Supplementary Information

Meta-analysis of the impacts of global change factors on soil microbial diversity and functionality

Zhou et al.

Includes:

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Supplementary Table 1 Summary of dominant drivers of soil microbial alpha diversity in terrestrial ecosystems from large-scale studies.

Driver	Effect	Involved mechanism or theory	Location (sample size)
Temperature	Positive	Metabolic theory: Elevated temperature increases biodiversity by accelerating the biochemical reactions that control speciation rate[1].	North America (126 soils)[2]
Soil resource content	Positive	Species energy theory: Species richness increases monotonically with the energy or resource[3]; It assumes that diversity mirrors productivity within microorganisms because soil microbial biomass much depends upon the soil carbon or nutrient contents[4,5].	Global (~600 soils)[4]
Soil carbon to nutrient ratios	Negative	Stoichiometry theory: Fast growing microorganisms require higher demand for nutrients than plants[6]; It assumes that microbial diversity mirrors its biomass, and thus lower carbon to nutrient ratios may result in higher microbial diversity[4].	Scotland (179 sites)[7]
Plant diversity	Positive	Aboveground–belowground interactions: Plant diversity promotes the diversity of soil microbes by increasing the diversity of soil exudates and litter, physical microhabitats and environmental conditions, and plant hosts for symbiotic and pathogenic microbes[8,9,10].	Four continents (25 temperate grassland sites)[9]
Soil pH	Unimodal	Niche imposes a physiological constraint, altering competitive outcomes or reducing net growth of individual taxa unable to survive if the soil pH falls outside a certain range[11,12,13].	North and South America (98 soils[11]; 88 soils[12]); Arctic (29 sites)[13]
Aridity	Negative	Aridity decreases microbial diversity by its negative impact on soil carbon contents.	Global (80 dryland sites)[14]
Latitude	Negative	Covariant factors with latitudinal gradients, especially temperature and precipitation.	Global (365 soils)[15]; Southern hemisphere (647 sites)[16]

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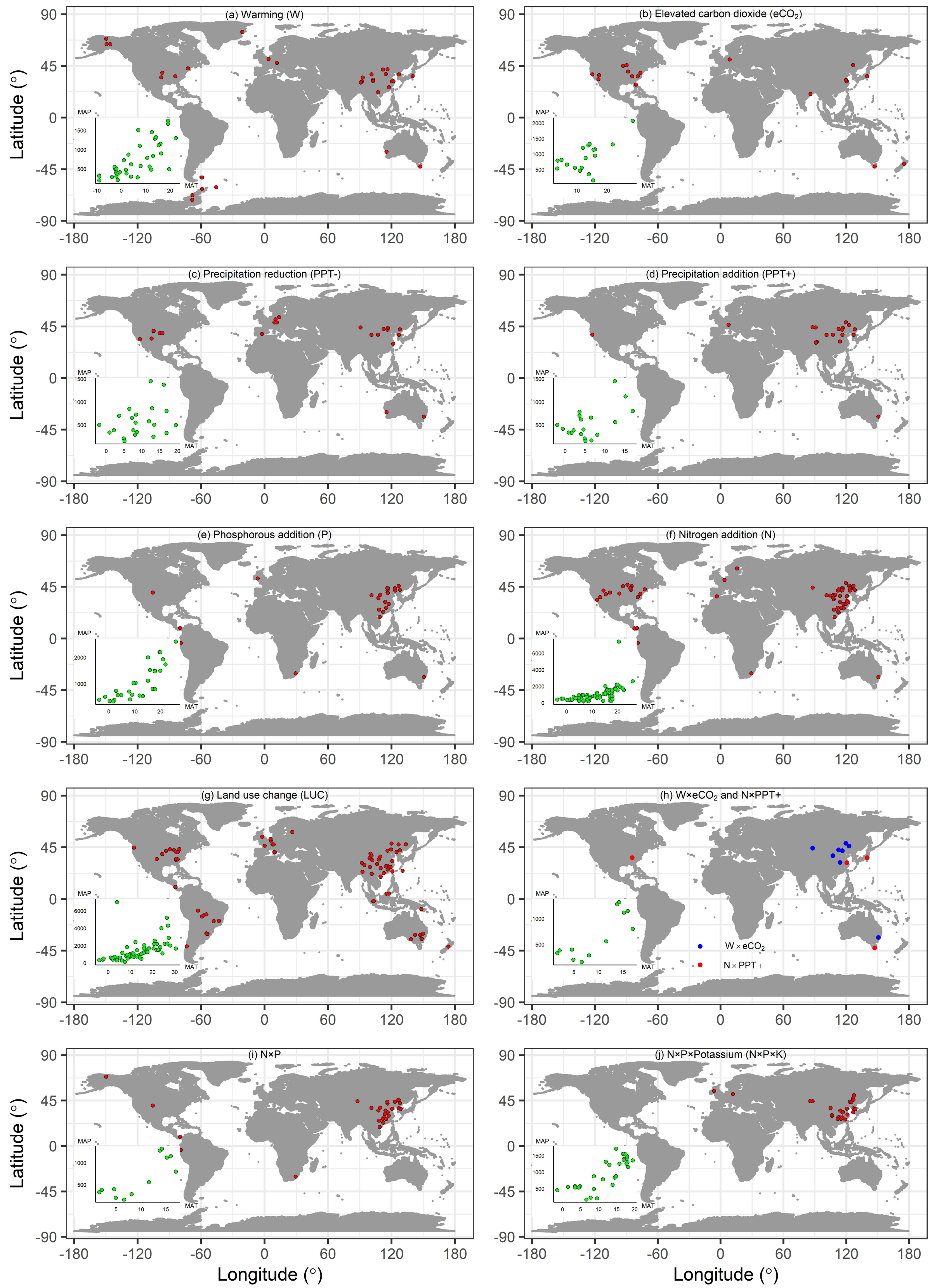
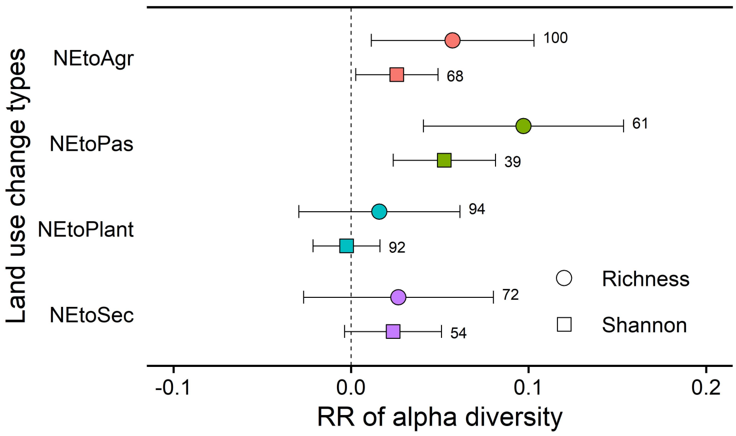
Supplementary Table 2 Correlation coefficients between response of microbial alpha diversity and climate factors.

GCFs	Climates	RR of richness	RR of Shannon index
W	MAT	-0.01(*n* = 100)	0.07(*n* = 73)
	MAP	-0.11(*n* = 100)	-0.05(*n* = 73)
eCO_2	MAT	-0.18(*n* = 39)	0.31(*n* = 22)
	MAP	-0.31(*n* = 39)	0.09(*n* = 22)
PPT-	MAT	-0.16(*n* = 47)	0.15(*n* = 59)
	MAP	0.00(*n* = 47)	0.03(*n* = 59)
PPT+	MAT	-0.25(*n* = 47)	-0.09(*n* = 44)
	MAP	-0.29(*n* = 47)	-0.1(*n* = 44)
P	MAT	-0.12(*n* = 62)	-0.29(*n* = 35)
	MAP	-0.07(*n* = 62)	0.13(*n* = 35)
N	MAT	**-0.14(*n* = 287)***	**-0.2(*n* = 199)****
	MAP	-0.07(*n* = 287)	0.07(*n* = 199)
LUC	MAT	-0.05(*n* = 291)	0.09(*n* = 246)
	MAP	0.00(*n* = 292)	0.07(*n* = 246)
W×eCO_2	MAT	-0.04(*n* = 9)	-0.38(*n* = 5)
	MAP	0.13(*n* = 9)	0.48(*n* = 5)
N×PPT+	MAT	**-0.51(*n* = 25)****	**-0.64(*n* = 23)*****
	MAP	**-0.71(*n* = 25)*****	**-0.71(*n* = 23)*****
N×P	MAT	**-0.28(*n* = 58)***	-0.16(*n* = 37)
	MAP	**-0.35(*n* = 58)****	-0.14(*n* = 37)
N×P×K	MAT	**-0.21(*n* = 101)***	0.05(*n* = 93)
	MAP	-0.08(*n* = 101)	0.07(*n* = 93)

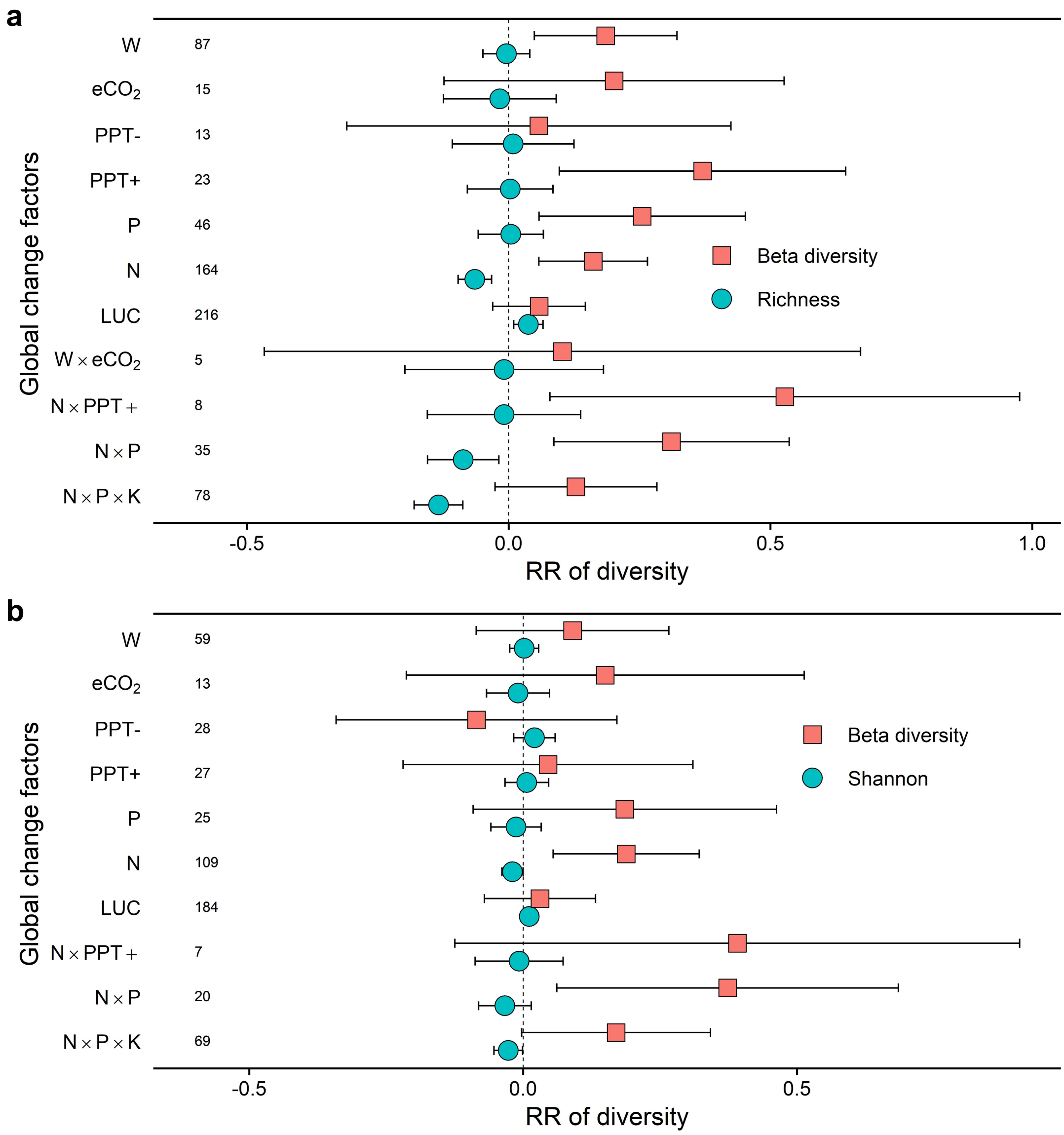
GCFs, global change factors (including warming (W), carbon dioxide enrichment (eCO_2), decreased precipitation (PPT-), increased precipitation (PPT+), phosphorous addition (P), nitrogen addition (N), land use change (LUC), W×eCO_2, N×PPT+, N plus P plus potassium addition (N×P×K)); MAT, mean annual temperature (℃); MAP, mean annual precipitation (mm). The significant correlations are marked by asterisk (*, P<0.05; **, P<0.01; ***, P<0.001).



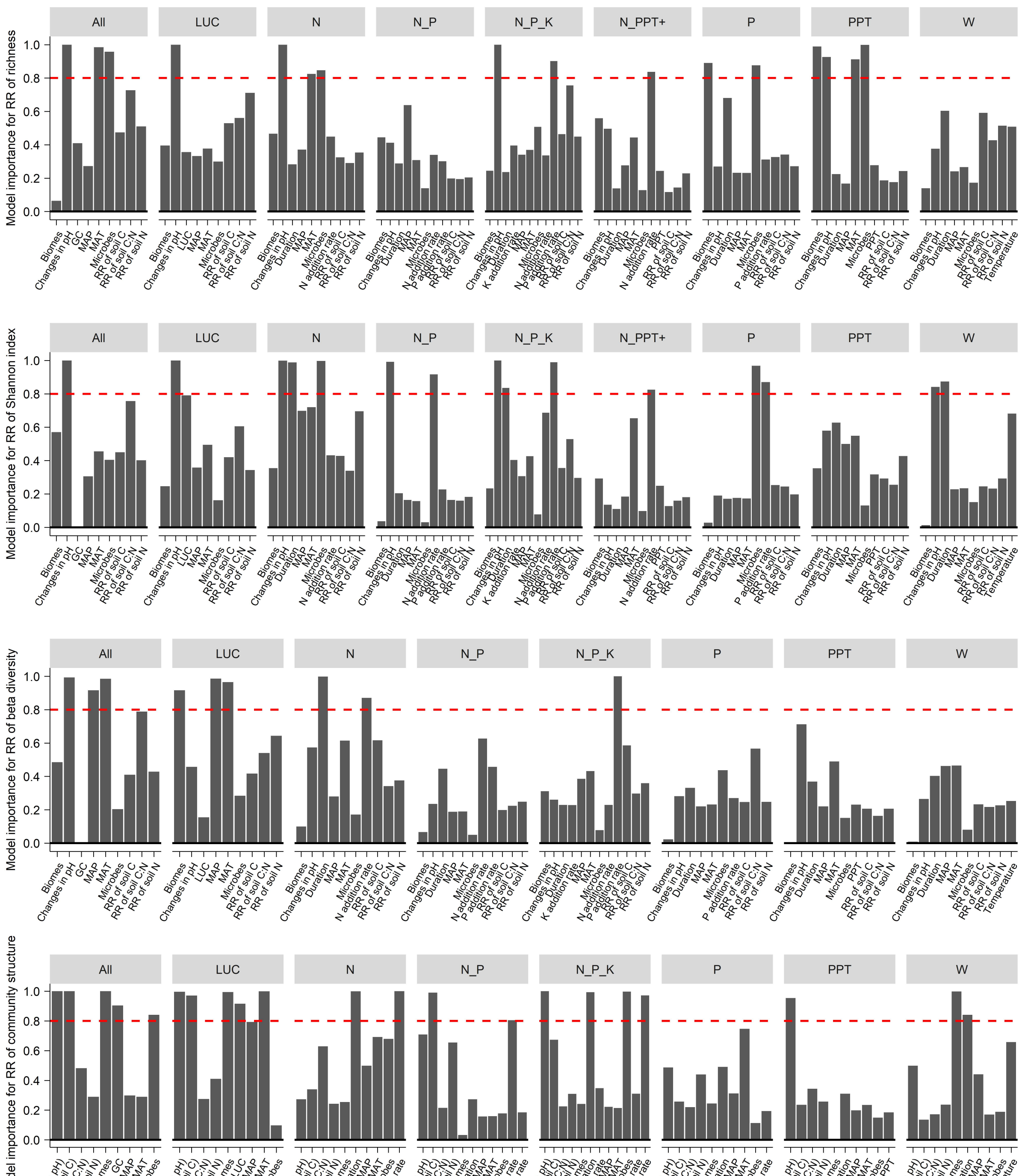
Supplementary Fig. 1 Distribution of the sampling sites for different global change factors. The inset scatter plots show the relationships between mean annual temperature (MAT, ℃) and mean annual precipitation (MAP, mm). Source data are provided as a Source Data file.



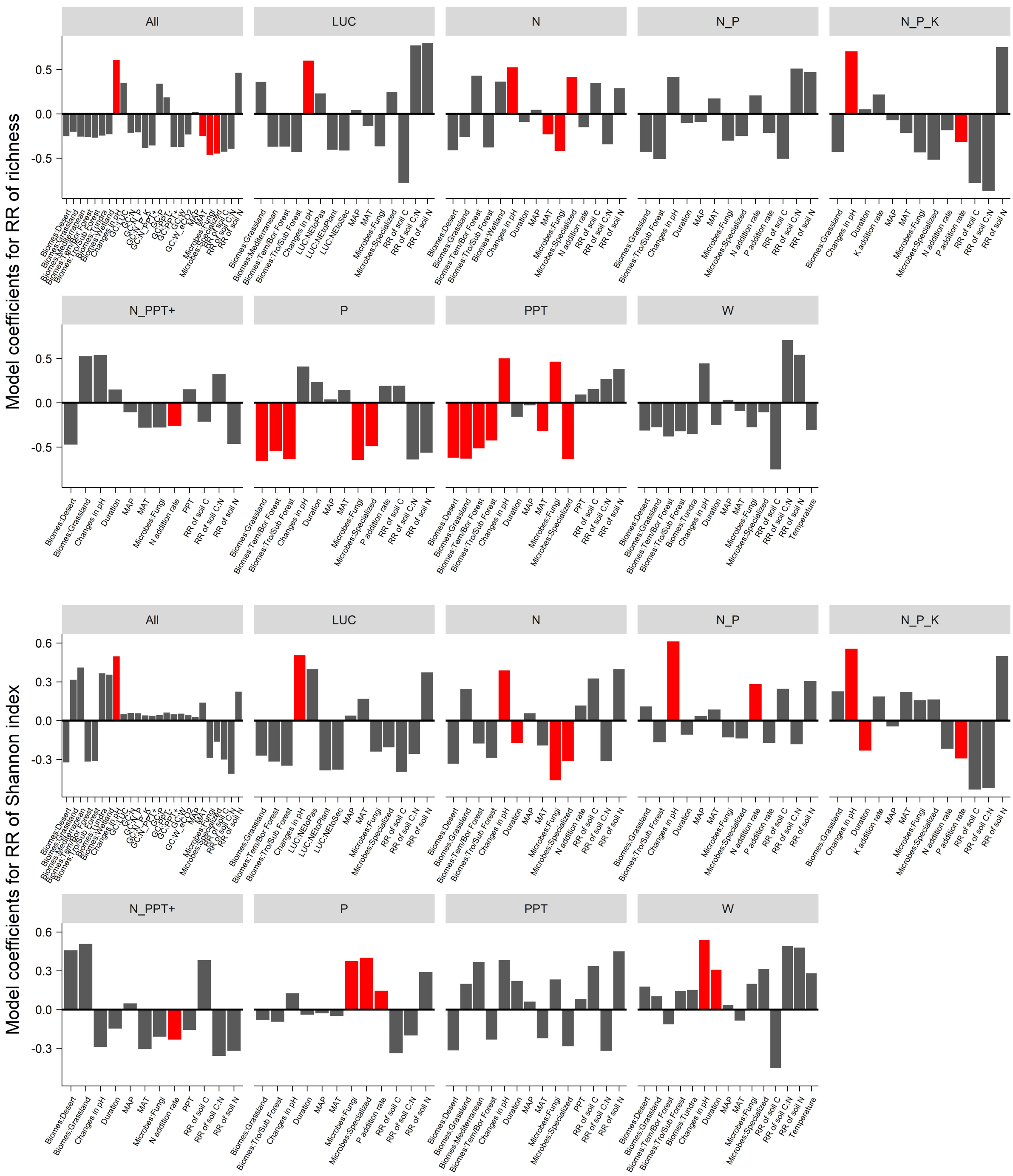
Supplementary Fig. 2 Responses of microbial alpha diversity to different land use change types. Weighted means and their 95% confidence intervals of response ratios (RR) are given. The numbers at the right side of the confidence intervals represent the sample sizes. NEtoAgr, conversion from native ecosystem to agriculture, NEtoPas, conversion from native ecosystem to pasture, NEtoPlant, conversion from native ecosystem to plantation, NEtoSec, conversion from native ecosystem to secondary ecosystem. Source data are provided as a Source Data file.



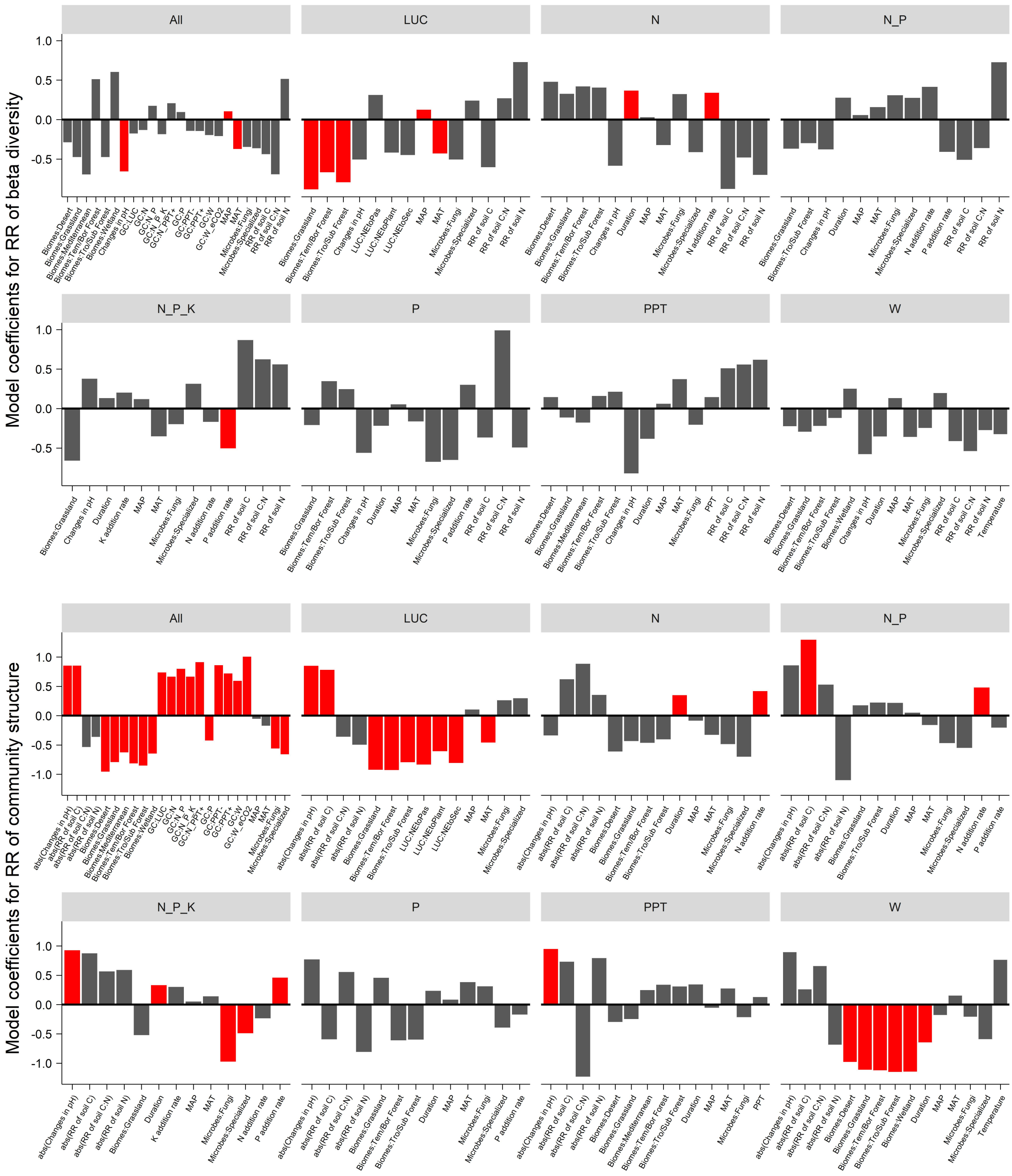
Supplementary Fig. 3 Paired comparisons of the responses of microbial alpha diversity and beta diversity to global change factors. **a** Comparisons between response ratio (RR) of richness and RR of beta diversity. **b** Comparisons between RR of Shannon index and RR of beta diversity. Weighted means and their 95% confidence intervals of RRs are given. The numbers at the left represent the sample sizes. W, warming; eCO_2, carbon dioxide enrichment; PPT-, decreased precipitation; PPT+, increased precipitation; P, phosphorous addition; N, nitrogen addition; LUC, land use change; W×eCO_2, warming plus carbon dioxide enrichment; N×PPT+, nitrogen addition plus increased precipitation; N×P, nitrogen plus phosphorous addition; N×P×K, nitrogen plus phosphorous plus potassium addition. Source data are provided as a Source Data file.



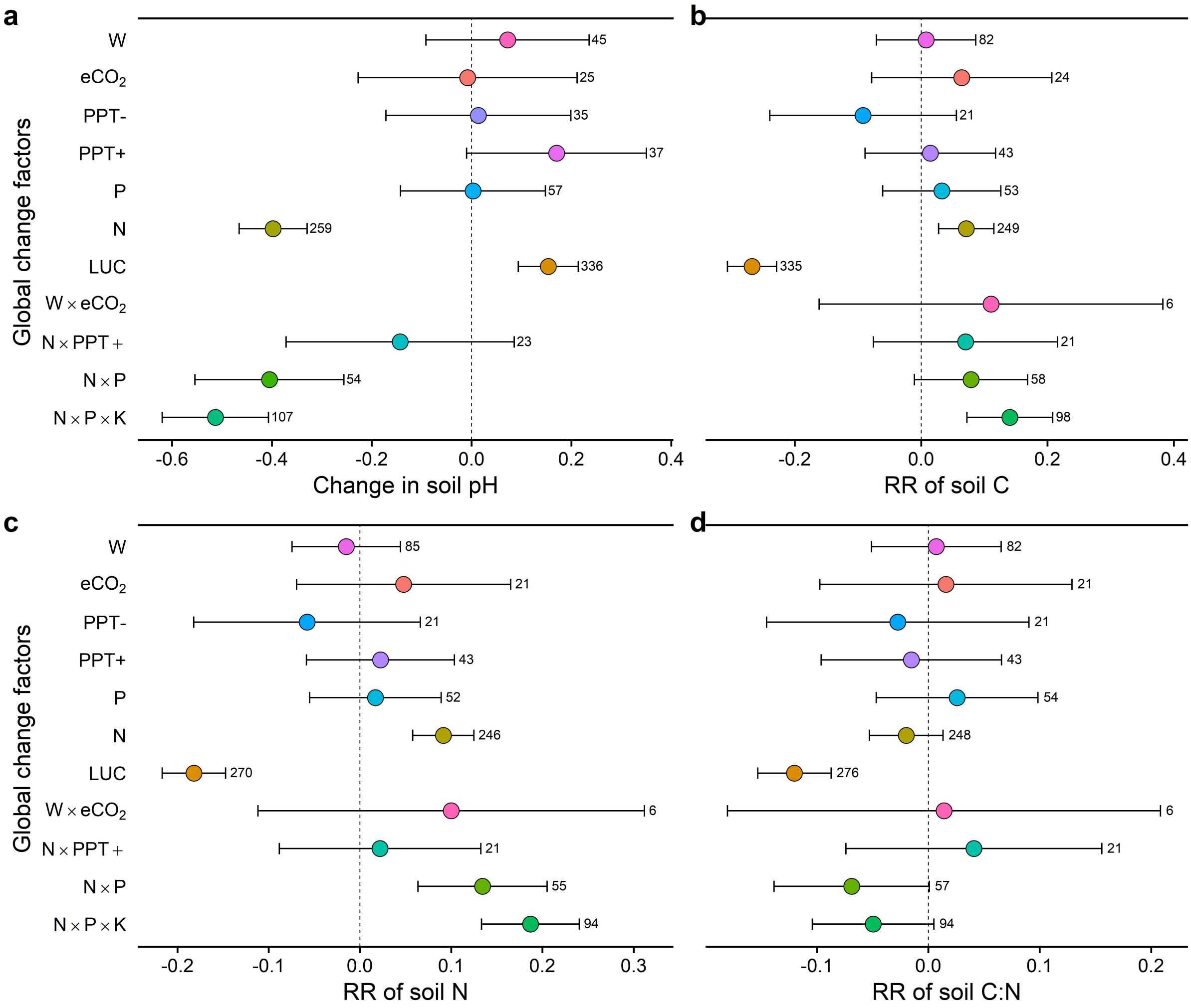
Supplementary Fig. 4 Model-averaged importance of the predictors of global changes effect on microbial communities. The importance is based on the sum of Akaike weights derived from the model selection using AIC (Akaike's Information Criteria corrected for small samples). A cutoff of 0.8 (the red dashed line) is set to differentiate between important and non-essential predictors. abs, absolute value. LUC, land use change; N, nitrogen addition; N_P, nitrogen plus phosphorous addition; N_P_K, nitrogen plus phosphorous plus potassium addition; N×PPT+, nitrogen addition plus increased precipitation; P, phosphorous addition; PPT, altered precipitation; W, warming. Source data are provided as a Source Data file.



Supplementary Fig. 5 Weighted averages of the model coefficients across various models for the responses of microbial alpha diversity to global change factors. The weights equal to the model probabilities. Model parameters are transferred by the fourth root for better visualization and ordered by increasing relative importance. The predictors in red bars are the ones with the sum of Akaike weights > 0.8. LUC, land use change; N, nitrogen addition; N_P, nitrogen plus phosphorous addition; N_P_K, nitrogen plus phosphorous plus potassium addition; N×PPT+, nitrogen addition plus increased precipitation; P, phosphorous addition; PPT, altered precipitation; W, warming. MAT, mean annual temperature (℃); MAP, mean annual precipitation (mm). The units for predictors of duration, N/P/K addition rates, altered PPT, and elevated temperature are year, g N/P/K m^{-2} $year^{-1}$, %, and ℃, respectively. Source data are provided as a Source Data file.



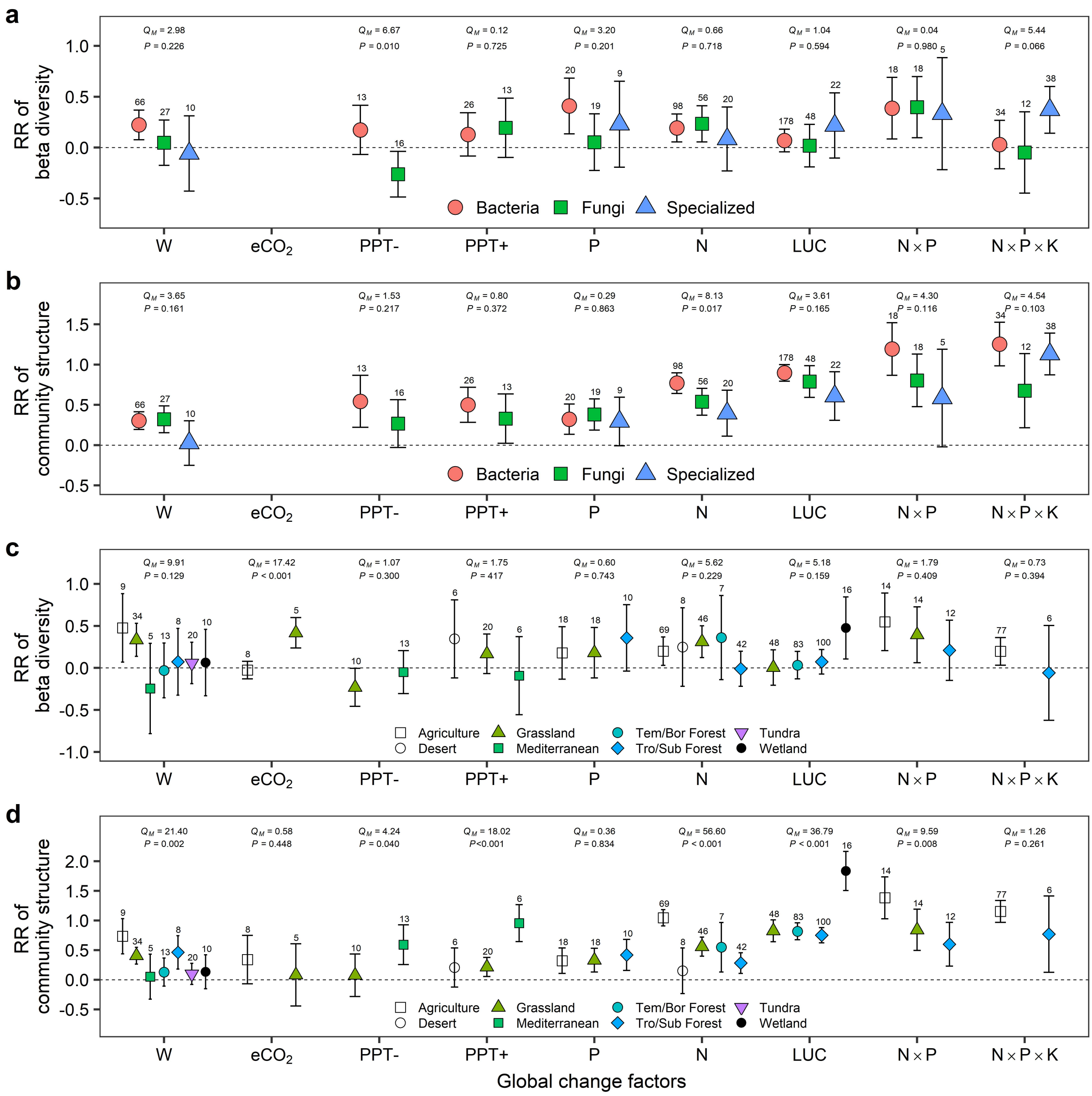
Supplementary Fig. 6 Weighted averages of the model coefficients across various models for the responses of microbial beta diversity and community structure to global change factors. The weights equal to the model probabilities. Model parameters are transferred by the fourth root for better visualization and ordered by increasing relative importance. The predictors in red bars are the ones with the sum of Akaike weights > 0.8. LUC, land use change; N, nitrogen addition; N_P, nitrogen plus phosphorous addition; N_P_K, nitrogen plus phosphorous plus potassium addition; N×PPT+, nitrogen addition plus increased precipitation; P, phosphorous addition; PPT, altered precipitation; W, warming. MAT, mean annual temperature (℃); MAP, mean annual precipitation (mm). The units for predictors of duration, N/P/K addition rates, altered PPT, and elevated temperature are year, g N/P/K m^{-2} $year^{-1}$, %, and ℃, respectively. Source Data are provided as a Source Data file.



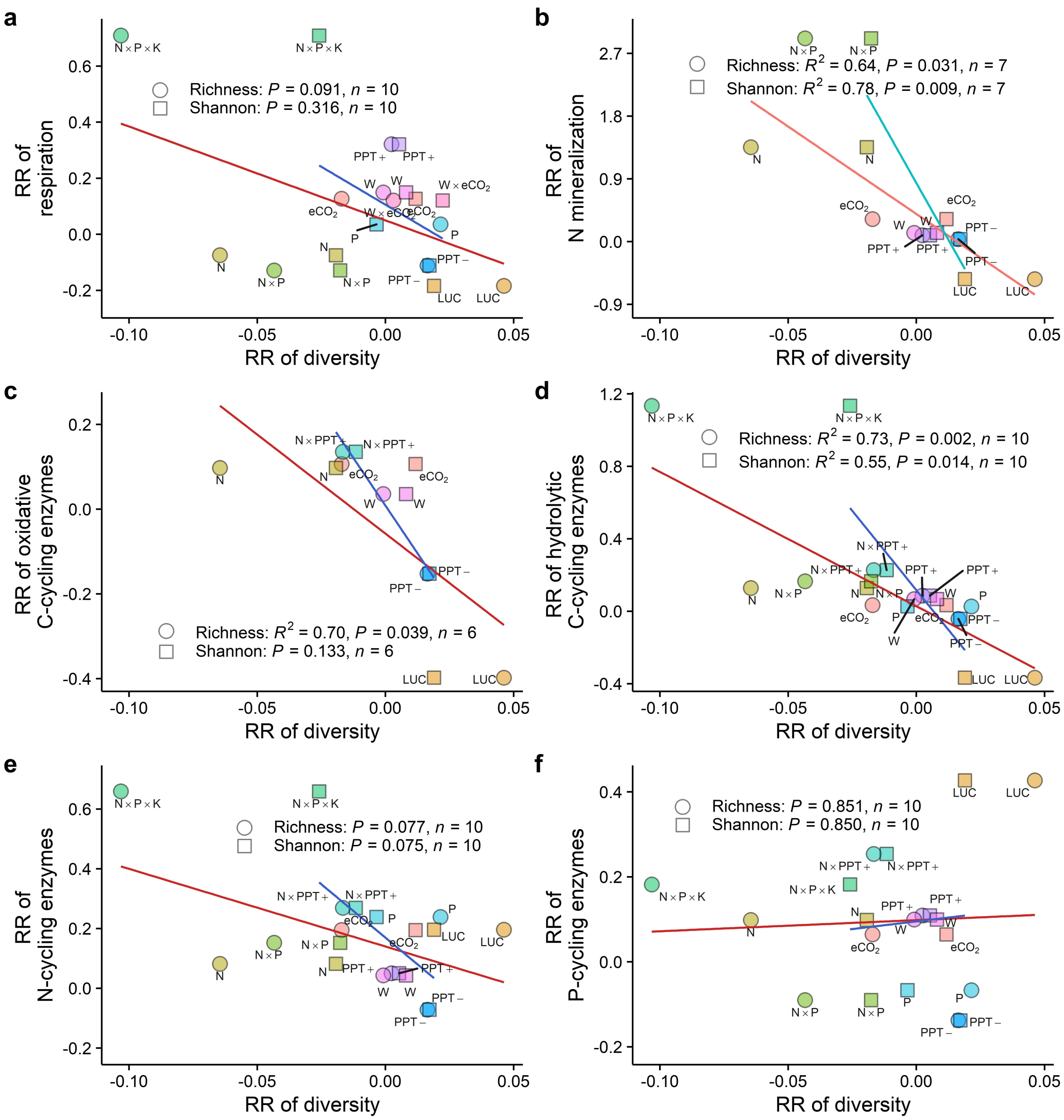
e

r values	RR of soil C	RR of soil N	RR of soil C:N
Change in soil pH	-0.37***(*n* = 910)	-0.20***(*n* = 831)	-0.18***(*n* = 843)
RR of soil C		0.72***(*n* = 911)	0.42***(*n* = 911)
RR of soil N			-0.33***(*n* = 911)

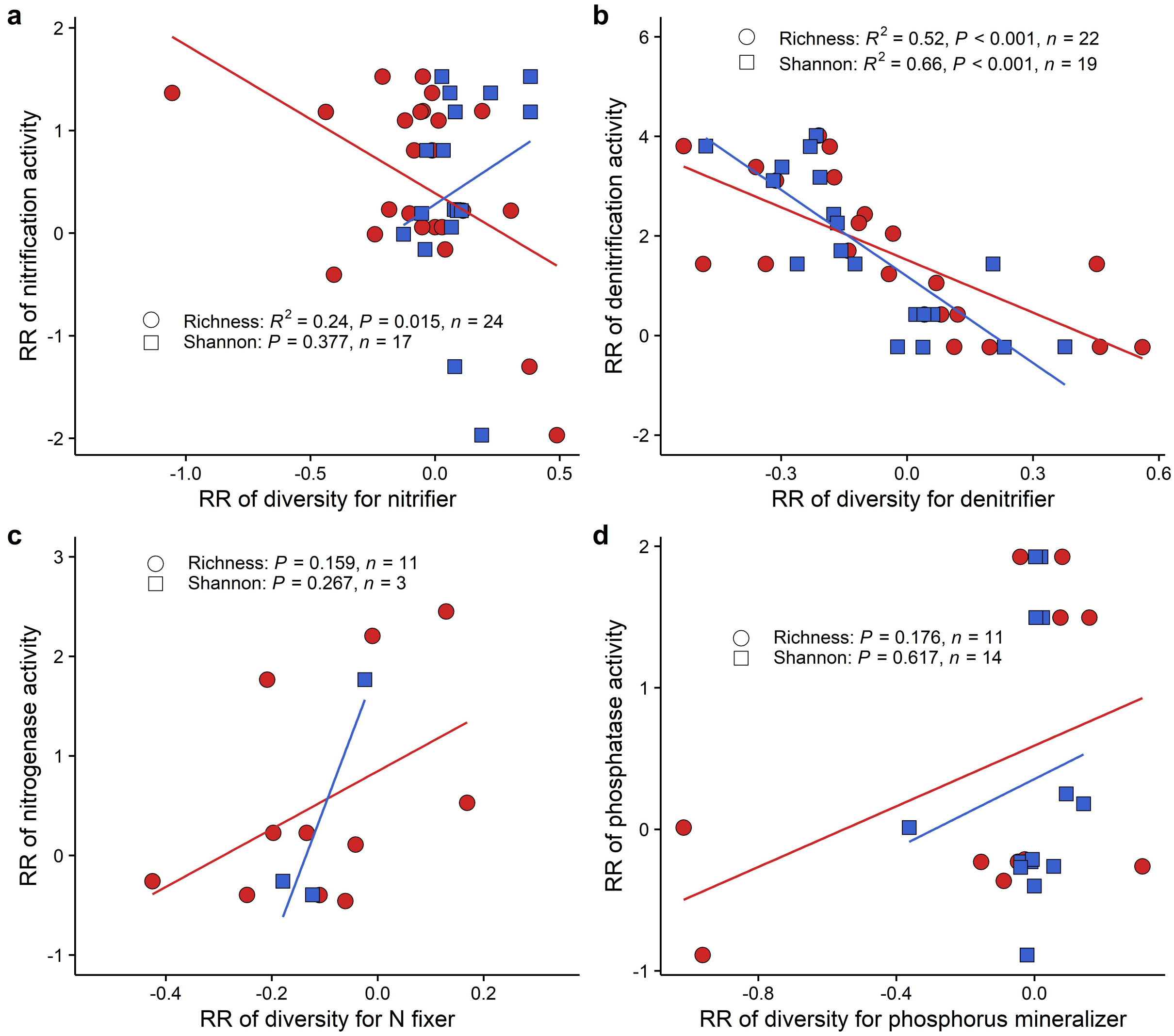
Supplementary Fig. 7 Global change factors (GCFs) induced changes in soil properties and their correlations. **a** GCFs induced change in soil pH. **b** Response ratio (RR) of soil C to GCFs. **c** RR of soil N to GCFs. **d** RR of soil C:N to GCFs. Weighted means and their 95% confidence intervals of RRs are given. The numbers at the right side of the confidence intervals represent the sample sizes. W, warming; eCO_2, carbon dioxide enrichment; PPT-, decreased precipitation; PPT+, increased precipitation; P, phosphorous addition; N, nitrogen addition; LUC, land use change; W×eCO_2, warming plus carbon dioxide enrichment; N×PPT+, nitrogen addition plus increased precipitation; N×P, nitrogen plus phosphorous addition; N×P×K, nitrogen plus phosphorous plus potassium addition. **e** Pearson's *r* correlation coefficients among GCFs induced shifts in soil properties. ***, P<0.001. Source data are provided as a Source Data file.



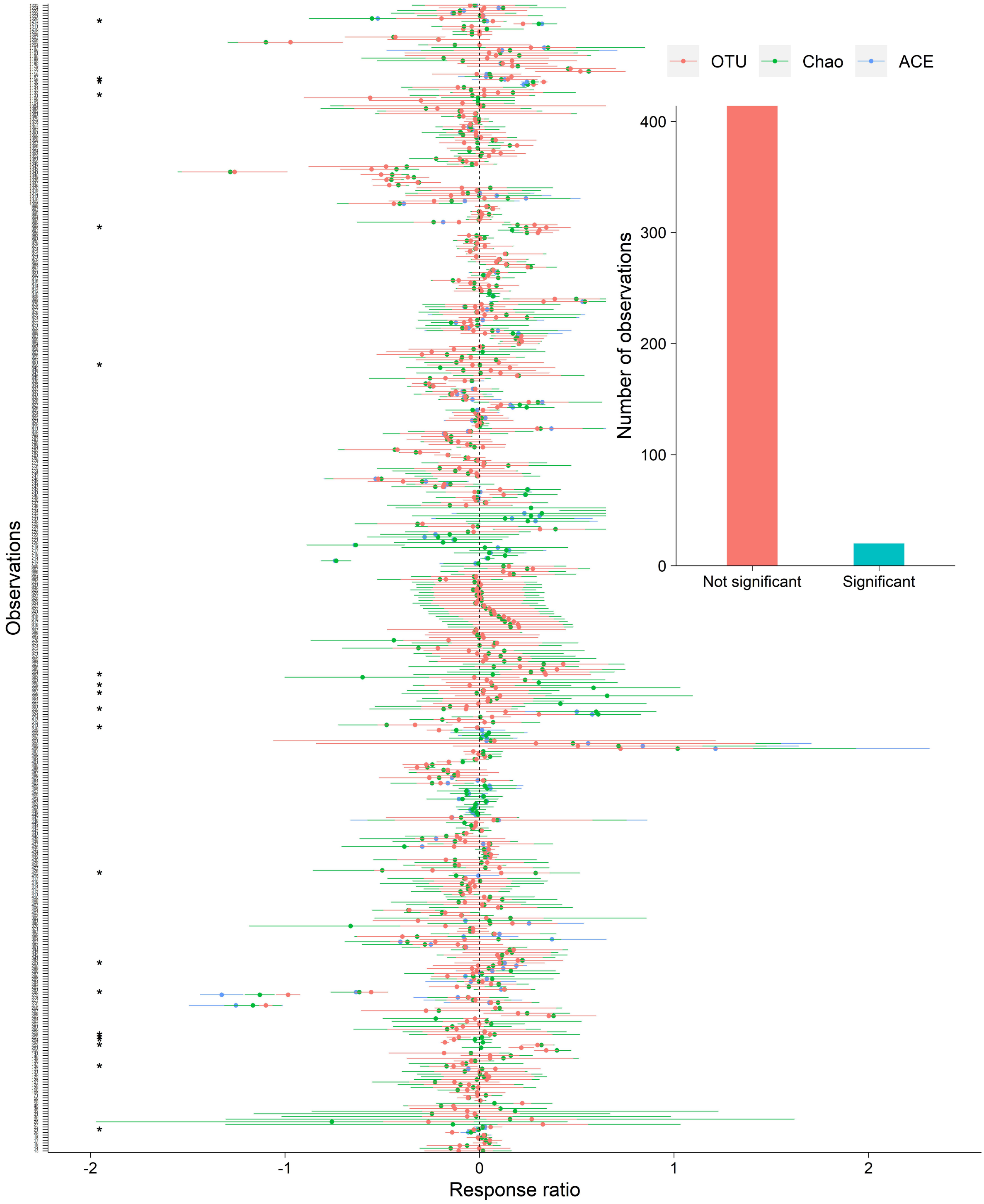
Supplementary Fig. 8 Responses of microbial beta diversity and community structure to global change factors by microbial groups and biomes. **a** Response ratio (RR) of beta diversity across microbial groups. **b** RR of community structure across microbial groups. **c** RR of beta diversity across biomes. **d** RR of community structure across biomes. Weighted means and their 95% confidence intervals of RRs are given. The numbers at the top of the confidence intervals represent the sample sizes. The significances of microbial groups and biome types are tested by omnibus test (Q_M). W, warming; eCO_2, carbon dioxide enrichment; PPT-, decreased precipitation; PPT+, increased precipitation; P, phosphorous addition; N, nitrogen addition; LUC, land use change; W×eCO_2, warming plus carbon dioxide enrichment; N×PPT+, nitrogen addition plus increased precipitation; N×P, nitrogen plus phosphorous addition; N×P×K, nitrogen plus phosphorous plus potassium addition. Tem/Bor, temperate/ boreal. Tro/Sub, tropical/subtropical. Source data are provided as a Source Data file.



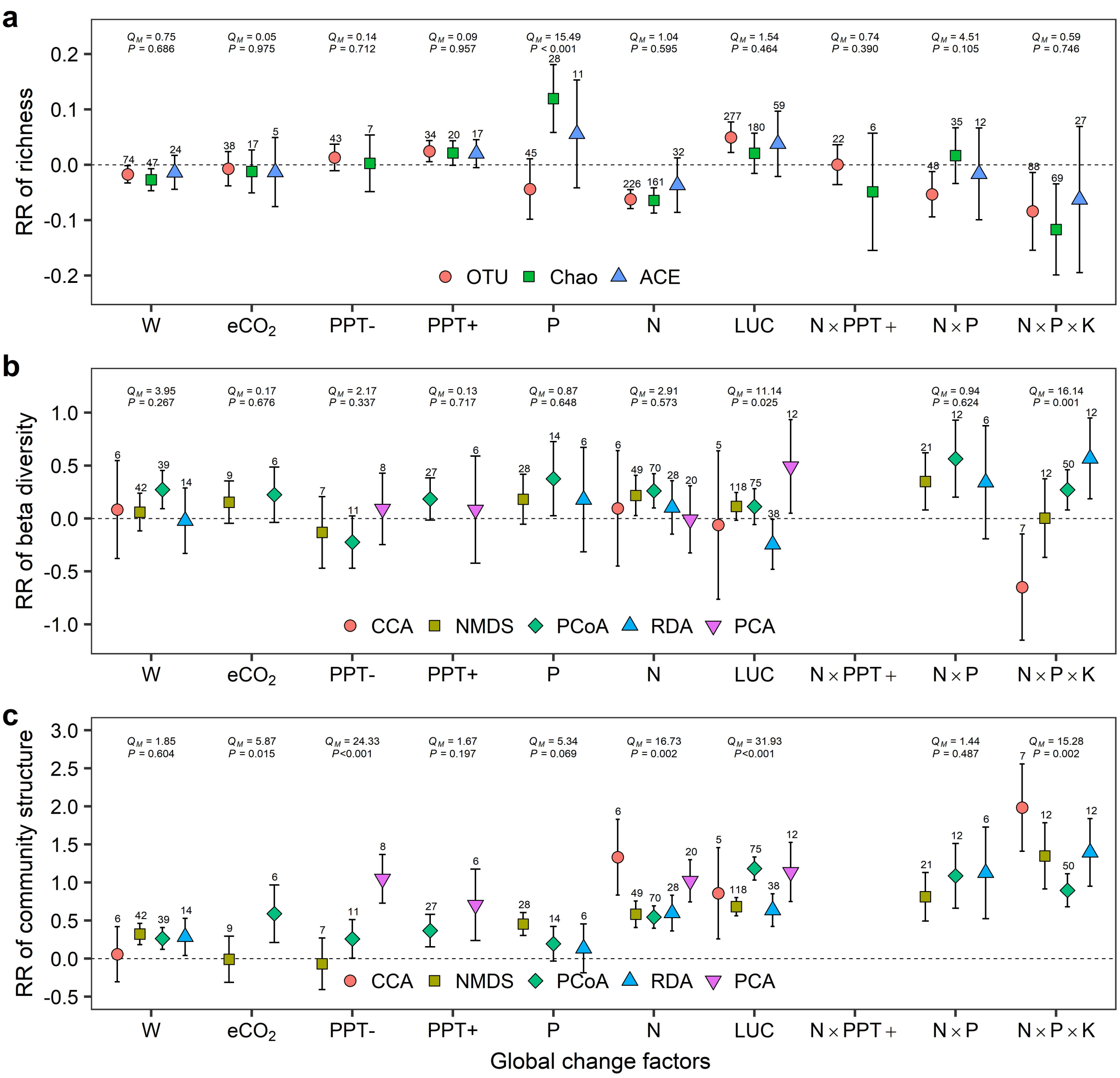
Supplementary Fig. 9 Linear relationships of the response ratios (RRs) between microbial alpha diversity response and different functional responses. **a** Linear relationship between RR of respiration and RR of richness or Shannon index (insignificant). **b** Linear relationship between RR of N mineralization and RR of richness ($y = -25.06x + 0.40$) or Shannon index ($y = -65.16x + 0.84$). **c** Linear relationship between RR of oxidative C-cycling enzymes and RR of richness ($y = -4.67x - 0.06$) or Shannon index (insignificant). **d** Linear relationship between RR of hydrolytic C-cycling enzymes and RR of richness ($y = -7.42x + 0.03$) or Shannon index ($y = -17.53x + 0.12$). **e** Linear relationship between RR of N-cycling enzymes and RR of richness or Shannon index (insignificant). **f** Linear relationship between RR of P-cycling enzymes and RR of richness or Shannon index (insignificant). Source data are provided as a Source Data file.



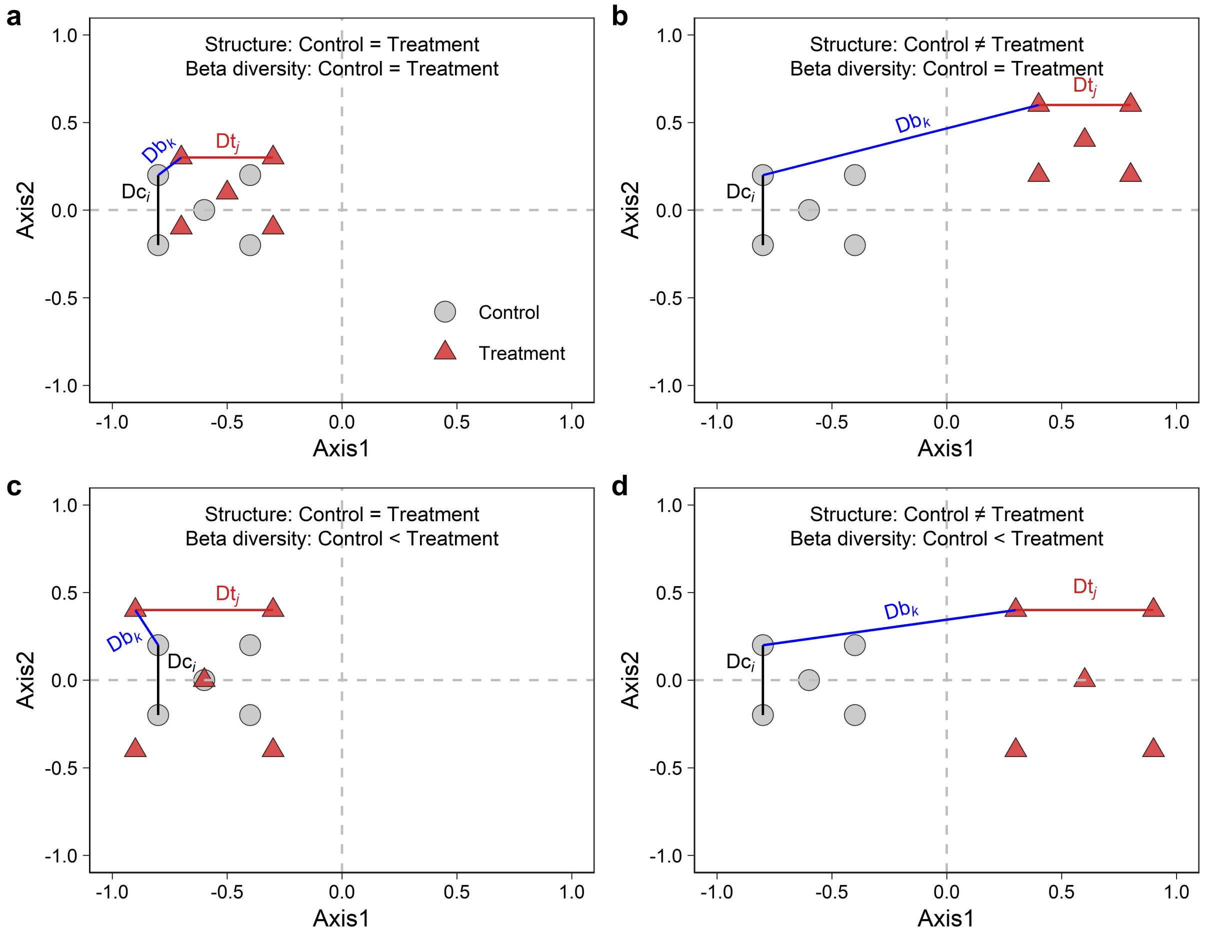
Supplementary Fig. 10 Coordinated changes between microbial alpha diversity and functions for specialized microbes. **a** Linear relationship between response ratio (RR) of nitrification activity and RRs of richness ($y = -1.44x + 0.39$) or Shannon index (insignificant) for nitrifier. **b** Linear relationship between RR of denitrification activity and RRs of richness ($y = -3.53x + 1.52$) or Shannon index ($y = -5.79x + 1.19$) for denitrifier. **c** Linear relationship between RR of nitrogenase activity and RRs of richness or Shannon index for nitrogen (N) fixer (insignificant). **d** Linear relationship between RR of phosphatase activity and RRs of richness or Shannon index for phosphorus mineralizer (insignificant). Source data are provided as a Source Data file.



Supplementary Fig. 11 Comparisons of response ratios of different richness metrics. The asterisks on the left indicate significant differences among the two/three metrics based on omnibus test (Q_M). The inset bar plot shows the total number of significant *vs.* insignificant observations. Source data are provided as a Source Data file.



Supplementary Fig. 12 Comparisons of microbial responses to global change factors by different data analytical methods. **a** Response ratios (RRs) of microbial richness from different metrics. **b** RRs of microbial beta diversity from canonical correspondence analysis (CCA), non-metric multidimensional scaling (NMDS), principal correspondence analysis (PCoA), redundancy analysis (RDA), and principal component analysis (PCA) plots. **c** RRs of microbial community structure from CCA, NMDS, PCoA, RDA, and PCA plots. The significances of methods are tested by omnibus test (Q_M). Weighted means and their 95% confidence intervals of RRs are given. The numbers at the top of the confidence intervals represent the sample sizes. W, warming; eCO2, carbon dioxide enrichment; PPT-, decreased precipitation; PPT+, increased precipitation; P, phosphorous addition; N, nitrogen addition; LUC, land use change; W×eCO2, warming plus carbon dioxide enrichment; N×PPT+, nitrogen addition plus increased precipitation; N×P, nitrogen plus phosphorous addition; N×P×K, nitrogen plus phosphorous plus potassium addition. Source data are provided as a Source Data file.



Supplementary Fig. 13 A diagrammatic sketch of the calculation of response of microbial community structure and beta diversity. Dc_i, the *i*th Euclidean distance within control, Dt_j, the *j*th Euclidean distance within treatment, Db_k, the *k*th Euclidean distance between control and treatment. The effect of global change factor on community composition is considered if the Euclidean distance between control and treatment is significantly greater than that within group. The effect of global change factor on beta diversity is considered if the Euclidean distance within treatment is significantly different from that within control.

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