

Figure S1: Concept map of the Evolutionary Distinctness Biased Markov Model (EDBMM). In this example, the tree is being simulated under a DE scenario ($-\sigma$, $+\epsilon$), meaning speciation and extinction rates are lower for ED tips and as such the resulting tree (in grey) has effectively the same shape as the original tree (in black).

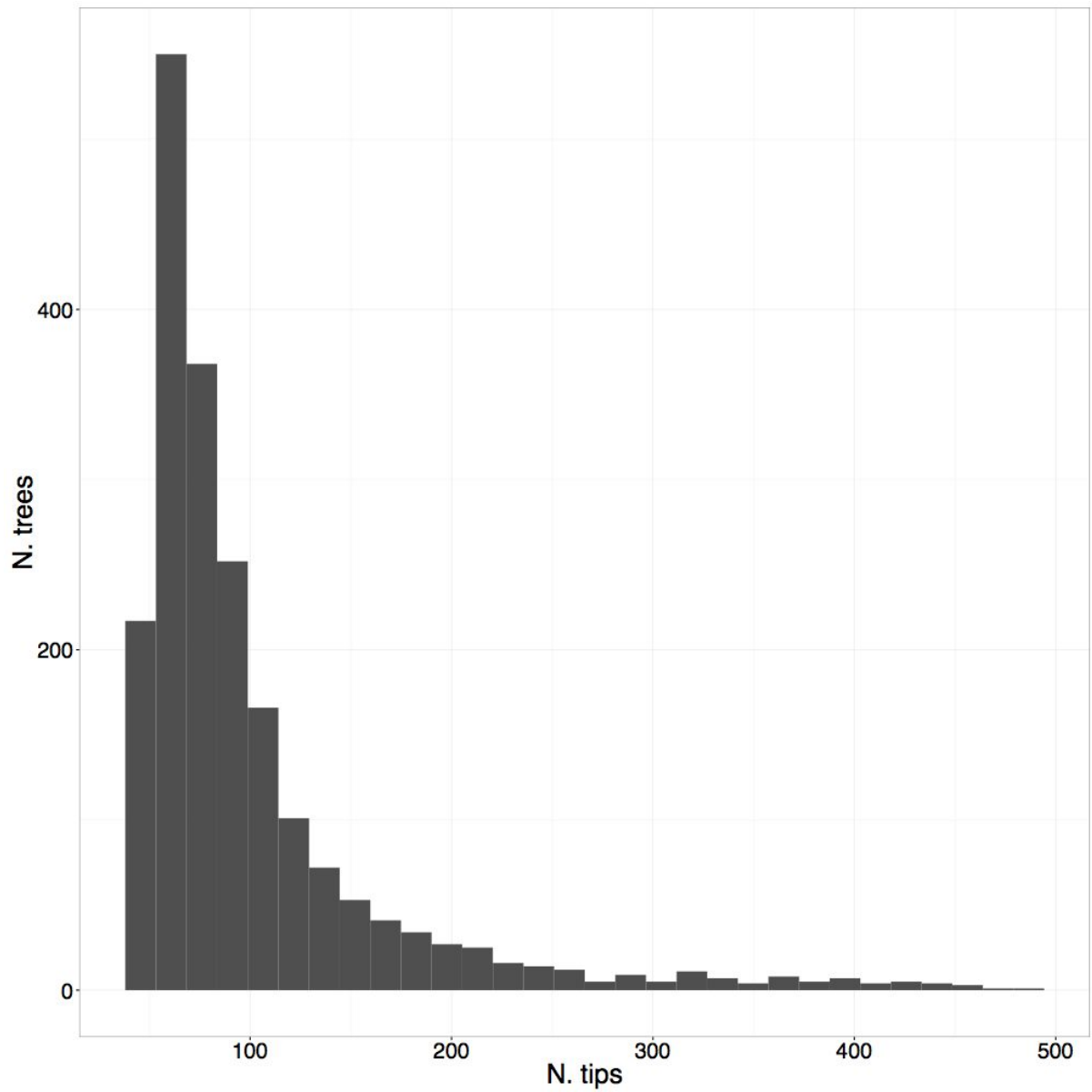


Figure S2. Number of tips represented by empirical sourced trees.

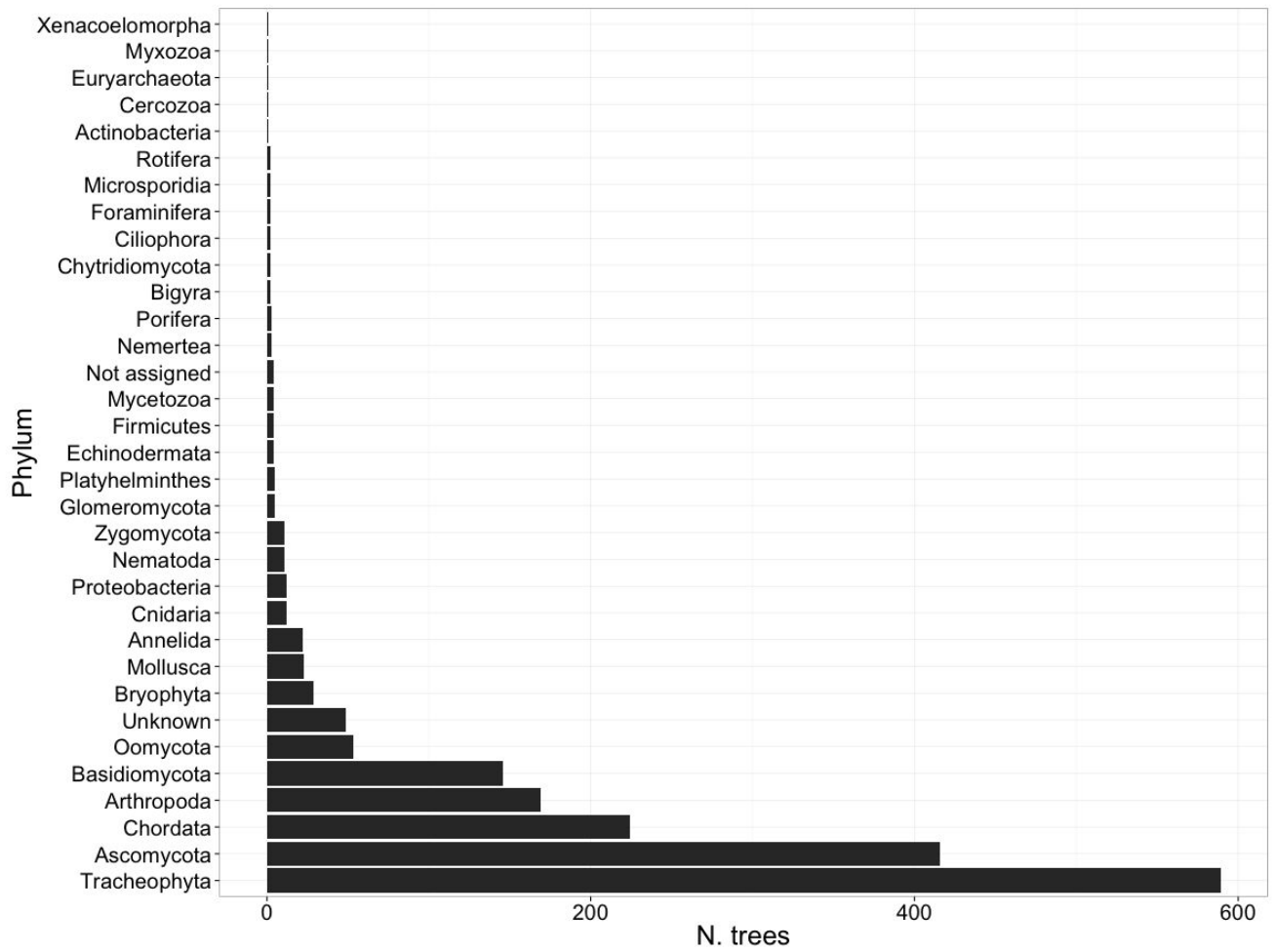
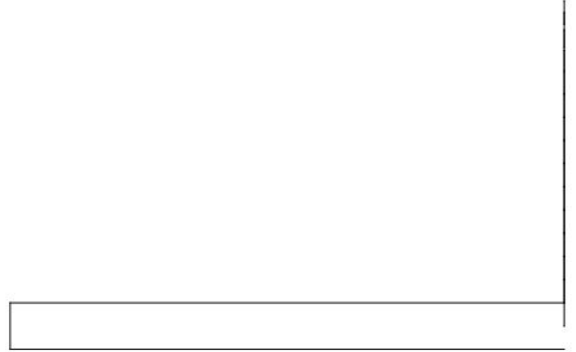


Figure S3: Number of sourced trees represented by each phylum.

PSV = 0.1



PSV = 1

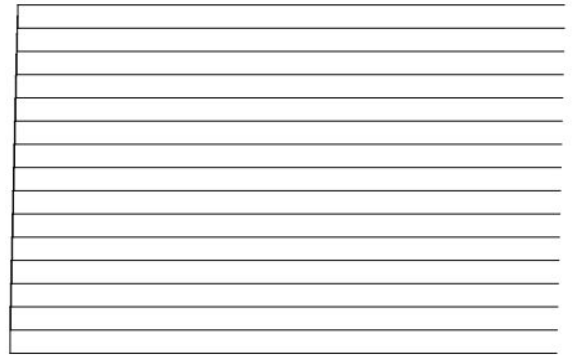
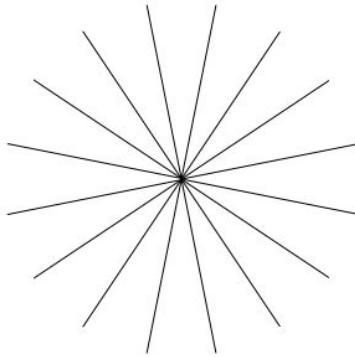


Figure S4. How PSV and phylogenetic gravity relate. (Top) A line/dot tree has a single cluster of highly related tips separated by a very distant tip, causing low phylogenetic species variability (PSV). When rooted on this long branch and keeping the tree ultrametric, internal nodes are clustered towards the tips. (Bottom) A star tree has all tips being equally distant and all internal nodes are distributed to the root.

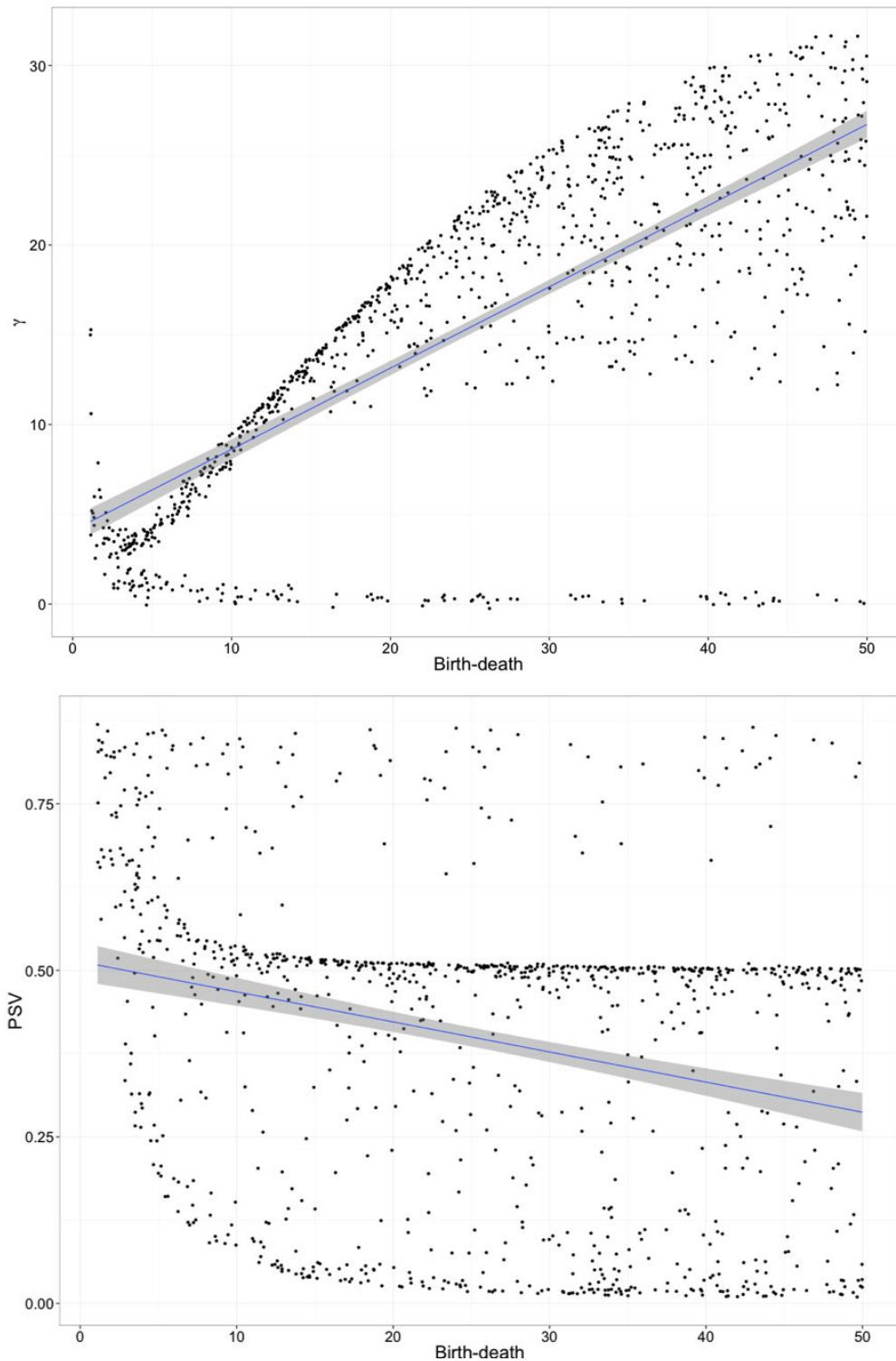


Figure S5. Correlations between birth-death parameters and γ (top) and PSV (bottom) for 1,000 simulated trees using random σ and ϵ parameters. PSV shows a weaker correlation to the birth-death parameter (Pearson's R -0.27) than γ (Pearson's R 0.78). The complex structuring of the points is caused by the interaction of birth-death, σ and ϵ with PSV and γ .

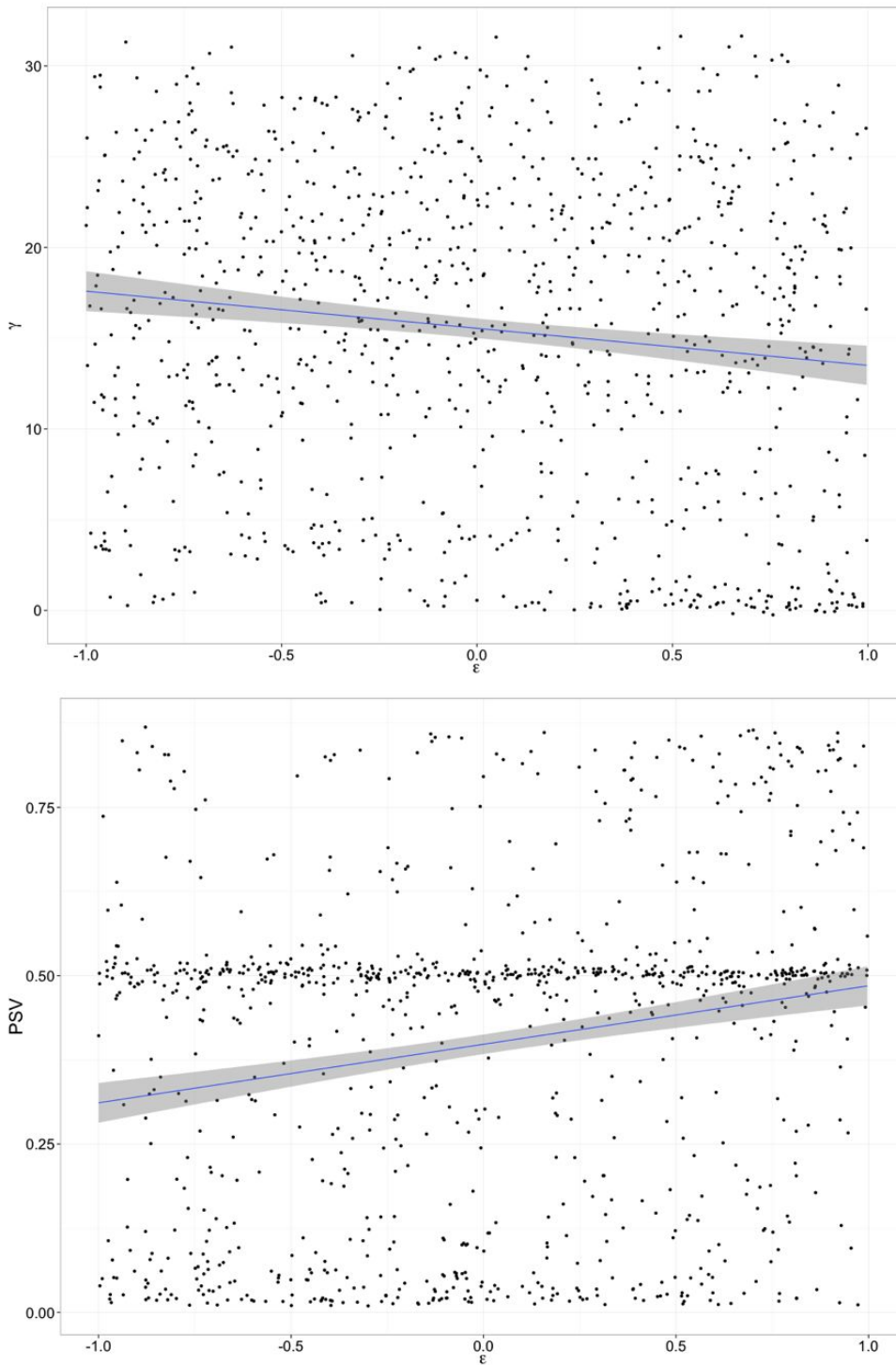


Figure S6. Correlations between ϵ parameters and γ (top) and PSV (bottom) for 1,000 simulated trees using random σ and ϵ parameters. Although weak, PSV shows a stronger correlation to the ϵ parameter (Pearson's R 0.20) than γ (Pearson's R -0.13). The structuring present in the PSV plot is indicative of a nonlinear interaction between σ and PSV.

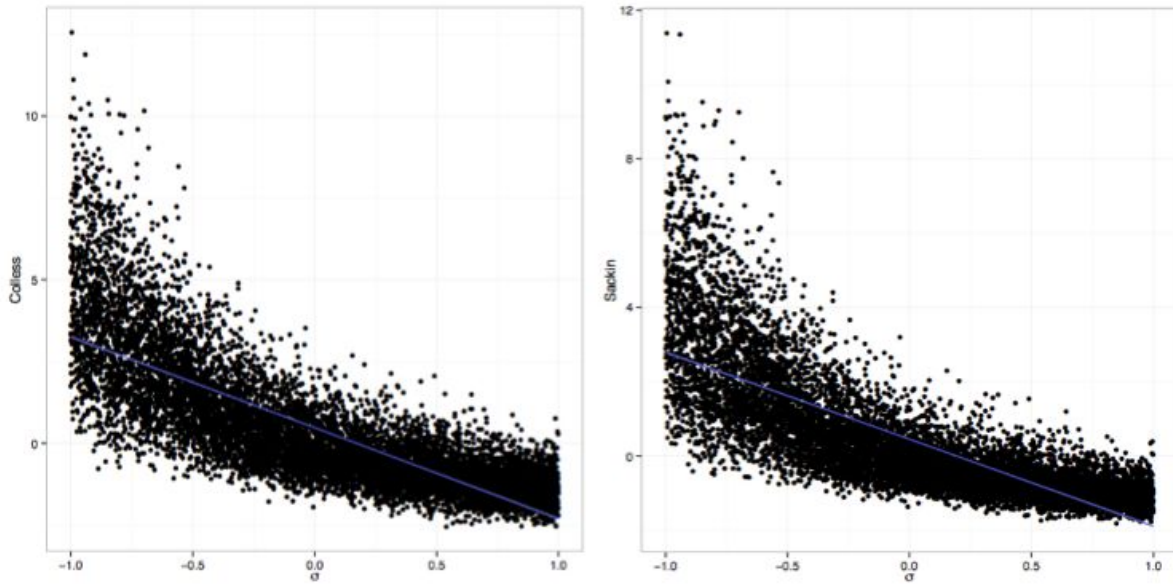


Figure S7: Yule normalised Colless (left) and Sackin (right) statistics against σ (“sigma”).

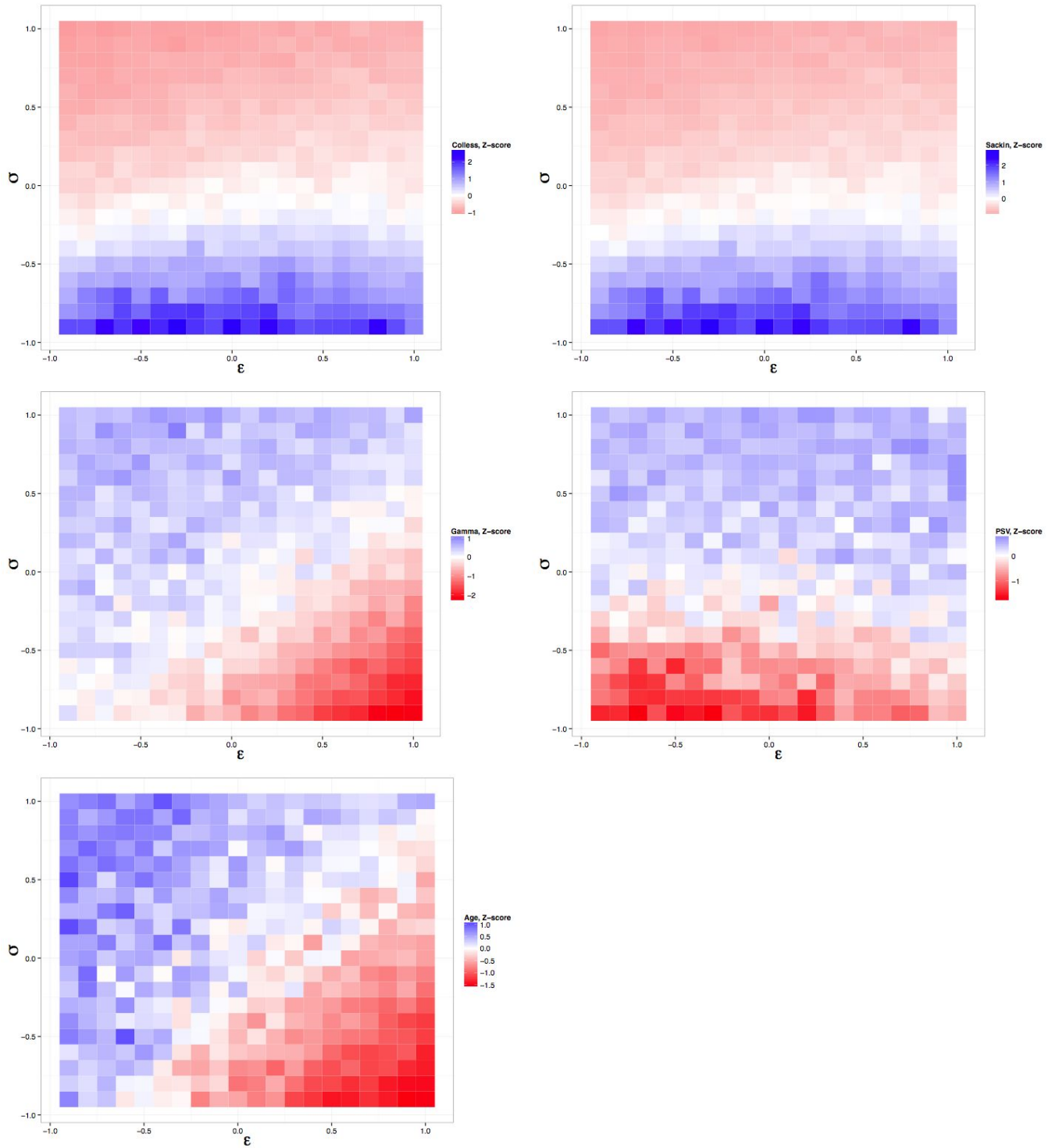


Figure S8: Z-scores for mean simulated tree statistics in σ - ϵ (“sigma”-“epsilon”) parameter space: (top-left) Yule normalised Colless, (top-right) Yule normalised Sackin, (middle-left) γ (“gamma”), (middle-right) phylogenetic species variability (PSV) and (bottom-left) age (root to tip distance).

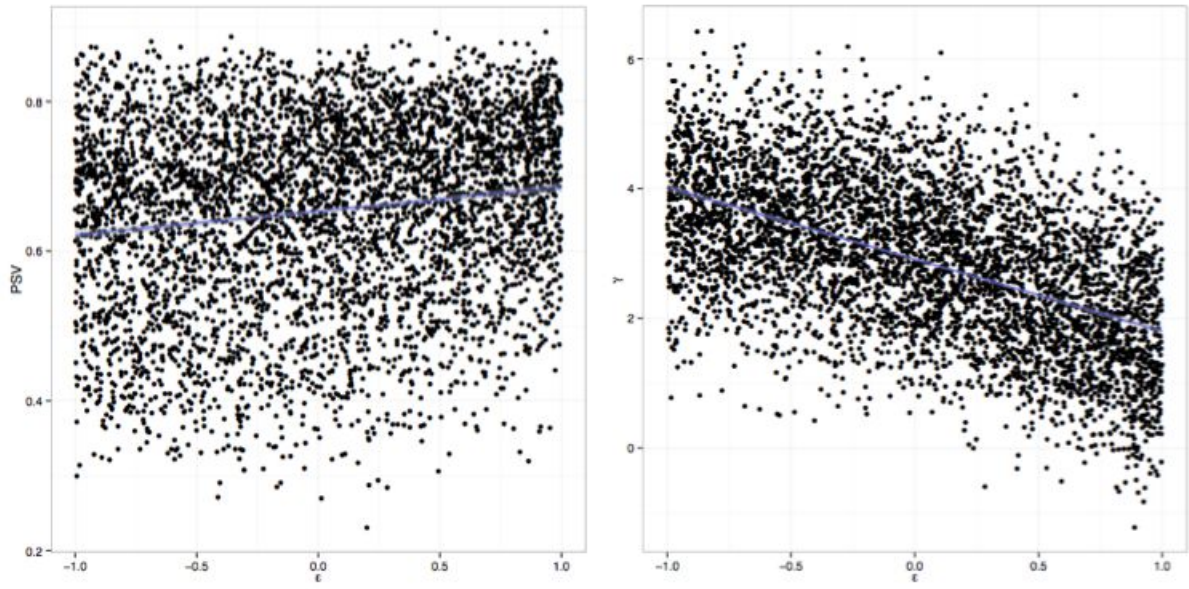


Figure S9: PSV (left) and γ (“gamma”) against ϵ (“epsilon”) for simulations with σ (“sigma”) < 0 .

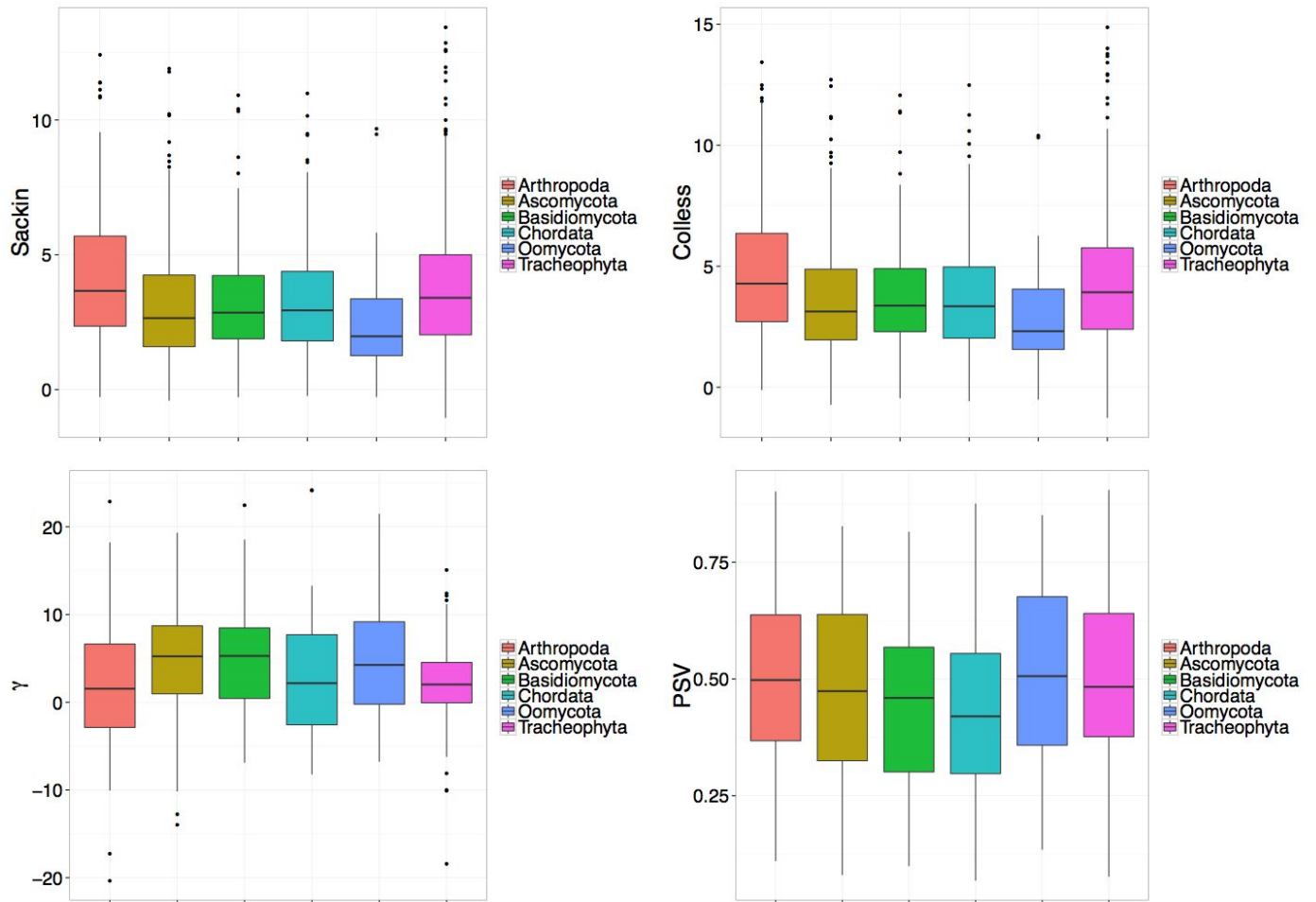


Figure S10. Shape metric ranges for different Phyla: Sackin (top-left), Colless (top-right), γ_{D8} (bottom-left) and PSV (bottom-right)

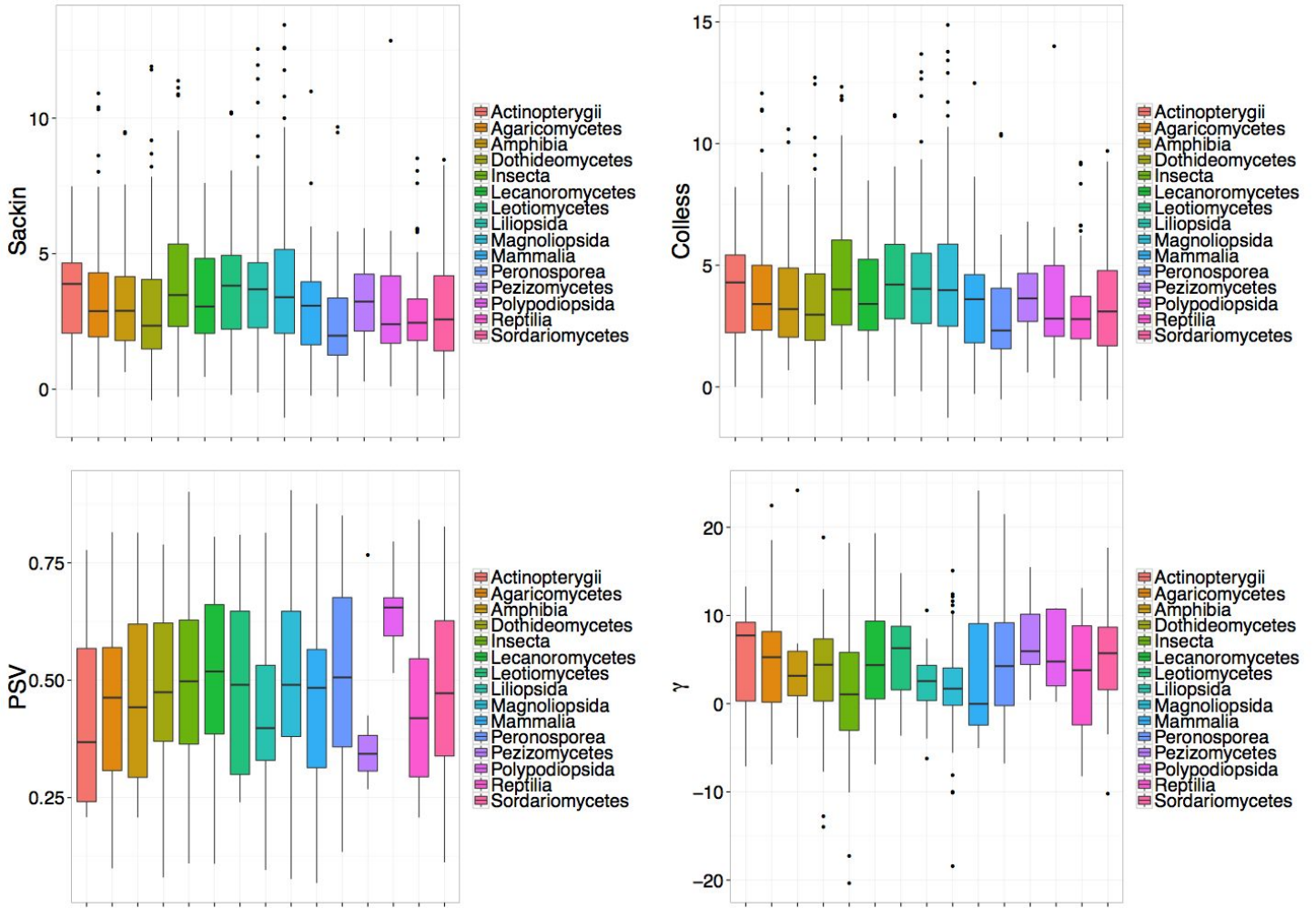


Figure S11. Shape metric ranges for different Classes: Sackin (top-left), Colless (top-right), γ_{D8} (bottom-left) and PSV (bottom-right)

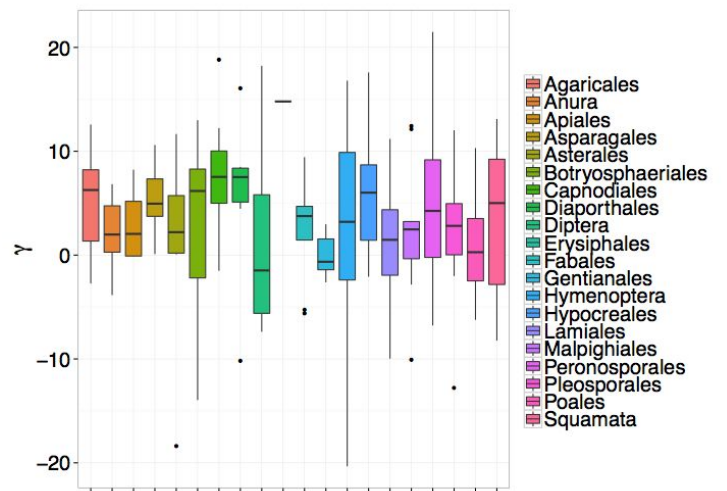
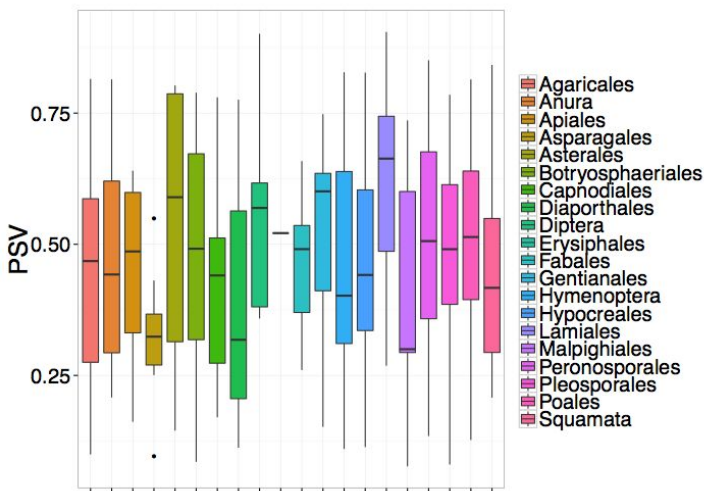
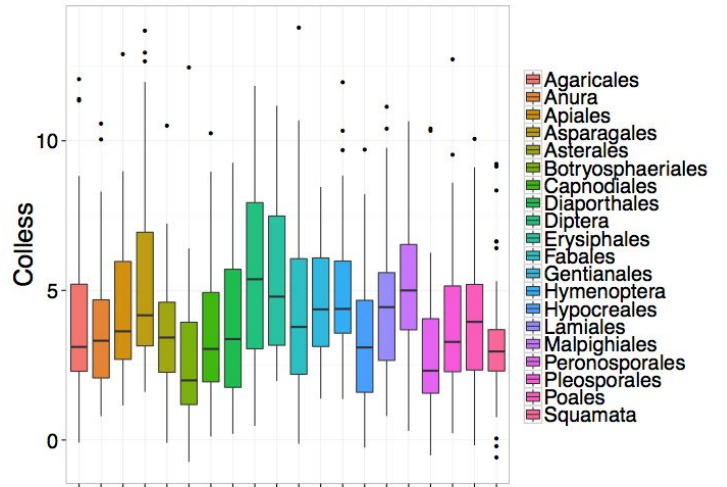
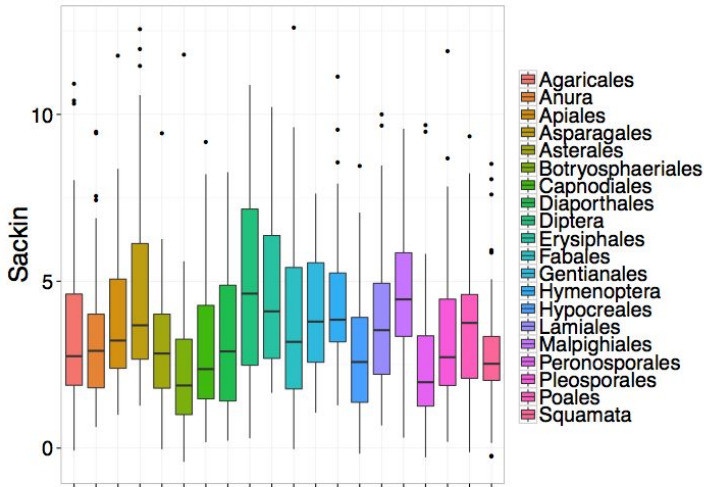


Figure S12. Shape metric ranges for top-ten most sourced Orders: Sackin (top-left), Colless (top-right), γ_{D8} (bottom-left) and PSV (bottom-right)

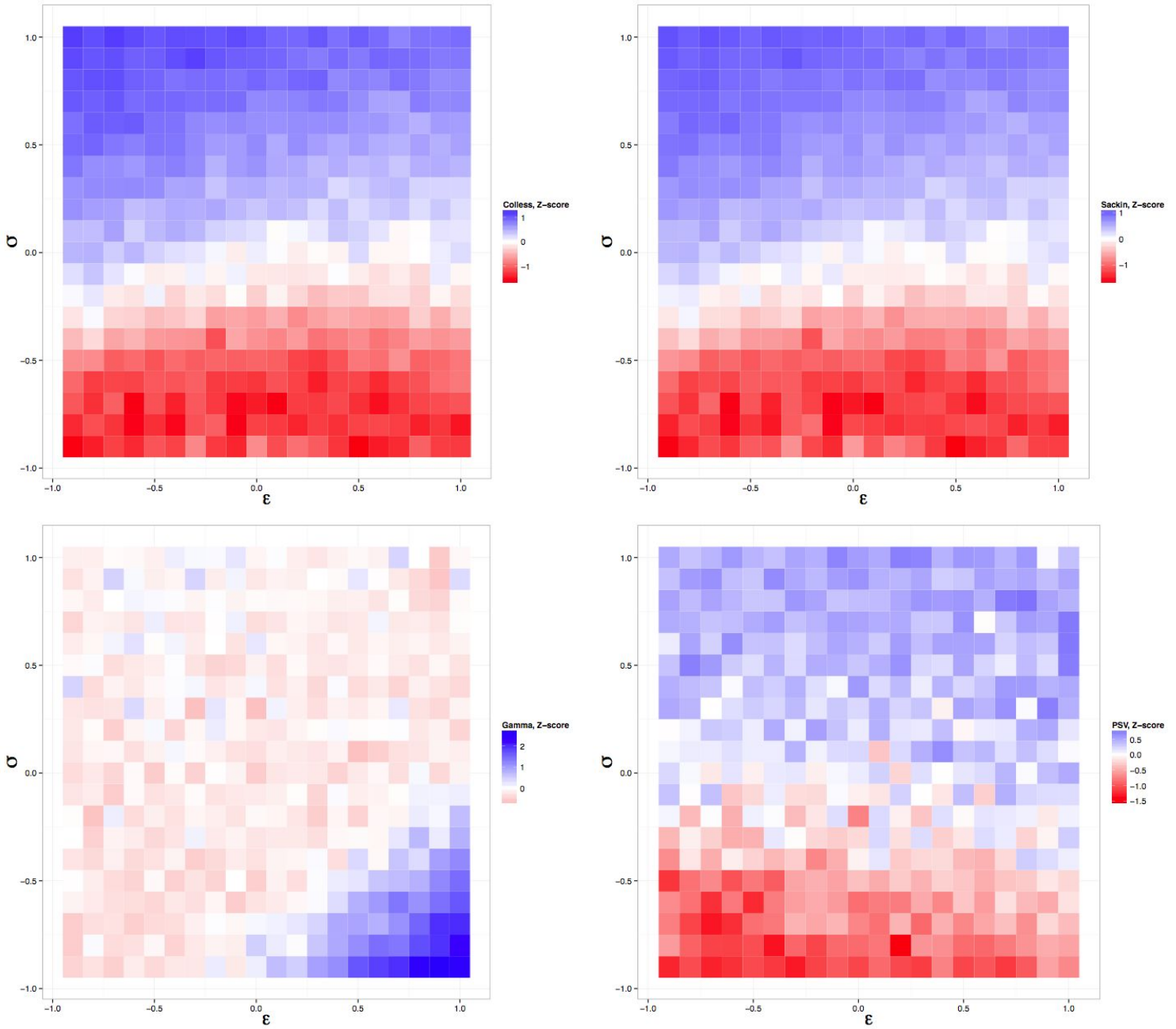


Figure S13: Z-scores for distance to empirical trees for mean simulated tree statistics in σ - ϵ ("sigma"- ϵ) parameter space, the lower the value the nearer the simulated is to the empirical: (top-right) Yule normalised Colless, (top-left) Yule normalised Sackin, (bottom-left) phylogenetic species variability (PSV_{D8}) and (bottom-right) γ_{D8} ("gamma").

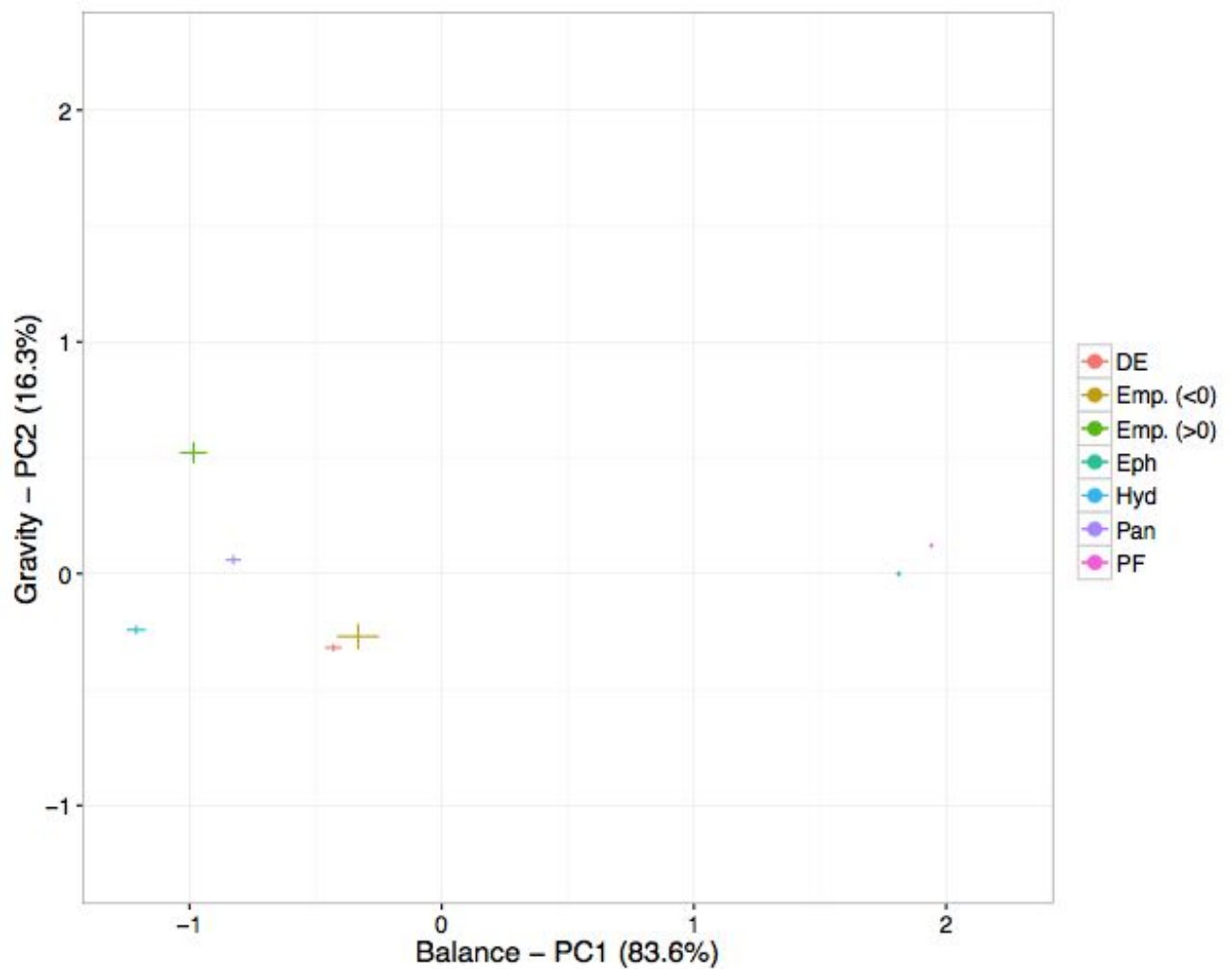


Figure S14: PCA of the extreme scenarios using Yule normalised Sackin, Colless and PSV. Colours indicate simulation scenario and whether tree is empirical with $\gamma > 0$ (high) or $\gamma < 0$ (low). ‘Low’ empirical tree shape is closer to the DE scenario, while ‘high’ has greater gravity than all simulated trees indicating that although Pan is closest in terms of gravity than any other simulation a diversity in birth-death rate is required to create the range of empirical gravity.

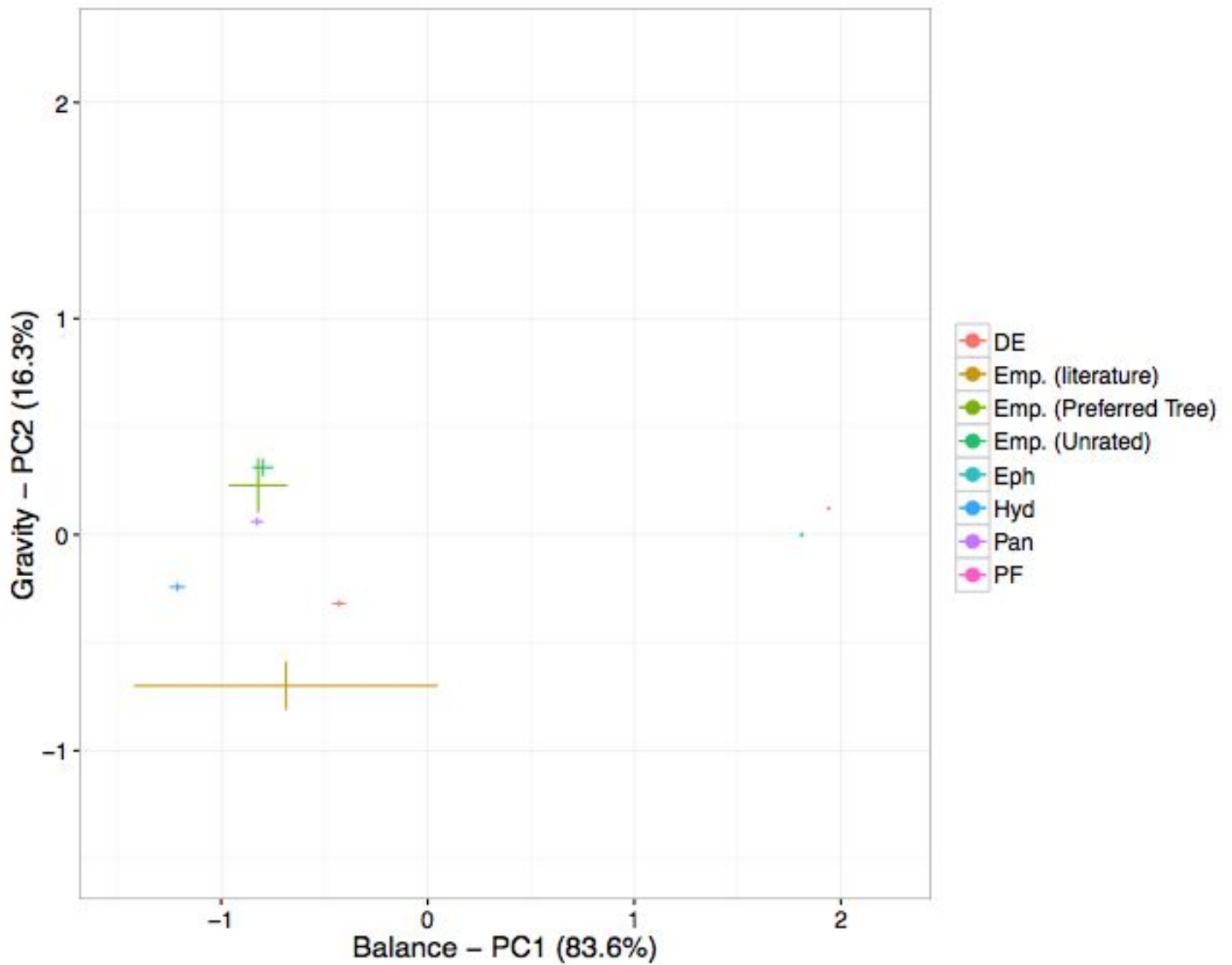


Figure S15: PCA of the extreme scenarios using Yule normalised Sackin, Colless and PSV. Colours indicate simulation scenario and empirical trees split between source/quality. 'Literature' refers to all the trees originating from Table S1, rate-smoothed with pathD8 if not already ultrametric. 'Preferred Tree' and 'Unrated' refer to quality tags for trees originating from TreeBase.

Table S1: Published trees taken from the literature

<i>Group</i>	<i>No. tips</i>	<i>Ultrametric</i>
Mammalia [1]	4510	Yes
Hymenoptera [2]	1376	No
Trachaeophyta [3]	5122	Yes
Aves* [4]	9993	Yes
Squamata [5]	4162	No

**Hackett backbone, 100 tree sample from 9,000-10,000*

posterior distribution

Table S2. Variance of means of taxonomic groups at Phylum, Class and Order for each shape metric (σ^2). Proportional change between variance of means between ranks (\pm). Significant differences between observed variance of means or change in variance of means generated using a permutation test are indicated with asterices (* < 0.05, ** < 0.01, * < 0.001).**

	Colless		Sackin		PSV ^{D8}		γ^{D8}	
Phylum (σ^2)	8.60E-01	***	6.00E-01	**	9.94E-05		2.36E+00	
Class (σ^2)	9.80E-01	***	7.70E-01	***	6.09E-03		5.91E+00	
Order (σ^2)	8.10E-01	***	6.60E-01	***	4.91E-03		9.85E+00	
Phylum-Class (\pm)	1.13E+00		1.28E+00		6.12E+00		2.50E+00	
Phylum-Order (\pm)	9.40E-01		1.11E+00		4.94E+00		4.17E+00	

References

- [1] Bininda-Emonds, O. R. P., Cardillo, M., Jones, K. E., MacPhee, R. D. E., Beck, R. M. D., Grenyer, R., ... Purvis, A. (2007). The delayed rise of present-day mammals. *Nature*, 446(7135), 507–12.
- [2] Danforth, B. N., Cardinal, S., Praz, C., Almeida, E. A. B., & Michez, D. (2013). The impact of molecular data on our understanding of bee phylogeny and evolution. *Annual Review of Entomology*, 58, 57–78.
- [3] Durka, W., & Michalski, S. G. (2012). Daphne: a dated phylogeny of a large European flora for phylogenetically informed ecological analyses. *Ecology*, 93(10), 2297–2297.
- [4] Jetz, W., Thomas, G. H. H., Joy, J. B. B., Hartmann, K., & Mooers, a. O. O. (2012). The global diversity of birds in space and time. *Nature*, 491(7424), 1–5.
- [5] Pyron, R. A., Burbrink, F. T., & Wiens, J. J. (2013). A phylogeny and revised classification of Squamata, including 4161 species of lizards and snakes. *BMC Evolutionary Biology*, 13(1), 93.