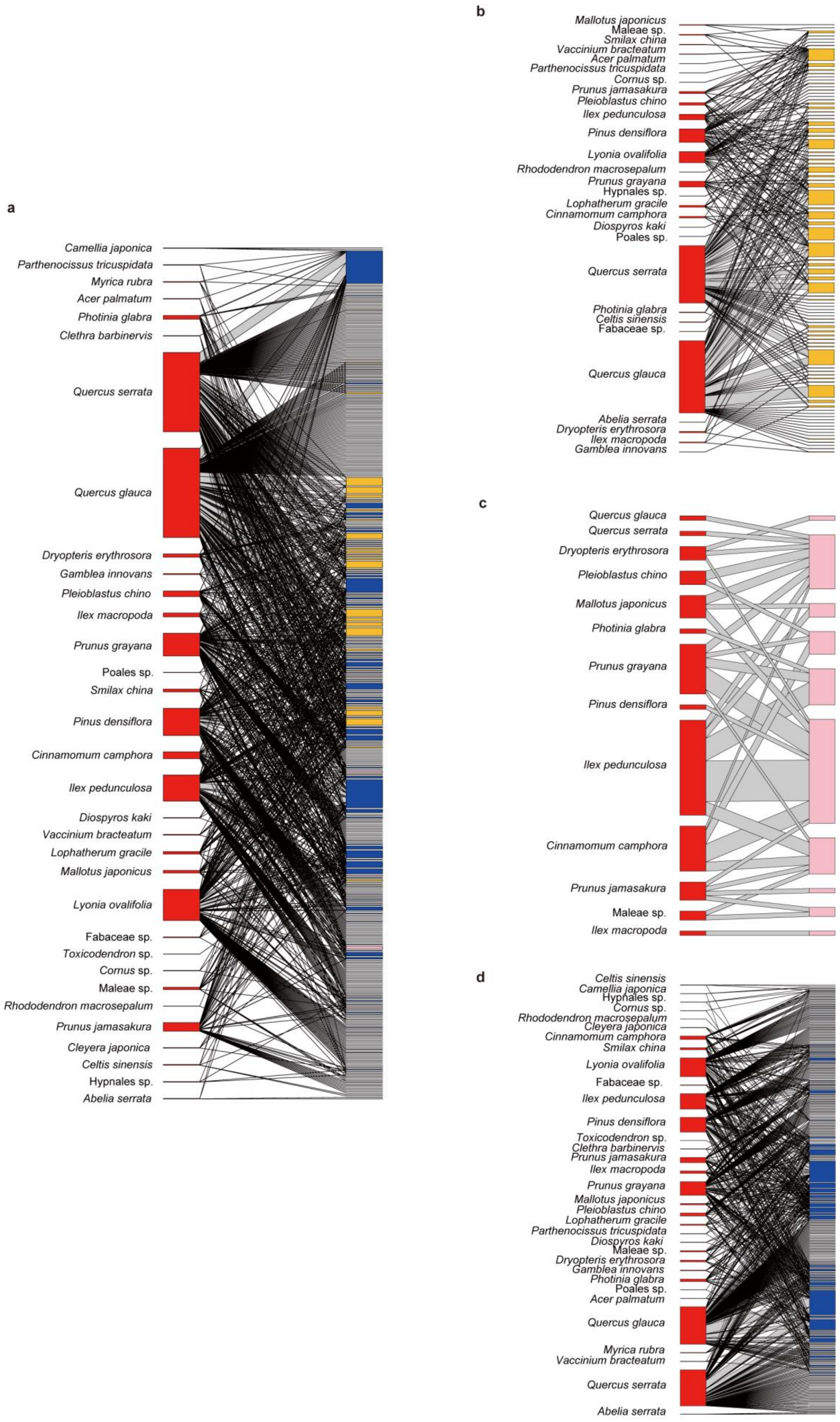
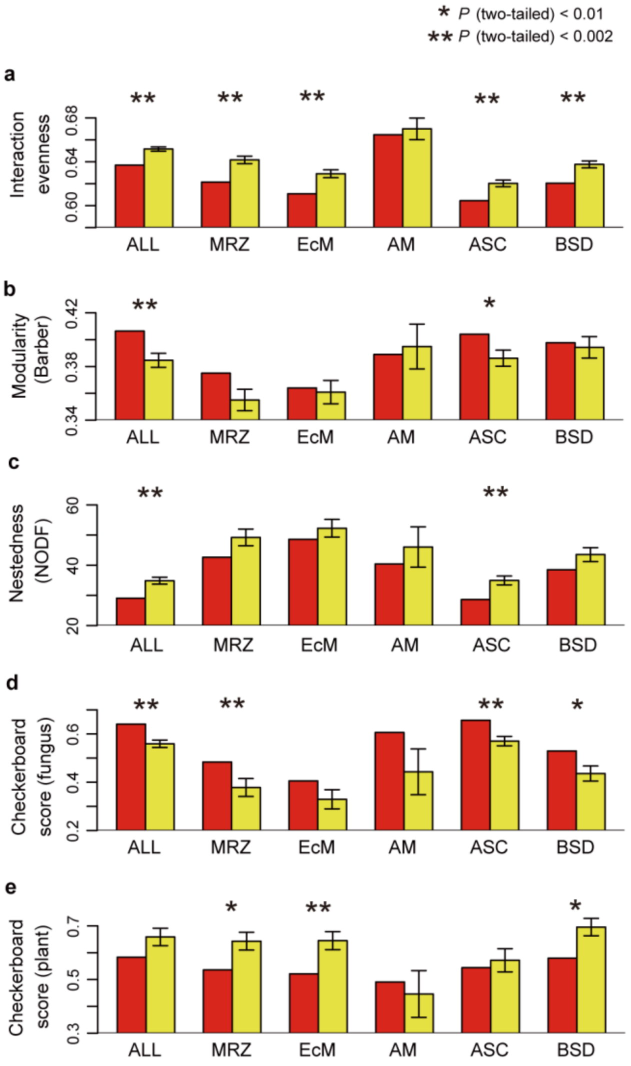
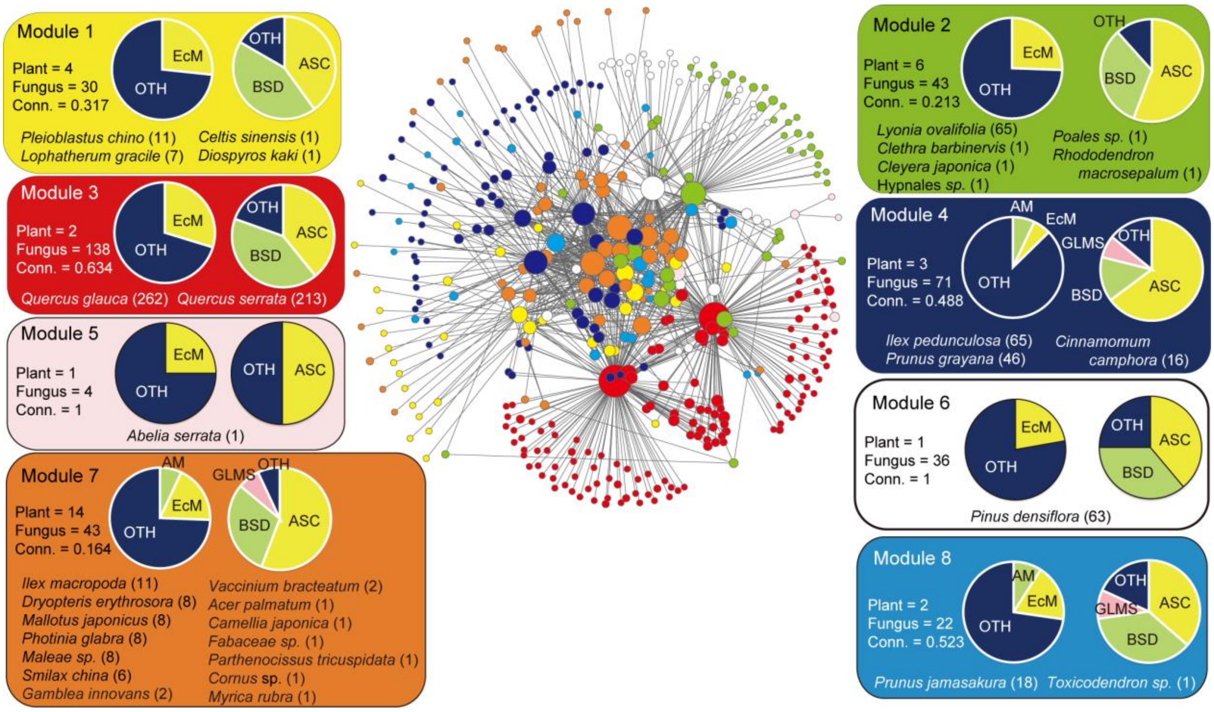

a
Camellia japonica
Parthenocissus tricuspidata
Myrica rubra
Acer palmatum
Photinia glabra
Clethra barbinervis
Quercus serrata
Quercus glauca
Dryopteris erythrosora
Gamblea innovans
Pleioblastus chino
Ilex macropoda
Prunus grayana
Poales sp.
Smilax china
Pinus densiflora
Cinnamomum camphora
Ilex pedunculosa
Diospyros kaki
Vaccinium bracteatum
Lophatherum gracile
Mallotus japonicus
Lyonia ovalifolia
Fabaceae sp.
Toxicodendron sp.
Cornus sp.
Maleae sp.
Rhododendron macrosepalum
Prunus jamasakura
Cleyera japonica
Celtis sinensis
Hypnales sp.
Abelia serrata
b
Mallotus japonicus
Maleae sp.
Smilax china
Vaccinium bracteatum
Acer palmatum
Parthenocissus tricuspidata
Cornus sp.
Prunus jamasakura
Pleioblastus chino
Ilex pedunculosa
Pinus densiflora
Lyonia ovalifolia
Rhododendron macrosepalum
Prunus grayana
Hypnales sp.
Lophatherum gracile
Cinnamomum camphora
Diospyros kaki
Poales sp.
Quercus serrata
Photinia glabra
Celtis sinensis
Fabaceae sp.
Quercus glauca
Abelia serrata
Dryopteris erythrosora
Ilex macropoda
Gamblea innovans
c
Quercus glauca
Quercus serrata
Dryopteris erythrosora
Pleioblastus chino
Mallotus japonicus
Photinia glabra
Prunus grayana
Pinus densiflora
Ilex pedunculosa
Cinnamomum camphora
Prunus jamasakura
Maleae sp.
Ilex macropoda
d
Celtis sinensis
Camellia japonica
Hypnales sp.
Cornus sp.
Rhododendron macrosepalum
Cleyera japonica
Cinnamomum camphora
Smilax china
Lyonia ovalifolia
Fabaceae sp.
Ilex pedunculosa
Pinus densiflora
Toxicodendron sp.
Clethra barbinervis
Prunus jamasakura
Ilex macropoda
Prunus grayana
Mallotus japonicus
Pleioblastus chino
Lophatherum gracile
Parthenocissus tricuspidata
Diospyros kaki
Maleae sp.
Dryopteris erythrosora
Gamblea innovans
Photinia glabra
Poales sp.
Acer palmatum
Quercus glauca
Myrica rubra
Vaccinium bracteatum
Quercus serrata
Abelia serrata

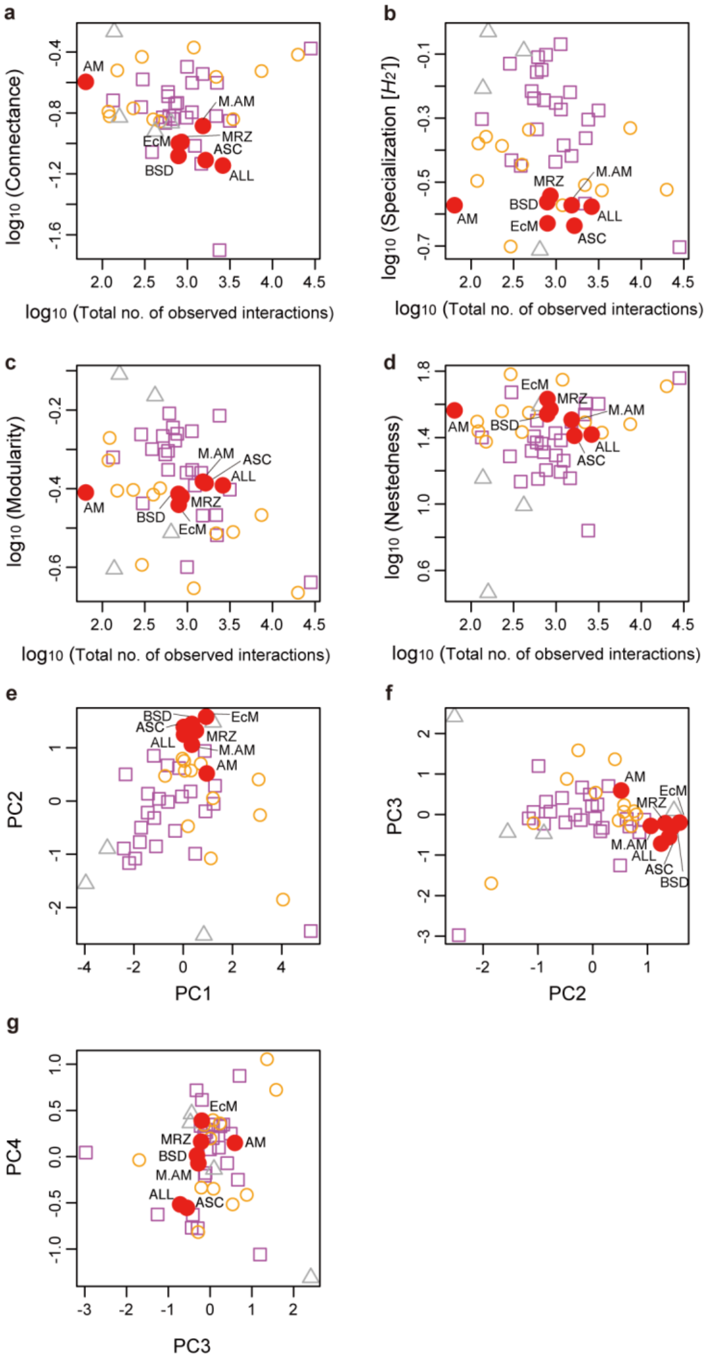
Supplementary Figure 1 | Bipartite display of the plant–fungus network. a, The entire network including all the 33 plant species (left side) and 387 fungal OTUs (right side). The thickness of lines and the size of rectangles represent the number of observed associations in the data matrix. Red, plant species; yellow, ectomycorrhizal fungal OTUs; pink, arbuscular mycorrhizal fungal OTUs; blue, fungal OTUs with unknown ecological functions. **b**, Partial network of ectomycorrhizal fungi and their host plants. **c**, Partial network of arbuscular mycorrhizal fungi and their host plants. **d**, Partial network of fungi with unknown functions and their host plants.



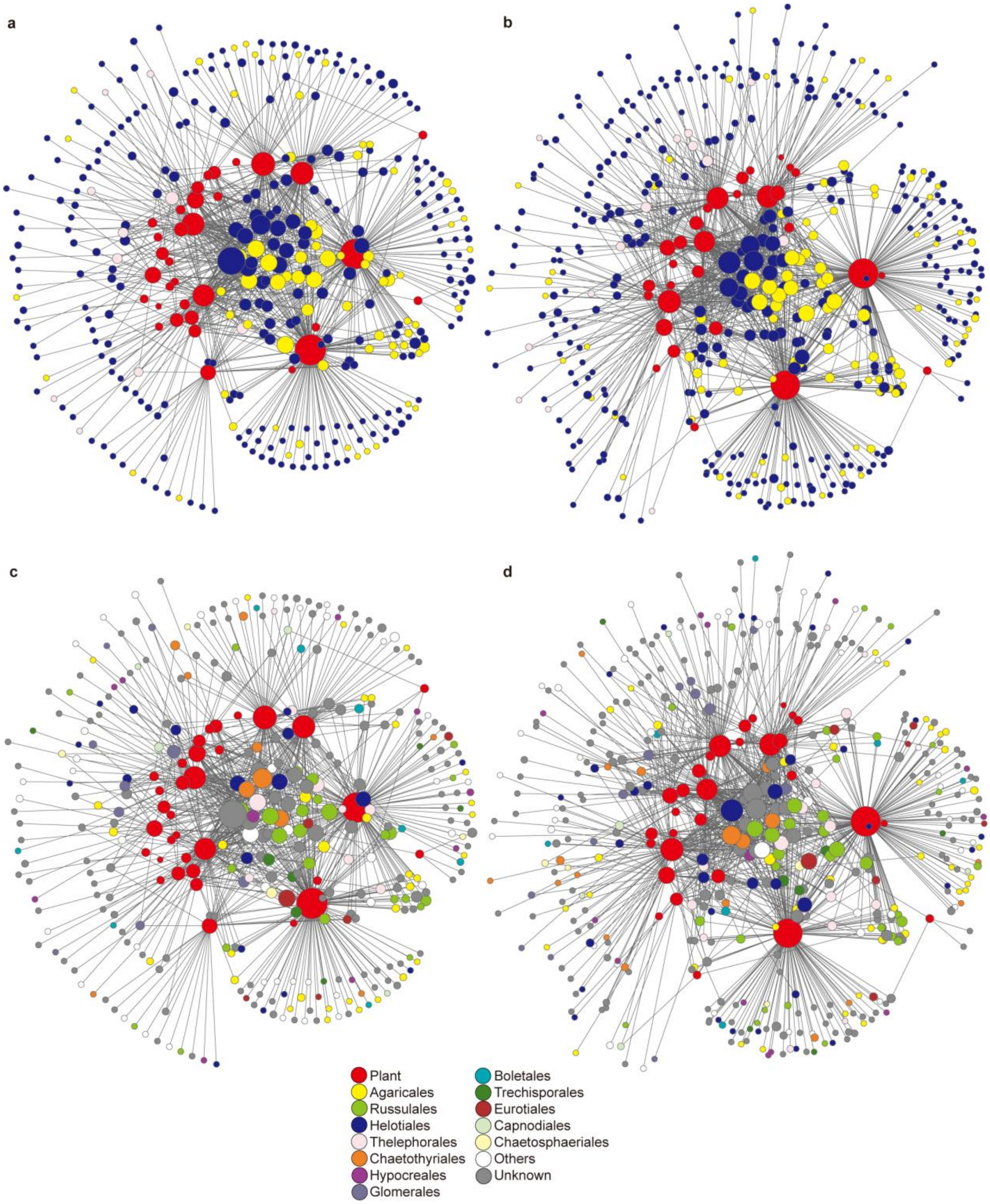
Supplementary Figure 2 | Supplementary analysis of network architecture. a, Interaction evenness evaluated by Shannon's evenness for network entries. The observed interaction evenness (left bar, red) is shown for each network or partial network. Asterisks indicate significant deviation of observed interaction evenness from that of randomized networks [right bar, yellow (mean ± SD)]. ALL, the entire network involving all plant species and fungal OTUs; MRZ, mycorrhizal partial network; EcM, ectomycorrhizal partial network; AM, arbuscular mycorrhizal partial network; ASC, ascomycete partial network; BSD, basidiomycete partial network. **b**, Modularity based on the Barber's metric for bipartite datasets. **c**, NODF nestedness for datasets in a binary (i.e., presence/absence) format. **d**, Checkerboard score as a measure of host plant differentiation within the fungal community. For the entire network, the composition of host plant species was more differentiated between fungal taxa than expected by chance. **e**, Checkerboard score as a measure of fungal symbiont differentiation within the plant community. The sign of partner differentiation was not observed within the plant community (see “ALL”), suggesting that competition for fungal symbionts was moderate or absent among plant species in the community.



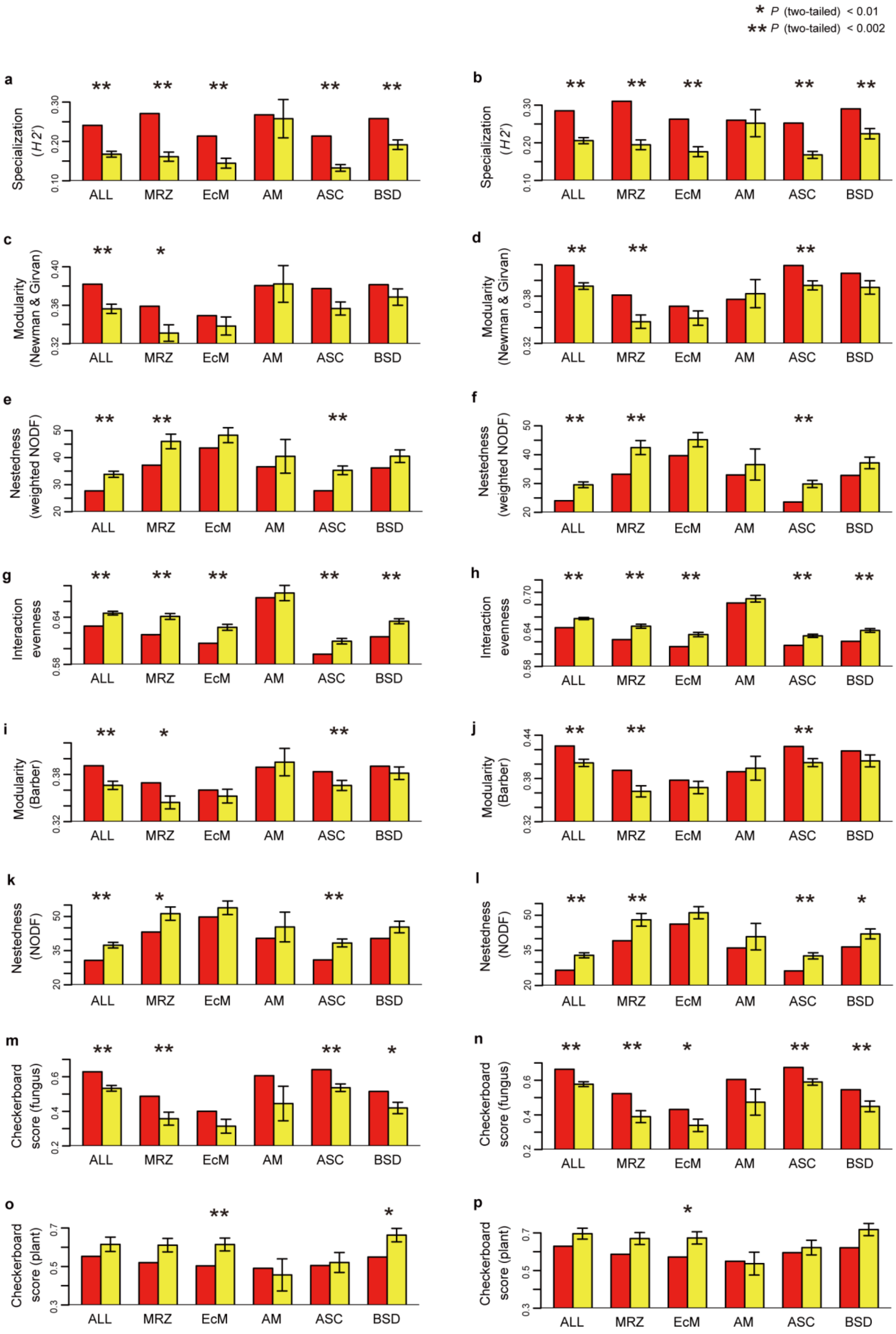
Supplementary Figure 3 | Statistical modules of the plant–fungus network. Based on the modularity analysis of the entire network (Fig. 3b), the members in different modules are indicated by colors. For each module, involved plant species are shown with the number of the root samples by which they were represented (i.e., the measure of relative abundance in the community). The pie charts in each module indicate the functional (left) and phylogenetic (right) composition of involved fungal OTUs. The numbers of plant species and fungal taxa, and connectance are shown for each module. AM, arbuscular mycorrhizal fungi; EcM, ectomycorrhizal fungi; ASC, ascomycete fungi; BSD, basidiomycete fungi; GLMS, glomeromycete fungi; OTH, others.



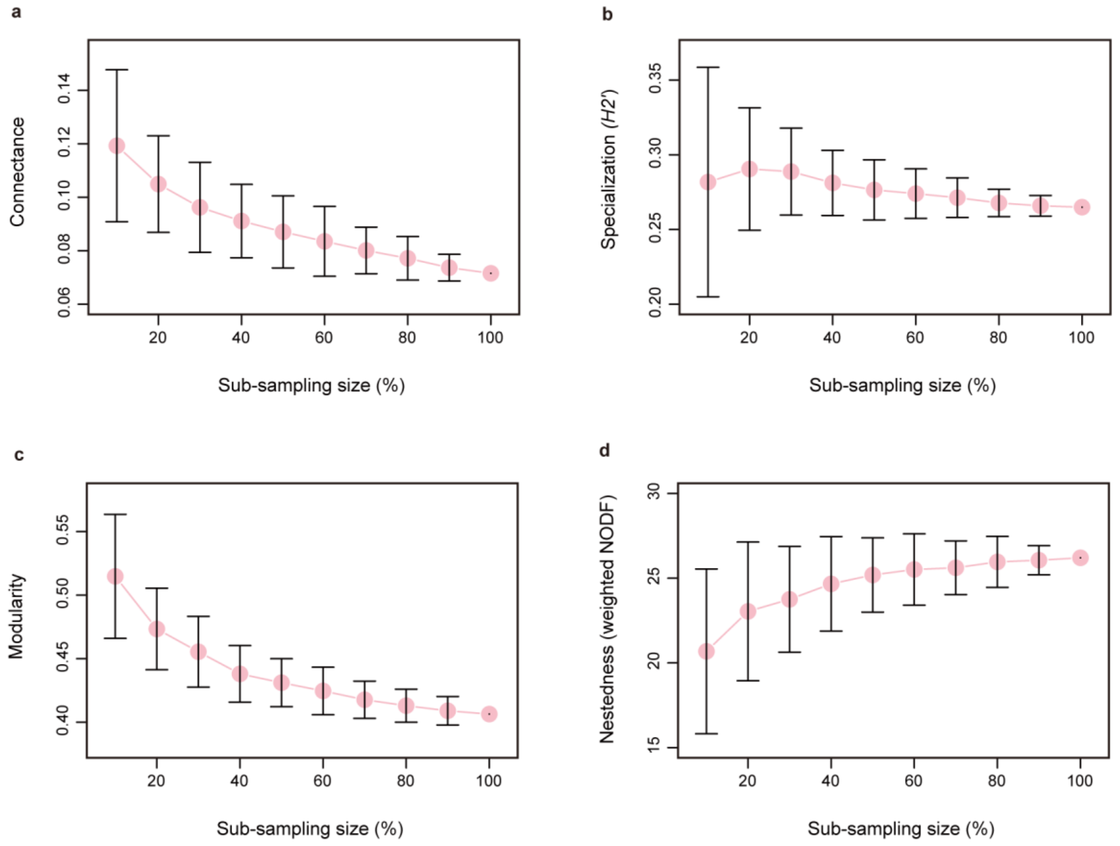
Supplementary Figure 4 | Total number of observed interactions and comparative analysis of network architecture. Across the 47 datasets with interaction frequency information (Supplementary Table 2), the dependence of network index values on the total number of observed interactions (i.e., the sum of interaction frequency) was examined. **a**, Network connectance. The symbols represent plant–pollinator (square), plant–seed disperser (open circle), myrmecophyte plant–ant (triangle), and plant–fungus (filled circle) networks. ALL, the entire network involving all plant species and fungal OTUs; MRZ, mycorrhizal partial network; EcM, ectomycorrhizal partial network; AM, arbuscular mycorrhizal partial network; ASC, ascomycete partial network; BSD, basidiomycete partial network; M.AM an arbuscular mycorrhizal network in Mexico. **b**, H_2' network-level specialization. **c**, Network modularity. **d**, Nestedness (weighted NODF). **e–g**, Principal component analysis. Larger values in the principal component (PC) axis 1 represent highly nested [factor loading (*r*) for modularity = 0.52] networks, while small values represent highly compartmentalized (*r* = -0.53) ones (Supplementary Table 4). High values in the PC axis 2 indicate low connectance (*r* = -0.65) and low specialization (*r* = -0.59). The PC axis 3 is negatively correlated with the total number of observed interactions (*r* = -0.82) and large values at the PC axis 4 represent high nestedness (*r* = 0.82).



Supplementary Figure 5 | Network topology at the cutoff fungal sequence similarities of 93% and 97%. The network data (Fig. 1) were re-analyzed with cutoff fungal ITS sequence similarities of 93% (**a**, **c**) and 97% (**b**, **d**), respectively (Supplementary Data 1). **a**, Distribution of fungal functional groups within the network (93%). In the bipartite network, plant species (red) interact with ectomycorrhizal (yellow) and arbuscular mycorrhizal (pink) fungal OTUs as well as OTUs with unknown ecological functions (blue). **b**, Distribution of fungal functional groups within the network (97%). **c**, Distribution of fungal taxonomic groups within the network (93%). Color represents the order-level taxonomy of fungal OTUs. **d**, Distribution of fungal taxonomic groups within the network (97%).


* P (two-tailed) < 0.01
** P (two-tailed) < 0.002
a
Specialization (H2')
0.10
0.20
0.30
** ** ** ** **
ALL MRZ EcM AM ASC BSD
b
Specialization (H2')
0.10
0.20
0.30
** ** ** ** **
ALL MRZ EcM AM ASC BSD
c
Modularity (Newman & Girvan)
0.32
0.36
0.40
** *
ALL MRZ EcM AM ASC BSD
d
Modularity (Newman & Girvan)
0.32
0.38
** ** **
ALL MRZ EcM AM ASC BSD
e
Nestedness (weighted NODF)
20
30
40
50
** ** **
ALL MRZ EcM AM ASC BSD
f
Nestedness (weighted NODF)
20
30
40
50
** ** **
ALL MRZ EcM AM ASC BSD
g
Interaction evenness
0.58
0.64
** ** ** ** **
ALL MRZ EcM AM ASC BSD
h
Interaction evenness
0.58
0.64
0.70
** ** ** ** **
ALL MRZ EcM AM ASC BSD
i
Modularity (Barber)
0.32
0.38
** * **
ALL MRZ EcM AM ASC BSD
j
Modularity (Barber)
0.32
0.38
0.44
** ** **
ALL MRZ EcM AM ASC BSD
k
Nestedness (NODF)
20
35
50
** * **
ALL MRZ EcM AM ASC BSD
l
Nestedness (NODF)
20
35
50
** ** ** *
ALL MRZ EcM AM ASC BSD
m
Checkerboard score (fungus)
0.2
0.4
0.6
** ** ** *
ALL MRZ EcM AM ASC BSD
n
Checkerboard score (fungus)
0.2
0.4
0.6
** ** * ** **
ALL MRZ EcM AM ASC BSD
o
Checkerboard score (plant)
0.3
0.5
0.7
** *
ALL MRZ EcM AM ASC BSD
p
Checkerboard score (plant)
0.3
0.5
0.7
*
ALL MRZ EcM AM ASC BSD

Supplementary Figure 6 | Detailed analysis of network indices at the cutoff fungal sequence similarities of 93% and 97%. For each network matrix based on a cutoff fungal sequence similarity of 93% (left-side panels) or 97% (right-side panels), randomization tests of network indices were conducted. **a-b**, H_2' metric of network-level specialization. The observed H_2' metric of interaction specialization (left bar) is shown for each network or partial network. Asterisks indicate significant deviation of observed H_2' values from those of randomized networks [right bar (mean ± SD)]. ALL, the entire network involving all plant species and fungal OTUs; MRZ, mycorrhizal partial network; EcM, ectomycorrhizal partial network; AM, arbuscular mycorrhizal partial network; ASC, ascomycete partial network; BSD, basidiomycete partial network. **c–d**, Newman and Girvan's metric of network modularity. **e–f**, Weighted NODF nestedness for network matrices with interaction frequency information. **g–h**, Interaction evenness evaluated by Shannon's evenness for network entries. **i–j**, Barber's metric of network modularity. **k–l**, NODF nestedness for datasets in a binary (i.e., presence/absence) format. **m–n**, Checkerboard score as a measure of host plant differentiation within the fungal community. **o–p**, Checkerboard score as a measure of fungal symbiont differentiation within the plant community.



Supplementary Figure 7 | Rarefaction analysis showing the potential influence of reduced sampling effort on network index estimates. At each level of reduced sampling effort (from 10% to 90%), 100 rarefaction trials were conducted. The mean of estimated network index values was shown with 95% confidence intervals based on the Student's *t*-distribution (df = 99). Estimates at the 100% rarefaction level represent those of the observed plant–fungus network (Fig. 3). **a**, Network connectance. **b**, H_2' network-level specialization. **c**, Network modularity. **d**, Nestedness (weighted NODF). See Supplementary Table 5 for the results of randomization tests of the examined network indices at each rarefaction level.

			P value		
Index	Data	Estimate	Model 1	Model 2	Model 3
Specialization (H_2')	ALL	0.265	< 0.001	< 0.001	< 0.001
	MRZ	0.287	< 0.001	< 0.001	< 0.001
	EcM	0.235	< 0.001	< 0.001	< 0.001
	AM	0.268	0.396	0.040	0.009
	ASC	0.231	< 0.001	< 0.001	< 0.001
	BSD	0.274	< 0.001	< 0.001	< 0.001
Modularity (Newman & Girvan)	ALL	0.397	< 0.001	< 0.001	< 0.001
	MRZ	0.366	0.006	< 0.001	< 0.001
	EcM	0.353	0.233	< 0.001	< 0.001
	AM	0.380	0.502	0.056	0.075
	ASC	0.397	0.002	< 0.001	< 0.001
	BSD	0.387	0.267	< 0.001	< 0.001
Nestedness (weighted NODF)	ALL	26.2	1.000	1.000	1.000
	MRZ	37.1	0.998	1.000	1.000
	EcM	42.9	0.924	1.000	0.996
	AM	36.6	0.764	0.971	0.985
	ASC	25.7	1.000	1.000	1.000
	BSD	34.7	0.965	1.000	1.000
Checkerboard score (fungus)	ALL	0.641	< 0.001	< 0.001	< 0.001
	MRZ	0.484	< 0.001	< 0.001	< 0.001
	EcM	0.405	0.024	< 0.001	0.195
	AM	0.606	0.022	0.004	0.006
	ASC	0.657	< 0.001	< 0.001	< 0.001
	BSD	0.529	0.002	< 0.001	0.012
Checkerboard score (plant)	ALL	0.583	0.986	0.056	0.037
	MRZ	0.536	0.998	0.743	0.535
	EcM	0.521	1.000	0.971	0.505
	AM	0.491	0.326	0.121	0.079
	ASC	0.544	0.738	0.003	< 0.001
	BSD	0.579	0.999	0.898	0.562
Interaction evenness	ALL	0.637	1.000	1.000	1.000
	MRZ	0.622	1.000	1.000	1.000
	EcM	0.611	1.000	1.000	1.000

	AM	0.665	0.717	0.959	0.874
	ASC	0.605	1.000	1.000	1.000
	BSD	0.621	1.000	1.000	1.000
Modularity (Barber)	ALL	0.406	< 0.001	< 0.001	< 0.001
	MRZ	0.375	0.009	< 0.001	< 0.001
	EcM	0.364	0.365	< 0.001	< 0.001
	AM	0.389	0.620	0.070	0.087
	ASC	0.404	0.002	< 0.001	< 0.001
	BSD	0.398	0.340	< 0.001	< 0.001
Nestedness (NODF)	ALL	29.1	1.000	1.000	1.000
	MRZ	42.6	0.994	1.000	1.000
	EcM	48.6	0.897	1.000	0.950
	AM	40.4	0.792	0.964	0.972
	ASC	28.6	1.000	1.000	1.000
	BSD	38.5	0.988	1.000	0.996

Supplementary Table 1 | Randomization tests based on three different null models. For each network index, randomization tests with three null models were conducted. A small *P* value indicates that the network index of the original matrix is larger than that of randomized matrices (1,000 permutations). ALL, the entire network involving all plant species and fungal OTUs; MRZ, mycorrhizal sub-network; EcM, ectomycorrhizal sub-network; AM, arbuscular mycorrhizal sub-network; ASC, ascomycete sub-network; BSD, basidiomycete sub-network.

Interaction	Dataset code name	Data type	Location	*N*	Ref.	Data repository*
Anemone–fish	anemonefish	binary	East coast of Africa and the Red Sea through the Indian Ocean to the western Pacific, and from southeastern Australia to the latitude of Tokyo	36	1	A
	Rich_Bahowo	binary	Manado region of Sulawesi, Indonesia	11	2	A
	Rich_Kopi	binary	Manado region of Sulawesi, Indonesia	10		A
Food web	AkatoreA	binary	Otago, New Zealand	84	3-9	A
	AkatoreB	binary	Otago, New Zealand	54		A
	Berwick	binary	Otago, New Zealand	77		A
	Blackrock	binary	Otago, New Zealand	86		A
	Broad	binary	Otago, New Zealand	94		A
	Canton	binary	Otago, New Zealand	108		A
	carpinteria	binary	Salt marsh	128	10	A
	Catlins	binary	Otago, New Zealand	48	3-9	A
	Coweeta1	binary	North Carolina, USA	58		A
	Coweeta17	binary	North Carolina, USA	71		A
	DempstersAu	binary	Otago, New Zealand	83		A
	DempstersSp	binary	Otago, New Zealand	93		A
	DempstersSu	binary	Otago, New Zealand	107		A
	German	binary	Otago, New Zealand	84		A

	Healy	binary	Otago, New Zealand	96		A
	Kyeburn	binary	Otago, New Zealand	98		A
	LilKyeburn	binary	Otago, New Zealand	78		A
	Martins	binary	Maine, USA	105		A
	Narrowdale	binary	Otago, New Zealand	71		A
	NorthCol	binary	Otago, New Zealand	78		A
	Powder	binary	Otago, New Zealand	78		A
	Stony	binary	Otago, New Zealand	112		A
	SuttonAu	binary	Otago, New Zealand	80		A
	SuttonSp	binary	Otago, New Zealand	74		A
	SuttonSu	binary	Otago, New Zealand	86		A
	Troy	binary	Maine, USA	77		A
	Venlaw	binary	Otago, New Zealand	66		A
Host–parasite	aishihik	binary	Yukon Territory, Canada	36	11-16	A
	cold	binary	Alberta, Canada	50		A
	mcgregor	binary	British Columbia, Canada	65		A
	parsnip	binary	British Columbia, Canada	70		A
	sbay_huron	binary	Labrador, Canada	130		A
	smallwood	binary	Ontario, Canada	31		A
	woods	binary	Ontario, Canada	175		A
Plant–ant	bluthgen_et_al_2004	binary	Australia	92	17,18	A
	davidson_et_al_1989	binary	Peru	24	19	A
	davidson&fisher_1991	binary	Peru	10	20	A
	fonseca&ganade	binary	Brazil	41	21	A

Plant–fungus	ALL	quantitative	Kyoto, Japan	420	22	B
	AM	quantitative	Kyoto, Japan	23		B
	ASC	quantitative	Kyoto, Japan	217		B
	BSD	quantitative	Kyoto, Japan	157		B
	EcM	quantitative	Kyoto, Japan	113		B
	MRZ	quantitative	Kyoto, Japan	123		B
	D.AM	binary	Koeru, Estonia	51	23	[14]
	M.AM	quantitative	Puebla, Mexico	60	24, 25	[15,54]
Plant–herbivore	joern_1979_altuda	binary	Altuda, Trans-Pecos, Texas, USA	74	26	A
	joern_1979_marathon	binary	Marathon,Trans-Pecos, Texas, USA	78		A
	leather_1991_britain	binary	Britain	94	27	A
	leather_1991inland	binary	Finland	69		A
Plant–pollinator	DIHI	quantitative	Hickling, Norfolk, UK	78	28	C
	DISH	quantitative	Shelfanger, Norfolk, UK	52		C
	EOLZ	binary	Zackenberg	107	29	C
	ESKI	binary	Mauritius Island	27	30	C
	HERR	binary	Doñana Nat. Park, Spain	205	31	C
	OFLO	binary	Flores, Açores	22	32	C
	OFST	binary	Hestehaven, Denmark	50		C
	OLAU	binary	Garajonay, Gomera, Spain	84		C
	PERC	binary	Jamaica	97	33	C
	PRAP	binary	Arthur's Pass, New Zealand	78	34	C

PRCA	binary	Cass, New Zealand	180		C
PRCG	binary	Craigieburn, New Zealand	167		C
PTND	binary	Daphní, Athens, Greece	797	35	C
RMRZ	binary	Canaima Nat. Park, Venezuela	97	36	C
SMRA	binary	Chiloe, Chile	154	37	C
arr_1	binary	Chile	186	38	A
arr_2	binary	Chile	103		A
arr_3	binary	Chile	69		A
barrett	quantitative	Canada	114	39	A
Bartomeus_Ntw_nceas	quantitative	Catalonia, Spain	151	40	A
bezerra-et-al-2009	quantitative	Pernambuco State, Brazil	26	41	A
cle	binary	USA	371	42	A
dupont	binary	Tenerife, Canary Islands	49	43	A
elb	quantitative	Sweden	141	44	A
hocking	binary	Canada	115	45	A
ino	quantitative	Australia	133	46	A
kaiser-bunbury_control	binary	Mauritius	158	47,48	A
kaiser-bunbury_restored	binary	Mauritius	208		A
kato	quantitative	Japan	767	49	A
mc_mullen	binary	Galápagos Islands	159	50	A
medan_ld	binary	Laguna Diamante, Mendoza, Argentina	66	51	A
medan_rb	binary	Río Blanco, Mendoza, Argentina	95		A

	mem	quantitative	Bristol, U.K.	104	52	A
	mos	quantitative	Canada	29	53	A
	mot	quantitative	USA	57	54	A
	ole_aigr	quantitative	Mauritius Island	27	55	A
	olelores	quantitative	Azores Islands	22		A
	ollerton	quantitative	KwaZulu-Natal region, South Africa	65	56	A
	ram	binary	Venezuela	81	57	A
	robertson_1929	binary	USA	1500	58	A
	santos-et-al-2010	binary	Bahia State, Brazil	76	59	A
	schemske	quantitative	USA	39	60	A
	small	quantitative	Canada	47	61	A
	vaz_ag	quantitative	Argentina	39	62-64	A
	vaz_cl	quantitative	Argentina	42		A
	vaz_ll	quantitative	Argentina	39		A
	vaz_mh	quantitative	Argentina	34		A
	vaz_mnh	quantitative	Argentina	43		A
	vaz_qh	quantitative	Argentina	35		A
	vaz_qnh	quantitative	Argentina	31		A
	vaz_s	quantitative	Argentina	36		A
Plant–seed disperser	CACG	quantitative	Caguana, Puerto Rico	41	65	C
	CACI	quantitative	Cialitos, Puerto Rico	54		C
	CACO	quantitative	Cordillera, Puerto Rico	38		C
	CAFR	quantitative	Fronton, Puerto Rico	36		C
	CROM	binary	Tropical rainforest.	79	66	C

		Queensland, Australia.			
FROS	binary	Mtunzini, South Africa	26	67	C
GEN1	quantitative	Santa Genebra Reserve T1. SE Brazil	25	68	C
GEN2	quantitative	Santa Genebra Reserve T2. SE Brazil	64		C
HAMM	binary	North Negros Forest Reserve, Central Philippine Islands	55	69	C
HRAT	binary	Hato Ratón, Sevilla. Spain	33	70	C
KANT	binary	Campeche state, Mexico	32	71	C
LAMB	binary	Kuala Lompat, Krau Game Reserve.	86	72	C
LOPE	binary	Gabon, Africa	27	73	C
MACK	binary	Crater Mountain Biological Research Station, Chimbu Province, Papua New Guinea	61	74	C
MONT	binary	Monteverde, Costa Rica	209	75	C
NCOR	binary	Nava Correhuelas. S. Cazorla, SE Spain.	58	76	C
NNOG	binary	Nava Noguera, Sierra de Cazorla, SE Spain	46		C
SAPF	binary	Yakushima Island, Japan	23	77	C
WES	binary	Intervales and Saibadela, São Paulo, Brazil	317	78	C

	beehler_1983	quantitative	Papa New Guinea	40	79	A
	poulin_1999	quantitative	Central Panama	24	80	A
	schleuning-et-al-2010	quantitative	Kakamega Forest, Western Province, Kenya	121	81	A
	snow&snow_1971	quantitative	Trinidad	79	82	A
	snow&snow_1988	quantitative	No information	48	83	A
	sorensen_1981	quantitative	Britain	25	84	A

Supplementary Table 2 | List of the datasets for the comparison of network architecture among different forms of interactions. The forms of interactions, dataset name, data type (binary or quantitative), sampling location, the number of species involved (*N*), source reference, and data repository are shown for each dataset.

*Data repository: A, Interaction Web DataBase[85] (http://www.nceas.ucsb.edu/interactionweb/index.html); B, Rezende et al. (2007) Nature[86]; C, Toju et al. (2013) Ecology and Evolution[22].

	Factor loading				Proportion of variance	Cumulative proportion
PC axis	Connectance	Specialization	Nestedness	Modularity		
PC1	0.365	-0.492	0.546	-0.571	0.68	0.68
PC2	-0.821	-0.554	0.118	0.066	0.23	0.91
PC3	0.038	-0.289	-0.813	-0.503	0.07	0.97
PC4	0.437	-0.606	-0.163	0.645	0.03	1.00

Supplementary Table 3 | Axes in the principal component analysis. The factor loading and the proportion of explained variance are shown for each principal component (PC) axis. See Figure 2 for the result of the principal component analysis.

	Factor loading					Proportion of variance	Cumulative proportion
PC axis	Total interaction	Connectance	Specialization	Nestedness	Modularity		
PC1	0.348	0.363	-0.446	0.515	-0.532	0.60	0.60
PC2	-0.445	-0.651	-0.585	0.177	-0.073	0.20	0.79
PC3	-0.816	0.500	0.098	0.000	-0.273	0.13	0.93
PC4	-0.125	-0.005	0.290	0.824	0.469	0.05	0.98
PC5	0.018	-0.441	0.604	0.155	-0.645	0.02	1.00

Supplementary Table 4 | Axes in the principal component analysis incorporating the total number of observed interactions. The factor loading and the proportion of explained variance are shown for each principal component (PC) axis. See Supplementary Figure 4 for the result of the principal component analysis.

		P value								
		Sub-sampling size (%)								
Index	Rarefaction trial	10	20	30	40	50	60	70	80	90
Specialization (*H2*’)	1	0.92	0.56	0.00	0.01	0.00	0.00	0.00	0.00	0.00
	2	0.87	0.74	0.21	0.00	0.00	0.00	0.00	0.00	0.00
	3	0.78	0.59	0.56	0.01	0.00	0.00	0.00	0.00	0.00
	4	0.90	0.52	0.12	0.03	0.00	0.00	0.00	0.00	0.00
	5	0.60	0.95	0.04	0.00	0.00	0.00	0.00	0.00	0.00
	6	0.77	0.08	0.51	0.02	0.00	0.00	0.00	0.00	0.00
	7	0.60	0.83	0.05	0.01	0.00	0.00	0.00	0.00	0.00
	8	0.79	0.41	0.06	0.00	0.02	0.00	0.00	0.00	0.00
	9	0.96	0.12	0.05	0.00	0.00	0.00	0.00	0.00	0.00
	10	0.93	0.27	0.01	0.04	0.00	0.00	0.00	0.00	0.00
	11	0.59	0.74	0.06	0.00	0.00	0.00	0.00	0.00	0.00
	12	0.88	0.59	0.14	0.00	0.00	0.00	0.00	0.00	0.00
	13	0.87	0.61	0.06	0.00	0.00	0.00	0.00	0.00	0.00
	14	0.42	0.11	0.00	0.01	0.00	0.00	0.00	0.00	0.00
	15	0.90	0.24	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	16	0.93	0.76	0.01	0.00	0.00	0.00	0.00	0.00	0.00
	17	0.93	0.18	0.02	0.00	0.00	0.00	0.00	0.00	0.00
	18	0.95	0.24	0.28	0.00	0.00	0.00	0.00	0.00	0.00
	19	0.57	0.28	0.03	0.04	0.00	0.00	0.00	0.00	0.00
	20	0.63	0.69	0.00	0.03	0.00	0.00	0.00	0.00	0.00
Modularity (Barber)	1	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.00	0.00
	2	0.12	0.00	0.01	0.10	0.00	0.00	0.00	0.00	0.00
	3	0.05	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	4	0.07	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	5	0.02	0.39	0.00	0.02	0.00	0.00	0.00	0.00	0.00
	6	0.00	0.09	0.01	0.00	0.00	0.00	0.00	0.00	0.00
	7	0.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	8	0.38	0.08	0.00	0.03	0.00	0.00	0.00	0.00	0.00
	9	0.11	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	10	0.10	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00
	11	0.20	0.00	0.15	0.04	0.00	0.00	0.04	0.00	0.00
	12	0.14	0.09	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	13	0.07	0.06	0.00	0.02	0.00	0.00	0.00	0.00	0.00

	14	0.12	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00
	15	0.03	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	16	0.00	0.01	0.02	0.00	0.00	0.00	0.00	0.02	0.00
	17	0.83	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00
	18	0.11	0.11	0.00	0.00	0.04	0.00	0.00	0.00	0.00
	19	0.14	0.12	0.08	0.00	0.00	0.00	0.00	0.00	0.00
	20	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nestedness (weighted NODF)	1	0.76	0.96	1.00	1.00	1.00	1.00	1.00	1.00	1.00
	2	0.60	0.94	1.00	0.99	1.00	1.00	1.00	1.00	1.00
	3	0.82	0.90	1.00	1.00	1.00	1.00	1.00	1.00	1.00
	4	0.88	0.98	0.99	0.96	0.99	1.00	1.00	1.00	1.00
	5	0.85	0.86	0.97	1.00	0.99	1.00	1.00	1.00	1.00
	6	0.68	0.93	0.99	1.00	1.00	1.00	1.00	1.00	1.00
	7	0.68	0.90	0.94	1.00	1.00	1.00	1.00	1.00	1.00
	8	0.32	0.95	0.99	1.00	1.00	1.00	1.00	1.00	1.00
	9	0.65	0.79	0.99	1.00	1.00	1.00	1.00	1.00	1.00
	10	0.74	0.97	0.94	1.00	1.00	0.98	1.00	1.00	1.00
	11	0.72	0.75	0.98	0.99	1.00	1.00	1.00	1.00	1.00
	12	0.41	0.77	1.00	1.00	0.93	1.00	1.00	1.00	1.00
	13	0.59	0.93	1.00	1.00	1.00	1.00	1.00	1.00	1.00
	14	0.75	0.97	1.00	1.00	1.00	1.00	1.00	1.00	1.00
	15	0.38	1.00	0.99	1.00	1.00	1.00	1.00	1.00	1.00
	16	0.65	0.61	0.99	1.00	1.00	1.00	1.00	1.00	1.00
	17	0.41	0.91	0.98	0.99	1.00	1.00	1.00	1.00	1.00
	18	0.87	0.85	0.89	1.00	1.00	1.00	1.00	1.00	1.00
	19	0.74	0.95	0.97	1.00	0.98	1.00	1.00	1.00	1.00
	20	0.69	0.76	1.00	1.00	1.00	1.00	1.00	1.00	1.00

Supplementary Table 5 | Randomization tests for the sub-sampled data. For 20 of the 100 rarefaction trials at each level of reduced sample size (Supplementary Fig. 7), a randomization test of each network index was performed. A small *P* value indicates that the network index of the original matrix is larger than that of randomized matrices (Model 1; 100 permutations).

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