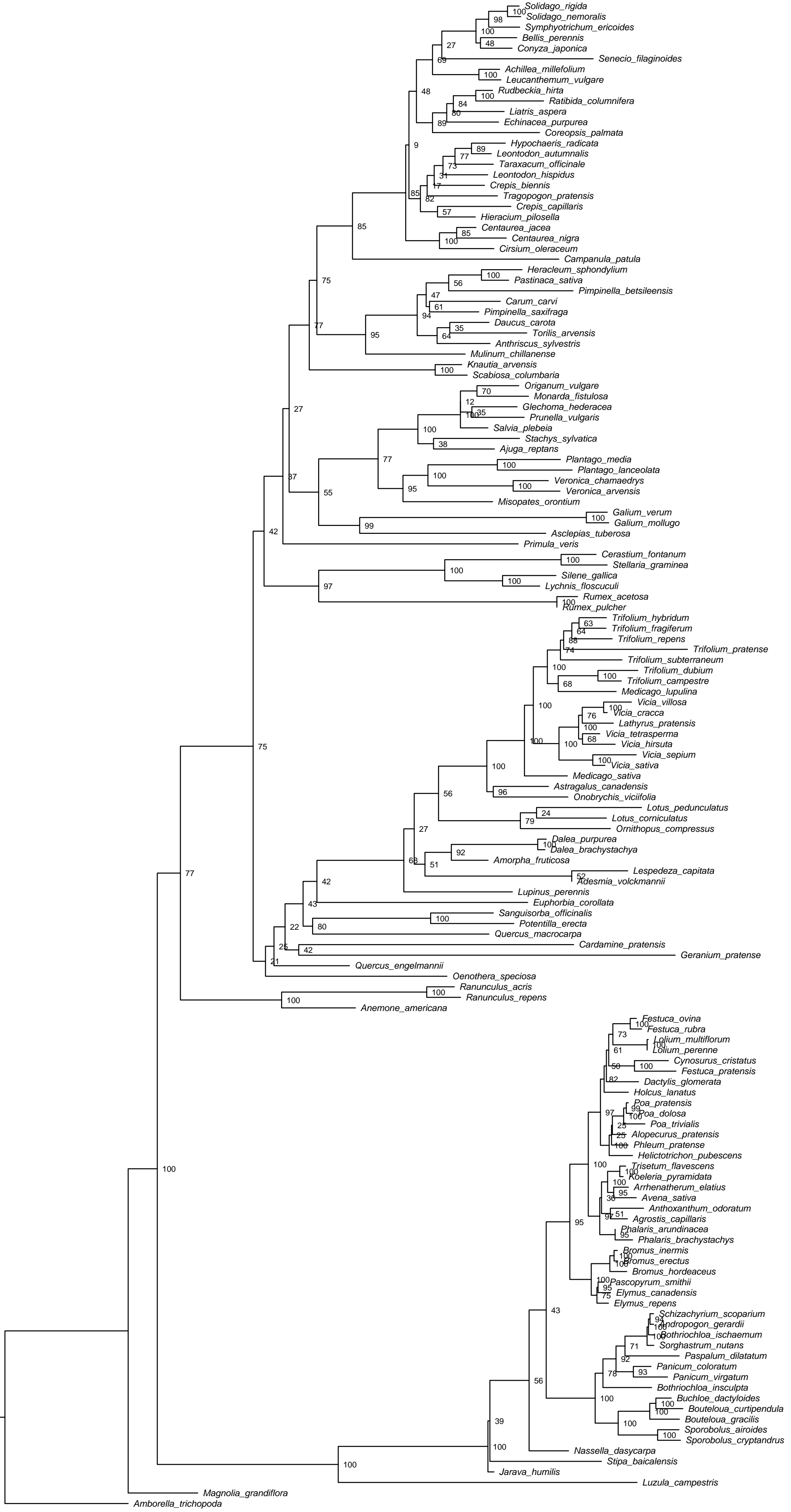


Fig S1: Phylogenetic relationship of the 141 plant species used in the current analysis and two outgroups (*Magnolia grandiflora* and *Amborella trichopoda*). Six gene sequences were used: *matk*, *rbcl*, *ndhf*, *its1*, *its2*, and *5.8s* (see **Table S2**). Sequences of each gene were aligned using MUSCLE (Edgar 2004), all genes were concatenated using phyloconcatenator (Oakley *et al.* 2014). This maximum likelihood phylogeny was estimated using RAxML (Stamatakis & Ott 2008), along with 100 bootstrap pseudoreplications to gauge nodal support. All phylogenetic analyses were conducted using the Osiris package (Oakley *et al.* 2014) of Galaxy.



0.1

Fig S2: Comparison of the four phylogenetic diversity measures estimated with the phylogenetic tree developed in the current study (**Fig. S1**, x-axis) and a recently published mega-tree (Zane *et al.* 2014, y-axis).

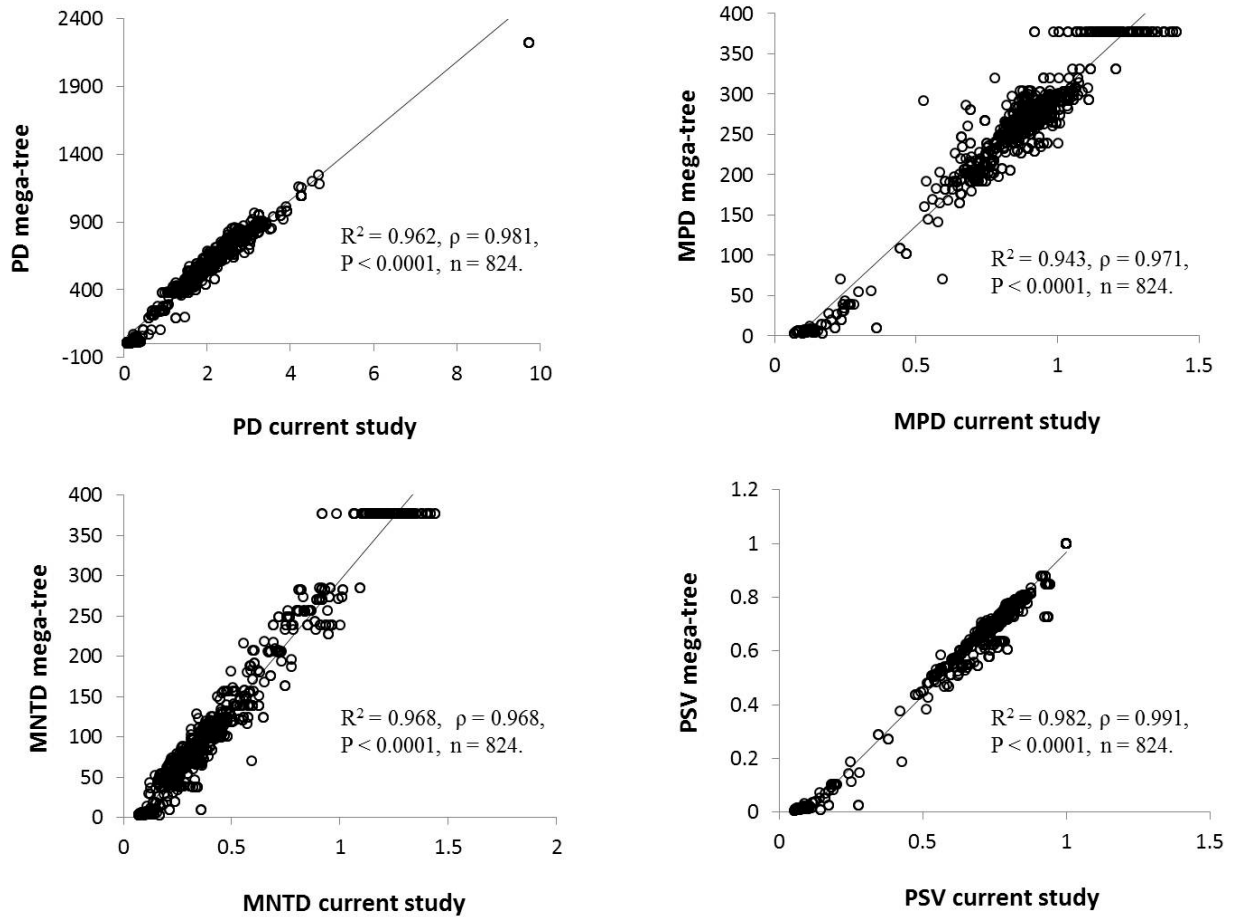


Table S1: List of the 16 studies included in this data synthesis presenting the reference study (authors and year of publication) with the name of the project and details on different treatments when available in parenthesis, the geographic location of the original study (locality or state and country), the number of time points over which biomass was measured and the total number of plots with different species compositions. Asterisks represent studies in which data for percentage coverage instead of biomass were available. n.a. refers to non-available project names.

	Reference study (name)	Location	Time points	Mixture plots
1	Reich <i>et al.</i> 2001 (BioCon)	Minnesota, USA	11	33
2	Reich <i>et al.</i> 2001 (BioCon, High N)	Minnesota, USA	11	31
3	Reich <i>et al.</i> 2001 (BioCon, High CO ₂)	Minnesota, USA	11	33
4	Reich <i>et al.</i> 2001 (BioCon , High CO ₂ , High N)	Minnesota, USA	11	29
5	Hector <i>et al.</i> 2010 (BioDepth)	Germany	3	40
6	Hector <i>et al.</i> 2010 (BioDepth)	Ireland	3	50
7	Hector <i>et al.</i> 2010 (BioDepth)	Portugal	3	28
8	Hector <i>et al.</i> 2010 (BioDepth)	Sheffield, England	3	30
9	Hector <i>et al.</i> 2010 (BioDepth)	Silwood, England	3	44
10	Hector <i>et al.</i> 2010 (BioDepth)	Sweden	3	34
11	Tilman <i>et al.</i> 2001 (Biodiversity II)	Minnesota, USA	8	123
12*	Tilman <i>et al.</i> 1996 (Biodiversity I)	Minnesota, USA	7	127
13	Van Ruijven & Berendse 2005 (n.a.)	The Netherlands	4	54
14	Isbell <i>et al.</i> 2009 (n.a.)	Texas, USA	10	36
15*	Flombaum & Sala 2008 (n.a.)	Patagonia, Argentina	3	66
16	Weigelt <i>et al.</i> 2010 (Jena)	Jena, Germany	6	66

Fig S3: For the *Type 2 analysis* we attempted to hold phylogenetic distance (PD) relatively constant and examine the impacts of species richness (SR) on community stability, biomass production, and the S.D. of biomass production through time. For this, we searched through all plots from all studies and found 1417 instances where PD was relatively similar among two plots in the same experiment, but where the two plots differed in species richness. For each of these 1417 contrasts, we calculated the log ratio of PD for the higher vs. lower PD species richness plots: $\ln(\text{Pd}_{\text{high}}/\text{Pd}_{\text{low}})$. The histogram of log ratios for the 1417 actual contrasts is plotted in blue (LRACT), which is a highly constrained range of variation in PD compared to the dataset as a whole (red histogram shows the log ratio of PD-values for 50,000 random draws among plots, LRRAND). Positive values represent larger PD in the plot with more species, and negative values the inverse. As such, these contrasts come as close as we can come to holding PD constant so that we can examine the impacts of SR on stability and its components.

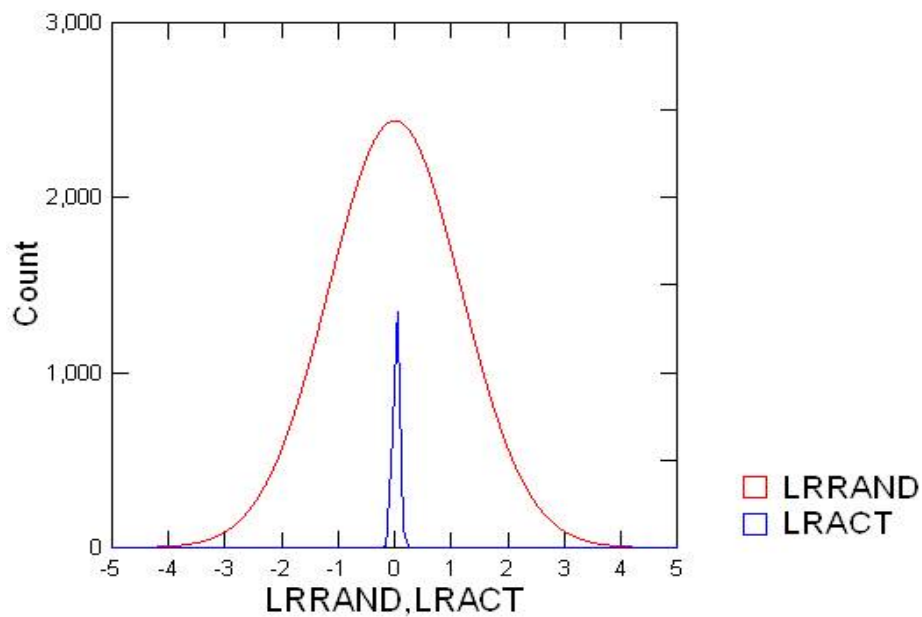


Fig S4: Correlations between 5 different metrics of biodiversity: species richness (SR); phylogenetic diversity (PD); mean phylogenetic distance (MPD); mean nearest taxon distance (MNTD) and phylogenetic species variability (PSV). Top left panels show correlation coefficients and significance values. Bottom right panels show actual correlation plots.

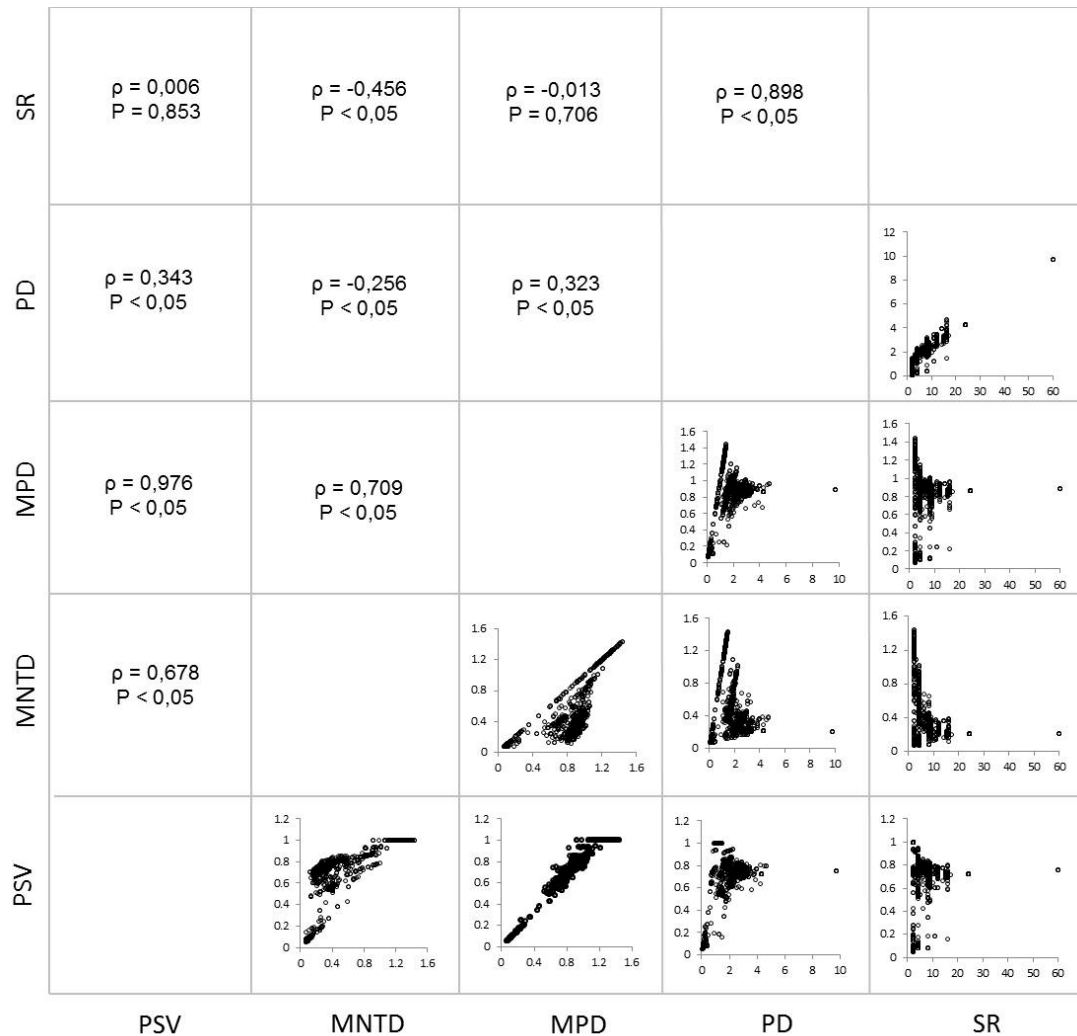


Table S2. GenBank Accession numbers for genes used in phylogenetic analyses.

Species	5.8s	its1	its2	matk	ndhf	rbcl
<i>Achillea_millefolium</i>	HE687356	AF046939	AF046939	JN894883	AF153633	L13641
<i>Adesmia_volckmannii</i>	U59893			AF142690		
<i>Agrostis_capillaris</i>	DQ146767	AF498395	AF498395	FJ231112		AY395527
<i>Ajuga_reptans</i>	JQ638909	EF508061	EF508061	AY840130	L36391	U32163
<i>Alopecurus_pratensis</i>				EU434293		AY395528
<i>Amborella_trichopoda</i>				DQ185522	AJ506156	L12628
<i>Amorpha_fruticosa</i>	JF491249	U59890		AY391785		U74212
<i>Andropogon_gerardii</i>				AF144577	AF117391	AJ784818
<i>Anemone_americana</i>				AF542590		EU053901
<i>Anthoxanthum_odoratum</i>	FJ010630	FJ010630	FJ010630	DQ786884	DQ786812	AJ746282
<i>Anthriscus_sylvestris</i>	AY548228	EU236159	EU236159	U58547		JN893702
<i>Arrhenatherum_elatius</i>	FM179388	DQ995405	DQ995405	EU434292	U71019	AY395529
<i>Asclepias_tuberosa</i>				GQ248084		GQ248553
<i>Astragalus_canadensis</i>		L10770	L10771	AY386875		
<i>Avena_sativa</i>	HQ600525	DQ995434	FJ794718	DQ786886	AF267663	L15300
<i>Bellis_perennis</i>	AF046950	JN315918	AF493996	JN893935	L39446	AY395530
<i>Bothriochloa_insculpta</i>	AF190756	AF190756	AF190756			
<i>Bothriochloa_ischaemum</i>				HE574006	AM849131	AM887873
<i>Bouteloua_curtipendula</i>	GU359281	GU359281	GU359281	AF144578	EF422911	JN681654
<i>Bouteloua_gracilis</i>	GU359285	GU359285	GU359285	HE575865	HE575771	AJ784829
<i>Bromus_erectus</i>	AY367907	AY367907	AY367907	AM234570	U71033	AJ746286
<i>Bromus_hordeaceus</i>	AF494347	AF494347	AF494346	JN895538	AM849134	AY395531
<i>Bromus_inermis</i>	HQ600546	AY367915	JN998985	AF164398	DQ786821	HQ600445
<i>Buchloe_dactyloides</i>				FR821320	FR821354	FR821337
<i>Campanula_patula</i>	FM212739			JN894553		JN892767
<i>Cardamine_pratensis</i>	X98637	AF265170	AF265191	HM850749		HM849848
<i>Carum_carvi</i>	AF077878	AF077878	AF077878	U58553		
<i>Centaurea_jacea</i>	JN808258	DQ319125	DQ319125	HQ593227		HQ590025
<i>Centaurea_nigra</i>	JQ360436	DQ319138	DQ319138	JN895934		JN892339
<i>Cerastium_fontanum</i>		AY936241	AY286525	JN894934		JN893675
<i>Cirsium_oleraceum</i>	AY780402	AY780402	AY780402			
<i>Conyza_japonica</i>	JN315938	JN315938	JN315938			
<i>Coreopsis_palmata</i>		AY553673	AY553674	AY551480		
<i>Crepis_biennis</i>	JF978846	AJ633355		JN895401	AF218345	JN891592
<i>Crepis_capillaris</i>	JF978846	AJ633381	HQ161936	AJ633142		HM849923

<i>Cynosurus cristatus</i>	HM453199	HM453199.1	HM453199	HM453075_pt9974	DQ786829	JN890889
<i>Dactylis glomerata</i>	AF393013	AF393013	AF393013	AM234595	AM849145	AJ746268
<i>Dalea brachystachya</i>				EU025886		
<i>Dalea purpurea</i>	AY426794.1	AY426794	AY426794.1	AY391798		
<i>Daucus carota</i>		JQ290121	GQ434704	DQ898156		DQ898156
<i>Echinacea purpurea</i>	EU785937	U73148	U74418		AB530929	AB530963
<i>Elymus canadensis</i>	EF396960	EF396960	EF396960	HM770807	HM770846	HM770840
<i>Elymus repens</i>	FJ793079	FJ793077	FJ793094	HQ593279	U71027	HQ600453
<i>Euphorbia corollata</i>	JQ750900.1	JQ750900.1	JQ750900.1		EU022038	
<i>Festuca ovina</i>	AF147170.2	AF147170.1	AF147170.3	JN894019	JX871940	JN891705
<i>Festuca pratensis</i>	AJ240151	HM453173	HM453173	HM850535	JN187627	AY395536
<i>Festuca rubra</i>	AJ240158	AF303422	JN999219	DQ786911	DQ786839	AJ746261
<i>Galium mollugo</i>	AM503885	AM503885		AM503814		AY395538
<i>Galium verum</i>				HQ593309		HQ590115
<i>Geranium pratense</i>				JN895981		JN892282
<i>Glechoma hederacea</i>	JQ280772	JQ669099		AY840143		AB266226
<i>Helictotrichon pubescens</i>	FM956100	AY870326		FM957003		JN891444
<i>Heracleum sphondylium</i>	EU169285	EU594914	EU169285	JN894478		AY395540
<i>Hieracium pilosella</i>	AM946982	HQ161945	HQ161945	JN896101		HQ590133
<i>Holcus lanatus</i>	HQ600532	HQ600531	HQ600533	JN894905	AM849157	AM235062
<i>Hypochaeris radicata</i>	AJ633310	GU011987	GU011987	AJ633231		AY395542
<i>Jarava humilis</i>	FN434548	EU489120	EU489120	EU489198		
<i>Knautia arvensis</i>				JN894671	AF161298	HE574586
<i>Koeleria pyramidata</i>		Z96912				AJ746262
<i>Lathyrus pratensis</i>				JN894102		AY395544
<i>Leontodon autumnalis</i>	HM627314	HQ161932		AJ633222		
<i>Leontodon hispidus</i>	GU116531	Z93830		AJ633218		AY395545
<i>Lespedeza capitata</i>	GU572172.1	GU572172.1	GU572172.1			
<i>Leucanthemum vulgare</i>	EF577315	AB359706	EF577315	HM850667	EU334481	AY395546
<i>Liatis aspera</i>	HQ416346	HQ416346	HQ416346		HQ416219	
<i>Lolium multiflorum</i>	HQ600550	EF379072				
<i>Lolium perenne</i>	AJ240138	AF303401	AF303401	JN895693		HQ600426
<i>Lotus corniculatus</i>	JN861088	DQ312207				U74213
<i>Lotus pedunculatus</i>	JQ858258	DQ166222				
<i>Lupinus perennis</i>		Z72162.1	Z72163.1			Z70058
<i>Luzula campestris</i>	FJ213882.1	FJ213882.1	FJ213882.1	HM850953		AY395548
<i>Lychnis flosculi</i>		U30957				AY395549
<i>Magnolia grandiflora</i>				AF548640	AF107940	AY008925
<i>Medicago lupulina</i>		AB546798				AY395551

<i>Medicago sativa</i>	JX017337	JX017335		AF522108		Z70173
<i>Misopates orontium</i>	AY707075	AY707075	AY707075	JN894172		JN893438
<i>Monarda fistulosa</i>	DQ667318.1	DQ667318.1	DQ667318.1			Z37419
<i>Mulinum chillanense</i>				AY188402		AY188428
<i>Nassella dasycarpa</i>		EU489148	EU489148	EU489222		
<i>Oenothera speciosa</i>	DQ075636.1	DQ075636.1	DQ075636.1			HQ644058
<i>Onobrychis viciifolia</i>	GQ246078	GQ246078	GQ246078	JQ669629		
<i>Origanum vulgare</i>	JQ389515	AY506647		AY840165		Z37427
<i>Ornithopus compressus</i>	HM468335	HM468335	HM468335	HM851142		HM850215
<i>Panicum coloratum</i>				HE574090		AM849415
<i>Panicum virgatum</i>	AM404348	AM404348				AY632368
<i>Pascopyrum smithii</i>					AF056172	
<i>Paspalum dilatatum</i>		AY771871	AY771904	HM850547		HM850238
<i>Pastinaca sativa</i>	EU169305	U30546	U30547	JN895118		JN893745
<i>Phalaris arundinacea</i>						AJ784827
<i>Phalaris brachystachys</i>	JF951057	JF951057	JF951057	HM850514		HM850250
<i>Phleum pratense</i>				AF164397		AY395554
<i>Pimpinella betsileensis</i>	DQ647626	DQ647626	DQ647626			
<i>Pimpinella saxifraga</i>	HM176655	AY581801		U58576		U50229
<i>Plantago lanceolata</i>	FJ024622	FJ024622				L36454
<i>Plantago media</i>	AJ548964	AJ548964		AY667474		AJ389596
<i>Poa dolosa</i>	GQ324502	GQ324502	GQ324502			
<i>Poa pratensis</i>	JF786337	JF786328	JF786337	AF164402		JN892391
<i>Poa trivialis</i>	AF532932	AF532932	AF532932	JN895711		AJ746301
<i>Potentilla erecta</i>	FN430780			JN896010		JN893738
<i>Primula veris</i>	AM920484	JX231022	AF323701	JN896058		JN893423
<i>Prunella vulgaris</i>	JQ669130	AY506653				AY395556
<i>Quercus engelmannii</i>	AF098420	AF098420	AF098420			
<i>Quercus macrocarpa</i>				EU749362		HQ590229
<i>Ranunculus acris</i>		FM242864		AY954199		AY395557
<i>Ranunculus repens</i>		AY680152		AY954182		
<i>Ratibida columnifera</i>		U73145	U74415			
<i>Rudbeckia hirta</i>			U74407	HQ593421		AB530973
<i>Rumex acetosa</i>						AY395559
<i>Rumex pulcher</i>				HM851087		HM850323
<i>Salvia plebeia</i>			FJ883524			HM590084
<i>Sanguisorba officinalis</i>	AY635041	AY635041	AY635041	AB073696		AY395560
<i>Scabiosa columbaria</i>	AY236188	AY236188	AY236188	AF446918	AF447038	AF446948
<i>Schizachyrium scoparium</i>				HE586094	AF117420	HE577863

Senecio_filaginoides	EF538334	EF538334	EF538334			
Silene_gallica	X86847	U30959	U30985	JN894574		M83544
Solidago_nemoralis	EU125357	HQ142596	HQ142596	EU749419		EU677026
Solidago_rigida	HQ142603	HQ142603	HQ142603			
Sorghastrum_nutans				FR821326	AF117421	EF125121
Sporobolus_airoides	AF019842	AF019842	AF019842	HE573973		
Sporobolus_cryptandrus	GU359208	GU359208	GU359208	HQ593457	GU359674	HQ590286
Stachys_sylvatica				JN895203		AF502022
Stellaria_graminea				JN895064		JN890625
Stipa_baicalensis	FN434508	FN434508.1	FN434508.1	FN434242		
Symphotrichum_ericoides	JQ360392	JQ360392	JQ360392	EU749432		EU677040
Taraxacum_officinale	JN407436	JN407436		AJ633157	AF218346	AY395562
Torilis_arvensis	FJ415110	FJ415110	AF164869	JN893950		AM234827
Tragopogon_pratensis	HQ456261	HQ456270	AY508167	JN893953		AY395563
Trifolium_campestre	DQ312025	AF154403	AF154627	HE970749		JN891072
Trifolium_dubium	DQ312047	DQ312047	DQ312047	JN894454		JN892755
Trifolium_fragiferum		AF154366	AF154590	JN894249		HM850413
Trifolium_hybridum	HM470609	EU348779	AF154600	AF522125		
Trifolium_pratense	FJ554461	EU348780	AF154620	FJ395384		AY395564
Trifolium_repens	HM470609	FJ980291_pt9958	AF053172	AF522131		HQ644078
Trifolium_subterraneum	EU348779	AF154407	AF053177	AF522135	EU849487	HM850426
Trisetum_flavescens		Z96898		JN895340		AY395565
Veronica_arvensis	DQ227328	DQ227328	DQ227328	AF052003		HQ619782
Veronica_chamaedrys	FJ024624	AF313003	AF313003	FJ395446		FJ395581
Vicia_cracca	JQ309787	AF335189	AF335190	JN894329		AY395566
Vicia_hirsuta	JQ309794	HM470620	DQ351827	AF522157		JN893460
Vicia_sativa	JQ309794	DQ312198	DQ312198	AF522160		JN893683
Vicia_sepium	JQ309794	AM087144		JN896142		JN891169
Vicia_tetrasperma	JQ309794	DQ351828	DQ351828	JN894335		HQ590329
Vicia_villosa	JQ309794	HM470637	DQ312199	AF522161		HM850464

Table S3: Detailed results of the structural equation model (Type 3 analysis, **Figure 4**) exploring the effect of phylogenetic diversity (PD) and species richness (SR) on average community biomass (biom) and standard deviation (sd) as components of community stability (stab). Values in bold correspond to the values included in **Figure 4**.

Number of observations						222	
Minimum Function Test Statistic						1.185	
Degrees of freedom						2	
P-value (Chi-square)						0.553	
Parameter estimates:							
	Information Standard Errors				Expected Standard		
		Estimate	Std. err	Z-value	P(> z)	Std. l v	Std. all
Regressions:							
biom ~							
SR	(a)	27.810	6.423	4.330	0.000	27.810	0.386
PD	(b)	0.843	24.402	0.035	0.972	0.843	0.003
sd ~							
SR	(c)	7.134	3.360	2.123	0.034	7.134	0.197
PD	(d)	14.009	12.765	1.098	0.272	14.009	0.102
stab ~							
biom	(e)	0.007	0.001	13.228	0.000	0.007	0.783
sd	(f)	-0.019	0.001	-18.061	0.000	-0.019	-1.069
Covariances:							
biom~sd		15856.694	1923.964	8.242	0.000	15856.694	0.664
SR~PD		1.966	0.226	8.710	0.000	1.966	0.721
Variances:							
biom		45653.645	4333.252			45653.645	0.849
sd		12492.508	1185.736			12492.508	0.922
stab		1.700	0.161			1.700	0.404
SR		10.368	0.984			10.368	1.000
PD		0.718	0.068			0.718	1.000
Defined parameters (Indirect effects of x -> y, via z):							
SR->Stab, Biom		0.192	0.047	4.115	0.000	0.192	0.302
SR->Stab, SD		-0.134	0.064	-2.109	0.035	-0.134	-0.211
PD->Stab, Biom		0.006	0.169	0.035	0.972	0.006	0.002
PD->Stab, SD		-0.264	0.241	-1.095	0.273	-0.264	-0.109
R-Square:							
biom		0.151					
sd		0.078					
stab		0.596					

Table S4: Results of linear models linking phylogenetic diversity (mean phylogenetic distance, MPD) and species richness (SR) to stability, average biomass, standard deviation (SD), sum of species variances (sum. var.) and synchrony (called *Type 4 analysis* in main text). Study was included as random effect. Cases with significant effects are in grey for visual clarity.

	Stability		Average biomass		S.D.		Sum. var.		Synchrony	
	F-value	P-value	F-value	P-value	F-value	P-value	F-value	P-value	F-value	P-value
SR	11.02	< 0.001	55.05	<0.0001	4.64	0.03	0.55	0.46	8.36	<0.01
MPD	1.52	0.22	2.83	0.09	6.58	0.01	6.09	0.01	2.93	0.07

Data S1: The current data-synthesis suggests that, after correcting for species richness, phylogenetic diversity is not a good predictor of community biomass (see Summary Table 2 in main document). This lack of effect was consistent over the three different statistical methods we used to test it. In contradiction, another meta-analysis using a similar dataset from grassland studies by Cadotte *et al.* (2008) showed that phylogenetic diversity was a good predictor of community biomass. In addition to a different dataset, both studies used different phylogenies to measure the phylogenetic diversity of each plot, used different measures of community biomass and applied different types of statistical analyses. These four factors may have influenced the observed differences. In order to determine the reasons for the discrepancies in the results among both studies we performed a series of permutations on: 1) the dataset, 2) the descriptive variables (x-variables), 3) the dependent variables (y-variables) and 4) the statistical analyses between Cadotte *et al.*'s study and ours. We started by collating data that contained the explanatory (phylogenetic diversity) and dependent variables (community biomass) from both studies, resulting in an overlapping dataset that included 318 plots. This collated dataset represents 24% of the 1318 plots included in Cadotte's paper and 39% of the 824 plots included in the current study.

Table S5: Summary of the results of a permutation exercise about the effect of phylogenetic diversity on community biomass.

Test	Dataset	Studies (plots)	x-variable	y-variable	Is PD significant?	
					LME	WZ _r
1	Cadotte	29 (1318)	ML_UM	Log ratios	Yes	Yes
2	Venail	16 (824)	PD	Average Biomass	Yes	No
3	Combined	12 (318)	ML_UM	Log ratios	Yes	Yes
4	Combined	12 (318)	ML_UM	Average Biomass	Yes	No
5	Combined	12 (318)	PD	Log ratios	Yes	Yes
6	Combined	12 (318)	PD	Average Biomass	Yes	No

We first tested if the reduced combined dataset reproduced Cadotte *et al.*'s main results. We ran all the same analyses as in their study (linear mixed effect models, LME models), using their same metric of phylogenetic diversity (ML_UM) and their same measure of community biomass (log ratios at the final point). We found exactly the same results as in their manuscript

(line 1 vs. line 3 in **Table S5**), which was a positive effect of phylogenetic diversity on community biomass.

Similarly, we also tested if this reduced dataset reproduces our main results. We ran the *Type 1* analyses using weighted Zr (WZ_r), PD values and the average biomass over time as measure of community biomass. We found the same results as in our main study (line 2 vs. line 6 in **Table S5**), which is no effect of phylogenetic diversity on community biomass. Thus, using a reduced combined dataset we were able to reproduce the results from both studies.

Then, we used this collated reduced dataset to perform three series of tests.

1) Testing the effect of “phylogenetic diversity”, the explanatory variable (x-variable).

Despite being based on two different phylogenies, the values of phylogenetic diversity from the two studies were highly correlated ($\rho = 0.946$, $P < 0.0001$, $n = 318$). A permutation of ML_UM by PD and vice-versa (line 3 vs. line 5 and line 4 vs. line 6 in **Table S5**) produced the same results as in the original studies, suggesting that changes in the measures of phylogenetic diversity were not responsible for the discrepancies among both studies.

2) Testing the effect of “community biomass”, the response variable (y-variable).

Cadotte *et al.* used as response variable the biomass of the entire community at a single final point converted into a log ratio relative to the average biomass as monocultures of the species present in a plot. In the current study we used community biomass averaged over time. The two measures of community biomass were poorly correlated ($\rho = 0.153$, $P = 0.006$, $n = 318$). A permutation of the response variable (average biomass instead of log ratio) using LME models (line 3 vs. line 4 in **Table S5**) produced the same result as in Cadotte *et al.*'s. However, a permutation of the response variable (log ratio instead of average biomass) using type 1 analysis (WZ_r , line 6 vs. line 5 in **Table S5**) led to a result that is different from the one in our main study. This suggests that the discrepancies in the results among both studies can be (at least partially) explained by differences in the response variable.

The fact that the type 1 analysis revealed a positive effect of PD on log ratios (last column in line 5 from **Table S5**) but not on average biomass (last column in line 6 from **Table S5**) raised another question. Were those differences in the results due to the log ratio transformation *per se*

or to the fact that log ratios were estimated only at the final point of a time series data? To answer this question, we ran a *type I analysis* (WZ_r) on the combined dataset using PD as explanatory variable and final biomass as response variable. As shown in the table below (test 5*), the *test I analysis* showed no effect of PD on final biomass. This means that it's the log ratio transformation and not the use of a single final time point that explains at least part of the differences in the results from both studies.

Test	Dataset	Studies (plots)	x-variable	y-variable	Is PD significant? (WZ_r)
5	Combined	12 (318)	PD	Average Biomass	No
5*	Combined	12 (318)	PD	Final biomass	No
6	Combined	12 (318)	PD	Log ratios	Yes

Indeed, Average biomass and Final biomass were highly correlated ($\rho = 0.752$, $P < 0.0001$, $n = 318$), whereas Average biomass and Log ratios were poorly correlated ($\rho = 0.153$, $P < 0.01$, $n = 318$).

3) Testing the effect of the statistical test.

Cadotte *et al.*'s results were based on linear mixed effect models (LME) whereas the results of the current study are based on weighted and averaged linear correlations between phylogenetic diversity and community biomass at each level of species richness (WZ_r). Switching statistical methods (WZ_r instead of LME) but keeping all other factors equal as in Cadotte *et al.* produced the same result as in their study (line 3 in **Table S5**). However, switching statistical methods (LME instead of WZ_r) but keeping all other factors equal as in our study led to a different result (line 6 in **Table S5**).

In conclusion, this permutation exercise revealed that using a different measure of community biomass (the log transformation *per se*) and a different statistical technique explain the observed differences in the results about the effect of phylogenetic diversity on community biomass among Cadotte *et al.*'s study and ours.