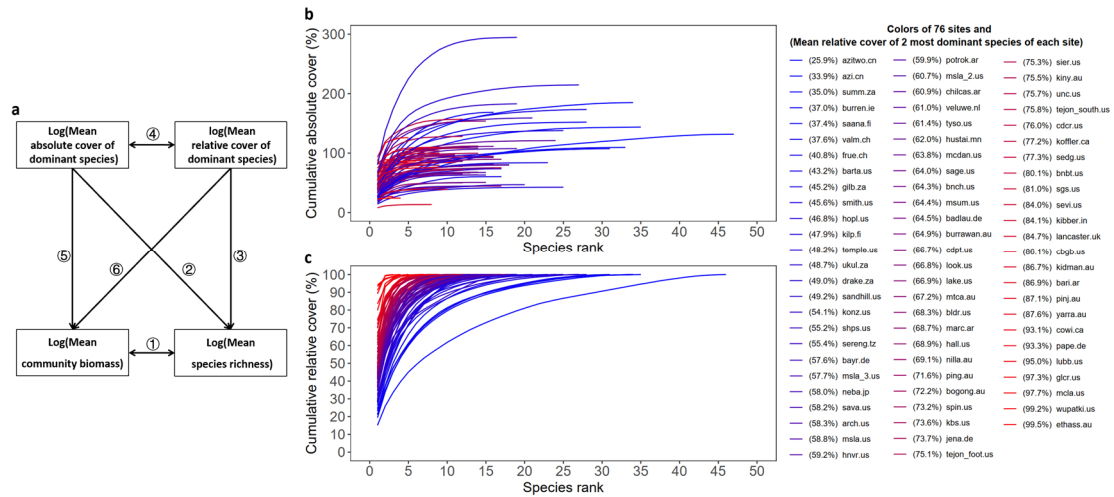


SUPPLEMENTARY INFORMATION:

Results directly based on the species-level absolute and relative cover data

3



4

Fig. S1 | (a) Structural equation meta-model and site-level patterns from 76 grassland sites throughout the world under ambient conditions of (b) cumulative absolute cover curve and (c) cumulative relative cover curve. Number in circles in (a) represent bivariate relationships. The x-axis in (b) and (c) is the rank of species from most to least abundant. Line colors in (b) and (c) represent the site-level mean relative cover of 2 most dominant species at each of the 76 sites under ambient conditions from low to high (from 25.9% to 99.5%). The words after the numbers in parentheses are the sites names.

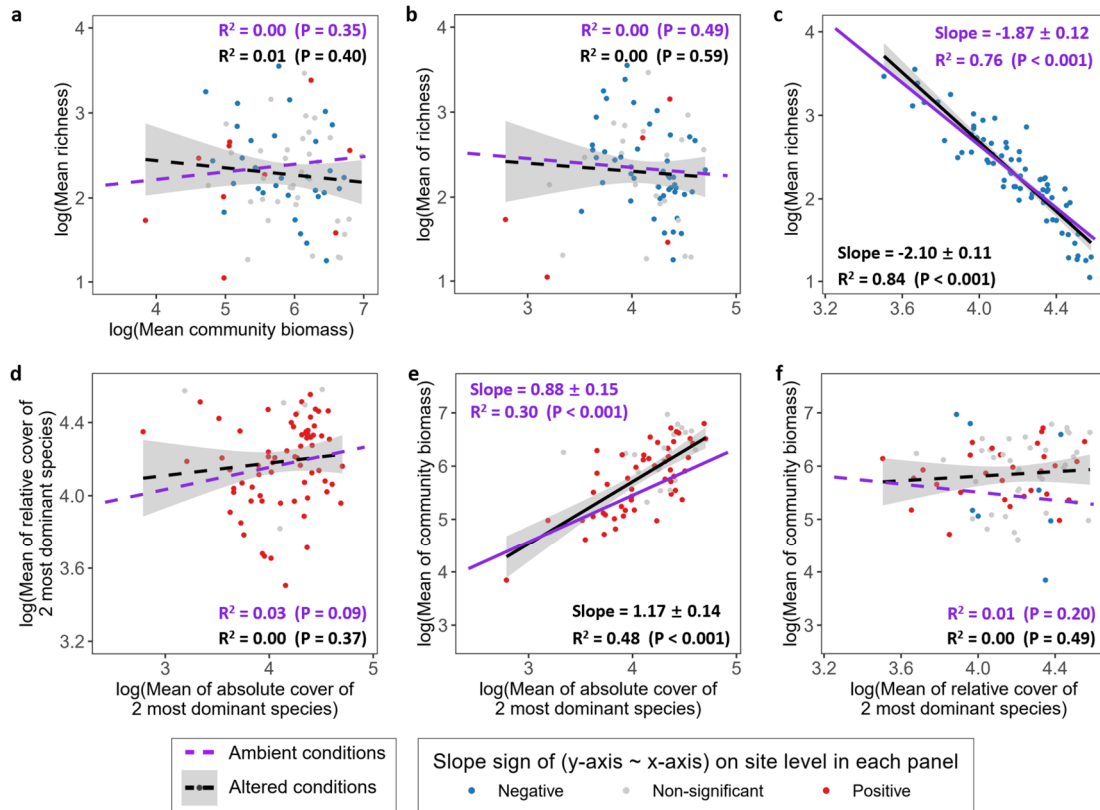


Fig. S3 | Grassland richness and biomass relationships under altered environmental conditions. The relationship between mean richness and (a) mean community biomass, and (b) mean absolute cover of the two most dominant species, and (c) mean relative cover of the two most dominant species; and (d) between mean relative cover and mean absolute cover of the two most dominant species; and between mean community level biomass and (e) mean absolute cover of the two most dominant species, and (f) mean relative cover of the two most dominant species, at 76 sites under altered environmental conditions (1-15 years; each site \approx 3 blocks; each block \approx 10 plots). All data were natural log-transformed. The correlation between the y-axis and x-axis variables of each panel on the site-level is indicated as significantly positive (red), uncorrelated (gray), and significantly negative (blue). The purple lines are regression curves for the ambient conditions in Fig.2. The purple fonts are R^2 and P values for the

39 ambient conditions in Fig.2. A dashed line indicates that the relationship is not
40 significant ($P > 0.05$), and a solid line indicates that the relationship is significant ($P <$
41 0.05).

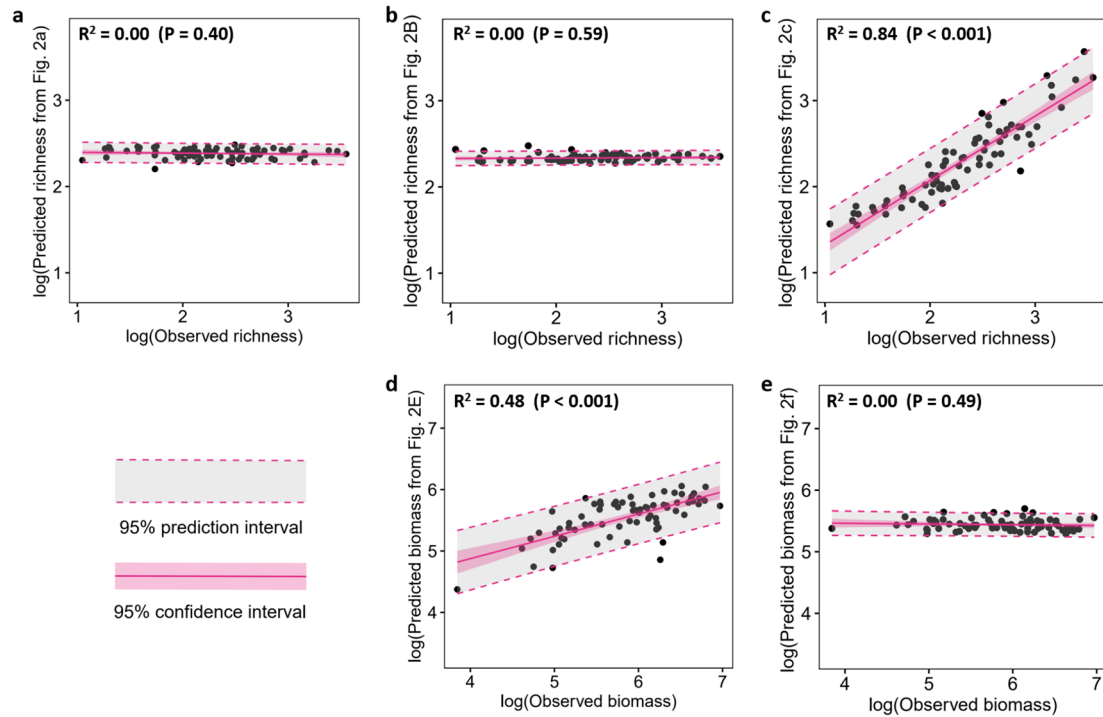


Fig. S4 | The regression model for ambient conditions predicts the outcome for global grasslands under altered environmental conditions. The relationship between (a, b, and c) the predicted species richness according to the regression model of the ambient conditions and the actual mean species richness of altered environmental conditions of each site, and between (d, e) the predicted community biomass according to the regression model of the ambient conditions and the actual mean community biomass of the altered environmental conditions of each site. The regression models used to predict the vertical axis variables in a, b, c, d, and e, are respectively from the model in a, b, c, e, and f of Fig. 2. In these five panels, the gray-shaded area is the 95% prediction interval, and the pink-shaded area represents the 95% confidence interval, around the regression line.

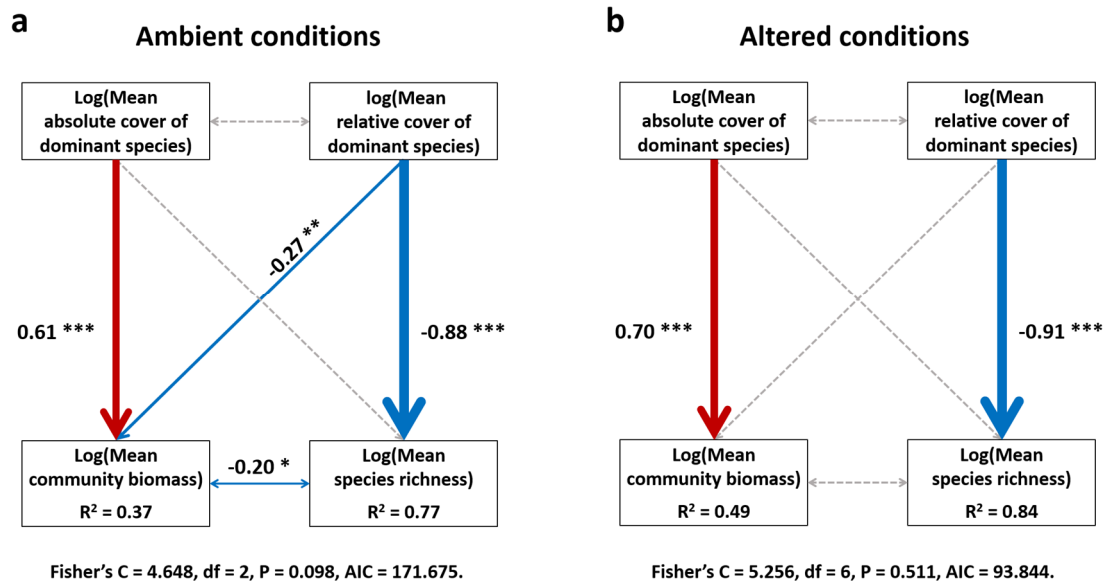


Fig. S5 | SEMs under (a) ambient and (b) altered environmental conditions from empirical grassland data. All data were natural log-transformed. The red and blue lines mean significantly positive and negative relationships, respectively. The dashed and solid lines indicate that the relationship is not significant ($P > 0.05$) and significant ($P < 0.05$), respectively.

Table S1 | (a) The R^2 of various relationships among four natural log-transformed variables, and (b) the R^2 of relationships between natural log-transformed gamma diversity and natural log-transformed mean relative cover of dominant species in the context of selecting different numbers of dominant species (from 1 to 5) from NutNet data under both ambient and altered conditions.

a.

		The number of dominant species (DS_n)				
		n = 1	n = 2	n = 3	n = 4	n = 5
The R^2 in ambient conditions	log(Mean richness) ~ log(Mean absolute cover of DS_n)	0.06 *	0.00 ^{NS}	0.00 ^{NS}	0.00 ^{NS}	0.02 ^{NS}
	log(Mean richness) ~ log(Mean relative cover of DS_n)	0.75 ***	0.76 ***	0.73 ***	0.70 ***	0.67 ***
	log(Mean relative cover of DS_n) ~ log(Mean absolute cover of DS_n)	0.15 ***	0.03 ^{NS}	0.00 ^{NS}	0.00 ^{NS}	0.00 ^{NS}
	log(Mean community biomass) ~ log(Mean absolute cover of DS_n)	0.24 ***	0.30 ***	0.32 ***	0.34 ***	0.34 ***
	log(Mean community biomass) ~ log(Mean relative cover of DS_n)	0.00 ^{NS}	0.01 ^{NS}	0.01 ^{NS}	0.01 ^{NS}	0.01 ^{NS}
The R^2 in altered environmental conditions	log(Mean richness) ~ log(Mean absolute cover of DS_n)	0.05 *	0.00 ^{NS}	0.00 ^{NS}	0.01 ^{NS}	0.03 ^{NS}
	log(Mean richness) ~ log(Mean relative cover of DS_n)	0.79 ***	0.84 ***	0.84 ***	0.82 ***	0.79 ***
	log(Mean relative cover of DS_n) ~ log(Mean absolute cover of DS_n)	0.11 **	0.00 ^{NS}	0.00 ^{NS}	0.00 ^{NS}	0.02 ^{NS}
	log(Mean community biomass) ~ log(Mean absolute cover of DS_n)	0.49 ***	0.48 ***	0.45 ***	0.42 ***	0.40 ***
	log(Mean community biomass) ~ log(Mean relative cover of DS_n)	0.00 ^{NS}	0.00 ^{NS}	0.00 ^{NS}	0.00 ^{NS}	0.00 ^{NS}

b.

		The number of dominant species (DS_n)				
		n = 1	n = 2	n = 3	n = 4	n = 5
The R^2 of log(Gamma diversity) ~ log(Mean relative cover of DS_n) in ambient conditions		0.45 ***	0.47 ***	0.43 ***	0.37 ***	0.31 ***
The R^2 of log(Gamma diversity) ~ log(Mean relative cover of DS_n) in altered environmental conditions		0.35 ***	0.39 ***	0.37 ***	0.33 ***	0.28 ***