

# Supplementary Material - Mujica et al.

## 1 Phylogenetic signal of Mycorrhizal types

Table 1: P-values for test of phylogenetic signal (D) of each mycorrhizal type. Significant values are highlighted in bold.

Threshold	model	AM	EM	MIX	NM
50	random	<b>0</b>	<b>0</b>	0.842	<b>0</b>
50	BM	0.899	0.969	<b>0.043</b>	0.832
60	random	<b>0</b>	<b>0</b>	<b>0.031</b>	<b>0</b>
60	BM	0.88	0.949	0.215	0.852
80	random	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>
80	BM	0.821	0.956	0.228	0.747
100	random	<b>0</b>	<b>0</b>	0.247	<b>0</b>
100	BM	0.083	0.958	<b>0</b>	0.643

## 2 Analysis per genera excluding 100% MIX families

### 2.1 Boxplots

#### 2.1.1 Threshold 50%

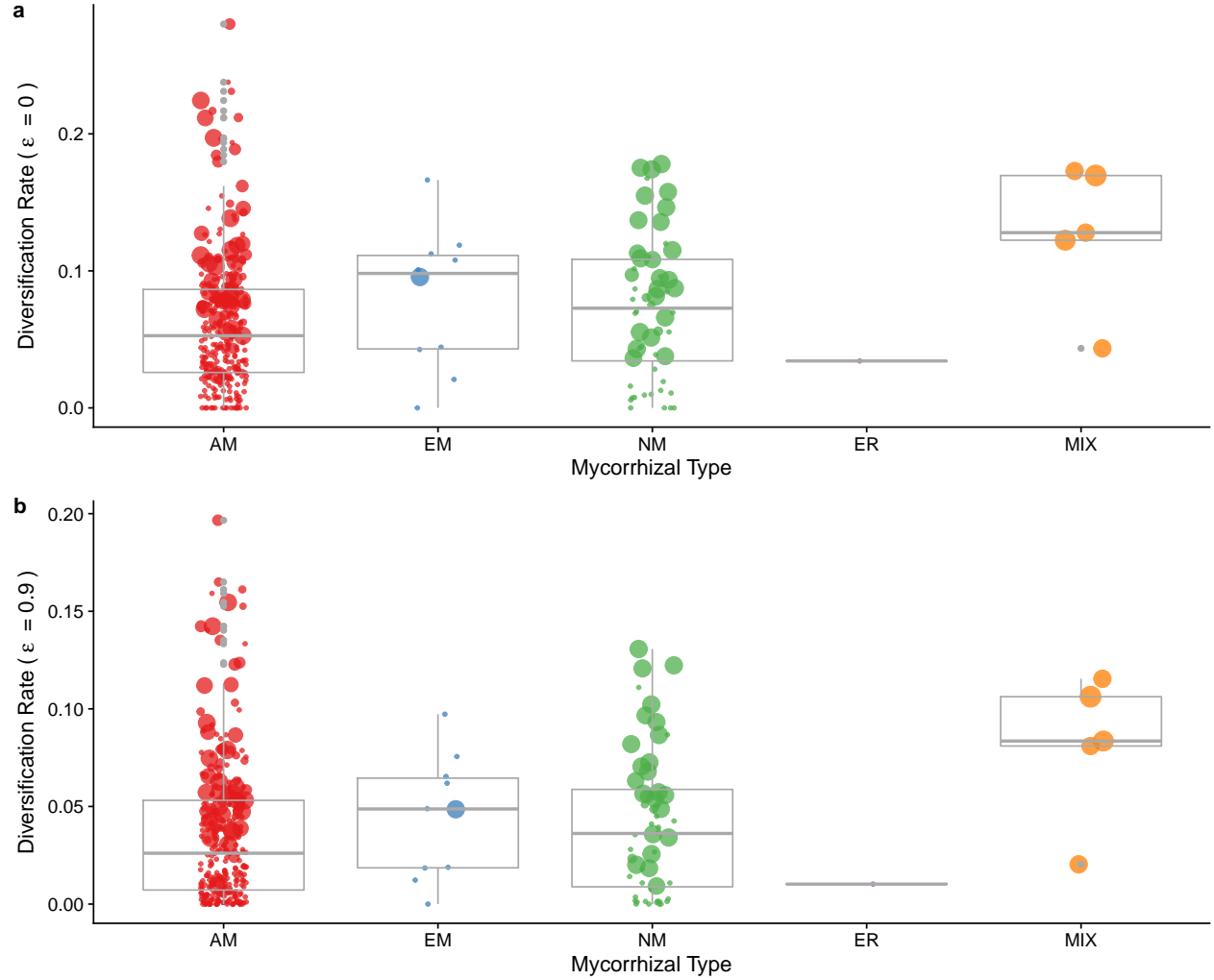


Figure 1: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with epsilon = 0 and b) diversification rate estimated with epsilon = 0.9. AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance of any specific mycorrhizal association). The size of the points indicates the Mycorrhizal Type Diversity Index value for each lineage, indicating a predominance of larger indices with higher diversification rates.

### 2.1.2 Threshold 60%

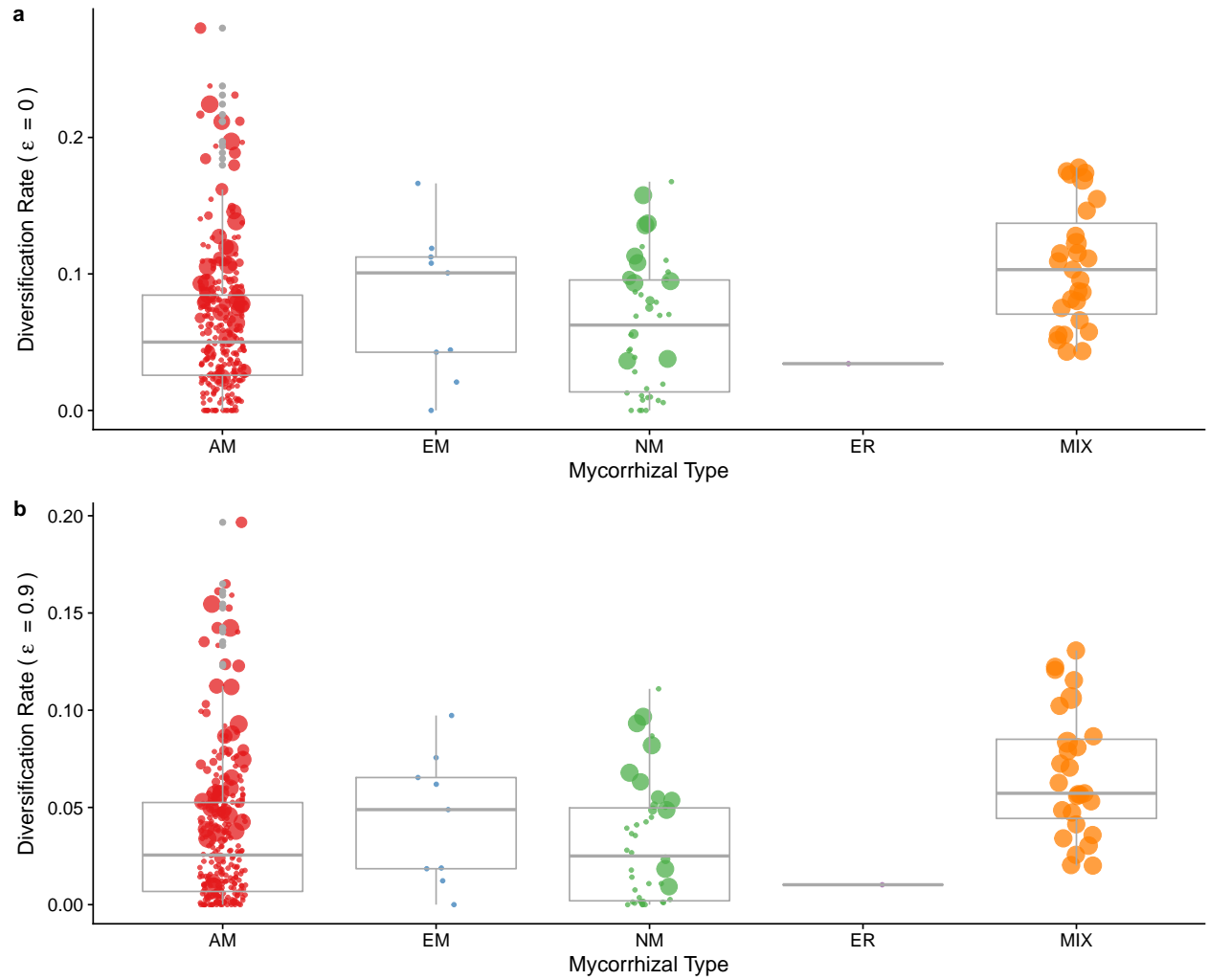


Figure 2: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with  $\epsilon = 0$  and b) diversification rate estimated with  $\epsilon = 0.9$ . AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance of any specific mycorrhizal association). The size of the points indicates the Mycorrhizal Type Diversity Index value for each lineage, indicating a predominance of larger indices with higher diversification rates.

### 2.1.3 Threshold 80%

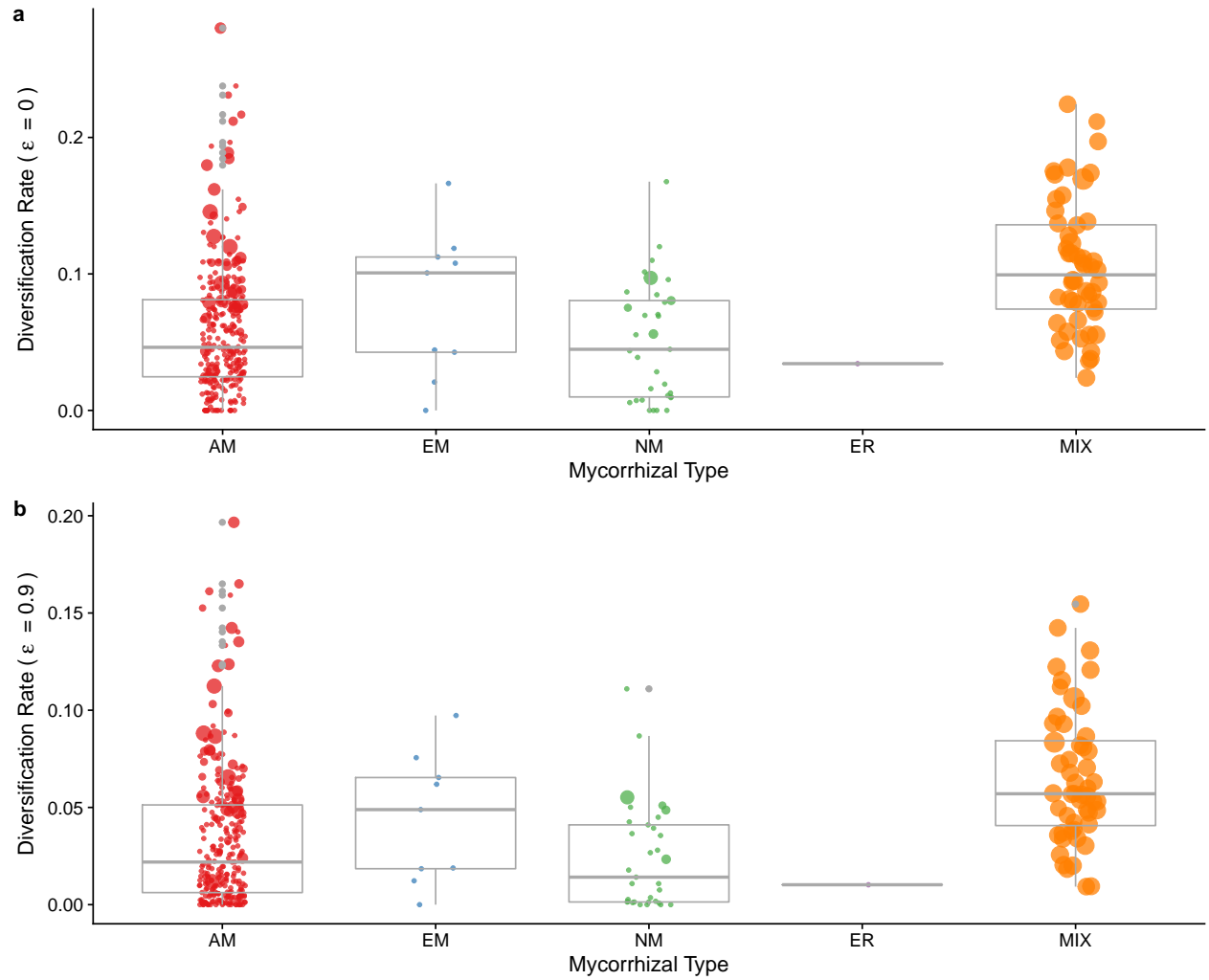


Figure 3: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with epsilon = 0 and b) diversification rate estimated with epsilon = 0.9. AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance of any specific mycorrhizal association). The size of the points indicates the Mycorrhizal Type Diversity Index value for each lineage, indicating a predominance of larger indices with higher diversification rates.

### 2.1.4 Threshold 100%

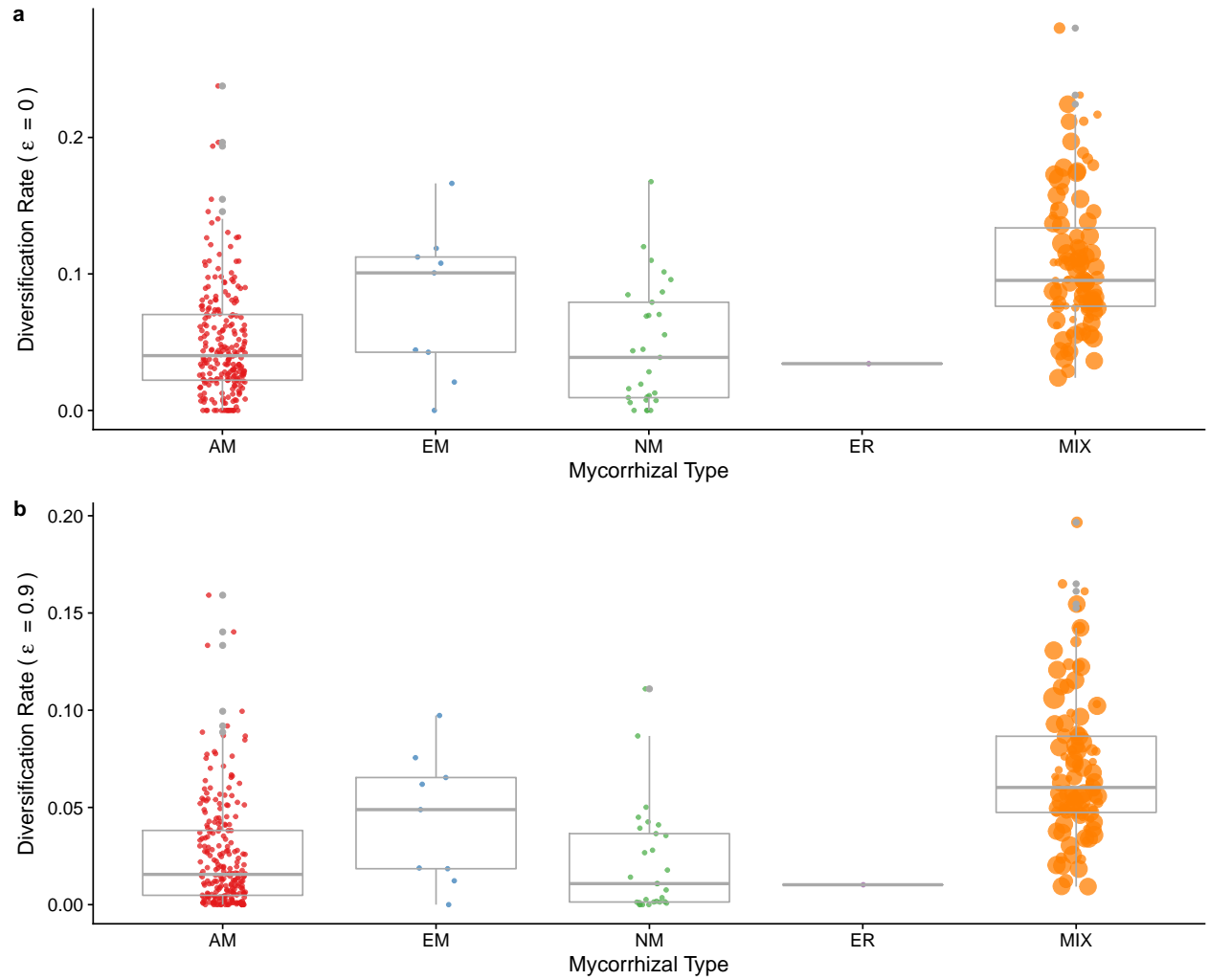


Figure 4: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with epsilon = 0 and b) diversification rate estimated with epsilon = 0.9. AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance of any specific mycorrhizal association). The size of the points indicates the Mycorrhizal Type Diversity Index value for each lineage, indicating a predominance of larger indices with higher diversification rates.

## 2.2 Summary statistics

### 2.2.1 phyANOVA

Table 2: Summary statistics for phyANOVA for both values of epsilon. Significant values are highlighted in bold.

Threshold	F.r0	pvalue.r0	F.r09	pvalue.r09
50	3.996	0.089	3.147	0.162
60	7.255	<b>0.013</b>	7.35	<b>0.007</b>
80	14.181	<b>0.001</b>	13.177	<b>0.001</b>
100	44.007	<b>0.001</b>	52.476	<b>0.001</b>

### 2.2.2 Standard ANOVA

Table 3: summary statistics for standard ANOVA for both values of epsilon. Significant values are highlighted in bold.

Threshold	F.r0	pvalue.r0	F.r09	pvalue.r09
50	3.996	<b>0.008</b>	3.147	<b>0.025</b>
60	7.255	<b>0</b>	7.35	<b>0</b>
80	14.181	<b>0</b>	13.177	<b>0</b>
100	44.007	<b>0</b>	52.476	<b>0</b>

## 2.3 Posthoc tests

### 2.3.1 phyANOVA

Table 4: Pairwise Corrected p-values for phyANOVA. Significant values are highlighted in bold.

Threshold	Mycorrhizal.Type	AM.r0	EM.r0	MIX.r0	NM.r0	AM.r09	EM.r09	MIX.r09	NM.r09
50	AM	1	0.858	<b>0.042</b>	0.747	1	1	<b>0.048</b>	1
50	EM	0.858	1	0.716	0.858	1	1	0.62	1
50	MIX	<b>0.042</b>	0.716	1	<b>0.042</b>	<b>0.048</b>	0.62	1	<b>0.048</b>
50	NM	0.747	0.858	<b>0.042</b>	1	1	1	<b>0.048</b>	1
60	AM	1	1	<b>0.006</b>	1	1	1	<b>0.006</b>	1
60	EM	1	1	1	1	1	1	0.952	1
60	MIX	<b>0.006</b>	1	1	<b>0.006</b>	<b>0.006</b>	0.952	1	<b>0.006</b>
60	NM	1	1	<b>0.006</b>	1	1	1	<b>0.006</b>	1
80	AM	1	1	<b>0.006</b>	1	1	1	<b>0.006</b>	1
80	EM	1	1	1	1	1	1	1	1
80	MIX	<b>0.006</b>	1	1	<b>0.006</b>	<b>0.006</b>	1	1	<b>0.006</b>
80	NM	1	1	<b>0.006</b>	1	1	1	<b>0.006</b>	1
100	AM	1	0.552	<b>0.006</b>	0.868	1	0.567	<b>0.006</b>	0.627
100	EM	0.552	1	0.552	0.552	0.567	1	0.468	0.567
100	MIX	<b>0.006</b>	0.552	1	<b>0.006</b>	<b>0.006</b>	0.468	1	<b>0.006</b>
100	NM	0.868	0.552	<b>0.006</b>	1	0.627	0.567	<b>0.006</b>	1

### 2.3.2 Standard ANOVA

Table 5: Pairwise Corrected p-values for standard ANOVA. Significant values are highlighted in bold.

Types	50.r0	60.r0	80.r0	100.r0	50.r09	60.r09	80.r09	100.r09
EM-AM	0.6181	6.86e-01	5.80e-01	1.54e-01	0.8536	8.66e-01	7.94e-01	0.2459
MIX-AM	<b>0.0175</b>	4.19e-05	8.91e-09	<b>0.00e+00</b>	<b>0.0253</b>	4.66e-05	7.23e-08	<b>0.0000</b>
NM-AM	0.3644	1.00e+00	7.83e-01	9.97e-01	0.6635	9.40e-01	4.56e-01	0.9239
MIX-EM	0.3148	4.92e-01	4.83e-01	2.51e-01	0.2476	3.30e-01	3.79e-01	0.0745
NM-EM	0.9704	7.53e-01	3.74e-01	1.98e-01	0.9934	7.65e-01	4.09e-01	0.1964
NM-MIX	0.0897	1.50e-03	4.83e-06	7.96e-10	0.0834	3.13e-04	1.98e-06	<b>0.0000</b>

## 2.4 Phylogenetic signal of diversification rates, age, and richness

Table 6: Phylogenetic signal of the four response variables.

Variable	Lambda
r.e0	0.475
r.e09	0.358
Stem.Age	1.000
Richness	0.000

### 3 Analysis per genera including all families

#### 3.1 Boxplots

##### 3.1.1 Threshold 50%

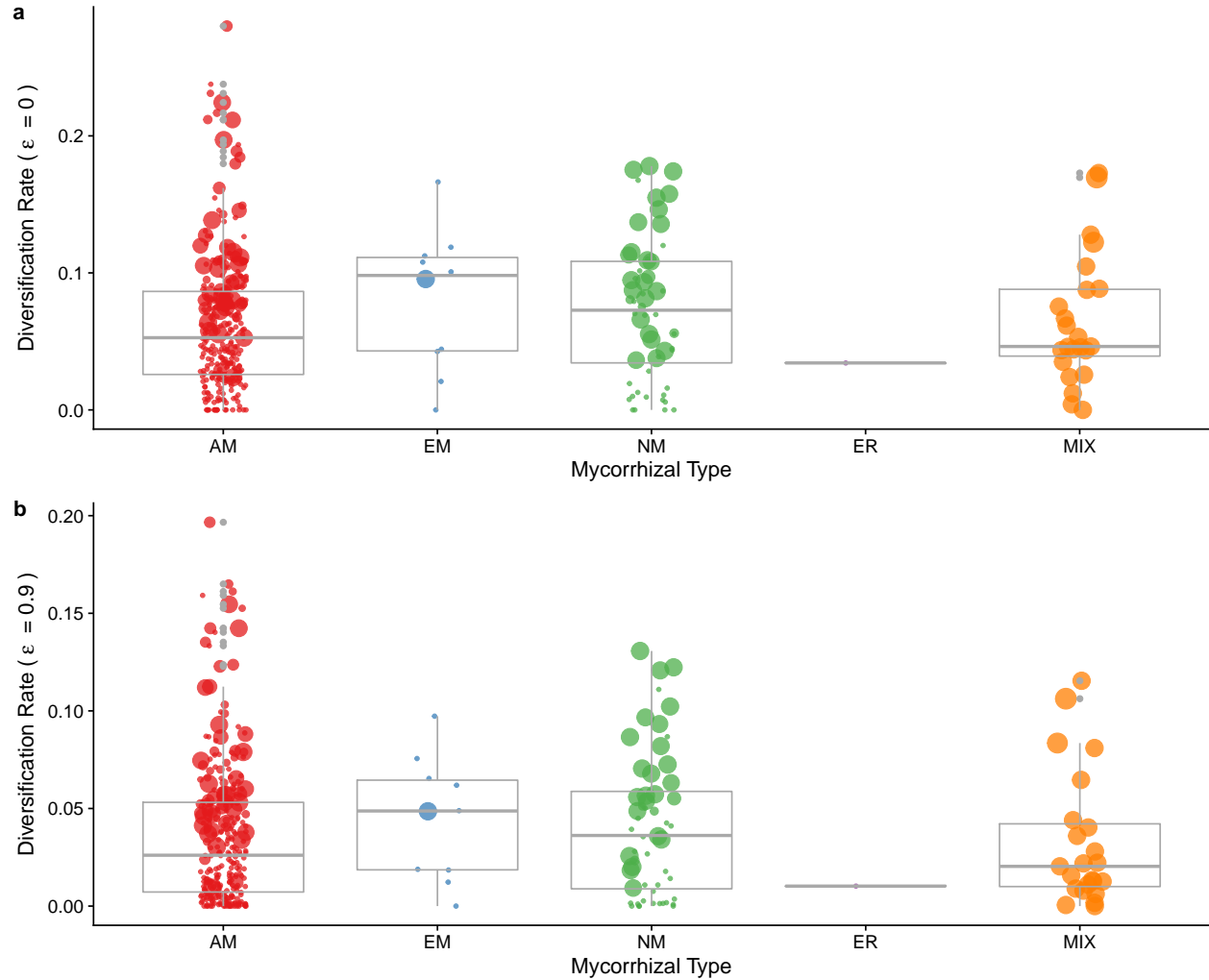


Figure 5: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with  $\epsilon = 0$  and b) diversification rate estimated with  $\epsilon = 0.9$ . AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance of any specific mycorrhizal association). The size of the points indicates the Mycorrhizal Type Diversity Index value for each lineage, indicating a predominance of larger indices with higher diversification rates.



### 3.1.2 Threshold 60%

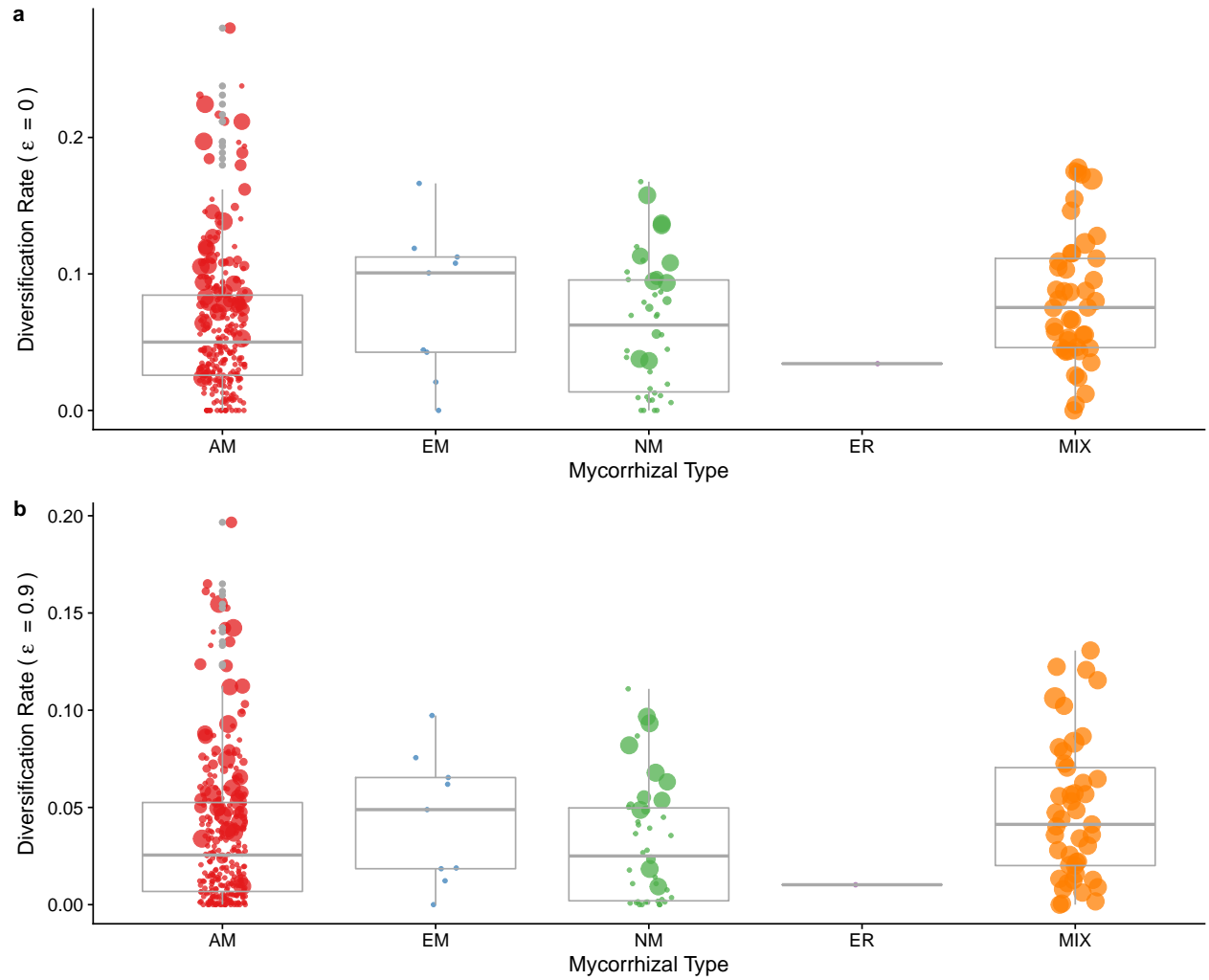


Figure 6: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with epsilon = 0 and b) diversification rate estimated with epsilon = 0.9. AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance of any specific mycorrhizal association). The size of the points indicates the Mycorrhizal Type Diversity Index value for each lineage, indicating a predominance of larger indices with higher diversification rates.

### 3.1.3 Threshold 80%

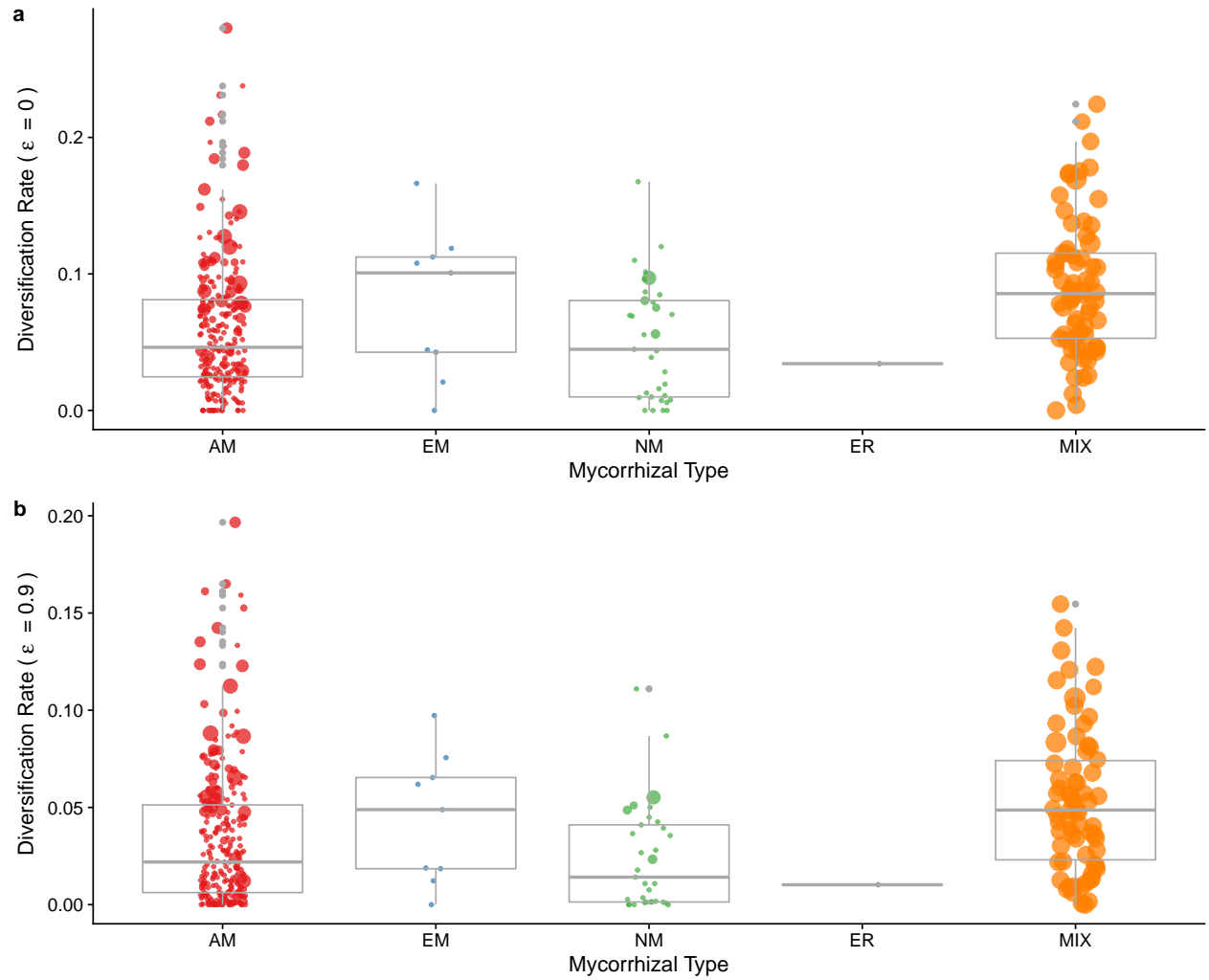


Figure 7: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with  $\epsilon = 0$  and b) diversification rate estimated with  $\epsilon = 0.9$ . AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance of any specific mycorrhizal association). The size of the points indicates the Mycorrhizal Type Diversity Index value for each lineage, indicating a predominance of larger indices with higher diversification rates.

### 3.1.4 Threshold 100%

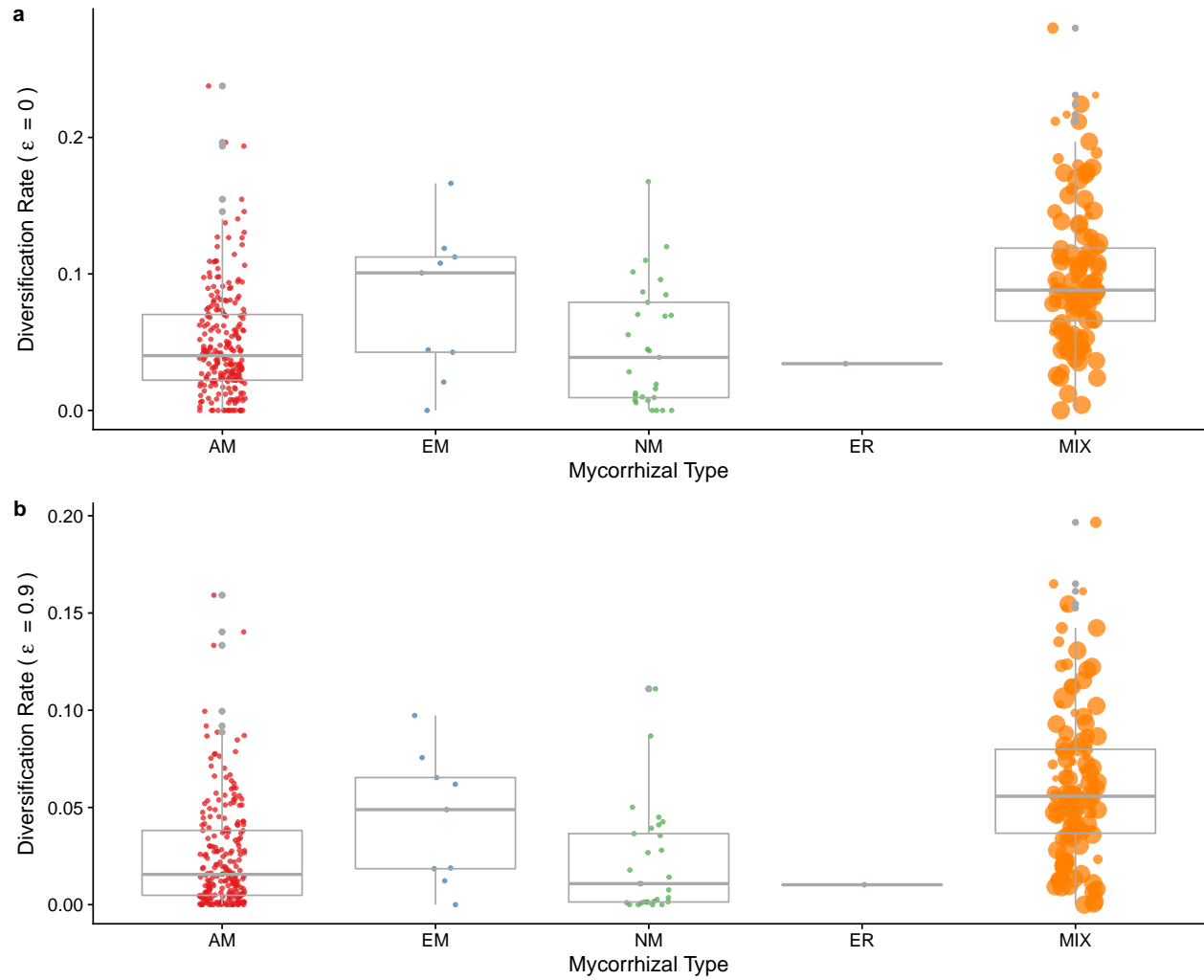


Figure 8: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with epsilon = 0 and b) diversification rate estimated with epsilon = 0.9. AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance of any specific mycorrhizal association). The size of the points indicates the Mycorrhizal Type Diversity Index value for each lineage, indicating a predominance of larger indices with higher diversification rates.

## 3.2 Summary statistics

### 3.2.1 phyANOVA

Table 7: summary statistics for phyANOVA for both values of epsilon. Significant values are highlighted in bold.

Threshold	F.r0	pvalue.r0	F.r09	pvalue.r09
50	1.295	0.631	0.696	0.825
60	2.842	0.244	2.153	0.402
80	8.598	<b>0.005</b>	7.033	<b>0.022</b>
100	33.621	<b>0.001</b>	37.429	<b>0.001</b>

### 3.2.2 Standard ANOVA

Table 8: summary statistics for standard ANOVA for both values of epsilon. Significant values are highlighted in bold.

Threshold	F.r0	pvalue.r0	F.r09	pvalue.r09
50	1.295	0.276	0.696	0.555
60	2.842	<b>0.038</b>	2.153	0.093
80	8.598	<b>0</b>	7.033	<b>0</b>
100	33.621	<b>0</b>	37.429	<b>0</b>

## 3.3 Posthoc tests

### 3.3.1 phyANOVA

Table 9: Pairwise Corrected p-values for phyANOVA. Significant values are highlighted in bold.

Threshold	Mycorrhizal.Type	AM.r0	EM.r0	MIX.r0	NM.r0	AM.r09	EM.r09	MIX.r09	NM.r09
50	AM	1	1	1	1	1	1	1	1
50	EM	1	1	1	1	1	1	1	1
50	MIX	1	1	1	1	1	1	1	1
50	NM	1	1	1	1	1	1	1	1
60	AM	1	1	0.355	1	1	1	0.665	1
60	EM	1	1	1	1	1	1	1	1
60	MIX	0.355	1	1	0.33	0.665	1	1	0.348
60	NM	1	1	0.33	1	1	1	0.348	1
80	AM	1	1	<b>0.01</b>	1	1	1	<b>0.03</b>	1
80	EM	1	1	1	1	1	1	1	1
80	MIX	<b>0.01</b>	1	1	<b>0.006</b>	<b>0.03</b>	1	1	<b>0.018</b>
80	NM	1	1	<b>0.006</b>	1	1	1	<b>0.018</b>	1
100	AM	1	0.64	<b>0.006</b>	0.878	1	0.796	<b>0.006</b>	0.796
100	EM	0.64	1	0.864	0.64	0.796	1	0.796	0.796
100	MIX	<b>0.006</b>	0.864	1	<b>0.006</b>	<b>0.006</b>	0.796	1	<b>0.006</b>
100	NM	0.878	0.64	<b>0.006</b>	1	0.796	0.796	<b>0.006</b>	1

### 3.3.2 Standard ANOVA

Table 10: Pairwise Corrected p-values for standard ANOVA. Significant values are highlighted in bold.

Pairs	50.r0	60.r0	80.r0	100.r0	50.r09	60.r09	80.r09	100.r09
EM.AM	0.616	0.689	5.87e-01	1.71e-01	0.852	0.869	0.799788	2.78e-01
MIX.AM	0.988	<b>0.032</b>	2.12e-05	<b>0.00e+00</b>	0.986	0.103	<b>0.000379</b>	<b>0.00e+00</b>
NM.AM	0.362	1.000	7.87e-01	9.97e-01	0.661	0.941	0.466891	9.31e-01
MIX.EM	0.833	0.998	9.37e-01	6.20e-01	0.815	0.991	0.909145	3.67e-01
NM.EM	0.970	0.755	3.82e-01	2.16e-01	0.993	0.769	0.419083	2.26e-01
NM.MIX	0.907	0.186	9.22e-04	2.98e-07	0.763	0.139	<b>0.000825</b>	8.54e-09

### 3.4 Scatterplots

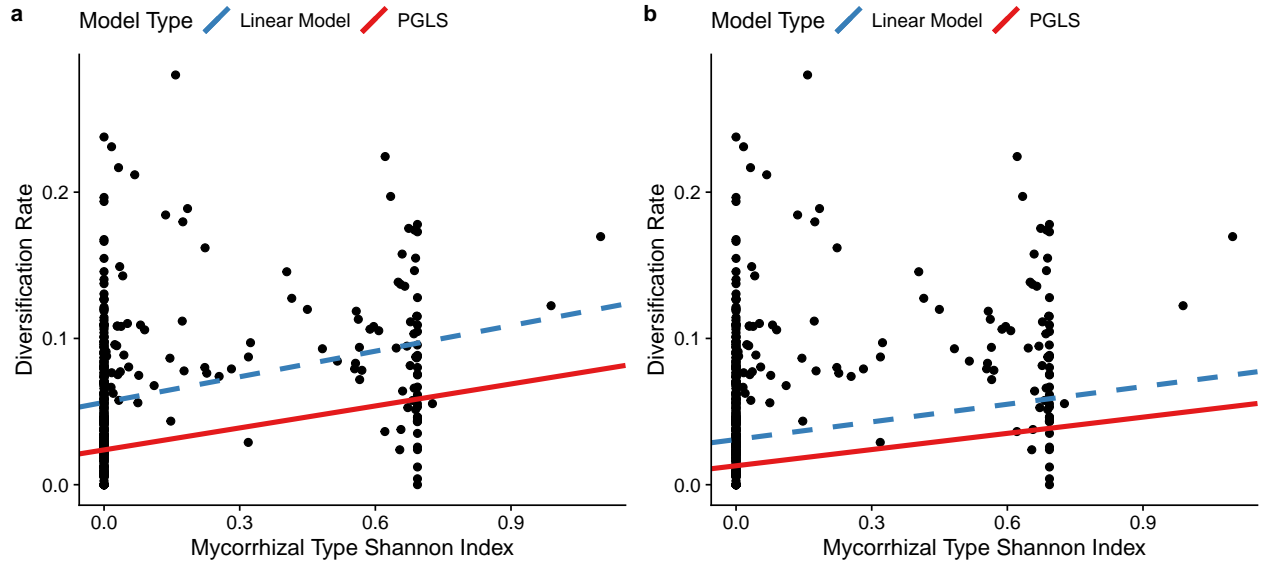


Figure 9: Scatterplots showing the relationship between mycorrhizal diversity index and diversification rates (a and c), species richness (b) and age family (d). Diversification rates were estimated with epsilon = 0 (a) and with epsilon = 0.9 (c). The red and blue lines indicate the results of a linear model and a phylogenetic generalized least squares (PGLS) fit, respectively.

Table 11: Summary statistics for the phylogenetic and parametric regressions using the full genus dataset. Significant values are highlighted in bold.

epsilon	pvalue.PGLS	R2.PGLS	pvalue.LM	R2.LM
0.0	<b>4.637e-08</b>	0.07343	<b>6.325e-10</b>	0.09319
0.9	<b>6.858e-08</b>	0.07157	<b>4.512e-09</b>	0.08402

## 4 Family classification based on different thresholds

Table 12: Mycorrhizal type assigned to each family based on 4 different percentage thresholds (50, 60, 80 and 100). Significant values are highlighted in bold.

Threshold	AM	EM	ER	MIX	NM
50	296	10	1	23	60
60	289	9	1	45	46
80	273	9	1	70	37
100	231	9	1	116	33

## 5 Species-level database

### 5.1 Clean database - excluding species with any remark

#### 5.1.1 Boxplots

##### 5.1.1.1 Threshold 50%

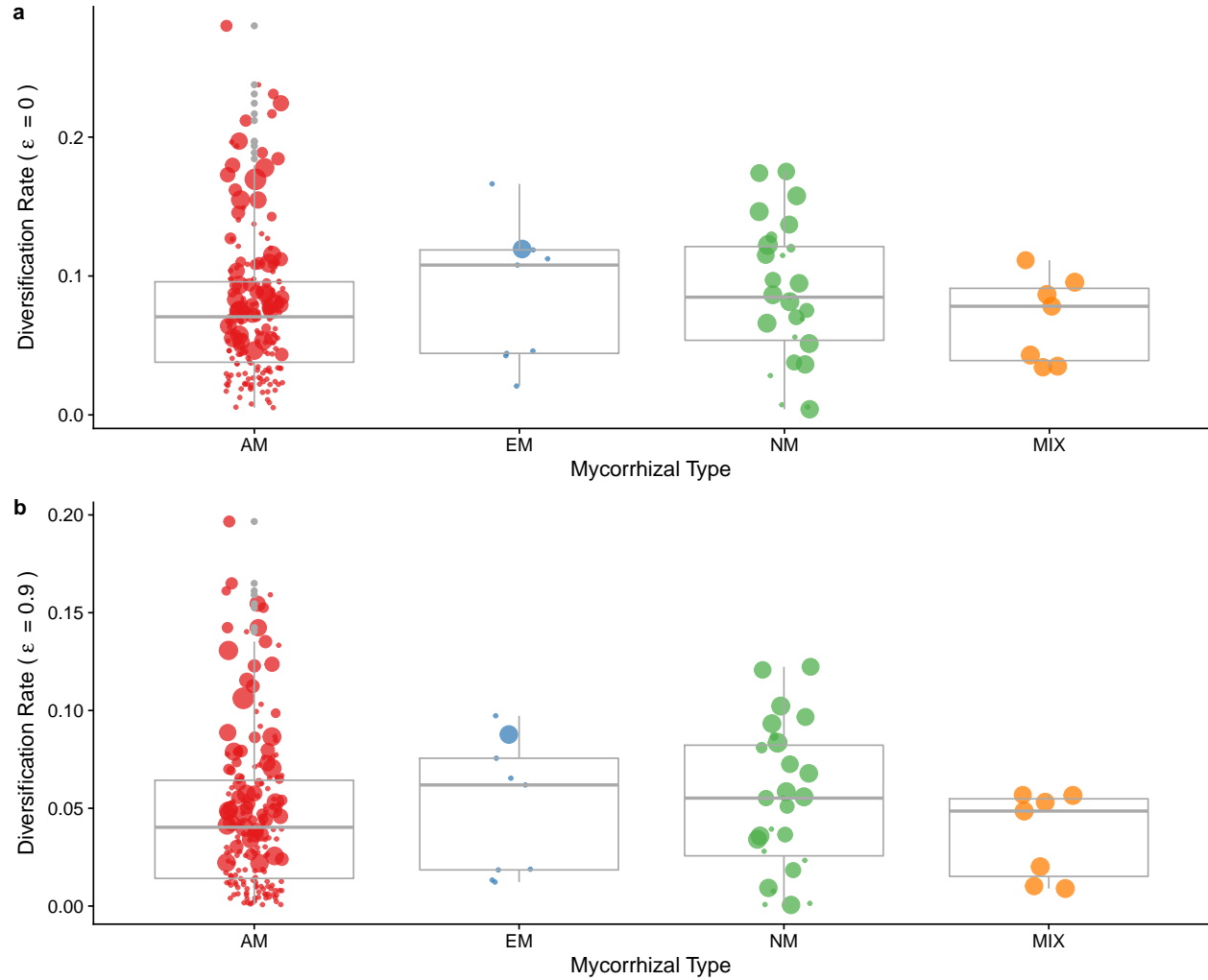


Figure 10: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with  $\epsilon = 0$  and b) diversification rate estimated with  $\epsilon = 0.9$ . AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance of any specific mycorrhizal association). The size of the points indicates the Mycorrhizal Type Diversity Index value for each lineage, indicating a predominance of larger indices with higher diversification rates.

### 5.1.1.2 Threshold 60%

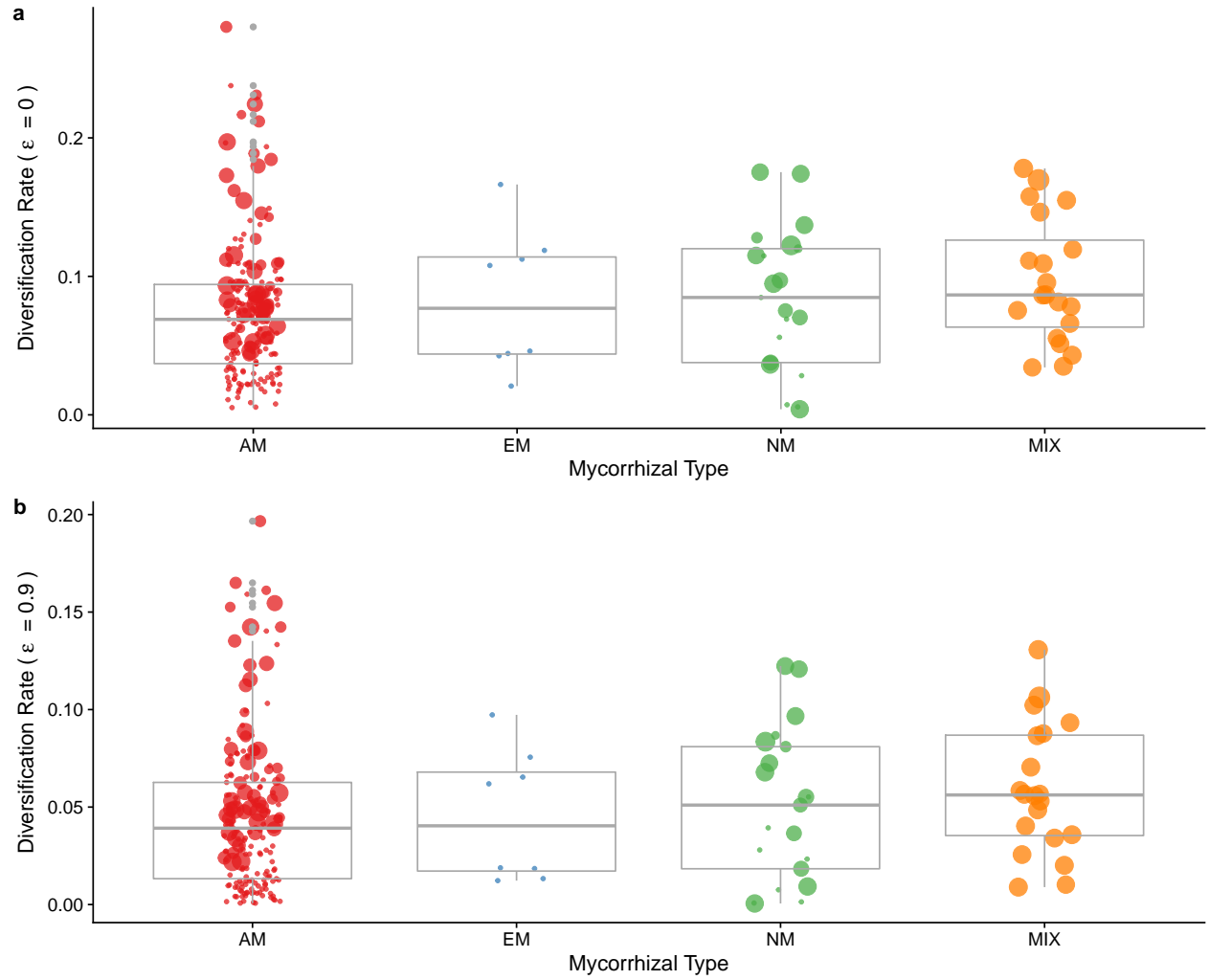


Figure 11: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with  $\epsilon = 0$  and b) diversification rate estimated with  $\epsilon = 0.9$ . AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance of any specific mycorrhizal association). The size of the points indicates the Mycorrhizal Type Diversity Index value for each lineage, indicating a predominance of larger indices with higher diversification rates.



### 5.1.1.3 Threshold 80%

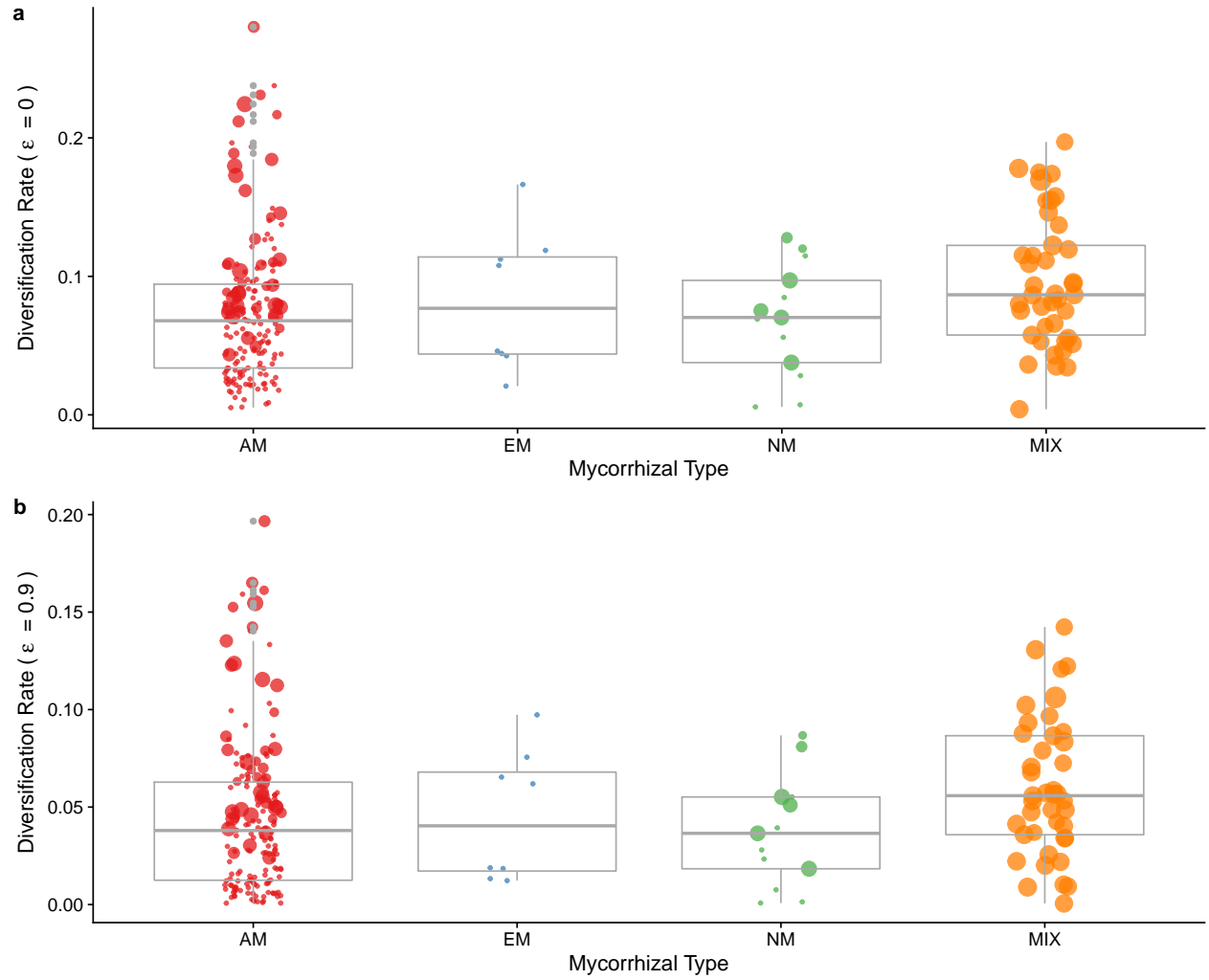


Figure 12: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with  $\epsilon = 0$  and b) diversification rate estimated with  $\epsilon = 0.9$ . AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance of any specific mycorrhizal association). The size of the points indicates the Mycorrhizal Type Diversity Index value for each lineage, indicating a predominance of larger indices with higher diversification rates.

#### 5.1.1.4 Threshold 100%

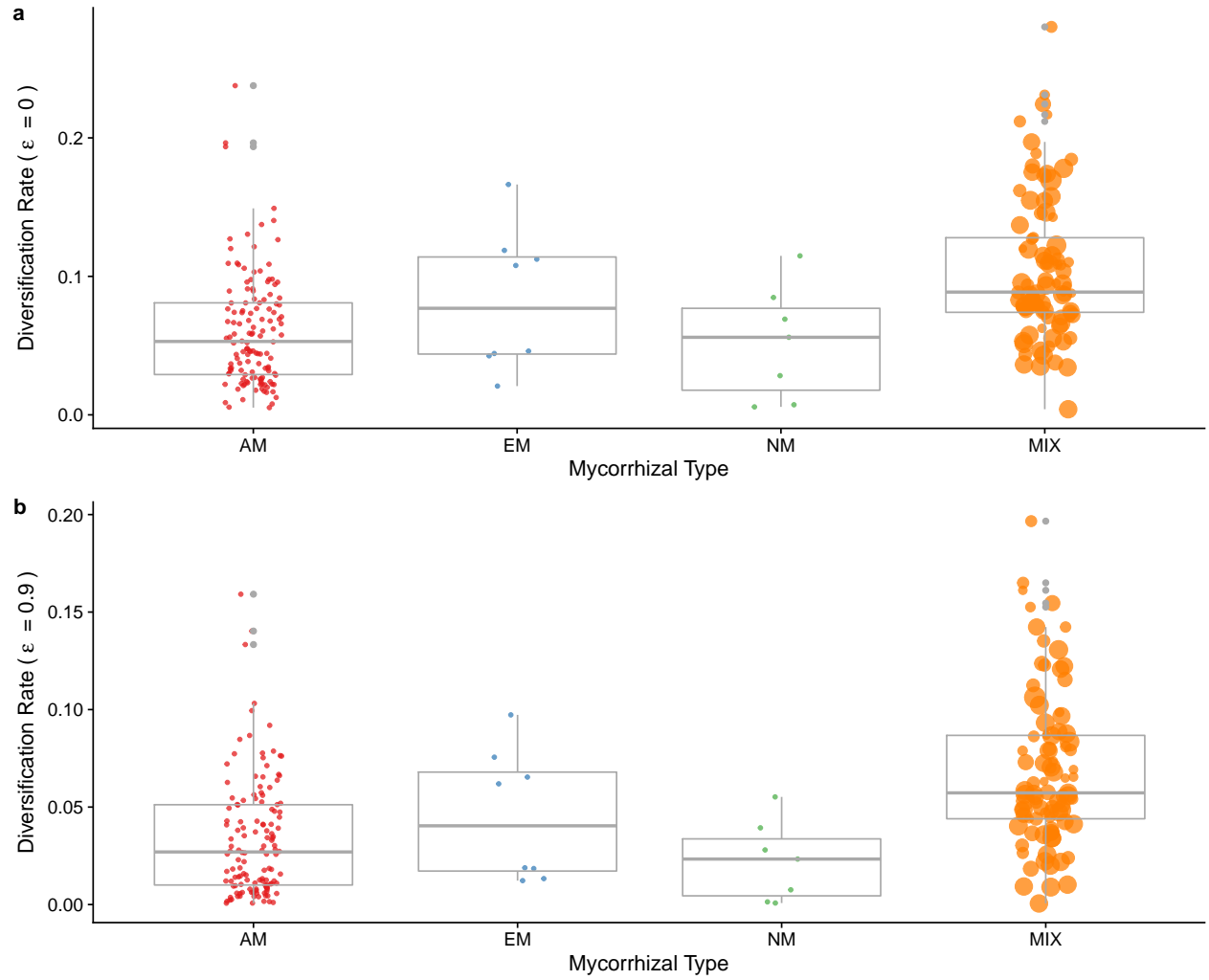


Figure 13: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with  $\epsilon = 0$  and b) diversification rate estimated with  $\epsilon = 0.9$ . AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance of any specific mycorrhizal association). The size of the points indicates the Mycorrhizal Type Diversity Index value for each lineage, indicating a predominance of larger indices with higher diversification rates.

## 5.2 Summary statistics

### 5.2.1 phyANOVA

Table 13: summary statistics for phyANOVA for both values of epsilon. Significant values are highlighted in bold.

Threshold	F.r0	pvalue.r0	F.r09	pvalue.r09
50	0.385	0.857	0.494	0.81
60	1.538	0.371	0.928	0.633
80	3.784	0.084	3.262	0.117
100	24.583	<b>0.001</b>	27.097	<b>0.001</b>

### 5.2.2 Standard ANOVA

Table 14: summary statistics for phyANOVA for both values of epsilon. Significant values are highlighted in bold.

Threshold	F.r0	pvalue.r0	F.r09	pvalue.r09
50	0.396	0.756	0.501	0.682
60	1.563	0.199	0.948	0.418
80	3.529	<b>0.015</b>	2.997	<b>0.031</b>
100	23.996	<b>0</b>	26.323	<b>0</b>

## 5.3 Posthoc tests

### 5.3.1 phyANOVA

Table 15: Pairwise Corrected p-values for phyANOVA. Significant values are highlighted in bold.

Threshold	Mycorrhizal.Type	AM.r0	EM.r0	MIX.r0	NM.r0	AM.r09	EM.r09	MIX.r09	NM.r09
50	AM	1	1	1	1	1	1	1	1
50	EM	1	1	1	1	1	1	1	1
50	MIX	1	1	1	1	1	1	1	1
50	NM	1	1	1	1	1	1	1	1
60	AM	1	1	0.264	1	1	1	0.69	1
60	EM	1	1	1	1	1	1	1	1
60	MIX	0.264	1	1	0.995	0.69	1	1	1
60	NM	1	1	0.995	1	1	1	1	1
80	AM	1	1	<b>0.036</b>	1	1	1	0.096	1
80	EM	1	1	1	1	1	1	1	1
80	MIX	<b>0.036</b>	1	1	0.1	0.096	1	1	0.096
80	NM	1	1	0.1	1	1	1	0.096	1
100	AM	1	0.726	<b>0.006</b>	0.726	1	0.747	<b>0.006</b>	0.747
100	EM	0.726	1	0.616	0.684	0.747	1	0.376	0.747
100	MIX	<b>0.006</b>	0.616	1	<b>0.006</b>	<b>0.006</b>	0.376	1	<b>0.006</b>
100	NM	0.726	0.684	<b>0.006</b>	1	0.747	0.747	<b>0.006</b>	1

### 5.3.2 Standard ANOVA

Table 16: Pairwise Corrected p-values for standard ANOVA. Significant values are highlighted in bold.

Types	50.r0	60.r0	80.r0	100.r0	50.r09	60.r09	80.r09	100.r09
EM.AM	0.964	0.992	0.9851	6.13e-01	0.993	1.000	1.0000	7.80e-01
MIX.AM	0.995	0.146	<b>0.0120</b>	1.75e-13	0.858	0.348	<b>0.0358</b>	1.22e-13
NM.AM	0.776	0.938	0.9112	8.08e-01	0.831	0.974	0.7779	6.26e-01
MIX.EM	0.954	0.769	0.7037	2.37e-01	0.866	0.768	0.6219	1.06e-01
NM.EM	1.000	1.000	0.8968	4.11e-01	0.996	0.993	0.9273	4.04e-01
NM.MIX	0.892	0.632	0.0896	3.04e-04	0.663	0.780	0.0810	5.05e-05

### 5.3.3 Scatterplots

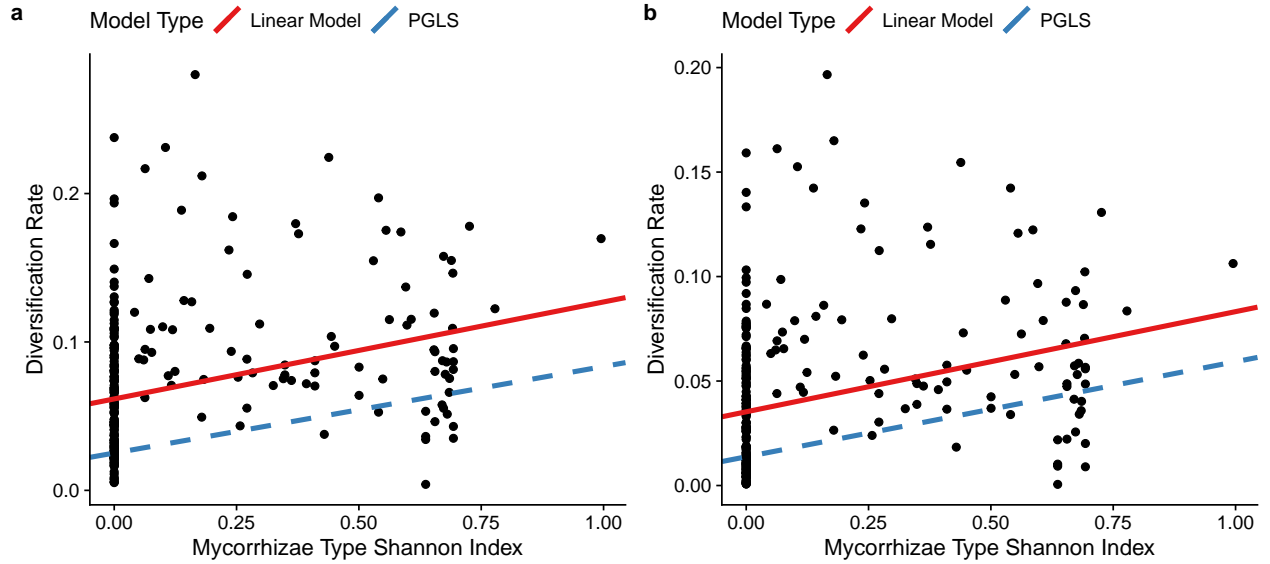


Figure 14: Scatterplots showing the relationship between mycorrhizal diversity index and diversification rates (a and c), species richness (b) and age family (d). Diversification rates were estimated with epsilon = 0 (a) and with epsilon = 0.9 (c). The red and blue lines indicate the results of a linear model and a phylogenetic generalized least squares (PGLS) fit, respectively.

Table 17: Summary statistics for the phylogenetic and parametric regressions using the full genus dataset. Significant values are highlighted in bold.

epsilon	pvalue.PGLS	R2.PGLS	pvalue.LM	R2.LM
0.0	<b>4.063e-07</b>	0.08904	<b>1.676e-07</b>	0.09458
0.9	<b>3.483e-07</b>	0.09007	<b>2.844e-07</b>	0.09109

## 5.4 More inclusive database - including species with any remark

### 5.4.1 Boxplots

#### 5.4.1.1 Threshold 50%

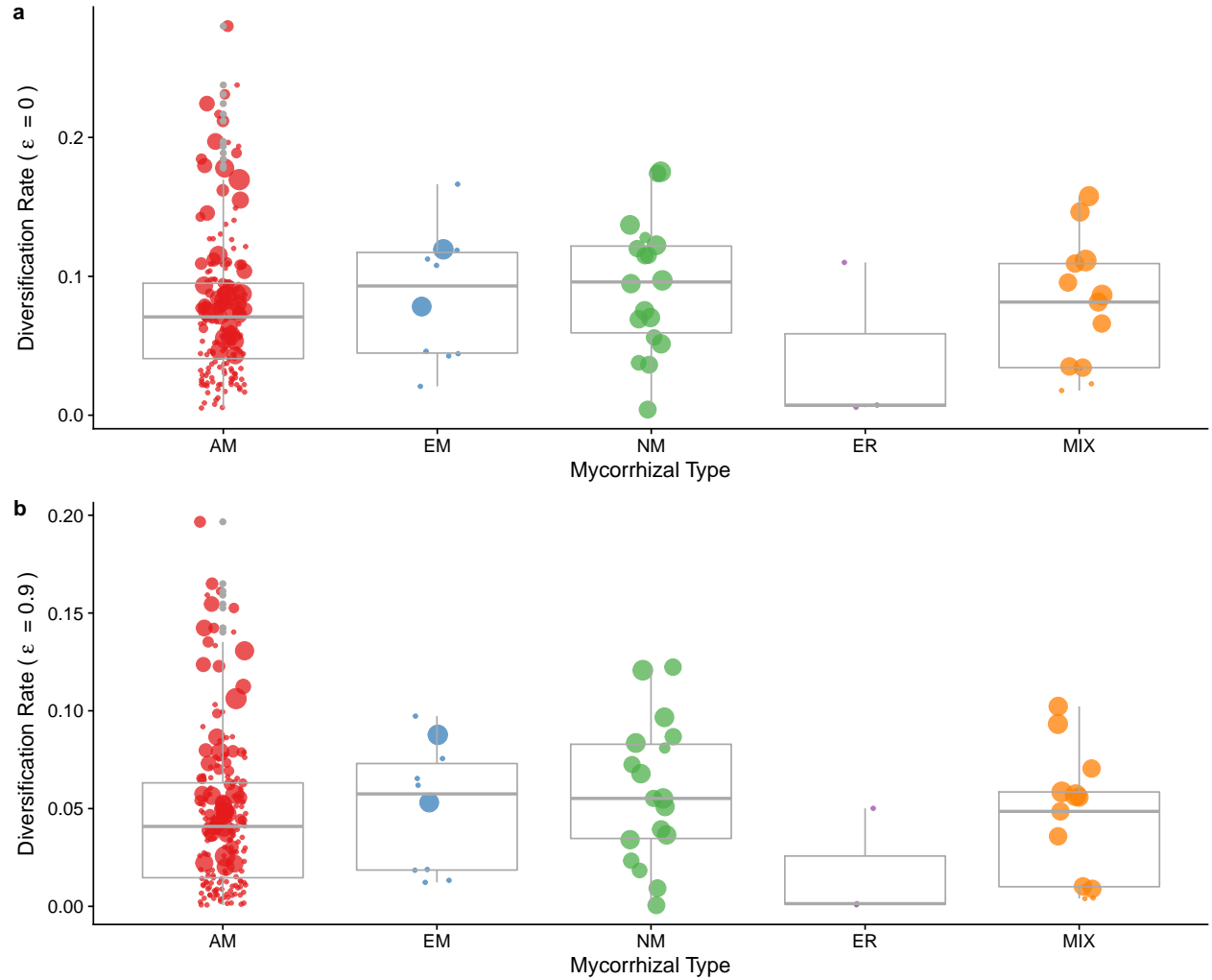


Figure 15: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with  $\epsilon = 0$  and b) diversification rate estimated with  $\epsilon = 0.9$ . AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance of any specific mycorrhizal association). The size of the points indicates the Mycorrhizal Type Diversity Index value for each lineage, indicating a predominance of larger indices with higher diversification rates.

#### 5.4.1.2 Threshold 60%

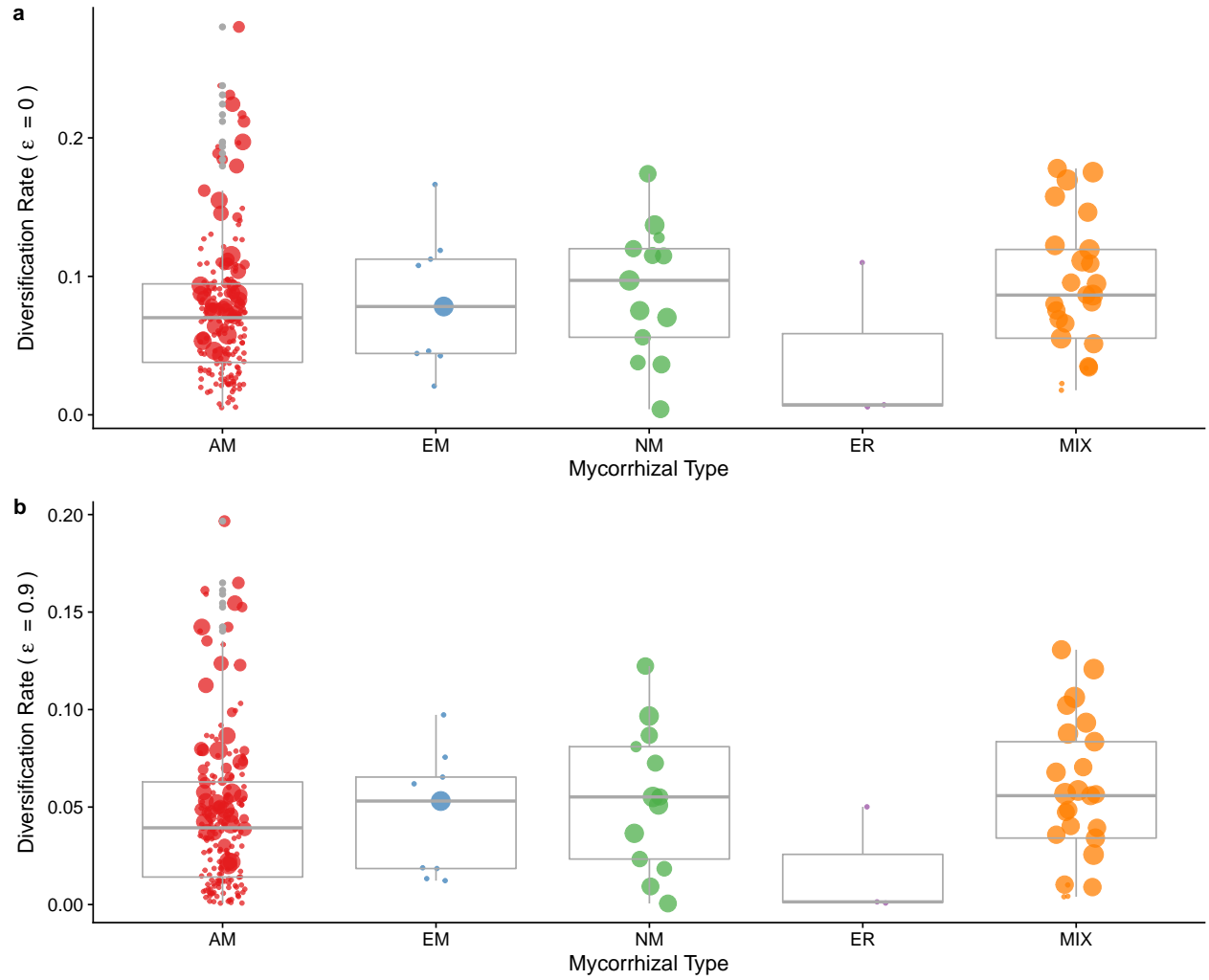


Figure 16: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with epsilon = 0 and b) diversification rate estimated with epsilon = 0.9. AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance of any specific mycorrhizal association). The size of the points indicates the Mycorrhizal Type Diversity Index value for each lineage, indicating a predominance of larger indices with higher diversification rates.

### 5.4.1.3 Threshold 80%

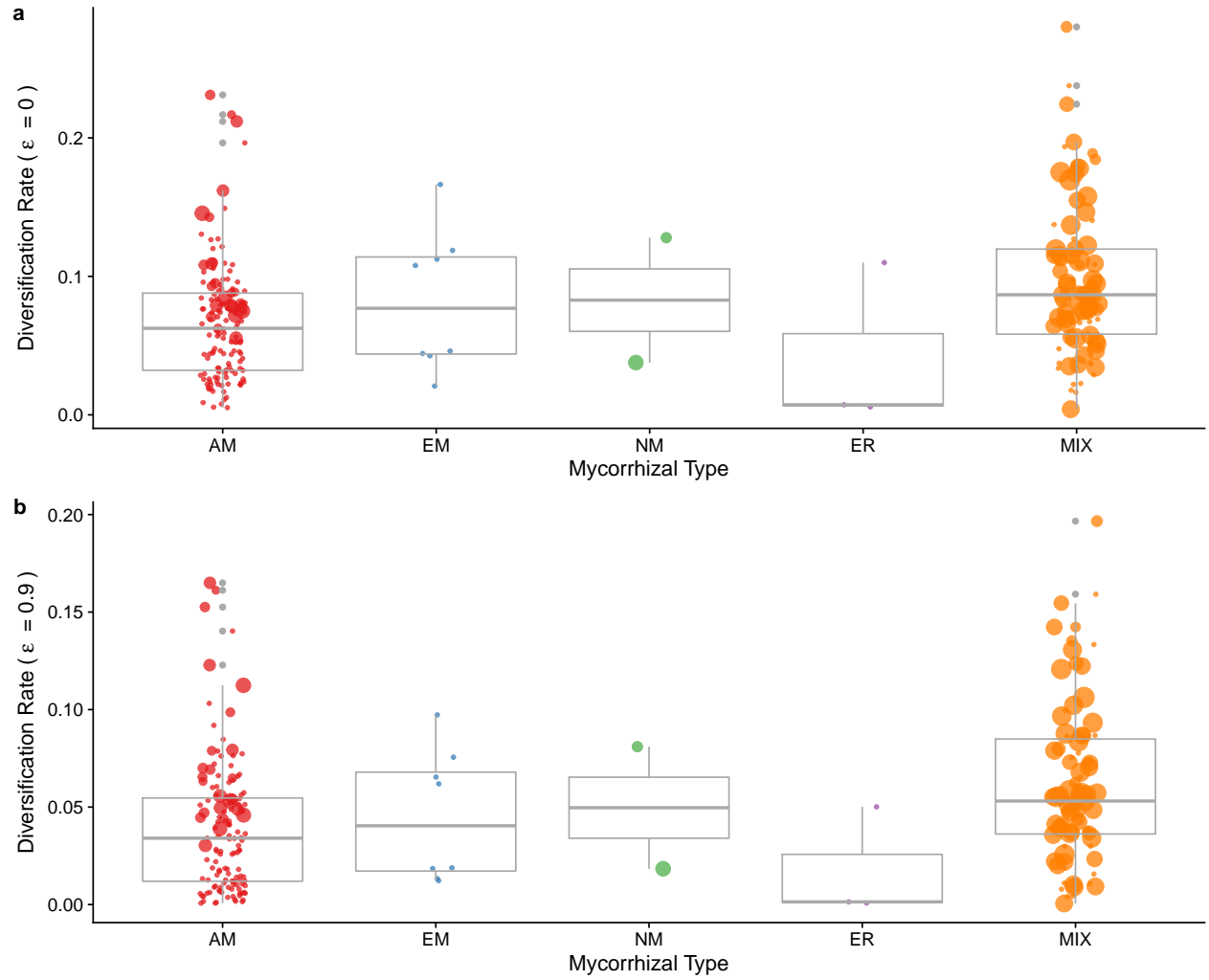


Figure 17: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with epsilon = 0 and b) diversification rate estimated with epsilon = 0.9. AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance of any specific mycorrhizal association). The size of the points indicates the Mycorrhizal Type Diversity Index value for each lineage, indicating a predominance of larger indices with higher diversification rates.

#### 5.4.1.4 Threshold 100%

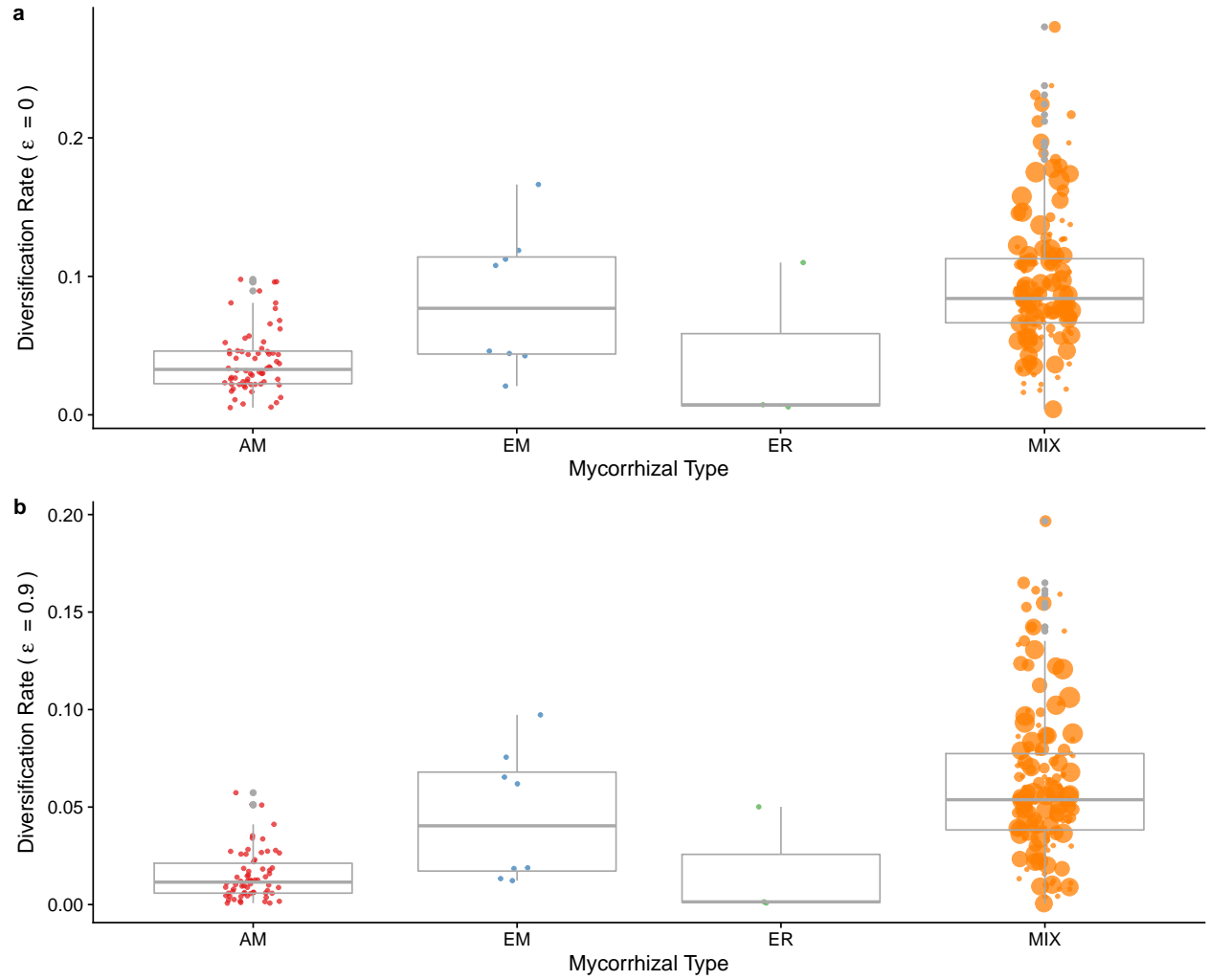


Figure 18: Relationship between mycorrhizal type and diversification rates. a) diversification rate estimated with  $\epsilon = 0$  and b) diversification rate estimated with  $\epsilon = 0.9$ . AM: Arbuscular mycorrhiza, EM: Ectomycorrhiza, NM: non-mycorrhizal and MIX (families with no dominance of any specific mycorrhizal association). The size of the points indicates the Mycorrhizal Type Diversity Index value for each lineage, indicating a predominance of larger indices with higher diversification rates.



## 5.5 Summary statistics

### 5.5.1 phyANOVA

Table 18: summary statistics for phyANOVA for both values of epsilon. Significant values are highlighted in bold.

Threshold	F.r0	pvalue.r0	F.r09	pvalue.r09
50	0.691	0.703	0.666	0.676
60	0.511	0.787	0.324	0.869
80	8.571	<b>0.001</b>	8.425	<b>0.001</b>
100	36.44	<b>0.001</b>	43.806	<b>0.001</b>

### 5.5.2 Standard ANOVA

Table 19: summary statistics for phyANOVA for both values of epsilon. Significant values are highlighted in bold.

Threshold	F.r0	pvalue.r0	F.r09	pvalue.r09
50	1.083	0.365	1.085	0.364
60	0.953	0.434	0.831	0.506
80	7.113	<b>0</b>	7.084	<b>0</b>
100	28.22	<b>0</b>	34.224	<b>0</b>

## 5.6 Posthoc tests

### 5.6.1 phyANOVA

Table 20: Pairwise Corrected p-values for phyANOVA. Significant values are highlighted in bold.

Threshold	Mycorrhizal.Type	AM.r0	EM.r0	MIX.r0	NM.r0	AM.r09	EM.r09	MIX.r09	NM.r09
50	AM	1	1	1	1	1	1	1	1
50	EM	1	1	1	1	1	1	1	1
50	MIX	1	1	1	0.918	1	1	1	0.924
50	NM	1	1	0.918	1	1	1	0.924	1
60	AM	1	1	1	1	1	1	1	1
60	EM	1	1	1	1	1	1	1	1
60	MIX	1	1	1	1	1	1	1	1
60	NM	1	1	1	1	1	1	1	1
80	AM	1	1	<b>0.006</b>	1	1	1	<b>0.006</b>	1
80	EM	1	1	1	1	1	1	1	1
80	MIX	<b>0.006</b>	1	1	0.255	<b>0.006</b>	1	1	0.145
80	NM	1	1	0.255	1	1	1	0.145	1
100	AM	1	0.18	<b>0.006</b>	0.922	1	0.2	<b>0.006</b>	0.742
100	EM	0.18	1	0.728	0.531	0.2	1	0.408	0.408
100	MIX	<b>0.006</b>	0.728	1	0.07	<b>0.006</b>	0.408	1	<b>0.015</b>
100	NM	0.922	0.531	0.07	1	0.742	0.408	<b>0.015</b>	1

### 5.6.2 Standard ANOVA

Table 21: Pairwise Corrected p-values for standard ANOVA. Significant values are highlighted in bold.

Types	50.r0	60.r0	80.r0	100.r0	50.r09
EM.AM	0.990633512621064	0.999066929741497	0.936868722793265	0.0668031153063937	0.998335123
ER.AM	0.59167799644029	0.620128699697407	0.807809909603096	0.999999925753053	0.562438984
MIX.AM	0.97044469654804	0.804996823389842	<b>9.60945215688902e-06</b>	<b>1.74860126378462e-13</b>	0.905942929
NM.AM	0.763273359186079	0.958094280569642	0.995627685586714	0.99997971946529	0.849762630
ER.EM	0.5610997307869	0.66332560965376	0.648683491922557	0.526651493003217	0.593050347
MIX.EM	0.936742971903572	0.995914486646062	0.778479187518824	0.674060482082851	0.928597622
NM.EM	0.997055565542504	0.999251070850478	0.934538146708019	0.582634773582996	0.995691997
MIX.ER	0.837524033937929	0.406862494515189	0.119528054154455	0.0500780239809808	0.869816527
NM.ER	0.351610960585478	0.50056469596149	0.979022885971943	0.999997287202152	0.367868322
NM.MIX	0.68358892614127	0.999943164896553	0.358349766894571	0.102452943553732	0.637221057

### 5.6.3 Scatterplots

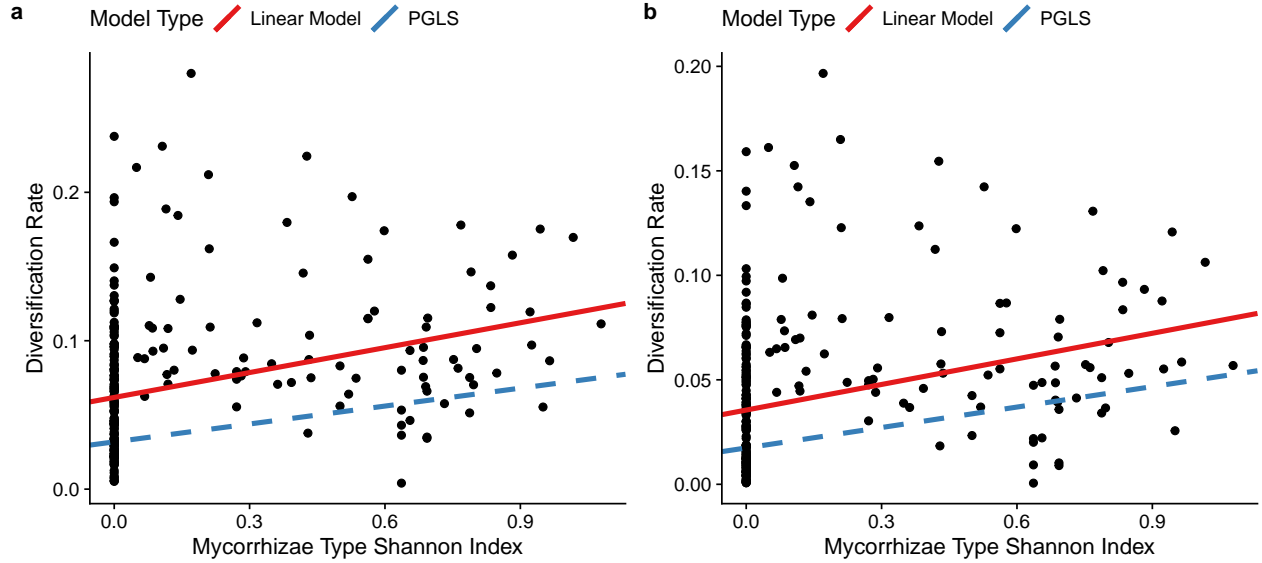


Figure 19: Scatterplots showing the relationship between mycorrhizal diversity index and diversification rates (a and c), species richness (b) and age family (d). Diversification rates were estimated with epsilon = 0 (a) and with epsilon = 0.9 (c). The red and blue lines indicate the results of a linear model and a phylogenetic generalized least squares (PGLS) fit, respectively.

Table 22: Summary statistics for the phylogenetic and parametric regressions using the full genus dataset. Significant values are highlighted in bold.

epsilon	pvalue.PGLS	R2.PGLS	pvalue.LM	R2.LM
0.0	<b>5.265e-05</b>	0.06444	<b>2.528e-07</b>	0.09354
0.9	<b>4.013e-05</b>	0.06653	<b>4.977e-07</b>	0.08898

## 6 Adding randomly 20% of misassignment of mycorrhizal type

### 6.1 Regressions

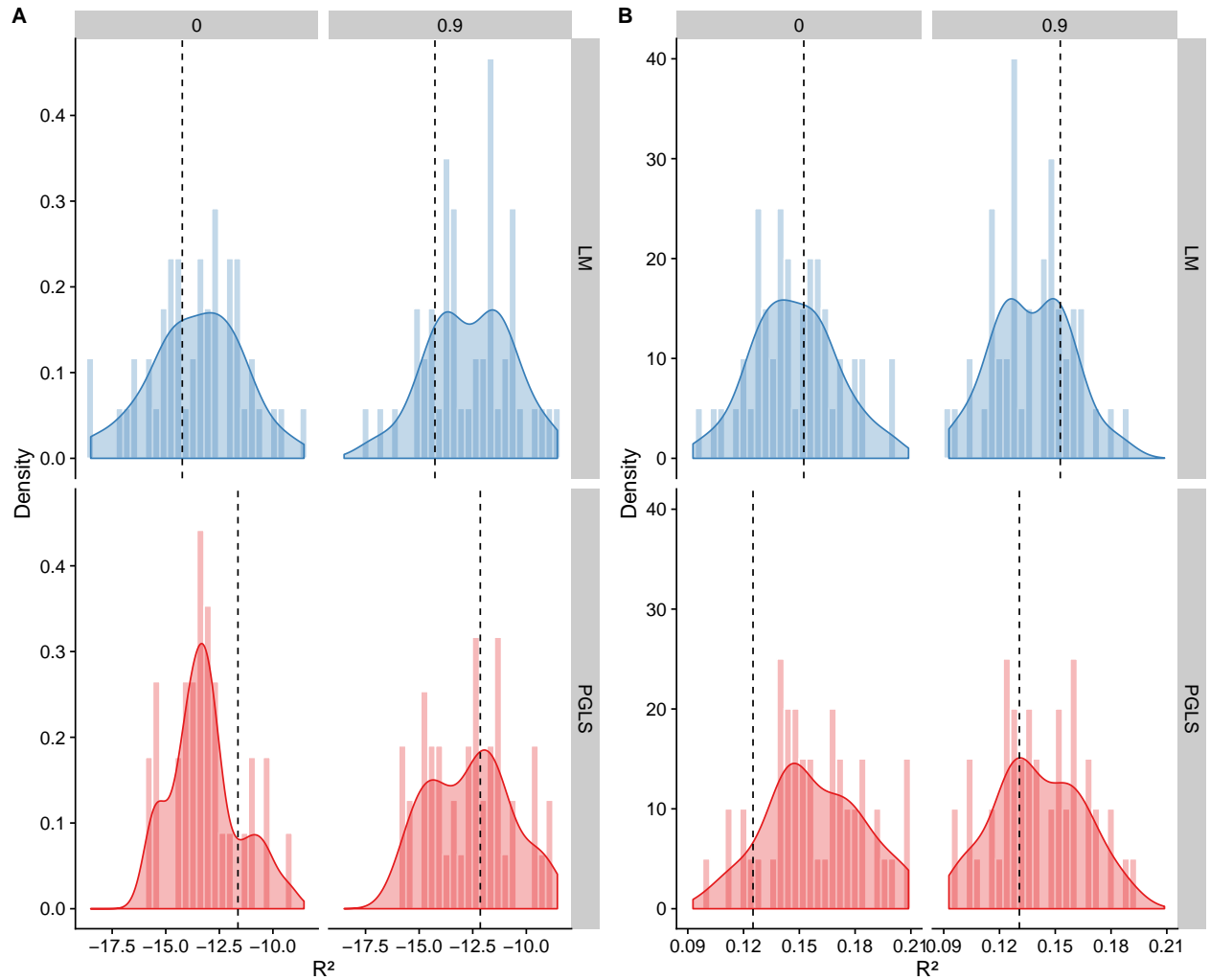


Figure 20: Distribution of (A) p-values and (B)  $R^2$  values for the same analyses of the main paper, but using all 50 replicate datasets with mycorrhizal types for 20% of species randomly sampled. Dashed vertical lines represent the corresponding empirical value from the main analysis.

## 6.2 ANOVAs

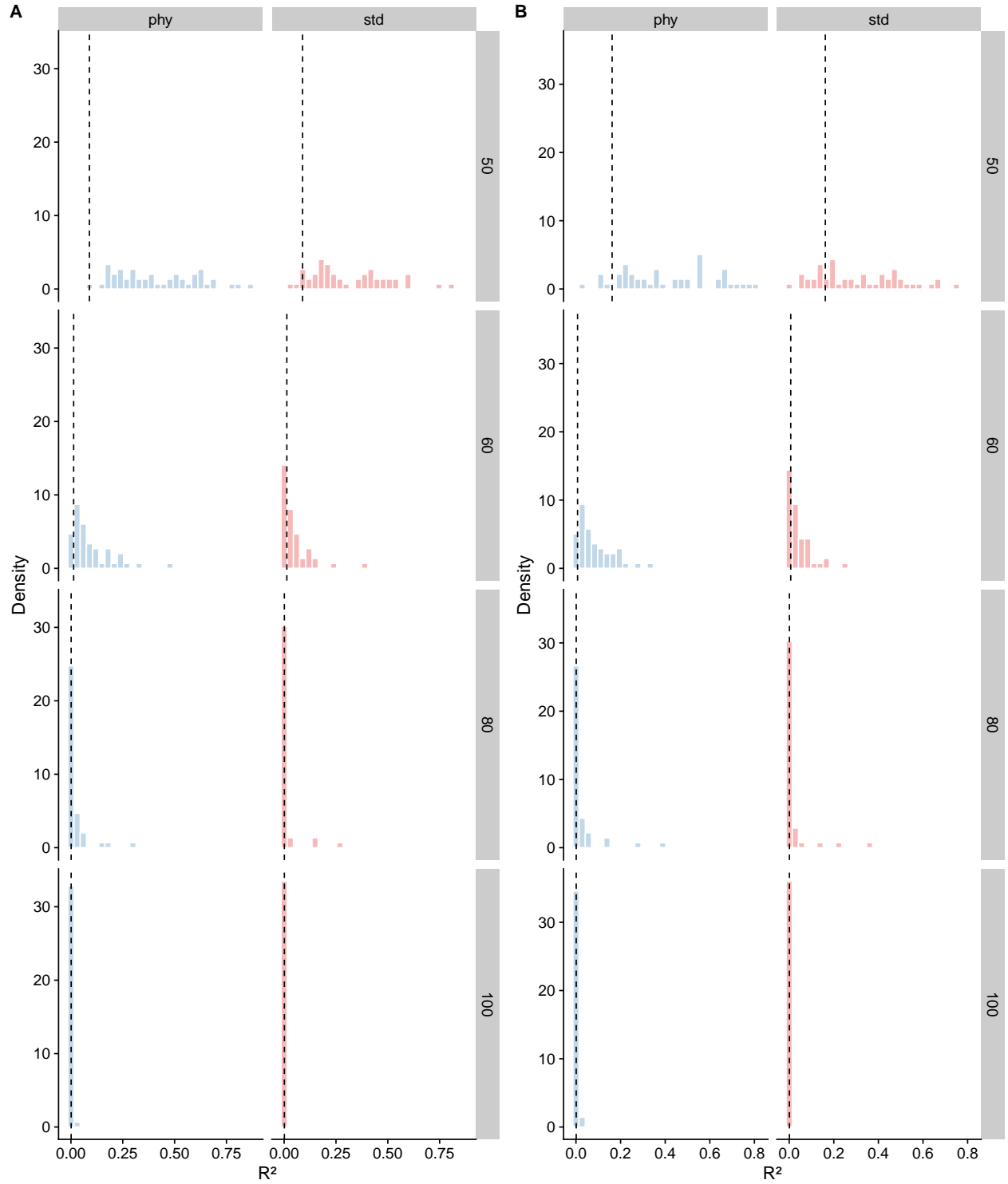


Figure 21: Distribution of p-values of (A) epsilon = 0 and (B) epsilon = 0.9 for the both phylogenetic and standard ANOVA, but using all 50 replicate datasets with mycorrhizal types for 20% of species randomly sampled. Dashed vertical lines represent the corresponding empirical value from the main analysis.