.001	0.075	0.054
Soil-borne plant pathogen control	0.11	0.011	0.001	0.002
ARG control	0.03	0.001	0.04	0.07

Supplementary Table 6. Linear and quadratic regressions between environmental factors and multifunctionality.

Variables	Direction	Response	Model	R square	F value	<i>Adjusted- P value</i>
			Linear	0.175	11.469	<0.001
Spatial	→→→	Multifunctionality	Quadratic	0.176	5.651	0.006
			Linear	0.007	0.395	0.533
Climate	→→→	Multifunctionality	Quadratic	0.008	0.222	0.802
			Linear	0.063	3.613	0.063
Plant cover	→→→	Multifunctionality	Quadratic	0.063	1.794	0.176
Plant richness	→→→	Multifunctionality	Linear	0.013	0.706	0.404
			Quadratic	0.023	0.632	0.536
			Linear	0.507	55.44	<0.001
N	→→→	Multifunctionality	Quadratic	0.584	37.149	<0.001
			Linear	0.186	12.373	<0.001
P	→→→	Multifunctionality	Quadratic	0.287	10.641	<0.001
			Linear	0.464	46.74	<0.001
SOC	→→→	Multifunctionality	Quadratic	0.582	36.83	<0.001
			Linear	0.079	4.616	0.036
C: N	→→→	Multifunctionality	Quadratic	0.081	2.329	0.107
			Linear	0.026	1.425	0.238
Soil pH	→→→	Multifunctionality	Quadratic	0.15	4.682	0.013
			Linear	0.032	1.813	0.184
% Sand	→→→	Multifunctionality	Quadratic	0.118	3.537	0.036

Supplementary Table 7. SEM boxes in the model. *P* values were indicated by asterisks. “*” represents adjusted $0.01 < P \leq 0.05$; “**” represents adjusted $P \leq 0.01$; *n* = 56 sites.

Boxes	Associations	Estimate
Box A	% Sand → Soil Biodiversity	0.296*
	Soil pH → Soil Biodiversity	0.106
	N → Soil Biodiversity	0.457**
	C: N → Soil Biodiversity	0.231
	P → Soil Biodiversity	0.229
Box B	Irrigated → P	-0.036
	Irrigated → N	-0.168
	Irrigated → Soil pH	0.308*
	Irrigated → C: N	-0.018
	Irrigated → % Sand	0.391**
	Fertilized → N	-0.141
	Fertilized → P	0.26
	Fertilized → C: N	-0.102
	Mowed → N	0.151
	Fertilized → Soil pH	-0.063
	Fertilized → % Sand	0.335**
	Mowed → P	0.17
	Mowed → C: N	0.113
Mowed → Soil pH	-0.16	
Mowed → % Sand	0.214	
Box C	% Sand → Multifunctionality	0.30*
	Soil pH → Multifunctionality	-0.097
	P → Multifunctionality	-0.078
	C: N → Multifunctionality	0.201
	N → Multifunctionality	0.461*
Box D	Mowed → Multifunctionality	0.384**
	Irrigated → Multifunctionality	-0.044
	Fertilized → Multifunctionality	0.264
Box E	Distance equator → P	0.35**
	Distance equator → Soil pH	0.091
	Distance equator → % Sand	-0.205
Box F	Fertilized → Soil Biodiversity	-0.33*
	Irrigated → Soil Biodiversity	0.15
	Mowed → Soil Biodiversity	0.24

Supplementary Table 8. The gene category of gene groups related to nutrient cycling (methane metabolism, nitrogen metabolism, phosphate metabolism, sulfur metabolism).

Methane Metabolism	Relative Abundance	Gene Names and Descriptions
K16158	0.006782629	mmoY; encodes methane monooxygenase component A beta chain [EC:1.14.13.25]
K16161	0.000788199	mmoC; encodes methane monooxygenase component C [EC:1.14.13.25]
K10944	0.008693892	pmoA; encodes methane monooxygenase subunit A [EC:1.14.18.3 1.14.99.39]
K10945	0.007302682	pmoB; encodes methane monooxygenase subunit B
K10946	0.000988152	pmoC; encodes methane monooxygenase subunit C
K16254	0.000350175	mxaj; encodes protein involved in methanol oxidation
K16260	0.002031333	mxad; encodes mxad protein
K00148	0.030178635	fdhA; encodes glutathione-independent formaldehyde dehydrogenase [EC:1.2.1.46]
K17067	0.002595589	mdo; encodes methanol dehydrogenase [EC:1.2.98.1 1.1.99.37]
K03396	0.00125672	gfa; encodes S-(hydroxymethyl) glutathione synthase [EC:4.4.1.22]
K01070	0.001701133	encodes S-formylglutathione hydrolase [EC:3.1.2.12]
K00317	0.00676302	encodes methylamine dehydrogenase [EC:1.5.8.1 1.5.8.2]
K18277	0.003174678	tmm; encodes trimethylamine monooxygenase [EC:1.14.13.148]
K03532	0.001484572	torC; encodes trimethylamine N-oxide (TMAO) reductase I, cytochrome c-type subunit
K07812	0.003819439	torZ; encodes trimethylamine-N-oxide reductase (cytochrome c) [EC:1.7.2.3]
K08685	0.001282375	qhpA; encodes quinohemoprotein amine dehydrogenase [EC:1.4.9.1]
K22081	0.010844341	mgsA; encodes methylamine---glutamate N-methyltransferase subunit A [EC:2.1.1.21]
K22082	0.009320283	mgsB; encodes methylamine---glutamate N-methyltransferase subunit B [EC:2.1.1.21]
K22083	0.032770066	mgsC; encodes methylamine---glutamate N-methyltransferase subunit C [EC:2.1.1.21]
K22085	0.000885594	mgdB; encodes methylglutamate dehydrogenase subunit B [EC:1.5.99.5]
K22086	0.001966974	mgdC; encodes methylglutamate dehydrogenase subunit C [EC:1.5.99.5]
K22087	0.001930929	mgdD; encodes methylglutamate dehydrogenase subunit D [EC:1.5.99.5]
K00200	0.001517323	fwdA, fmdA; encodes formylmethanofuran dehydrogenase subunit A [EC:1.2.7.12]
K00201	0.002084424	fwdB, fmdB; encodes formylmethanofuran dehydrogenase subunit B [EC:1.2.7.12]
K00203	0.006881575	fwdD, fmdD; encodes formylmethanofuran dehydrogenase subunit D [EC:1.2.7.12]
K00205	0.001335264	fwdF, fmdF; encodes 4Fe-4S ferredoxin
K11261	0.008698389	fwdE, fmdE; encodes formylmethanofuran dehydrogenase subunit E [EC:1.2.7.12]
K00672	0.001301414	fr; encodes formylmethanofuran--tetrahydromethanopterin N-formyltransferase [EC:2.3.1.101]
K01499	0.006208519	mch; encodes methenyltetrahydromethanopterin cyclohydrolase [EC:3.5.4.27]
K00441	0.007350342	frhB; encodes coenzyme F420 hydrogenase subunit beta [EC:1.12.98.1]
K10714	0.01187951	mtdB; encodes methylene-tetrahydromethanopterin dehydrogenase [EC:1.5.1.-]
K10713	0.00124611	encodes aldehyde-activating protein [EC:4.2.1.147]
K00320	0.014049891	encodes LLM class F420-dependent oxidoreductase [EC:1.5.98.2]
K00577	0.00283747	mtrA; encodes tetrahydromethanopterin S-methyltransferase subunit A [EC:2.1.1.86]
K03388	0.002752191	hdrA2; encodes heterodisulfide reductase subunit A2 [EC:1.8.7.3 1.8.98.4 1.8.98.5 1.8.98.6]

K03389	0.000417141	hdrB2; encodes heterodisulfide reductase subunit B2 [EC:1.8.7.3 1.8.98.4 1.8.98.5 1.8.98.6]
K03390	9.21512E-05	hdrC2; encodes heterodisulfide reductase subunit C2 [EC:1.8.7.3 1.8.98.4 1.8.98.5 1.8.98.6]
K08264	0.005868733	hdrD; encodes heterodisulfide reductase subunit D [EC:1.8.98.1]
K00058	0.089398498	serA, PHGDH; encodes D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95 1.1.1.399]
K00831	0.01785258	serC, PSAT1; encodes phosphoserine aminotransferase [EC:2.6.1.52]
K01079	0.014140451	serB, PSPH; encodes phosphoserine phosphatase [EC:3.1.3.3]
K22305	0.032778605	psp; encodes phosphoserine phosphatase [EC:3.1.3.3]
K14083	0.013821843	mttB; encodes trimethylamine methyltransferase family protein [EC:2.1.1.250]
K08097	0.010265136	comA; encodes phosphosulfolactate synthase [EC:4.4.1.19]
K05979	0.00576282	comB; encodes 2-phosphosulfolactate phosphatase [EC:3.1.3.71]
K06034	0.00136925	comD; encodes sulfopyruvate decarboxylase subunit alpha [EC:4.1.1.79]
K13039	0.000493137	comE; encodes sulfopyruvate decarboxylase subunit beta [EC:4.1.1.79]
K11779	0.037220347	fbiC; encodes 7,8-didemethyl-8-hydroxy-5-deazariboflavin synthase [EC:2.5.1.147 4.3.1.32] cofH; encodes 5-amino-6-(D-ribitylamino)uracil--L-tyrosine 4-hydroxyphenyl transferase [EC:2.5.1.147]
K11781	0.03652379	
K11780	0.034117146	cofG; encodes 7,8-didemethyl-8-hydroxy-5-deazariboflavin synthase [EC:4.3.1.32]
K14941	0.010027295	cofC; encodes 2-phospho-L-lactate guanylyltransferase [EC:2.7.7.68 2.7.7.105]
K11212	0.017977254	cofD; encodes LPPG:FO 2-phospho-L-lactate transferase [EC:2.7.8.28]
K12234	0.019970057	cofE; encodes coenzyme F420-0:L-glutamate ligase [EC:6.3.2.31 6.3.2.34]
K14940	0.003529812	cofF; encodes gamma-F420-2:alpha-L-glutamate ligase [EC:6.3.2.32]
K16792	0.005551652	aksD; encodes methanogen homoaconitase large subunit [EC:4.2.1.114]
K16793	0.004764616	aksE; encodes methanogen homoaconitase small subunit [EC:4.2.1.114]
K07144	0.000481075	mfnE; encodes 5-(aminomethyl)-3-furanmethanol phosphate kinase [EC:2.7.4.31]

Nitrogen Metabolism	Relative Abundance	Gene Names and Descriptions
K02575	0.016274666	NRT, narK, nrtP, nasA; encodes MFS transporter, NNP family, nitrate/nitrite transporter
K15576	0.000469833	nrtA; encodes nitrate/nitrite transport system substrate-binding protein
K15578	0.000371547	nrtC; encodes nitrate/nitrite transport system ATP-binding protein [EC:7.3.2.4]
K00367	0.004307401	narB; encodes ferredoxin-nitrate reductase [EC:1.7.7.2]
K00370	0.020685964	narG; encodes nitrate reductase A subunit alpha [EC:1.7.5.1 1.7.99.-]
K00371	0.022738819	narH; encodes nitrate reductase A subunit beta [EC:1.7.5.1 1.7.99.-]
K00374	0.00588144	narI; encodes nitrate reductase A subunit gamma [EC:1.7.5.1 1.7.99.-]
K00372	0.019978235	nasA; encodes assimilatory nitrate reductase catalytic subunit [EC:1.7.99.-]
K00360	0.003147265	nasB; encodes assimilatory nitrate reductase electron transfer subunit [EC:1.7.99.-]
K00362	0.057289148	nirB; encodes nitrite reductase (NADH) large subunit [EC:1.7.1.15]
K00363	0.02721847	nirD; encodes nitrite reductase (NADH) small subunit [EC:1.7.1.15]
K00366	0.03924645	nirA; encodes ferredoxin-nitrite reductase [EC:1.7.7.1]
K03385	0.001296001	nrfA; encodes nitrite reductase (cytochrome c-552) [EC:1.7.2.2]
K15876	0.000940033	nrfH; encodes cytochrome c nitrite reductase small subunit
K00368	0.066226866	nirK; encodes nitrite reductase (NO-forming) [EC:1.7.2.1]
K04561	0.009177835	norB; encodes nitric oxide reductase subunit B [EC:1.7.2.5]

K02305	0.004088686	norC; encodes nitric oxide reductase subunit C
K00376	0.000521435	nosZ; encodes nitrous-oxide reductase [EC:1.7.2.4]
K02586	0.000123849	nifD; encodes nitrogenase molybdenum-iron protein alpha chain [EC:1.18.6.1]
K02588	0.000247698	nifH; encodes nitrogenase iron protein NifH
K10535	0.000110581	hao; encodes hydroxylamine dehydrogenase [EC:1.7.2.6]
K00459	0.025246193	ncd2; encodes probable 2-nitropropane dioxygenase [EC:1.13.12.16]
K01501	0.008224692	nitrilase [EC:3.5.5.1]
K15371	0.037072369	GDH2; encodes glutamate dehydrogenase (NAD(+)) [EC:1.4.1.2]
K00260	0.006626771	gudB; encodes putative glutamate/leucine/phenylalanine/valine dehydrogenase [EC:1.4.1.2]
K00261	0.027730637	GLUD1_2; encodes glutamate dehydrogenase (NAD(P)+) [EC:1.4.1.3]
K00262	0.023818441	gdhA; encodes glutamate dehydrogenase (NADP+) [EC:1.4.1.4]
K00265	0.073372347	gltB; encodes glutamate synthase (NADPH) large chain [EC:1.4.1.13]
K00266	0.028286676	gltD; encodes glutamate synthase (NADPH) small chain [EC:1.4.1.13]
K01725	0.000110581	cynS; encodes cyanate lyase [EC:4.2.1.104]
K00926	0.021406174	arcC; encodes carbamate kinase [EC:2.7.2.2]
K01673	0.029958864	cynT; encodes carbonic anhydrase 1 [EC:4.2.1.1]
K01674	0.003186111	cah; encodes carbonic anhydrase [EC:4.2.1.1]

Phosphate Metabolism	Relative Abundance	Gene Names and Descriptions
K01841	0.00024938	pepM; encodes phosphoenolpyruvate phosphomutase [EC:5.4.2.9]
K09459	0.000584605	encodes phosphonopyruvate decarboxylase [EC:4.1.1.82]
K05306	0.001026239	phnX; encodes phosphonoacetaldehyde phosphonohydrolase [EC:3.11.1.1]
K03430	0.005913099	phnW; encodes 2-aminoethylphosphonate-pyruvate transaminase [EC:2.6.1.37]
K21195	0.004355771	phnY; encodes 2-aminoethylphosphonate dioxygenase [EC:1.14.11.46]
K03823	0.023113197	pat, bar; encodes phosphinothricin acetyltransferase [EC:2.3.1.183]
K06162	0.000172007	phnM; encodes alpha-D-ribose 1-methylphosphonate 5-triphosphate diphosphatase [EC:3.6.1.63]
K06167	0.012657144	phnP; encodes phosphoribosyl 1,2-cyclic phosphate phosphodiesterase [EC:3.1.4.55]
K01113	0.000680178	phoD; encodes alkaline phosphatase D [EC:3.1.3.1]
K01524	0.0136717	ppx; encodes exopolyphosphatase [EC:3.6.1.11 3.6.1.40]
K05781	0.012172455	phnK; encodes putative phosphonate transport system ATP-binding protein
K06137	0.03569628	pqqC; encodes pyrroloquinoline-quinone synthase [EC:1.3.3.11]
K00937	0.006990919	ppk1; encodes polyphosphate kinase 1 [EC:2.7.4.1]
K22468	0.012193291	ppk2; encodes polyphosphate kinase 2 [EC:2.7.4.34]

Sulfur Metabolism	Relative Abundance	Gene Names and Descriptions
K02048	0.010044231	cysP; encodes sulfate/thiosulfate transport system substrate-binding protein
K02046	0.017925168	cysU; encodes sulfate/thiosulfate transport system permease protein
K02047	0.014635578	cysW; encodes sulfate transport system permease protein cysW
K02045	0.013199915	cysA; encodes sulfate/thiosulfate transport system ATP-binding protein [EC:7.3.2.3]
K15551	0.000738209	tauA; encodes taurine ABC transporter periplasmic binding protein

K15552	0.00484234	tauC; encodes taurine ABC transporter membrane subunit
K10831	0.002540815	tauB; encodes taurine transport system ATP-binding protein [EC:7.6.2.7]
K03119	0.016015559	tauD; encodes taurine dioxygenase [EC:1.14.11.17]
K15553	0.003072479	ssuA; encodes sulfonate transport system substrate-binding protein
K15554	0.002031891	ssuC; encodes sulfonate transport system permease protein
K15555	0.007871372	ssuB; encodes sulfonate transport system ATP-binding protein [EC:7.6.2.14]
K04091	0.012704512	ssuD; encodes alkanesulfonate monooxygenase [EC:1.14.14.5]
K00299	0.015720978	ssuE; encodes FMN reductase [EC:1.5.1.38]
K13811	0.018302163	PAPSS; encodes 3'-phosphoadenosine 5'-phosphosulfate synthase [EC:2.7.7.4 2.7.1.25]
K00955	0.033714914	cysNC; encodes bifunctional enzyme CysN/CysC [EC:2.7.7.4 2.7.1.25]
K00956	0.034779159	cysN; encodes sulfate adenylyltransferase subunit 1 [EC:2.7.7.4]
K00957	0.035239378	cysD; encodes sulfate adenylyltransferase subunit 2 [EC:2.7.7.4]
K00958	0.039566809	sat, met3; encodes sulfate adenylyltransferase [EC:2.7.7.4]
K00860	0.044459231	cysC; encodes adenylylsulfate kinase [EC:2.7.1.25]
K01082	0.006918101	cysQ; encodes 3'(2'), 5'-bisphosphate nucleotidase [EC:3.1.3.7]
		nrnA; encodes bifunctional oligoribonuclease and PAP phosphatase NrnA [EC:3.1.3.7 3.1.13.3]
K06881	0.018844518	
K00395	0.000628173	aprB; encodes adenylylsulfate reductase, subunit B [EC:1.8.99.2]
K00390	0.102435058	cysH; encodes phosphoadenosine phosphosulfate reductase [EC:1.8.4.8 1.8.4.10]
K00387	0.014258679	SUOX; encodes sulfite oxidase [EC:1.8.3.1]
K05301	0.008697478	sorA; encodes sulfite dehydrogenase (cytochrome) subunit A [EC:1.8.2.1]
K21307	0.002732775	soeA; encodes molybdopterin dinucleotide binding domain protein [EC:1.8.5.6]
K21308	0.004262118	soeB; encodes dmsO reductase chain B
K21309	0.000516047	soeC; encodes DMSO reductase anchor subunit family protein
K17222	0.000922833	soxA; encodes L-cysteine S-thiosulfotransferase [EC:2.8.5.2]
K17223	0.033483564	soxX; encodes sulfur oxidation c-type cytochrome SoxX [EC:2.8.5.2]
K17226	0.003036432	soxY; encodes sulfur-oxidizing protein SoxY
K17227	0.002243932	soxZ; encodes sulfur-oxidizing protein SoxZ
K17224	0.003892037	soxB; encodes S-sulfosulfanyl-L-cysteine sulfohydrolase [EC:3.1.6.20]
K17225	0.000958372	soxC; encodes sulfane dehydrogenase subunit SoxC
K11180	0.000534477	dsrA; encodes dissimilatory sulfite reductase alpha subunit [EC:1.8.99.5]
K11181	0.000843119	dsrB; encodes dissimilatory sulfite reductase beta subunit [EC:1.8.99.5]
K00380	0.003592595	cysJ; encodes sulfite reductase (NADPH) flavoprotein alpha-component [EC:1.8.1.2]
K00381	0.021987159	cysI; encodes sulfite reductase (NADPH) hemoprotein beta-component [EC:1.8.1.2]
K16950	0.001984598	asrA; encodes anaerobic sulfite reductase subunit A
K00392	0.033600871	sir; encodes sulfite reductase (ferredoxin) [EC:1.8.7.1]
K17218	0.012629469	sqr; encodes sulfide:quinone oxidoreductase [EC:1.8.5.4]
K17229	0.006264294	fccB; encodes sulfide dehydrogenase [flavocytochrome c] flavoprotein chain [EC:1.8.2.3]
K17230	0.000605765	fccA; encodes cytochrome subunit of sulfide dehydrogenase
K16937	0.006726892	doxD; encodes thiosulfate dehydrogenase (quinone) large subunit [EC:1.8.5.2]
K08358	0.000202733	ttrB; encodes tetrathionate reductase subunit B

K08359	0.00246118	ttrC; encodes tetrathionate reductase subunit C
K08352	0.000497616	psrA; encodes polysulfide reductase chain A [EC:1.8.5.5]
K08354	0.000294884	phsC; encodes thiosulfate reductase cytochrome b subunit
K01011	0.072911889	TST; encodes 3-mercaptopyruvate sulfurtransferase [EC:2.8.1.1 2.8.1.2]
K02439	0.004104072	glpE; encodes thiosulfate sulfurtransferase GlpE [EC:2.8.1.1]
K00640	0.018811064	cysE; encodes serine O-acetyltransferase [EC:2.3.1.30]
K10150	0.005724285	cysO; encodes O-phosphoserine sulfhydrylase [EC:2.5.1.47 2.5.1.65 4.2.1.22]
K01738	0.073382239	cysK; encodes cysteine synthase [EC:2.5.1.47]
K00641	0.027516423	metX; encodes homoserine O-acetyltransferase [EC:2.3.1.31 2.3.1.46]
K01739	0.046622212	metB; encodes cystathionine gamma-synthase [EC:2.5.1.48]
K10764	0.016118168	metZ; encodes O-succinylhomoserine sulfhydrylase [EC:2.5.1.-]
K17217	0.003434793	mccB; encodes homocysteine desulfhydrase [EC:4.4.1.1 4.4.1.2]
K17285	0.014739932	SELENBP1; encodes methanethiol oxidase [EC:1.8.3.4]
K17228	0.002586555	sfnG; encodes dimethylsulfone monooxygenase [EC:1.14.14.35]
K16968	0.000134099	msmA; encodes methanesulfonate monooxygenase subunit alpha [EC:1.14.13.111]
K15762	0.005605951	tmoC; encodes Toluene-4-monooxygenase system ferredoxin subunit
K15765	0.000123849	tmoF; encodes Toluene-4-monooxygenase electron transfer component [EC:1.18.1.3]
K07306	0.003819439	dmsA; encodes anaerobic dimethyl sulfoxide reductase subunit A [EC:1.8.5.3]
K07308	0.000995233	dmsC; encodes anaerobic dimethyl sulfoxide reductase subunit C
K00184	0.0123484	dmsB; encodes dimethyl sulfoxide reductase iron-sulfur subunit
K00185	0.010133785	dmsC; encodes dimethyl sulfoxide reductase membrane subunit
K16964	0.00061087	ddhA; encodes dimethylsulfide dehydrogenase subunit alpha [EC:1.8.2.4]
K16953	0.000100521	dddL; encodes dimethylpropiothetin dethiomethylase [EC:4.4.1.3]
K20034	0.006277829	dmdB; encodes 3-(methylthio)propionyl--CoA ligase [EC:6.2.1.44]
K20035	0.005273446	dmdC; encodes 3-(methylthio)propanoyl-CoA dehydrogenase [EC:1.3.8.-]
K20036	0.000100521	dmdD; encodes (methylthio)acryloyl-CoA hydratase [EC:4.2.1.155]
K21310	0.020769017	mddA; encodes methanethiol S-methyltransferase [EC:2.1.1.334]
K16955	0.007621168	mtsB; encodes methylated-thiol--corrinoid protein

Supplementary Table 9. The gene category of gene groups associated with human diseases and antibiotic resistance (infectious diseases, biosynthesis of vancomycin group antibiotics, drug resistance, antimicrobial resistance).

Infectious Diseases	Relative Abundance	Gene Names and Descriptions
K15490	0.000216	lgt1_2_3; encodes glucosyltransferase Lgt1/2/3
K12688	0.000313	sphB1; encodes autotransporter serine protease [EC:3.4.21.-]
K14475	0.000325	ICP; encodes inhibitor of cysteine peptidase
K14196	0.000455	spa; encodes immunoglobulin G-binding protein A
K14956	0.000464	esxA; encodes 6 kDa early secretory antigenic target
K15477	0.000748	vipD; encodes VPS inhibitor protein D
K03191	0.000768	ureI; encodes acid-activated urea channel
K15349	0.000831	sseJ; encodes secreted effector protein SseJ
K10954	0.000934	zot; encodes zona occludens toxin
K14955	0.001098	lprA; encodes lipoprotein LprA
K15845	0.001203	hopZ; encodes outer membrane protein HopZ
K14954	0.001227	lprG; encodes lipoprotein LprG
K14953	0.00123	lpqH; encodes lipoprotein LpqH
K01401	0.00202	aur; encodes aureolysin [EC:3.4.24.29]
K14949	0.002044	pknG; encodes serine/threonine-protein kinase PknG [EC:2.7.11.1]
K14201	0.002049	clfA; encodes clumping factor A
K15492	0.002238	lepB; encodes effector protein B
K11089	0.00242	TROVE2; encodes 60 kDa SS-A/Ro ribonucleoprotein
K15842	0.002736	cagA; encodes cytotoxicity-associated immunodominant antigen
K15719	0.00276	NCOAT; encodes protein O-GlcNAcase [EC:3.2.1.169 2.3.1.48]
K14197	0.003233	sbi; encodes immunoglobulin G-binding protein Sbi
K07347	0.003707	fimD; encodes outer membrane usher protein
K13963	0.004395	SERPINB; encodes serpin B
K14952	0.004797	namH; encodes UDP-MurNAc hydroxylase
K17680	0.006297	PEO1; encodes twinkle protein [EC:3.6.4.12]
K14194	0.006753	sdrC_D_E; encodes serine-aspartate repeat-containing protein C/D/E
K12567	0.007318	TTN; encodes titin [EC:2.7.11.1]
K13730	0.007655	inlA; encodes internalin A
K01354	0.013895	ptrB; encodes oligopeptidase B [EC:3.4.21.83]
K13735	0.054618	yeeJ; encodes adhesin/invasin
K03596	0.097149	lepA; encodes GTP-binding protein LepA
K15125	0.114814	fhaB; encodes filamentous hemagglutinin
Biosynthesis of Vancomycin Group Antibiotics	Relative Abundance	Gene Names and Descriptions
K16421	0.025779	hmaS; encodes 4-hydroxymandelate synthase [EC:1.13.11.46]

K16422	0.008054	hmo; encodes 4-hydroxymandelate oxidase [EC:1.1.3.46] hpgT, nocG; encodes (S)-3,5-dihydroxyphenylglycine transaminase [EC:2.6.1.103]
K16423	0.001847	
K16425	0.002123	dpgB; encodes isomerase DpgB dpgC; encodes (3,5-dihydroxyphenyl) acetyl-CoA 1,2-dioxygenase [EC:1.13.11.80]
K16427	0.000719	
K16434	0.000442	cepJ; encodes thioesterase CepJ
K16437	0.000743	evaC; encodes methylation protein EvaC
K16440	9.62E-05	gtfA; encodes chloroorienticin B synthase [EC:2.4.1.311]
K16444	0.002301	gtfB; encodes vancomycin aglycone glucosyltransferase [EC:2.4.1.310]

Drug Resistance	Relative Abundance	Gene Names and Descriptions
K08218	0.008585	ampG; encodes muropeptide transporter
K02172	0.004463	blaR1; encodes bla regulator protein blaR1
K02171	0.001888	blaI; encodes BlaI family transcriptional regulator, penicillinase repressor
K18148	0.001128	rtcB; encodes release factor H-coupled RctB family protein nalD; encodes TetR/AcrR family transcriptional regulator, repressor of the mexAB-oprM multidrug resistance operon
K18135	0.000332	
K03585	0.014725	acrA, mexA, adeI, smeD, mtrC, cmeA; encodes membrane fusion protein, multidrug efflux system
K18138	0.014674	acrB, mexB, adeJ, smeE, mtrD, cmeB; encodes multidrug efflux pump adeS; encodes two-component system, OmpR family, sensor histidine kinase AdeS [EC:2.7.13.3]
K18143	0.016566	
K18767	0.000129	blaCTX-M; encodes beta-lactamase class A CTX-M [EC:3.5.2.6]
K18768	0.000129	blaKPC; encodes beta-lactamase class A KPC [EC:3.5.2.6]
K17837	0.001817	bla2; encodes metallo-beta-lactamase class B [EC:3.5.2.6]
K12962	0.001085	arnE; encodes undecaprenyl phosphate-alpha-L-ara4N flippase subunit ArnE arnF; encodes undecaprenyl phosphate-alpha-L-ara4N flippase subunit ArnF
K12963	0.002562	
K01406	0.025799	prtC; encodes serralyisin [EC:3.4.24.40]
K01448	0.043516	amiABC; encodes N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28] dsbA; encodes protein dithiol oxidoreductase (disulfide-forming) [EC:1.8.4.15]
K03673	0.001863	
K13632	0.002305	marA; encodes AraC family transcriptional regulator, mar-sox-rob regulon activator

Antimicrobial Resistance	Relative Abundance	Gene Names and Descriptions
K17882	3.69E-05	aadD; encodes kanamycin nucleotidyltransferase [EC:2.7.7.-]
K19278	8.05E-05	aac6-Ib; encodes aminoglycoside 6'-N-acetyltransferase Ib [EC:2.3.1.82]
K19301	8.05E-05	aac6-II; encodes aminoglycoside 6'-N-acetyltransferase II [EC:2.3.1.82]
K17910	0.000124	aphD; encodes aminoglycoside 2"-phosphotransferase [EC:2.7.1.190]

K00638	0.000249	catB; encodes chloramphenicol O-acetyltransferase type B [EC:2.3.1.28]
K05593	0.000262	aadK; encodes aminoglycoside 6-adenylyltransferase [EC:2.7.7.-]
K00662	0.000331	aacC; encodes aminoglycoside 3-N-acetyltransferase [EC:2.3.1.81]
K21267	0.000331	encodes FAD-dependent oxidoreductase [EC:1.14.13.211]
K21252	0.00035	fosX; encodes fosfomicin resistance protein FosX
K18236	0.000412	lnuB_F; encodes lincosamide nucleotidyltransferase B/F
K19273	0.000464	sat4; encodes streptothricin acetyltransferase [EC:2.3.-.-]
K19299	0.000944	aph3-III; encodes aminoglycoside 3'-phosphotransferase III [EC:2.7.1.95]
K00897	0.000944	aphA; encodes kanamycin kinase [EC:2.7.1.95]
K17880	0.000979	hyg; encodes hygromycin-B 7"-O-kinase [EC:2.7.1.119]
K18234	0.001191	vat; encodes virginiamycin A acetyltransferase [EC:2.3.1.-]
K18844	0.001402	spcN; encodes spectinomycin phosphotransferase
K19545	0.001617	lnuA_C_D_E; encodes lincosamide nucleotidyltransferase A/C/D/E
K18220	0.001934	tetM; encodes tetracycline resistance ribosomal protection protein Tet(M)
K19279	0.002281	ant9; encodes aminoglycoside 9-adenylyltransferase [EC:2.7.7.-]
K00984	0.002557	aadA; encodes streptomycin 3"-adenylyltransferase [EC:2.7.7.47]
K04343	0.003358	strB; encodes streptomycin 6-kinase [EC:2.7.1.72]
K18815	0.003545	aac6-I; encodes aminoglycoside 6'-N-acetyltransferase I [EC:2.3.1.82]
K18554	0.003578	cpt; encodes chloramphenicol 3-O phosphotransferase [EC:2.7.1.-]
K06880	0.005913	ereA_B; encodes erythromycin esterase [EC:3.1.1.-]
K19062	0.0061	arr; encodes rifampin ADP-ribosylating transferase
K21288	0.0061	arr2; encodes rifampin ADP-ribosylating transferase
K18816	0.006905	aac6-I, aacA7; encodes aminoglycoside 6'-N-acetyltransferase I [EC:2.3.1.82]
K17840	0.007361	aac2-I; encodes aminoglycoside 2'-N-acetyltransferase I [EC:2.3.1.59]
K18235	0.018871	vgb; encodes virginiamycin B lyase [EC:4.2.99.-]
K00663	0.019356	aacA; encodes aminoglycoside 6'-N-acetyltransferase [EC:2.3.1.82]

Supplementary Table 10. The soil biota category selected by random forest model.

ASVs Numbers	%IncMSE	Taxonomy
bacteria46212	0.018621458	Bacteria; Proteobacteria; Deltaproteobacteria; Desulfarculales; Desulfarculaceae
protist8618	0.039316297	Eukaryota; Amoebozoa; Lobosa; Lobosa_X; Centramoebida; Acanthamoebidae; Acanthamoeba; pustulosa
bacteria9638	0.100935297	Bacteria; Actinobacteria; Actinobacteria; Micrococcales; Intrasporangiaceae; Lapillicoccus
invertebrate1982	0.142930734	Eukaryota; Opisthokonta; Metazoa
bacteria56813	0.176185109	Bacteria; Verrucomicrobia; Verrucomicrobiae; Pedosphaerales; Pedosphaeraceae
bacteria12199	0.327273741	Bacteria; Actinobacteria; Thermoleophilia; Gaiellales; Gaiellaceae; Gaiella
bacteria40626	0.394463088	Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae; Caulobacter
bacteria3922	0.433223646	Bacteria; Acidobacteria; Blastocatellia; Pyrinomonadales; Pyrinomonadaceae; RB41
invertebrate2902	0.440455861	Eukaryota; Opisthokonta; Metazoa; Nematoda; Chromadorea; Chromadorea; Plectus
bacteria6885	0.462237575	Bacteria; Acidobacteria; Subgroup_6
bacteria52466	0.505162141	Bacteria; Proteobacteria; Gammaproteobacteria; R7C24
bacteria44843	0.541730462	Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Altererythrobacter
bacteria7551	0.640770632	Bacteria; Actinobacteria; Acidimicrobiia; IMCC26256
bacteria5359	0.653195294	Bacteria; Acidobacteria; Subgroup_6
bacteria9587	0.700535423	Bacteria; Actinobacteria; Actinobacteria; Micrococcales; Cellulomonadaceae; Cellulomonas
bacteria50201	0.773204573	Bacteria; Proteobacteria; Gammaproteobacteria; Betaproteobacteriales; Burkholderiaceae; Paucibacter
bacteria5692	0.811565931	Bacteria; Acidobacteria; Subgroup_6
bacteria14744	0.831946988	Bacteria; Actinobacteria; Thermoleophilia; Solirubrobacterales; Solirubrobacteraceae; Solirubrobacter
bacteria15868	0.839470385	Bacteria; Bacteroidetes; Bacteroidia; Chitinophagales; Chitinophagaceae; Ferruginibacter
bacteria9129	0.840776056	Bacteria; Actinobacteria; Actinobacteria; Frankiales; Frankiaceae; Jatrophihabitans
bacteria46853	1.006170155	Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; BIRii41
bacteria10836	1.010902731	Bacteria; Actinobacteria; Actinobacteria; Pseudonocardiales; Pseudonocardaceae; Actinomycetospora
bacteria51022	1.028693739	Bacteria; Proteobacteria; Gammaproteobacteria; Betaproteobacteriales; SC-I-84
bacteria24254	1.071874553	Bacteria; Chloroflexi; Gitt-GS-136
protist8927	1.074142914	Eukaryota; Stramenopiles; Ochrophyta; Chrysophyceae; Chrysophyceae_X; Chrysophyceae_Clade-C; Spumella
bacteria53496	1.119038905	Bacteria; Verrucomicrobia; Verrucomicrobiae; Chthoniobacterales; Chthoniobacteraceae; Candidatus_Udaeobacter
bacteria40517	1.202128388	Bacteria; Proteobacteria; Alphaproteobacteria; Azospirillales; Azospirillaceae; Skermanella
bacteria7042	1.236139531	Bacteria; Acidobacteria; Subgroup_6; Unknown_Order; Unknown_Family;

		Vicinamibacter
bacteria10542	1.296715085	Bacteria; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideae; Marmoricola
bacteria51257	1.307799769	Bacteria; Proteobacteria; Gammaproteobacteria; Betaproteobacteriales; TRA3-20
bacteria44210	1.311565713	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Xanthobacteraceae; Rhodoplanes
bacteria52424	1.317673398	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas
protist8419	1.327115419	Eukaryota; Amoebozoa; Lobosa; Tubulinea; Arcellinida; Arcellinida_X; Cryptodiffugia; oviformis
bacteria18788	1.361070262	Bacteria; Bacteroidetes; Bacteroidia; Cytophagales; Hymenobacteraceae; Adhaeribacter
bacteria16964	1.363476881	Bacteria; Bacteroidetes; Bacteroidia; Chitinophagales; Chitinophagaceae
protist8154	1.369033995	Eukaryota; Amoebozoa; Conosa; Mycetozoa-Myxogastrea; Trichiales; Trichiaceae; Trichia
bacteria5263	1.389630319	Bacteria; Acidobacteria; Subgroup_6
fungi30541	1.398467177	Fungi; Mortierellomycota; Mortierellomycetes; Mortierellales; Mortierellaceae; Mortierella; Mortierella_alpina
protist7978	1.40537656	Eukaryota; Amoebozoa; Lobosa; Tubulinea; Echinamoebida; Vermamoebidae; Hartmannella; vermiformis
bacteria52298	1.413762944	Bacteria; Proteobacteria; Gammaproteobacteria; PLTA13
bacteria10602	1.415752832	Bacteria; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioideae; Nocardioides
bacteria12249	1.41655458	Bacteria; Actinobacteria; Thermoleophilia; Gaiellales
protist8802	1.433879566	Eukaryota; Amoebozoa; Lobosa; Lobosa_X; Centramoebida; Acanthamoebidae; Acanthamoeba
bacteria50209	1.475501406	Bacteria; Proteobacteria; Gammaproteobacteria; Betaproteobacteriales; Burkholderiaceae; Piscinibacter
bacteria13090	1.479974567	Bacteria; Actinobacteria; Thermoleophilia; Solirubrobacterales; 67-14
protist9267	1.524900257	Eukaryota; Stramenopiles; Ochrophyta; Chrysophyceae; Chrysophyceae_X; Chrysophyceae_CladeC; Spumella
protist9124	1.526725541	Eukaryota; Stramenopiles; Ochrophyta; Chrysophyceae; Chrysophyceae_X; Chrysophyceae_Clade_C; Ochromonas
protist9105	1.58513443	Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia; Oxytrichidae
bacteria5573	1.607248795	Bacteria; Acidobacteria; Subgroup_6
protist8947	1.65343784	Eukaryota; Rhizaria; Cercozoa; Filosa-Sarcomonadea; Glissomonadida; Allapsidae; Viridiraptor; invadens
protist9323	1.671922635	Eukaryota; Rhizaria; Cercozoa; Filosa-Thecofilosea; Cryomonadida; Rhogostoma-lineage; Capsellina
bacteria43702	1.674263602	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Xanthobacteraceae
bacteria14804	1.677526196	Bacteria; Actinobacteria; Thermoleophilia; Solirubrobacterales; Solirubrobacteraceae; Solirubrobacter
protist9236	1.694208323	Eukaryota; Amoebozoa; Conosa; Variosea; Variosea_X; Mb5C-lineage; Mb5C-

		lineage_X
bacteria42452	1.713506476	Bacteria; Proteobacteria; Alphaproteobacteria; Reyranelles; Reyranelleaceae; Reyranelle
invertebrate2680	1.720061756	Eukaryota; Opisthokonta; Metazoa; Nematoda; Chromadorea; Chromadorea_X
protist8985	1.720665383	Eukaryota; Alveolata; Ciliophora; Litostomatea; Litostomatea_X; Litostomatea
fungi30534	1.730101893	Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae; Ilyonectria; Ilyonectria_macrodidyma
bacteria19519	1.74179456	Bacteria; Bacteroidetes; Bacteroidia; Cytophagales; Microscillaceae; OLB12
protist9170	1.814598083	Eukaryota; Amoebozoa; Lobosa; Lobosa_X; Lobosa_XX; LKM74-lineage
bacteria11944	1.882312603	Bacteria; Actinobacteria; Thermoleophilia; Gaiellales; Gaiellaceae; Gaiella
bacteria29085	1.97760192	Bacteria; Gemmatimonadetes; Gemmatimonadetes; Gemmatimonadales; Gemmatimonadaceae; Gemmatimonas
bacteria45499	1.998391813	Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas
bacteria10671	2.04981081	Bacteria; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioidaceae; Nocardioidea
protist8421	2.087093673	Eukaryota; Rhizaria; Cercozoa; Filosa-Thecofilosea; Cryomonadida
bacteria24431	2.093089999	Bacteria; Chloroflexi; KD4-96
bacteria53622	2.176132895	Bacteria; Verrucomicrobia; Verrucomicrobiae; Chthoniobacteriales; Chthoniobacteraceae; Candidatus_Udaeobacter
bacteria10447	2.246276601	Bacteria; Actinobacteria; Actinobacteria; Propionibacteriales; Nocardioidaceae; Aeromicrobium
bacteria6923	2.287068776	Bacteria; Acidobacteria; Subgroup_6
bacteria24538	2.43717489	Bacteria; Chloroflexi; KD4-96
protist9309	2.437269639	Eukaryota; Rhizaria; Cercozoa; Filosa Sarcomonadea; Cercomonadida; Cercomonadidae; Eocercomonas
protist8913	2.536539595	Eukaryota; Rhizaria; Cercozoa; Filosa-Sarcomonadea; Cercomonadida; Cercomonadidae; Cercomonas
bacteria9523	2.711379824	Bacteria; Actinobacteria; Actinobacteria; Kineosporiales; Kineosporiaceae; Kineosporia
protist9077	2.944651071	Eukaryota; Rhizaria; Cercozoa; Endomyxa; Vampyrellida; Leptophryidae; Platyreta; Platyreta_germanica
bacteria7938	3.497150393	Bacteria; Actinobacteria; Acidimicrobiia; Microtrichales; Ilumatobacteraceae
bacteria24601	6.59076502	Bacteria; Chloroflexi; KD4-96
bacteria50212	9.056035343	Bacteria; Proteobacteria; Gammaproteobacteria; Betaproteobacteriales; Burkholderiaceae; Piscinibacter

Supplementary Table 11. The microbial functional genes category selected by random forest model.

KEGG Number	%IncMSE	Gene Name and Descriptions
K03817	10.52399947	rimL; encodes ribosomal-protein-serine acetyltransferase [EC:2.3.1.-]
K03412	9.433292501	cheB; encodes two-component system, chemotaxis family, protein-glutamate encodes methyltransferase/glutaminase [EC:3.1.1.61 3.5.1.44]
K05715	8.416117867	2PGK; encodes 2-phosphoglycerate kinase [EC:2.7.2.16]
K11070	7.218036525	potC; encodes spermidine/putrescine transport system permease protein
K15526	7.030536354	mshC; encodes L-cysteine:1D-myo-inositol 2-amino-2-deoxy-alpha-D- encodes glucopyranoside ligase [EC:6.3.1.13]
K01575	6.798186697	alsD; encodes alpha-acetolactate decarboxylase [EC:4.1.1.5]
K01613	5.800810401	psd, PISD; encodes phosphatidylserine decarboxylase [EC:4.1.1.65]
K15724	5.609084204	erpA; encodes iron-sulfur cluster insertion protein
K22348	5.551351062	moxA; encodes manganese oxidase [EC:1.16.3.3]
K00382	5.011819425	DLD, lpd, pdhD; encodes dihydrolipoamide dehydrogenase [EC:1.8.1.4]
K13979	4.872099662	yahK; encodes alcohol dehydrogenase (NADP+) [EC:1.1.1.2]
K06944	4.556027745	DRG; encodes developmentally regulated GTP binding protein
K03147	4.440759519	thiC; encodes phosphomethylpyrimidine synthase [EC:4.1.99.17]
K06223	4.3458947	dam; encodes DNA adenine methylase [EC:2.1.1.72]
K10716	4.253146944	kch, trkA, mthK, pch; encodes voltage-gated potassium channel encodes site-specific DNA-methyltransferase (cytosine-N4-specific) [EC:2.1.1.113]
K00590	4.238042263	tadA; encodes tRNA(adenine34) deaminase [EC:3.5.4.33]
K11991	4.151510885	rfk; encodes riboflavin kinase, archaea type [EC:2.7.1.161]
K07732	3.984098921	whiEII; encodes putative monooxygenase
K14673	3.977842835	etbAc; encodes ethylbenzene dioxygenase ferredoxin component
K14750	3.87412085	rnd; encodes ribonuclease D [EC:3.1.13.5]
K03684	3.735205474	gadB; encodes glutamate decarboxylase [EC:4.1.1.15]
K01580	3.698756656	udg; encodes uracil-DNA glycosylase [EC:3.2.2.27]
K21929	3.615160658	lsrF; encodes 3-hydroxy-5-phosphonooxypentane-2,4-dione thiolase [EC:2.3.1.245]
K08321	3.614818934	tilS-hprT; encodes bifunctional protein TilS/HprT [EC:6.3.4.19 2.4.2.8]
K15780	3.58217425	CPOX, hemF; encodes coproporphyrinogen III oxidase [EC:1.3.3.3]
K00228	3.575177699	cysD; encodes sulfate adenylyltransferase subunit 2 [EC:2.7.7.4]
K00957	3.572391684	folP; encodes dihydropteroate synthase [EC:2.5.1.15]
K00796	3.495569583	manC, cpsB; encodes mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]
K00971	3.472561101	encodes hypothetical protein
K07005	3.388788214	udp, UPP; encodes uridine phosphorylase [EC:2.4.2.3]
K00757	3.356521311	flgD; encodes flagellar basal-body rod modification protein FlgD
K02389	3.346527042	yafP; encodes putative acetyltransferase [EC:2.3.1.-]
K03830	3.334485945	phoD; encodes alkaline phosphatase D [EC:3.1.3.1]
K01113	3.318044764	encodes AraC family transcriptional regulator
K07506	3.30159563	

K11074	3.285839268	potI; encodes putrescine transport system permease protein
K02477	3.217251375	encodes two-component system, LytTR family, response regulator
K02372	3.182110552	fabZ; encodes 3-hydroxyacyl-[acyl-carrier-protein] dehydratase [EC:4.2.1.59]
K01429	3.108783424	ureB; encodes urease subunit beta [EC:3.5.1.5]
K07978	3.048503008	plmA; encodes GntR family transcriptional regulator
K02067	3.020237719	mldA; encodes ABC-type organic solvent transporter
K02834	3.01826527	rbfA; encodes ribosome-binding factor A
K03888	2.987447973	MQCRC, qcrC, bfcC, petD; encodes menaquinol-cytochrome c reductase cytochrome b/c subunit
K18369	2.955104382	adh2; encodes alcohol dehydrogenase [EC:1.1.1.-]
K05375	2.924607257	mbtH; encodes MbtH protein
K09123	2.890147147	lhpI; encodes cis-L-3-hydroxyproline dehydratase [EC:4.2.1.171]
K14260	2.887967719	alaA; encodes alanine-synthesizing transaminase [EC:2.6.1.66 2.6.1.2]
K05995	2.854918216	pepE; encodes dipeptidase E [EC:3.4.13.21]
K00992	2.82311476	murU; encodes N-acetyl-alpha-D-muramate 1-phosphate uridylyltransferase [EC:2.7.7.99]
K10944	2.807431162	pmoA; encodes methane monooxygenase subunit A [EC:1.14.18.3 1.14.99.39]
K07402	2.789823794	xdhC; encodes xanthine dehydrogenase accessory factor
K07358	2.770916732	fimE; encodes type 1 fimbriae regulatory protein FimE
K01703	2.719912562	leuC, IPMI-L; encodes 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit [EC:4.2.1.33 4.2.1.35]
K16370	2.71093342	pfkB; encodes 6-phosphofructokinase 2 [EC:2.7.1.11]
K03306	2.709234673	TC.PIT; encodes inorganic phosphate transporter, PiT family
K08281	2.667119113	pncA; encodes nicotinamidase/pyrazinamidase [EC:3.5.1.19 3.5.1.-]
K00975	2.639688639	glgC; encodes glucose-1-phosphate adenylyltransferase [EC:2.7.7.27]
K01847	2.637186861	MUT; encodes methylmalonyl-CoA mutase [EC:5.4.99.2]
K00917	2.630221232	lacC; encodes tagatose 6-phosphate kinase [EC:2.7.1.144]
K00203	2.620503789	fwdD, fmdD; encodes formylmethanofuran dehydrogenase subunit D [EC:1.2.7.12]
K22015	2.61706471	fdhF; encodes formate dehydrogenase (hydrogenase) [EC:1.17.98.4 1.17.98.-]
K21636	2.582485256	nrdD; encodes ribonucleoside-triphosphate reductase (formate) [EC:1.1.98.6]
K20140	2.581408995	cfiA; encodes 2-oxoglutarate carboxylase large subunit [EC:6.4.1.7]
K11312	2.573223281	encodes cupin 2 domain-containing protein
K10233	2.56958235	aglF, ggtC; encodes alpha-glucoside transport system permease protein
K07577	2.560830353	encodes putative mRNA 3-end processing factor
K00174	2.559074415	korA, oorA, oforA; encodes 2-oxoglutarate/2-oxoacid ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3 1.2.7.11]
K20238	2.546304553	encodes sphingolipid C9-methyltransferase [EC:2.1.1.317]
K18292	2.528824726	encodes (S)-citramalyl-CoA lyase [EC:4.1.3.25]
K09726	2.521239828	encodes hypothetical protein
K02621	2.516457255	parC; encodes topoisomerase IV subunit A [EC:5.6.2.2]
K01854	2.514008556	glf; encodes UDP-galactopyranose mutase [EC:5.4.99.9]
K04800	2.512776149	rflC; encodes replication factor C large subunit

K03428	2.484661461	bchM, chlM; encodes magnesium-protoporphyrin O-methyltransferase [EC:2.1.1.11]
K02453	2.461494043	gspD; encodes general secretion pathway protein D
K00663	2.445403182	aacA; encodes aminoglycoside 6'-N-acetyltransferase [EC:2.3.1.82]
K02626	2.410025578	pdaD; encodes arginine decarboxylase [EC:4.1.1.19]
K18566	2.40418576	thnF, cmmF; encodes N-acetyltransferase [EC:2.3.1.-]
K09779	2.363063754	encodes hypothetical protein
K00609	2.355028382	pyrB, PYR2; encodes aspartate carbamoyltransferase catalytic subunit [EC:2.1.3.2]
K00001	2.348317313	adh; encodes alcohol dehydrogenase [EC:1.1.1.1]
K13052	2.327364833	divIC, divA; encodes cell division protein DivIC
K00652	2.319547906	bioF; encodes 8-amino-7-oxononanoate synthase [EC:2.3.1.47]
K03427	2.315433648	hsdM; encodes type I restriction enzyme M protein [EC:2.1.1.72]
K11102	2.304651592	gltP, gltT; encodes proton glutamate symport protein
K10530	2.30313178	lctO; encodes L-lactate oxidase [EC:1.1.3.2]
K05337	2.285102019	fer; encodes ferredoxin
K03416	2.282991496	encodes methylmalonyl-CoA carboxyltransferase 5S subunit [EC:2.1.3.1]
K00615	2.277915174	tktA, tktB; encodes transketolase [EC:2.2.1.1]
K06872	2.277404831	ygcG; encodes hypothetical protein
K21470	2.273828758	ycbB; encodes L,D-transpeptidase YcbB
K00568	2.25562054	ubiG; encodes 2-polyprenyl-6-hydroxyphenyl methylase / 3-demethylubiquinone-9 3-methyltransferase [EC:2.1.1.222 2.1.1.64]
K00410	2.243950535	fbcH; encodes ubiquinol-cytochrome c reductase cytochrome b/c1 subunit
K01997	2.236041488	livH; encodes branched-chain amino acid transport system permease protein
K19517	2.222217494	MIK; encodes 1D-myo-inositol 3-kinase [EC:2.7.1.64]
K20712	2.208158286	glnA; encodes 3-(hydroxyamino)phenol mutase [EC:5.4.4.3]
K01724	2.206233878	PCBD, phhB; encodes 4a-hydroxytetrahydrobiopterin dehydratase [EC:4.2.1.96]
K07180	2.205208043	prkA; encodes serine protein kinase
K00362	2.196495629	nirB; encodes nitrite reductase (NADH) large subunit [EC:1.7.1.15]
K02914	2.19387589	RP-L34, MRPL34, rpmH; encodes large subunit ribosomal protein L34
K05565	2.187636219	mnhA, mrpA; encodes multicomponent Na ⁺ :H ⁺ antiporter subunit A
K03667	2.186754584	hslU; encodes ATP-dependent HslUV protease ATP-binding subunit HslU
K04088	2.184511329	hflK; encodes modulator of FtsH protease HflK
K07039	2.182399732	yecA; encodes conserved metal-binding protein
K11689	2.176131895	dctQ; encodes C4-dicarboxylate transporter, DctQ subunit
K00625	2.152332877	pta; encodes phosphate acetyltransferase [EC:2.3.1.8]
K00367	2.129932068	narB; encodes ferredoxin-nitrate reductase [EC:1.7.7.2]
K19286	2.128005106	nfrA2; encodes FMN reductase [NAD(P)H] [EC:1.5.1.39]
K07095	2.123895903	yfcE; encodes phosphodiesterase YfcE
K09143	2.105335904	encodes hypothetical protein
K02406	2.080609046	fliC, hag; encodes flagellin
K03089	2.075020892	rpoH; encodes RNA polymerase sigma-32 factor

K16147	2.069873354	glgE; encodes starch synthase (maltosyl-transferring) [EC:2.4.99.16]
K02666	2.065668625	pilQ; encodes type IV pilus assembly protein PilQ
K22024	2.06535006	pdxA2; encodes 4-phospho-D-threonate 3-dehydrogenase / 4-phospho-D-erythronate 3-dehydrogenase [EC:1.1.1.408 1.1.1.409]
K07357	2.057975025	fimB; encodes type 1 fimbriae regulatory protein FimB
K06076	2.055225931	fadL; encodes long-chain fatty acid transport protein
K00758	2.053611009	deoA; encodes thymidine phosphorylase [EC:2.4.2.4]
K03781	2.048667511	katE; encodes hydroperoxidase HP(III) [EC:1.11.1.6]
K00255	2.045879474	ACADL; encodes long-chain-acyl-CoA dehydrogenase [EC:1.3.8.8]
K03878	2.04358103	ND1; encodes NADH-ubiquinone oxidoreductase chain 1 [EC:7.1.1.2]
K01602	2.039622971	rbcS, cbbS; encodes ribulose-bisphosphate carboxylase small chain [EC:4.1.1.39]
K02904	2.033753571	RP-L29, rpmC; encodes large subunit ribosomal protein L29
K03772	2.027828078	fkpA; encodes FKBP-type peptidyl-prolyl cis-trans isomerase FkpA [EC:5.2.1.8]
K15777	2.021191774	DOPA; encodes 4,5-DOPA dioxygenase extradiol [EC:1.13.11.-]
K20074	2.016506977	prpC, phpP; encodes PPM family protein phosphatase [EC:3.1.3.16]
K13421	2.014628016	UMPS; encodes uridine monophosphate synthetase [EC:2.4.2.10 4.1.1.23]
K02992	2.007886492	RP-S7; encodes small subunit ribosomal protein S7
K10215	2.006879283	ethA; encodes monooxygenase [EC:1.14.13.-]
K09128	2.005917129	acnX2; encodes mevalonate 5-phosphate dehydratase small subunit
K04618	1.997916988	GAOA; encodes galactose oxidase [EC:1.1.3.9]
K13853	1.9957333	aroG, aroA; encodes 3-deoxy-7-phosphoheptulonate synthase / chorismate mutase [EC:2.5.1.54 5.4.99.5]
K03940	1.992669213	NDUFS7; encodes NADH dehydrogenase (ubiquinone) Fe-S protein 7 [EC:7.1.1.2]
K00215	1.987658552	dapB; encodes 4-hydroxy-tetrahydrodipicolinate reductase [EC:1.17.1.8]
K00406	1.969372654	ccoP; encodes cytochrome c oxidase cbb3-type subunit III
K08744	1.958530126	CRLS; encodes cardiolipin synthase (CMP-forming) [EC:2.7.8.41]
K03976	1.925340894	ybaK, ebsC; encodes Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase [EC:3.1.1.-]
K19700	1.924316958	sap; encodes 3-succinoylsemialdehyde-pyridine dehydrogenase [EC:1.2.1.83]
K03040	1.922836353	rpoA; encodes DNA-directed RNA polymerase subunit alpha [EC:2.7.7.6]
K13277	1.920041435	epr; encodes minor extracellular protease Epr [EC:3.4.21.-]
K02674	1.915431502	pilY1; encodes type IV pilus assembly protein PilY1
K00801	1.914671266	FDFT1; encodes farnesyl-diphosphate farnesyltransferase [EC:2.5.1.21]
K03881	1.912742478	ND4; encodes NADH-ubiquinone oxidoreductase chain 4 [EC:7.1.1.2]
K15738	1.911918497	uup; encodes ABC transport system ATP-binding/permease protein
K03305	1.90644192	TC.POT; encodes proton-dependent oligopeptide transporter, POT family
K01057	1.906054566	devB; encodes 6-phosphogluconolactonase [EC:3.1.1.31]
K03536	1.900238336	rnpA; encodes ribonuclease P protein component [EC:3.1.26.5]
K01555	1.900154886	fahA; encodes fumarylacetoacetase [EC:3.7.1.2]
K06370	1.899674437	safA; encodes morphogenetic protein associated with SpoVID
K11325	1.889687896	encodes L-cysteine/cystine lyase

K01759	1.88942466	gloA; encodes lactoylglutathione lyase [EC:4.4.1.5]
K04757	1.887874953	rsbW; encodes serine/threonine-protein kinase RsbW [EC:2.7.11.1]
K22100	1.877903525	trpF; encodes 2,5-diamino-6-(5-phospho-D-ribosylamino)pyrimidin-4(3H)-one isomerase/dehydratase [EC:4.2.1.160]
K07140	1.877104427	encodes molybdenum cofactor sulfurase isoform X1
K11735	1.874093628	encodes gabP; GABA permease
K00337	1.867740082	nuoH; encodes NADH-quinone oxidoreductase subunit H [EC:7.1.1.2]
K04760	1.867390523	greB; encodes transcription elongation factor GreB
K00790	1.851318869	murA; encodes UDP-N-acetylglucosamine 1-carboxyvinyltransferase [EC:2.5.1.7]
K04079	1.850587818	htpG; encodes molecular chaperone HtpG

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