SUPPLEMENTAL MATERIAL

for

Conserving phylogenetic diversity can be a poor strategy for conserving functional diversity

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List of supplemental Materials

Type	α	r	# traits	# species	# selected species	Yule Tree FD ratio metric Mean	Sd	Yule Tree Phylo. Signal Mean	Sd	Coalescent Tree FD ratio metric Mean	Sd	Coalescent Tree Phylo. Signal Mean	Sd
BM			1	32	8	0.53	0.08	0.99	0.46	0.54	0.08	1	0.85
			1	64	8	0.53	0.09	0.98	0.43	0.54	0.09	1.04	0.93
			1	32	16	0.51	0.05	1.01	0.48	0.52	0.05	0.97	0.78
			1	64	16	0.52	0.06	1	0.41	0.53	0.05	1.02	0.96
			2	32	8	0.56	0.12	0.99	0.34	0.6	0.12	0.99	0.59
			2	64	8	0.55	0.13	1	0.31	0.6	0.12	1.01	0.64
			2	32	16	0.53	0.07	0.97	0.31	0.55	0.06	1	0.57
			2	64	16	0.54	0.08	1	0.28	0.56	0.08	0.98	0.61
			4	32	8	0.63	0.18	1	0.24	0.73	0.16	0.99	0.42
			4	64	8	0.61	0.19	1	0.21	0.74	0.17	1.01	0.45
			4	32	16	0.58	0.09	1	0.24	0.62	0.1	1	0.42
			4	64	16	0.59	0.11	1	0.21	0.66	0.11	0.97	0.41
EB		-5	1	32	8	0.56	0.09	3.42	1.91	0.55	0.1	6.56	4.7
		-5	1	64	8	0.55	0.09	4.32	2.51	0.56	0.11	9.18	7.36
		-5	1	32	16	0.52	0.05	3.37	1.86	0.52	0.06	6.6	4.69
		-5	1	64	16	0.54	0.06	4.28	2.56	0.53	0.07	8.86	7.37
		-1	1	32	8	0.53	0.08	1.3	0.65	0.54	0.08	1.44	1.25
		-1	1	64	8	0.53	0.09	1.34	0.62	0.55	0.09	1.52	1.33
		-1	1	32	16	0.52	0.05	1.31	0.68	0.52	0.04	1.42	1.29
		-1	1	64	16	0.52	0.05	1.34	0.64	0.53	0.06	1.54	1.4
		-5	2	32	8	0.62	0.12	3.35	1.35	0.63	0.14	6.57	3.58
		-5	2	64	8	0.62	0.13	4.33	1.83	0.66	0.15	9.32	5.55
		-5	2	32	16	0.56	0.08	3.22	1.25	0.56	0.09	6.69	3.54
		-5	2	64	16	0.58	0.08	4.26	1.84	0.58	0.1	9.33	5.58
		-1	2	32	8	0.57	0.12	1.29	0.45	0.6	0.12	1.44	0.94
		-1	2	64	8	0.57	0.12	1.33	0.43	0.61	0.13	1.52	1.01
		-1	2	32	16	0.54	0.07	1.28	0.44	0.55	0.07	1.4	0.9
		-1	2	64	16	0.55	0.08	1.32	0.45	0.57	0.08	1.5	0.95
		-5	4	32	8	0.77	0.16	3.36	1.1	0.79	0.17	6.45	2.61
		-5	4	64	8	0.77	0.16	4.23	1.36	0.82	0.16	9.23	4.17
		-5	4	32	16	0.65	0.11	3.35	1.08	0.65	0.12	6.24	2.52
		-5	4	64	16	0.69	0.12	4.4	1.54	0.69	0.13	9.42	4.09
		-1	4	32	8	0.67	0.17	1.28	0.33	0.73	0.17	1.42	0.62
		-1	4	64	8	0.65	0.17	1.34	0.35	0.74	0.17	1.49	0.67
		-1	4	32	16	0.6	0.09	1.28	0.33	0.62	0.1	1.41	0.64
		-1	4	64	16	0.62	0.11	1.33	0.31	0.67	0.11	1.44	0.66
OU	1.4	0	1	32	8	0.51	0.09	0.6	0.21	0.53	0.08	0.47	0.33
	1.4	0	1	64	8	0.51	0.09	0.54	0.16	0.54	0.09	0.44	0.3
	1.4	0	1	32	16	0.51	0.05	0.59	0.23	0.52	0.04	0.46	0.3
	1.4	0	1	64	16	0.51	0.06	0.54	0.16	0.52	0.05	0.45	0.3
	7	0	1	32	8	0.5	0.09	0.28	0.1	0.51	0.09	0.17	0.08
	7	0	1	64	8	0.51	0.1	0.24	0.06	0.52	0.09	0.14	0.06
	7	0	1	32	16	0.5	0.05	0.28	0.1	0.52	0.05	0.17	0.07
	7	0	1	64	16	0.5	0.07	0.24	0.06	0.51	0.06	0.14	0.06
	1.4	0	2	32	8	0.53	0.12	0.59	0.16	0.57	0.12	0.47	0.23
	1.4	0	2	64	8	0.53	0.13	0.53	0.12	0.59	0.13	0.45	0.22
	1.4	0	2	32	16	0.52	0.07	0.58	0.16	0.54	0.06	0.47	0.23
	1.4	0	2	64	16	0.52	0.08	0.54	0.12	0.56	0.08	0.43	0.2
	7	0	2	32	8	0.51	0.13	0.28	0.08	0.54	0.13	0.16	0.06
	7	0	2	64	8	0.51	0.13	0.24	0.04	0.55	0.13	0.14	0.04
	7	0	2	32	16	0.51	0.07	0.28	0.07	0.53	0.06	0.17	0.06
	7	0	2	64	16	0.51	0.09	0.24	0.05	0.54	0.08	0.14	0.04
	1.4	0	4	32	8	0.57	0.18	0.58	0.11	0.69	0.17	0.48	0.17
	1.4	0	4	64	8	0.56	0.2	0.54	0.08	0.7	0.17	0.45	0.16
	1.4	0	4	32	16	0.56	0.1	0.59	0.11	0.61	0.09	0.48	0.17
	1.4	0	4	64	16	0.55	0.11	0.55	0.09	0.64	0.11	0.44	0.15
	7	0	4	32	8	0.52	0.19	0.28	0.06	0.6	0.19	0.17	0.04
	7	0	4	64	8	0.51	0.2	0.23	0.03	0.59	0.19	0.14	0.03
	7	0	4	32	16	0.51	0.1	0.28	0.06	0.58	0.1	0.17	0.04
	7	0	4	64	16	0.52	0.12	0.23	0.03	0.59	0.11	0.14	0.03

Supplemental Table 1. For common trait macroevolution models, sets of species that maximize PD always harbour, on average, at least as much FD (Convex hull measure) as random sets of species of the same size. The table presents, for each combination of macroevolutionnary models (column 1), specific set of parameters (column 2-3), number of independent traits (column 4), tree size (column 5) and number of selected species (column 6) a measure of the relative amount of FD between PD_{max} and random sets of species for pure birth Yule trees (column 7-8) and coalescent trees (column 11-12).The comparison of FD (<u>as measured by the convex hull measure</u>) between the two sets of species is quantified with the following metric: $FD_{maxPD}/(FD_{Randome} + FD_{maxPD})$. A value <.5 means PD is doing worse than random, a value >.5 means PD is doing better than random and a value of .5 means PD is doing the same as random. The phylogenetic signal for Yule trees (column 9-10) and coalescent trees (column 13-14) is measured with the Bloomberg K (for multiple traits, the mean across traits is given). All statistics are based on 1000 simulations in each case.

Evolutionary Model			Traits and Species			Type of Trees							
						Yule Tree				Coalescent Tree			
						FD ratio metric		Phylo. Signal		FD ratio metric		Phylo. Signal	
Type	α	r	# traits	# species	# selected species	Mean	Sd	Mean	Sd	Mean	Sd	Mean	Sd
BM	0	0	1	32	8	0.54	0.15	0.99	0.46	0.57	0.15	1	0.85
BM	0	0	1	64	8	0.55	0.16	0.98	0.43	0.57	0.15	1.04	0.93
BM	0	0	1	32	16	0.52	0.08	1.01	0.48	0.52	0.09	0.97	0.78
BM	0	0	1	64	16	0.52	0.1	1	0.41	0.54	0.1	1.02	0.96
BM	0	0	2	32	8	0.54	0.11	0.99	0.34	0.57	0.11	0.99	0.59
BM	0	0	2	64	8	0.54	0.12	1	0.31	0.56	0.12	1.01	0.64
BM	0	0	2	32	16	0.52	0.06	0.97	0.31	0.52	0.06	1	0.57
BM	0	0	2	64	16	0.53	0.07	1	0.28	0.54	0.08	0.98	0.61
BM	0	0	4	32	8	0.54	0.08	1	0.24	0.56	0.08	0.99	0.42
BM	0	0	4	64	8	0.54	0.08	1	0.21	0.57	0.09	1.01	0.45
BM	0	0	4	32	16	0.52	0.04	1	0.24	0.53	0.05	1	0.42
BM	0	0	4	64	16	0.52	0.05	1	0.21	0.54	0.06	0.97	0.41
EB	0	-5	1	32	8	0.59	0.15	3.42	1.91	0.57	0.16	6.56	4.7
EB	0	-5	1	64	8	0.58	0.16	4.32	2.51	0.59	0.18	9.18	7.36
EB	0	-5	1	32	16	0.53	0.09	3.37	1.86	0.53	0.1	6.6	4.69
EB	0	-5	1	64	16	0.55	0.11	4.28	2.56	0.55	0.12	8.86	7.37
EB	0	-1	1	32	8	0.55	0.14	1.3	0.65	0.57	0.14	1.44	1.25
EB	0	-1	1	64	8	0.54	0.16	1.34	0.62	0.57	0.15	1.52	1.33
EB	0	-1	1	32	16	0.52	0.08	1.31	0.68	0.52	0.09	1.42	1.29
EB	0	-1	1	64	16	0.52	0.1	1.34	0.64	0.53	0.11	1.54	1.4
EB	0	-5	2	32	8	0.58	0.12	3.35	1.35	0.58	0.14	6.57	3.58
EB	0	-5	2	64	8	0.58	0.12	4.33	1.83	0.6	0.15	9.32	5.55
EB	0	-5	2	32	16	0.54	0.07	3.22	1.25	0.53	0.09	6.69	3.54
EB	0	-5	2	64	16	0.54	0.08	4.26	1.84	0.54	0.11	9.33	5.58
EB	0	-1	2	32	8	0.55	0.11	1.29	0.45	0.57	0.12	1.44	0.94
EB	0	-1	2	64	8	0.55	0.11	1.33	0.43	0.57	0.12	1.52	1.01
EB	0	-1	2	32	16	0.52	0.06	1.28	0.44	0.53	0.07	1.4	0.9
EB	0	-1	2	64	16	0.53	0.07	1.32	0.45	0.54	0.08	1.5	0.95
EB	0	-5	4	32	8	0.58	0.1	3.36	1.1	0.58	0.13	6.45	2.61
EB	0	-5	4	64	8	0.59	0.1	4.23	1.36	0.59	0.14	9.23	4.17
EB	0	-5	4	32	16	0.53	0.06	3.35	1.08	0.53	0.08	6.24	2.52
EB	0	-5	4	64	16	0.55	0.07	4.4	1.54	0.55	0.1	9.42	4.09
EB	0	-1	4	32	8	0.55	0.08	1.28	0.33	0.57	0.1	1.42	0.62
EB	0	-1	4	64	8	0.55	0.08	1.34	0.35	0.57	0.1	1.49	0.67
EB	0	-1	4	32	16	0.52	0.05	1.28	0.33	0.53	0.06	1.41	0.64
EB	0	-1	4	64	16	0.53	0.05	1.33	0.31	0.54	0.07	1.44	0.66
OU	1.4	0	1	32	8	0.52	0.15	0.6	0.21	0.56	0.14	0.47	0.33
OU	1.4	0	1	64	8	0.52	0.16	0.54	0.16	0.56	0.16	0.44	0.3
OU	1.4	0	1	32	16	0.52	0.09	0.59	0.23	0.53	0.08	0.46	0.3
OU	1.4	0	1	64	16	0.52	0.11	0.54	0.16	0.53	0.1	0.45	0.3
OU	7	0	1	32	8	0.51	0.16	0.28	0.1	0.52	0.16	0.17	0.08
OU	7	0	1	64	8	0.51	0.17	0.24	0.06	0.53	0.16	0.14	0.06
OU	7	0	1	32	16	0.5	0.09	0.28	0.1	0.52	0.09	0.17	0.07
OU	7	0	1	64	16	0.5	0.11	0.24	0.06	0.52	0.1	0.14	0.06
OU	1.4	0	2	32	8	0.52	0.11	0.59	0.16	0.55	0.1	0.47	0.23
OU	1.4	0	2	64	8	0.52	0.12	0.53	0.12	0.56	0.11	0.45	0.22
OU	1.4	0	2	32	16	0.52	0.06	0.58	0.16	0.52	0.06	0.47	0.23
OU	1.4	0	2	64	16	0.51	0.07	0.54	0.12	0.53	0.07	0.43	0.2
OU	7	0	2	32	8	0.51	0.11	0.28	0.08	0.53	0.11	0.16	0.06
OU	7	0	2	64	8	0.51	0.12	0.24	0.04	0.53	0.12	0.14	0.04
OU	7	0	2	32	16	0.51	0.06	0.28	0.07	0.52	0.06	0.17	0.06
OU	7	0	2	64	16	0.5	0.08	0.24	0.05	0.52	0.07	0.14	0.04
OU	1.4	0	4	32	8	0.52	0.08	0.58	0.11	0.55	0.08	0.48	0.17
OU	1.4	0	4	64	8	0.52	0.09	0.54	0.08	0.56	0.08	0.45	0.16
OU	1.4	0	4	32	16	0.51	0.04	0.59	0.11	0.52	0.04	0.48	0.17
OU	1.4	0	4	64	16	0.51	0.05	0.55	0.09	0.53	0.06	0.44	0.15
OU	7	0	4	32	8	0.51	0.08	0.28	0.06	0.53	0.08	0.17	0.04
OU	7	0	4	64	8	0.5	0.08	0.23	0.03	0.53	0.08	0.14	0.03
OU	7	0	4	32	16	0.5	0.04	0.28	0.06	0.52	0.04	0.17	0.04
OU	7	0	4	64	16	0.51	0.05	0.23	0.03	0.52	0.05	0.14	0.03

Supplemental Table 2. For common trait macroevolution models, sets of species that maximize PD always harbour, on average, at least as much FD (Rao quadratic entropy measure) as random sets of species of the same size. The table presents, for each combination of macroevolutionnary models (column 1), specific set of parameters (column 2-3), number of independent traits (column 4), tree size (column 5) and number of selected species (column 6) a measure of the relative amount of FD between PD_{max} and random sets of species for pure birth Yule trees (column 7-8) and coalescent trees (column 11-12). The comparison of FD (<u>as measured by the Rao quadratic entropy</u>) between the two sets of species is quantified with the following metric: $FD_{maxPD}/(FD_{Randome} + FD_{maxPD})$. A value <.5 means PD is doing worse than random, a value >.5 means PD is doing better than random and a value of .5 means PD is doing the same as random. The phylogenetic signal for Yule trees (column 9-10) and coalescent trees (column 13-14) is measured with the Bloomberg K (for multiple traits, the mean across traits is given). All statistics are based on 1000 simulations in each case.
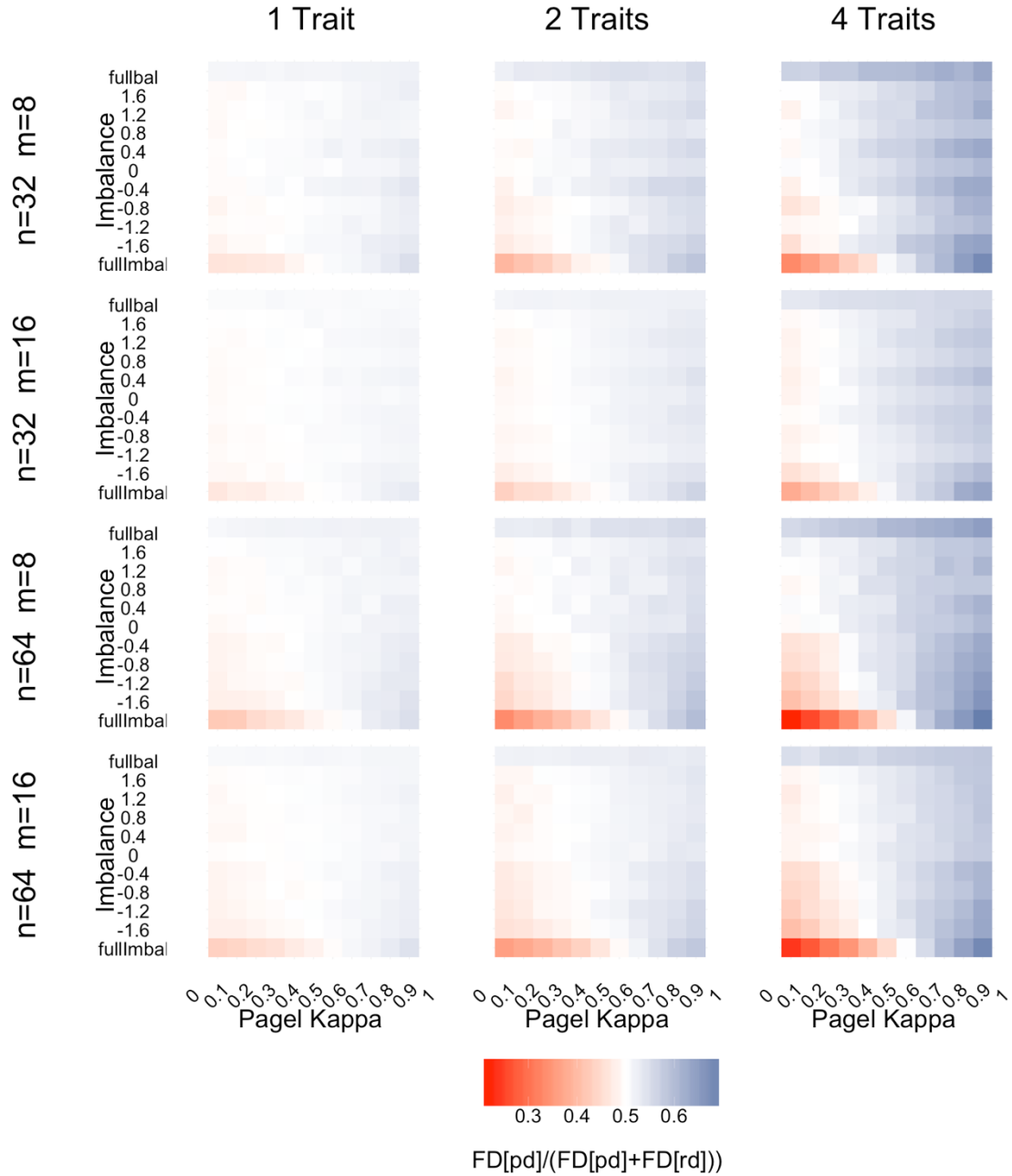
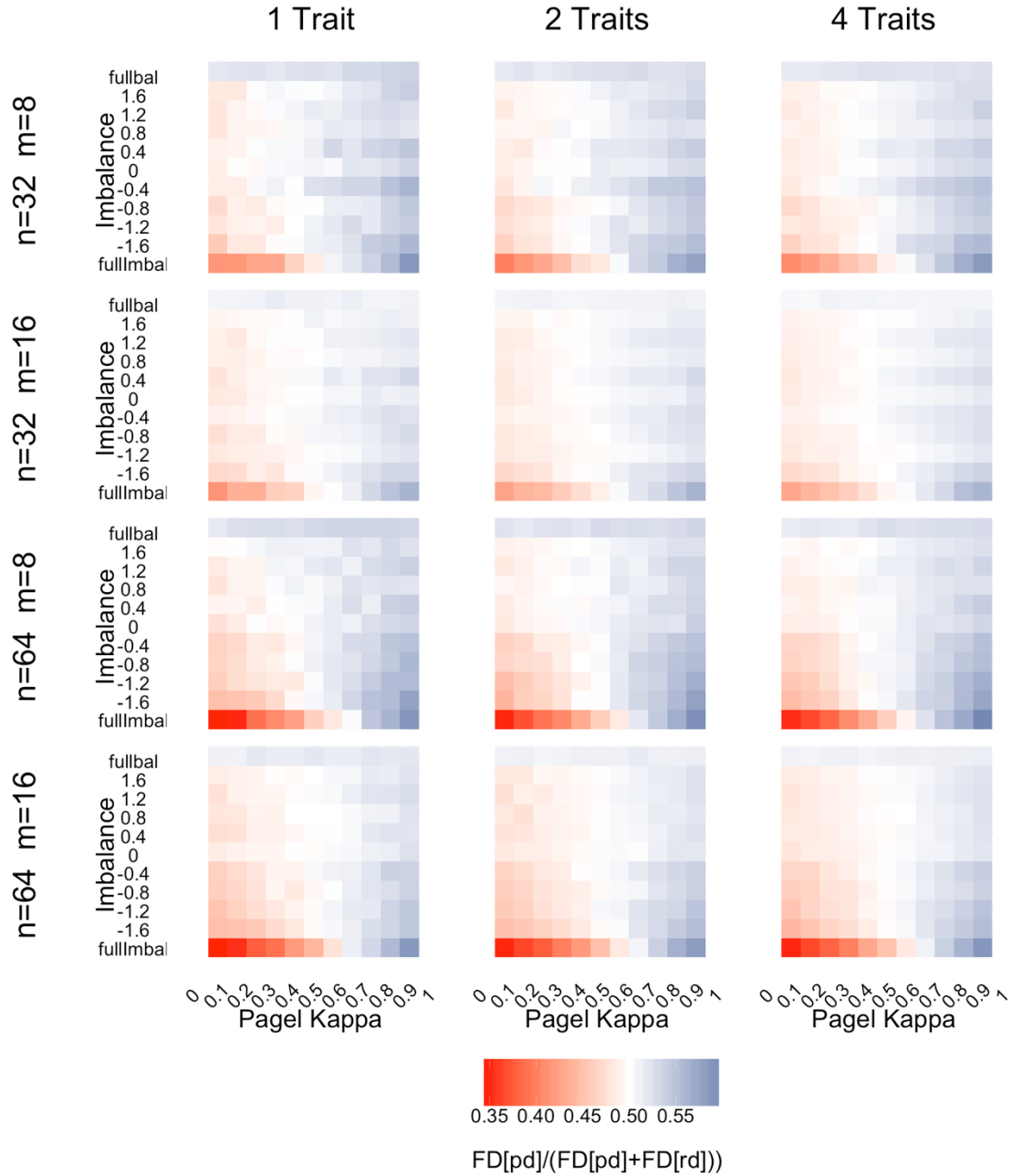**Figure S1. Extension of our results to multiple traits and varying tree sizes and selected species number using Convex Hull as a measure of FD.** The figure present the variation of a measure of the relative amount of FD (as measured by the convex Hull measure) between PD-maximized and random set of species (see legend) in function of tree imbalance (as measured by β, Y-axis, "fullbal" refers to fully balanced tree and "fullImbal" refers to fully imbalanced tree) and the degree of speciational vs. gradual evolution (as measured by Pagel κ, X-axis). The color of each grid cell reflects the mean value of the metric over 100 trait simulations on 10 different trees (for a total of 1000 simulations) or, in the case of fully balanced and fully imbalanced trees, 1000 simulations on one single tree. Each panel corresponds to a different set of parameters (tree size (n), selected number of species (m) and number of traits).
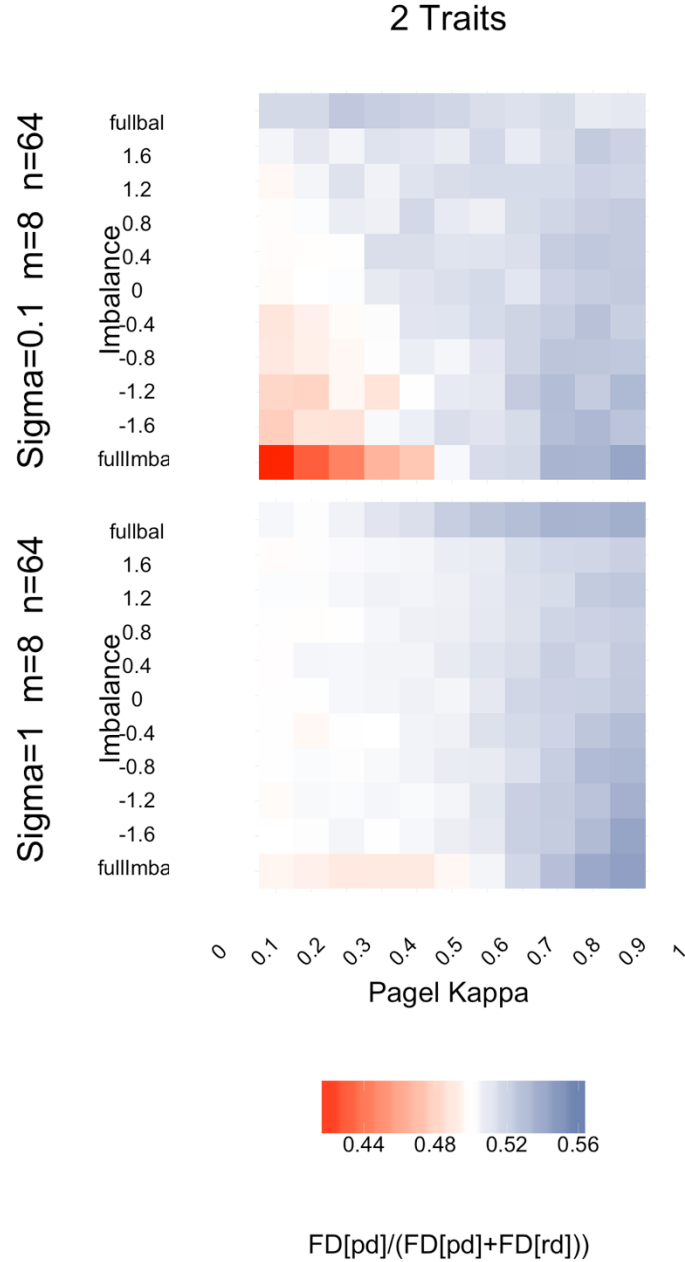
Figure S2. Extension of our results to multiple traits and varying tree sizes and selected species number using Rao quadratic entropy as a measure of FD. The figure presents the variation of a measure of the relative amount of FD (as measured by Rao quadratic entropy) between PD-maximized and random set of species (see legend) in function of tree imbalance (as measured by β, Y-axis, "fullbal" refers to fully balanced tree and "fullImbal" refers to fully imbalanced tree) and the degree of speciational vs. gradual evolution (as measured by Pagel κ, X-axis). The color of each grid cell reflects the mean value of the metric over 100 trait simulations on 10 different trees (for a total of 1000 simulations) or, in the case of fully balanced and fully imbalanced trees, 1000 simulations on one single tree. Each panel corresponds to a different set of parameters (tree size (n), selected number of species (m) and number of traits).

Figure S3. Extension of our results to discrete trait evolution. The figure presents the variation of a measure of the relative amount of FD (as measured by the number of character state combinations) between PD-maximized and random set of species (see legend) in function of tree imbalance (as measured by β, Y-axis, "fullbal" refers to fully balanced tree and "fullImbal" refers to fully imbalanced tree) and the degree of speciational vs. gradual evolution (as measured by Pagel κ, X-axis). The color of each grid cell reflects the mean value of the metric over 100 trait simulations on 10 different trees (for a total of 1000 simulations) or, in the case of fully balanced and fully imbalanced trees, 1000 simulations on one single tree. Results are based on sets of 8 species out of 64 (tree size). The different panels correspond to different values of the transition rate parameter of the Markov model.
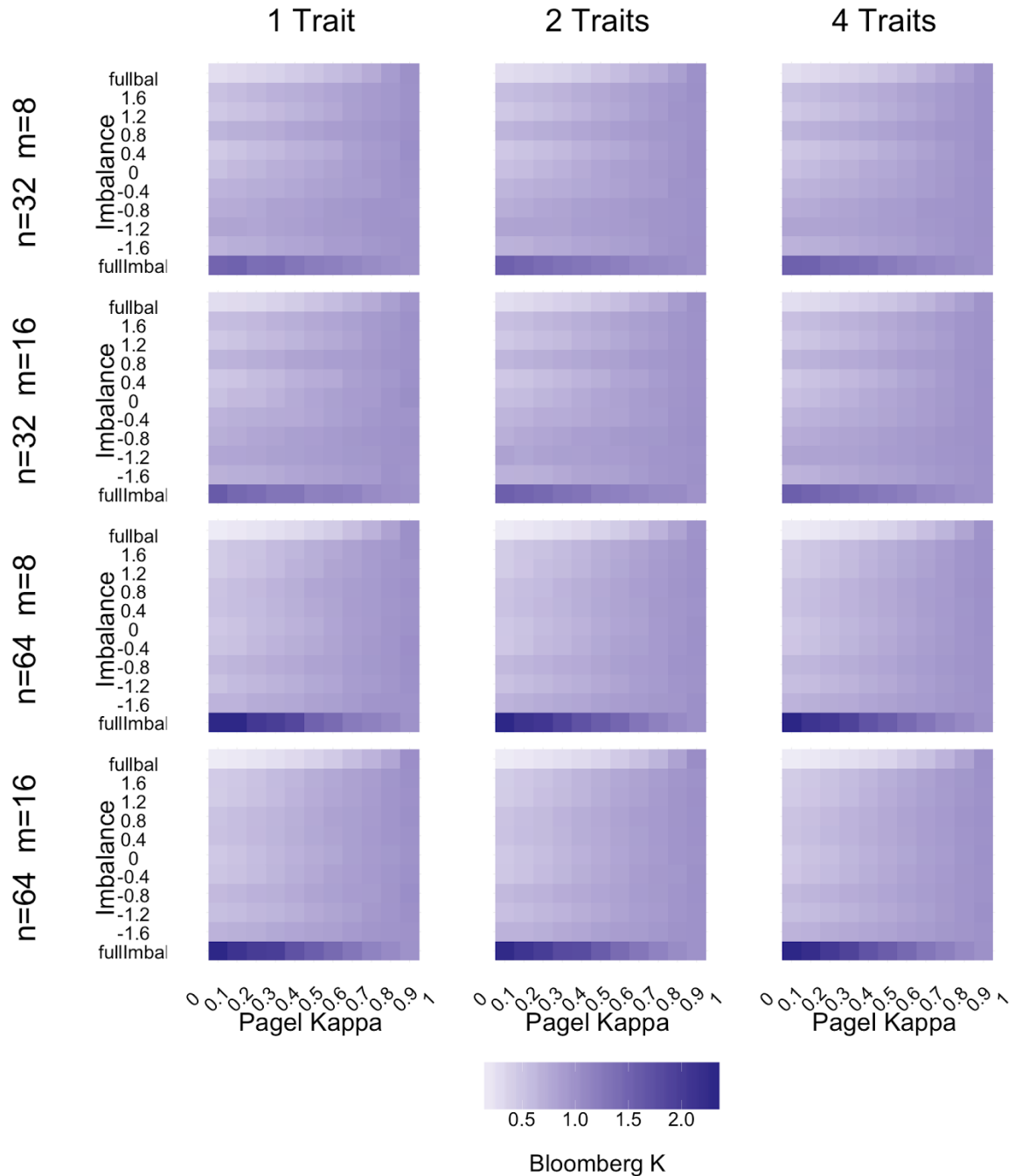
Figure S4. Variability of the phylogenetic signal as measured by the Bloomberg K. The figure presents the variation of phylogenetic signal across the parameter space presented on figure 1 of the main text. Mean Bloomberg K statistic (see legend) are presented in function of tree imbalance (as measured by β, Y-axis, "fullbal" refers to fully balanced tree and "fullImbal" refers to fully imbalanced tree) and the degree of speciational vs. gradual evolution (as measured by Pagel κ, X-axis). Each panel corresponds to a different set of parameters (tree size (n), selected number of species (m) and number of traits). The color of each grid cell reflects the mean value of the metric over 100 trait simulations on 10 different trees (for a total of 1000 simulations) or, in the case of fully balanced and fully imbalanced trees, 1000 simulations on one single tree.
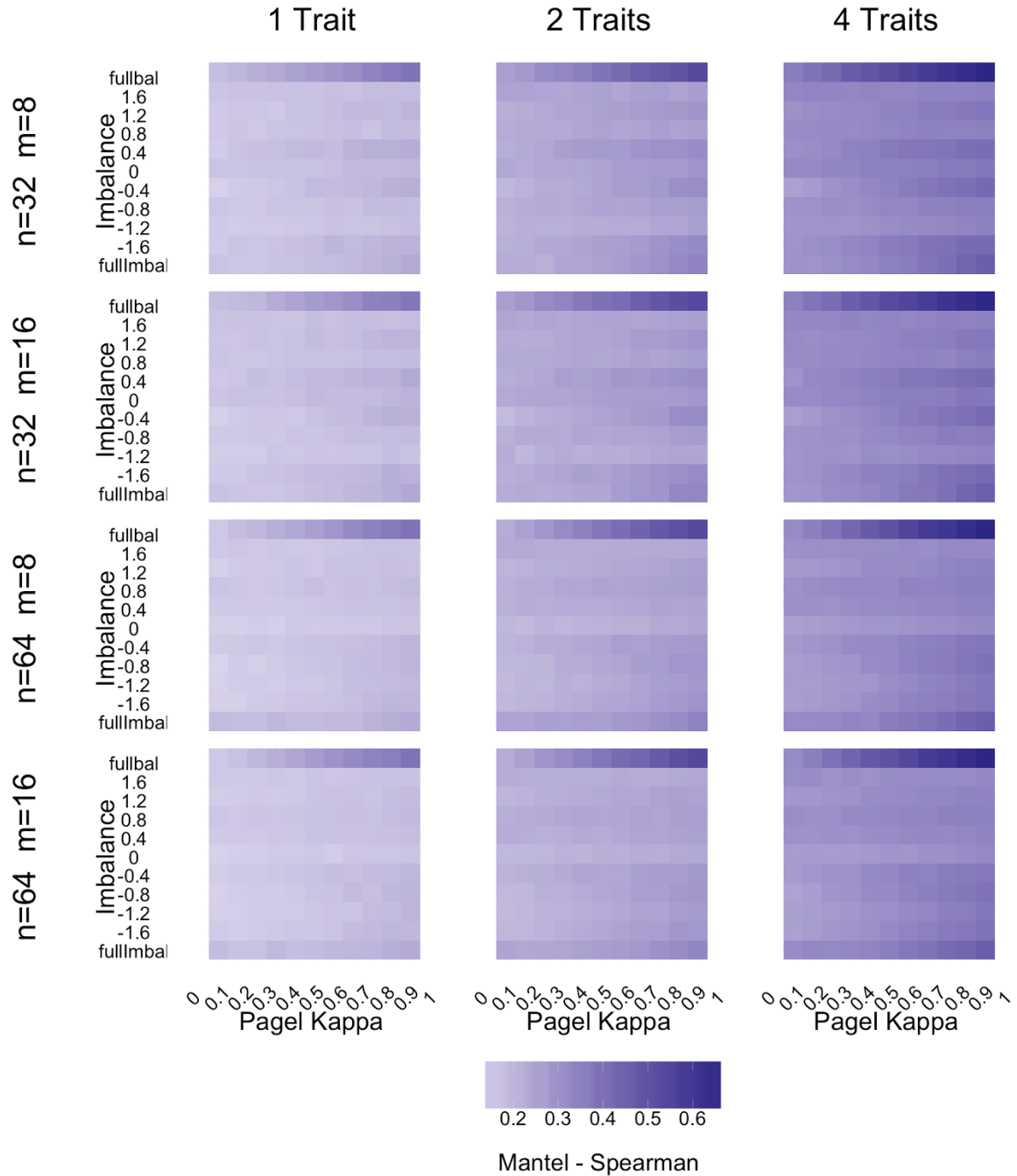
Figure S5. Variability of the phylogenetic signal as measured by the Spearman correlation between trait and phylogenetic distances. The figure presents the variation of phylogenetic signal across the parameter space presented on figure 1 of the main text. Mean mantel (spearman) statistic (see legend) are presented in function of tree imbalance (as measured by β, Y-axis, "fullbal" refers to fully balanced tree and "fullImbal" refers to fully imbalanced tree) and the degree of speciational vs. gradual evolution (as measured by Pagel κ, X-axis). Each panel corresponds to a different set of parameters (tree size (n), selected number of species (m) and number of traits). The color of each grid cell reflects the mean value of the metric over 100 trait simulations on 10 different trees (for a total of 1000 simulations) or, in the case of fully balanced and fully imbalanced trees, 1000 simulations on one single tree.