Open Access

Earth System
Science
Data

Supplement of

The biogeography of relative abundance of soil fungi versus bacteria in surface topsoil

Kailiang Yu et al.

Correspondence to: Kailiang Yu (kai86liang@gmail.com) and Thomas W. Crowther (tom.crowther@usys.ethz.ch)

Classification of vegetation biomes and vegetation types

Following the approach by Olson et al. 2006, vegetation biomes where the soil samples were collected were classified into tundra, boreal forests, montane grasslands, temperate conifer forests, temperate grasslands, temperate broadleaf forests, tropical forests, and Mediterranean & deserts. Mediterranean and deserts had low sample sizes and thus were combined into one vegetation biome. To determine the vegetation types in locations where the soil samples were collected, we used the Global 1-km Consensus Land Cover map[2]. The land cover map classifies vegetation or land cover types into Evergreen/Deciduous Needleleaf Trees, Evergreen Broadleaf Trees, Deciduous Broadleaf Trees, Mixed/Other Trees, Shrubs, Herbaceous Vegetation, Cultivated and Managed Vegetation, Regularly Flooded Vegetation, Urban/Built-up, Snow/Ice, Barren, and Open Water. We summed up the vegetation types of Evergreen/Deciduous Needleleaf Trees, Evergreen Broadleaf Trees, Deciduous Broadleaf Trees, Mixed/Other Trees and Shrubs to derive the total woody plant cover. To represent human activities (or land usage change), we used land cover of Cultivated and Managed Vegetation to derive the managed cover. Total vegetation cover is the sum of woody, herbaceous and managed vegetation cover. Then we classified our soil sample locations into vegetation types or ecosystems dominated by woody vegetation, managed vegetation, and herbaceous vegetation. To this end, we tested various thresholds of vegetation cover values and chose the one without overlaps among different vegetation types. That is, if the total vegetation cover was less than 20% or the cover of barren soil was greater than 50%, it was classified as barren soil. If the woody vegetation cover was larger than 20% and larger than the managed vegetation cover, it was classified into the vegetation type or ecosystem dominated by woody vegetation. If the managed vegetation cover was larger than 20% and larger than the woody vegetation cover, it was classified into the vegetation type or ecosystem

25 dominated by managed vegetation. The rest of sample sites were classified into herbaceous

26 vegetation dominated ecosystem, if herbaceous vegetation cover was larger than 20%.

Environmental drivers

29 Based on previous studies[3–5], variables or covariates of climate, soil and human activities

30 which likely affect F:B ratio or fungal proportion were selected for this study. They include

31 climate conditions (aridity index, mean annual precipitation-MAP, mean annual temperature-

32 MAT), soil properties (clay, silt and sand content, soil organic carbon-SOC, soil C:N ratio,

33 pH, cation exchange capacity), vegetation index (net primary productivity-NPP, woody

34 vegetation cover, herbaceous vegetation cover), and human activities (managed vegetation

35 cover). All of these variables were derived from the global layers based on georeferenced

36 coordinates of aggregated soil sample at 30 arc-seconds resolution. Machine-learning

37 algorithm Random Forest was then used to determine variable importance for these 12

38 variable (Breiman 2001). We ran 1000 simulations of machine-learning algorithm random

39 forest and reported mean values of mean decrease in accuracy (%IncMSE) and mean decrease

40 gini (IncNodePurity) with 95% confidence interval. The greater the values of %IncMSE and

41 IncNodePurity are, the more important the variables are.

Machine learning

44 Fungal proportion has the largest sample size (n = 3224 samples) and is the focus of our

45 study. Because of better predictive strength, we used machine learning (random forest) to

46 generate a spatially explicit map of fungal proportion at a global scale. The distinct soil

47 samples (n = 3224) falling within the same 30 arc-seconds (~1-km^2) pixel were aggregated as

48 an average, thus resulting in a total of 946 unique pixels across global as inputs into the

49 geospatial modelling.

50   To generate a quantitative and mechanistic understanding of environmental controls on

51 fungal proportion across landscapes, we used a stack of ecologically relevant, global map

2

52   layers including climatic, soil nutrient, soil chemical, soil physical, vegetative indices,

53   radiation and topographic variables and anthropogenic covariates (Supplementary Table 1).

54   All of these covariate map layers were standardized at 30 arc-seconds resolution (≈1km at the

55   equator). When these global layers' resolution is higher than 30 arc-seconds, we

56   downsampled these layers using a mean aggregation method. In contrast, if layers have a

57   lower original resolution, we resampled these layers using simple upsampling (i.e., without

58   interpolation) to align with the higher resolution grid. Each sample (plot)-specific

59   independent variables were then derived from these ecologically relevant, global map layers

60   based on each sample' georeferenced location.

61   The soil samples used for measuring soil microbes were collected from top soil surface

62   (0-10/15 cm). To approximate the sampling soil depth, we thus used the soil variable at soil

63   depth of 15 cm, thus resulting in a total of 90 ecologically relevant, global map layers.

64   Geospatial modelling was used to investigate the dependence of fungal proportion on the 90

65   covariates. We followed recent advancements in machine learning for spatial prediction[6], and

66   used random forest with a variety of parameters (i.e., variablesPerSplit 2, 3, 4, 5, 8, 10) to

67   train the models and assessed each model using k-fold cross validation (with k = 10). This

68   allowed us to quantify the coefficient of determination values for each fold of data in each

69   model. Then we determined the mean and standard deviation values for the cross validated

70   models. The model with the highest coefficient of determination values and lowest standard

71   deviation were selected as the best model. The results showed that the final (best) model had a

72   remarkably high strength of prediction (mean cross-validation R^2 = 0.43, standard deviation =

73   0.09). The "best model" with the highest coefficient of determination values and lowest

74   standard deviation were then used to spatially explanate the fungal proportion at a global

75   scale, with the derived 90 covariates on all the soil samples (n = 946). The results showed

76   again that the best performing model had remarkably high predictive strength at a global scale

77 (overall $R^2 = 0.90$).

78   To account for the potential role of land usage change, we used the subset of data

79 including only natural ecosystems (n = 1795) and aggregated the samples at 30 arc-seconds

80 (~1-km^2) resolution as an average. We then used machine learning (random forest) to

81 generate a spatially explicit map of fungal proportion at a global scale, using the derived 90

82 covariates on all the soil samples (n = 716) (Fig. S1). The predictive strength of using data of

83 natural ecosystems was lower than the case of using full dataset. But it still had good

84 predictive strength with mean cross-validation $R^2 = 0.35$ and a final best model $R^2 = 0.91$

85 (Fig. S9). In view of the minimal difference of the two scenarios, the main text reported

86 results from the full dataset, whereas results from only the natural ecosystems was reported in

87 the supplementary materials.

88

89

90

91

92

93

94

95

96

97

98 **References**

99 1. Olson, D. M. *et al.* Terrestrial Ecoregions of the World: A New Map of Life on Earth.

100 *Bioscience* **51**, 933 (2006).

101 2. Tuanmu, M. N. & Jetz, W. A global 1-km consensus land-cover product for

102 biodiversity and ecosystem modelling. *Glob. Ecol. Biogeogr.* **23**, 1031–1045 (2014).

103 3. de Vries, F. T. *et al.* Abiotic drivers and plant traits explain landscape-scale patterns in

104 soil microbial communities. *Ecol. Lett.* **15**, 1230–1239 (2012).

105 4. Chen, Y. L. *et al.* Patterns and drivers of soil microbial communities in Tibetan alpine

106 and global terrestrial ecosystems. *J. Biogeogr.* **43**, 2027–2039 (2016).

107 5. Drenovsky, R. E., Steenwerth, K. L., Jackson, L. E. & Scow, K. M. Land use and

108 climatic factors structure regional patterns in soil microbial communities. *Glob. Ecol.*

109 *Biogeogr.* **19**, 27–39 (2010).

110 6. Hengl, T., Nussbaum, M., Wright, M. N., Heuvelink, G. B. M. & Gräler, B. Random

111 forest as a generic framework for predictive modeling of spatial and spatio-temporal

112 variables. *PeerJ* **6**, e5518 (2018).
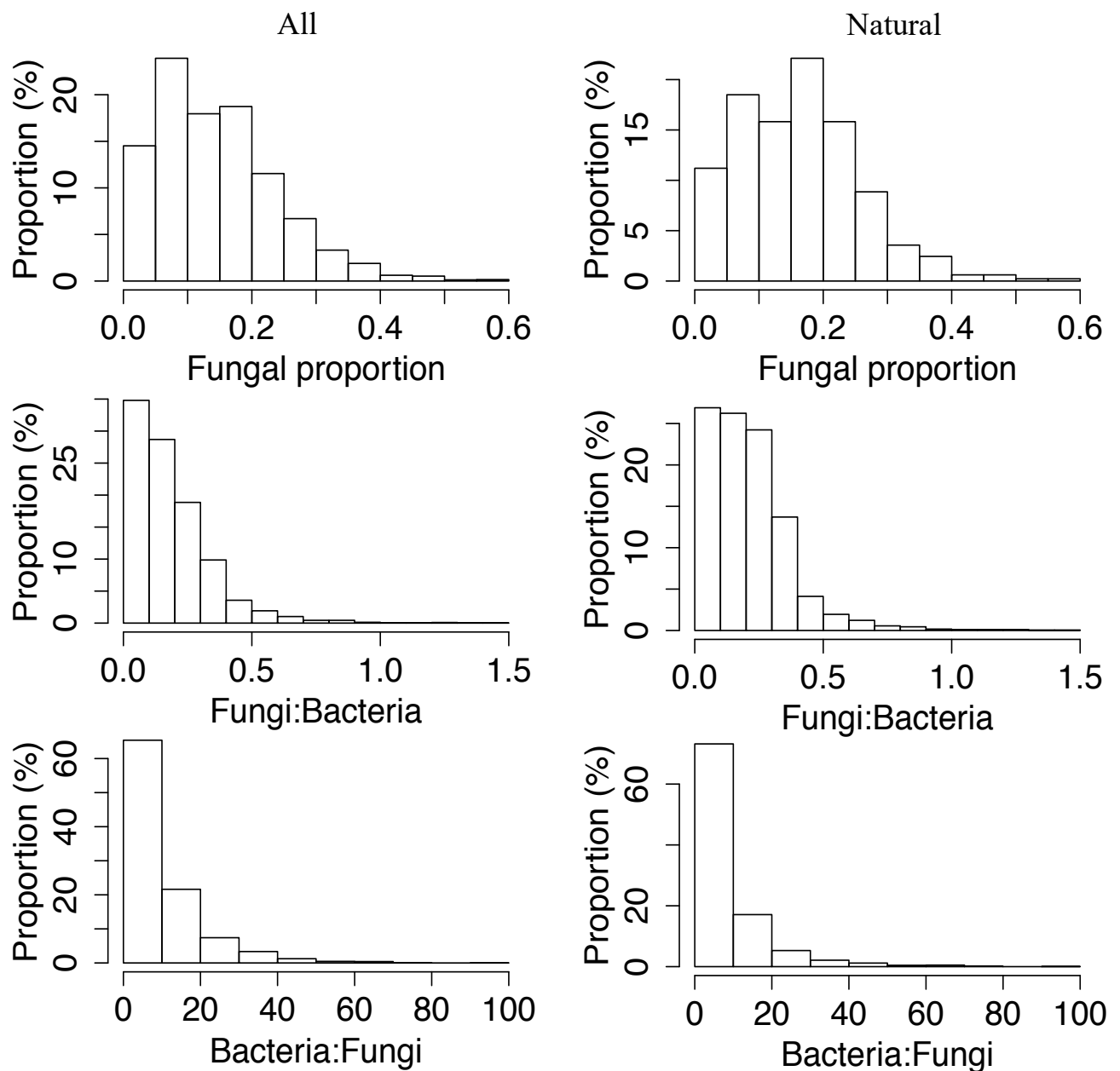
113

114

115

116

117

Fig. S1 Frequency distribution (%) of proportion of fungi, fungal and bacterial ratio and bacterial and fungal ratio. The data is derived from the original distinct soil samples (n = 3224 for all data and n = 1795 for natural ecosystems) before aggregation.
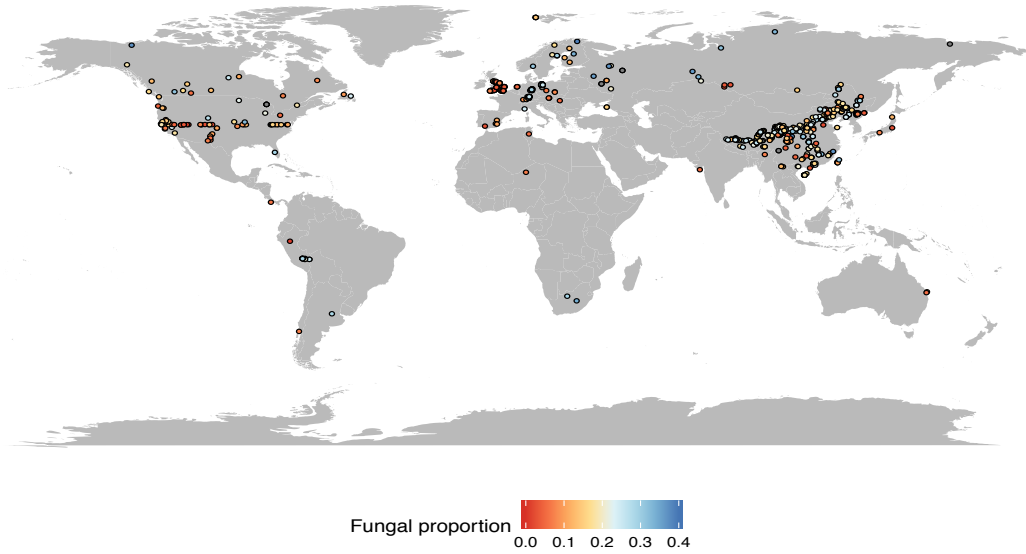
Fig. S2 Map of sample locations for fungal proportion using natural ecosystems. All data points (n = 1795) falling within the same 30 arc-seconds (~1-km^2) pixel were aggregated via an average (n = 716).
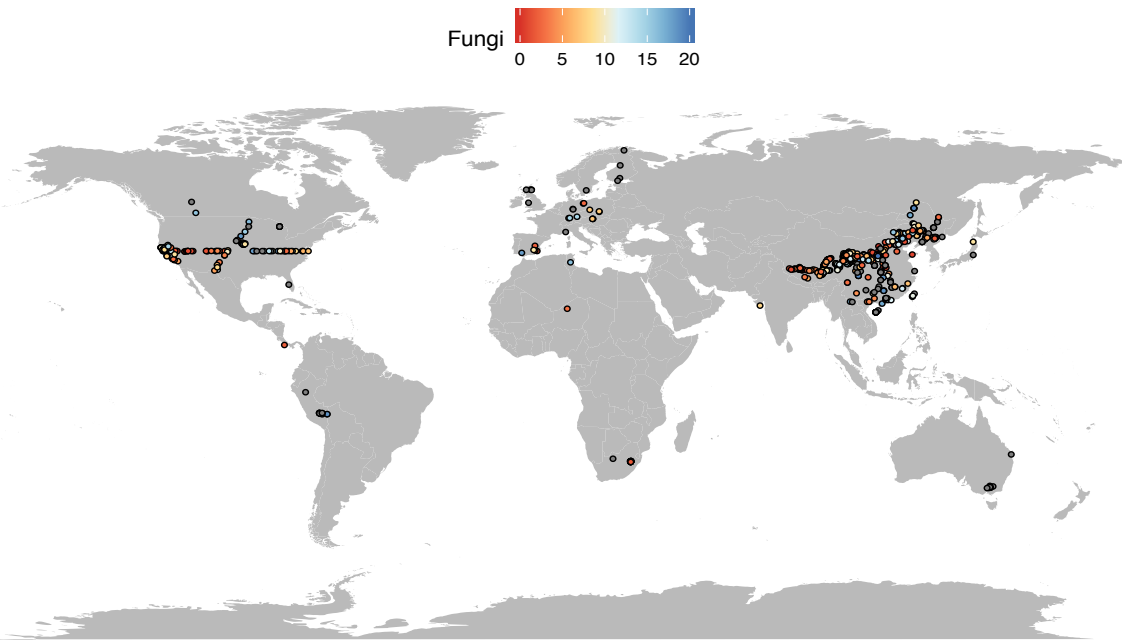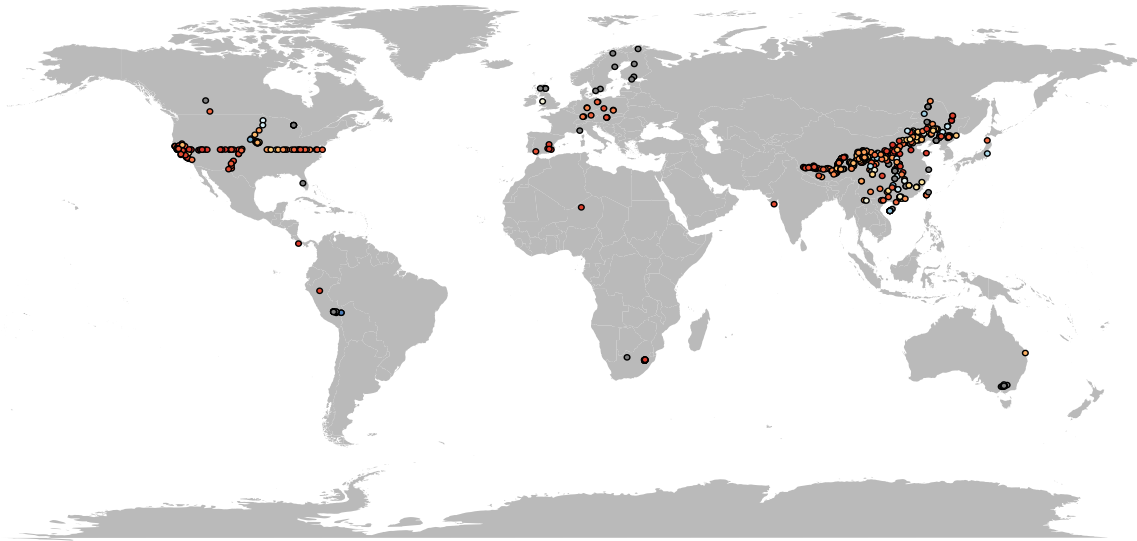
Fig. S3 Map of sample locations for abundance of fungi and bacteria. All data points (n = 2753 for fungi and n = 2759 for bacteria) falling within the same 30 arc-seconds (~1-km²) pixel were aggregated via an average (n = 646 and n = 647 for both fungi and bacteria, respectively).
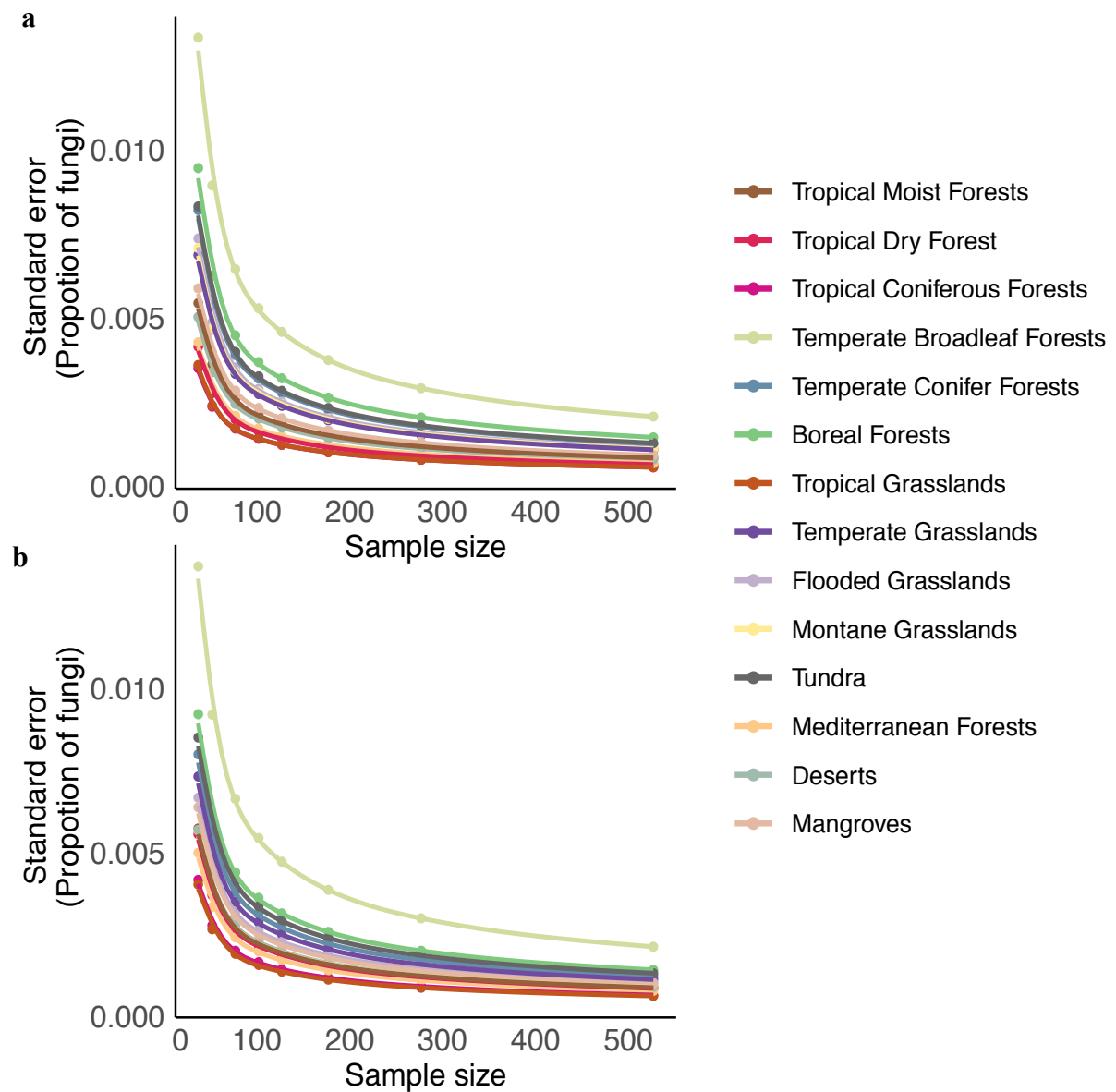
Fig. S4 The standard error of the predicted mean values of fungal proportion decrease with increasing sample size, quantified by the 1000 bootstrapping. a, the scenario of using full dataset. b, the scenario of using dataset with natural ecosystems.
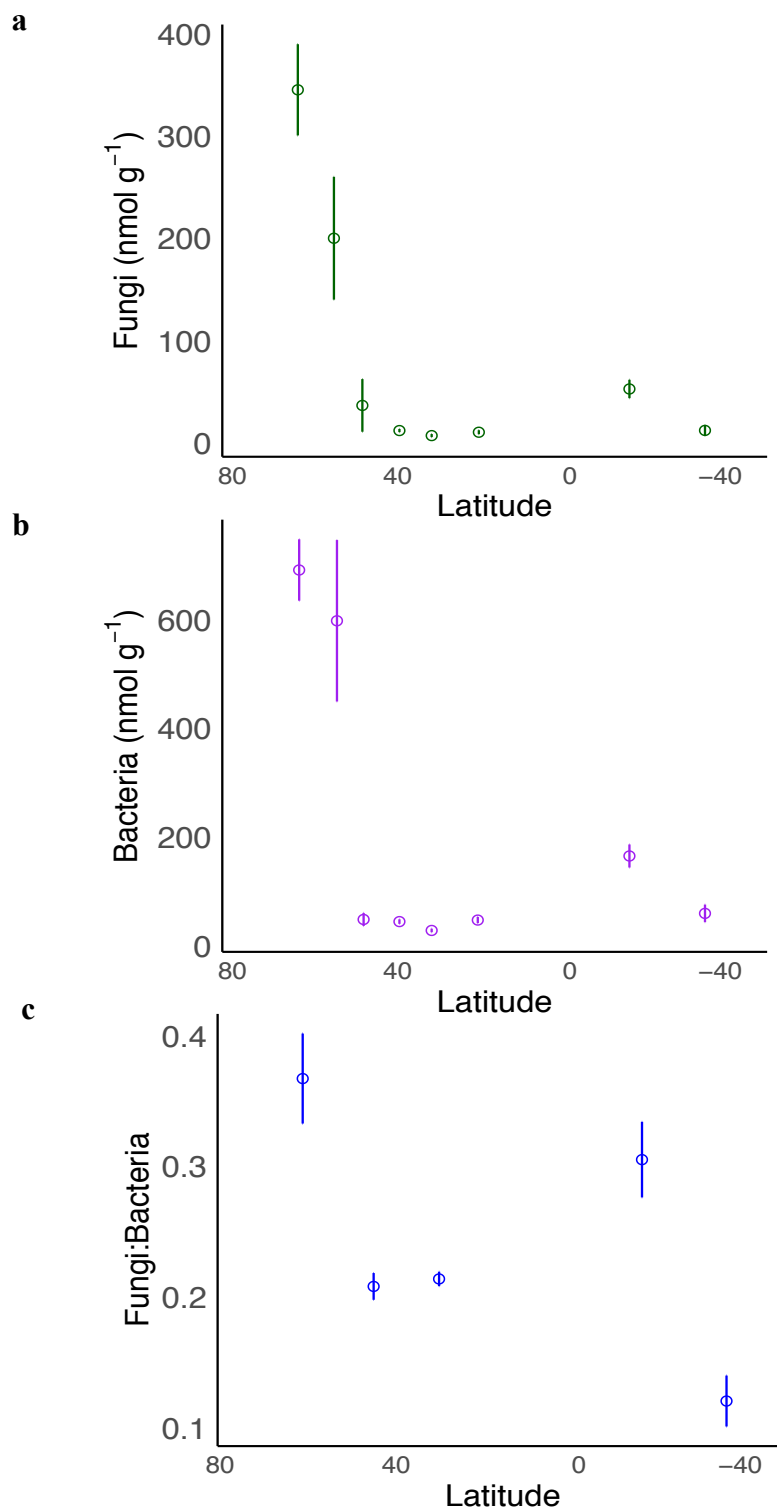
Fig. S5 Abundance of fungi (a), bacteria (b), and fungi and bacteria ratio (c) derived from PLFA as affected by latitude.
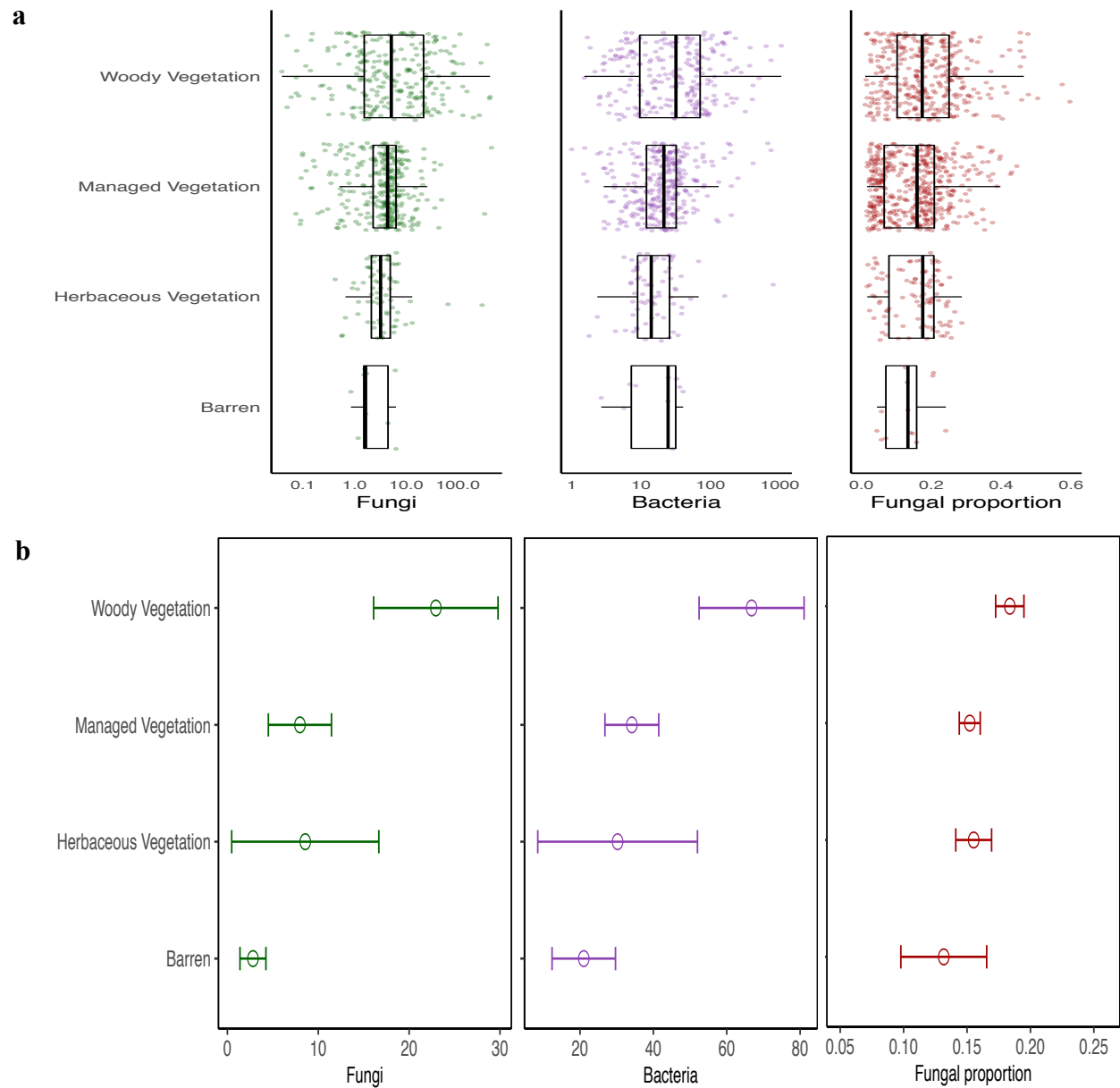
Fig. S6 The median and interquartile range (a) and mean ± 95 CIs (b) of abundance of fungi and bacteria and fungal proportion across vegetation types. Mediterranean and desert have low sample sizes (<25) and thus were combined.
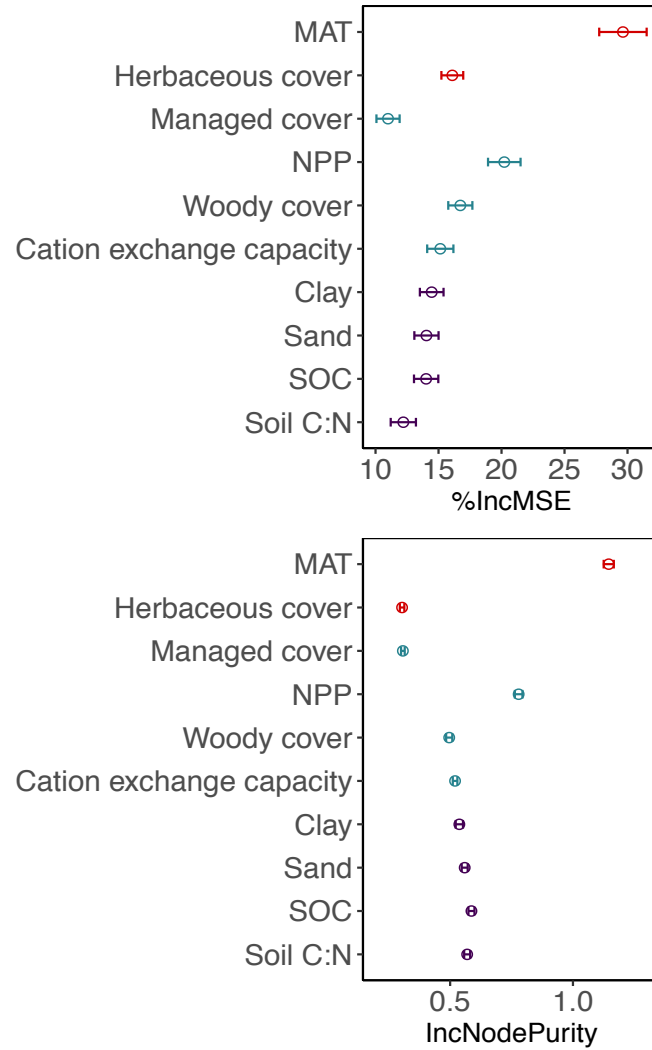
Fig. S7 Mean decrease in accuracy (%IncMSE, mean and SD) and mean decrease gini (IncNodePurity, mean and SD) estimated from 1000 simulations of random forests. This is used to evaluate the importance of top environmental drivers on proportion of fungi derived from natural ecosystems.
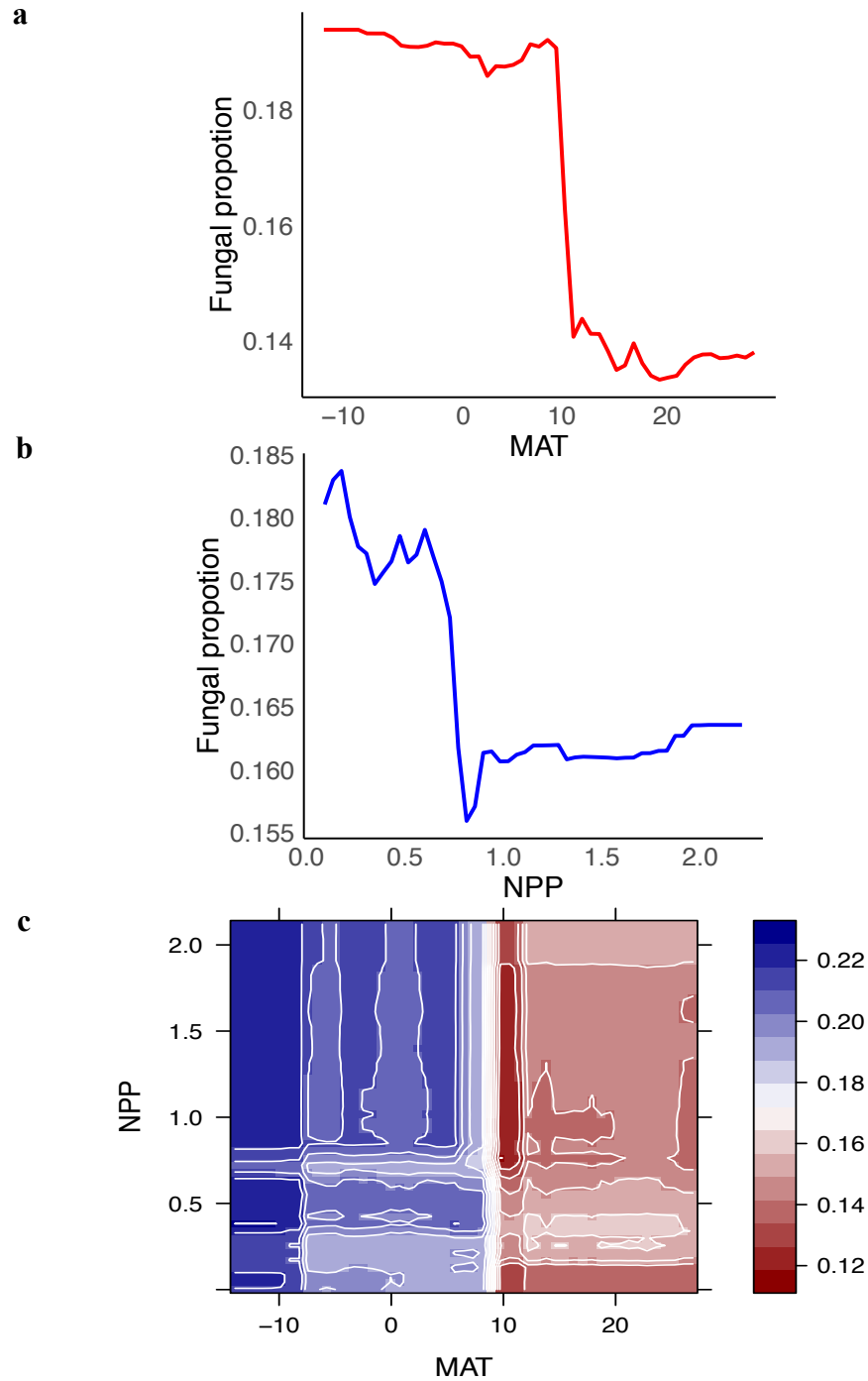
Fig. S8 Fungal proportion is primarily associated with net primary productivity and climate using data set of natural ecosystems. a–b, Partial feature contributions of primary environmental variables (**a**, MAT; **b**, NPP) to proportion of fungi. **c**, Partial feature contributions of primary environmental variable interactions (MAT vs NPP) to proportion of fungi.

333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
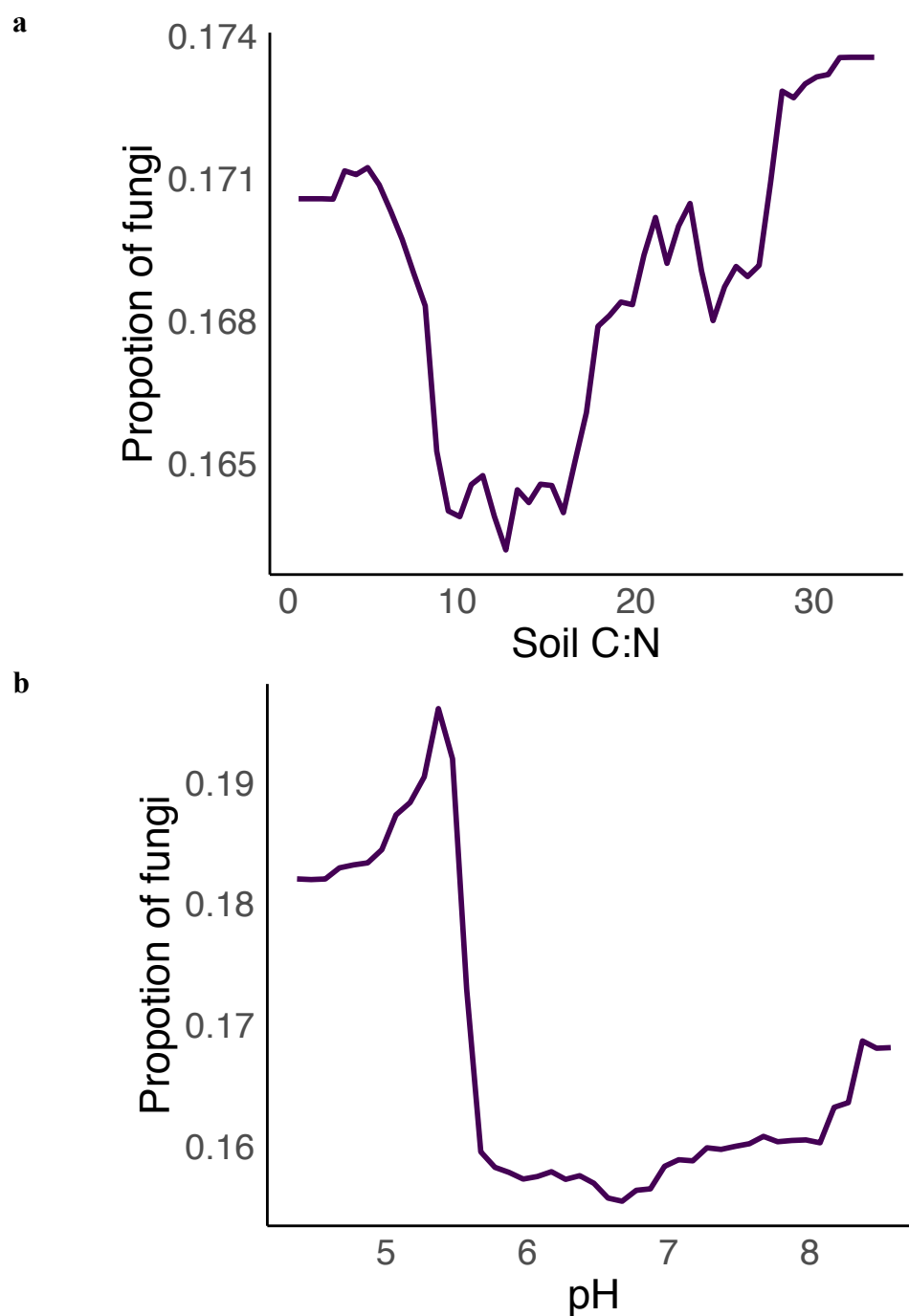
Fig. S9 Partial feature contributions of soil C:N (a) and pH (b) to fungal proportion.
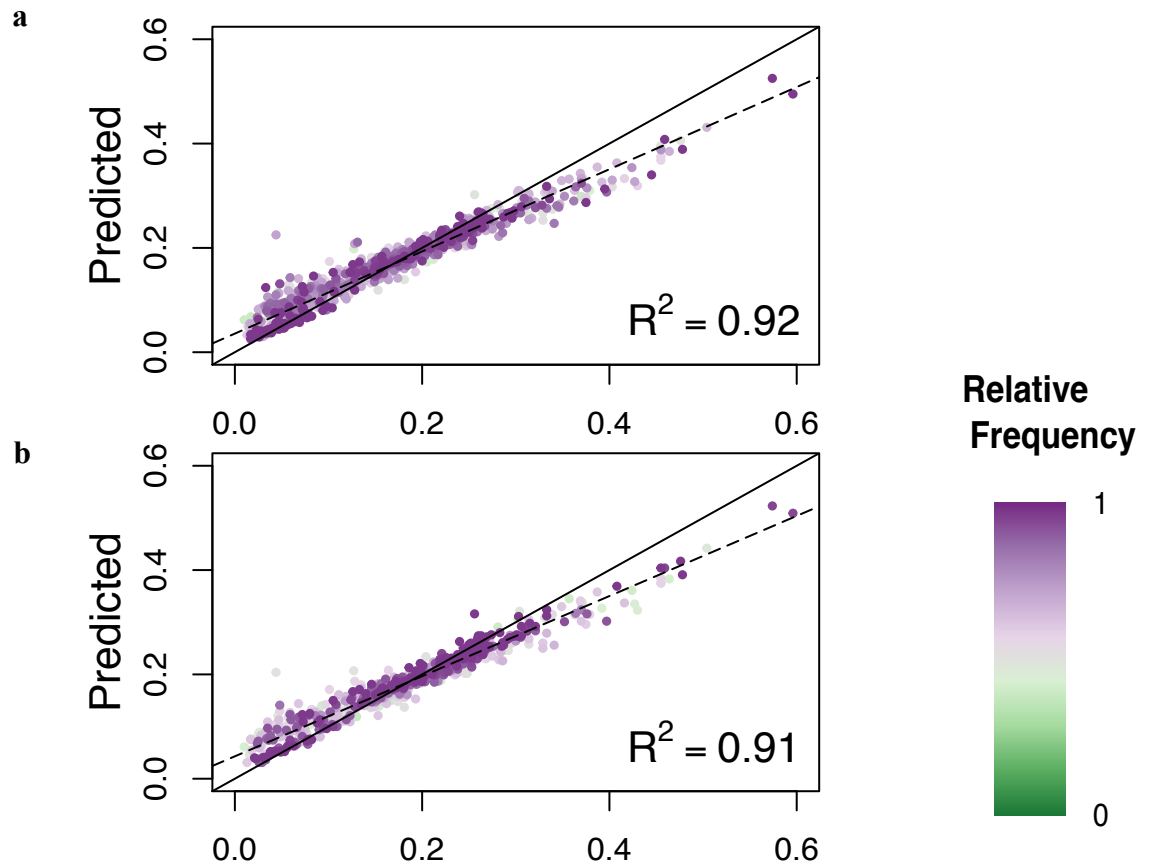
Fig. S10 Model and data validation in the final model. a, the scenario of using full dataset for fungal proportion; b, the scenario of using dataset from natural ecosystems for fungal proportion; C. Heat plots showing the relationships between predicted versus observed values of fungal proportion for the best final models. Dashed diagonal lines indicate fitted relationships, while solid diagonal lines indicate a 1:1 relationship between predicted and observed points.

15

a

Fungal proportion

0.1   0.3

b

Coefficient of variation
(% sd)

0%   20%
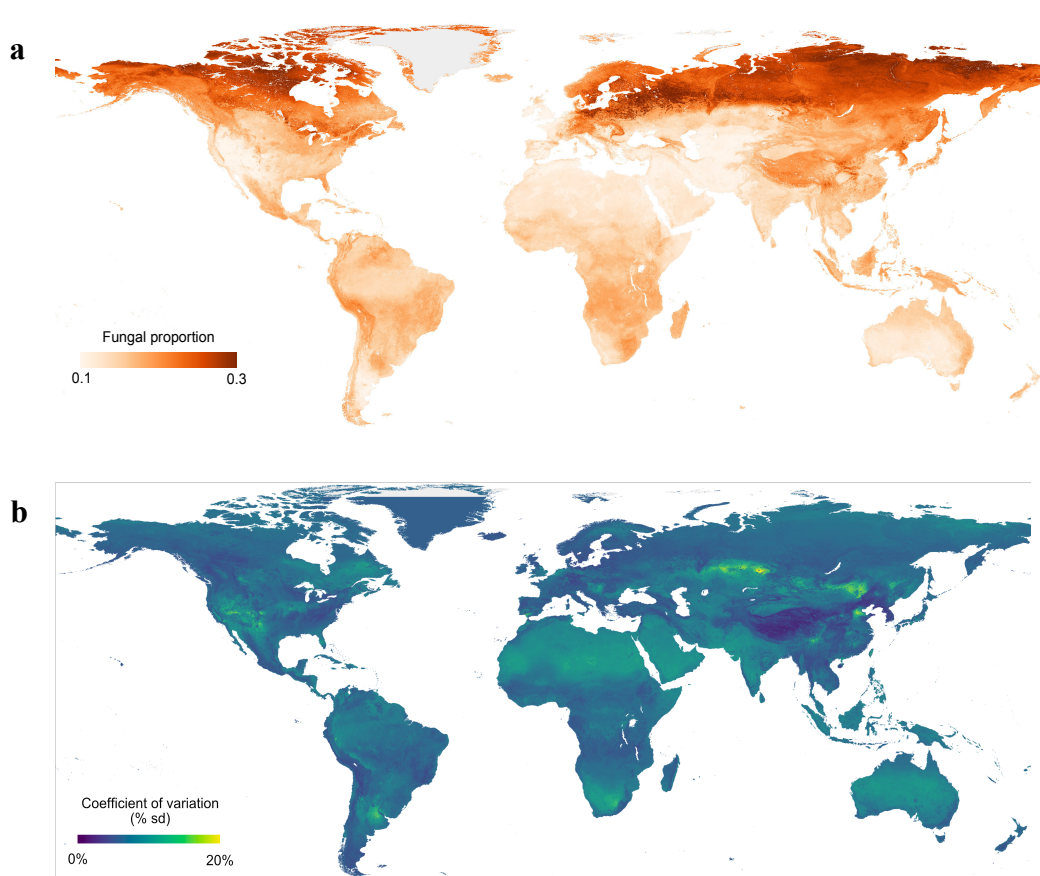
Fig. S11 Global map of fungal proportion (a) and bootstrapped (100 iterations) coefficient of variation (b) at the 30 arcsec (approximately 1 km) pixel scale using the data with natural ecosystems. Bootstrapped coefficient of variation is standard deviation divided by the mean predicted value as a measure of prediction accuracy. Sampling was stratified by biome.

423

a

424

425

426

427

428

Fungal proportion

429

0.1   0.3

430

b

431

432

433

434

435

Coefficient of variation
(% mean)

436

0%   8%

437

438

439   **Fig. S12 Global map of fungal proportion (a) and bootstrapped (100 iterations)**

440   **coefficient of variation (b) at the 30 arcsec (approximately 1 km) pixel scale using full**

441   **data.** Bootstrapped coefficient of variation is standard deviation divided by the mean

442   predicted value as a measure of prediction accuracy. Samples were selected by randomly

443   sampling 90% full datasets with replacement to account for the unbalanced sample

444   distribution.

445

446

447

448   Supplementary references for PLFA

449   1.   Schnecker, J. *et al.* Effects of soil organic matter properties and microbial community

450   composition on enzyme activities in cryoturbated arctic soils. *PLoS One* (2014).

451   doi:10.1371/journal.pone.0094076

452   2.   Birkhofer, K. *et al.* General relationships between abiotic soil properties and soil biota

453   across spatial scales and different land-use types. *PLoS One* (2012).

454   doi:10.1371/journal.pone.0043292

455   3.   Niu, J., Zhou, X., Jiang, N. & Wang, Y. Characteristics of soil microbial communities

456   under dry and wet conditionin Zoige alpine wetland. *Shengtai Xuebao/ Acta Ecol. Sin.*

457   (2011).

458   4.   de Vries, F. T. *et al.* Abiotic drivers and plant traits explain landscape-scale patterns in
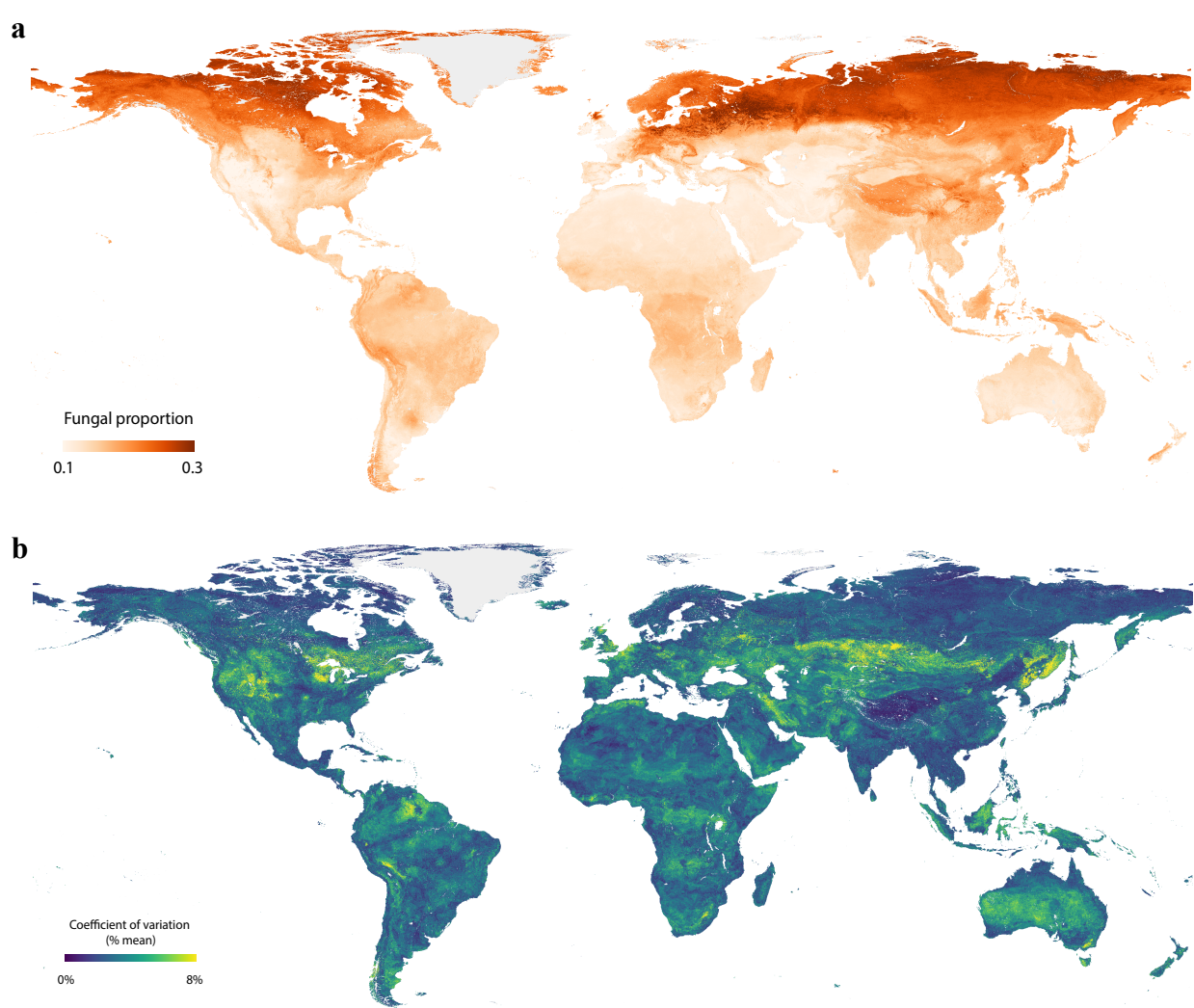
459   soil microbial communities. *Ecol. Lett.* **15**, 1230–1239 (2012).

460   5.   Drenovsky, R. E., Steenwerth, K. L., Jackson, L. E. & Scow, K. M. Land use and

461   climatic factors structure regional patterns in soil microbial communities. *Glob. Ecol.*

462   *Biogeogr.* **19**, 27–39 (2010).

463   6.   Bardgett, R. D., Lovell, R. D., Hobbs, P. J. & Jarvis, S. C. Seasonal changes in soil

464   microbial communities along a fertility gradient of temperate grasslands. *Soil Biol.*

465   *Biochem.* (1999). doi:10.1016/S0038-0717(99)00016-4

466   7.   Boot, C. M., Hall, E. K., Denef, K. & Baron, J. S. Long-term reactive nitrogen loading

467   alters soil carbon and microbial community properties in a subalpine forest ecosystem.

468   *Soil Biol. Biochem.* (2016). doi:10.1016/j.soilbio.2015.10.002

469   8.   Boyle, S. A., Yarwood, R. R., Bottomley, P. J. & Myrold, D. D. Bacterial and fungal

470   contributions to soil nitrogen cycling under Douglas fir and red alder at two sites in

471   Oregon. *Soil Biol. Biochem.* (2008). doi:10.1016/j.soilbio.2007.09.007

472   9.   Brant, J. B., Myrold, D. D. & Sulzman, E. W. Root controls on soil microbial

473   community structure in forest soils. *Oecologia* (2006). doi:10.1007/s00442-006-0402-7

474   10.   Chang, E. H. & Chiu, C. Y. Changes in soil microbial community structure and activity

475   in a cedar plantation invaded by moso bamboo. *Appl. Soil Ecol.* (2015).

476   doi:10.1016/j.apsoil.2015.02.001

477   11.   Chang, E. H., Tian, G. & Chiu, C. Y. The effect of re-planting trees on soil microbial

478   communities in a wildfire-induced subalpine grassland. *Forests* (2017).

479   doi:10.3390/f8100385

480   12.   Chang, E. H., Chen, C. P., Tian, G. & Chiu, C. Y. Replacement of natural hardwood

481   forest with planted bamboo and cedar in a humid subtropical mountain affects soil

482   microbial community. *Appl. Soil Ecol.* (2018). doi:10.1016/j.apsoil.2017.11.006

483   13.   Cui, H. jun *et al.* Soil microbial community composition and its driving factors in

484   alpine grasslands along a mountain elevational gradient. *J. Mt. Sci.* (2016).

485   doi:10.1007/s11629-015-3614-7

486   14.   Dong, W. Y. *et al.* Responses of soil microbial communities and enzyme activities to

487   nitrogen and phosphorus additions in Chinese fir plantations of subtropical China.

488   *Biogeosciences* (2015). doi:10.5194/bg-12-5537-2015

489   15.   He, R. *et al.* Effects of forest conversion on soil microbial communities depend on soil

490   layer on the eastern Tibetan Plateau of China. *PLoS One* (2017).

491   doi:10.1371/journal.pone.0186053

492   16.   Guo, J. *et al.* Conversion of a natural evergreen broadleaved forest into coniferous

493   plantations in a subtropical area: effects on composition of soil microbial communities

494   and soil respiration. *Biol. Fertil. Soils* (2016). doi:10.1007/s00374-016-1120-x

495   17.   Herold, N. *et al.* Soil property and management effects on grassland microbial

496   communities across a latitudinal gradient in Germany. *Appl. Soil Ecol.* (2014).

497   doi:10.1016/j.apsoil.2013.07.009

498   18.   Hsiao, C. J., Sassenrath, G. F., Zeglin, L. H., Hettiarachchi, G. M. & Rice, C. W.

499   Vertical changes of soil microbial properties in claypan soils. *Soil Biol. Biochem.*

500   (2018). doi:10.1016/j.soilbio.2018.03.012

501   19.   Huang, Y. M., Michel, K., An, S. shan & Zechmeister-Boltenstern, S. Changes in

502   microbial-community structure with depth and time in a chronosequence of restored

503   grassland soils on the Loess Plateau in northwest China. *J. Plant Nutr. Soil Sci.* (2011).

504   doi:10.1002/jpln.201000397

505   20.   KUMAR, C. M. & GHOSHAL, N. Impact of Land-Use Change on Soil Microbial

506   Community Composition and Organic Carbon Content in the Dry Tropics. *Pedosphere*

507   (2017). doi:10.1016/S1002-0160(17)60404-1

508   21.   Labidi, S., Nasr, H., Zouaghi, M. & Wallander, H. Effects of compost addition on

509   extra-radical growth of arbuscular mycorrhizal fungi in Acacia tortilis ssp. raddiana

510   savanna in a pre-Saharan area. *Appl. Soil Ecol.* (2007).

511   doi:10.1016/j.apsoil.2006.04.009

512   22.   Li, H. *et al.* Shift in soil microbial communities with shrub encroachment in Inner

513   Mongolia grasslands, China. *Eur. J. Soil Biol.* (2017). doi:10.1016/j.ejsobi.2017.02.004

514   23.   Liu, L., Gundersen, P., Zhang, T. & Mo, J. Effects of phosphorus addition on soil

515   microbial biomass and community composition in three forest types in tropical China.

516   *Soil Biol. Biochem.* (2012). doi:10.1016/j.soilbio.2011.08.017

517   24.   Ma, L., Guo, C., Xin, X., Yuan, S. & Wang, R. Effects of belowground litter addition,

518   increased precipitation and clipping on soil carbon and nitrogen mineralization in a

519   temperate steppe. *Biogeosciences* (2013). doi:10.5194/bg-10-7361-2013

520   25.   Merilä, P. *et al.* Soil organic matter quality as a link between microbial community

521   structure and vegetation composition along a successional gradient in a boreal forest.

522   *Appl. Soil Ecol.* (2010). doi:10.1016/j.apsoil.2010.08.003

523   26.   Monkai, J. *et al.* Natural forests maintain a greater soil microbial diversity than that in

524   rubber plantations in Southwest China. *Agric. Ecosyst. Environ.* (2018).

525   doi:10.1016/j.agee.2018.06.009

526   27.   Schnecker, J. *et al.* Microbial community composition shapes enzyme patterns in

527   topsoil and subsoil horizons along a latitudinal transect in Western Siberia. *Soil Biol.*

528   *Biochem.* (2015). doi:10.1016/j.soilbio.2015.01.016

529   28.   Smyth, C. E., Macey, D. & Trofymow, J. A. Long-term litter decay in Canadian forests

530   and the influence of soil microbial community and soil chemistry. *Soil Biol. Biochem.*

531   (2015). doi:10.1016/j.soilbio.2014.09.027

532   29.   Sun, D. di *et al.* Effects of experimental warming on soil microbial communities in two

533   contrasting subalpine forest ecosystems, eastern Tibetan Plateau, China. *J. Mt. Sci.*

534   (2016). doi:10.1007/s11629-015-3733-1

535   30.   Teurlincx, S., Heijboer, A., Veraart, A. J., Kowalchuk, G. A. & Steven, S. A. Local

536   functioning, landscape structuring: Drivers of soil microbial community structure and

537   function in peatlands. *Front. Microbiol.* (2018). doi:10.3389/fmicb.2018.02060

538   31.   Wang, M., Xue, J., Horswell, J., Kimberley, M. O. & Huang, Z. Long-term biosolids

539   application alters the composition of soil microbial groups and nutrient status in a pine

540   plantation. *Biol. Fertil. Soils* **53**, 799–809 (2017).

541   32.   Wei, Y., Cao, W., Li, J., Zhang, A. & Li, X. Phospholipidfatty acid (PLFA) analysis of

542   soil microbial community structure with different intensities of grazing and fencing in

543   alpine shrubland. *Shengtai Xuebao/ Acta Ecol. Sin.* (2018).

544   doi:10.5846/stxb201706301182

545   33.   Whitaker, J. *et al.* Microbial community composition explains soil respiration

546   responses to changing carbon inputs along an Andes-to-Amazon elevation gradient. *J.*

547   *Ecol.* **102**, 1058–1071 (2014).

548   34.   Xiao, L., Liu, G. Bin & Xue, S. Effects of vegetational type and soil depth on soil

549   microbial communities on the Loess Plateau of China. *Arch. Agron. Soil Sci.* (2016).

550   doi:10.1080/03650340.2016.1170811

551   35.   Xu, G. *et al.* Labile, recalcitrant, microbial carbon and nitrogen and the microbial

552   community composition at two Abies faxoniana forest elevations under elevated

553   temperatures. *Soil Biol. Biochem.* (2015). doi:10.1016/j.soilbio.2015.08.016

554   36.   Xu, Z. *et al.* The variations in soil microbial communities, enzyme activities and their

555   relationships with soil organic matter decomposition along the northern slope of

556   Changbai Mountain. *Appl. Soil Ecol.* (2014). doi:10.1016/j.apsoil.2014.09.015

557   37.   Yang, Y., Geng, Y., Zhou, H., Zhao, G. & Wang, L. Effects of gaps in the forest

558   canopy on soil microbial communities and enzyme activity in a Chinese pine forest.

559   *Pedobiologia (Jena).* (2017). doi:10.1016/j.pedobi.2017.03.001

560   38.   Yokobe, T., Hyodo, F. & Tokuchi, N. Seasonal effects on microbial community

561   structure and nitrogen dynamics in temperate forest soil. *Forests* (2018).

562   doi:10.3390/f9030153

563   39.   Zhang, X., Wang, W., Chen, W., Zhang, N. & Zeng, H. Comparison of seasonal soil

564   microbial process in snow-covered temperate ecosystems of northern China. *PLoS One*

565   (2014). doi:10.1371/journal.pone.0092985

566   40.   Zhao, Q. *et al.* Altered precipitation seasonality impacts the dominant fungal but rare

567   bacterial taxa in subtropical forest soils. *Biol. Fertil. Soils* (2017). doi:10.1007/s00374-

568   016-1171-z

569   41.   Zhou, Y., Clark, M., Su, J. & Xiao, C. Litter decomposition and soil microbial

570   community composition in three Korean pine (Pinus koraiensis) forests along an

571   altitudinal gradient. *Plant Soil* (2014). doi:10.1007/s11104-014-2254-y

572   42.   Ananyeva, N. D., Castaldi, S., Stolnikova, E. V., Kudeyarov, V. N. & Valentini, R.

573   Fungi-to-bacteria ratio in soils of European Russia. *Arch. Agron. Soil Sci.* (2015).

574   doi:10.1080/03650340.2014.940916

575   43.   Chen, Y. L. *et al.* Patterns and drivers of soil microbial communities in Tibetan alpine

576   and global terrestrial ecosystems. *J. Biogeogr.* (2016). doi:10.1111/jbi.12806

577   44.   Bischoff, N. *et al.* Land-use change under different climatic conditions: Consequences

578   for organic matter and microbial communities in Siberian steppe soils. *Agric. Ecosyst.*

579   *Environ.* (2016). doi:10.1016/j.agee.2016.10.022

580   45.   Chang, E. H., Chen, T. H., Tian, G. L., Hsu, C. K. & Chiu, C. Y. Effect of 40 and 80

581   years of conifer regrowth on soil microbial activities and community structure in

582   subtropical low mountain forests. *Forests* (2016). doi:10.3390/f7100244

583   46.   Chang, E. H., Tian, G. & Chiu, C. Y. Soil microbial communities in natural and

584   managed cloud montane forests. *Forests* (2017). doi:10.3390/f8010033

585   47.   Chen, Y. *et al.* Large amounts of easily decomposable carbon stored in subtropical

586   forest subsoil are associated with r-strategy-dominated soil microbes. *Soil Biol.*

587   *Biochem.* (2016). doi:10.1016/j.soilbio.2016.01.004

588   48.   Cheng, S., Fang, H. & Yu, G. Threshold responses of soil organic carbon concentration

589   and composition to multi-level nitrogen addition in a temperate needle-broadleaved

590   forest. *Biogeochemistry* (2018). doi:10.1007/s10533-017-0412-z

591   49.   Demoling, F., Ola Nilsson, L. & Bååth, E. Bacterial and fungal response to nitrogen

592   fertilization in three coniferous forest soils. *Soil Biol. Biochem.* (2008).

593   doi:10.1016/j.soilbio.2007.08.019

594   50.   Ebersberger, D., Wermbter, N., Niklaus, P. A. & Kandeler, E. Effects of long term

595   CO_2 enrichment on microbial community structure in calcareous grassland. *Plant Soil*

596   (2004). doi:10.1023/B:PLSO.0000047768.89268.8c

597   51.   Grayston, S. J. & Rennenberg, H. Assessing effects of forest management on microbial

598   community structure in a central European beech forest. *Can. J. For. Res.* (2006).

599   doi:10.1139/X06-154

600   52. Hoogmoed, M., Cunningham, S. C., Baker, P. J., Beringer, J. & Cavagnaro, T. R.

601   Effects of wetting frequency and afforestation on carbon, nitrogen and the microbial

602   community in soil. *Agric. Ecosyst. Environ.* (2016). doi:10.1016/j.agee.2016.06.024

603   53. Huang, X. *et al.* Changes of soil microbial biomass carbon and community

604   composition through mixing nitrogen-fixing species with Eucalyptus urophylla in

605   subtropical China. *Soil Biol. Biochem.* (2014). doi:10.1016/j.soilbio.2014.01.021

606   54. Huygens, D. *et al.* Microbial nitrogen dynamics in south central Chilean agricultural

607   and forest ecosystems located on an Andisol. *Nutr. Cycl. Agroecosystems* (2011).

608   doi:10.1007/s10705-010-9386-0

609   55. Jangid, K. *et al.* Land-use history has a stronger impact on soil microbial community

610   composition than aboveground vegetation and soil properties. *Soil Biol. Biochem.* **43**,

611   2184–2193 (2011).

612   56. Jangid, K. *et al.* Development of soil microbial communities during tallgrass prairie

613   restoration. *Soil Biol. Biochem.* (2010). doi:10.1016/j.soilbio.2009.11.008

614   57. The Microbial Community of Three Mountains Pingding, Changbai and Saihanwula

615   Based on the Analysis of Phospholipid Fatty Acids(PLFAs). Ecology and

616   Environmental Sciences (2014).

617   58. Liu, L. *et al.* Interactive Effects of Nitrogen and Phosphorus on Soil Microbial

618   Communities in a Tropical Forest. *PLoS One* (2013).

619   doi:10.1371/journal.pone.0061188

620   59. Ma, Z., Zhang, M., Xiao, R., Cui, Y. & Yu, F. Changes in soil microbial biomass and

621   community composition in coastal wetlands affected by restoration projects in a

622   Chinese delta. *Geoderma* (2017). doi:10.1016/j.geoderma.2016.11.037

623   60.   Richter, A., Schöning, I., Kahl, T., Bauhus, J. & Ruess, L. Regional environmental

624   conditions shape microbial community structure stronger than local forest management

625   intensity. *For. Ecol. Manage.* (2018). doi:10.1016/j.foreco.2017.11.027

626   61.   Romaniuk, R., Costantini, A., Giuffré, L. & Nannipieri, P. Catabolic response and

627   phospholipid fatty acid profiles as microbial tools to assess soil functioning. *Soil Use*

628   *Manag.* (2016). doi:10.1111/sum.12293

629   62.   Royer-Tardif, S., Bradley, R. L. & Parsons, W. F. J. Evidence that plant diversity and

630   site productivity confer stability to forest floor microbial biomass. *Soil Biol. Biochem.*

631   (2010). doi:10.1016/j.soilbio.2010.01.018

632   63.   Stevenson, B. A., Hunter, D. W. F. & Rhodes, P. L. Temporal and seasonal change in

633   microbial community structure of an undisturbed, disturbed, and carbon-amended

634   pasture soil. *Soil Biol. Biochem.* (2014). doi:10.1016/j.soilbio.2014.04.010

635   64.   Wang, Q., He, T., Wang, S. & Liu, L. Carbon input manipulation affects soil

636   respiration and microbial community composition in a subtropical coniferous forest.

637   *Agric. For. Meteorol.* (2013). doi:10.1016/j.agrformet.2013.04.021

638   65.   Wang, C. *et al.* Effects of long-term experimental warming on plant community

639   properties and soil microbial community composition in an alpine meadow. *Isr. J.*

640   *Ecol. Evol.* (2017). doi:10.1080/15659801.2017.1281201

641   66.   Wang, R. *et al.* Sensitivities to nitrogen and water addition vary among microbial

642   groups within soil aggregates in a semiarid grassland. *Biol. Fertil. Soils* (2017).

643   doi:10.1007/s00374-016-1165-x

644   67.   Xu, Z. *et al.* Divergence of dominant factors in soil microbial communities and

645   functions in forest ecosystems along a climatic gradient. *Biogeosciences* (2018).

646   doi:10.5194/bg-15-1217-2018

647   68.   Yang, B., Pang, X., Hu, B., Bao, W. & Tian, G. Does thinning-induced gap size result

648 in altered soil microbial community in pine plantation in eastern Tibetan Plateau? *Ecol.*

649 *Evol.* (2017). doi:10.1002/ece3.2714

650 69. Yang, S. *et al.* Variations in soil microbial community composition and enzymatic

651 activities in response to increased N deposition and precipitation in Inner Mongolian

652 grassland. *Appl. Soil Ecol.* (2017). doi:10.1016/j.apsoil.2017.06.041

653 70. Yang, F. *et al.* Spatial heterogeneity of microbial community and enzyme activities in a

654 broad-leaved Korean pine mixed forest. *Eur. J. Soil Biol.* (2018).

655 doi:10.1016/j.ejsobi.2018.07.001

656 71. Zhao, C. *et al.* Soil microbial community composition and respiration along an

657 experimental precipitation gradient in a semiarid steppe. *Sci. Rep.* (2016).

658 doi:10.1038/srep24317

659 72. Baer, S. G., Bach, E. M., Meyer, C. K., Du Preez, C. C. & Six, J. Belowground

660 Ecosystem Recovery During Grassland Restoration: South African Highveld

661 Compared to US Tallgrass Prairie. *Ecosystems* **18**, 390–403 (2015).

662 73. Liang, A. *et al.* Investigations of relationships among aggregate pore structure,

663 microbial biomass, and soil organic carbon in a Mollisol using combined non-

664 destructive measurements and phospholipid fatty acid analysis. *Soil Tillage Res.*

665 (2019). doi:10.1016/j.still.2018.09.003

666 74. Kou, L. *et al.* Nitrogen additions inhibit nitrification in acidic soils in a subtropical pine

667 plantation: effects of soil pH and compositional shifts in microbial groups. *J. For. Res.*

668 (2019). doi:10.1007/s11676-018-0645-2

669 75. Li, Q. *et al.* Spatial variation in soil microbial community structure and its relation to

670 plant distribution and local environments following afforestation in central China. *Soil*

671 *Tillage Res.* (2019). doi:10.1016/j.still.2019.05.015

672 76. Zhou, J. *et al.* Nitrogen addition affects soil respiration primarily through changes in

673   microbial community structure and biomass in a subtropical natural forest. *Forests*

674   (2019). doi:10.3390/f10050435

675 77. Chen, L. *et al.* Differential responses of net n mineralization and nitrification to

676   throughfall reduction in a castanopsis hystrix plantation in southern china. *For.*

677   *Ecosyst.* (2019). doi:10.1186/s40663-019-0174-2

678 78. Zhang, Q. *et al.* Nitrogen addition accelerates the nitrogen cycle in a young subtropical

679   Cunninghamia lanceolata (Lamb.) plantation. *Ann. For. Sci.* (2019).

680   doi:10.1007/s13595-019-0817-z

681 79. Liu, D., Huang, Y., Sun, H. & An, S. The restoration age of Robinia pseudoacacia

682   plantation impacts soil microbial biomass and microbial community structure in the

683   Loess Plateau. *Catena* (2018). doi:10.1016/j.catena.2018.02.001

684 80. Wei, K., Sun, T., Tian, J., Chen, Z. & Chen, L. Soil microbial biomass, phosphatase

685   and their relationships with phosphorus turnover under mixed inorganic and organic

686   nitrogen addition in a Larix gmelinii plantation. *For. Ecol. Manage.* (2018).

687   doi:10.1016/j.foreco.2018.04.035

688 81. Yang, M., Yang, D. & Yu, X. Soil microbial communities and enzyme activities in sea-

689   buckthorn (Hippophae rhamnoides) plantation at different ages. *PLoS One* (2018).

690   doi:10.1371/journal.pone.0190959

691 82. Li, J. *et al.* Response of soil organic carbon fractions, microbial community

692   composition and carbon mineralization to high-input fertilizer practices under an

693   intensive agricultural system. *PLoS One* (2018). doi:10.1371/journal.pone.0195144

694 83. Kang, H. *et al.* Changes in soil microbial community structure and function after

695   afforestation depend on species and age: Case study in a subtropical alluvial island. *Sci.*

696   *Total Environ.* (2018). doi:10.1016/j.scitotenv.2017.12.180

697 84. Fan, Y. *et al.* Decreased soil organic P fraction associated with ectomycorrhizal fungal

698   activity to meet increased P demand under N application in a subtropical forest

699   ecosystem. *Biol. Fertil. Soils* (2018). doi:10.1007/s00374-017-1251-8

700 85. Yu, X. *et al.* Effect of soil layer and plant-soil interaction on soil microbial diversity

701   and function after canopy gap disturbance. *Forests* (2018). doi:10.3390/f9110680

702 86. Liu, D. *et al.* Dynamics of soil nitrogen fractions and their relationship with soil

703   microbial communities in two forest species of northern China. *PLoS One* (2018).

704   doi:10.1371/journal.pone.0196567

705 87. Li, D., Liu, J., Chen, H., Zheng, L. & Wang, K. Soil microbial community responses to

706   forage grass cultivation in degraded karst soils, Southwest China. *L. Degrad. Dev.*

707   (2018). doi:10.1002/ldr.3188

708 88. Liao, H., Zheng, C., Li, J. & Long, J. Dynamics of soil microbial recovery from

709   cropland to orchard along a 20-year chronosequence in a degraded karst ecosystem.

710   *Sci. Total Environ.* (2018). doi:10.1016/j.scitotenv.2018.05.246

711 89. Zhao, Q. *et al.* Spring drying and intensified summer rainfall affected soil microbial

712   community composition but not enzyme activity in a subtropical forest. *Appl. Soil*

713   *Ecol.* (2018). doi:10.1016/j.apsoil.2018.06.014

714 90. Kim, S. *et al.* Tree species and recovery time drives soil restoration after mining: A

715   chronosequence study. *L. Degrad. Dev.* (2018). doi:10.1002/ldr.2951

716 91. van Leeuwen, J. P. *et al.* Effects of land use on soil microbial biomass, activity and

717   community structure at different soil depths in the Danube floodplain. *Eur. J. Soil Biol.*

718   (2017). doi:10.1016/j.ejsobi.2017.02.001

719 92. Gunina, A., Smith, A. R., Godbold, D. L., Jones, D. L. & Kuzyakov, Y. Response of

720   soil microbial community to afforestation with pure and mixed species. *Plant Soil*

721   (2017). doi:10.1007/s11104-016-3073-0

722 93. Liu, Z., Rong, Q., Zhou, W. & Liang, G. Effects of inorganic and organic amendment

723 on soil chemical properties, enzyme activities, microbial community and soil quality in

724 yellow clayey soil. *PLoS One* (2017). doi:10.1371/journal.pone.0172767

725 94. Fang, X. *et al.* Forest-type shift and subsequent intensive management affected soil

726 organic carbon and microbial community in southeastern China. *Eur. J. For. Res.*

727 (2017). doi:10.1007/s10342-017-1065-0

728 95. Lupwayi, N. Z., Larney, F. J., Blackshaw, R. E., Kanashiro, D. A. & Pearson, D. C.

729 Phospholipid fatty acid biomarkers show positive soil microbial community responses

730 to conservation soil management of irrigated crop rotations. *Soil Tillage Res.* (2017).

731 doi:10.1016/j.still.2016.12.003

732 96. Dai, X., Wang, H. & Fu, X. Soil microbial community composition and its role in

733 carbon mineralization in long-term fertilization paddy soils. *Sci. Total Environ.* (2017).

734 doi:10.1016/j.scitotenv.2016.11.212

735 97. Rathore, A. P., Chaudhary, D. R. & Jha, B. Seasonal Patterns of Microbial Community

736 Structure and Enzyme Activities in Coastal Saline Soils of Perennial Halophytes. *L.*

737 *Degrad. Dev.* (2017). doi:10.1002/ldr.2710

738 98. Wang, C. *et al.* The effect of simulated warming on root dynamics and soil microbial

739 community in an alpine meadow of the Qinghai-Tibet Plateau. *Appl. Soil Ecol.* (2017).

740 doi:10.1016/j.apsoil.2017.03.005

741 99. Zhao, Q. *et al.* Asymmetric effects of litter removal and litter addition on the structure

742 and function of soil microbial communities in a managed pine forest. *Plant Soil* (2017).

743 doi:10.1007/s11104-016-3115-7

744 100. Sun, S. *et al.* Response of soil microbial community structure to increased precipitation

745 and nitrogen addition in a semiarid meadow steppe. *Eur. J. Soil Sci.* (2017).

746 doi:10.1111/ejss.12441

747 101. Kotzé, E., Sandhage-Hofmann, A., Amelung, W., Oomen, R. J. & du Preez, C. C. Soil

748   microbial communities in different rangeland management systems of a sandy savanna

749   and clayey grassland ecosystem, South Africa. *Nutr. Cycl. Agroecosystems* (2017).

750   doi:10.1007/s10705-017-9832-3

751 102. Swarzenski, C. M., Song, C., Meng, H., Wang, X. & Tan, W. Nitrogen additions affect

752   litter quality and soil biochemical properties in a peatland of Northeast China. *Ecol.*

753   *Eng.* (2017). doi:10.1016/j.ecoleng.2016.12.025

754 103. Zhang, J., Li, M. & Zheng, G. Effect of stand age on soil microbial community

755   structure in wolfberry (Lycium barbarum L.) fields. *Shengtai Xuebao/ Acta Ecol. Sin.*

756   (2017). doi:10.1016/j.chnaes.2016.12.003

757 104. Xu, S. *et al.* Comparison of Microbial Community Composition and Diversity in

758   Native Coastal Wetlands and Wetlands that Have Undergone Long-Term Agricultural

759   Reclamation. *Wetlands* (2017). doi:10.1007/s13157-016-0843-7

760 105. Xiang, Y., Cheng, M., Huang, Y., An, S. & Darboux, F. Changes in soil microbial

761   community and its effect on carbon sequestration following afforestation on the Loess

762   Plateau, China. *Int. J. Environ. Res. Public Health* (2017). doi:10.3390/ijerph14080948

763 106. Veen, G. F. C. *et al.* Coordinated responses of soil communities to elevation in three

764   subarctic vegetation types. *Oikos* (2017). doi:10.1111/oik.04158

765 107. Faust, S. *et al.* Effect of biodynamic soil amendments on microbial communities in

766   comparison with inorganic fertilization. *Appl. Soil Ecol.* (2017).

767   doi:10.1016/j.apsoil.2017.03.006

768 108. Qi, L. & Yang, J. Microbial community composition regulates SOC decomposition

769   response to forest conversion in a Chinese temperate forest. *Ecol. Res.* (2017).

770   doi:10.1007/s11284-016-1428-x

771 109. Chang, E. H., Chen, T. H., Tian, G. & Chiu, C. Y. The effect of altitudinal gradient on

772   soil microbial community activity and structure in moso bamboo plantations. *Appl. Soil*

773   *Ecol.* (2016). doi:10.1016/j.apsoil.2015.10.018

774   110.   Cavagnaro, T. R., Cunningham, S. C. & Fitzpatrick, S. Pastures to woodlands: Changes

775   in soil microbial communities and carbon following reforestation. *Appl. Soil Ecol.* **107**,

776   24–32 (2016).

777   111.   Guo, X. *et al.* Effects of land use change on the composition of soil microbial

778   communities in a managed subtropical forest. *For. Ecol. Manage.* (2016).

779   doi:10.1016/j.foreco.2016.03.048

780   112.   Jia, S. *et al.* Long-term conservation tillage influences the soil microbial community

781   and its contribution to soil CO_2 emissions in a Mollisol in Northeast China. *J. Soils*

782   *Sediments* (2016). doi:10.1007/s11368-015-1158-7

783   113.   Xiao, L., Liu, G. Bin, Zhang, J. Y. & Xue, S. Long-term effects of vegetational

784   restoration on soil microbial communities on the Loess Plateau of China. *Restor. Ecol.*

785   (2016). doi:10.1111/rec.12374

786   114.   Perkiömäki, J. & Fritze, H. Short and long-term effects of wood ash on the boreal

787   forest humus microbial community. *Soil Biol. Biochem.* (2002). doi:10.1016/S0038-

788   0717(02)00079-2

789   115.   Perkiömäki, J., Tom-Petersen, A., Nybroe, O. & Fritze, H. Boreal forest microbial

790   community after long-term field exposure to acid and metal pollution and its potential

791   remediation by using wood ash. *Soil Biol. Biochem.* (2003). doi:10.1016/S0038-

792   0717(03)00250-5

793   116.   Niwa, S., Kaneko, N., Okada, H. & Sakamoto, K. Effects of fine-scale simulation of

794   deer browsing on soil micro-foodweb structure and N mineralization rate in a

795   temperate forest. *Soil Biol. Biochem.* (2008). doi:10.1016/j.soilbio.2007.10.004

796   117.   Campbell, C. D., Cameron, C. M., Bastias, B. A., Chen, C. & Cairney, J. W. G. Long

797   term repeated burning in a wet sclerophyll forest reduces fungal and bacterial biomass

798   and responses to carbon substrates. *Soil Biol. Biochem.* (2008).

799   doi:10.1016/j.soilbio.2008.04.020

800   118. Unger, I. M., Kennedy, A. C. & Muzika, R. M. Flooding effects on soil microbial

801   communities. *Appl. Soil Ecol.* (2009). doi:10.1016/j.apsoil.2009.01.007

802   119. Zhang, Q. *et al.* Alterations in soil microbial community composition and biomass

803   following agricultural land use change. *Sci. Rep.* (2016). doi:10.1038/srep36587

804   120. Deng, Q. *et al.* Soil microbial community and its interaction with soil carbon and

805   nitrogen dynamics following afforestation in central China. *Sci. Total Environ.* (2016).

806   doi:10.1016/j.scitotenv.2015.09.080

807   121. Wang, C. *et al.* Responses of soil microbial community to continuous experimental

808   nitrogen additions for 13 years in a nitrogen-rich tropical forest. *Soil Biol. Biochem.*

809   (2018). doi:10.1016/j.soilbio.2018.03.009

810   122. Zheng, S. *et al.* Effect of nitrogen and acid deposition on soil respiration in a temperate

811   forest in China. *Geoderma* (2018). doi:10.1016/j.geoderma.2018.05.022

812   123. Wang, J. *et al.* Conversion of rainforest into agroforestry and monoculture plantation in

813   China: Consequences for soil phosphorus forms and microbial community. *Sci. Total*

814   *Environ.* (2017). doi:10.1016/j.scitotenv.2017.04.012

815   124. Bastida, F. *et al.* Differential sensitivity of total and active soil microbial communities

816   to drought and forest management. *Glob. Chang. Biol.* (2017). doi:10.1111/gcb.13790

817   125. Buyer, J. S., Baligar, V. C., He, Z. & Arévalo-Gardini, E. Soil microbial communities

818   under cacao agroforestry and cover crop systems in Peru. *Appl. Soil Ecol.* (2017).

819   doi:10.1016/j.apsoil.2017.09.009

820   126. Borymski, S., Cycon, M., Beckmann, M., Mur, L. A. J. & Piotrowska-Seget, Z. Plant

821   species and heavy metals affect biodiversity of microbial communities associated with

822   metal-tolerant plants in metalliferous soils. *Front. Microbiol.* (2018).

823   doi:10.3389/fmicb.2018.01425

824   127.   Montiel-Rozas, M. M. *et al.* Long-term effects of organic amendments on bacterial and

825   fungal communities in a degraded Mediterranean soil. *Geoderma* (2018).

826   doi:10.1016/j.geoderma.2018.06.022

827   128.   Huang, J. *et al.* Effects of phosphorus addition on soil microbial biomass and

828   community composition in a subalpine spruce plantation. *Eur. J. Soil Biol.* (2016).

829   doi:10.1016/j.ejsobi.2015.12.007

830   129.   Chen, L. *et al.* Regulation of priming effect by soil organic matter stability over a broad

831   geographic scale. *Nat. Commun.* (2019). doi:10.1038/s41467-019-13119-z

832   130.   Zhang, C. *et al.* Soil microbial communities response to herbicide 2,4-

833   dichlorophenoxyacetic acid butyl ester. *Eur. J. Soil Biol.* (2010).

834   doi:10.1016/j.ejsobi.2009.12.005

835   131.   Bezemer, T. M. *et al.* Plant species and functional group effects on abiotic and

836   microbial soil properties and plant-soil feedback responses in two grasslands. *J. Ecol.*

837   (2006). doi:10.1111/j.1365-2745.2006.01158.x

838   132.   Bi, J., Zhang, N., Liang, Y., Yang, H. & Ma, K. Interactive effects of water and

839   nitrogen addition on soil microbial communities in a semiarid steppe. *J. Plant Ecol.*

840   (2012). doi:10.1093/jpe/rtr046

841   133.   Chen, D. *et al.* Effects of plant functional group loss on soil biota and net ecosystem

842   exchange: A plant removal experiment in the Mongolian grassland. *J. Ecol.* (2016).

843   doi:10.1111/1365-2745.12541

844   134.   Högberg, M. N., Högberg, P. & Myrold, D. D. Is microbial community composition in

845   boreal forest soils determined by pH, C-to-N ratio, the trees, or all three? *Oecologia*

846   (2007). doi:10.1007/s00442-006-0562-5

847   135.   Niu, L., Liu, Y. H., Li, Y. & Ouyang, S. N. Microbial community structure of the

848   alpine meadow under different grazing styles in Naqu prefecture of Tibet. *Chinese J.*

849   *Appl. Ecol.* (2015).

850   136. Qin, H. *et al.* Rapid soil fungal community response to intensive management in a

851   bamboo forest developed from rice paddies. *Soil Biol. Biochem.* (2014).

852   doi:10.1016/j.soilbio.2013.09.031

853   137. Yan, H., Huang, Y., Jiang, Y. & Zhao, T. Seasonal variation of PLFA during soil

854   mineralization under two kinds of shrub lands in mountainous area of southern

855   Ningxia, Northwest China. *Huanjing Kexue Xuebao/Acta Sci. Circumstantiae* (2014).

856   doi:10.13671/j.hjkxxb.2014.0538

857   138. Yang, Q. *et al.* Structure and function of soil microbial community in artificially

858   planted Sonneratia apetala and S. caseolaris forests at different stand ages in Shenzhen

859   Bay, China. *Mar. Pollut. Bull.* (2014). doi:10.1016/j.marpolbul.2014.02.024

860   139. Hu, Y. *et al.* Soil organic carbon and soil structure are driving microbial abundance and

861   community composition across the arid and semi-arid grasslands in northern China.

862   *Soil Biol. Biochem.* (2014). doi:10.1016/j.soilbio.2014.06.014

863   140. Ma, L., Guo, C., Lü, X., Yuan, S. & Wang, R. Do climate factors govern soil microbial

864   community composition and biomass at a regional scale? *Biogeosciences Discussions*

865   (2014). doi:10.5194/bgd-11-17729-2014

866   141. Frey, B., Stemmer, M., Widmer, F., Luster, J. & Sperisen, C. Microbial activity and

867   community structure of a soil after heavy metal contamination in a model forest

868   ecosystem. *Soil Biol. Biochem.* (2006). doi:10.1016/j.soilbio.2005.11.032

869   142. Jiang, Y., Sun, B., Jin, C. & Wang, F. Soil aggregate stratification of nematodes and

870   microbial communities affects the metabolic quotient in an acid soil. *Soil Biol.*

871   *Biochem.* (2013). doi:10.1016/j.soilbio.2013.01.006

872   143. Joner, E. J., Eldhuset, T. D., Lange, H. & Frostegård, Å. Changes in the microbial

873   community in a forest soil amended with aluminium in situ. in *Plant and Soil* (2005).

874   doi:10.1007/s11104-005-2287-3

875   144. Li, Q. *et al.* Nitrogen Addition and Warming Independently Influence the Belowground

876   Micro-Food Web in a Temperate Steppe. *PLoS One* (2013).

877   doi:10.1371/journal.pone.0060441

878   145. Mitchell, R. J., Campbell, C. D., Chapman, S. J. & Cameron, C. M. The ecological

879   engineering impact of a single tree species on the soil microbial community. *J. Ecol.*

880   (2010). doi:10.1111/j.1365-2745.2009.01601.x

881   146. Potthoff, M. *et al.* Soil microbial community composition as affected by restoration

882   practices in California grassland. *Soil Biol. Biochem.* (2006).

883   doi:10.1016/j.soilbio.2005.12.009

884   147. Shanmugam, S. G. & Kingery, W. L. Changes in soil microbial community structure in

885   relation to plant succession and soil properties during 4000 years of pedogenesis. *Eur.*

886   *J. Soil Biol.* (2018). doi:10.1016/j.ejsobi.2018.07.003

887   148. Xu, M. *et al.* Soil microbial community structure and activity along a montane

888   elevational gradient on the Tibetan Plateau. *Eur. J. Soil Biol.* (2014).

889   doi:10.1016/j.ejsobi.2014.06.002

890   149. Waldrop, M. P. *et al.* The interacting roles of climate, soils, and plant production on

891   soil microbial communities at a continental scale. *Ecology* (2017).

892   doi:10.1002/ecy.1883

893   150. Ma, et al. Plants regulate the effects of experimental warming on the soil microbial

894   community in an alpine scrub ecosystem. PLoS One, 13, e0195079 (2018).

895

896   151. Xu. Influence of elevation and land use on soil organic carbon and microbial

897   community on Southeast Tibetan Plateau. PhD Dissertation, China Agricultural

898   University, (2016).

899

900   152.   Zhu. Study on the effects of microorganisms on phosphorus transformation in the

901   rhizosphere of wetland plants. Masters Dissertation, Beijing Forestry University,

902   (2016).

903   153.   Zhao, et al. Changes in soil microbial community, enzyme activities and organic matter

904   fractions under long-term straw return in north-central China. Agriculture, Ecosystmes

905   & Environment, 216, 82-88 (2016).

906   154.   Wu, et al. The Effect of Forest Thinning on Soil Microbial Community Structure and

907   Function. Forests, 10, 352 (2019).

908   155.   Si, et al. Changes in soil microbial community composition and organic carbon

909   fractions in an integrated ricecrayfish farming system in subtropical China. Scientific

910   Reports, 7, 2856 (2017).

911   156.   Peltoniemi, et al. Microbial ecology in a future climate: effects of temperature and

912   moisture on microbial communities of two boreal fens. Fems Microbiology Ecology, 7,

913   54-61 (2015).

914   157.   Jing. The spatial heterogeneity of soil microorganism and organic matter in broad-

915   leaved korean pine forest in Changbai mountain. Masters Dissertation, Shanxi

916   University, (2016).

917   158.   Huang, et al. Effects of phosphorus addition on soil microbial biomass and community

918   composition in a subalpine spruce plantation. European Journal of Soil Biology, 72,

919   35-41 (2016).

920   159.   Yu, et al. Effect of monospecific and mixed seabuckthorn (Hippophae rhamnoides)

921   plantattion s on the structure and acitivity of soil microbial communities. PLoS One,

922   10, e0117505 (2015).

923

924 160.   Zhang Responses of soil microbial communities to typical artificial plantations with

925   different ages in a loess area. Masters Dissertation, Northwest A & F University,

926   (2017).

927 161.   Zang et al. Effects of grazing on microbial community structure diversity in

928   rhizosphere soil of Artemisiafrigida. Acta Agrestia Sinica, 25, 982-992 (2017).

929 162.   Yang et al. Comparison of soil microbial communtiy composition and structure in

930   Tricholoma matsutake shiro and non-shiro soils in Quercus semecarpifolia and Pinus

931   densata forests. Acta Ecologica Sinica, 38, 1630-1638 (2018).

932 163.   Wu. The research on soil nutrition and relationship with the composition of the

933   microbial communities in different forests of Changbai mountain. Masters Dissertation,

934   Northeast Forestry University, (2012).

935 164.   Sun. Interactions of water and nitrogen addition on soil microbial community

936   composition and functional diversity depending on the inter-annual precipitation in a

937   Chinese steppe. Journal of Integrative Agriculture, 14, 788-799 (2015).

938 165.   Wang et al. Soil microbial community composition rather than litter quality is linked

939   with soil organic carbon chemical composition in plantations in subtropical China.

940   Journal of Soils Sediments, 15, 1094-1103 (2015).

941 166.   Pan. Soil carbon and nitrogen transfromation process research of relationship between

942   soil microbial community sturcture of Michelia maclurei, Pinus massoniana plantation

943   Masters Dissertation, Guangxi University, (2015).

944 167.   Qin et al. Effects of wetland vegetation on soil microbial composition: a case study in

945   Tumen river basin, Northeast China. Chinese Geographical Science, 27, 239-247

946   (2017).

947 168.   Huang. Soil microbial indices response to vegetation natural rehabilitation on the loess

948   hilly-gully area. PhD Dissertation, Northwest A & F University, (2008).

949

950   169.   Brant et al. Microbial community utilization of added carbon substrates in response to

951   long-term carbon input manipulation. Soil Biology & Biochemistry, 38, 2219-2232

952   (2006).

953   170.   Chang. The study of microbial community diversity and function along glacier

954   foreland in Ny-Alesund, Arctic. PhD Dissertation, Wuhan University, (2016).

955   171.   Chen et al. Microbial community structure of three typical gymnosperms soil in scenic

956   area of Maijishan, Gansu Province. Microbiology China, 43, 1939-1944 (2016).

957   172.   Chi et al. Research on soil microbial community structure of different forest-wetland

958   ecotones in Xiaoxing'an Mountain. Forest Engineering, 3, 6-13 (2018).

959   173.   Gu et al. Soil microbial community structure, enzyme activities, and their influencing

960   factors along different altitudes of Changbai Mountain. Acta Ecologica Sinica, 37,

961   8347-8384 (2017).

962   174.   Li et al. Effects of nitrogen and phosphorus addition on soil microbial community in a

963   secondary tropical forest of China. Biology & Fertility of Soils, 51, 207-215 (2015).

964   175.   Liu et al. Soil microbial community structure and functional diversity marked by PLFA

965   in forestland. Masters Dissertation, Beijing Forestry University, (2016).

966   176.   Liu et al. Effect of different land use types on soil aggregates microbial biomass and

967   community composition in the loess hilly region of west Henan. Pratacultural Science,

968   35, 771-780 (2018).

969   177.   Lu et al. Soil labile organic carbon and nitrogen pools and associated microbial process

970   under three forest types in Australia. PhD Dissertation, Jiangxi Agricultural University,

971   (2011).

972   178.   Luo et al. Characteristics of carbon and nitrogen in monoculture and mixed young

stands of Erythrophleum fordii and Pinus massoniana in southern subtropical China.

PhD Dissertation, Chinese Academy of Forestry, (2014).

179. Wu et al. Effects of precipitation change on soil microbial community of the monsoon

evergreen leaved forest in Dinghushan biosphere reserve. Masters Dissertation,

Guangzhou University, (2017).