

Supporting Information File 4

Supplementary Figures

The grass was greener: Repeated evolution of specialized morphologies and habitat shifts in ghost spiders following grassland expansion in South America

F.S. Ceccarelli, N. Mongiardino Koch, E.M. Soto, M.L. Barone, M.A. Arnedo, M.J. Ramírez

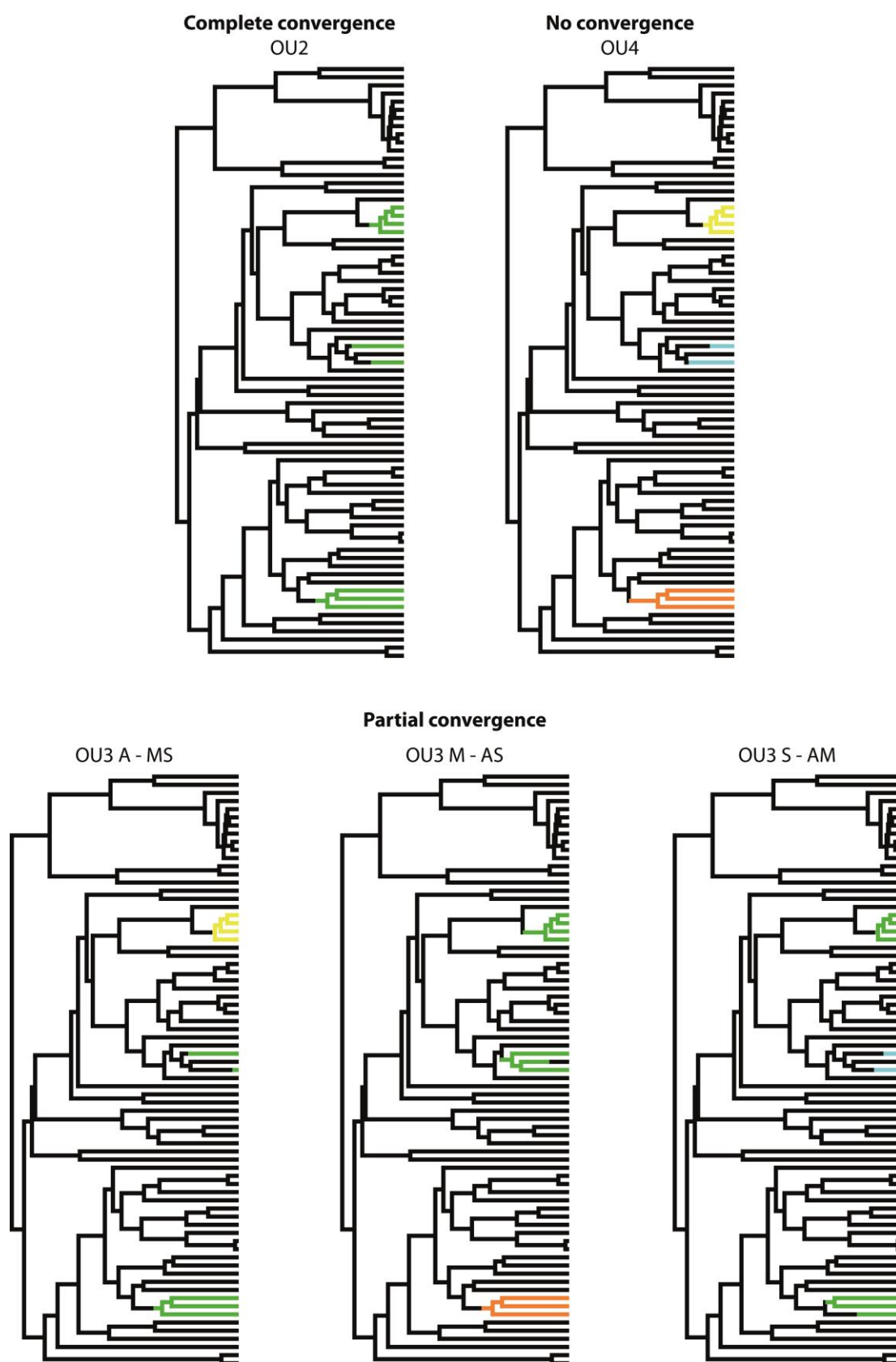


Figure S1. Graphical representation of the five explored multi-OU models. Selective regimes are painted on the tree using stochastic character mapping, with black denoting the general peak, and colors used for the grassland peaks. Green is always used for convergent regimes, other colors represent clade-specific regimes.

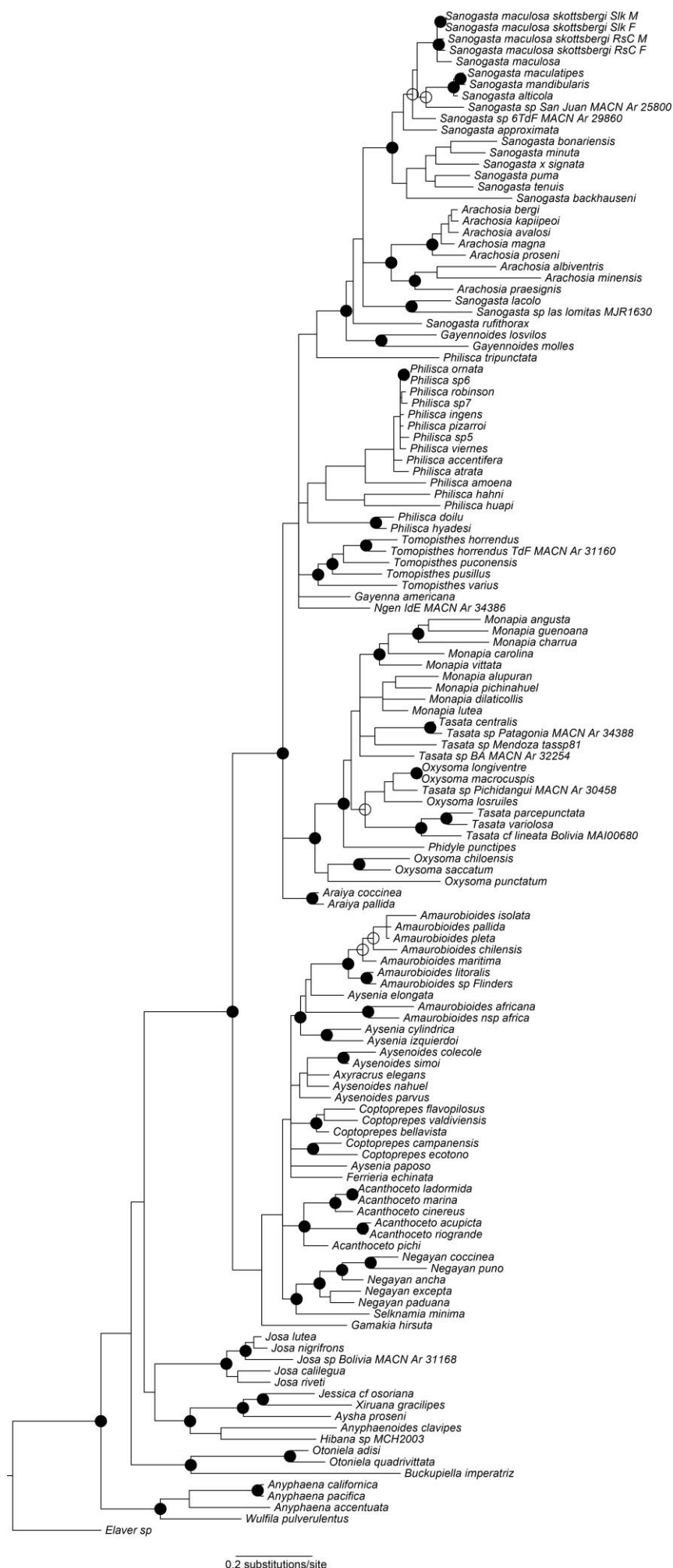


Figure S2. 50% majority rule tree obtained from MrBayes using the mitochondrial COI and 16S matrix. Node support is represented as full (0.95 < PP < 1) or empty (0.9 < PP < 0.94) circles.

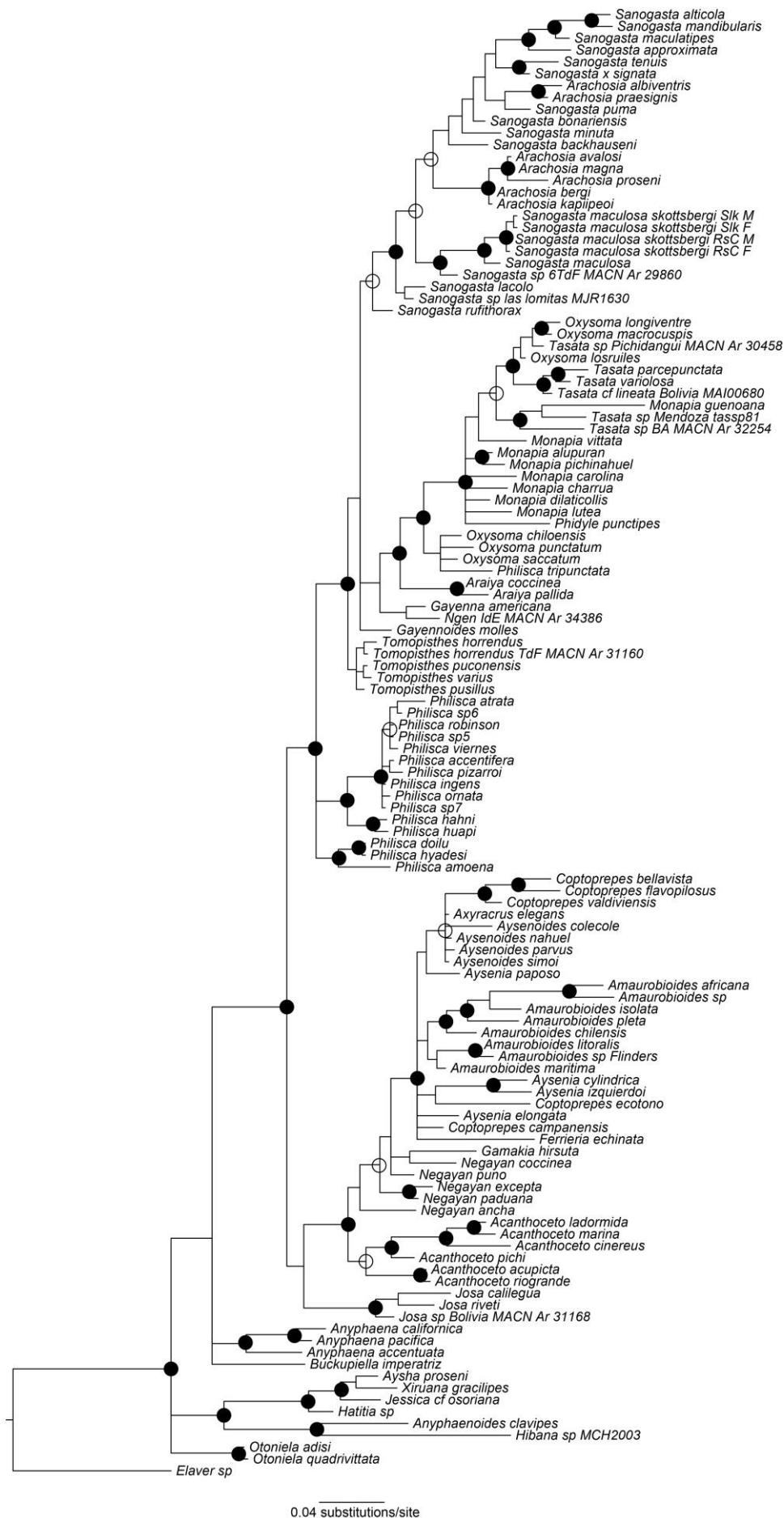


Figure S3. 50% majority rule tree obtained from MrBayes using the 28S matrix. Node support is represented as full (0.95 < PP < 1) or empty (0.9 < PP < 0.94) circles.

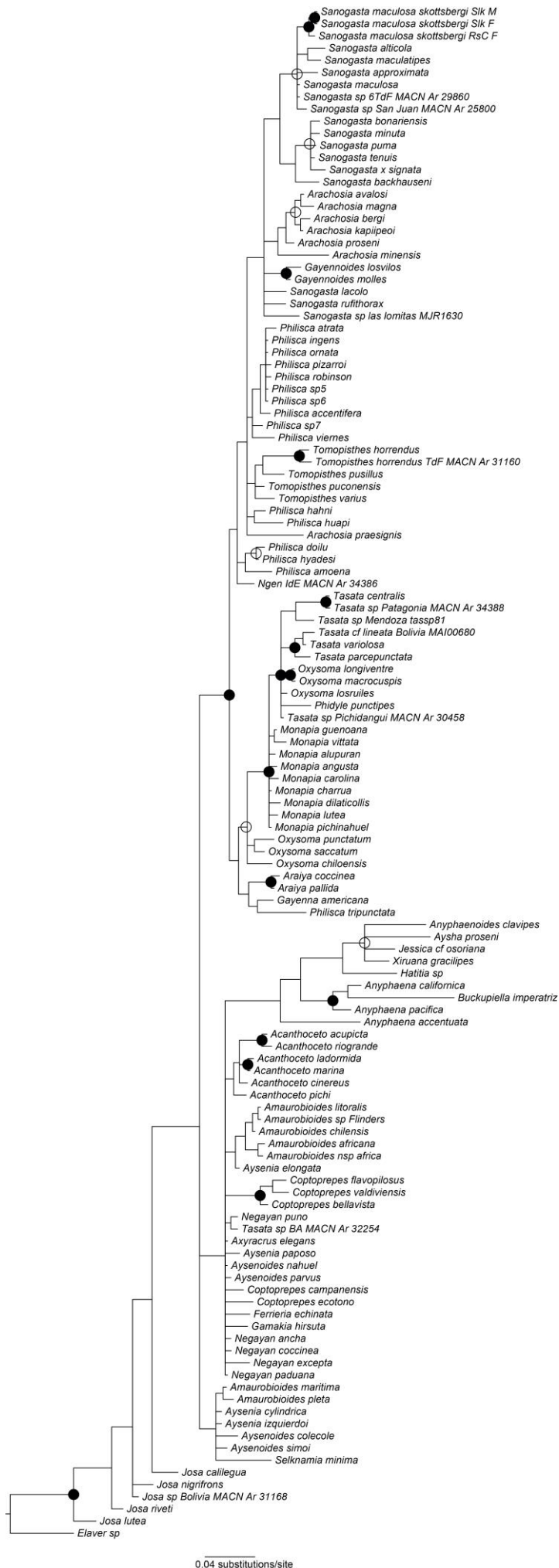


Figure S4. 50% majority rule tree obtained from MrBayes using the H3a matrix. Node support is represented as full ($0.95 < PP < 1$) or empty ($0.9 < PP < 0.94$) circles.

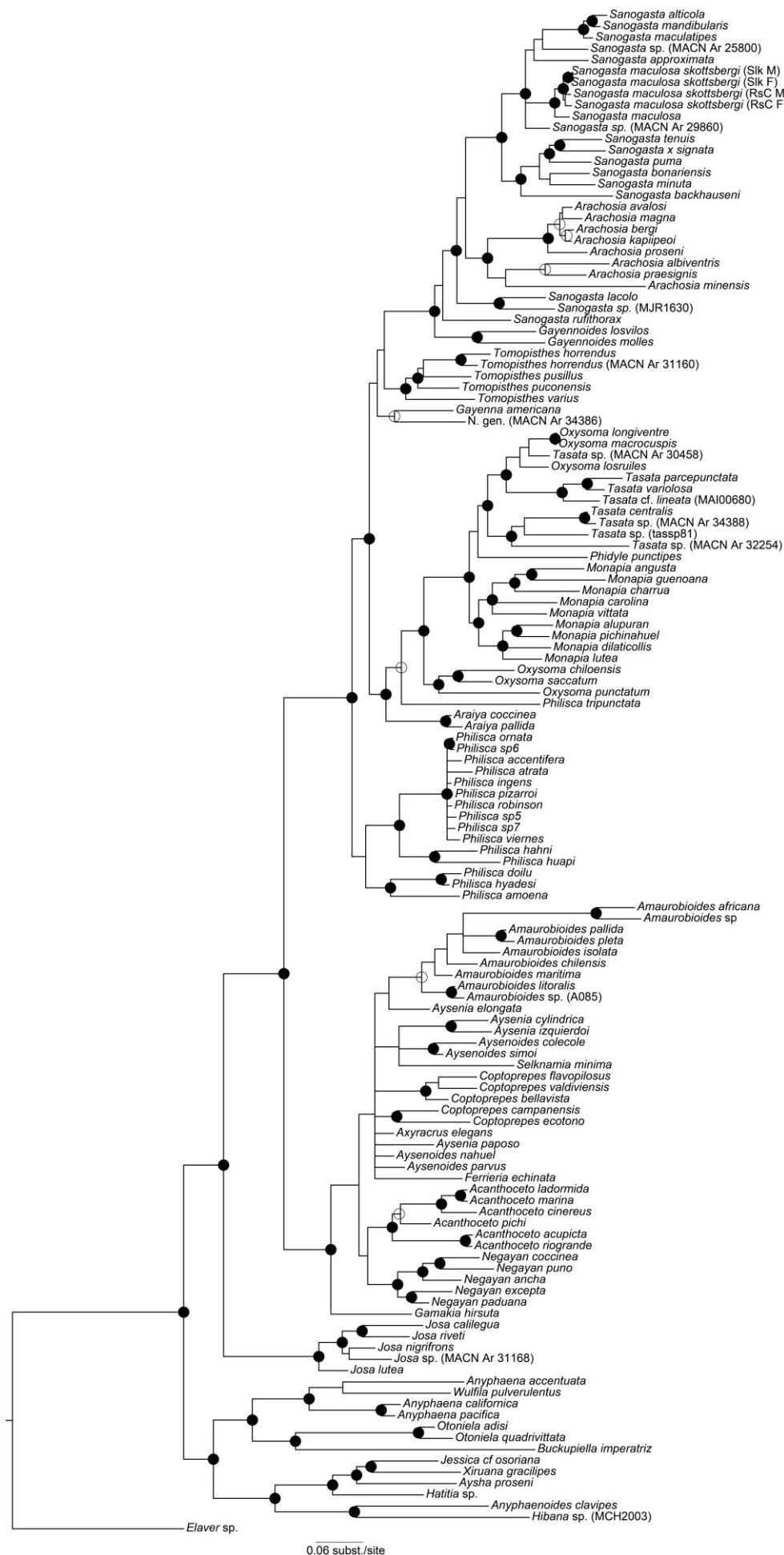


Figure S5. 50% majority rule tree obtained from MrBayes using concatenated COI, 16S, H3a and 28S matrices. Node support is represented as full (0.95 < PP < 1) or empty (0.9 < PP < 0.94) circles. For undescribed or duplicate taxa, the voucher numbers are given in brackets (cross-reference with Supplementary Table S1).



Figure S6. Maximum Likelihood tree obtained from RAXML using concatenated COI, 16S, H3a and 28S matrices. Nodal support values are based on 1000 bootstrap replicates and are shown as black circles (values above 75%).

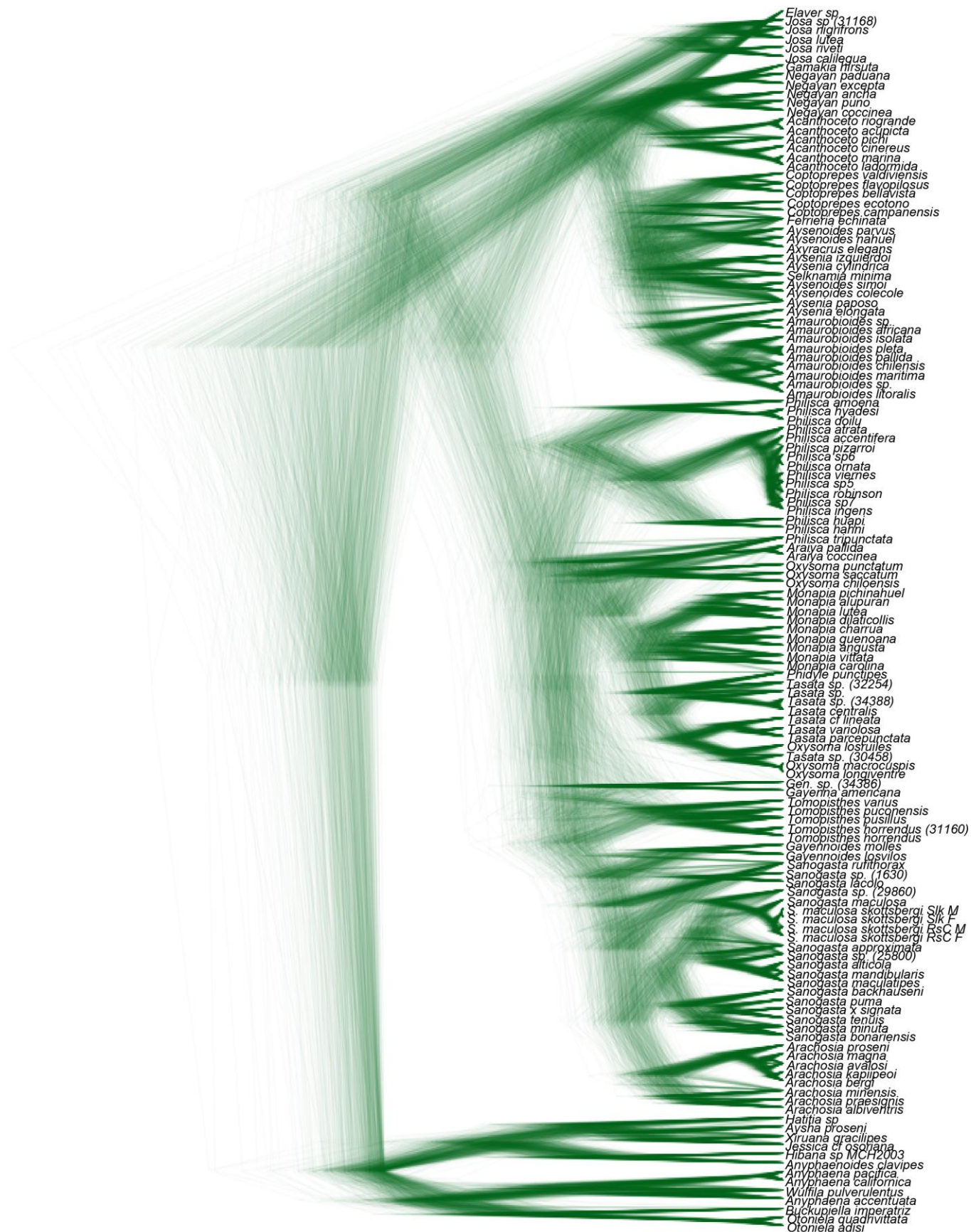


Figure S7. DensiTree representation of the topologies of the post-burnin posterior trees from the analysis in BEAST.

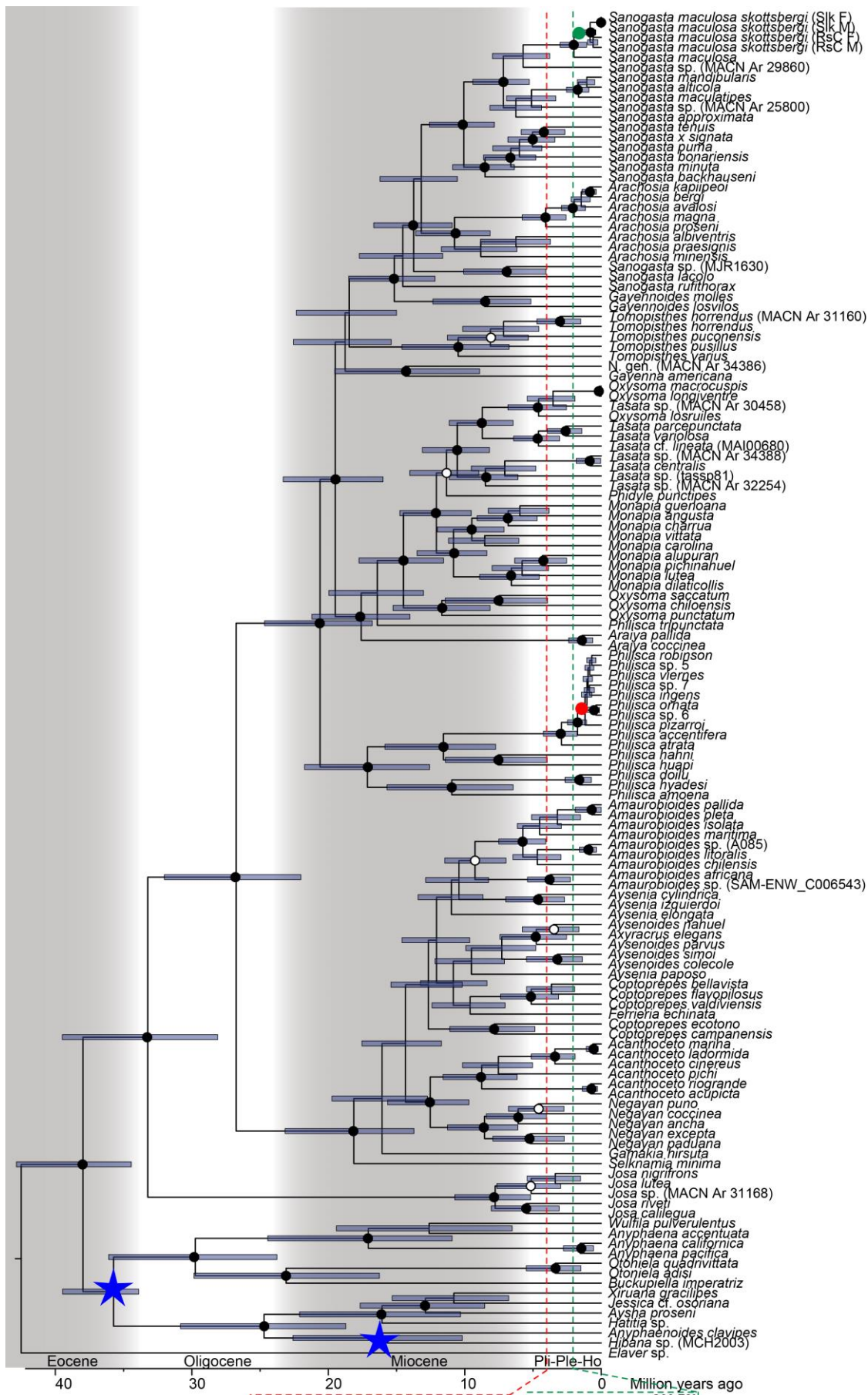


Figure S8. Maximum clade credibility tree from BEAST using concatenated COI, 16S, H3a and 28S matrices, with node age estimates based on fossil calibration points (indicated by the blue stars). Node support is represented as full ($0.95 < PP < 1$) or white ($0.9 < PP < 0.94$) circles at the nodes and blue bars represent the 95% Highest Posterior Densities for the node ages. Scale bar is shown below the tree, with geological epochs shown (Pli-Ple-Ho = Pliocene, Pleistocene and Holocene). Dashed vertical lines indicate the approximate emergence of the Juan Fernandez Archipelago islands Robinson Crusoe (red dashed line and box) and Selkirk (green dashed line and box), which in turn harbor the clades marked with red and green circles on the branches, respectively.

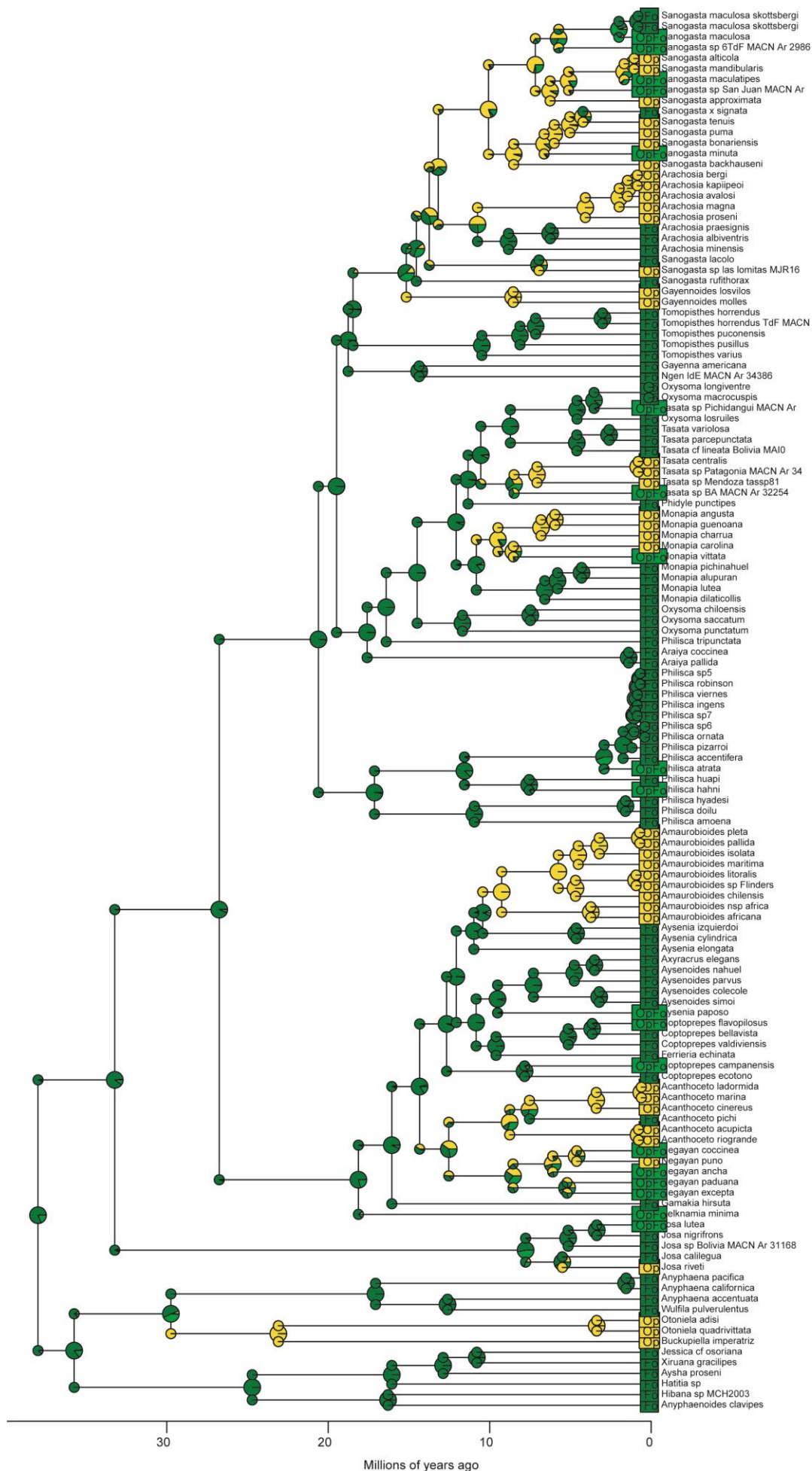


Figure S9. Ancestral habitat estimation based on the DEC+J algorithm in BioGeoBEARS with relative probabilities of ancestral habitat states (open=Op, forest=Fo) shown as pies at nodes.

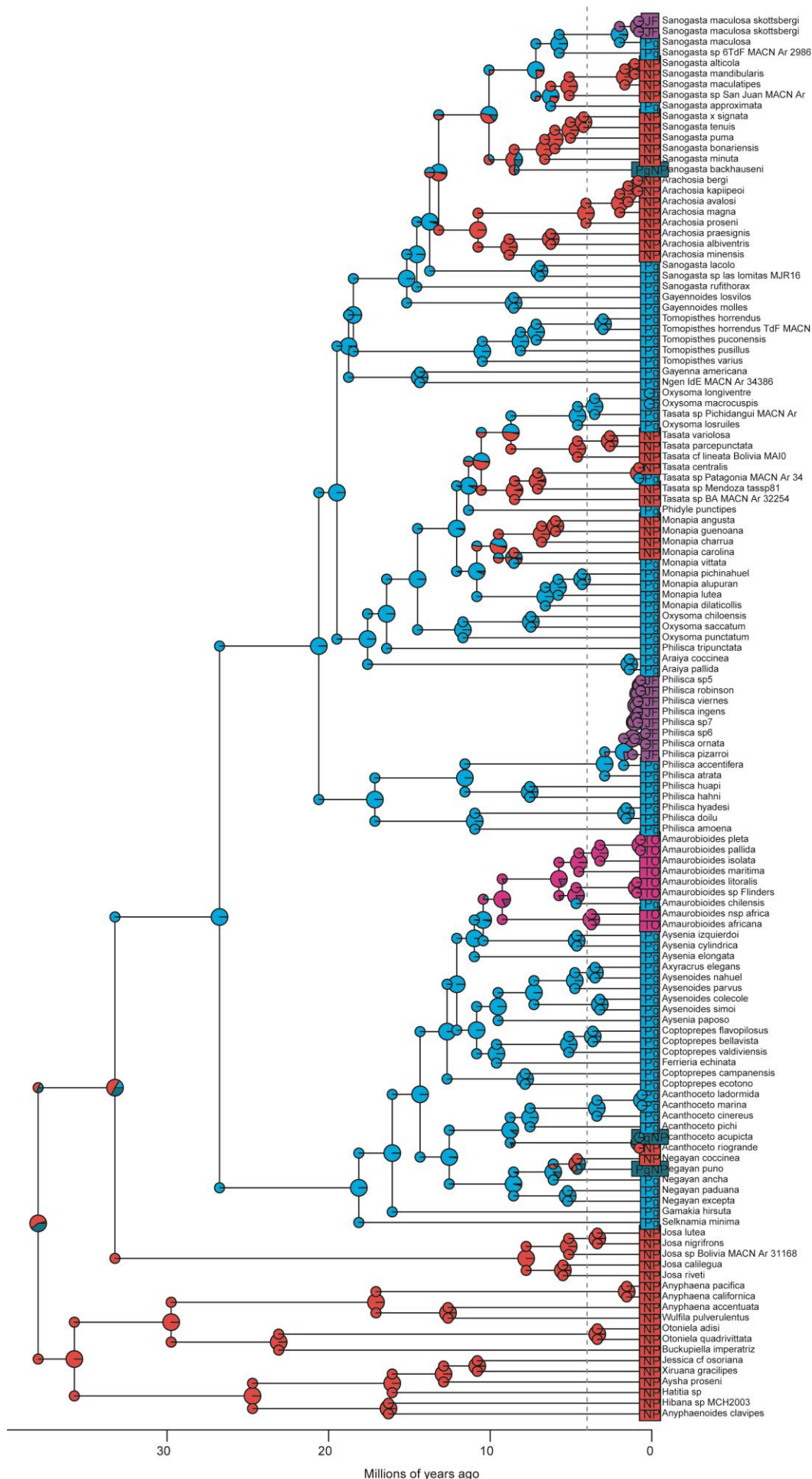


Figure S10. Ancestral area estimation based on the DEC+J algorithm with relative probabilities of ancestral states (Patagonia=Pg, non-Patagonian Neotropics=NP, Juan Fernandez=JF, trans-oceanic=TO) shown as pies at nodes.

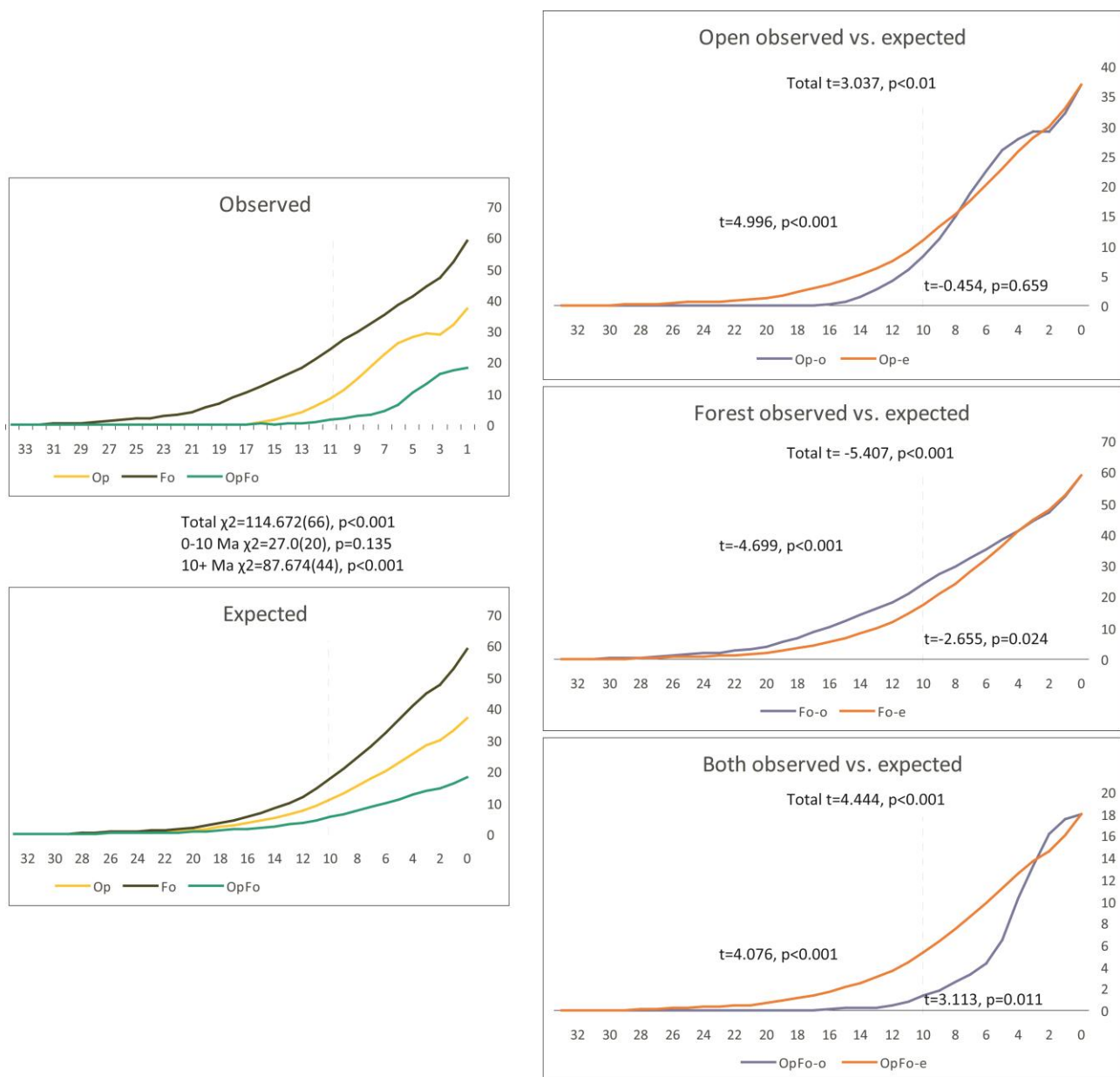


Figure S11. Accumulation curves of number of lineages (y-axis) through time (x-axis; million years ago) occupying open (Op) and forest (Fo) habitats, based on average values of the 100 Bayesian (observed) trees used for ancestral area and habitat estimations in BioGeoBEARS and proportionally down-scaled (expected) values.

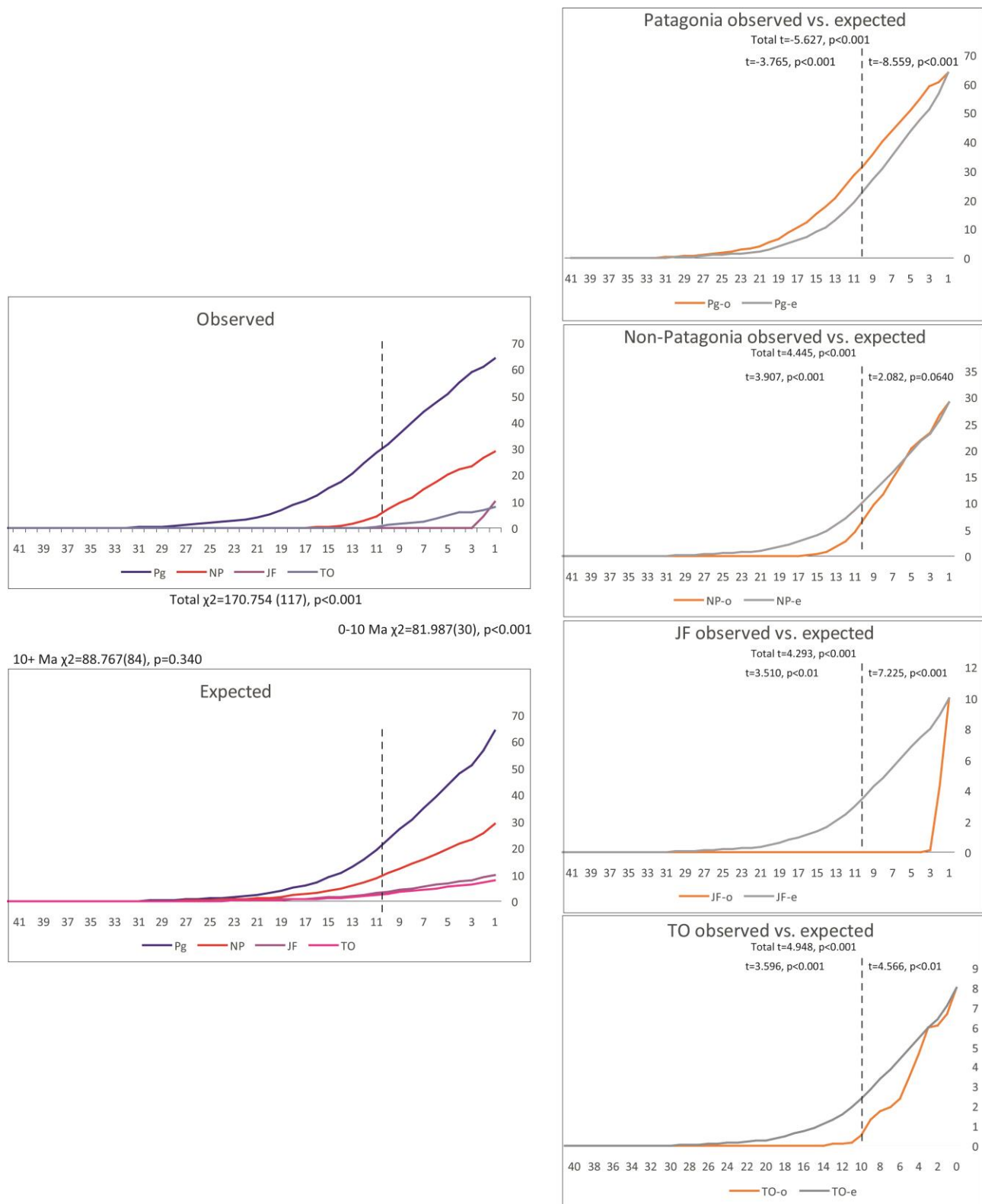


Figure S12. Accumulation curves of number of lineages (y-axis) through time (x-axis; million years ago) found in different areas, based on average values of the 100 Bayesian (observed) trees used for ancestral area and habitat estimations in BioGeoBEARS and proportionally down-scaled (expected) values.

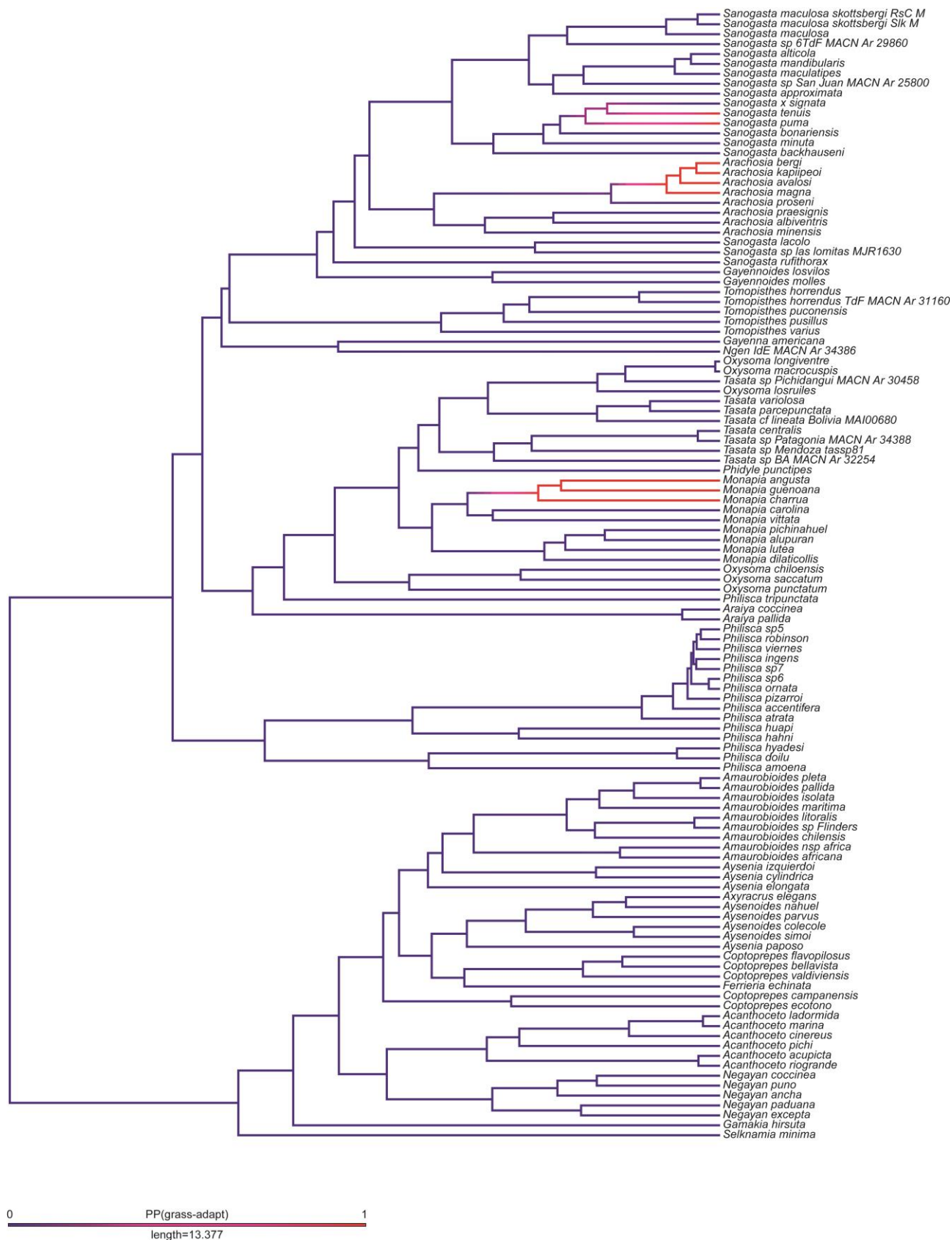


Figure S13. Density map obtained from Bayesian stochastic mapping of 100 replicates of the BEAST mcc tree's A+G clade, showing the posterior probabilities along the branches of grass-adaptation, color-coded as in the legend.

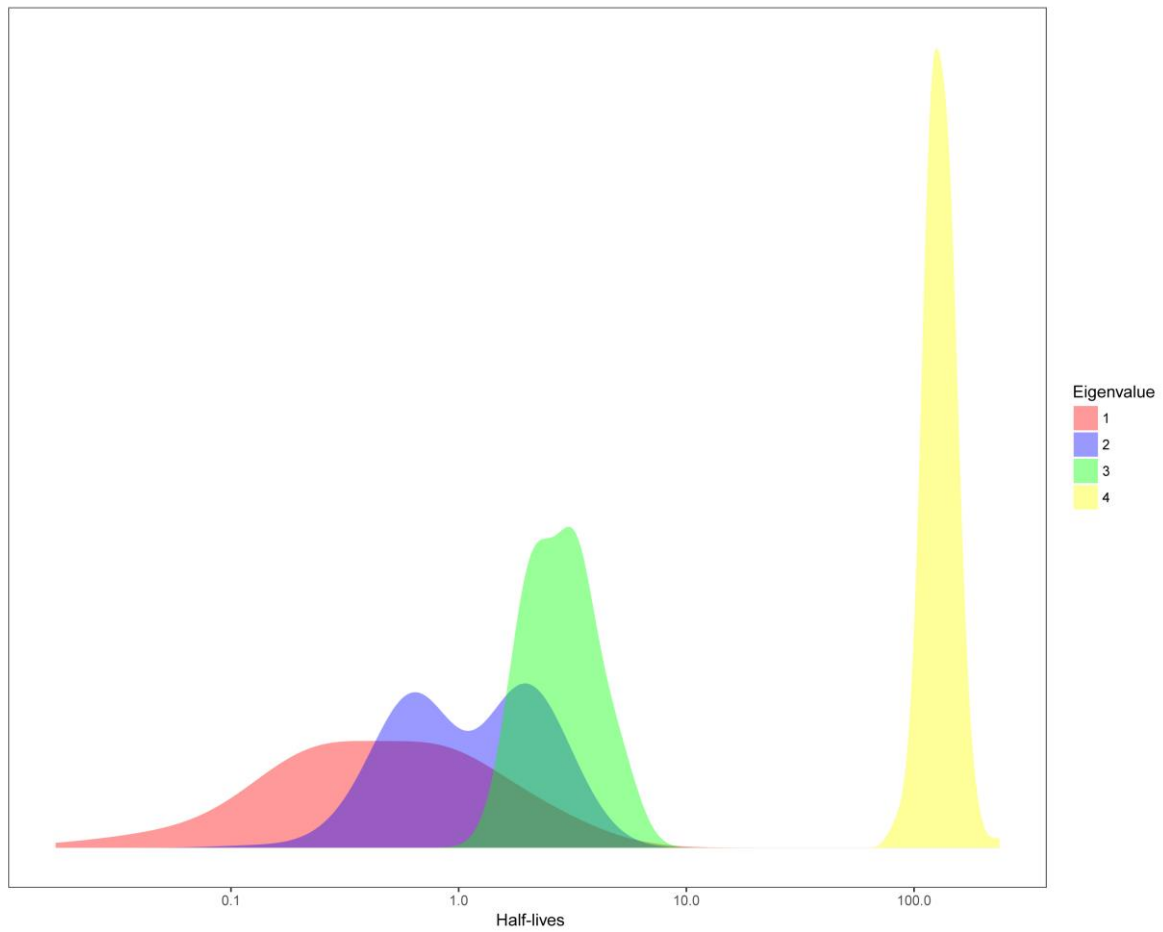


Figure S14. Estimated half-lives for the eigenvalues of the α matrix across replicates. X axis is shown in log scale.

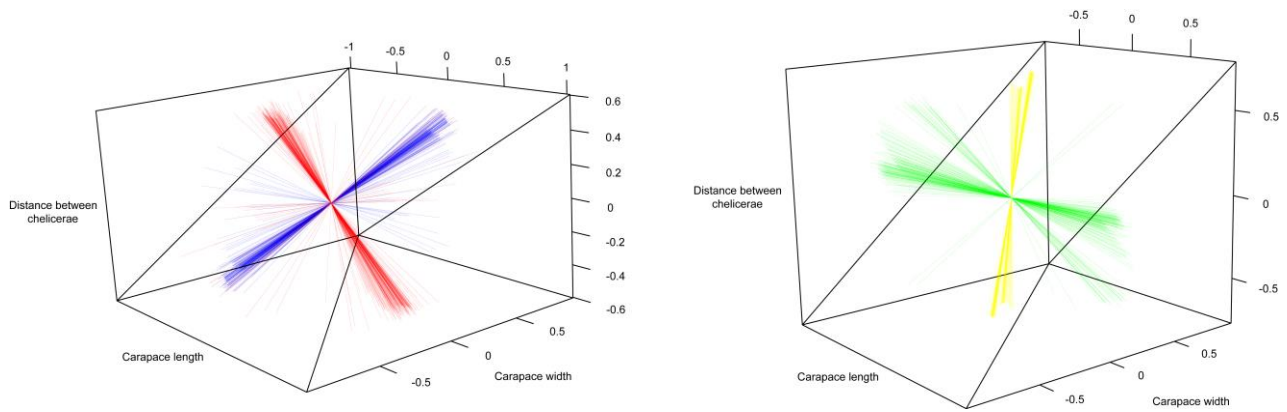


Figure S15. Visualization of eigenvectors of the α matrix across replicates (see also Table S14 of SI File 1). Given the ambiguity in the location of the peaks corresponding to the length of tibia III, this dimension was excluded. Colors are as in Fig. S14, and vectors are centered at 0. Left: Eigenvector 1 shows a strong decrease in the distance between chelicerae as size increases, while eigenvector 2 shows allometric scaling of all traits, corresponding to changes in size but not shape. Right: Eigenvector 3 and 4 seem to capture reductions of the carapace width and the distance between the chelicerae, respectively, with minor changes to the remaining traits. Data and code to reproduce this figure in 3D can be found in SI File 3.