Table S1. Plant Diversity Index Calculation

Plant Diversity Index	equation
1.Magalef richness index(R)	$R = S$
2.Shannon–Wiener diversity index(H')	$H' = \sum_{i=1}^{S} p_i \ln p_i$
3.Simpson diversity index(D)	$D = 1 - \sum_{i=1}^{S} p_i{}^2$
4.Pielou evenness index(E)	$E = \dfrac{H'}{lnS}$
5.FRic richness index	$FRic = \dfrac{\cup_{s \in S_c R_{ts}}}{\cup_{s \cup s_c R_{ts}}} = \dfrac{\int_{s \in S_c}^{max}[I_{st}(x)]\,dx}{\int_{s \cup s_c}^{max}[I_{st}(x)]\,dx}$
6.FEve evenness index	$FE_{ve} = \dfrac{\sum_{i=1}^{s-1} min\left(PEW_I \dfrac{1}{s-1}\right) - \dfrac{1}{s-1}}{1 - \dfrac{1}{s-1}}$
7.FDiv divergence index	$FD_{iv} = \dfrac{\Delta d + \overline{dG}}{\Delta|d| + \overline{dG}}$
8.RaoQ quadratic entropy index	$Rao = \sum_{i=1}^{s}\sum_{j>1}^{s} d_{ij} w_i w_j$
9.mean nearest interspecific distance (MNTD)	$MNTD = \sum_{m}^{S} min\,(d_{mn})a_m$
10.mean interspecific distance index (MPD)	$MPD = \dfrac{\sum m \sum n\, d_{mn} a_m a_n}{\sum m \sum n\, a_m a_n}$
11.Faith diversity index (PD)	$PD = B \times \dfrac{\sum_i^B L_i A_i}{\sum_i^B A_i}$

In equations 1-4, S represents the number of species, pi represents the proportion of the i-th species in the total.

In the equation 5, S represents the number of species, t is the trait, x is the trait value, and $I_{st}(x)$ is the trait correlation function of S. S_c is the community of S, and R_{ts} is the range of traits of S.

In the equation 6, S represents the number of species, i is the i-th species in the community, I is the branch length and PEW_I is the branch length weight.

In the equation 7, S represents the number of species, i is the i-th species in the community, $\overline{dG}$ is the average distance of species i from the center of gravity, and d is the weight dispersion of abundance, whose value varies between 0 and 1.

In the equation 8, S represents the number of species, i is the i-th species in the community, d_{ij} is the Euclidean distance between species i and species j, and w_i is the relative abundance of species i.

In the equations 9-11, n refers to the node-based index, B refers to the number of branches in the tree, and L_i refers to the length of branch i. A_i refers to the average abundance of species sharing branch i, d_{mn} refers to the phylogenetic distance between species m and species n, and a_m is the abundance of species m.