

Supplementary Information for

**Bacterial biogeography in China and its association to land use and
soil organic carbon**

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This file includes: Supplemental Figures. S1-S7

Table S1-S4

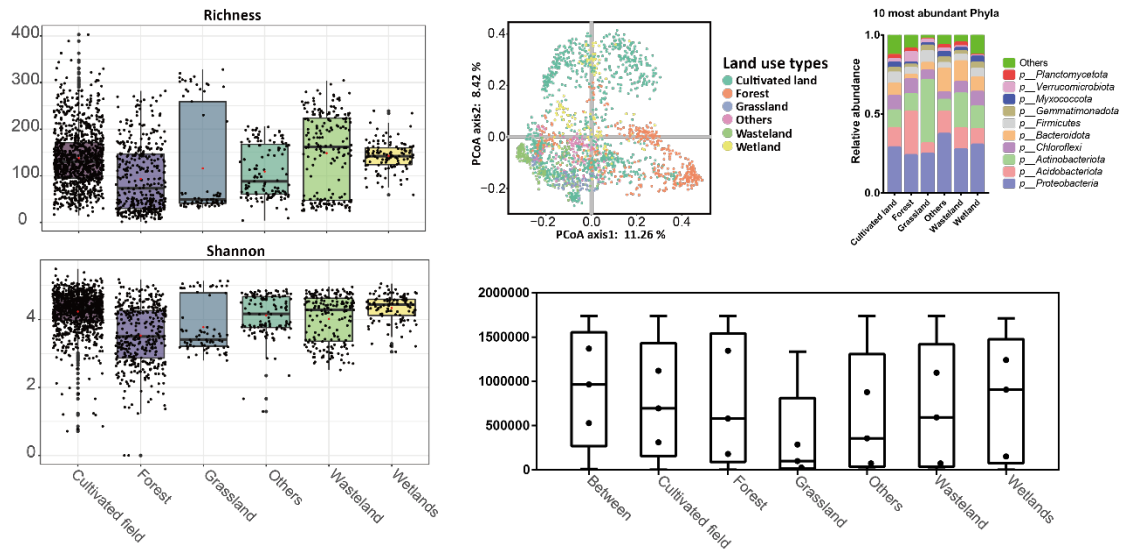


Figure S1 (a, b) Shannon index and richness calculated at the genus level. Different letters represent significant differences between land-use types (Kruskal-Wallis test, $P < 0.05$). The red dot of the boxplot represents the mean value. (c, d) PCoA of Bray-Curtis dissimilarities of the microbial communities at the genus level. The between represent the difference of multiple land use types. Statistical significance was evaluated using a PERMANOVA. The black line of the boxplot represents the mean value. (e) Effects of land-use type on the community composition of the main bacterial phyla.

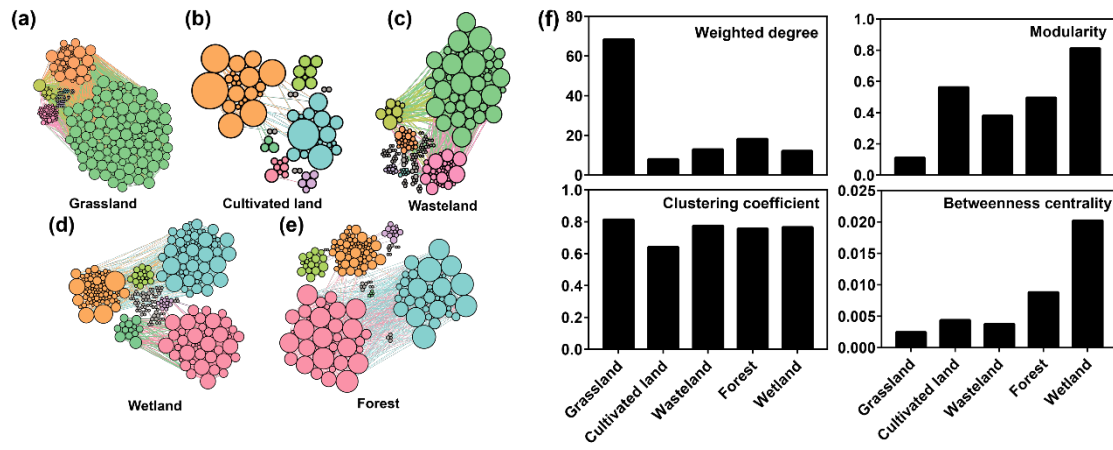


Figure S2 (a-e) Co-occurrence patterns of genera in the land-use types. Each node represents a genus. (f) Weighted degree, modularity, clustering coefficient and centrality of the co-occurrence networks.

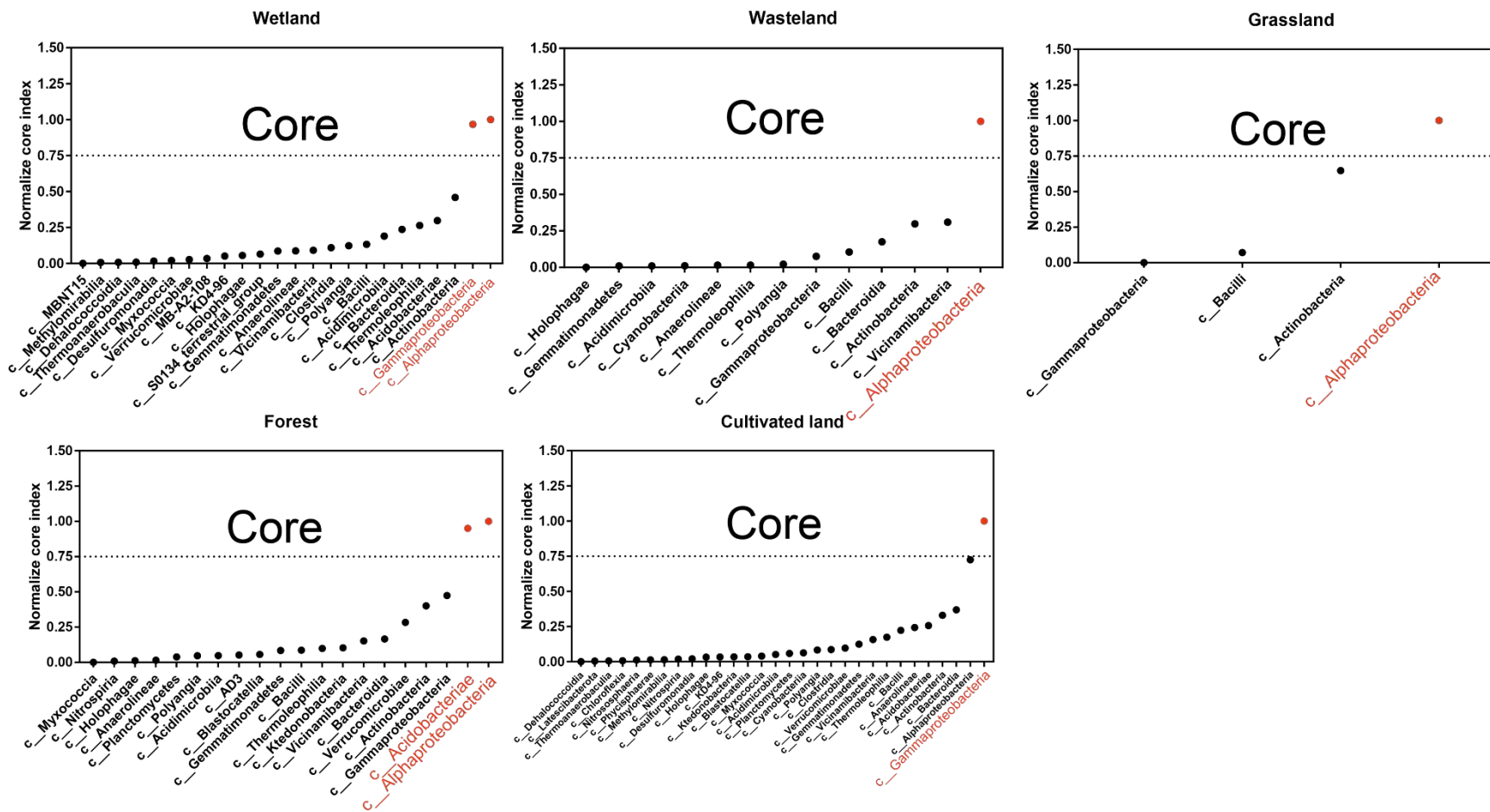


Figure S3 Core microbes at the class level in the land-use types. Core microbes with a core index >0.75 are shown in red.

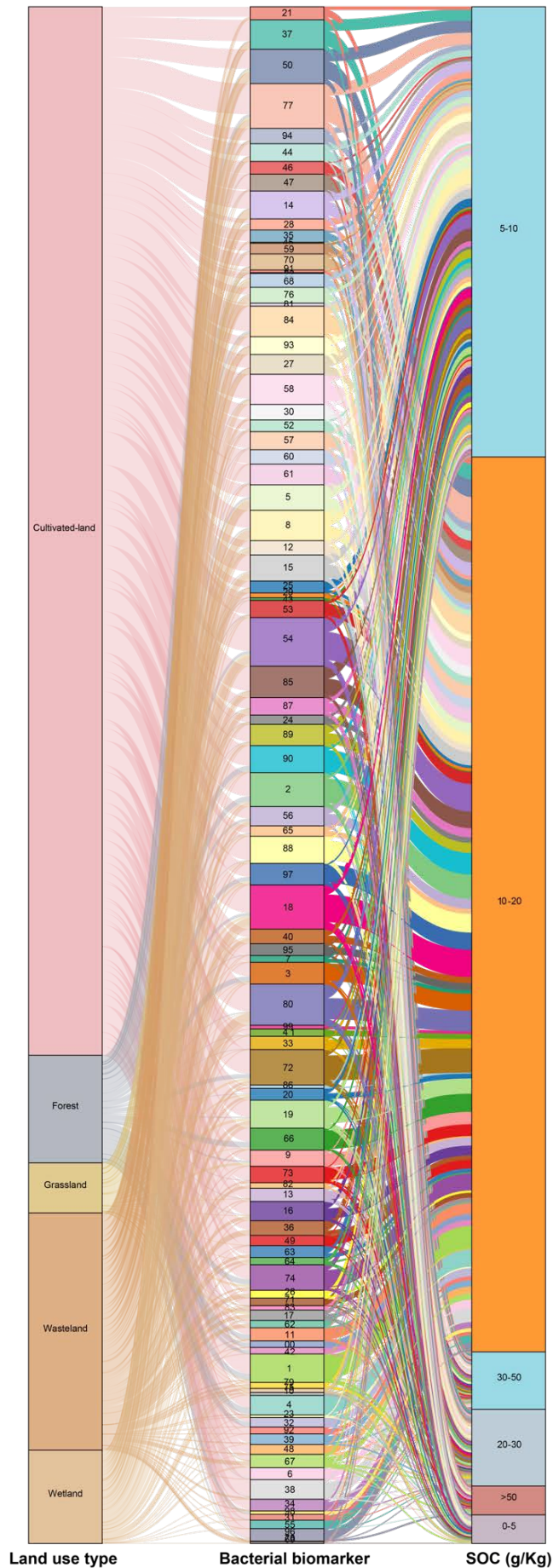


Figure S4 Sankey diagram demonstrating the relationship between the land-use type, 100 most important biomarkers and SOC concentration in China. The colors of the lines indicate the level of the 100 most important biomarkers.

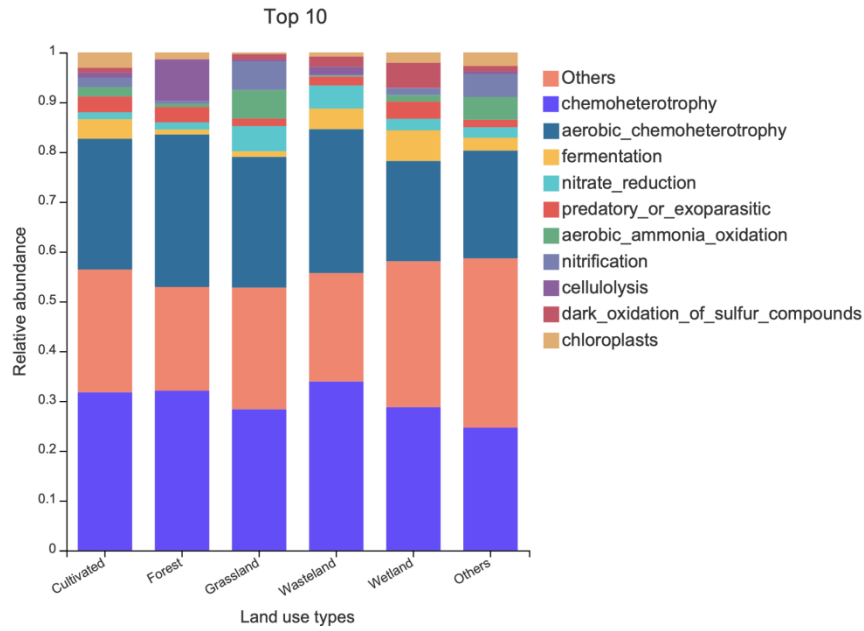


Figure S6 Functional potential of all microorganisms associated with soil nutrient cycling (top 10 abundant cycles) in different land uses. The functional analysis of microorganisms associated with nutrient cycling was achieved using the FAPROTAX (<http://www.cloud.biomicroclass.com/CloudPlatform/SoftPage/FAP>).

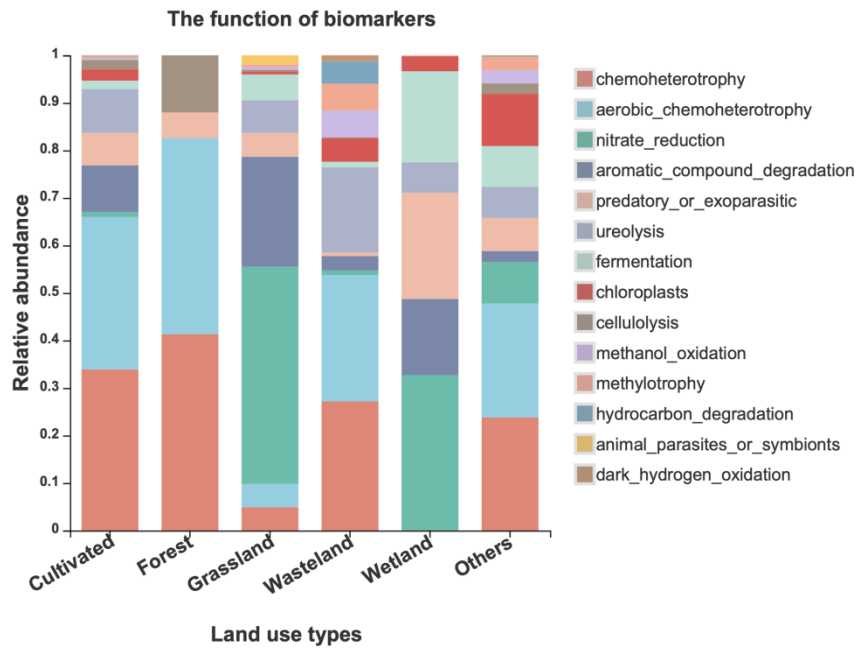


Figure S7 Functional potential of 100 biomarkers (100 most important genera calculated by random forest model and sorted by increase node purity) associated with soil nutrient cycling in different land uses. The functional analysis of microorganisms associated with nutrient cycling was achieved using the FAPROTAX (<http://www.cloud.biomicroclass.com/CloudPlatform/SoftPage/FAP>).

Table S1 The 269 bioproject accession numbers of the high-throughput sequencing data from 218 studies.

Index	Bioproject	Sample size	Paper Title	DOI
1	PRJNA316041	266	Climate change and human activities altered the diversity and composition of soil microbial community in alpine grasslands of the Qinghai-Tibetan Plateau	doi.org/10.1016/j.scitotenv.2016.03.221
2	PRJNA310322	27	The influence of soil properties on the size and structure of bacterial and fungal communities along a paddy soil chronosequence	doi.org/10.1016/j.ejsobi.2016.06.002
3	PRJNA315177	27	The influence of soil properties on the size and structure of bacterial and fungal communities along a paddy soil chronosequence	doi.org/10.1016/j.ejsobi.2016.06.002
5	PRJNA279223	24	Responsiveness of soil nitrogen fractions and bacterial communities to afforestation in the Loess Hilly Region (LHR) of China	10.1038/srep28469
6	PRJNA245065	26	Soil carbon content drives the biogeographical distribution of fungal communities in the black soil zone of northeast China	doi.org/10.1016/j.soilbio.2015.01.009
7	PRJNA213163	26	High throughput sequencing analysis of biogeographical distribution of bacterial communities in the black soils of northeast China	doi.org/10.1016/j.soilbio.2013.12.014
9	PRJNA298379	26	Diversity and distribution patterns of acidobacterial communities in the black soil zone of northeast China	doi.org/10.1016/j.soilbio.2015.12.021
10	PRJNA253903	15	Long-term balanced fertilization increases the soil microbial functional diversity in a phosphorus-limited paddy soil	10.1111/mec.13010
11	PRJNA255542	44	Responses of Soil Bacterial Communities to Nitrogen Deposition and Precipitation Increment Are Closely Linked with Aboveground Community Variation	10.1007/s00248-016-0730-z
12	PRJNA210332	226	Drivers of bacterial beta diversity in two temperate forests; Soil bacterial communities of different natural forest types in Northeast China; Aboveground-belowground biodiversity linkages differ in early and late successional temperate forests	doi.org/10.1007/s11284-015-1313-z; 10.1038/srep12234 10.1007/s11104-014-2165-y;
13	PRJNA291544	100	Changes of soil microbial community under different degraded gradients of alpine meadow	doi.org/10.1016/j.agee.2016.02.020
14	PRJNA295634	136	Scale-dependent effects of climate and geographic distance on bacterial diversity patterns across northern China's grasslands	10.1093/femsec/fiv133
15	PRJNA312997	115	Biogeographic Distribution Patterns of Bacteria in Typical Chinese Forest Soils	doi.org/10.3389/fmicb.2016.01106
16	PRJEB8961	40	Nitrogen fertilization directly affects soil bacterial diversity and indirectly affects bacterial community composition	doi.org/10.1016/j.soilbio.2015.09.018

17	PRJEB6148	42	Rate-specific responses of prokaryotic diversity and structure to nitrogen deposition in the <i>Leymus chinensis</i> steppe	doi.org/10.1016/j.soilbio.2014.09.009
18	PRJNA595442	24	Diminished rhizosphere and bulk soil microbial abundance and diversity across succession stages in Karst area, southwest China	doi.org/10.1016/j.apsoil.2020.103799
19	PRJNA598790	24	Diminished rhizosphere and bulk soil microbial abundance and diversity across succession stages in Karst area, southwest China	doi.org/10.1016/j.apsoil.2020.103799
20	PRJNA640847	200	Biogeographical patterns and mechanisms of microbial community assembly that underlie successional biocrusts across northern China	doi.org/10.1038/s41522-021-00188-6
21	PRJNA640833	20	Effects of growth-promoting rhizobacteria on maize growth and rhizosphere microbial community under conservation tillage in Northeast China	doi.org/10.1111/1751-7915.13693
22	PRJNA450260	60	Microbial communities in rare earth mining soil after in-situ leaching mining	doi.org/10.1016/j.scitotenv.2020.142521
23	PRJNA611054	135	The stronger impact of inorganic nitrogen fertilization on soil bacterial community than organic fertilization in short-term condition	doi.org/10.1016/j.geoderma.2020.114752
24	PRJNA476847	52	Biogeographic patterns and co-occurrence networks of diazotrophic and arbuscular mycorrhizal fungal communities in the acidic soil ecosystem of southern China	doi.org/10.1016/j.apsoil.2020.103798
25	PRJNA506324	66	Comparison of soil microbial community between planted woodland and natural grass vegetation on the Loess Plateau	doi.org/10.1016/j.foreco.2019.117817
26	PRJNA506313	33	Comparison of soil microbial community between planted woodland and natural grass vegetation on the Loess Plateau	doi.org/10.1016/j.foreco.2019.117817
27	PRJNA422172	30	Salinity controls soil microbial community structure and function in coastal estuarine wetlands	doi.org/10.1111/1462-2920.15281
28	PRJNA657738	24	Effects of disturbance to moss biocrusts on soil nutrients, enzyme activities, and microbial communities in degraded karst landscapes in southwest China	doi.org/10.1016/j.soilbio.2020.108065
29	PRJNA340057	20	Changes in soil microbial community structure during long-term secondary succession	doi.org/10.1002/ldr.3505
30	PRJNA340058	20	Changes in soil microbial community structure during long-term secondary succession	doi.org/10.1002/ldr.3505
31	PRJNA437231	144	Effects of long-term no-tillage with different straw mulching frequencies on soil microbial community and the abundances of two soil-borne pathogens	doi.org/10.1016/j.apsoil.2019.103488
32	PRJNA573412	18	The diversity of microbial community and function varied in response to different agricultural residues composting	doi.org/10.1016/j.scitotenv.2020.136983

33	PRJNA560408	36	Long term effects of management practice intensification on soil microbial community structure and co-occurrence network in a non-timber plantation	doi.org/10.1016/j.foreco.2019.117805
35	PRJNA437336	144	Long-term no-tillage and different residue amounts alter soil microbial community composition and increase the risk of maize root rot in northeast China	doi.org/10.1016/j.still.2019.104452
36	PRJNA592248	24	Characteristics of the soil microbial community in the forestland of <i>Camellia oleifera</i>	doi.org/10.7717/peerj.9117
37	PRJNA640885	27	Peat-vermiculite alters microbiota composition towards increased soil fertility and crop productivity	doi.org/10.1007/s11104-021-04851-x
38	PRJNA429554	228	Tight coupling of fungal community composition with soil quality in a Chinese fir plantation chronosequence	doi.org/10.1002/ldr.3771
39	PRJNA564116	72	Fertilization regime has a greater effect on soil microbial community structure than crop rotation and growth stage in an agroecosystem	doi.org/10.1016/j.apsoil.2020.103510
40	PRJNA564154	72	Fertilization regime has a greater effect on soil microbial community structure than crop rotation and growth stage in an agroecosystem	doi.org/10.1016/j.apsoil.2020.103510
41	PRJNA637813	24	Profiling multiple heavy metal contamination and bacterial communities surrounding an iron tailing pond in Northwest China	doi.org/10.1016/j.scitotenv.2020.141827
42	PRJNA522864	27	Interactions between biochar and nitrogen impact soil carbon mineralization and the microbial community	doi.org/10.1016/j.still.2019.104437
43	PRJNA522870	27	Interactions between biochar and nitrogen impact soil carbon mineralization and the microbial community	doi.org/10.1016/j.still.2019.104437
44	PRJEB29291	18	Fifteen-Year Application of Manure and Chemical Fertilizers Differently Impacts Soil ARGs and Microbial Community Structure	doi.org/10.3389/fmicb.2020.00062
45	PRJNA600330	18	Seasonal Microbial Community Characteristic and Its Driving Factors in a Copper Tailings Dam in the Chinese Loess Plateau	doi.org/10.3389/fmicb.2020.01574
46	PRJNA605500	18	Seasonal Microbial Community Characteristic and Its Driving Factors in a Copper Tailings Dam in the Chinese Loess Plateau	doi.org/10.3389/fmicb.2020.01574
47	PRJNA575814	72	Spatiotemporal vanadium distribution in soils with microbial community dynamics at vanadium smelting site	doi.org/10.1016/j.envpol.2020.114782
48	PRJNA527630	33	Spatiotemporal vanadium distribution in soils with microbial community dynamics at vanadium smelting site	doi.org/10.1016/j.envpol.2020.114782
49	PRJNA526110	41	Soil bacterial communities vary with grassland degradation in the Qinghai Lake watershed	doi.org/10.1007/s11104-020-04823-7

50	PRJNA593866	32	Soil microbial communities and their relationships to soil properties at different depths in an alpine meadow and desert grassland in the Qilian mountain range of China	
51	PRJNA593869	32	Soil microbial communities and their relationships to soil properties at different depths in an alpine meadow and desert grassland in the Qilian mountain range of China	
52	PRJNA661140	12	Variations in the diversity of the soil microbial community and structure under various categories of degraded wetland in Sanjiang Plain, northeastern China	doi.org/10.1002/ldr.3872
53	PRJNA578945	30	Crop rotation suppresses soil-borne Fusarium wilt of banana and alters microbial communities	doi.org/10.1080/03650340.2020.1839058
54	PRJNA578172	30	Crop rotation suppresses soil-borne Fusarium wilt of banana and alters microbial communities	doi.org/10.1080/03650340.2020.1839058
55	PRJNA549054	12	Dissecting the effect of continuous cropping of potato on soil bacterial communities as revealed by high-throughput sequencing	doi.org/10.1371/journal.pone.0233356
56	PRJNA588718	27	The responses of soil bacterial communities and enzyme activities to the edaphic properties of coal mining areas in Central China	doi.org/10.1371/journal.pone.0231198
57	PRJNA507126	48	Soil chemical properties and geographical distance exerted effects on arbuscular mycorrhizal fungal community composition in pear orchards in Jiangsu Province, China	10.1016/j.apsoil.2019.05.017
58	PRJNA647612	20	Bacterial richness is negatively related to potential soil multifunctionality in a degraded alpine meadow	doi.org/10.1016/j.ecolind.2020.106996
59	PRJNA647603	20	Bacterial richness is negatively related to potential soil multifunctionality in a degraded alpine meadow	doi.org/10.1016/j.ecolind.2020.106996
60	PRJNA573484	32	Long-term nitrogen input alters plant and soil bacterial, but not fungal beta diversity in a semiarid grassland	10.1111/gcb.15681
61	PRJNA573488	32	Long-term nitrogen input alters plant and soil bacterial, but not fungal beta diversity in a semiarid grassland	10.1111/gcb.15681
62	PRJNA507935	21	Driving forces linking microbial community structure and functions to enhanced carbon stability in biochar-amended soil	10.1016/j.envint.2019.105211
63	PRJNA512875	48	A Rhizosphere-Derived Consortium of <i>Bacillus subtilis</i> and <i>Trichoderma harzianum</i> Suppresses Common Scab of Potato and Increases Yield	10.1016/j.csbj.2019.05.003
64	PRJNA319330	14	Microbial Community Responses to Vanadium Distributions in Mining Geological Environments and Bioremediation Assessment	10.1029/2018JG004670

65	PRJNA376077	18	Soil microbial community assemblage and its seasonal variability in alpine treeline ecotone on the eastern Qinghai-Tibet Plateau	10.1007/s42832-019-0006-x
66	PRJNA532487	12	Effect of Drought Stress and Developmental Stages on Microbial Community Structure and Diversity in Peanut Rhizosphere Soil	10.3390/ijms20092265
67	PRJNA397171	2	A plant growth-promoting bacterium alters the microbial community of continuous cropping poplar trees' rhizosphere	10.1111/jam.14194
68	PRJNA477767	39	The occurrence of potato common scab correlates with the community composition and function of the geocaulosphere soil microbiome	10.1186/s40168-019-0629-2
69	PRJNA552653	24	Bacterial shifts during in-situ mineralization bio-treatment to nonferrous metal(loid) tailings	10.1016/j.envpol.2019.113165
70	PRJNA503944	16	Microbial response to CaCO ₃ application in an acid soil in southern China	10.1016/j.jes.2018.12.007
71	PRJNA419588	54	Effects of soil properties, heavy metals, and PBDEs on microbial community of e-waste contaminated soil	10.1016/j.ecoenv.2019.05.027
72	PRJNA530114	26	Co-occurrence patterns of microbial communities affected by inoculants of plant growth-promoting bacteria during phytoremediation of heavy metal-contaminated soils	10.1016/j.ecoenv.2019.109504
73	PRJNA394928	24	Salinity is a key determinant for soil microbial communities in a desert ecosystem	10.1128/mSystems.00225-18
74	PRJNA286946	1	Variations in Soil Bacterial Composition and Diversity in Newly Formed Coastal Wetlands	10.3389/fmicb.2018.03256
75	PRJNA478705	31	Response of freshwater sediment archaeal community to metal spill; Pyrosequencing-based assessment of soil microbial community structure and analysis of soil properties with vegetable planted at different years under greenhouse conditions	10.1016/j.chemosphere.2018.11.054; 10.1016/j.still.2018.11.008
76	PRJNA487518	20	Diversity and function of soil bacterial communities in response to long-term intensive management in a subtropical bamboo forest	10.1016/j.geoderma.2019.113894
77	PRJNA505996	8	Distinct Successions of Common and Rare Bacteria in Soil Under Humic Acid Amendment - A Microcosm Study	10.3389/fmicb.2019.02271
78	PRJNA427384	50	Distinct methanotrophic communities exist in habitats with different soil water contents	10.1016/j.soilbio.2019.02.007
79	PRJNA486259	24	Differential responses of the acidobacterial community in the topsoil and subsoil to fire disturbance in Pinus tabulaeformis stands	10.7717/peerj.8047
80	PRJNA430782	84	Biofertilizers regulate the soil microbial community and enhance Panax ginseng yields	10.1186/s13020-019-0241-1

81	PRJNA494298	18	Changes in the soil microbial community are associated with the occurrence of <i>Panax quinquefolius</i> L. root rot diseases	10.1007/s11104-018-03928-4
82	PRJNA397343	3	The effect of <i>Glomus intraradices</i> on the physiological properties of <i>Panax ginseng</i> and on rhizospheric microbial diversity	10.1016/j.jgr.2017.08.005
83	PRJNA438424	37	Deterministic processes dominate soil microbial community assembly in subalpine coniferous forests on the Loess Plateau	10.7717/peerj.6746
84	PRJNA307123	2	The inhibitory effect of cadmium and/or mercury on soil enzyme activity, basal respiration, and microbial community structure in coal mine-affected agricultural soil	10.1007/s13213-019-01478-3
85	PRJNA472201	24	Change of soil microbial community under long-term fertilization in a reclaimed sandy agricultural ecosystem	10.7717/peerj.6497
86	PRJNA479702	20	Characterization of iron-metabolizing communities in soils contaminated by acid mine drainage from an abandoned coal mine in Southwest China	10.1007/s11356-019-04336-6
87	PRJNA403998	118	Impact of long-term grazing exclusion on soil microbial community composition and nutrient availability	10.1007/s00374-018-01336-5
88	PRJNA388719	54	Tropical rainforest conversion into rubber plantations results in changes in soil fungal composition, but underlying mechanisms of community assembly remain unchanged	10.1016/j.geoderma.2020.114505
89	PRJNA492504	234	Soil bacterial and eukaryotic co-occurrence networks across a desert climate gradient in northern China	10.1002/ldr.3844
90	PRJNA510006	42	Effects of organic fertilizer on soil nutrient status, enzyme activity, and bacterial community diversity in <i>Leymus chinensis</i> steppe in Inner Mongolia, China	10.1371/journal.pone.0240559
91	PRJNA516026	80	The microbial network property as a bio-indicator of antibiotic transmission in the environment.	10.1016/J.SCITOTENV.2020.143712
92	PRJNA521835	61	Vegetation type impacts microbial interaction with antimony contaminants in a mining-contaminated soil environment	10.1016/j.envpol.2019.06.070
93	PRJNA525286	42	The mechanisms of improving coastal saline soils by planting rice	10.1016/j.scitotenv.2019.135529
94	PRJNA525518	40	Long-term phosphorus deficiency decreased bacterial-fungal network complexity and efficiency across three soil types in China as revealed by network analysis	10.1016/j.apsoil.2020.103506
95	PRJNA526139	27	Continuous application of conservation tillage affects in situ N ₂ O emissions and nitrogen cycling gene abundances following nitrogen fertilization	10.1016/j.soilbio.2021.108239
96	PRJNA527660	27	Rhizosphere bacterial community in watermelon-wheat intercropping was more stable than in watermelon monoculture system under <i>Fusarium oxysporum</i> f. sp. <i>niveum</i> invasion	10.1007/s11104-019-04321-5

98	PRJNA528368	482	The Rhizosphere Microbiome of <i>Mikania micrantha</i> Provides Insight Into Adaptation and Invasion	10.3389/FMICB.2020.01462
99	PRJNA531335	45	High Aluminum Drives Different Rhizobacterial Communities Between Aluminum-Tolerant and Aluminum-Sensitive Wild Soybean	10.3389/fmicb.2020.01996
100	PRJNA532293	30	Zokor disturbances indicated positive soil microbial responses with carbon cycle and mineral encrustation in alpine grassland	10.1016/j.ecoleng.2019.105702
101	PRJNA533708	191	Changes in assembly processes of soil microbial communities during secondary succession in two subtropical forests	10.1016/j.soilbio.2021.108144
102	PRJNA533930	42	Contrasting bacterial communities and their assembly processes in karst soils under different land use.	10.1016/j.scitotenv.2020.142263
103	PRJNA544819	24	Responses of bacterial <i>phoD</i> gene abundance and diversity to crop rotation and feedbacks to phosphorus uptake in wheat	10.1016/j.apsoil.2020.103604
104	PRJNA550348	60	Fertility-related interplay between fungal guilds underlies plant richness-productivity relationships in natural grasslands	10.1111/nph.16390
105	PRJNA550310	60	Fertility-related interplay between fungal guilds underlies plant richness-productivity relationships in natural grasslands	10.1111/nph.16390
106	PRJNA551144	220	Mycorrhizal symbiosis modulates the rhizosphere microbiota to promote rhizobia-legume symbiosis	10.1016/j.molp.2020.12.002
107	PRJNA551722	41	Response of bacterial community in composition and function to the various DOM at river confluences in the urban area.	10.1177/1934578X20972518
108	PRJNA552986	660	Local community assembly mechanisms shape soil bacterial β diversity patterns along a latitudinal gradient	10.1038/s41467-020-19228-4
109	PRJNA553654	80	Bacterial Community Selection of <i>Russula griseocarnosa</i> Mycosphere Soil.	10.3389/fmicb.2020.00347
110	PRJNA554565	24	Effects of Continuous Cropping of Sweet Potatoes on the Bacterial Community Structure in Rhizospheric Soil	10.21203/rs.3.rs-61006/v3
111	PRJNA557316	128	Contrasting Biogeographic Patterns of Bacterial and Archaeal Diversity in the Top- and Subsoils of Temperate Grasslands	10.1128/mSystems.00566-19
112	PRJNA559440	60	Distinct microbial communities among different tissues of citrus tree <i>Citrus reticulata</i> cv. <i>Chachiensis</i>	10.1038/s41598-020-62991-z
113	PRJNA561469	45	Rhizosphere Soil Fungal Communities of Aluminum-Tolerant and -Sensitive Soybean Genotypes Respond Differently to Aluminum Stress in an Acid Soil	10.3389/fmicb.2020.01177

114	PRJNA563235	39	Periphyton improves soil conditions and offers a suitable environment for rice growth in coastal saline alkali soil	10.1002/ldr.3944
116	PRJNA563500	69	Soil bacterial taxonomic diversity is critical to maintaining the plant productivity	10.1016/J.ENVINT.2020.105766
117	PRJNA563974	48	The Responses to Long-Term Water Addition of Soil Bacterial, Archaeal, and Fungal Communities in a Desert Ecosystem	10.3390/microorganisms9050981
118	PRJNA563998	30	Effects of foliar selenium application on growth and rhizospheric soil micro-ecological environment of <i>Atractylodes macrocephala</i> Koidz	10.1016/j.sajb.2020.09.032
119	PRJNA574017	45	SOIL MICROBIAL COMMUNITY CHANGE DURING NATURAL FOREST CONVERSION TO RUBBER PLANTATIONS	10.15666/aeer/1803_43714382
120	PRJNA574849	90	Community Composition and Co-Occurrence Patterns of Diazotrophs along a Soil Profile in Paddy Fields of Three Soil Types in China	10.1007/S00248-021-01716-9
121	PRJNA579018	66	Assessing Chromium Contamination in Red Soil: Monitoring the Migration of Fractions and the Change of Related Microorganisms	10.3390/ijerph17082835
122	PRJNA579032	48	Exploring the key microbial changes in the rhizosphere that affect the occurrence of tobacco root-knot nematodes	10.1186/s13568-020-01006-6
123	PRJNA587576	42	Increasing methane (CH ₄) emissions and altering rhizosphere microbial diversity in paddy soil by combining Chinese milk vetch and rice straw	10.7717 / peerj.9653
124	PRJNA588346	61	Comparative characterization of microbial communities that inhabit arsenic-rich and antimony-rich contaminated sites: Responses to two different contamination conditions	10.1016/j.envpol.2020.114052
125	PRJNA588741	21	Indigenous Bacteria Have High Potential for Promoting <i>Salix integra</i> Thunb. Remediation of Lead-Contaminated Soil by Adjusting Soil Properties	10.3389/fmicb.2020.00924
126	PRJNA589245	162	Chemolithoautotrophic diazotrophy dominates the nitrogen fixation process in mine tailings.	10.1021/acs.est.9b07835
127	PRJNA592575	80	Changes in microbial biomass, community composition and diversity, and functioning with soil depth in two alpine ecosystems on the Tibetan plateau	10.1007/s11104-020-04712-z
128	PRJNA592716	208	Microbes changed their carbon use strategy to regulate the priming effect in an 11-year nitrogen addition experiment in grassland	https://doi.org/10.1016/j.scitotenv.2020.138645
129	PRJNA592724	208	Microbes changed their carbon use strategy to regulate the priming effect in an 11-year nitrogen addition experiment in grassland	https://doi.org/10.1016/j.scitotenv.2020.138645
130	PRJNA594154	32	Nitrate-assisted biodegradation of polycyclic aromatic hydrocarbons (PAHs) in the water-level-fluctuation zone of the three Gorges Reservoir, China: Insights from in situ microbial interaction analyses and a microcosmic experiment	10.1016/j.envpol.2020.115693

131	PRJNA594249	32	Utilization of marigold (<i>Tagetes erecta</i>) flower fermentation wastewater as a fertilizer and its effect on microbial community structure in maize rhizosphere and non-rhizosphere soil	10.1080/13102818.2020.1781548
132	PRJNA595717	20	Fencing decreases microbial diversity but increases abundance in grassland soils on the Tibetan Plateau	10.1002/ldr.3626
133	PRJNA597436	36	Metagenomics Reveal Correlations Between Microbial Organisms in Soils and the Health of <i>Populus euphratica</i>	10.3389/FMICB.2020.02095
134	PRJNA598057	36	Short-term lime application impacts microbial community composition and potential function in an acid black soil	10.1007/S11104-021-04913-0
135	PRJNA598095	36	Short-term lime application impacts microbial community composition and potential function in an acid black soil	10.1007/S11104-021-04913-0
136	PRJNA598736	178	Soil microbial community dynamics mediate the priming effects caused by in situ decomposition of fresh plant residues	10.1016/j.scitotenv.2020.139708
137	PRJNA600371	96	Seasonal effects of river flow on microbial community coalescence and diversity in a riverine network	10.1093/femsec/fiaa132
138	PRJNA600772	24	Long-Term Fertilization Shapes the Putative Electrotrophic Microbial Community in Paddy Soils Revealed by Microbial Electrosynthesis Systems	10.1021/acs.est.0c08022
139	PRJNA602554	160	Livestock overgrazing disrupts the positive associations between soil biodiversity and nitrogen availability	10.1111/1365-2435.13575
140	PRJNA606926	72	Revealing Microbiome Structure and Assembly Process in Three Rhizocompartments of <i>Achyranthes bidentata</i> Under Continuous Monoculture Regimes	10.3389/fmicb.2021.677654
141	PRJNA609530	36	Regulating soil bacterial diversity, community structure and enzyme activity using residues from golden apple snails	10.1038/s41598-020-73184-z
142	PRJNA611953	24	Changes in soil organic carbon and microbial community under varying straw incorporation strategies	10.1016/j.still.2020.104735
143	PRJNA611878	24	Changes in soil organic carbon and microbial community under varying straw incorporation strategies	10.1016/j.still.2020.104735
144	PRJNA613534	120	Halosulfuron methyl did not have a significant effect on diversity and community of sugarcane rhizosphere microflora.	10.1016/J.JHAZMAT.2020.123040
145	PRJNA622661	24	Underlying Mechanism of Wild <i>Radix pseudostellariae</i> in Tolerance to Disease Under the Natural Forest Cover	10.3389/fmicb.2020.01142

146	PRJNA623479	21	Behaviors of cadmium in rhizosphere soils and its interaction with microbiome communities in phytoremediation.	10.1016/j.chemosphere.2020.128765
147	PRJNA624250	24	Fungi are more sensitive than bacteria to drainage in the peatlands of the Zoige Plateau	10.1016/j.ecolind.2021.107367
148	PRJNA624794	24	Fungi are more sensitive than bacteria to drainage in the peatlands of the Zoige Plateau	10.1016/j.ecolind.2021.107367
149	PRJNA625373	138	Revegetation approach and plant identity unequally affect structure, ecological network and function of soil microbial community in a highly acidified mine tailings pond	doi.org/10.1016/j.scitotenv.2020.140793
150	PRJNA630545	24	A new strategy using nanoscale zero-valent iron to simultaneously promote remediation and safe crop production in contaminated soil	10.1038/s41565-020-00803-1
151	PRJNA631128	52	Diverse Bacterial Communities From Qaidam Basin of the Qinghai–Tibet Plateau: Insights Into Variations in Bacterial Diversity Across Different Regions	10.3389/fmicb.2020.554105
152	PRJNA631145	27	Bacillus circulans GN03 Alters the Microbiota, Promotes Cotton Seedling Growth and Disease Resistance, and Increases the Expression of Phytohormone Synthesis and Disease Resistance-Related Genes	10.3389/fpls.2021.644597
153	PRJNA631473	180	Synthetic community with six Pseudomonas strains screened from garlic rhizosphere microbiome promotes plant growth	10.1111/1751-7915.13640
154	PRJNA633985	21	Contribution of environmental factors on the distribution of antibiotic resistance genes in agricultural soil	10.1016/J.EJSOBI.2020.103269
155	PRJNA640527	35	The Invasion of Alternanthera philoxeroides Increased Soil Organic Carbon in a River and a Constructed Wetland With Different Mechanisms	10.3389/FEVO.2020.574528
156	PRJNA641981	39	Grassland fairy rings of Leucocalocybe mongolica represent the center of a rich soil microbial community	10.1007/s42770-021-00478-3
157	PRJNA642251	90	Soil pH has a stronger effect than arsenic content on shaping plastisphere bacterial communities in soil	10.1016/j.envpol.2021.117339
158	PRJNA643678	31	Microbial Flow Within an Air-Phyllosphere-Soil Continuum.	10.3389/FMICB.2020.615481
159	PRJNA660301	48	Disentangling Responses of the Subsurface Microbiome to Wetland Status and Implications for Indicating Ecosystem Functions	10.3390/microorganisms9020211
160	PRJNA660325	48	Disentangling Responses of the Subsurface Microbiome to Wetland Status and Implications for Indicating Ecosystem Functions	10.3390/microorganisms9020211
161	PRJNA660862	24	Nitrogen Deposition Reduces the Diversity and Abundance of cbbL Gene-Containing CO ₂ -Fixing Microorganisms in the Soil of the Stipa baicalensis Steppe	10.3389/fmicb.2021.570908

162	PRJNA663422	106	Soil properties and root traits jointly shape fine-scale spatial patterns of bacterial community and metabolic functions within a Korean pine forest	10.7717/peerj.10902
163	PRJNA715960	54	Effects of plant cultivars on the structure of bacterial and fungal communities associated with ginseng	10.1007/s11104-021-05000-0
164	PRJNA515213	36	Changes in plant Rhizosphere Microbial Communities under Different Vegetation Restoration patterns in Karst and Non-karst ecosystems	10.1038/s41598-019-44985-8
165	PRJNA515337	36	Changes in plant Rhizosphere Microbial Communities under Different Vegetation Restoration patterns in Karst and Non-karst ecosystems	10.1038/s41598-019-44985-8
166	PRJNA578995	36	Plant Taxonomic Diversity Better Explains Soil Fungal and Bacterial Diversity than Functional Diversity in Restored Forest Ecosystems	10.3390/plants8110479
167	PRJNA578999	36	Plant Taxonomic Diversity Better Explains Soil Fungal and Bacterial Diversity than Functional Diversity in Restored Forest Ecosystems	10.3390/plants8110479
168	PRJNA656119	60	Effects of vegetation type, season, and soil properties on soil microbial community in subtropical forests	10.1016/j.apsoil.2020.103813
169	PRJNA656346	60	Effects of vegetation type, season, and soil properties on soil microbial community in subtropical forests	10.1016/j.apsoil.2020.103813
170	PRJNA588667	15	Long-term effects of maize straw return and manure on the microbial community in cinnamon soil in Northern China using 16S rRNA sequencing	10.1371/journal.pone.0249884
171	PRJNA700061	24	Analysis of Soil Fungal and Bacterial Communities in Tianchi Volcano Crater, Northeast China	10.3390/life11040280
173	PRJNA670299	25	Shifts in composition and function of soil fungal communities and edaphic properties during the reclamation chronosequence of an open-cast coal mining dump	10.1016/j.scitotenv.2020.144465
174	PRJNA630558	112	Succession of the Resident Soil Microbial Community in Response to Periodic Inoculations	10.1128/AEM.00046-21
175	PRJNA559597	48	Soil Microbial Composition and phoD Gene Abundance Are Sensitive to Phosphorus Level in a Long-Term Wheat-Maize Crop System	10.3389/fmicb.2020.605955
176	PRJNA562601	429	A latitudinal gradient of microbial β -diversity in continental paddy soils	10.1111/geb.13267
177	PRJNA597112	60	Dynamics of methane emission and archaeal microbial community in paddy soil amended with different types of biochar	10.1016/j.apsoil.2021.103892
178	PRJNA681439	9	Diversity of microbial communities and soil nutrients in sugarcane rhizosphere soil under water soluble fertilizer	10.1371/journal.pone.0245626

179	PRJNA615072	48	Soil microbial community responses to shortterm nitrogen addition in China's Horqin Sandy Land	10.1371/journal.pone.0242643
180	PRJNA657994	48	Effects of Living Cover on the Soil Microbial Communities and Ecosystem Functions of Hazelnut Orchards	10.3389/fpls.2021.652493
181	PRJNA639362	72	Soil pH and nutrients shape the vertical distribution of microbial communities in an alpinewetland	10.1016/j.scitotenv.2021.145780
182	PRJNA612170	18	Yak excreta-induced changes in soil microbial communities increased the denitrification rate of marsh soil under warming conditions	10.1016/j.apsoil.2021.103935
183	PRJNA631362	40	Strong agricultural management effects on soil microbial community in a non-experimental agroecosystem	10.1016/j.apsoil.2021.103970
184	PRJNA577740	36	Benzoic acid plays a part in rhizosphere microbial composition of peach seedlings grown in replanted soil	10.1016/j.rhisph.2021.100364
185	PRJNA643002	15	Crop Rotation With Cress Increases Cucumber Yields by Regulating the Composition of the Rhizosphere Soil Microbial Community	10.3389/fmicb.2021.631882
186	PRJNA644465	15	Crop Rotation With Cress Increases Cucumber Yields by Regulating the Composition of the Rhizosphere Soil Microbial Community	10.3389/fmicb.2021.631882
187	PRJNA683770	54	Comparison of Microbial Communities in Colorado Potato Beetles (<i>Leptinotarsa decemlineata</i> Say) Collected From Different Sources in China	10.3389/fmicb.2021.639913
188	PRJNA632992	40	Higher Sensitivity of Soil Microbial Network Than Community Structure under Acid Rain	10.3390/microorganisms9010118
189	PRJNA664270	48	Differential microbial assemblages associated with shikonin-producing <i>Borage</i> species in two distinct soil types	10.1038/s41598-021-90251-1
190	PRJNA685114	48	The Effects of Microbial Inoculants on Bacterial Communities of the Rhizosphere Soil of Maize	10.3390/agriculture11050389
191	PRJNA634745	66	Herbicide Selection Promotes Antibiotic Resistance in Soil Microbiomes	10.1093/molbev/msab029
192	PRJNA681095	36	Diversity and composition of the <i>Panax ginseng</i> rhizosphere microbiome in various cultivation modes and ages	10.1186/s12866-020-02081-2
193	PRJNA664653	90	Microbial assembly and association network in watermelon rhizosphere after soil fumigation for <i>Fusarium</i> wilt control	10.1016/j.agee.2021.107336
194	PRJNA600081	18	Linkage between soil ectoenzyme stoichiometry ratios and microbial diversity following the conversion of cropland into grassland	10.1016/j.agee.2021.107418

195	PRJNA707614	18	Influence of Peanut, Sorghum, and Soil Salinity on Microbial Community Composition in Interspecific Interaction Zone	10.3389/fmicb.2021.678250
196	PRJNA661057	29	Variations in Soil Enzyme Activities and Microbial Communities along an Altitudinal Gradient on the Eastern Qinghai-Tibetan Plateau	10.3390/f12060681
197	PRJNA615284	130	Temperature sensitivity of SOM decomposition is linked with a K-selected microbial community	10.1111/gcb.15593
198	PRJNA692029	36	Effects of antimony on anaerobic methane oxidization and microbial community in an antimony-contaminated paddy soil: A microcosm study	10.1016/j.scitotenv.2021.147239
199	PRJNA626484	24	Agricultural land-use change and rotation system exert considerable influences on the soil antibiotic resistome in Lake Tai Basin	10.1016/j.scitotenv.2020.144848
200	PRJNA693142	24	Microbial community structure and co-occurrence are essential for methanogenesis and its contribution to phenanthrene degradation in paddy soil	10.1016/j.jhazmat.2021.126086
201	PRJNA693175	12	Microbial community structure and co-occurrence are essential for methanogenesis and its contribution to phenanthrene degradation in paddy soil	10.1016/j.jhazmat.2021.126086
202	PRJNA630855	48	Nitrogen and water addition regulate fungal community and microbial co-occurrence network complexity in the rhizosphere of <i>Alhagi sparsifolia</i> seedlings	10.1016/j.apsoil.2021.103940
203	PRJNA685959	30	Intercropping With Aromatic Plants Increased the Soil Organic Matter Content and Changed the Microbial Community in a Pear Orchard	10.3389/fmicb.2021.616932
204	PRJNA586741	210	Exploration of Intrinsic Microbial Community Modulators in the Rice Endosphere Indicates a Key Role of Distinct Bacterial Taxa Across Different Cultivars	10.3389/fmicb.2021.629852
205	PRJNA675153	48	Livestock Manure Type Affects Microbial Community Composition and Assembly During Composting	10.3389/fmicb.2021.621126
206	PRJNA454514	120	Clomazone improves the interactions between soil microbes and affects C and N cycling functions	10.1016/j.scitotenv.2020.144730
208	PRJNA705274	15	Succession of the microbial communities and function prediction during short-term peach sawdust-based composting	10.1016/j.biortech.2021.125079
209	PRJNA705286	15	Succession of the microbial communities and function prediction during short-term peach sawdust-based composting	10.1016/j.biortech.2021.125079
211	PRJNA631871	20	Changes of acid and alkaline phosphatase activities in long-term chemical fertilization are driven by the similar soil properties and associated microbial community composition in acidic soil	10.1016/j.ejsobi.2021.103312
214	PRJNA400124	129	Microbial communities associated with Feammox in paddy soils from Southern China	//doi.org/10.1016/j.envpol.2017.08.027

215	PRJNA392724	9	Only mass migration of fungi runs through the biotopes of soil, phyllosphere, and feces	10.1007/s11368-020-02873-z
216	PRJNA359373	36	Effects of heavy metals on soil microbial community structure and diversity in the rice (<i>Oryza sativa</i> L. subsp. Japonica, Food Crops Institute of Jiangsu Academy of Agricultural Sciences) rhizosphere	//doi.org/10.1080/00380768.2016.1247385
217	PRJNA358439	30	Soil organic matter quantity and quality shape microbial community compositions of subtropical broadleaved forests	//doi-org.cam.80599.net/10.1111/mec.13384
218	PRJNA287864	12	Effect of 35 years inorganic fertilizer and manure amendment on structure of bacterial and archaeal communities in black soil of northeast China	//doi.org/10.1016/j.apsoil.2016.04.010
219	PRJNA312735	20	Soil Bacterial Communities Under Different Vegetation Types in the Loess Plateau	10.13227/j.hjxk.2016.10.035
220	PRJNA397796	16	Altitudinal distribution pattern and formation mechanism of forest soil fungi in Shennongjia National Park, China	
221	PRJNA397354	51	Root-induced changes in aggregation characteristics and potentially toxic elements (PTEs) speciation in a revegetated artificial zinc smelting waste slag site	10.1016/j.chemosphere.2019.125414
222	PRJNA391010	48	Ammonia-Oxidizing Archaea Are More Resistant Than Denitrifiers to Seasonal Precipitation Changes in an Acidic Subtropical Forest Soil	//doi.org/10.3389/fmicb.2017.01384
223	PRJNA322587	10	Effects of continuous cropping on the number and bacterial community of <i>Verticillium</i> wilt in cotton field soil	doi: Y2015/V27/I1/62
224	PRJNA351285	13	High-resolution analyses reveal structural diversity patterns of microbial communities in Chromite Ore Processing Residue (COPR) contaminated soils	//doi.org/10.1016/j.chemosphere.2017.05.105
225	PRJNA339655	33	Effects of wetland reclamation on soil microbial community structure in Sanjiang Plain	10.13227/j.hjxk.201809204
226	PRJNA313250	36	Thirty-one years of rice-rice-green manure rotations shape the rhizosphere microbial community and enrich beneficial bacteria	doi.org/10.1016/j.soilbio.2016.10.023
227	PRJNA422505	24	Resource Availability Drives Responses of Soil Microbial Communities to Short-term Precipitation and Nitrogen Addition in a Desert Shrubland	doi.org/10.3389/fmicb.2018.00186
228	PRJNA387214	32	Arbuscular mycorrhizal fungi influence decomposition and the associated soil microbial community under different soil phosphorus availability	//doi.org/10.1016/j.soilbio.2018.02.010
229	PRJNA328121	40	Insight into the effects of different cropping systems on soilbacterial community and tobacco bacterial wilt rate	10.1002/jobm.201600222
230	PRJNA350374	36	Influence of flm mulching on soil microbial community in a rainfed region of northeastern China	10.1038/s41598-017-08575-w

231	PRJNA339364	36	Changes in soil microbial communities after 10 years of winter wheat cultivation versus fallow in an organic-poor soil in the Loess Plateau of China	doi.org/10.1371/journal.pone.0184223
232	PRJNA291799	36	Fertilization Shapes Bacterial Community Structure by Alteration of Soil pH	doi.org/10.3389/fmicb.2017.01325
233	PRJNA352638	48	Distinct soil bacterial communities in response to the cropping system in a Mollisol of northeast China	doi.org/10.1016/j.apsoil.2017.07.013
234	PRJNA336100	36	Fungal Communities in Rhizosphere Soil under Conservation Tillage Shift in Response to Plant Growth	doi.org/10.3389/fmicb.2017.01301
235	PRJNA278919	21	Distinct roles for soil fungal and bacterial communities associated with the suppression of vanilla Fusarium wilt disease	doi.org/10.1016/j.soilbio.2017.01.010
236	PRJNA360659	66	Bacterial and Fungal Community Structures in Loess Plateau Grasslands with Different Grazing Intensities	doi.org/10.3389/fmicb.2017.00606
237	PRJNA406989	96	Effects of tillage and residue management on soil quality in a wheat-maize cropping system	
238	PRJNA353518	135	Rhizosphere-associated bacterial network structure and spatial distribution differ significantly from bulk soil in wheat crop fields	doi.org/10.1016/j.soilbio.2017.06.020
239	PRJNA403772	162	Effect of Conservation Tillage Practices on Soil Microbial Spatial Distribution and Soil Physico-Chemical Properties of the Northwest Dryland	
240	PRJNA317785	48	Three years of biochar amendment alters soil physiochemical properties and fungal community composition in a black soil of northeast China	doi.org/10.1016/j.soilbio.2017.03.005
241	PRJNA347897	48	Changes of bacterial community compositions after three years of biochar application in a black soil of northeast China	doi.org/10.1016/j.apsoil.2017.01.007
242	PRJNA348840	135	Environment and geographic distance differ in relative importance for determining fungal community of rhizosphere and bulk soil	10.1111/1462-2920.13865
243	PRJNA422960	70	Differences of soil biological characteristics and bacterial diversity of sugarcane fields in red soil region affected by long-term single chemical fertilization and chemical organic combined application	10.11674/zwyf.15506
244	PRJNA427653	81	Comparative analysis of human and animal gut microbiota diversity and soil microbiota diversity in Xinlinguole pasture	10.1360/N972018-00822
245	PRJNA376845	24	Understanding the variation of microbial community in heavy metals contaminated soil using high throughput sequencing	doi.org/10.1016/j.ecoenv.2017.06.048
246	PRJNA287861	30	Microbial Taxa Distribution Is Associated with Ecological Trophic Cascades along an Elevation Gradient	doi.org/10.3389/fmicb.2017.02071

247	PRJNA292998	36	Influence of inorganic fertilizer and organic manure application on fungal communities in a long-term field experiment of Chinese Mollisols	doi.org/10.1016/j.apsoil.2016.12.003
248	PRJEB21751	115	The responses and adaptations of microbial communities to salinity in farmland soils: A molecular ecological network analysis	//doi.org/10.1016/j.apsoil.2017.08.019
249	PRJNA301752	30	Divergent taxonomic and functional responses of microbial communities to field simulation of aeolian soil erosion and deposition	10.1111/mec.14194
250	PRJNA308897	24	Bacterial succession along a long-term chronosequence of paddy soil in the Yangtze River Delta, China	doi.org/10.1016/j.soilbio.2016.10.013
251	PRJNA316533	29	Long-term nitrogen fertilization decreased the abundance of inorganic phosphate solubilizing bacteria in an alkaline soil	10.1038/srep42284
252	PRJNA324751	24	Methane Emissions and Microbial Communities as Influenced by Dual Cropping of Azolla along with Early Rice	10.1038/srep40635
253	PRJNA330793	48	Impacts of replanting American ginseng on fungal assembly and abundance in response to disease outbreaks	doi.org/10.1007/s00203-019-01638-8
254	PRJNA342521	30	Soil bacterial community responses to revegetation of moving sand dune in semi-arid grassland	10.1007/s00253-017-8336-z
255	PRJNA347427	36	Development of bacterial communities in biological soil crusts along a revegetation chronosequence in the Tengger Desert, northwest China	10.5194/bg-14-3801-2017
256	PRJNA352102	36	Effects of over 30-year of different fertilization regimes on fungal community compositions in the black soils of northeast China	doi.org/10.1016/j.agee.2017.07.031
257	PRJNA342077	24	Different impacts of manure and chemical fertilizers on bacterial community structure and antibiotic resistance genes in arable soils	doi.org/10.1016/j.chemosphere.2017.08.162
258	PRJNA352677	20	Soil bacterial quantification approaches coupling with relative abundances reflecting the changes of taxa	10.1038/s41598-017-05260-w
259	PRJNA354810	26	Response of Soil Microbial Communities to Elevated Antimony and Arsenic Contamination Indicates the Relationship between the Innate Microbiota and Contaminant Fractions	doi.org/10.1021/acs.est.7b00294
260	PRJNA360476	143	Greater diversity of soil fungal communities and distinguishable seasonal variation in temperate deciduous forests compared with subtropical evergreen forests of eastern China	10.1093/femsec/fix069
261	PRJNA361046	60	Response of soil microbial communities and microbial interactions to long-term heavy metal contamination	doi.org/10.1016/j.envpol.2017.08.057

262	PRJNA388250	29	Prokaryotic Community Distribution along an Ecological Gradient of Salinity in Surface and Subsurface Saline Soils	10.1038/s41598-017-13608-5
263	PRJNA392375	97	EFFECTS OF MULCHING MANAGERMENTS ON SOIL MICROBIAL COMMUNITIES IN AN UNIRRIGATED APPLE ORCHARD OF WEIBEI LOESS PLATEAU	//journals.im.ac.cn/actamicrocn/ch/index.aspx
264	PRJNA402087	32	Impact of tropical forest conversion on soil bacterial diversity in tropical region of China	doi.org/10.1016/j.ejsobi.2017.10.007
265	PRJNA414757	36	Structural and functional differentiation of the microbial community in the surface and subsurface peat of two minerotrophic fens in China	//doi-org.zdt.80599.net/10.1007/s11104-019-03962-w
266	PRJNA421849	36	Spatial and seasonal variations of chloramphenicol resistance genes and their co-occurring analysis with bacteria in a typical mangrove area of Hainan island, China	//doi.org/10.1016/j.ecss.2019.106541
267	PRJNA427653	81	Comparative analysis of human and animal gut microbiota diversity and soil microbiota diversity in Xilinguole pasture	10.1360/N972018-00822
268	PRJNA414324	62	The Patterns and Drivers of Bacterial and Fungal β -Diversity in a Typical Dryland Ecosystem of Northwest China	doi.org/10.3389/fmicb.2017.02126
269	PRJNA414325	62	The Patterns and Drivers of Bacterial and Fungal β -Diversity in a Typical Dryland Ecosystem of Northwest China	doi.org/10.3389/fmicb.2017.02126
		15128		

Table S2 Most important genera (top 100) calculated by random forest model and sorted by increase node purity.

Taxonomy	Serial Number	Cultivated land	Forest	Grassland	Others	Wasteland	Wetland	MeanDecreaseAccuracy
d__Bacteria;p__Actinobacteriota;c__Rubrobacteria;o__Rubrobacterales;f__Rubrobacteriaceae;g__Rubrobacter	1	0.008961239	0.009090817	0.079953322	0.004478344	0.033978963	0.004156524	0.014544481
d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Subgroup_2;f__Subgroup_2;g__Subgroup_2	2	0.005926833	0.025849396	0.013626461	0.008080628	0.011464045	0.006290101	0.011342108
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Nitrosomonadaceae;g__MND1	3	0.00445257	0.022016363	0.011126246	0.005137393	0.009608946	0.008023897	0.009332947
d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	4	0.004289955	0.018406107	0.009308582	0.011487738	0.007524966	0.00737209	0.008509269
d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__uncultured	5	0.00680831	0.011033409	0.025553356	0.007999526	0.005348324	0.005495608	0.008291706
d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Streptomycetales;f__Streptomycetaceae;g__Streptomyces	6	0.004699758	0.017826394	0.002494626	0.008650039	0.006975047	0.008074734	0.008159867
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Comamonadaceae;__	7	0.000900939	0.024132146	0.007016236	0.00819265	0.008426686	0.006973433	0.007940648
d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Chthoniobacterales;f__Xiphinematobacteraceae;g__Candidatus_Xiphinematobacter	8	0.006679475	0.012776168	0.002145172	0.008450766	0.007033907	0.006214893	0.007917995
d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae;__	9	0.001165805	0.020414548	0.00959428	0.003475802	0.016693807	0.004234876	0.007716531
d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Chthoniobacterales;f__Chthoniobacteraceae;g__Candidatus_Udaeobacter	10	0.00556004	0.01412161	0.007302249	0.008261998	0.005726324	0.005618151	0.007620525
d__Bacteria;p__Chloroflexi;c__Anaerolineae;o__Anaerolineales;f__Anaerolineaceae;g__uncultured	11	0.003249987	0.016306343	0.003428	0.003490005	0.009951588	0.010169806	0.007256747
d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Frankiales;f__Acidothermaceae;g__Acidothermus	12	0.005242426	0.013306348	0.009273068	0.004961514	0.007088813	0.003709741	0.007204788
d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Frankiales;f__Geodermatophilaceae;g__Blastococcus	13	0.003152238	0.012391741	0.015278904	0.002699365	0.015128188	0.002268901	0.007196662
d__Bacteria;p__Chloroflexi;c__Anaerolineae;o__RBG-13-54-9;f__RBG-13-54-9;g__RBG-13-54-9	14	0.005486973	0.012104087	0.007117868	0.008052636	0.005165133	0.004410491	0.006984759

d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;g__Microvirga	15	0.002004811	0.010239605	0.029976969	0.005365887	0.013168489	0.004372239	0.006835203
d__Bacteria;p__Nitrospirota;c__Thermodesulfovibrionia;o__uncultured;f__uncultured;g__uncultured	16	0.005776985	0.009561457	0.006129871	0.005171982	0.006238527	0.005111584	0.006544509
d__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus	17	0.001300833	0.015937484	0.016456137	0.005618989	0.009296586	0.004621009	0.00638529
d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingomonas	18	0.003936447	0.010670445	0.007465174	0.001281128	0.0104103	0.006579668	0.006294756
d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;__	19	0.00388504	0.006600347	0.013830069	0.005453684	0.013988422	0.00531095	0.006256043
d__Bacteria;p__Bacteroidota;c__Kryptonia;o__Kryptoniales;f__BSV26;g__BSV26	20	0.003485327	0.01143794	0.006335443	0.004980112	0.006209484	0.009005292	0.006064436
d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__Solirubrobacterales;f__67-14;g__67-14	21	0.00266279	0.003443738	0.06440593	0.005303684	0.005758705	0.004898981	0.005882184
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Oxalobacteraceae;g__Massilia	22	0.001624043	0.016032957	0.000724422	0.003678325	0.008350874	0.0070852	0.005879519
d__Bacteria;p__Nitrospirota;c__4-29-1;o__4-29-1;f__4-29-1;g__4-29-1	23	0.004346394	0.009209876	0.005652277	0.006093661	0.006533485	0.00192462	0.005697431
d__Bacteria;p__Desulfobacterota;c__Desulfuromonadia;o__Geobacterales;f__Geobacteraceae;__	24	0.004028438	0.00811434	0.005763193	0.007958223	0.008055461	0.002512778	0.005567632
d__Bacteria;p__Chloroflexi;c__Anaerolineae;o__Anaerolineales;f__Anaerolineaceae;g__Anaerolinea	25	0.003472258	0.010579001	0.006796507	0.00492465	0.006395958	0.001730543	0.005480286
d__Bacteria;p__Chloroflexi;c__Chloroflexia;o__Thermomicrobiales;f__JG30-KF-CM45;g__JG30-KF-CM45	26	0.002046697	0.012381585	0.002311723	0.003267707	0.012552208	0.001679134	0.005428292
d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Devosiaceae;g__Devosia	27	0.003474539	0.011664211	0.006796359	0.0025936	0.004585236	0.000848536	0.005329546
d__Bacteria;p__Desulfobacterota;c__Syntrophorhabdia;o__Syntrophorhabdiales;f__Syntrophorhabdaceae;g__Syntrophorhabdus	28	0.003200562	0.009598053	0.006307325	0.004636264	0.006590467	0.006828515	0.005328694
d__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;__;__	29	0.001840852	0.014177049	0.002408449	0.005242703	0.005795192	0.003098777	0.005254241
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Methylophilaceae;g__Methylotenera	30	0.003111643	0.00354717	0.002198824	0.002399849	0.02173722	0.003186523	0.005204635

d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__SC-I-84;g__SC-I-84	31	0.002739707	0.00921716	0.007560766	0.003395801	0.009980298	0.00098366	0.005134428
d__Bacteria;p__Myxococcota;c__Polyangia;o__Polyangiales;f__BIRii41;g__BIRii41	32	0.00112205	0.011254987	0.005594574	0.015098803	0.004702971	0.005593287	0.005040439
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__Ferruginibacter	33	0.004116784	0.003929986	0.009951498	0.01874146	0.002464837	0.001732422	0.005024367
d__Bacteria;p__Cyanobacteria;c__Cyanobacteriia;o__Chloroplast;f__Chloroplast;g__Chloroplast	34	0.002151396	0.009255922	0.007592757	0.010778705	0.005005183	0.003869504	0.004928131
d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Propionibacteriales;f__Nocardioideae;g__Nocardioideae	35	0.002008142	0.012688649	0.004705366	0.003768156	0.003443019	0.00452913	0.004921026
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidetes_vadinHA17;g__Bacteroidetes_vadinHA17	36	0.001980289	0.00778796	0.005266929	0.003678897	0.005098001	0.018139988	0.004820728
d__Bacteria;p__Chloroflexi;c__Ktedonobacteria;o__Ktedonobacteriales;f__Ktedonobacteraceae;g__HSB_OF53-F07	37	0.003294923	0.01011792	0.003747635	0.003702037	0.003309991	0.003177796	0.004782503
d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Opitutales;f__Opitutaceae;g__Opitutus	38	0.001877968	0.003109223	0.002575101	0.043354148	0.001807981	0.002172574	0.004590867
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;__	39	0.000967493	0.011505579	0.008926254	0.011283954	0.002953526	0.002301236	0.00447171
d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Acidobacteriales;f__uncultured;g__uncultured	40	0.00271142	0.004669853	0.009919939	0.006479287	0.009196535	0.002557316	0.004447716
d__Bacteria;p__Myxococcota;c__Polyangia;o__Haliangiales;f__Haliangiaceae;g__Haliangium	41	0.001116047	0.005881803	0.0078098	0.00487107	0.011446695	0.009173701	0.004400574
d__Bacteria;p__Myxococcota;c__Myxococcia;o__Myxococcales;f__Anaeromyxobacteraceae;g__Anaeromyxobacter	42	0.002350368	0.007093197	0.006014977	0.005151336	0.007722752	0.00188519	0.00433675
d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Micrococcales;f__Intrasporangiaceae;__	43	0.000428807	0.013314926	0.005454893	0.004739866	0.005452676	0.002355034	0.00432603
d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;__	44	0.002091362	0.006174925	0.002349431	0.004345208	0.011092503	0.000770147	0.004325952
d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Elsterales;f__uncultured;g__uncultured	45	0.003174199	0.007176767	0.000387061	0.003510719	0.004276981	0.005999578	0.004239786
d__Bacteria;p__Methylomirabilota;c__Methylomirabilia;o__Methylomirabilales;f__Methylomirabilaceae;g__Sh765B-TzT-35	46	0.002574238	0.008338274	0.003693489	0.004897752	0.004503405	0.000894839	0.004107407

d__Bacteria;p__Acidobacteriota;c__Blastocatellia;o__Pyrinomonadales;f__Pyrinomonadaceae;g__RB41	47	0.003146508	0.003618593	0.000578867	0.002407414	0.010811332	0.003399012	0.003958888
d__Bacteria;p__Acidobacteriota;c__Acidobacteriales;o__Solibacterales;f__Solibacteraceae;g__Candidatus_Solibacter	48	0.002172295	0.005440845	0.007329932	0.001850855	0.008722943	0.00378976	0.003943155
d__Bacteria;p__Chloroflexi;c__AD3;o__AD3;f__AD3;g__AD3	49	0.002630978	0.006612826	0.005711592	0.002908253	0.005036432	0.002894139	0.003942296
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Cytophagales;f__Microscillaceae;g__uncultured	50	0.000899038	0.002620508	0.001625711	0.002332694	0.023329844	0.001280232	0.003807728
d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Tistrellales;f__Geminococcaceae;g__uncultured	51	0.002188427	0.002637488	0.000281861	0.00328751	0.012539862	0.008468147	0.003763704
d__Bacteria;p__Acidobacteriota;c__Subgroup_25;o__Subgroup_25;f__Subgroup_25;g__Subgroup_25	52	0.002374594	0.0057593	0.00156581	0.006324059	0.004132827	0.00516481	0.003706201
d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__Pseudolabrys	53	0.001648226	0.007888609	0.007930642	0.000396629	0.002904408	0.006292843	0.003559012
d__Bacteria;p__Chloroflexi;c__Anaerolineae;o__Anaerolineales;f__Anaerolineaceae;g__UTCFX1	54	0.001186699	0.003234791	0.001649873	0.002151463	0.017030271	0.001989664	0.003477393
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__TRA3-20;g__TRA3-20	55	0.001236581	0.007791633	0.003033595	0.003176198	0.006005715	0.00136091	0.003390736
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	56	0.001240151	0.00417509	0.005216397	0.007021536	0.009919192	0.002126227	0.003360532
d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Azospirillales;f__Azospirillaceae;g__Skermanella	57	0.001357248	0.004362715	0.002991193	0.001296911	0.009503527	0.003777145	0.003332829
d__Bacteria;p__Desulfobacterota;c__Desulfobactria;o__Desulfobactriales;f__Desulfobactriaceae;g__Desulfobactria	58	0.002614832	0.005193094	0.002528195	0.003115098	0.003851429	0.002438027	0.003310485
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Cytophagales;f__Microscillaceae;g__uncultured	59	0.001380307	0.004618021	0.004288036	0.0046316	0.008543184	0.001668788	0.00320888
d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Euzebyales;f__Euzebyaceae;g__uncultured	60	0.002032264	0.001406288	0.001511238	0.001088949	0.006225317	0.015411565	0.003133271
d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__Gemmatimonadales;f__Gemmatimonadaceae;g__Gemmatimonas	61	0.00213433	0.003453278	0.005142059	0.005363647	0.006316612	0.001157041	0.003116243
d__Bacteria;p__WPS-2;c__WPS-2;o__WPS-2;f__WPS-2;g__WPS-2	62	0.002600723	0.004166416	0.006020905	-	0.004883005	0.00224382	0.003088243

d__Bacteria;p__Actinobacteriota;c__Thermoleophila;o__Solirubrobacterales;f__Solirubrobacteraceae;g__Solirubrobacter	63	0.001586294	0.004273298	0.015464113	0.001406681	0.004198395	0.001493295	0.003064698
d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Rubellimicrobium	64	0.002244177	0.001494299	0.005513852	0.001052841	0.007923551	0.000823478	0.003022605
d__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__uncultured	65	0.001341342	0.001268583	0.000354267	0.029985358	0.000988195	0.000776092	0.002873452
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__Flavobacterium	66	0.00173922	0.001533754	0.002786379	0.004029495	0.010353733	0.002055859	0.002857827
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Steroidobacterales;f__Steroidobacteraceae;g__uncultured	67	0.001498556	0.004180906	0.00283251	0.001191814	0.003208573	0.008282828	0.002749922
d__Bacteria;p__Acidobacteriota;c__Vicinamibacteria;o__Vicinamibacterales;f__Vicinamibacteraceae;g__Vicinamibacteraceae	68	0.001869972	0.00395762	0.002295938	0.001987706	0.005755022	0.001717961	0.00274474
d__Bacteria;p__Chloroflexi;c__Anaerolineae;__;__;__	69	0.002008801	0.003747864	0.001119284	0.004316808	0.003763824	0.002713564	0.00273837
d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;__	70	0.001731827	0.003324955	0.002698446	0.001069238	0.004492264	0.004000076	0.002716875
d__Bacteria;p__Methylomirabilota;c__Methylomirabilia;o__Rokubacterales;f__Rokubacterales;g__Rokubacterales	71	0.00162789	0.005732209	0.003427228	0.00132409	0.002326316	0.002228834	0.002676037
d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;g__uncultured	72	0.001726062	0.001283905	0.00165666	0.000949306	0.008743502	0.001009448	0.002622774
d__Bacteria;p__Chloroflexi;c__Anaerolineae;o__Anaerolineales;f__Anaerolineaceae;__	73	0.00056167	0.005574327	0.003192872	0.004052085	0.002785529	0.005898508	0.002604032
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Nitrosomonadaceae;g__Ellin6067	74	0.001670266	0.002231926	0.004528524	0.001842987	0.007457012	0.001320355	0.002599613
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__Aurantisolimonas	75	0.001581737	0.001298857	0.001470691	0.022679653	0.000919804	0.00072711	0.002578211
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter	76	0.00088653	0.006458956	0.004059505	0.003840267	0.001849857	0.001646208	0.002551415
d__Bacteria;p__Chloroflexi;c__Anaerolineae;o__SJA-15;f__SJA-15;g__SJA-15	77	0.000955337	0.004287985	0.002374066	0.002840546	0.00256434	0.007602368	0.002466817
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__Flavisolibacter	78	0.000775614	0.007712463	0.00141442	0.002986896	0.000751266	0.001084847	0.002440449

d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Corynebacteriales;f__Mycobacteriaceae;g__Mycobacterium	79	0.001079792	0.001766934	0.017751601	0.003744953	0.003396339	0.001025814	0.002287953
d__Bacteria;p__Chloroflexi;c__Ktedonobacteria;o__C0119;f__C0119;g__C0119	80	0.001074181	0.006259979	0.001183491	0.001197634	0.00116654	0.001521457	0.00228466
d__Bacteria;p__Chloroflexi;c__OLB14;o__OLB14;f__OLB14;g__OLB14	81	0.000913861	0.005597173	0.004125773	0.001558871	0.002250762	0.00121121	0.002271697
d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__Gemmatimonadales;f__Gemmatimonadaceae;g__uncultured	82	0.002147652	0.002963082	0.002983322	0.003378182	0.001029827	0.00143474	0.002246594
d__Bacteria;p__Actinobacteriota;c__Thermoleophilia;o__Gaiellales;f__uncultured;g__uncultured	83	0.000922078	0.003403667	0.012417953	0.001559465	0.002991897	0.001992247	0.002235921
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Gammaproteobacteria_Incertae_Sedis;f__Unknown_Family;g__Acidibacter	84	0.001478907	0.001831935	0.001614385	0.001773931	0.006269603	0.003008543	0.002233545
d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Donogiales;f__Dongiaceae;g__Dongia	85	0.000790537	0.004726752	0.004407673	0.00261567	0.002524951	0.001581474	0.002150781
d__Bacteria;p__Planctomycetota;c__Planctomycetes;o__Pirellulales;f__Pirellulaceae;g__Pir4_lineage	86	0.000623371	0.000824664	0.002303225	0.000904563	0.013407895	0.00060307	0.002148938
d__Bacteria;p__Bacteroidota;c__SJA-28;o__SJA-28;f__SJA-28;g__SJA-28	87	0.001297366	0.003332316	0.003699641	0.002919211	0.00318078	0.001565451	0.00214599
d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Methyloligellaceae;g__Methyloligellaceae	88	0.000692388	0.00518132	0.002230313	0.003005168	0.002016948	0.002634525	0.002123641
d__Bacteria;p__Planctomycetota;c__Planctomycetes;o__Pirellulales;f__Pirellulaceae;g__Pirellula	89	0.000934453	0.004757912	0.003666213	-7.86573E-05	0.002599199	0.002432983	0.002084867
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Hydrogenophaga	90	0.000922799	0.001170081	0.001328419	0.000292745	0.010728714	0.002110323	0.00207504
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Nitrosomonadaceae;g__Nitrospira	91	0.000448449	0.004698442	0.002633527	0.001481279	0.005392607	0.000998702	0.002055
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Oceanospirillales;f__Halomonadaceae;g__Halomonas	92	0.001480846	0.001407047	0.000987044	0.000173384	0.000777629	0.013545189	0.002047228
d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Bryobacteriales;f__Bryobacteraceae;g__Bryobacter	93	0.001256726	0.001919732	0.001833786	0.002977398	0.004879644	0.002647336	0.002036971
d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingorhabdus	94	0.001506399	0.000907651	0.000777274	0.00034516	0.00834971	0.000635853	0.001994954

d__Bacteria;p__Sva0485;c__Sva0485;o__Sva0485;f__Sva0485;g__Sva0485	95	0.000965871	0.003041022	0.002345028	0.001375689	0.002229384	0.006791387	0.001994801
d__Bacteria;p__Bacteroidota;c__Kapabacteria;o__Kapabacteriales;f__Kapabacteriales;g__Kapabacteriales	96	0.0005167	0.003155451	0.001248898	0.00883721	0.002755377	0.002180001	0.001967802
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__Terrimonas	97	0.000391573	0.002936264	0.001043757	0.000705236	0.008568566	0.001204247	0.001963253
d__Bacteria;p__Dadabacteria;c__Dadabacteriia;o__Dadabacteriales;f__Dadabacteriales;g__Dadabacteriales	98	0.000290068	0.001498522	0.001432247	0.001498611	0.011350318	0.000985201	0.001933949
d__Bacteria;p__Acidobacteriota;c__Subgroup_18;o__Subgroup_18;f__Subgroup_18;g__Subgroup_18	99	0.000987162	0.00387063	0.001450077	0.002544975	0.002173519	0.00166022	0.001912858
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Methylophilaceae;__	100	0.000308195	0.000986782	0.001644802	5.62673E-05	0.012795423	0.00031694	0.001882829

Table S3 Standardized total effect from structural equation modeling.

	TP	TN	TK	pH	Latitude	Land use	Climate	Shannon	Richness
Shannon	0.144	-0.101	-0.243	-0.223	0.171	-0.049	-0.385	0	0
Richness	0.079	-0.05	-0.217	0.067	0.173	-0.007	-0.213	0	0
SOC	-0.038	0.953	-0.07	0.123	-0.066	0.012	-0.009	-0.012	-0.011

Table S4 Detailed parameters of structural equation modeling for describing the negative and positive effects of geographic conditions, microbial-community characteristics and soil chemical properties on the SOC concentration.

Label	R²	P	S.E.	C.R.
Climate --->TP	0.015	0.582	0.004	0.55
Climate --->TN	0.145	***	0.02	5.591
Climate --->TK	-0.39	***	0.084	-15.21
Climate --->pH	-0.29	***	0.028	-11.16
Climate --->Shannon	-0.28	***	0.021	-9.317
Climate --->Richness	-0.16	***	2.114	-5.33
Land use --->TP	0.159	***	0.003	7.296
Land use --->TN	0.451	***	0.014	21.793
Land use --->TK	0.223	***	0.06	11.055
Land use --->pH	-0.04	0.087	0.02	-1.709
Land use --->Shannon	-0.13	***	0.015	-5.447
Land use --->Richness	-0.07	0.006	1.513	-2.773
Latitude --->TP	0.472	***	0.008	16.903
Latitude --->TN	0.309	***	0.045	11.611
Latitude --->TK	0.391	***	0.186	15.041
Latitude --->pH	0.479	***	0.061	17.963
Latitude --->Shannon	0.022	0.466	0.047	0.73
Latitude --->Richness	0.149	***	4.699	4.744
Climate --->SOC	-0.02	0.087	0.105	-1.712
Latitude --->SOC	-0.06	***	0.263	-5.577
Land use --->SOC	0.011	0.132	0.077	1.506
pH --->SOC	0.108	***	0.129	8.923
Shannon --->SOC	-0.01	0.339	0.18	-0.956
Richness --->SOC	-0.01	0.326	0.002	-0.983
TP --->SOC	-0.04	***	0.672	-4.282
TN --->SOC	0.984	***	0.163	87.914
TK --->SOC	-0.07	***	0.028	-8.419

*** means < 0.05