

Supplementary Files for the Manuscript:

The evolution of fungal substrate specificity in a widespread group of crustose lichens.
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Information

This document includes supplementary information to accompany the manuscript.

Extended Materials and Methods

Study system

We focused on lichens formed by members of the ascomycete families Trapeliaceae and Xylographaceae (hereafter: trapelioid lichens). The constituent fungi of trapelioid lichens form a monophyletic group, which has been well studied from taxonomic and phylogenetic perspectives [1-5]. Trapelioid fungi began diversifying about 150-200 Ma BP [6-7]. The lichens in which they occur are exclusively crust-forming and establish physical bonds with a wide range of mineral and organic substrates. They can occur on multiple (generalist) or only one (specialist) substrate type, which can be carbohydrate-rich (e.g. wood and bark) or carbohydrate-poor (rock). Our taxon set consists mostly of specimens and sequences published by [3] and [4], augmented with some new data (Suppl. Table 1). In *Placopsis* we have considered as separate species the OTUs estimated by [4] although they have yet to be formally described as species. Sequences were generated following methods and primers described in [3].

Estimating taxon sampling completeness

To account for bias in species capture, we estimated the number of known species in each group using one of the largest databases for fungal taxonomy, Index Fungorum (www.indexfungorum.org; accessed Jan. 2018). We checked every trapelioid genus except the recently described *Ducatina* and recorded the total number of described species. Additionally, taxonomic and evolutionary knowledge on trapelioid lichens accumulated over the years [8, 1-5]) allows us to estimate the expected total species number of the group with confidence. We then calculated percent ratios of total known versus included species per genus in our dataset (Figure S1). Whenever possible, we performed analyses under multiple sampling regimes.

Chronogram estimation

We assembled a data set of eight fungal loci including mitochondrial ribosomal (mtSSU), nuclear ribosomal (ITS, SSU, LSU) and nuclear protein-coding genes (RPB1, RPB2, MCM7 and EF1alpha; abbreviations following [3]). DNA isolation, PCR and Sanger sequencing were performed as in [3] and [4]. Alignments were generated for each locus using MAFFT [9] following our phylo-scripts pipeline [3, 10]. Using BEAST 2.2.4 [11] we estimated time-calibrated phylogenies for the concatenated dataset using under locus-independent site and clock models and a birth-death tree prior. We chose the best substitution models according to the Akaike Information Criterion (AIC) for each locus with JModelTest 2 [12]. We used relaxed log-normal clocks for ITS, SSU, LSU, RPB2, MCM7 and EF1alpha. For RPB1 we set a strict clock rate as estimated for Lecanoromycetes [13]. We set a normally distributed root prior for the studied group with a mean of 150 million years as estimated by [6] and [7]. After discarding a burn-in of 15%, we combined the log and tree files from two independent 108 generation runs (sampling every 20000th tree) with LogCombiner. Using Tracer 1.5 [14] we investigated convergence diagnostics and estimated sample size (ESS>200) of model parameters.

Tree selection and phylogenetic uncertainty

For downstream analyses we consistently used either a) a random subset of 100 trees selected from the BEAST posterior distribution for analyses using multiple trees to account for phylogenetic uncertainty, or b) a maximum clade credibility (MCC) tree when only single topologies could be used (BAMM). The MCC topology was estimated in TreeAnnotator 2.2.1 after discarding the first 15% of trees as burn-in.

Coding ecological and substrate preference characters

We coded ecological strategies as two sets of categorical variables. Specialization (GS) was treated as binary (generalist: growing on multiple substrates; specialist: growing on single substrate), while the preferred substrate (PS) was coded as multistate (rock, soil, bark, wood, other lichens). We derived substrate use data from our own collections as well as from herbarium collections (BG, GZU, UPS), species catalogs [15], identification keys [16-17] and recent monographs (Placopsis: [18], Xylographa: [2]). A species was considered a specialist when >95% of its global occurrences were from one substrate.

Testing for phylogenetic signal

We estimated phylogenetic signal of the PS variable using two simulation-based multi-tree approaches: a) recursive use of Pagel's λ [19], and b) comparison of the distribution of cophenetic distances. In the first approach, we transformed each tree for eleven different values of Pagel's λ given our own character data (Table S1), and retained a distribution of AIC scores of fitted maximum likelihood models of trait evolution [20] with the R package geiger [21]. To obtain null models, we simulated 100 random character distributions for each tree while maintaining the number of individuals with different character states and repeatedly fitted a model of trait evolution. We compared the AIC score of the original model to the distribution of AIC scores from simulations with one-sided Mann-Whitney tests (considered significant if $p < 0.05$) and created density plots of the obtained p values. We consider phylogenetic signal strong when the real character distribution has better fitting models than the simulated datasets even for small values of λ (when the tree topology gets more star-like). λ tree transformations and model fitting were performed using rescale() and fitDiscrete() from geiger [21].

As a second measure for phylogenetic signal, we assume that closely related species are ecologically similar [22-23] due to shared evolutionary histories. When species with the same phenotypic character are clustered in the tree, their mean tip-to-tip distance should be smaller compared to when they are randomly dispersed. First, we calculated the mean per-tree distances between all species pairs having the same character state. Next, we shuffled the original character assignments to create randomly distributed tip states and calculated means as above. We repeated this procedure 100 times per tree and compared the obtained distributions to the mean distribution from the true character assignment with Mann-Whitney tests (significance considered for $p < 0.05$). We calculated tip-to-tip distances for each tree with the function cophenetic.phylo from the R package ape [24] and summarized the obtained p -values in density plots.

Ancestral state reconstruction

Different methods of ancestral state reconstruction as well as the parametrization of the different models may result in divergent or contradictory results [25]. We used three alternative multi-tree methods to be able to compare reconstruction of the ancestral states for the GS and PS variables at the main 19 internal nodes of the Trapeliales phylogeny (Figure 1). (1) We employed a maximum likelihood approach based on [26] and implemented in the ace function in ape [24], imposing models with equal (ER), symmetric (SYM) and asymmetric rates (ASR) of character evolution. Ancestral states on internal nodes were estimated jointly [27] as well as marginally using only information from the tip states. (2) We used a second maximum likelihood approach described in [28] and implemented in function rayDISC of the R package corHMM [28]. rayDISC allows uncertainty of tip states to be incorporated by imposing probabilities on tip state distributions, in this case allowing us to account for species colonizing multiple substrates (Table S1). Again we used ER, SYM and ASR models as well as joint and marginal estimations of ancestral states. Furthermore, we employed methods proposed by [20], [29] and [30] to weight the probability of ancestral states at the root of the tree, as well as rayDISC's default, which assumes equal weighting among all states. (3) We used stochastic character mapping [31] to infer posterior probabilities of ancestral states using phytools [32]. Again we used models with equal, symmetric and asymmetric rates and we estimated rate parameters for each tree using a Markov Chain Monte Carlo (MCMC) approach ($Q = "mcmc"$) and a time-continuous Markov model ($Q = "empirical"$). For each character set we created 100 maps per tree.

To provide a summary of ancestral character reconstruction while accounting for bias introduced by methods, models and tree topologies, we developed a recursive strategy. First we fitted models with all possible parameter combinations available for each method to each tree. Then we only considered as the most probable ancestral state the one recovered most often across all analyses and tree topologies. The most probable ancestral states identified across all 24 different simulations are shown with the maximum clade credibility tree. For each node we created a plot indicating the number of trees for which a particular ancestral character state was estimated under all possible models for one method.

Reconstructing transitions between substrates

To investigate the evolutionary transitions between substrate types we used stochastic character mappings created for ancestral state reconstructions (see above) under an unconstrained model (ARD). Transitions between the different character states were counted and relativized by the total number of character transitions for each tree. The cumulative results of the 10,000 alternative transition histories were summarized numerically and are presented as histograms for binary ecological strategy characters (GS) and as circle plots for multi-state substrate characters (PS).

Testing substrate “no-switch” scenarios

To test whether models prohibiting certain substrate transitions are more likely given our set of trees, we created thirty transition rate matrices describing different scenarios of character change. We compared these constrained models on each of the 100 trees from the BEAST posterior distribution of trees. The tested models include all possible combinations of no-switch scenarios for our multistate substrate character. Each model and each tree was subjected to a maximum likelihood ancestral state estimation with `ace()` from `ape` [24]. We then calculated AIC scores and ranked models from best to worst according to AIC score comparisons for each tree. To see which models scored best over all trees, we calculated for how many trees a specific model would be the best, second best, third best and so on. Then we searched for the models for which the majority of trees were recovered in the first five ranks.

Modeling of diversification rates

To characterize the diversification dynamics of the trapezoid clade we used character-independent Bayesian analysis of macroevolutionary mixtures (BAMM) [33] as well as character-dependent SSE models [29-30]. Using BAMM 2.6.0 we studied the speciation rate dynamics of the MCC tree topology. The priors and initial values for λ , λ -shifts and μ used to initialize the Bayesian BAMM analyses were estimated with `setBAMMpriors` [34]. BAMM was run for 107 generations saving every 1000th step. We ran three independent analyses assuming different sampling regimes (100% and two more; see above). We analysed the BAMM output with `BAMMtools` [34] discarding a 20% burn-in. Finally, we summarized results graphically by plotting the 95% credibility sets of rate-shift configurations and rate through time plots for individual clades as well as for the whole tree.

To investigate effects of character realizations on diversification dynamics we utilized multi-state speciation extinction models (MuSSE; [29]) implemented in `diversitree` [35]. Unlike BAMM, MuSSE can be used as a multi-tree method, and we took advantage of this to analyse our sample of 100 tree topologies randomly chosen from the BEAST posterior distribution. For each tree we fitted a MuSSE model using an MCMC run of 1000 generations under exponential priors and sampling every 10th generation. We combined the posterior samples from all 100 runs and created density plots for λ , μ and diversification rate ($\lambda\cdot\mu$). We repeated the analysis for different sampling scenarios according to our species completeness information. To identify significantly different speciation rates, we compared the obtained probability distributions with Mann-Whitney tests for all possible combinations of characters. The lack of consensus on the performance and suitability of the SSE approach to model evolutionary trends [36] led us to test the extent to which the modelled diversification rates respond to the phylogenetic tree alone without a further connection to

the distribution of characters on the tree. For this we implemented the method and scripts developed by [36] to simulate 100 neutral binary characters on our MCC tree under different transition rate parameters ($q=0.01/0.1/1/10$). We tested if these neutral characters are associated with a speciation rate increase using likelihood ratio tests on models with $\lambda_0 = \lambda_1$ and λ_0, λ_1 , respectively. We also simulated an alternative null distribution of pure-birth trees of the same size as our MCC tree without rate heterogeneity. We performed simulations for 100 neutral binary characters for different values of q as above and tested if the character distributions were associated with speciation rate changes.

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Figure S1 - Relative sampling completeness

Sampling completeness of sampled taxa used in this study. (a) Relative number of species sampled and grouped by substrates. Numbers above bars indicate number of species sampled in our dataset and total number of known trapezoid species growing on a particular substrate. (b) Relative number of species sampled per genus. Numbers above bars indicate sampled number of species per genus and total number of species per genus according to different information sources.

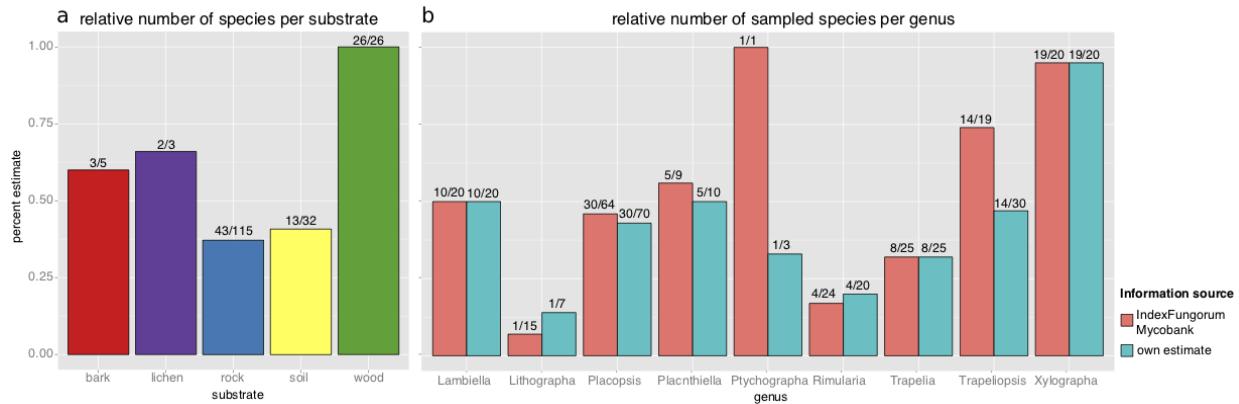


Figure S2 - Phylogenetic informativeness simulation 1: Pagel's Lambda

p-value distributions of phylogenetic signal analyses relying on Pagel's lambda: We transformed each of the 100 trees from the BEAST posterior tree distribution for eleven values of lambda and fitted models using tip distributions of the preferred substrate character on each. To obtain a null-model we simulated 100 random character distributions and fitted models for each simulated character on each tree. We then compared AIC scores of fitted models for the preferred substrate character set to the distribution of AIC scores obtained from random character sets for each tree with a Mann-Whitney test. p-values < 0.05 indicate significantly better fit (higher phylogenetic signal) for the real character distribution compared to simulated characters. y-axis = number of trees, x-axis = p-value

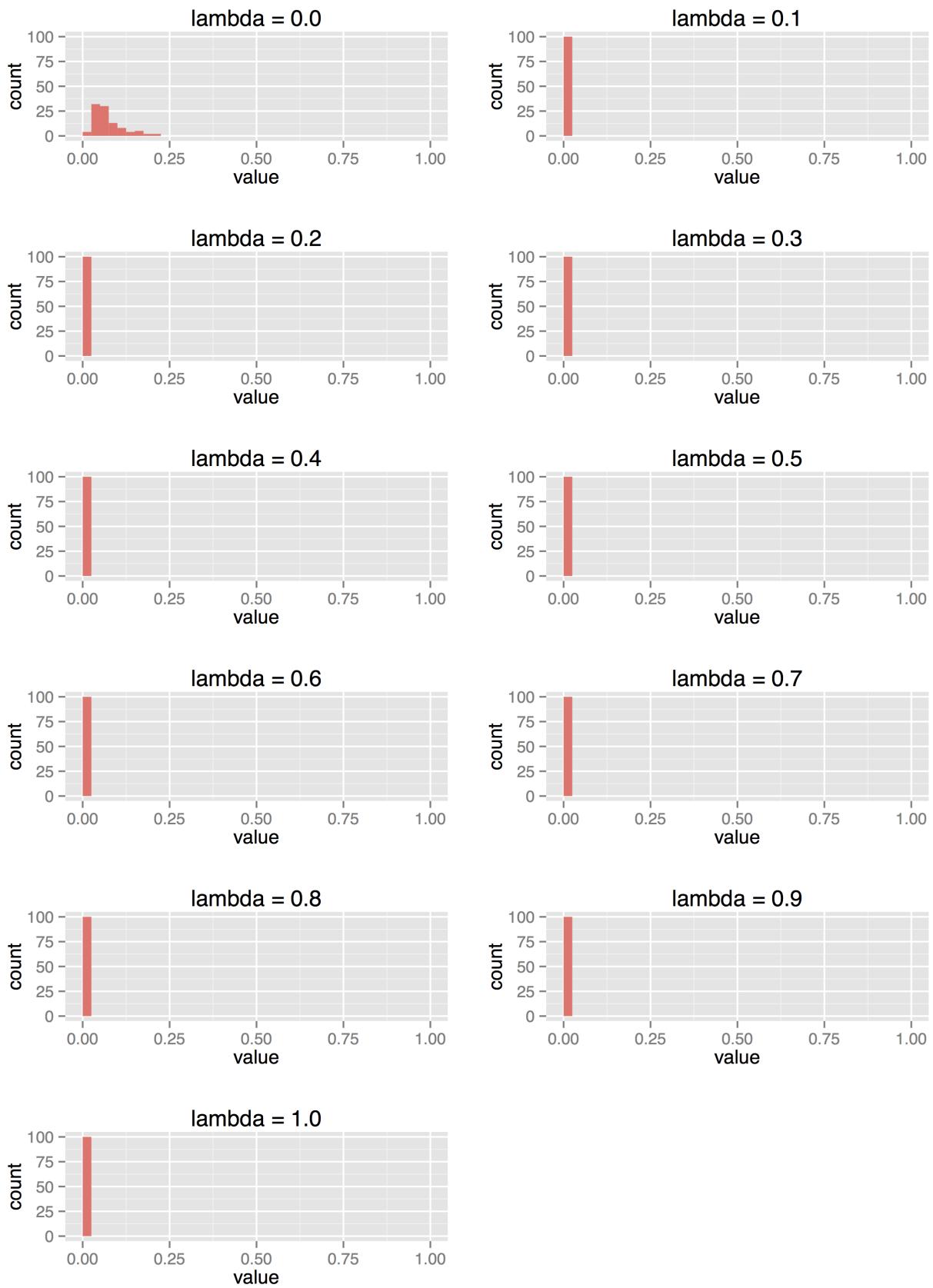


Figure S3 - Phylogenetic informativeness simulation 2: Distance method

Results of phylogenetic signal test assuming that closely related species are ecologically more similar than distantly related species. Plots show p-value distributions of Mann-Whitney tests of differences between mean tip-to-tip distances of real character distribution and simulated character distributions for each tree. blue = rock, yellow= soil, green= wood, red = bark, purple= lichen.

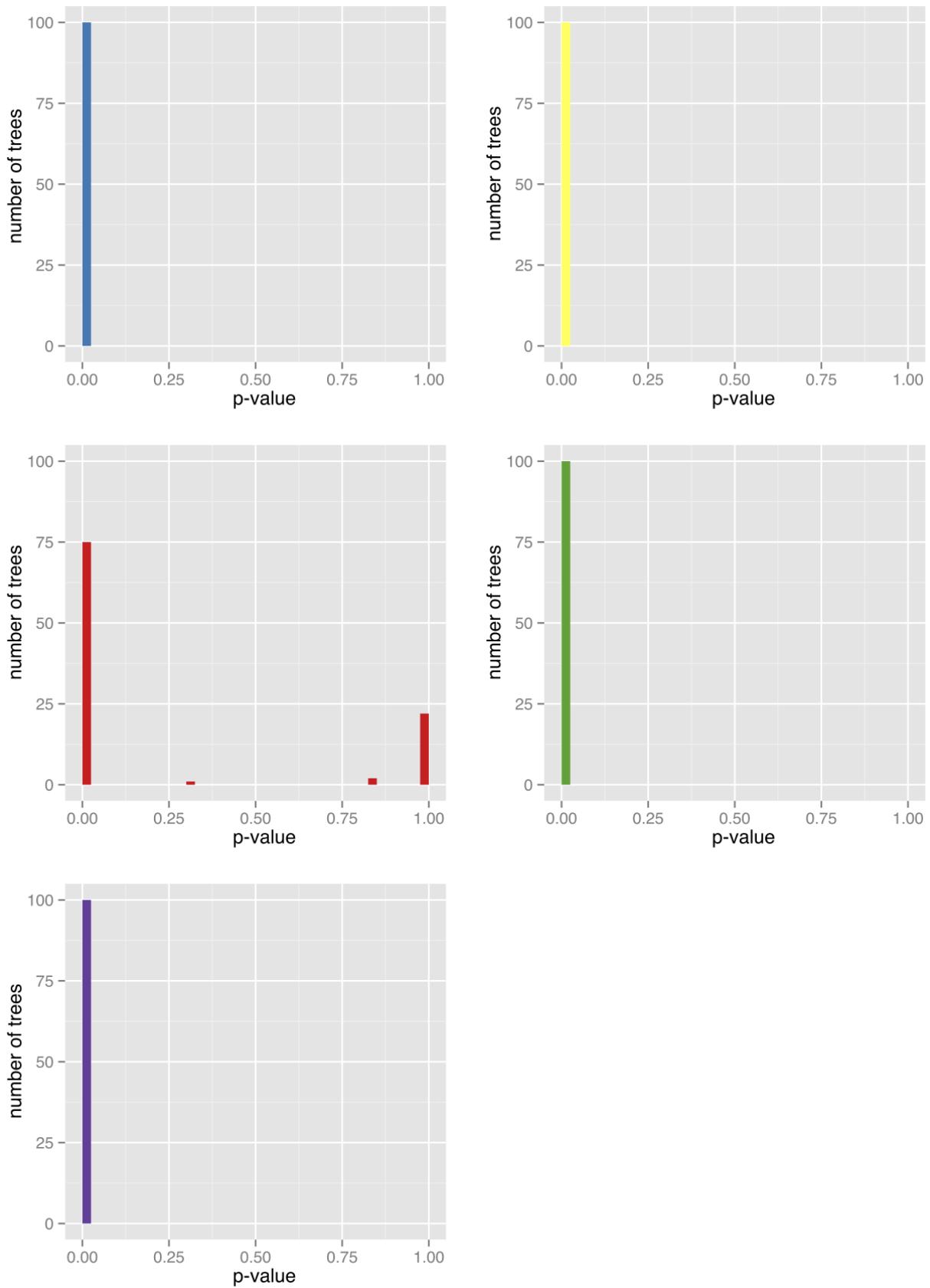
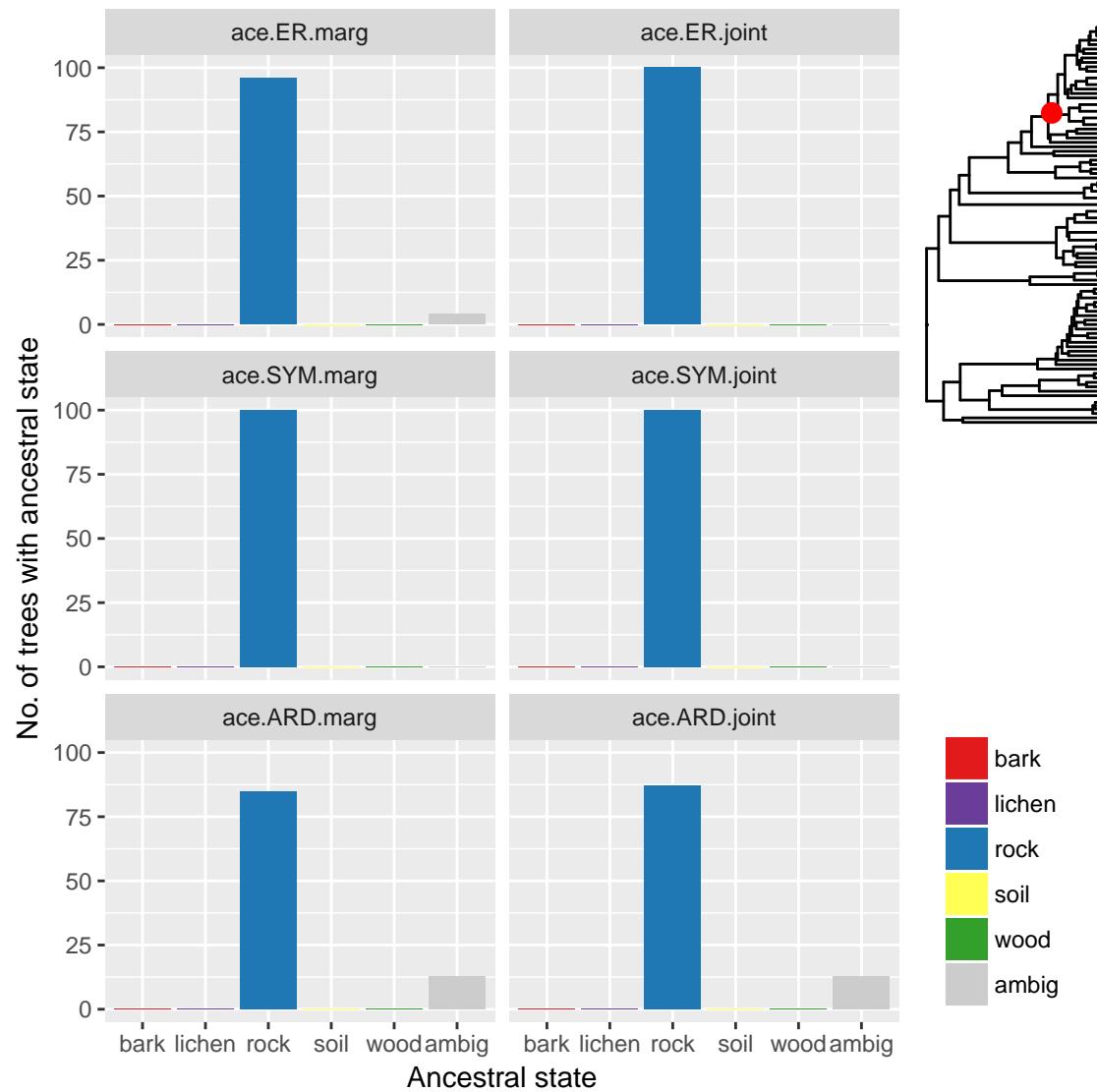


Figure S4-S22 - Results of ancestral state estimation of the preferred substrate character with ace for 19 nodes of the trapezoid phylogeny

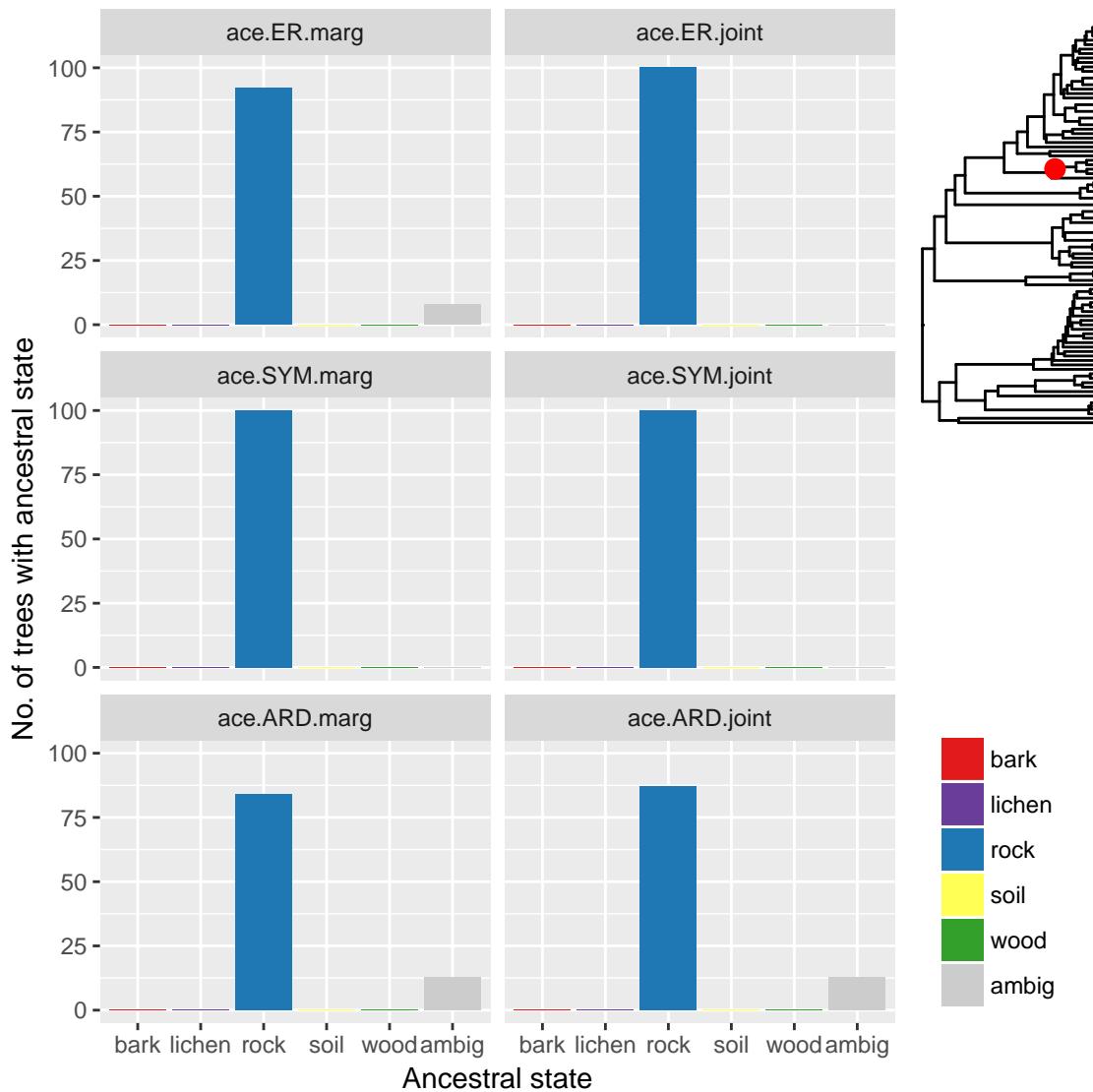
Ancestral state estimations of the preferred substrate character for 19 nodes of the trapezoid phylogeny based on the method implemented in the ace function in the R package ape imposing 6 different models. Please refer to the main text for details.

Figure S4: Ancestral states for node 1



- █ bark
- █ lichen
- █ rock
- █ soil
- █ wood
- █ ambig

Figure S5: Ancestral states for node 2



- █ bark
- █ lichen
- █ rock
- █ soil
- █ wood
- █ ambig

Figure S6: Ancestral states for node 3

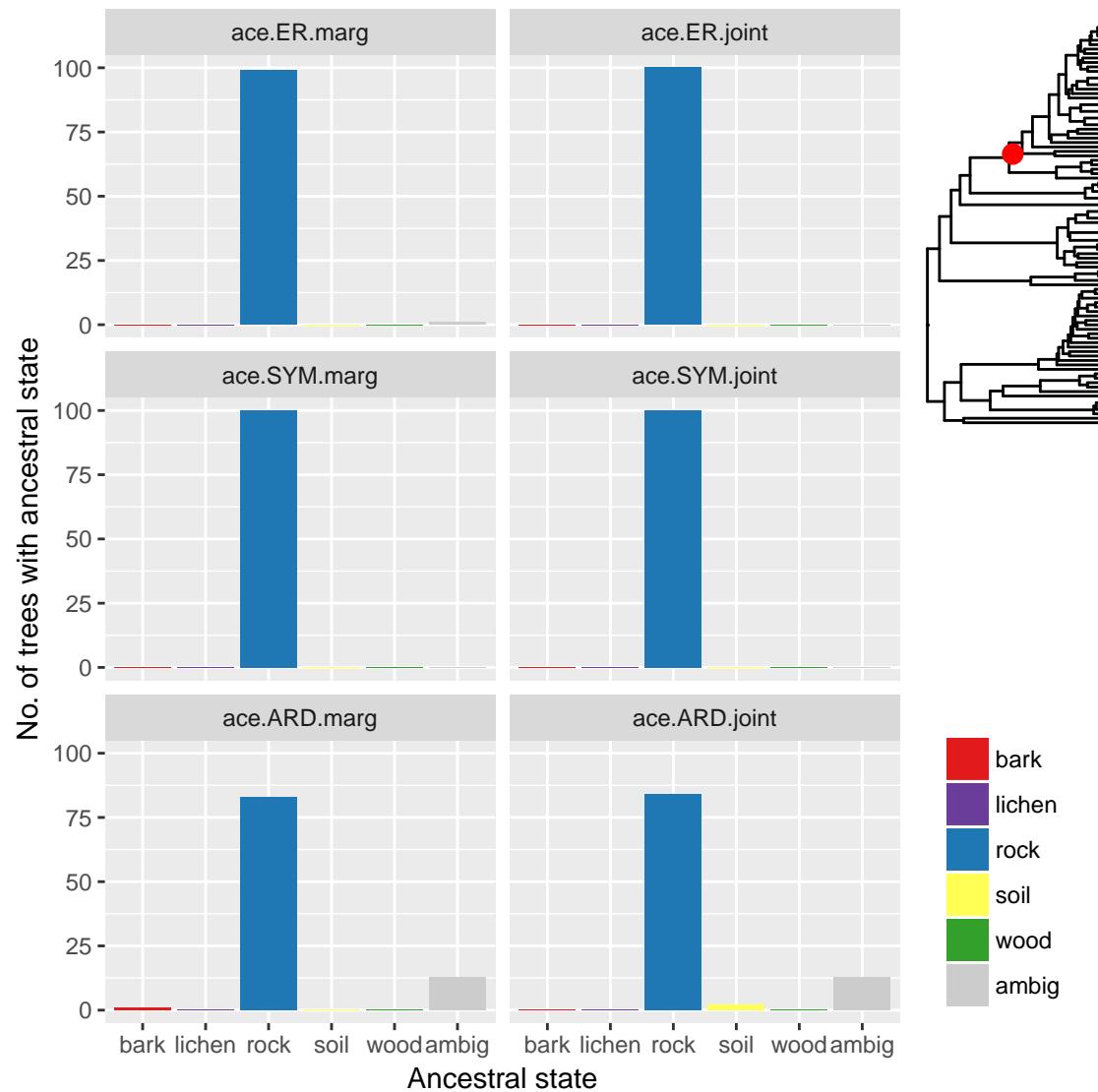


Figure S7: Ancestral states for node 4

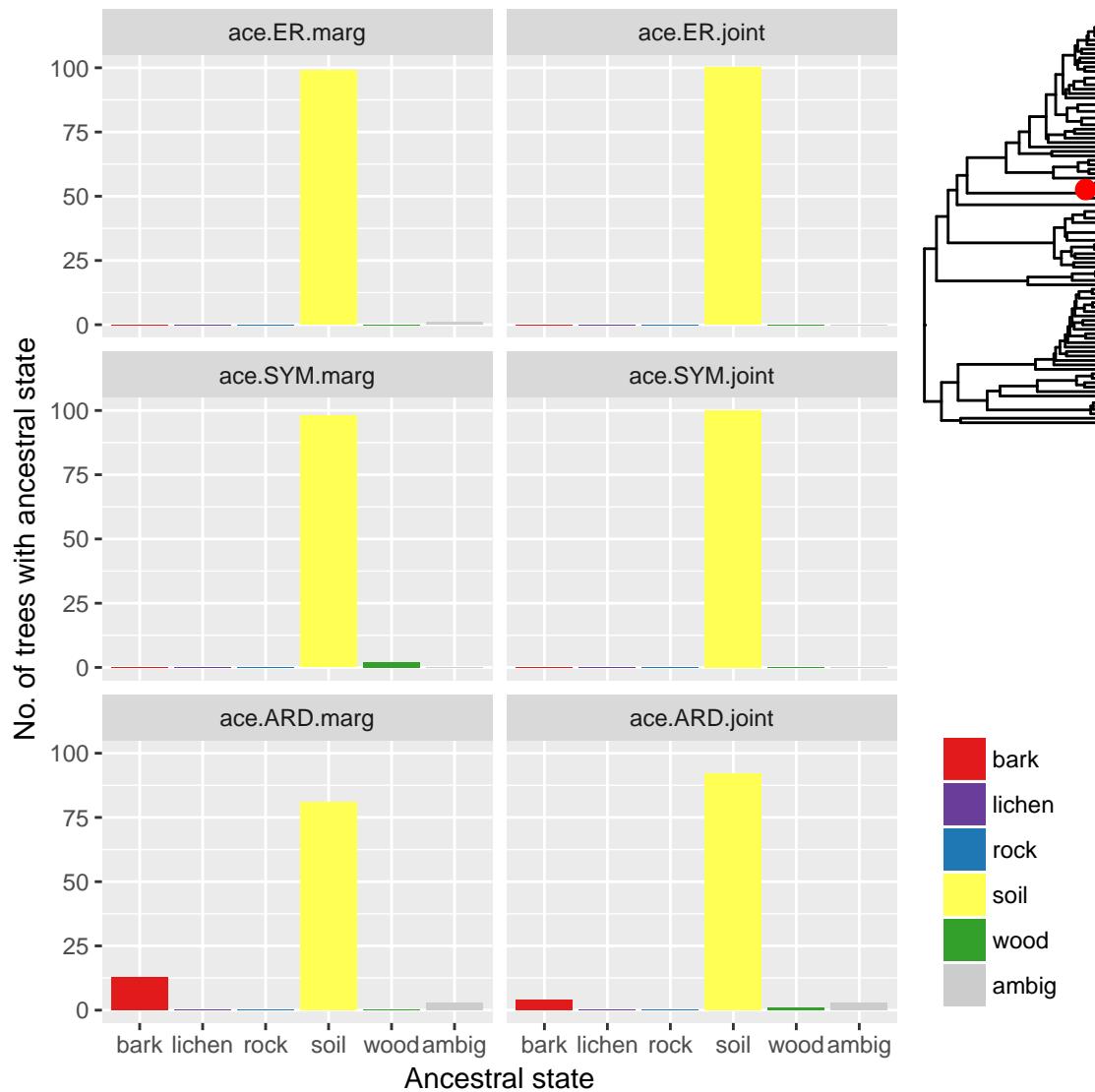


Figure S8: Ancestral states for node 5

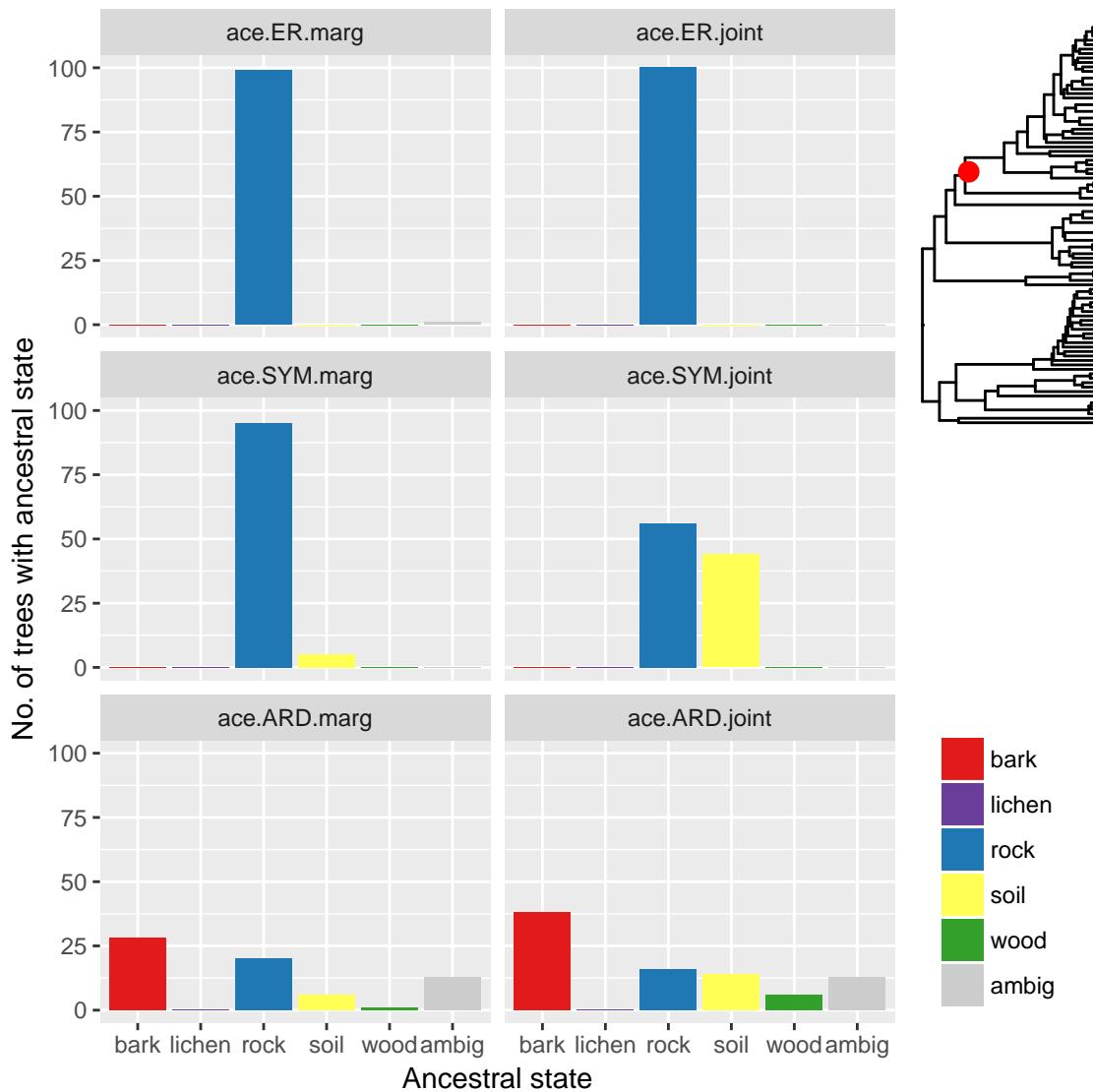


Figure S9: Ancestral states for node 6

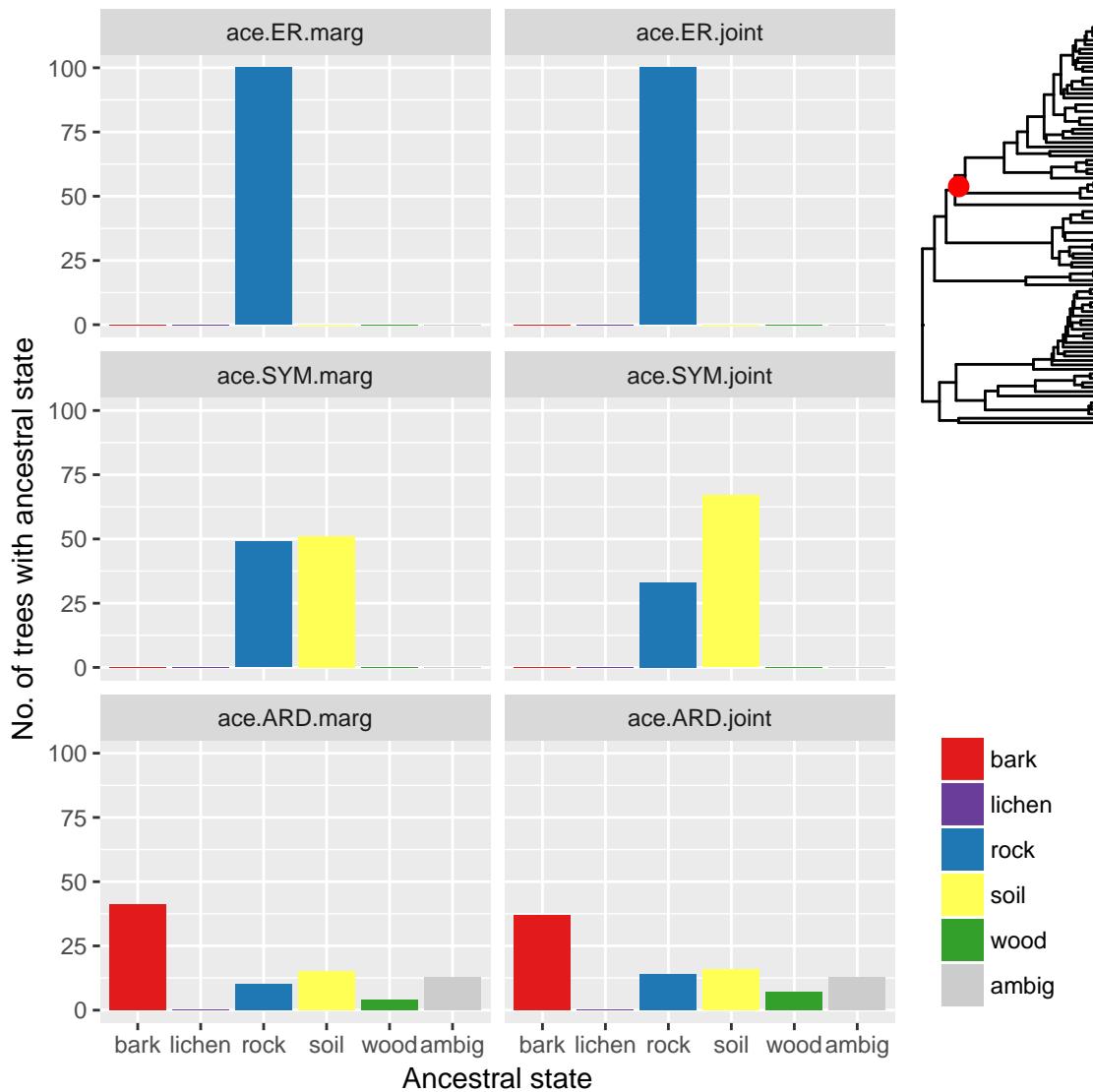


Figure S10: Ancestral states for node 7

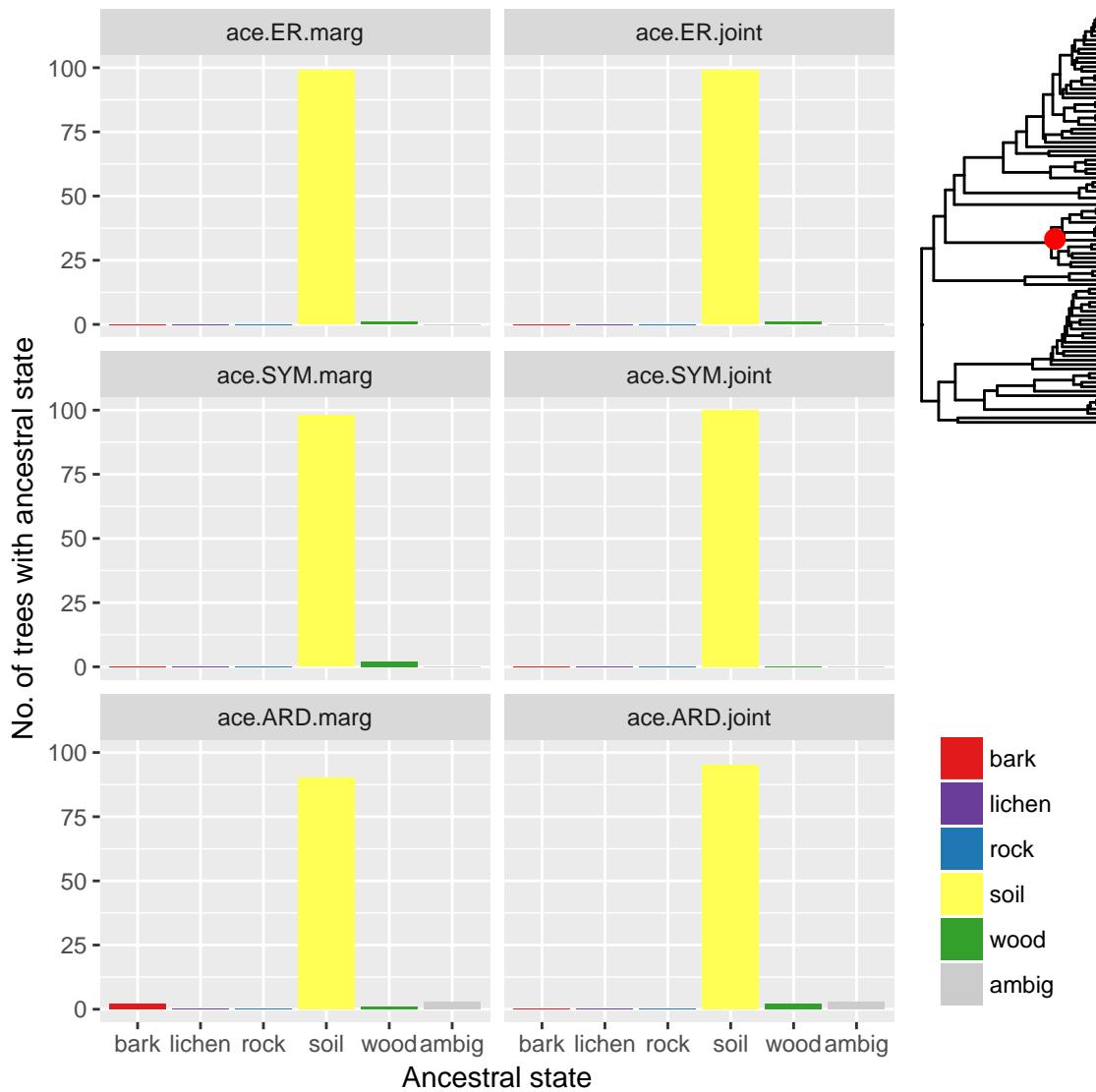


Figure S11: Ancestral states for node 8

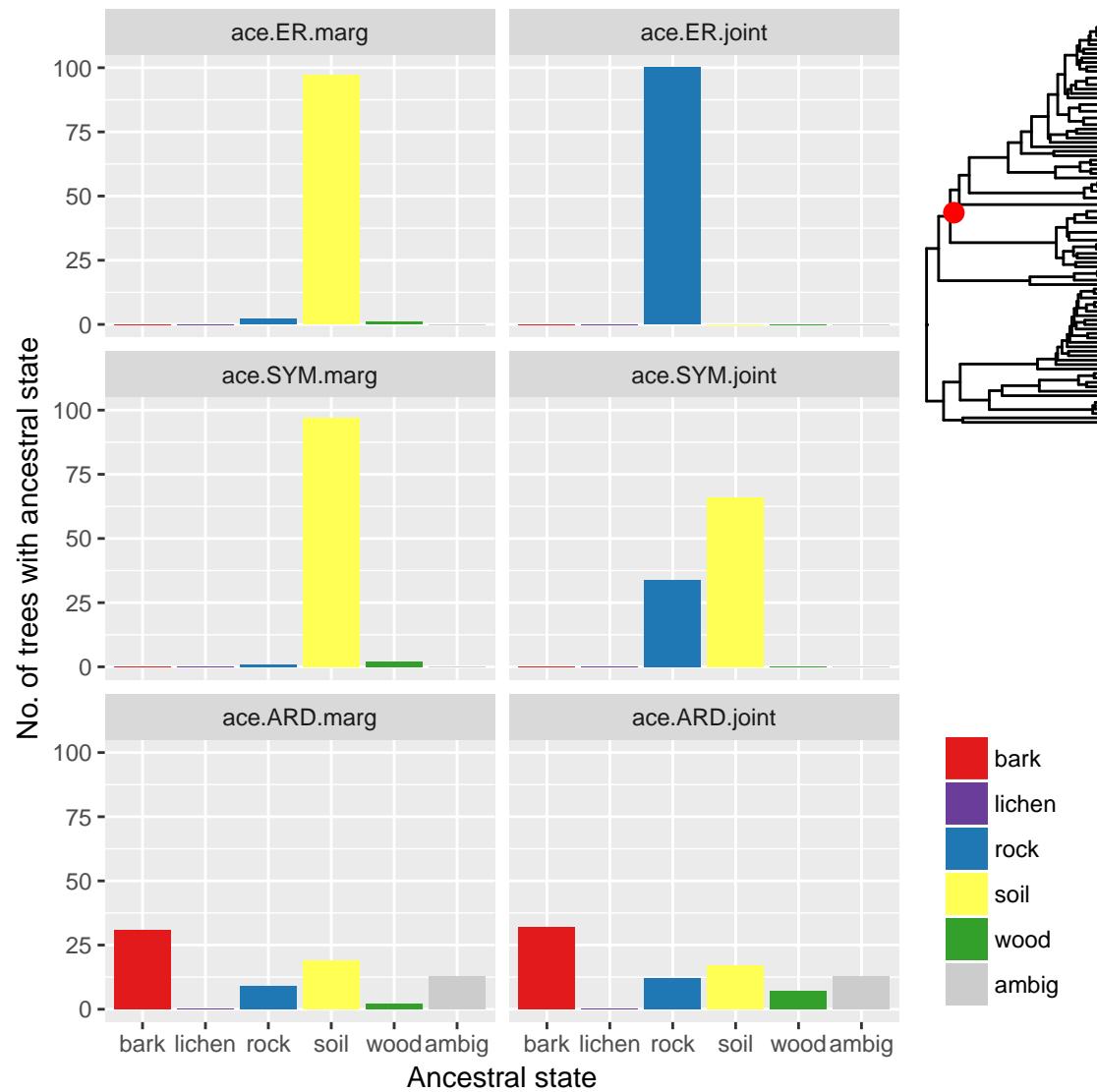


Figure S12: Ancestral states for node 9

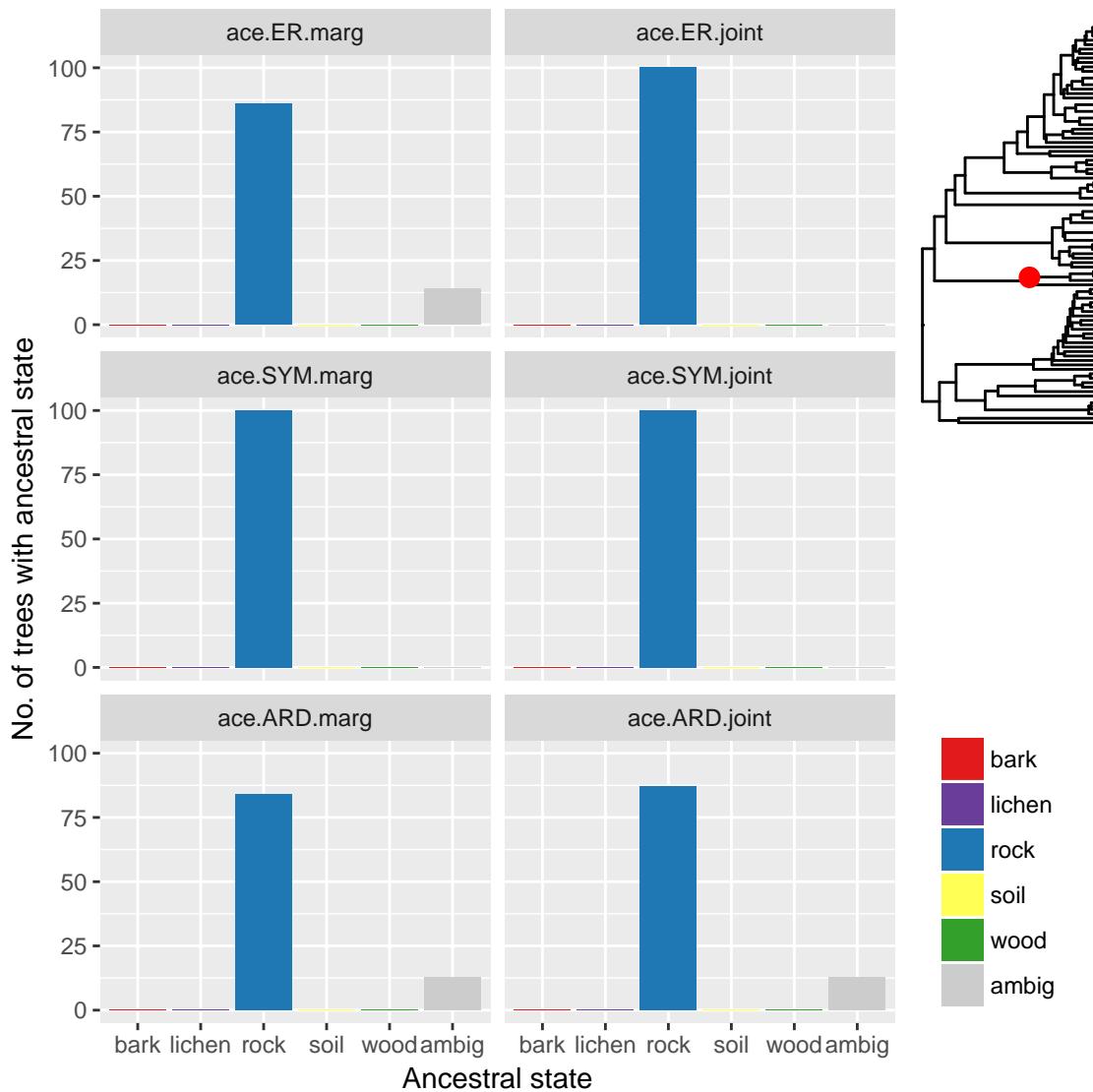


Figure S13: Ancestral states for node 10

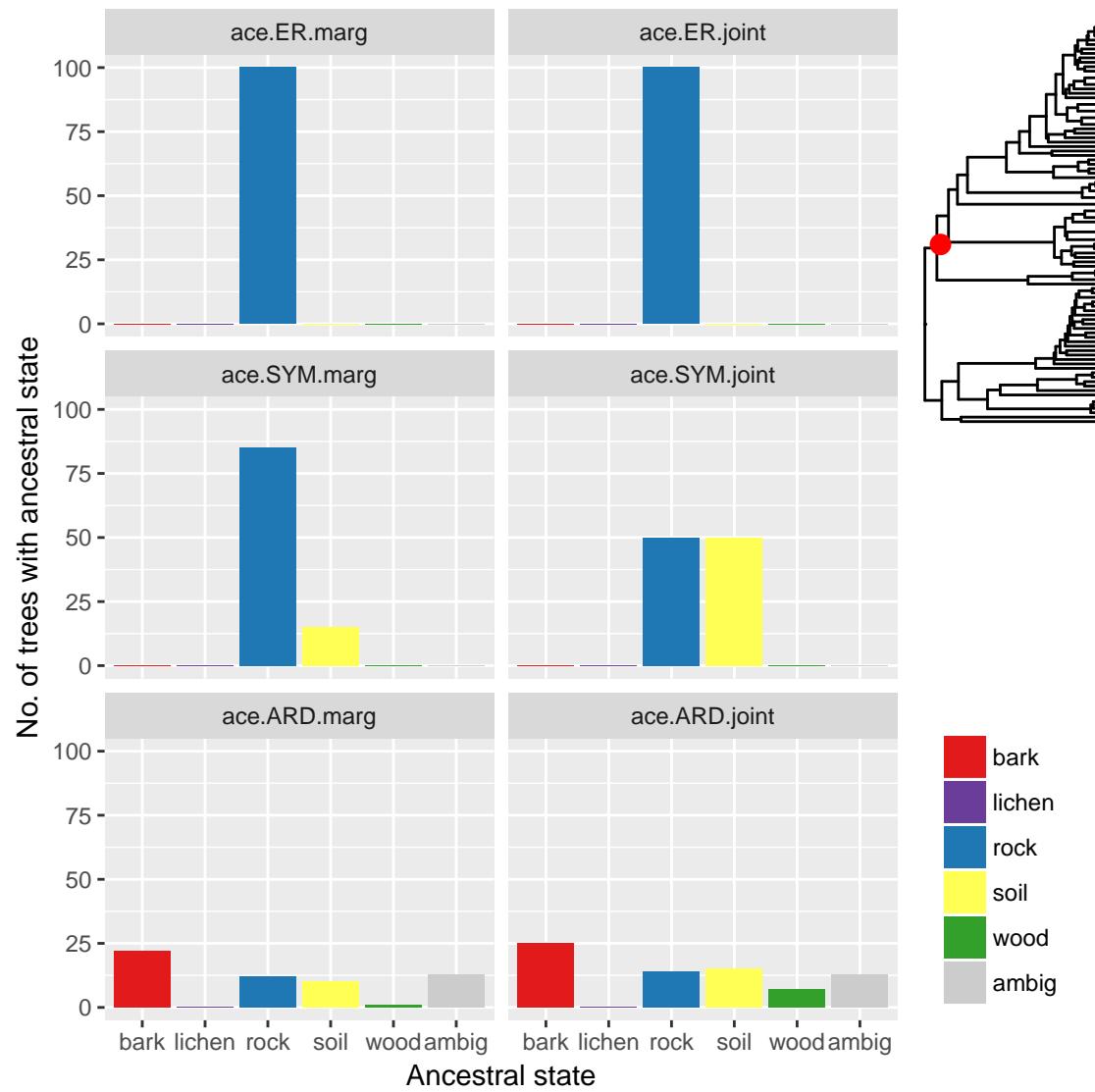


Figure S14: Ancestral states for node 11

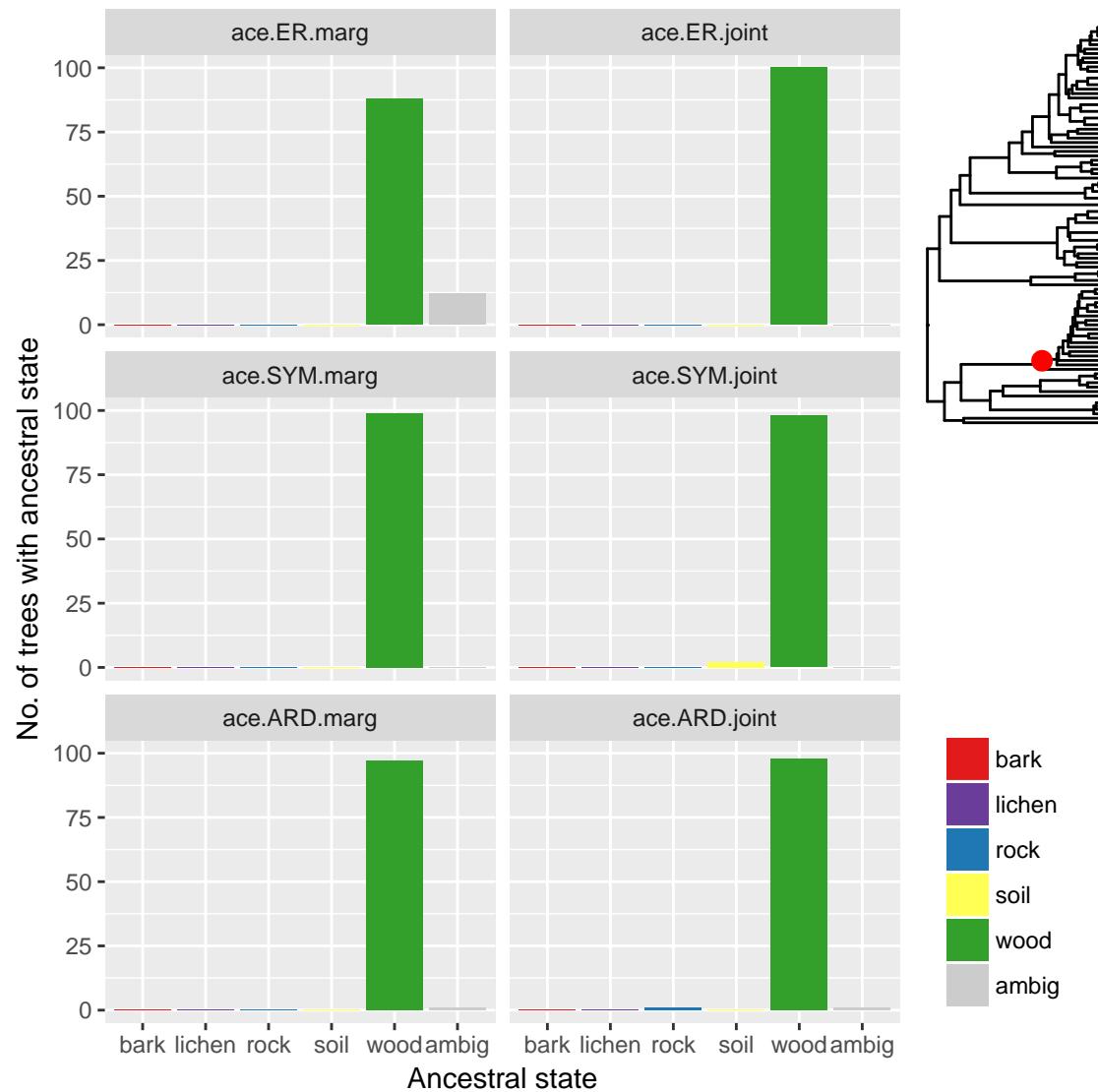


Figure S15: Ancestral states for node 12

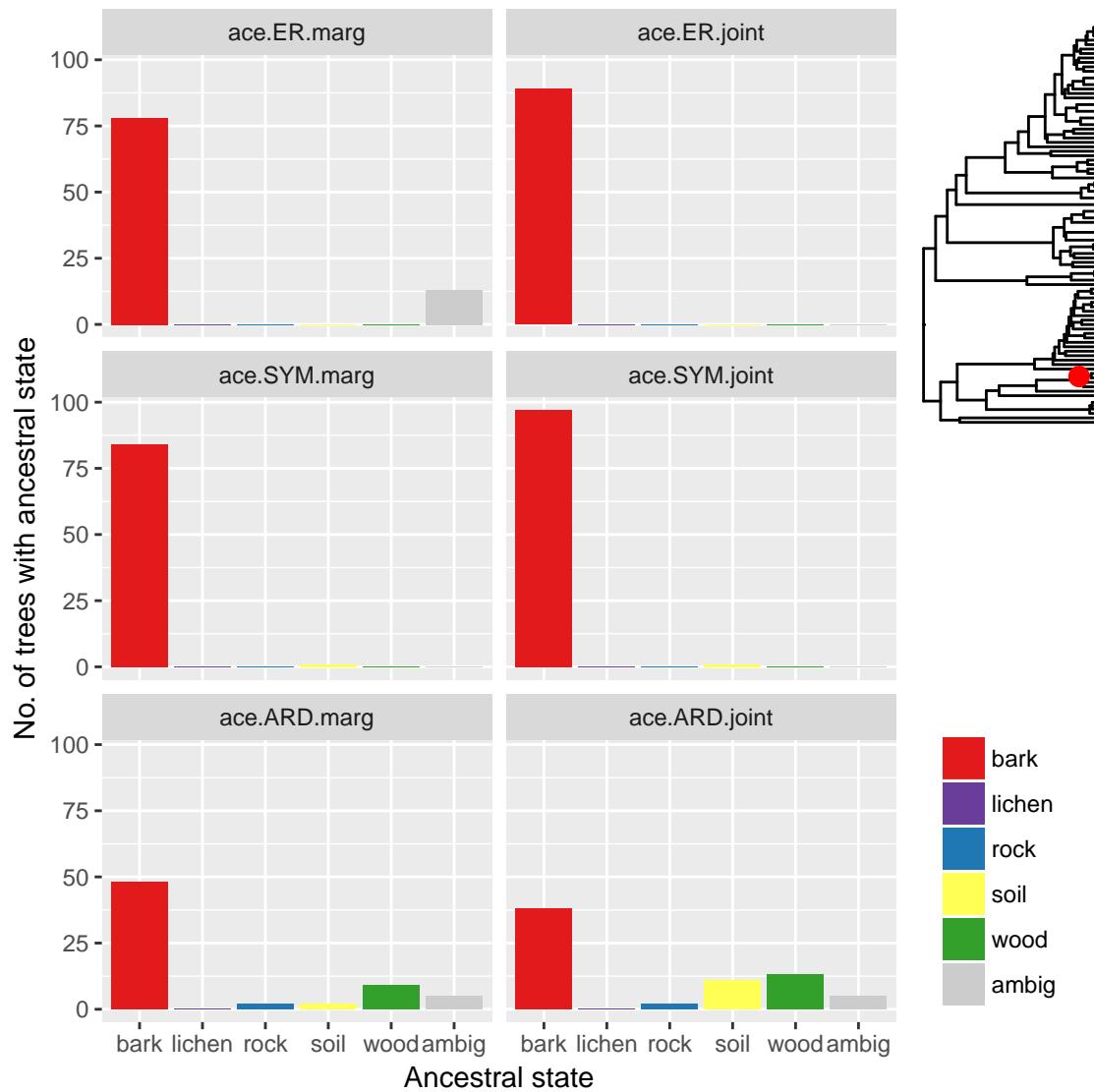


Figure S16: Ancestral states for node 13

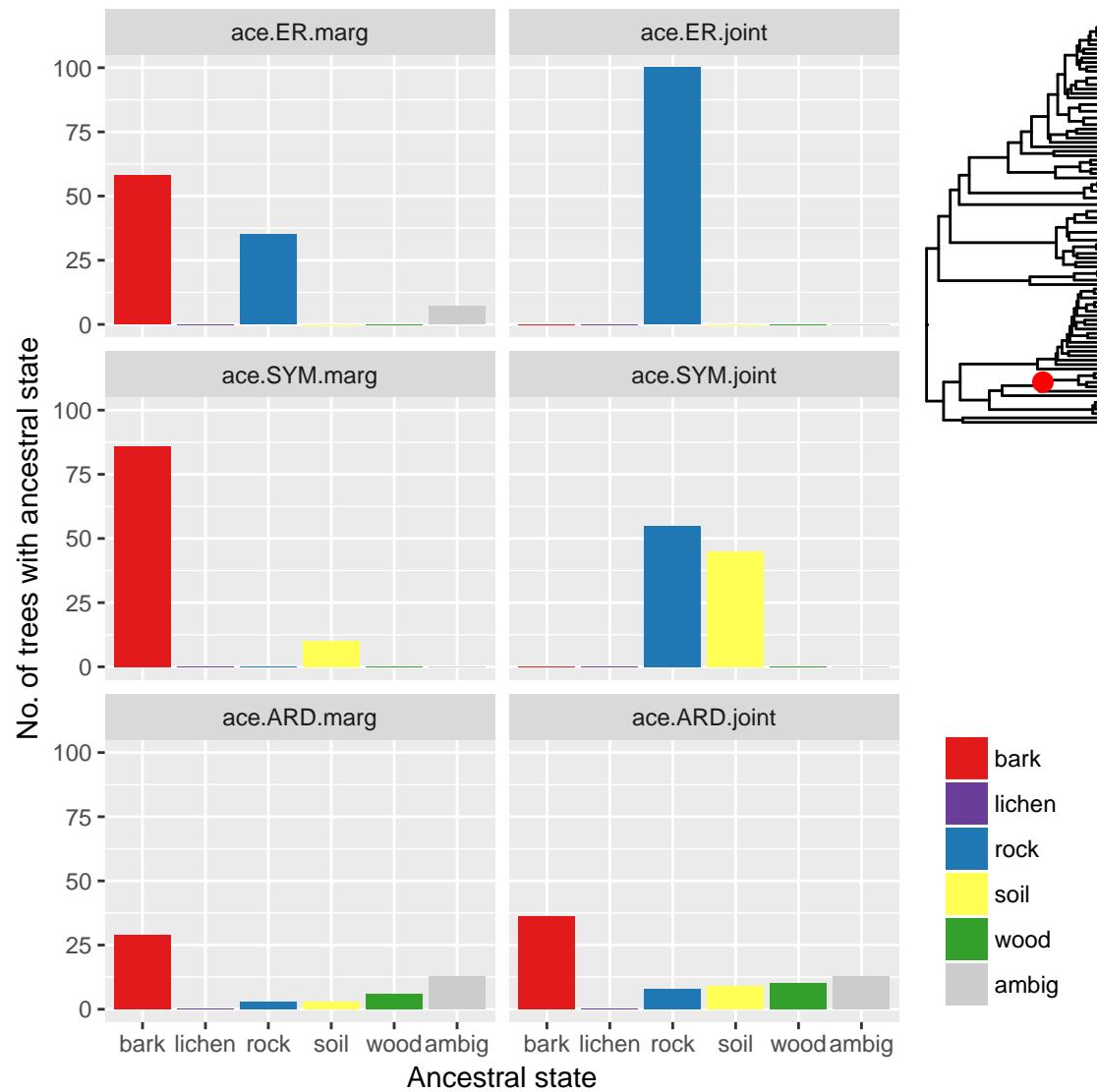


Figure S17: Ancestral states for node 14

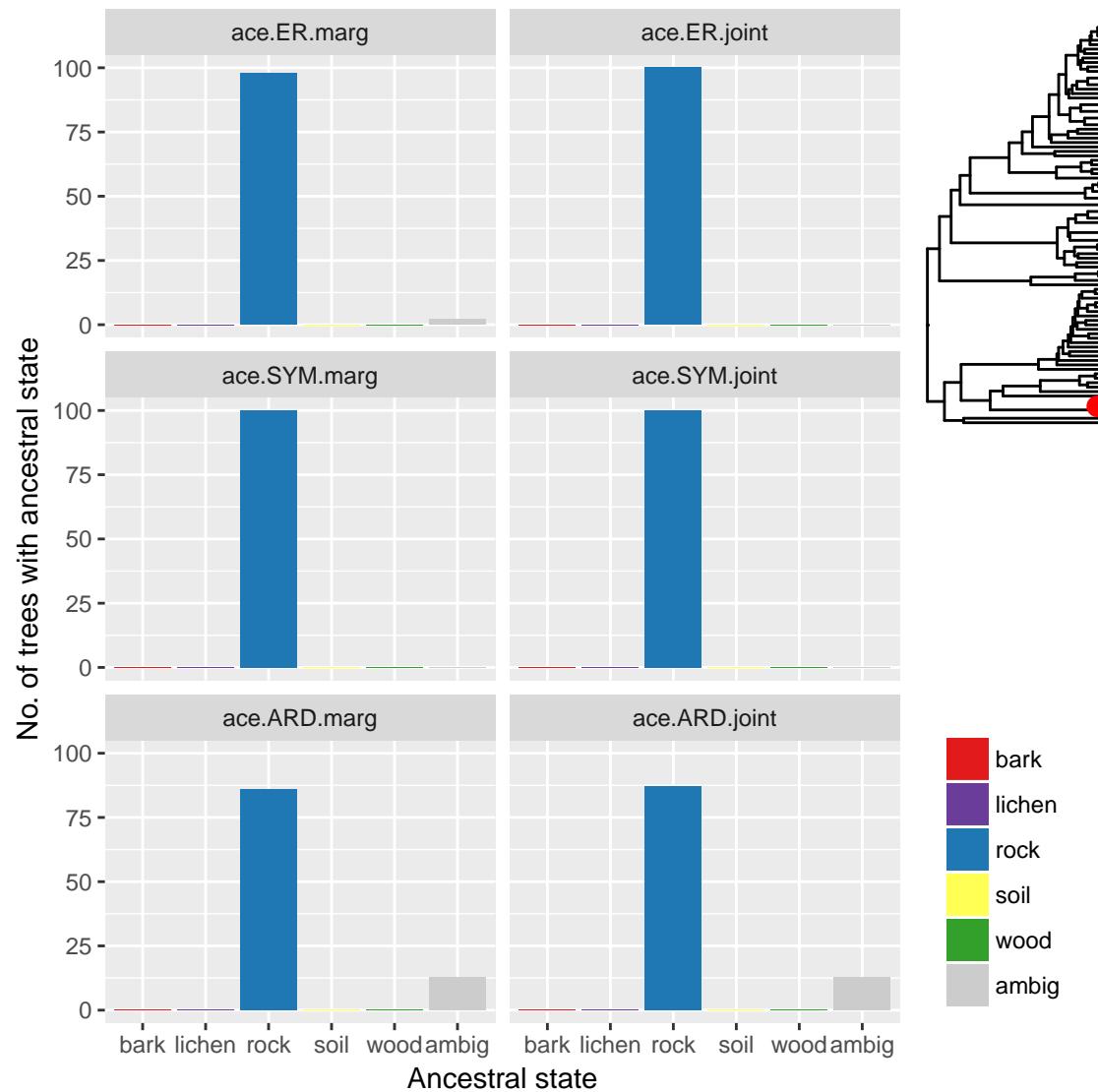


Figure S18: Ancestral states for node 15

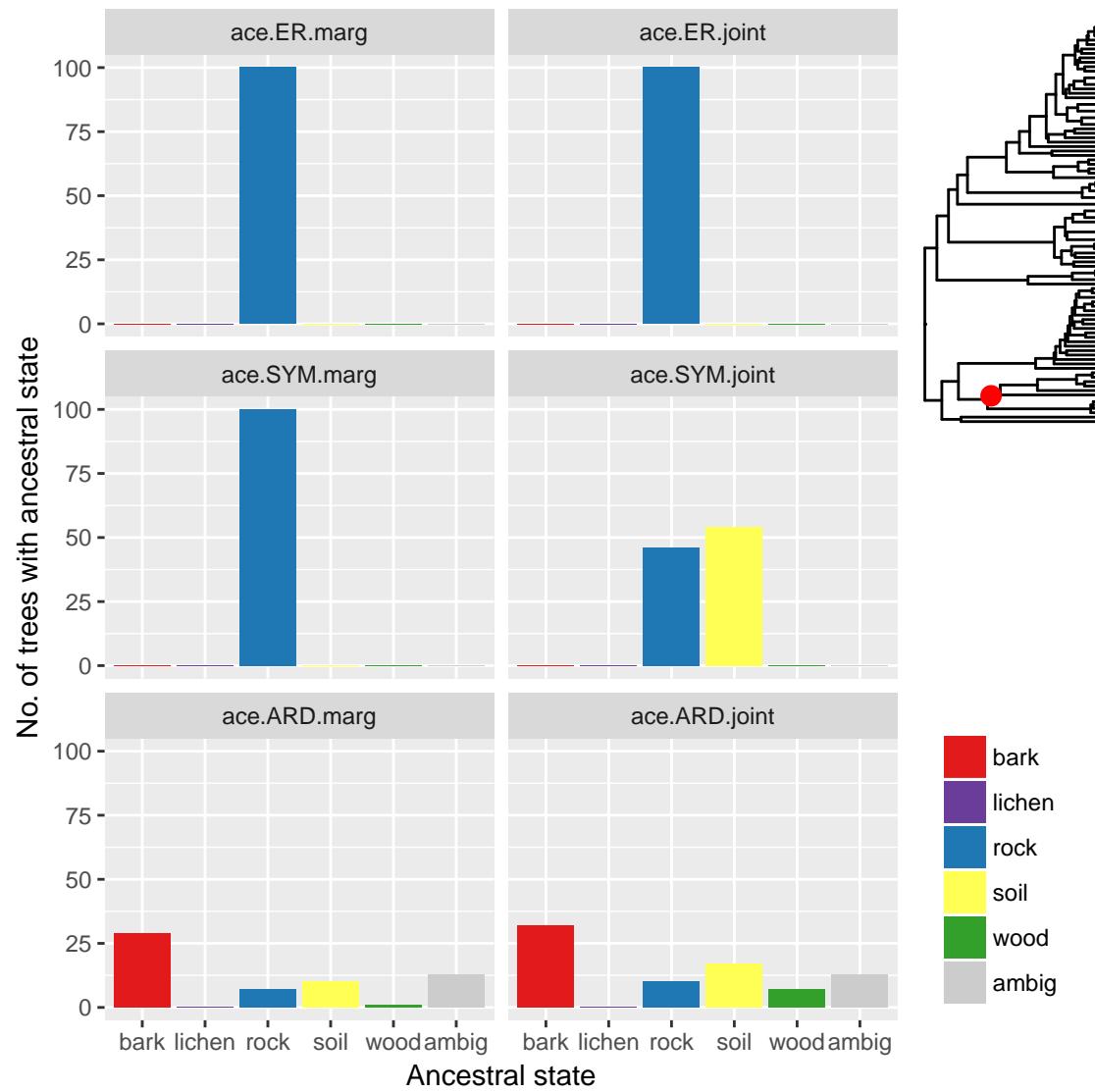


Figure S19: Ancestral states for node 16

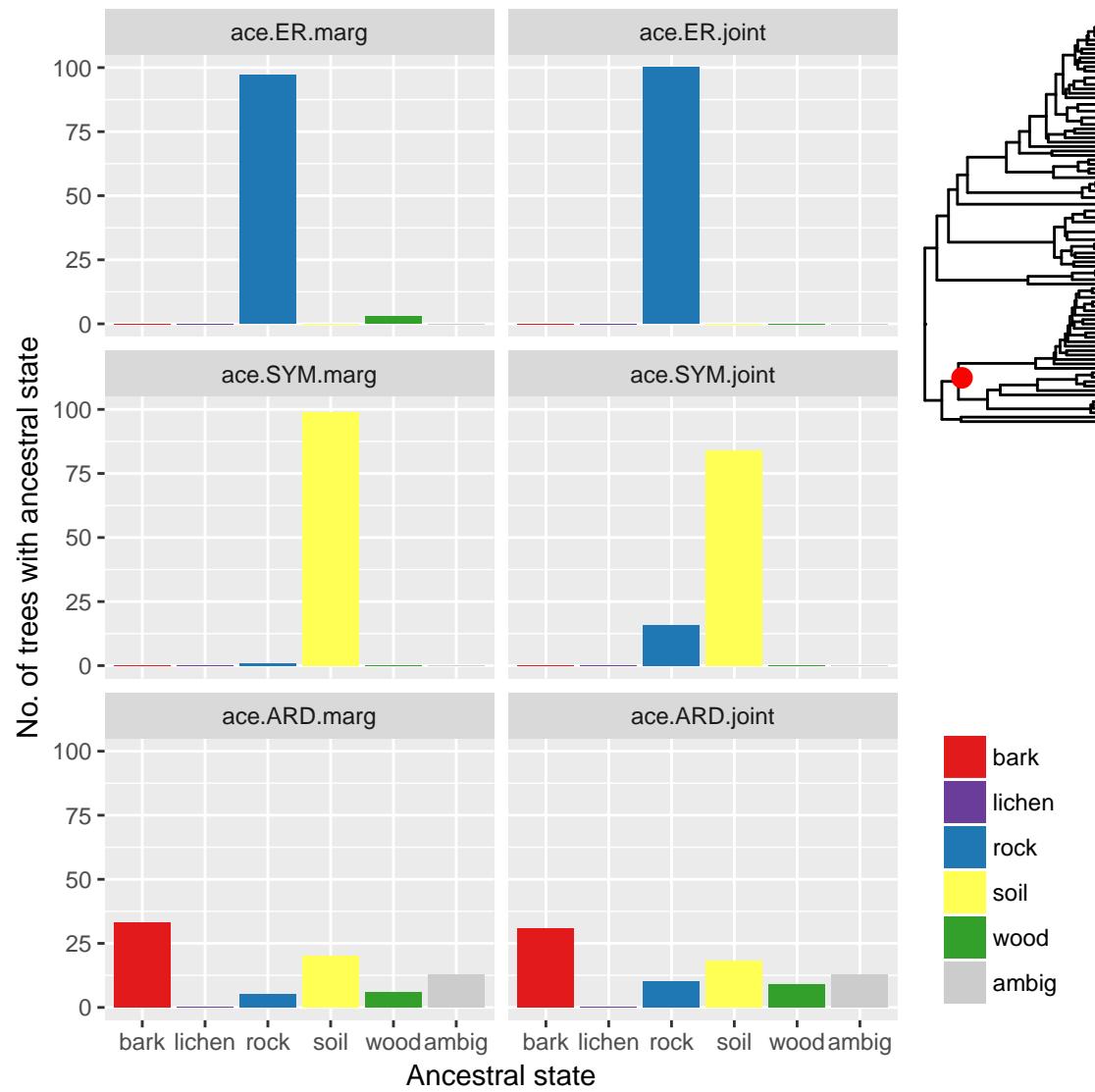


Figure S20: Ancestral states for node 17

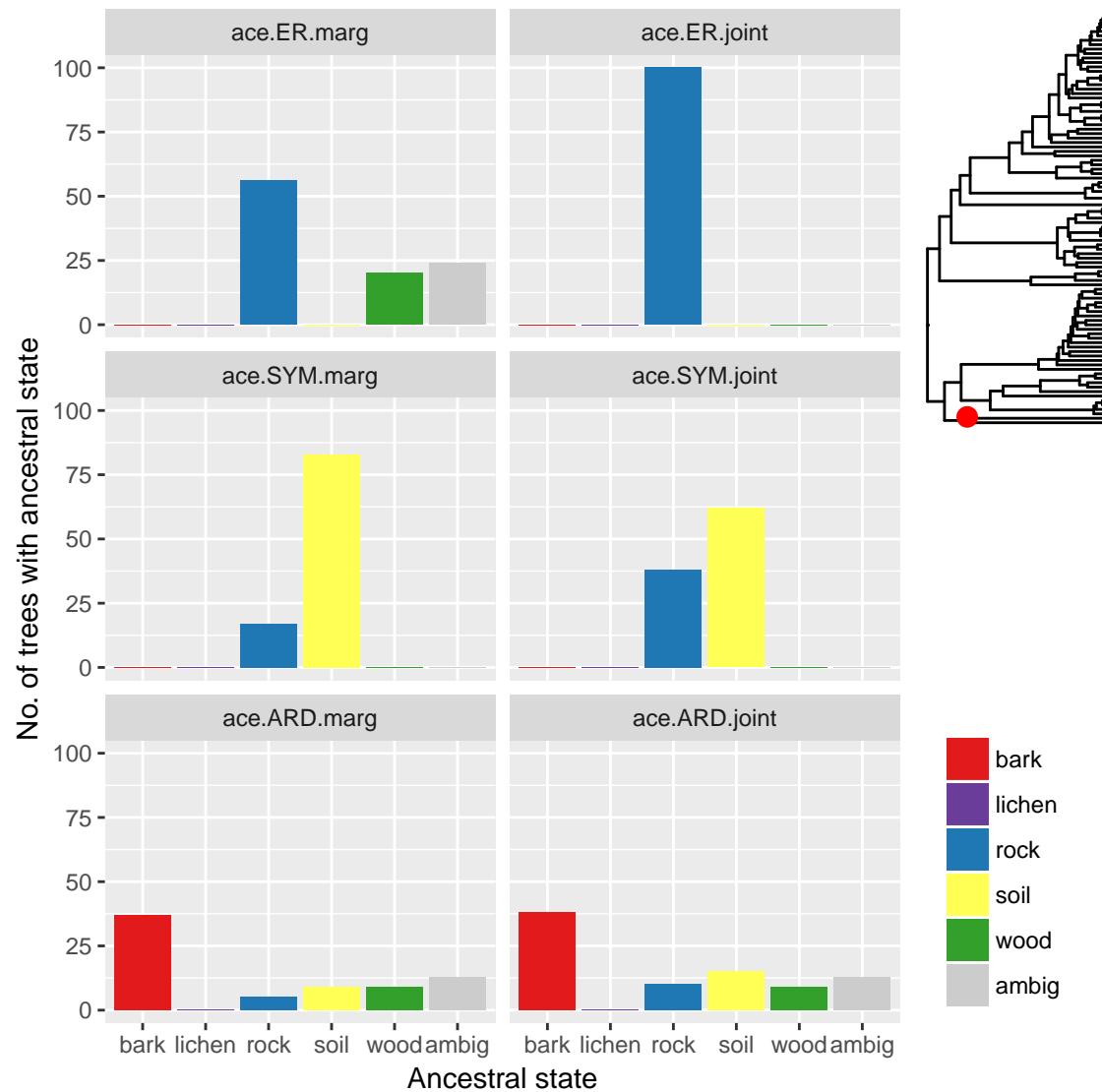


Figure S21: Ancestral states for node 18

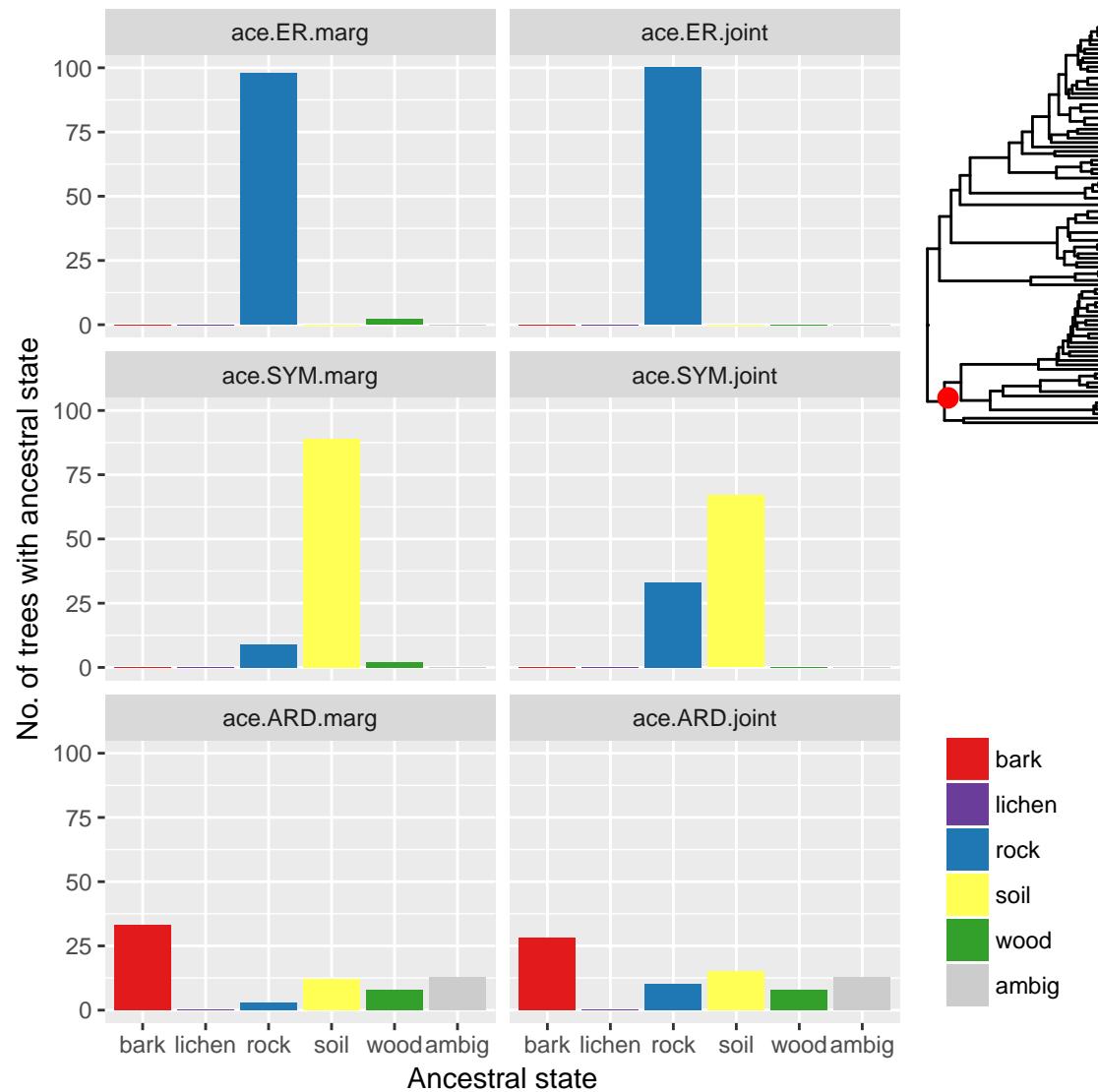


Figure S22: Ancestral states for node 19

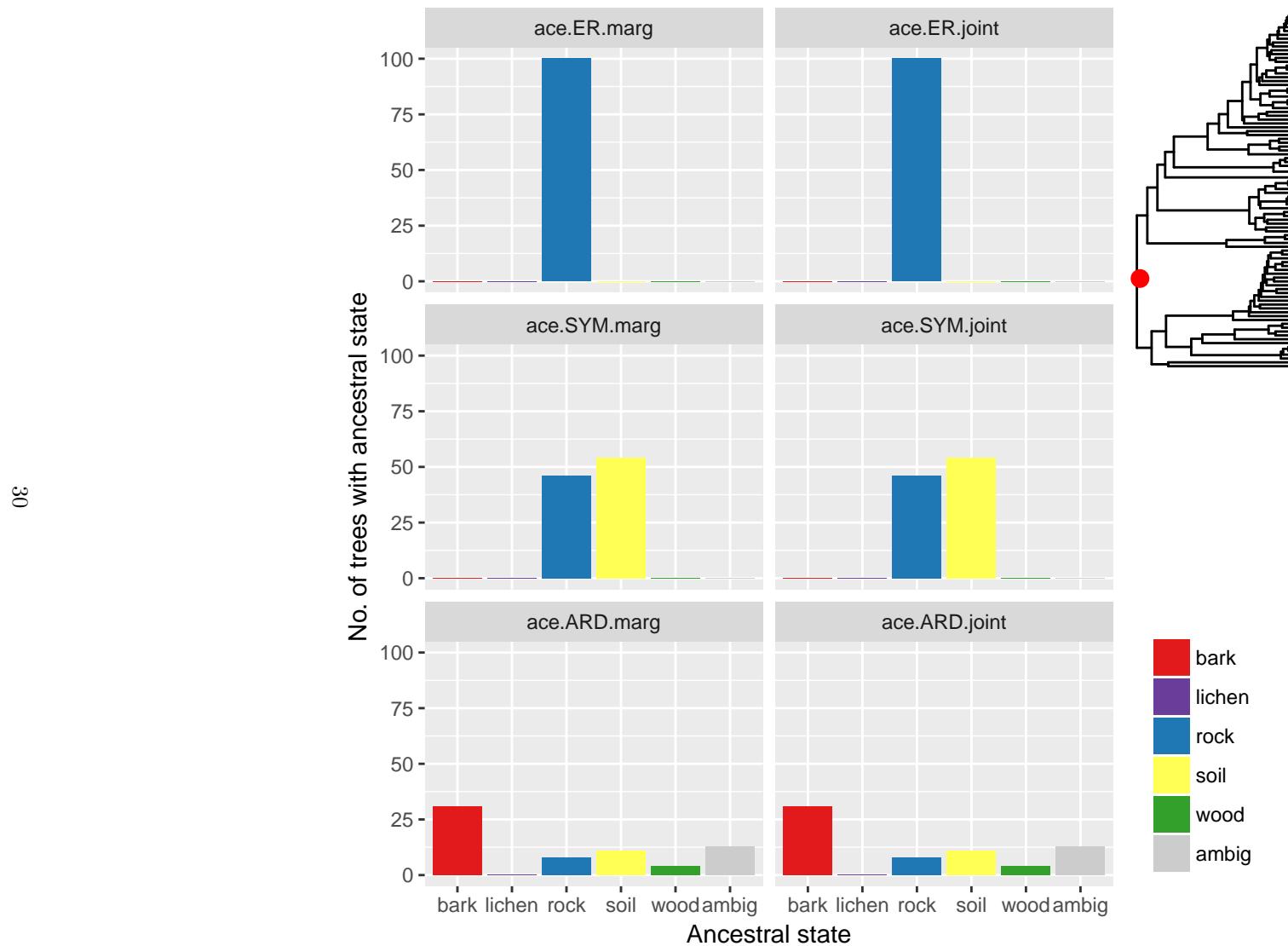


Figure S23-S41 - Results of ancestral state estimation of the preferred substrate character with rayDISC for 19 nodes of the trapeliod phylogeny

Ancestral state estimations of the preferred substrate character for 19 nodes of the trapeliod phylogeny based on the method implemented in rayDISC in the R package corHMM imposing 18 different models. Please refer to the main text for details.

Figure S23: Ancestral states for node 1

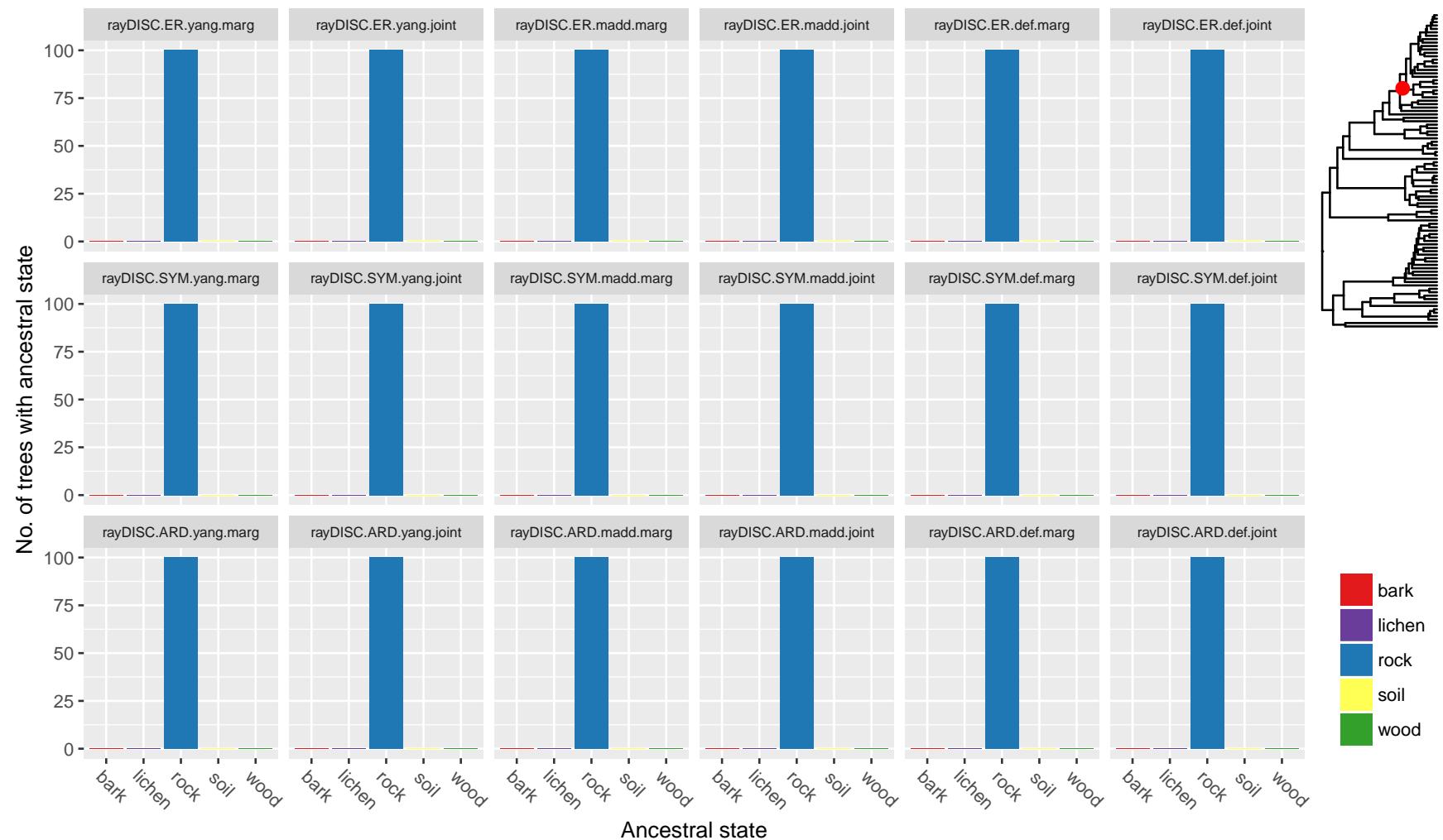


Figure S24: Ancestral states for node 2

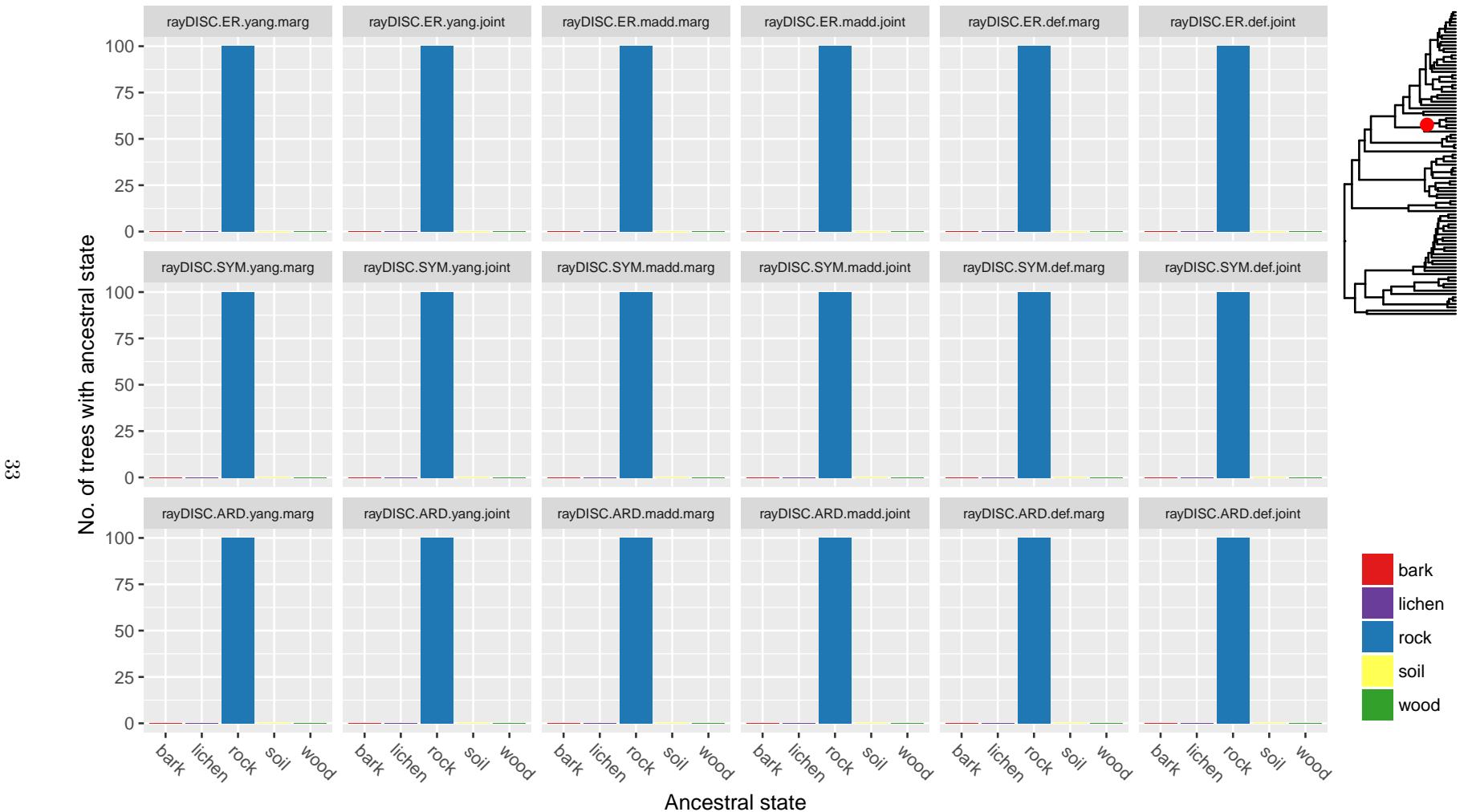


Figure S25: Ancestral states for node 3

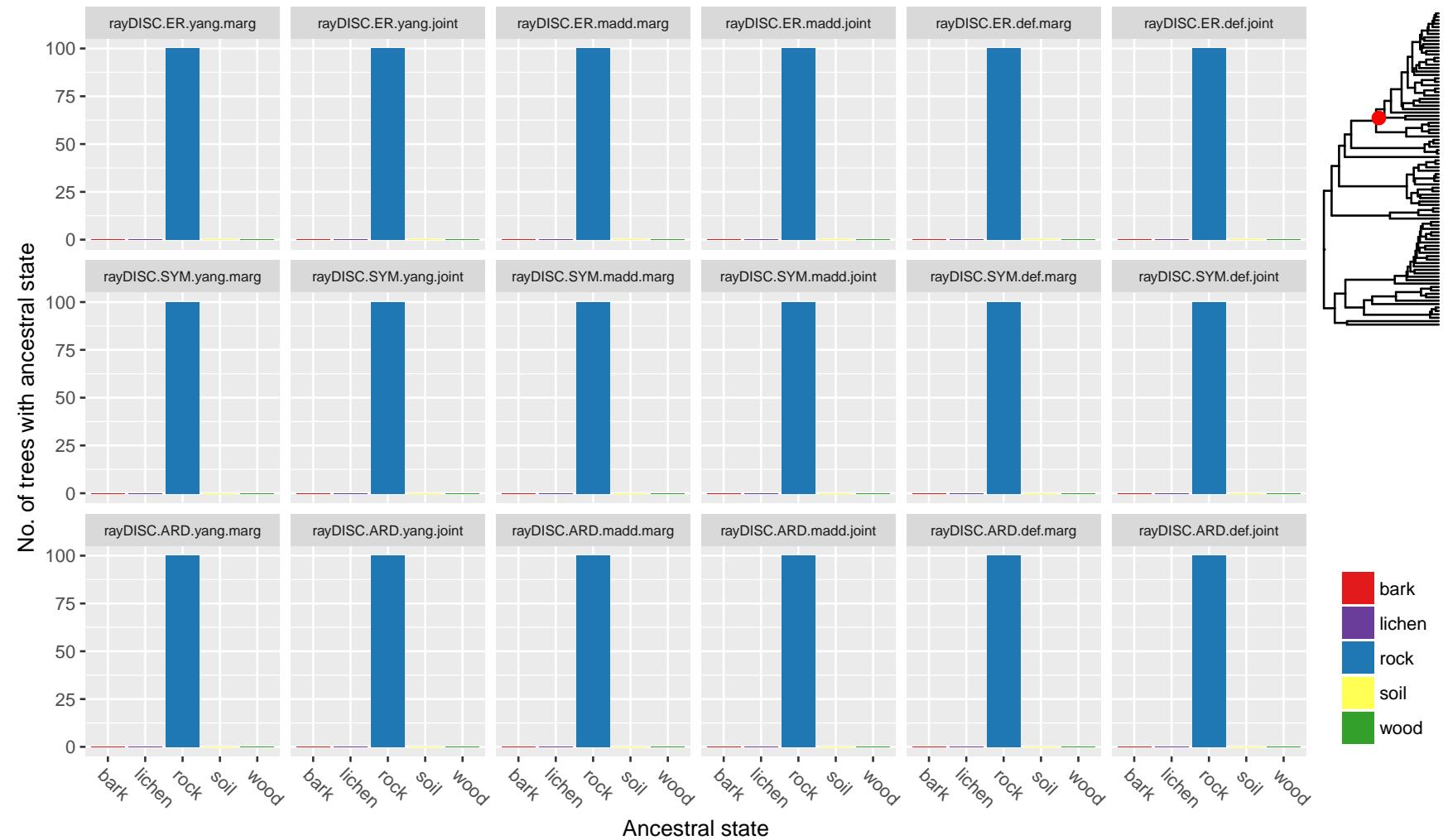


Figure S26: Ancestral states for node 4

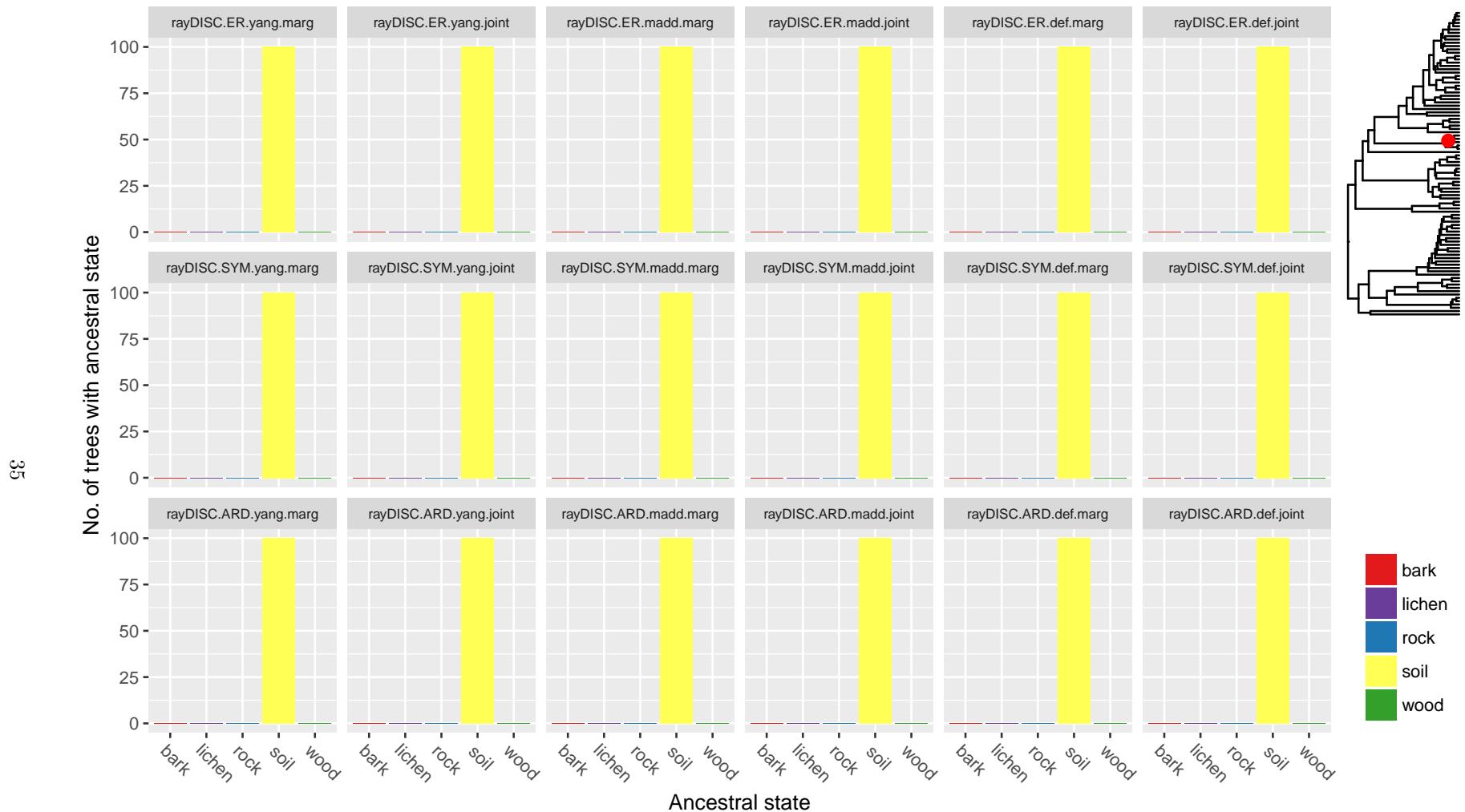


Figure S27: Ancestral states for node 5

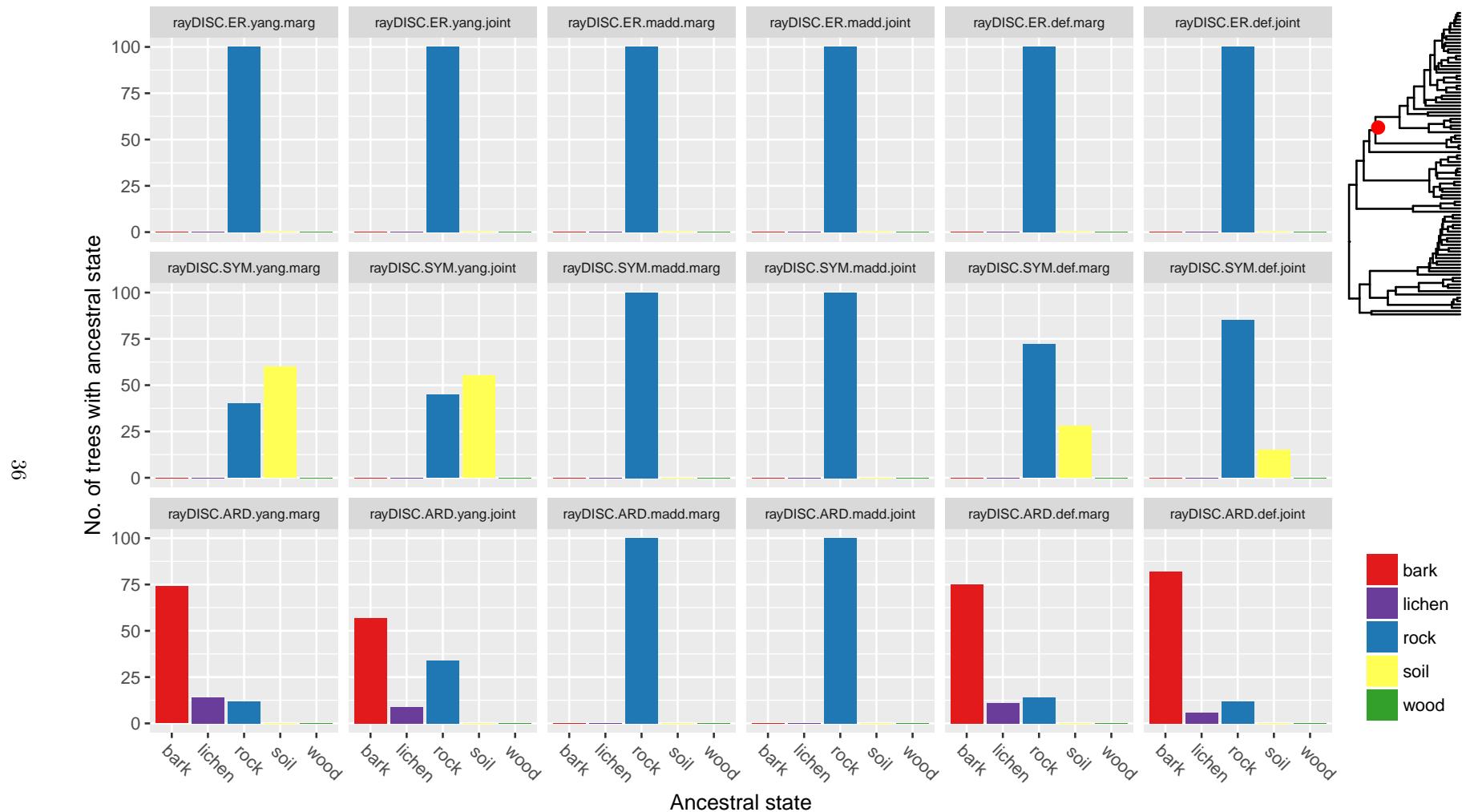


Figure S28: Ancestral states for node 6

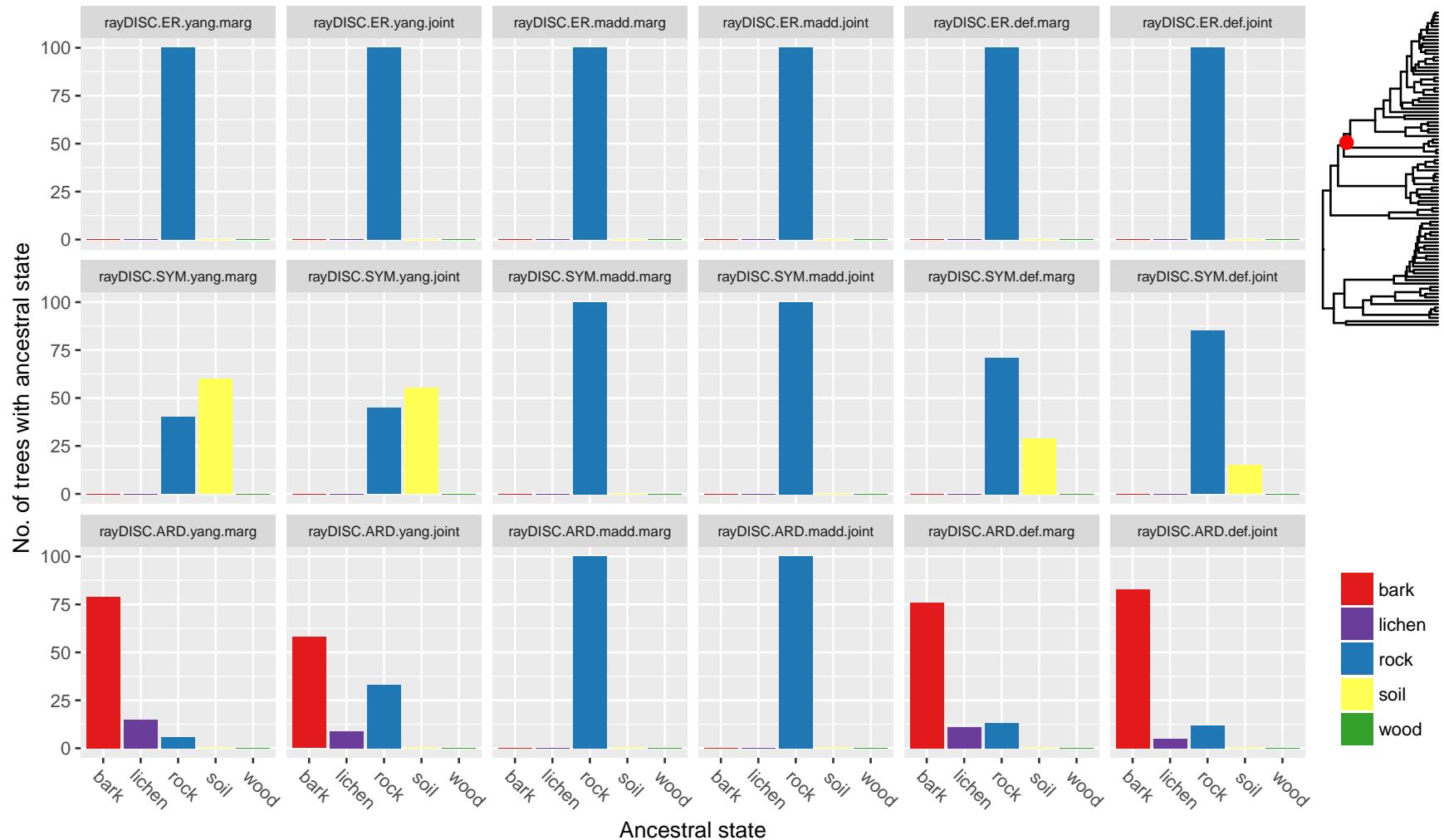


Figure S29: Ancestral states for node 7

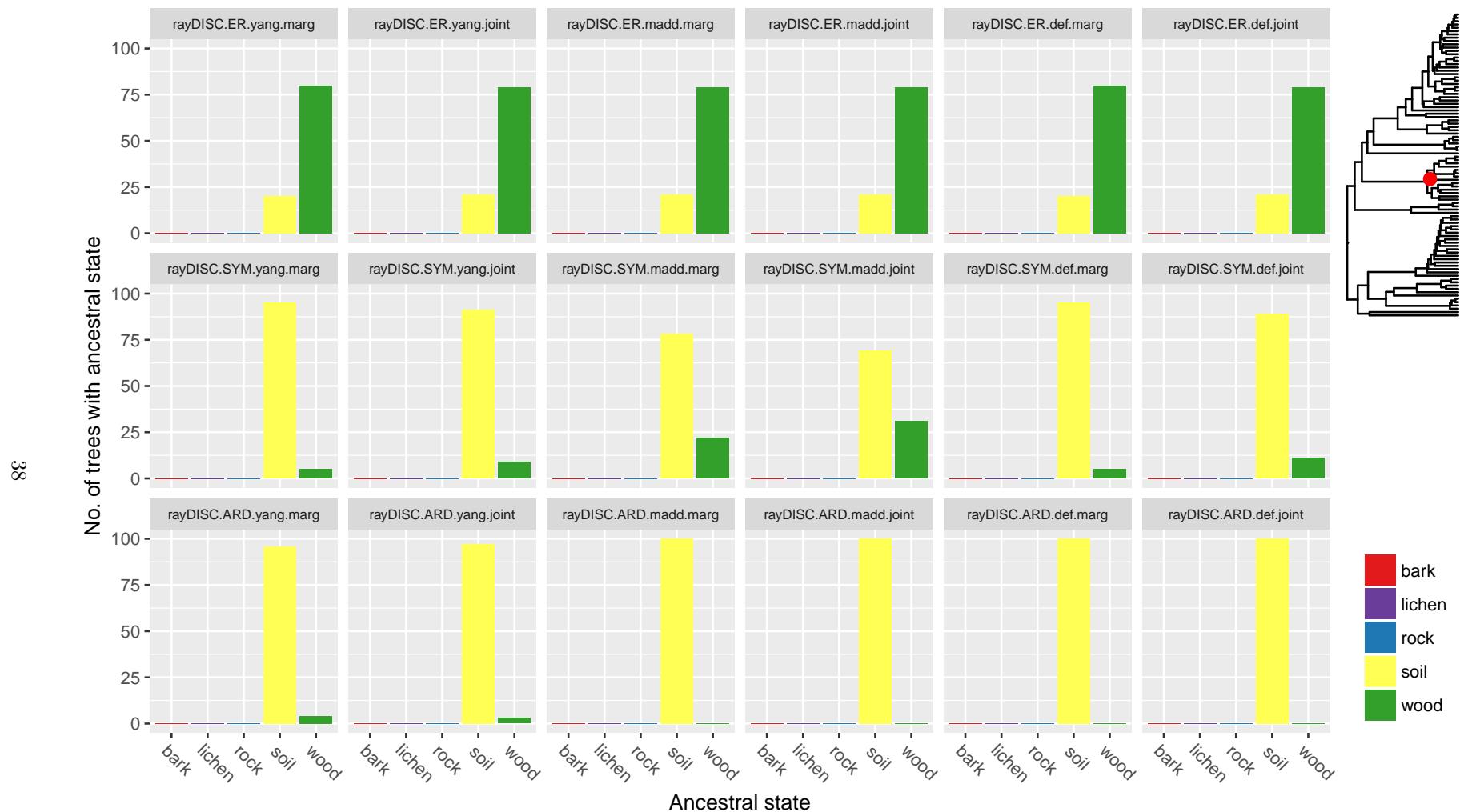


Figure S30: Ancestral states for node 8

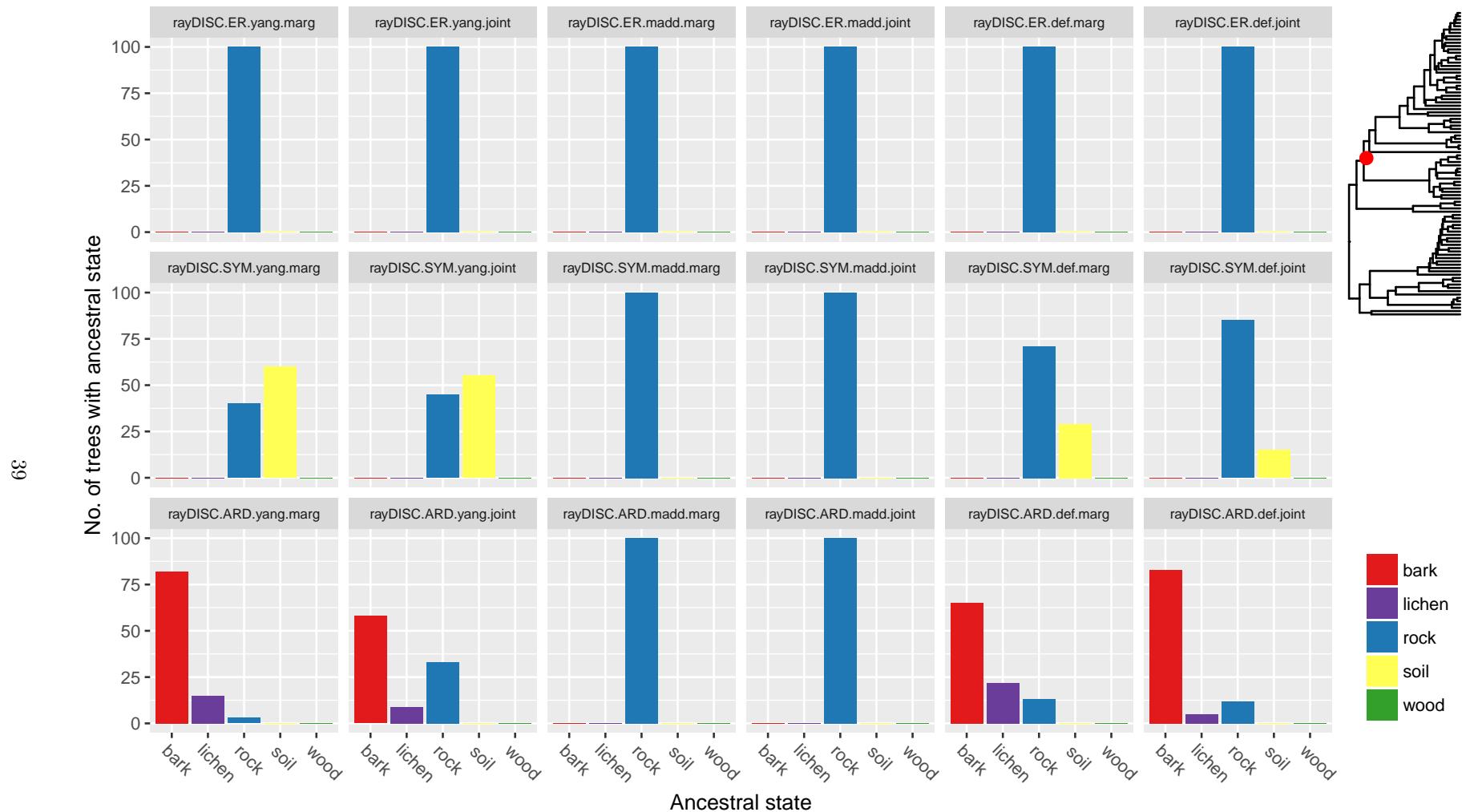


Figure S31: Ancestral states for node 9

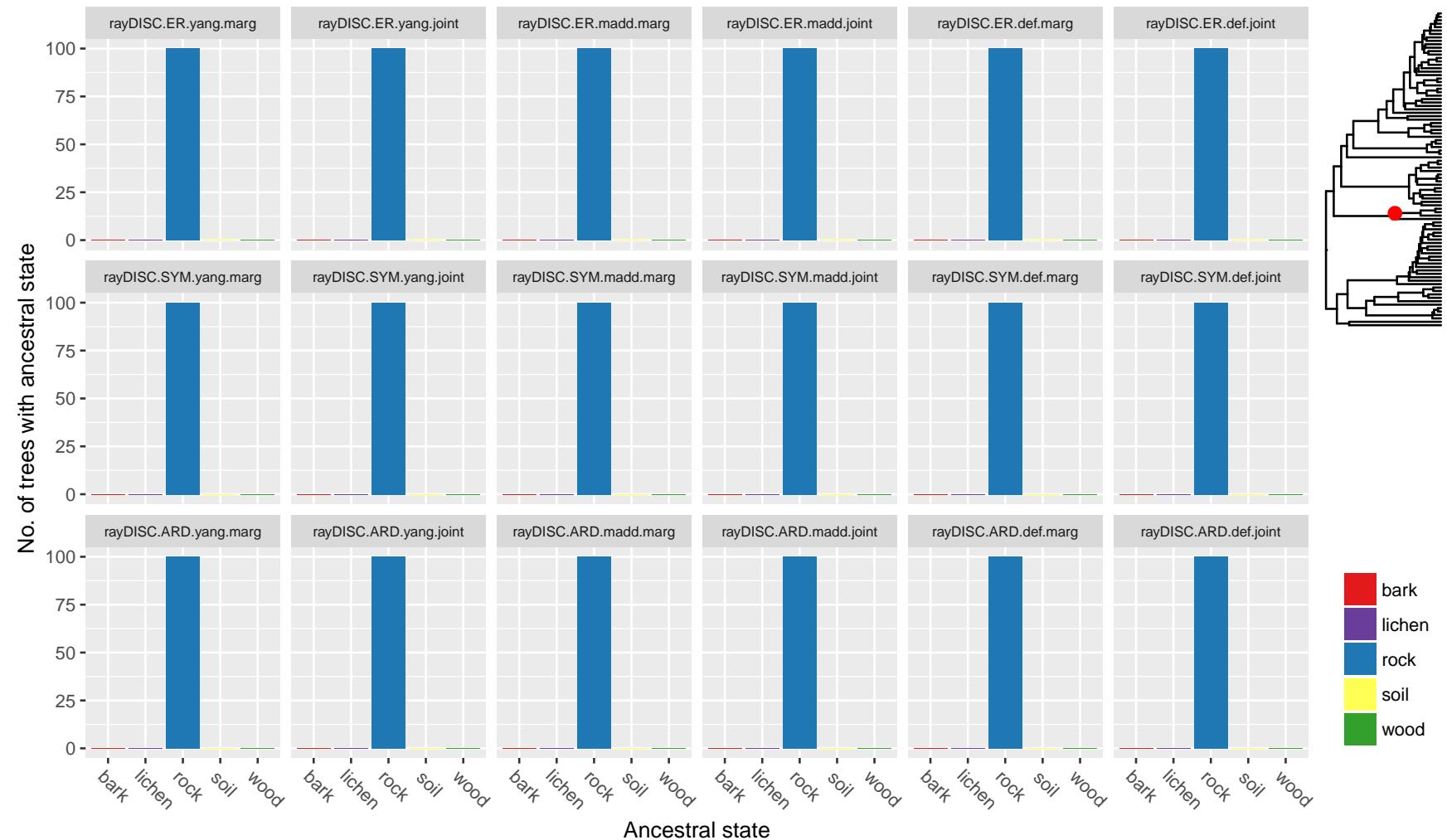


Figure S32: Ancestral states for node 10

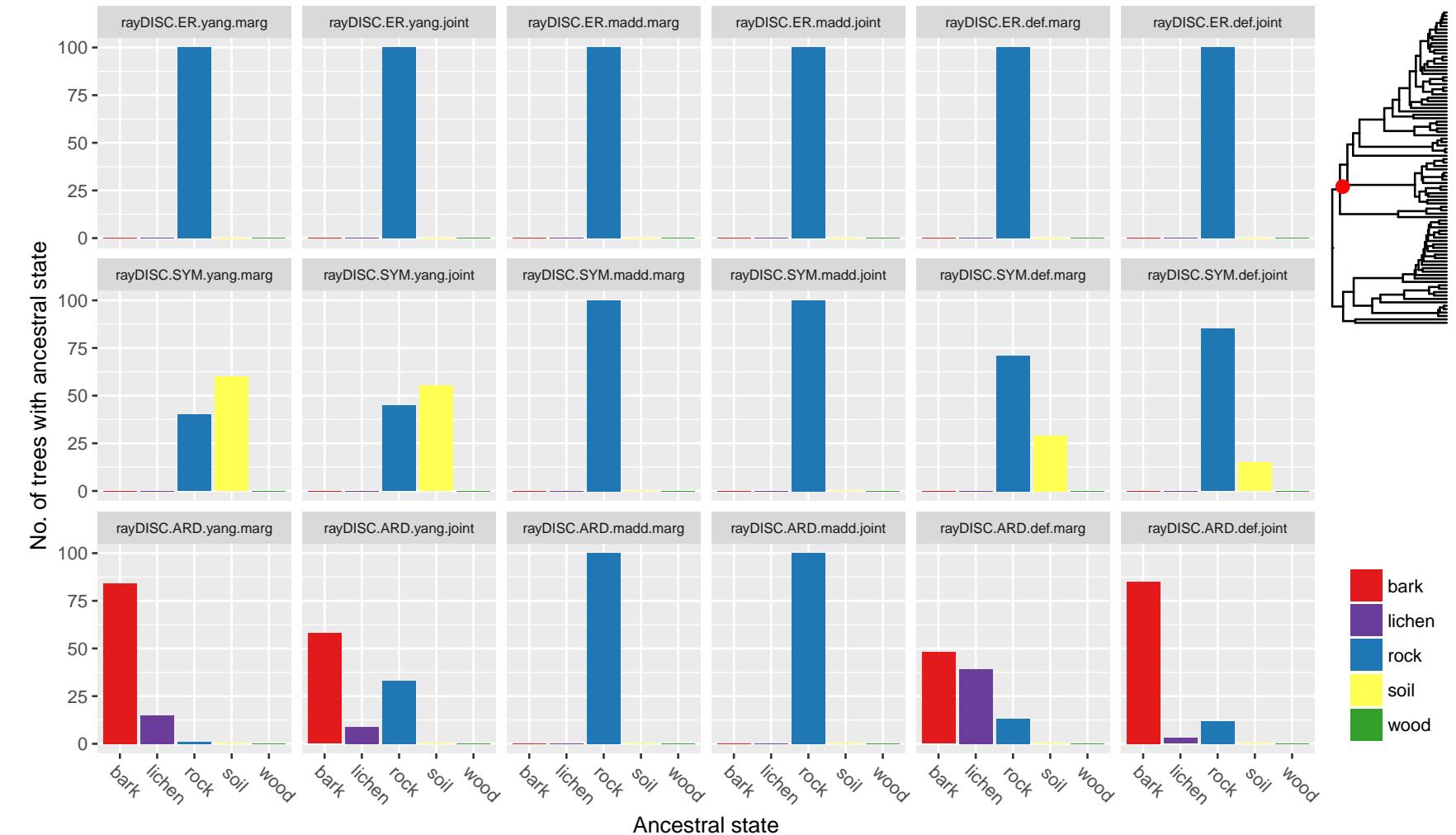


Figure S33: Ancestral states for node 11

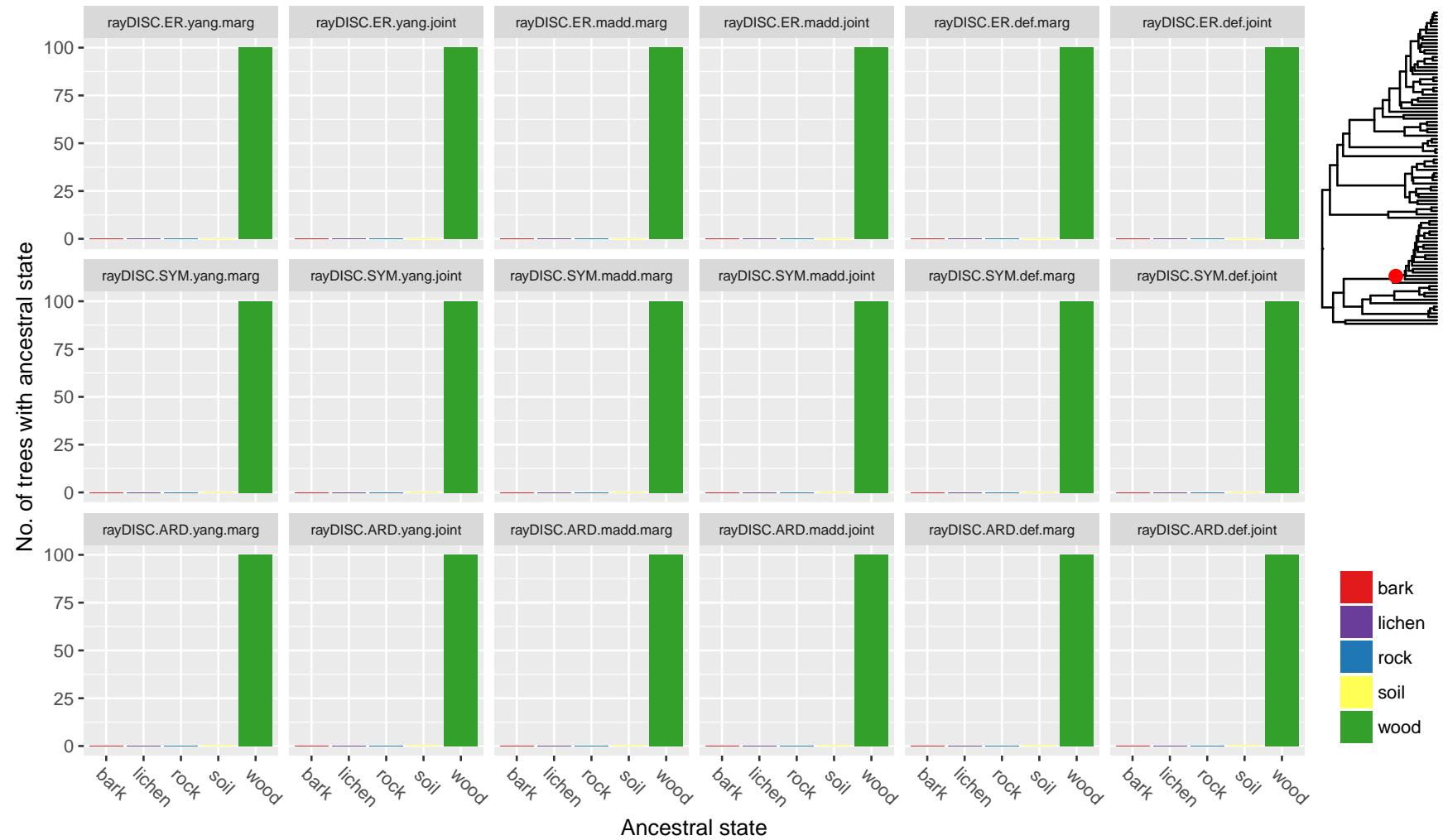


Figure S34: Ancestral states for node 12

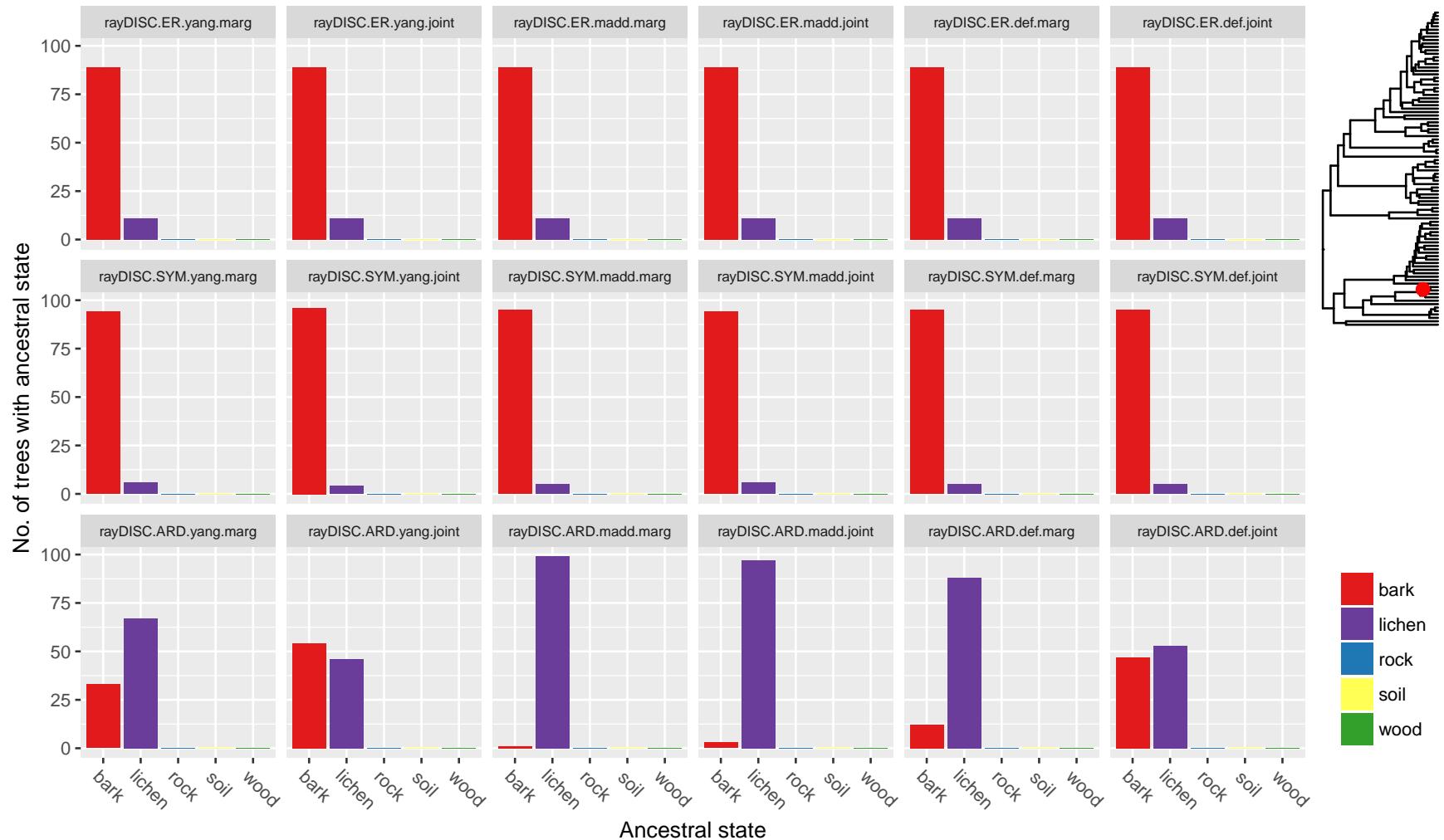


Figure S35: Ancestral states for node 13

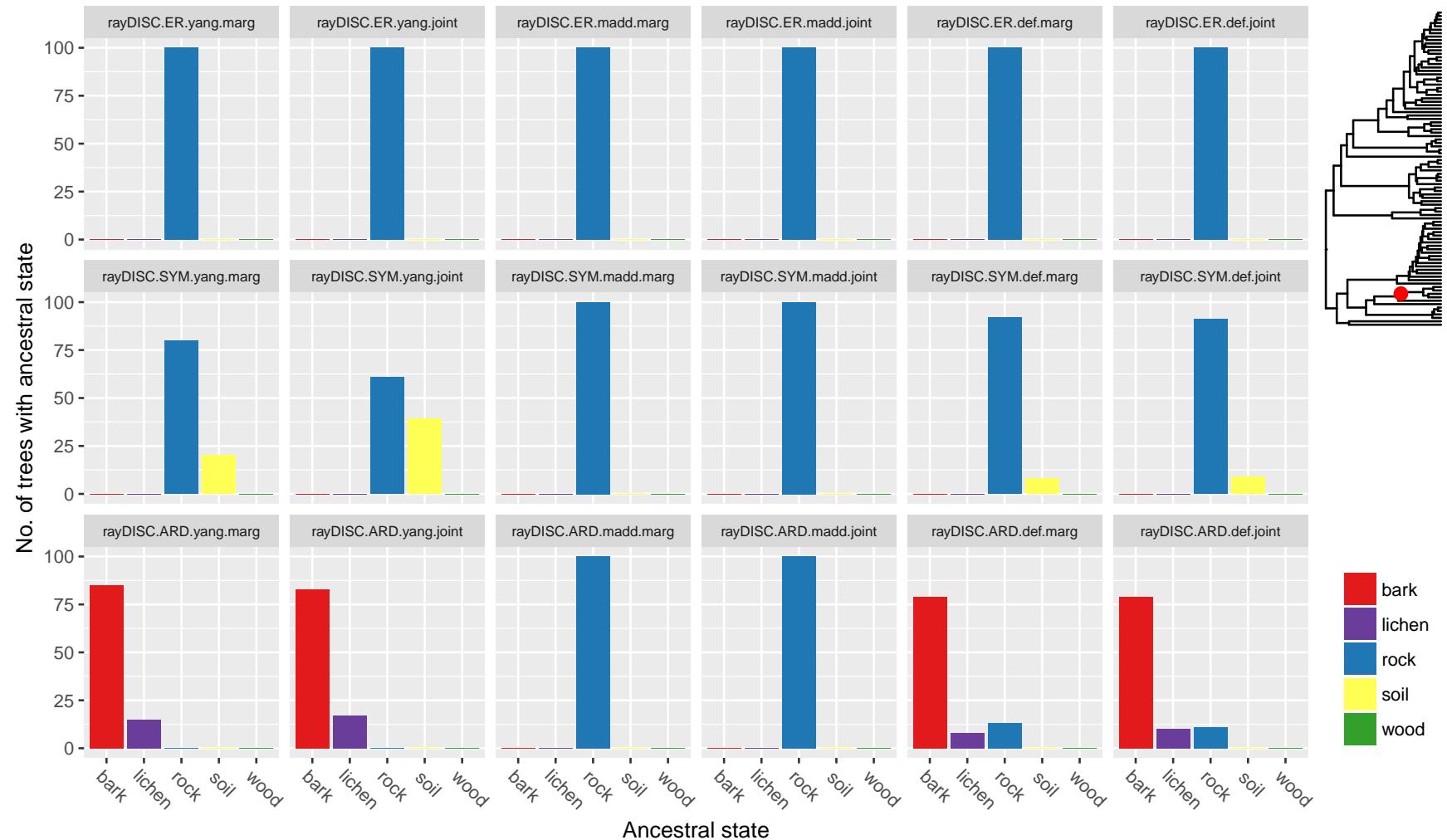


Figure S36: Ancestral states for node 14

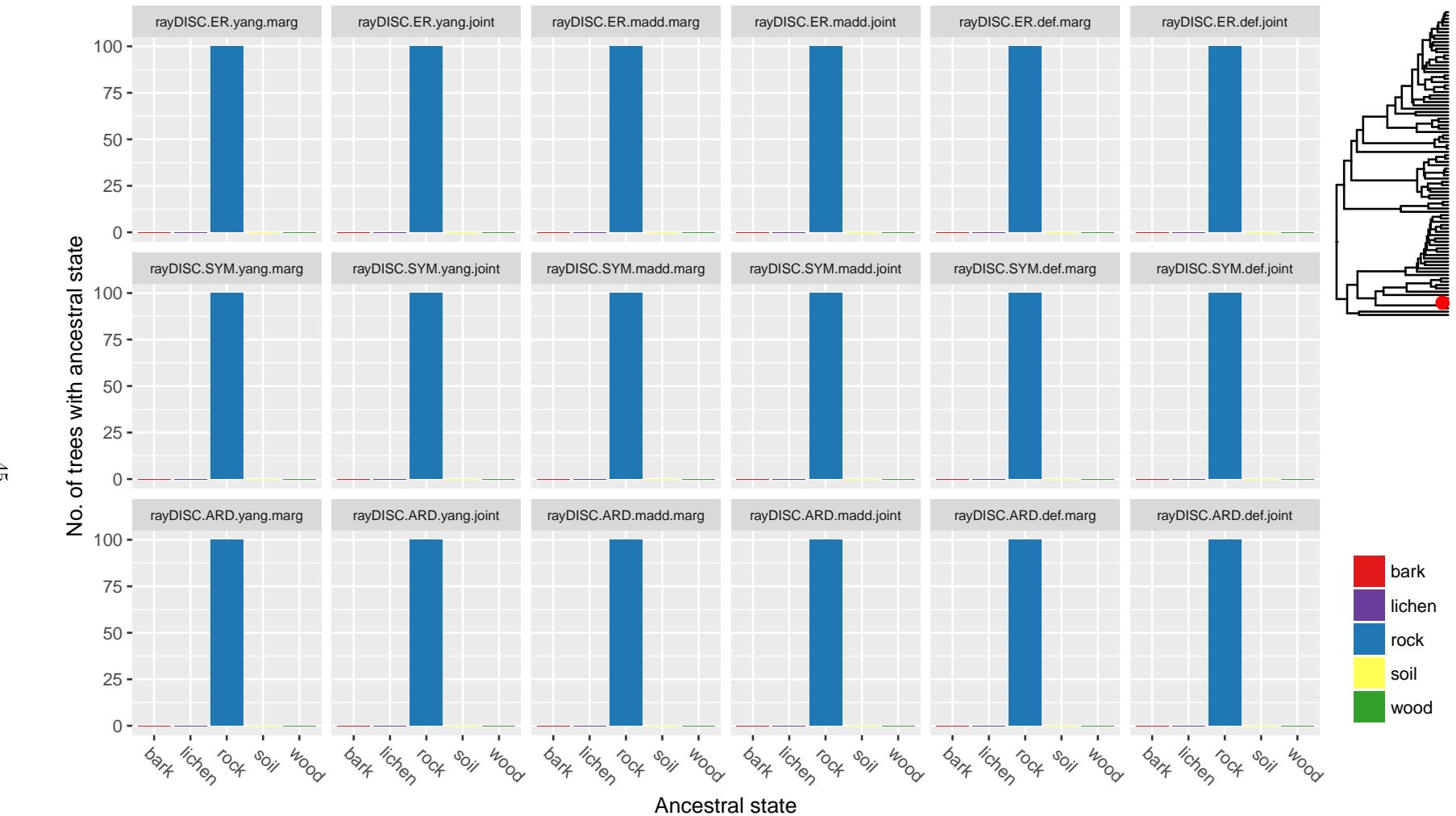


Figure S37: Ancestral states for node 15

46

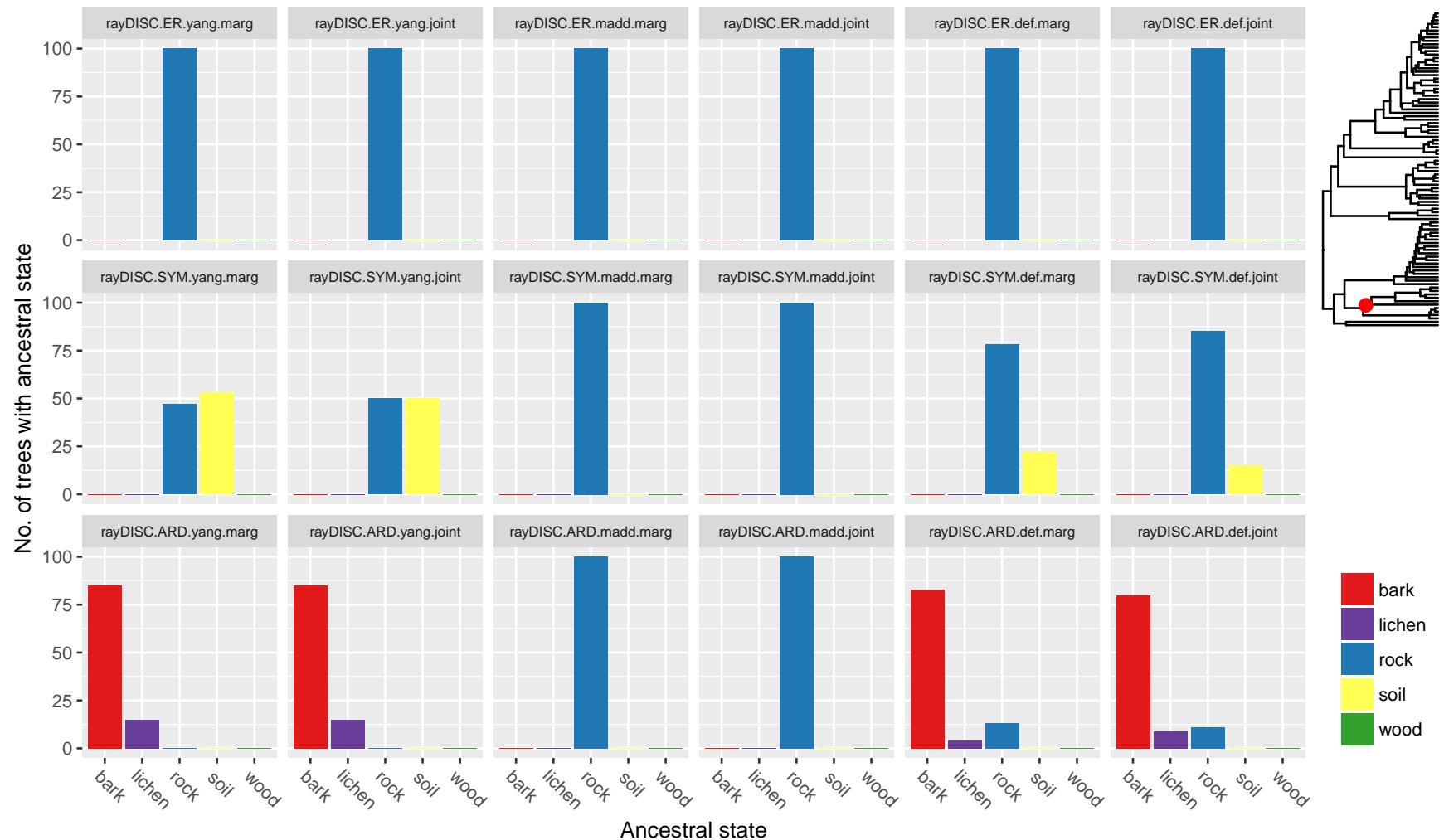


Figure S38: Ancestral states for node 16

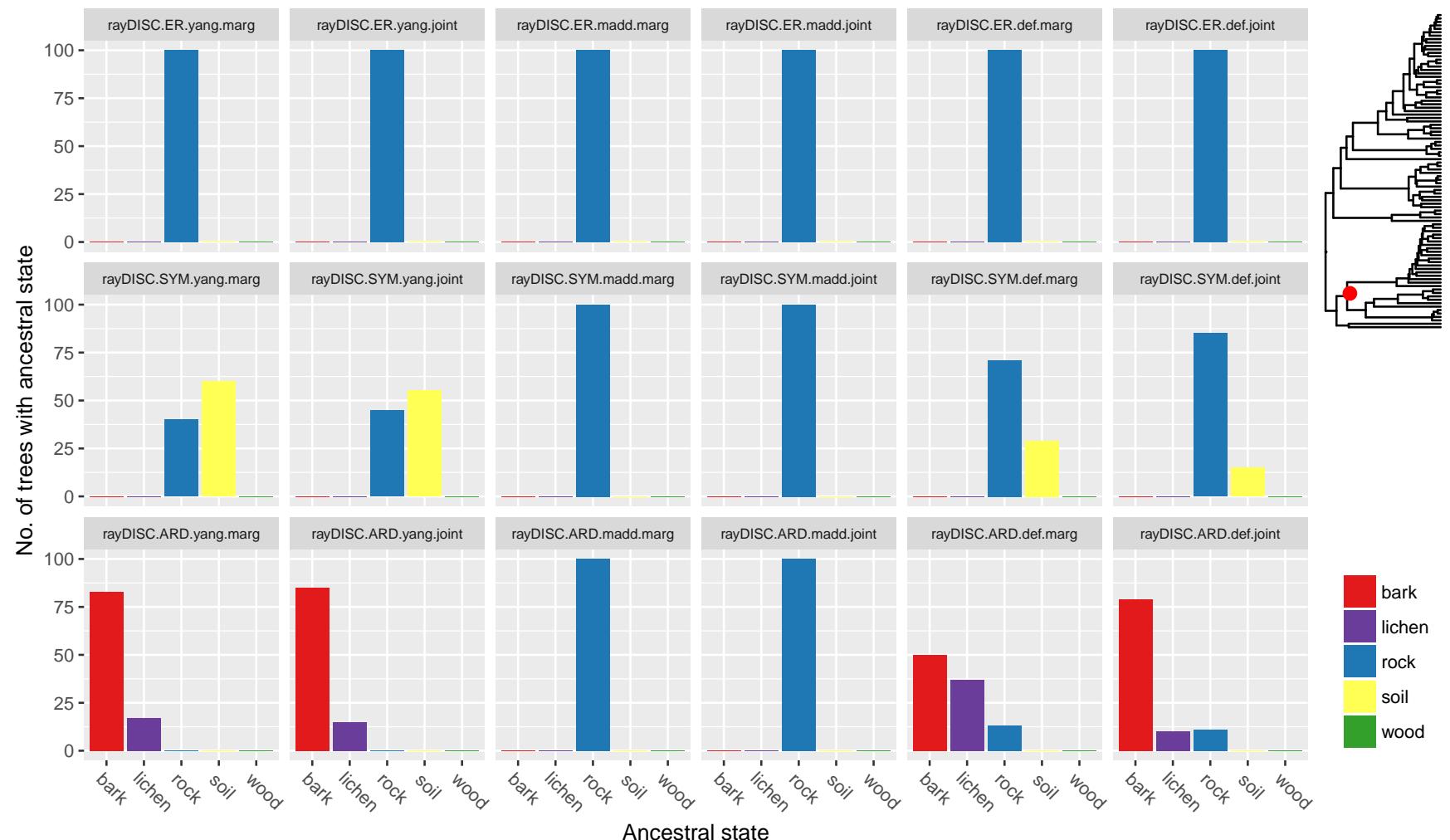


Figure S39: Ancestral states for node 17

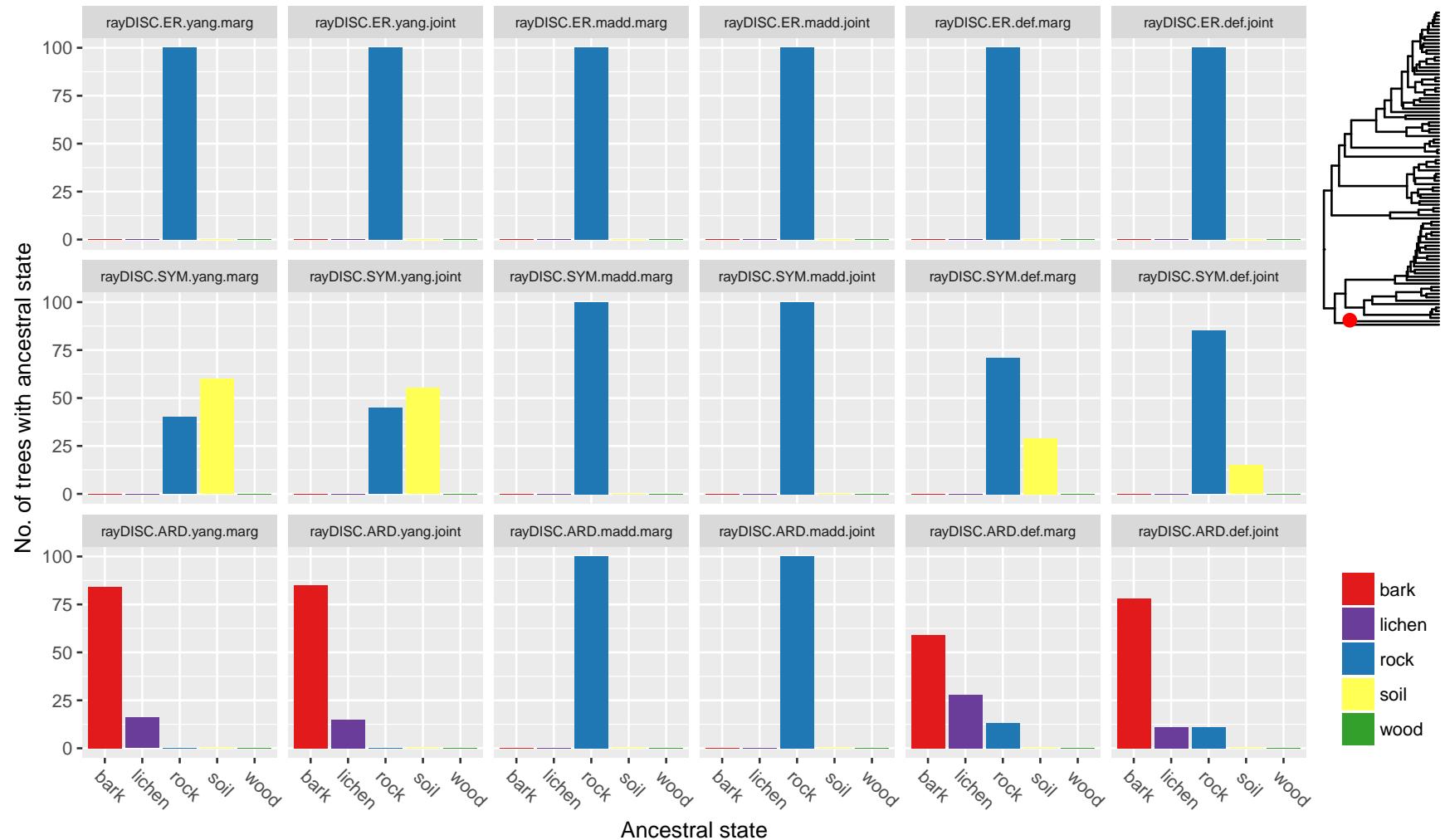


Figure S40: Ancestral states for node 18

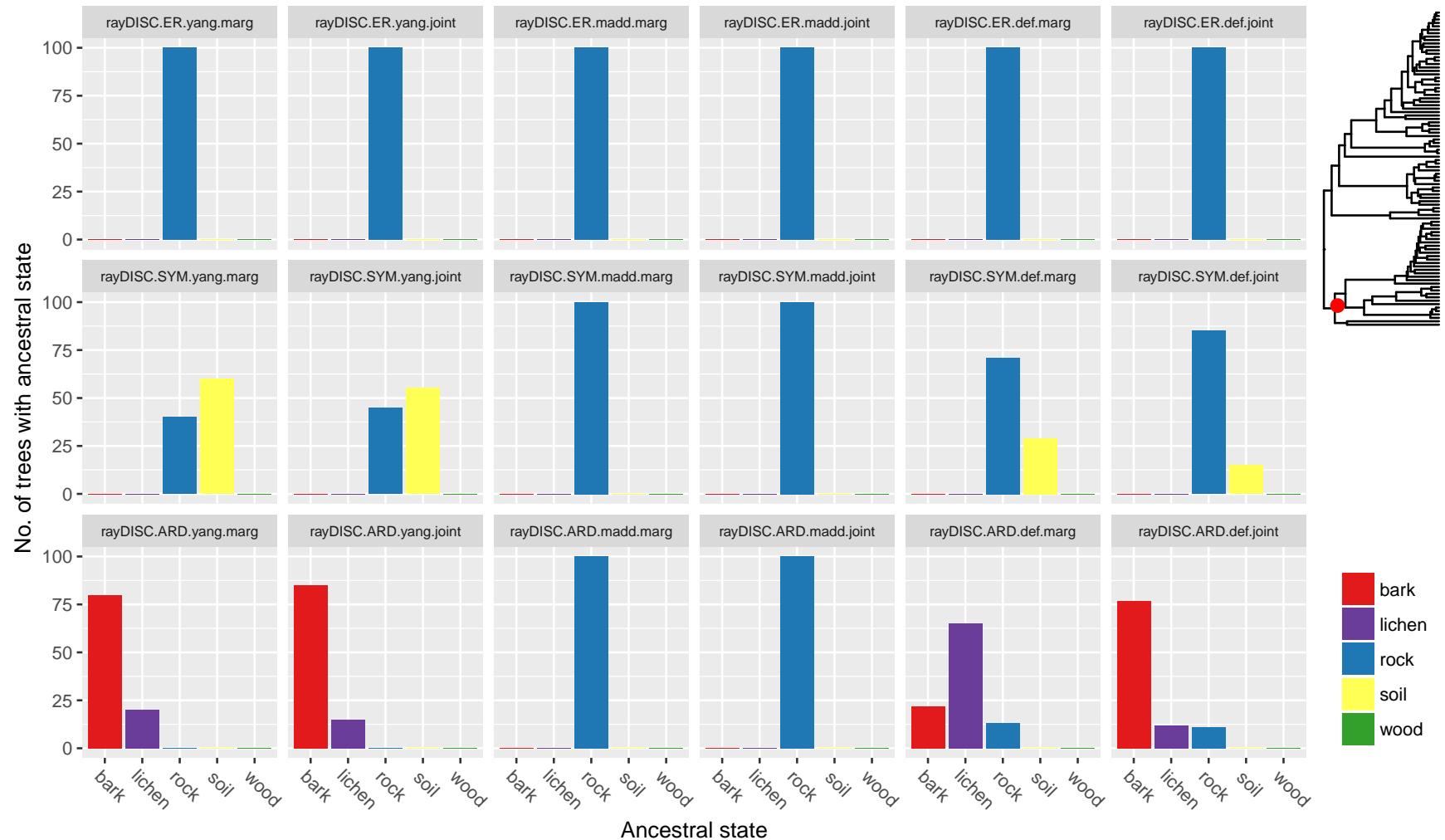


Figure S41: Ancestral states for node 19

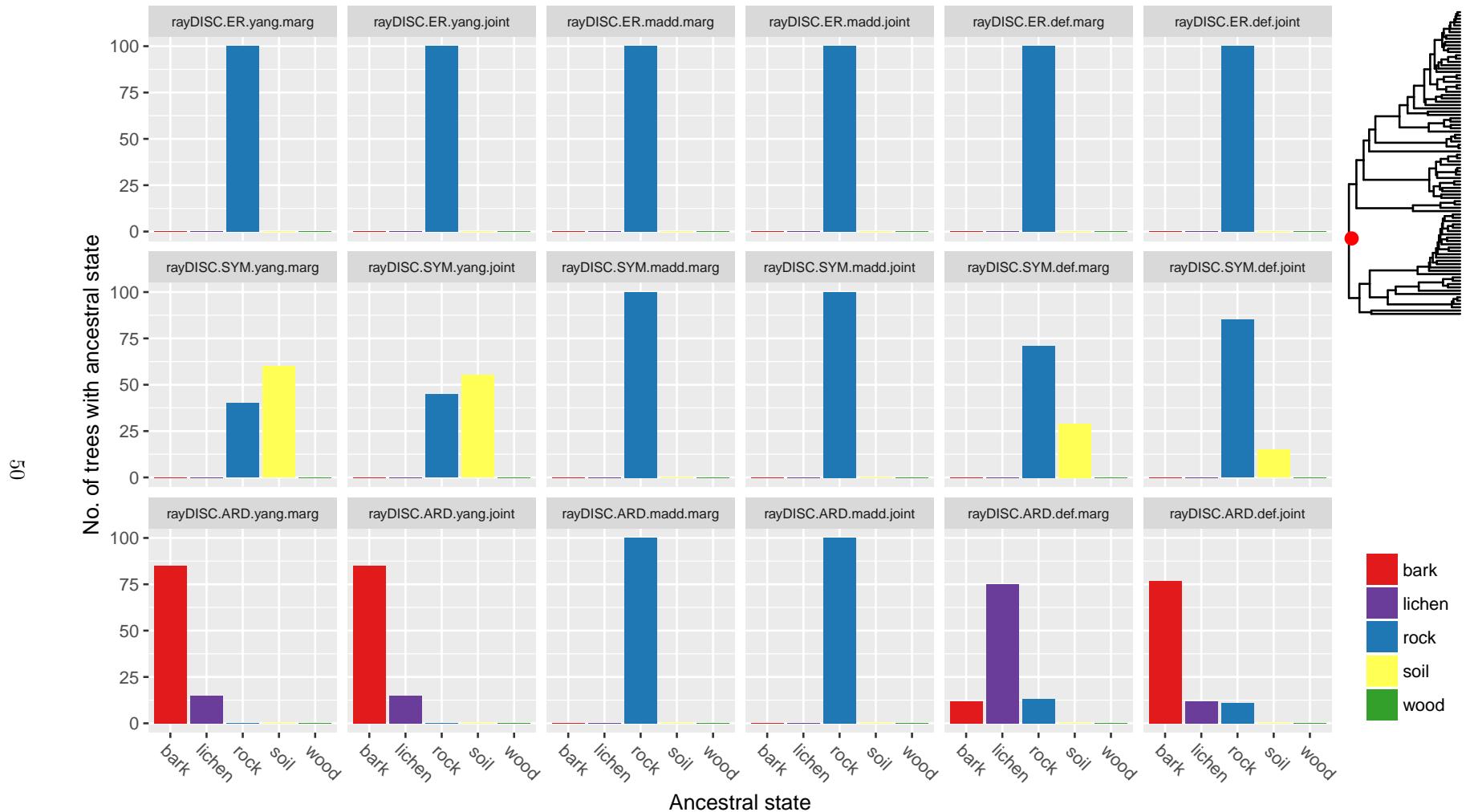


Figure S42-S60 - Results of ancestral state estimation of the preferred substrate character with make.simmap for 19 nodes of the trapelioid phylogeny

Ancestral state estimations of the preferred substrate character for 19 nodes of the trapelioid phylogeny based on stochastic character mapping using phytools imposing 6 different models. Please refer to the main text for details.

Figure S42: Ancestral states for node 1

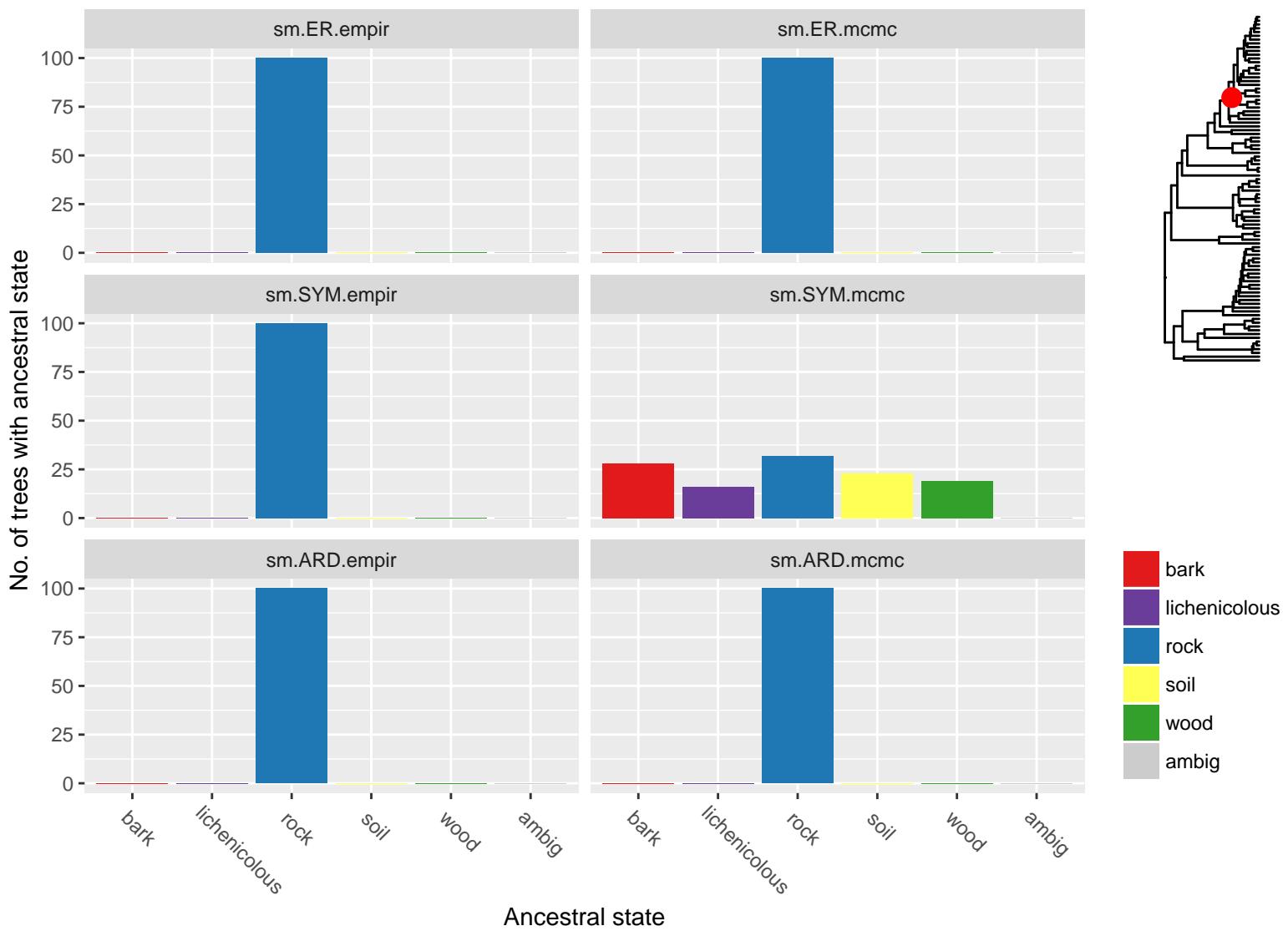


Figure S43: Ancestral states for node 2

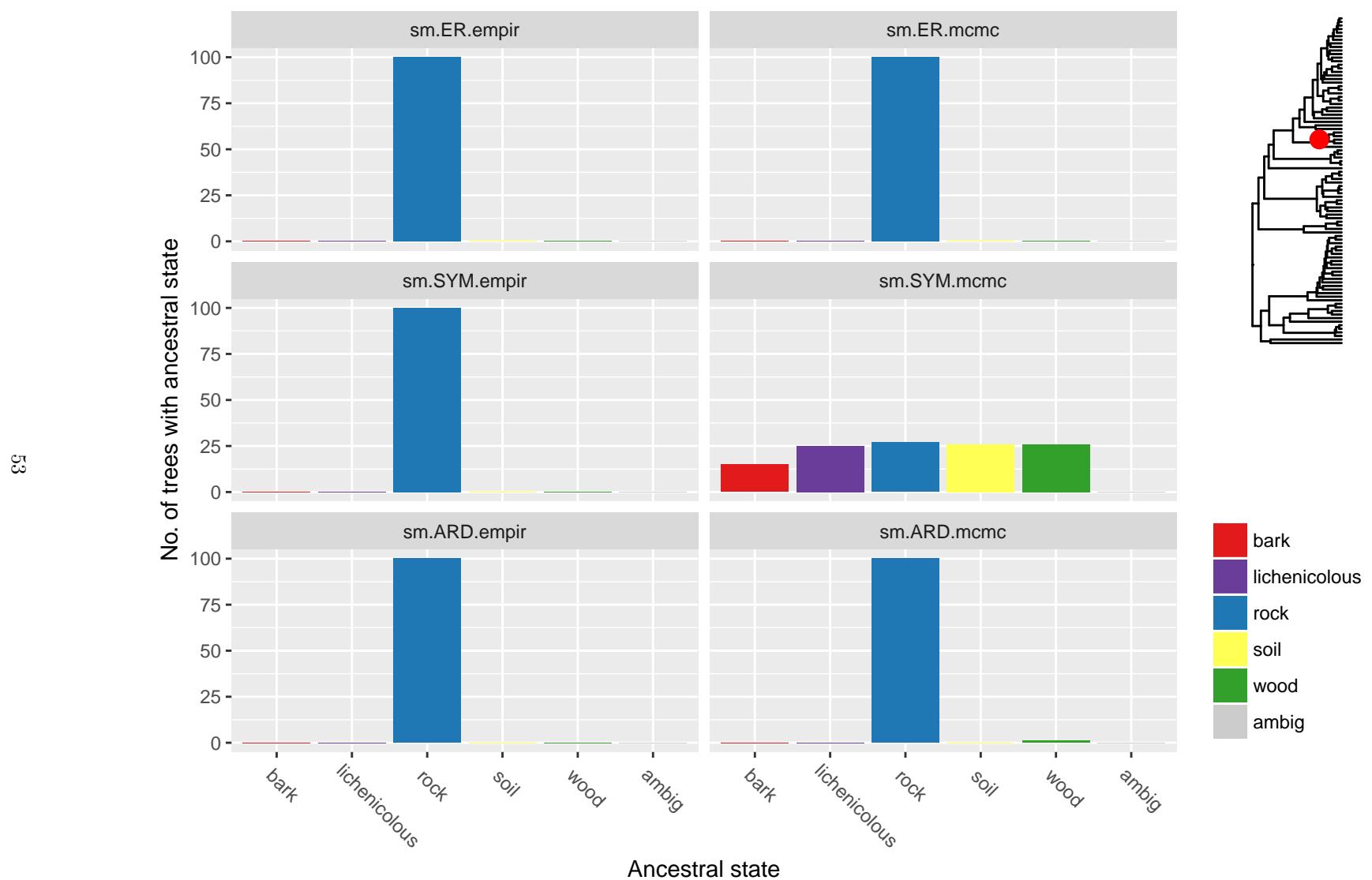


Figure S44: Ancestral states for node 3

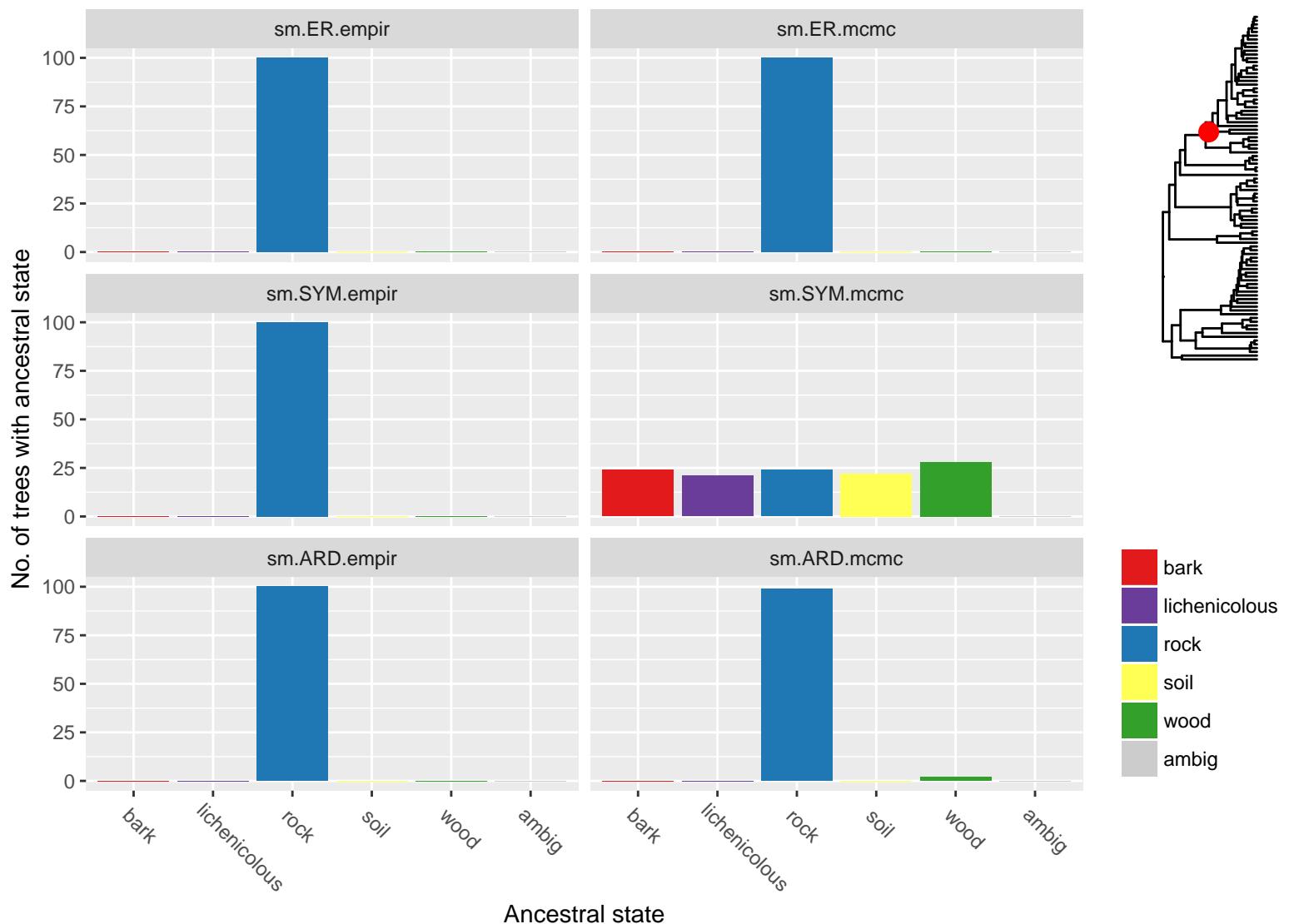


Figure S45: Ancestral states for node 4

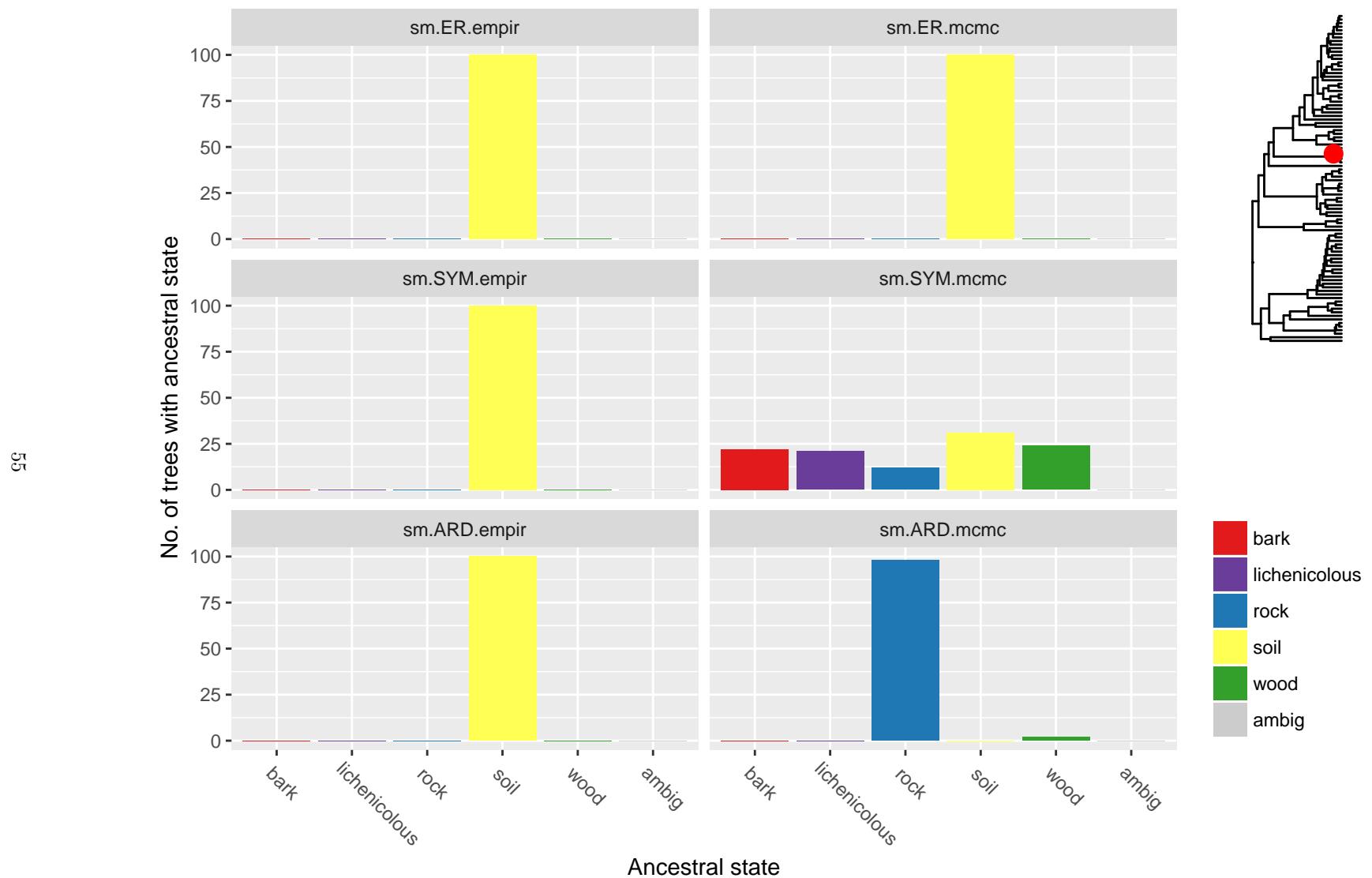


Figure S46: Ancestral states for node 5

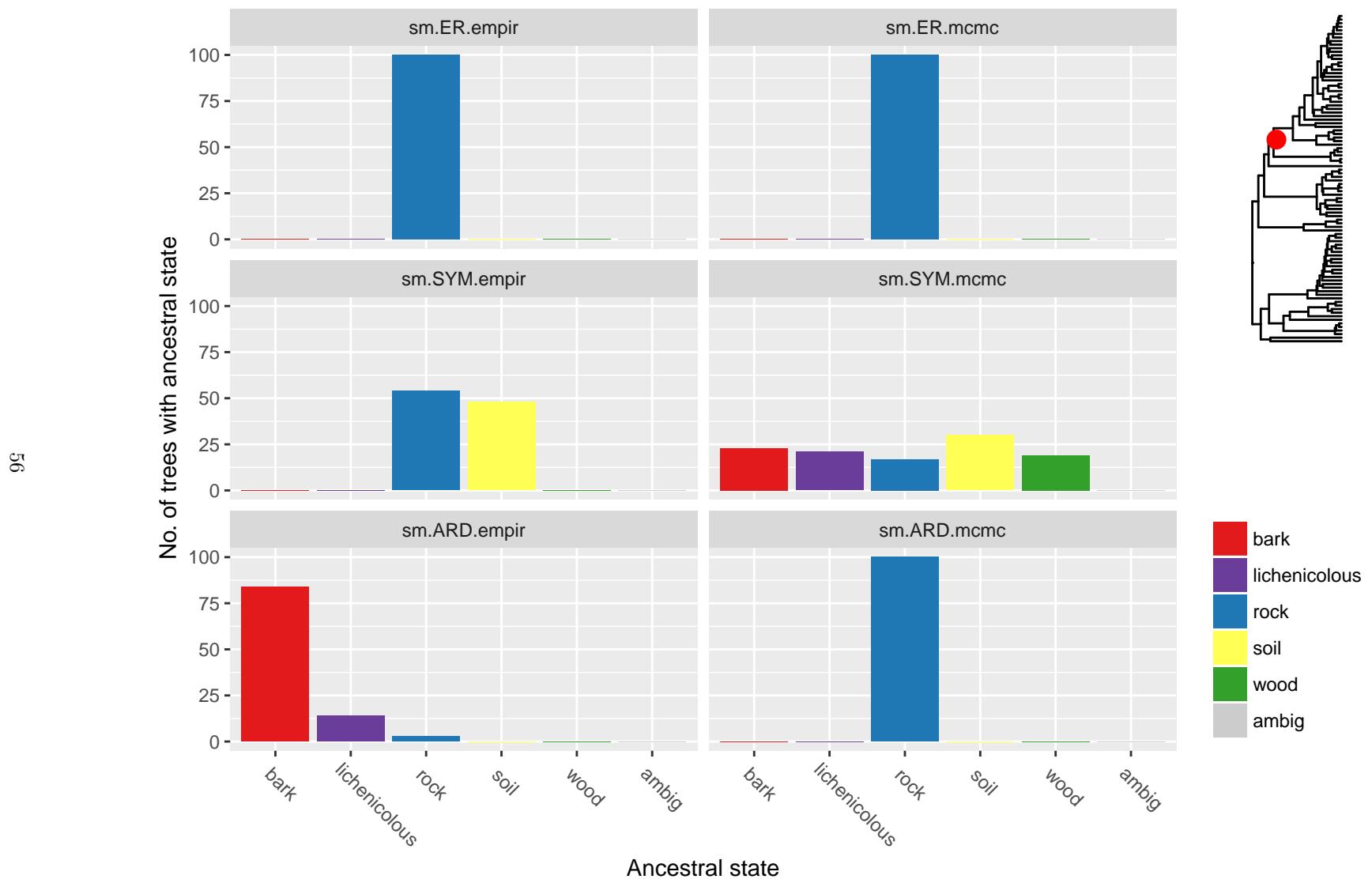
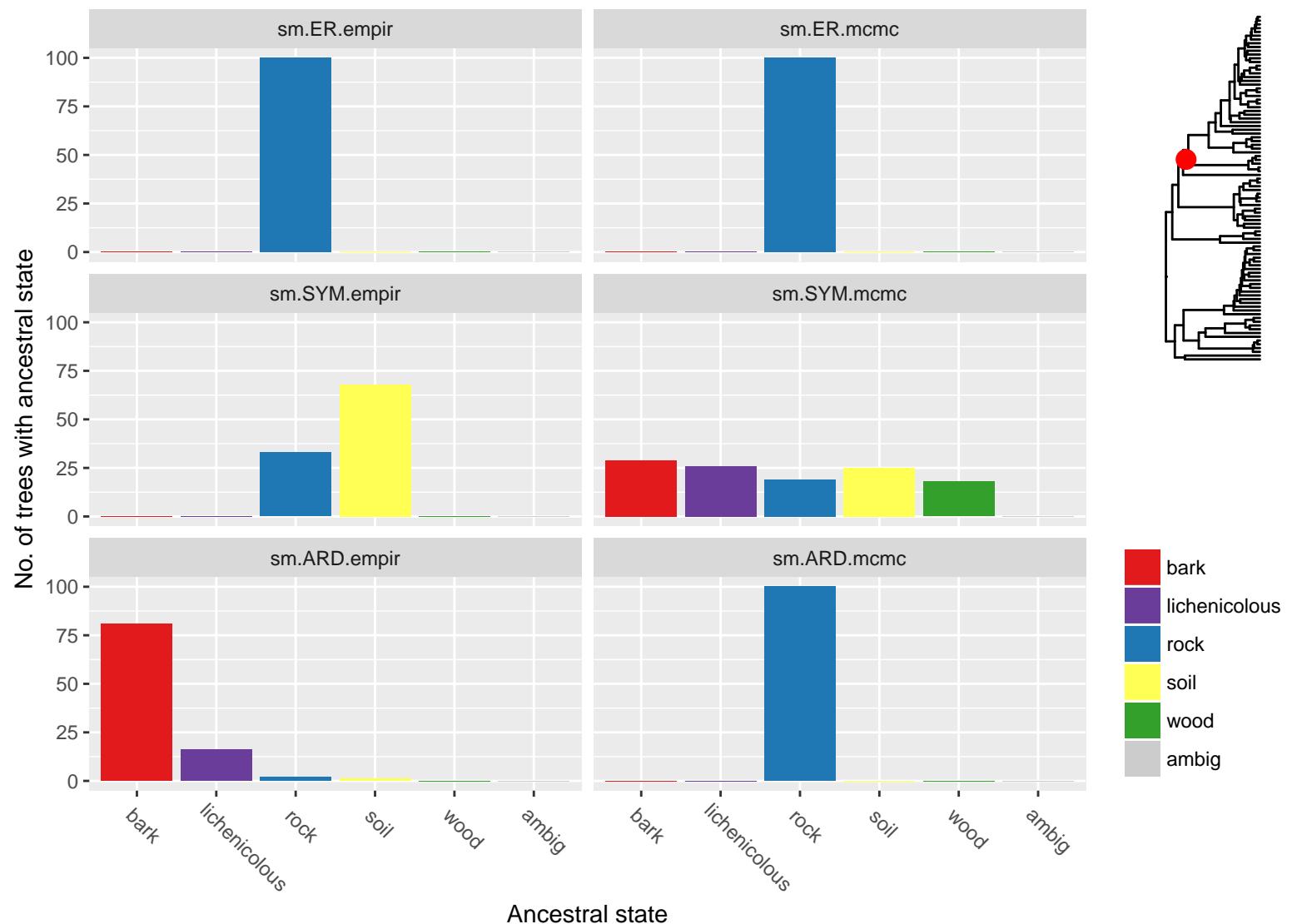


Figure S47: Ancestral states for node 6



8c

Figure S48: Ancestral states for node 7

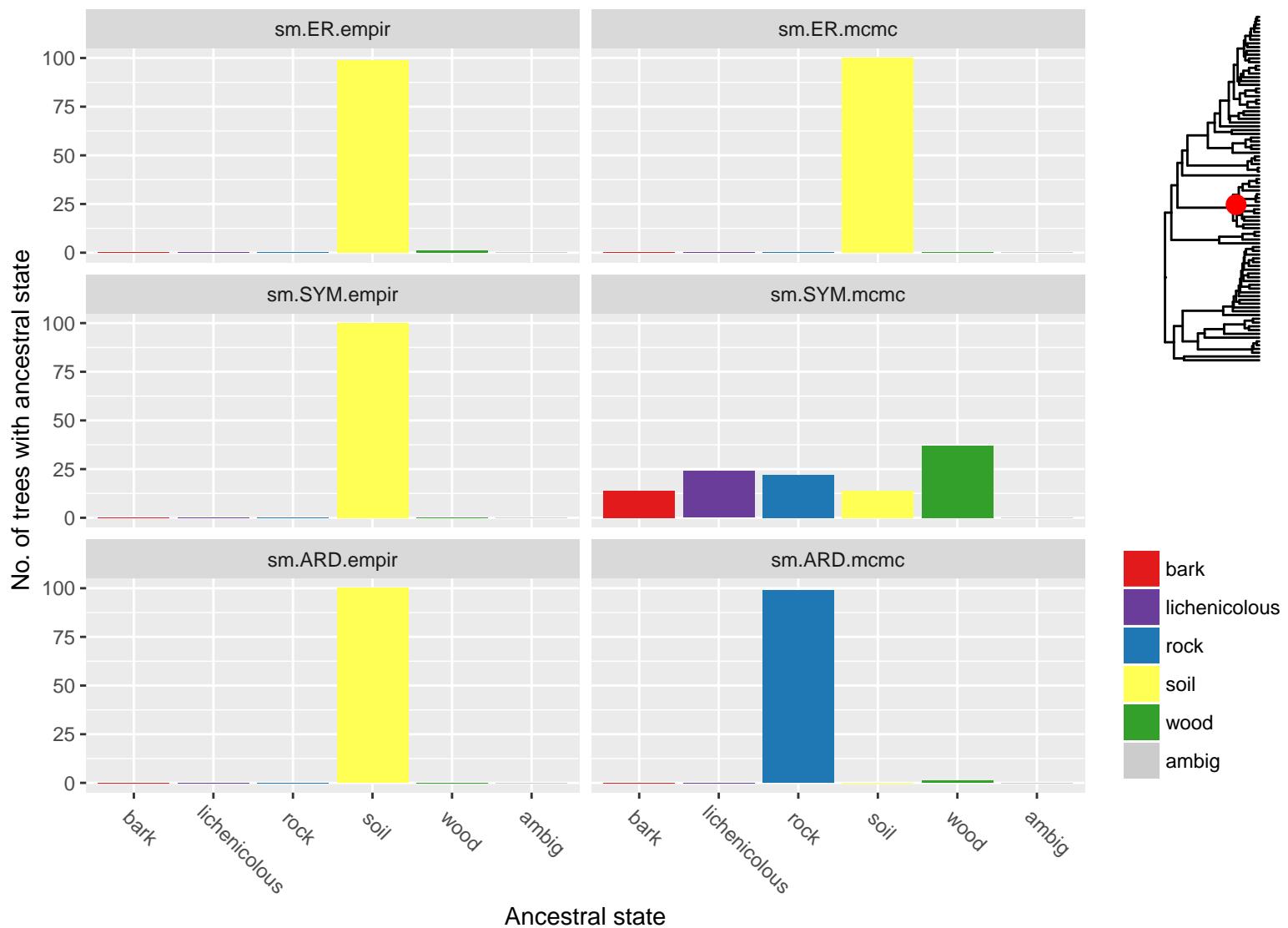
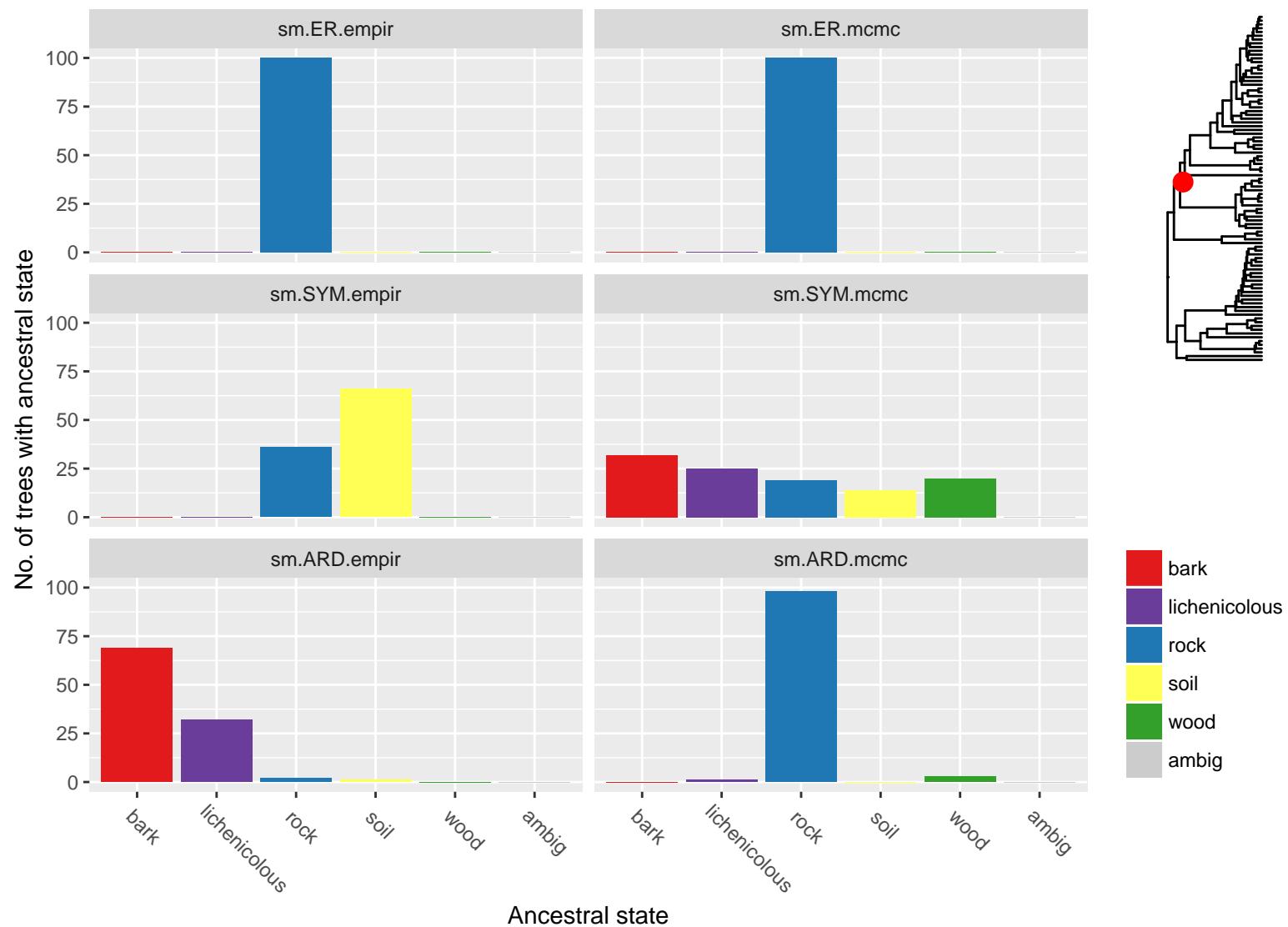


Figure S49: Ancestral states for node 8

6c



09

Figure S50: Ancestral states for node 9

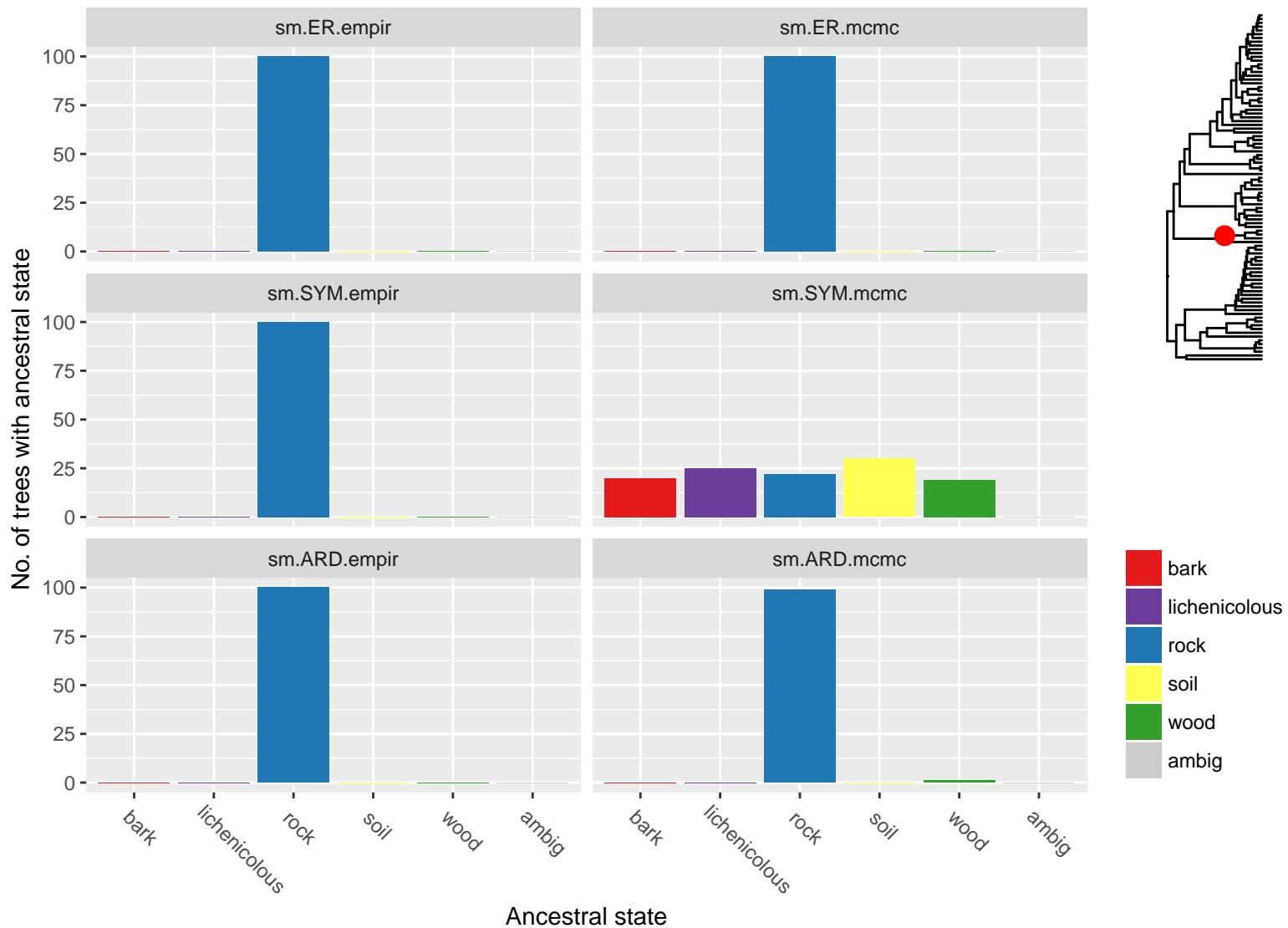


Figure S51: Ancestral states for node 10

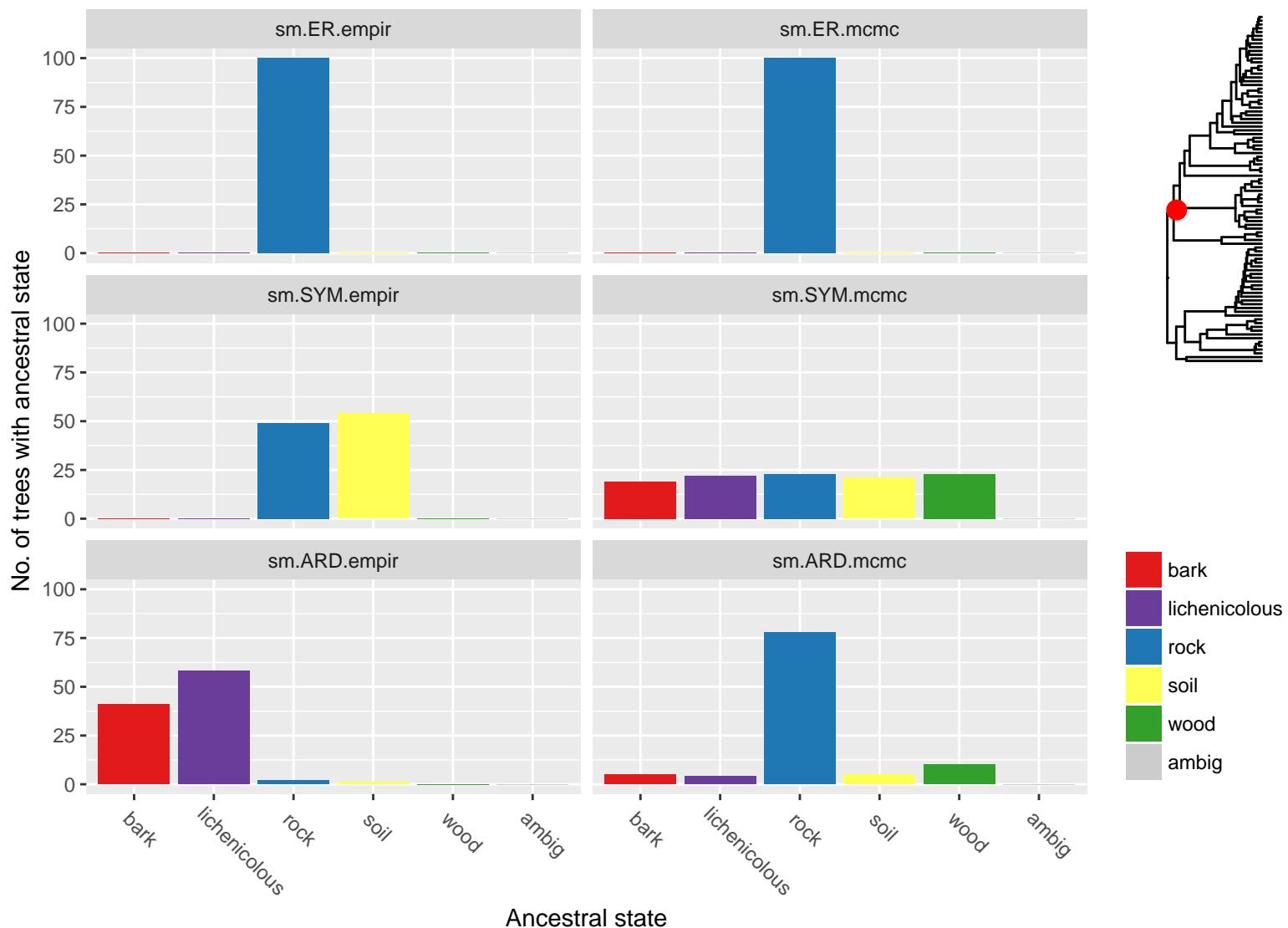
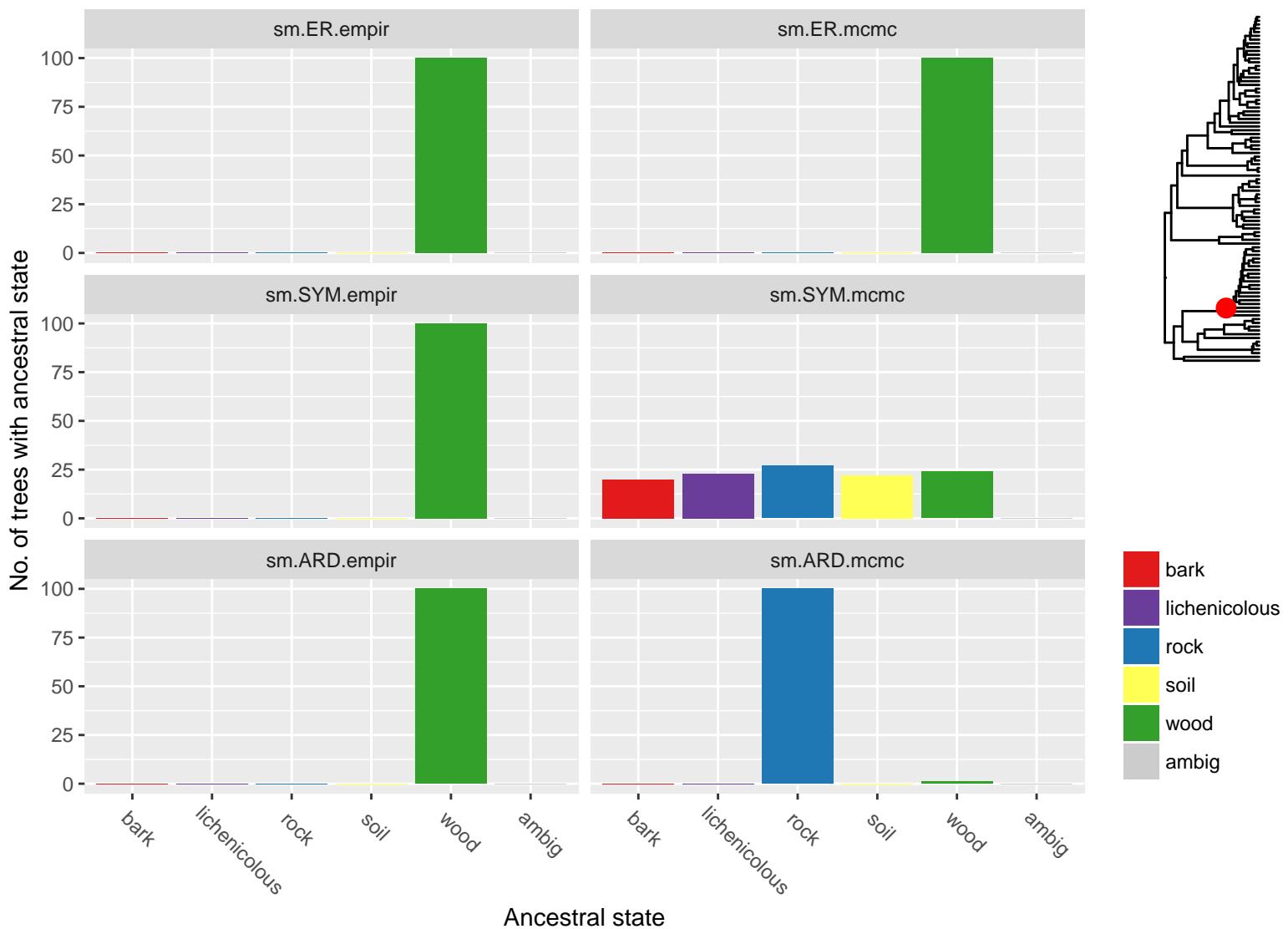


Figure S52: Ancestral states for node 11



ε9

Figure S53: Ancestral states for node 12

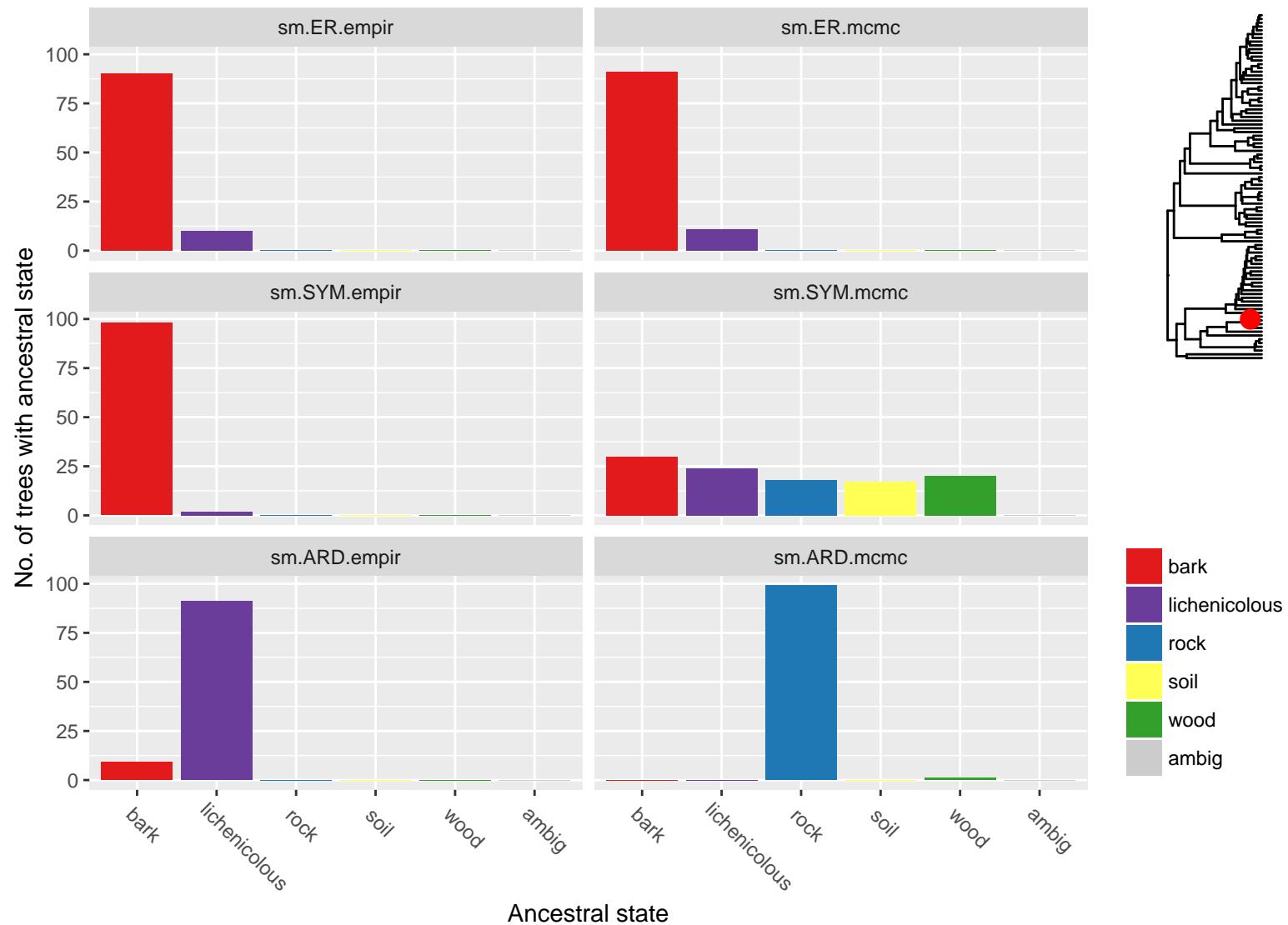


Figure S54: Ancestral states for node 13

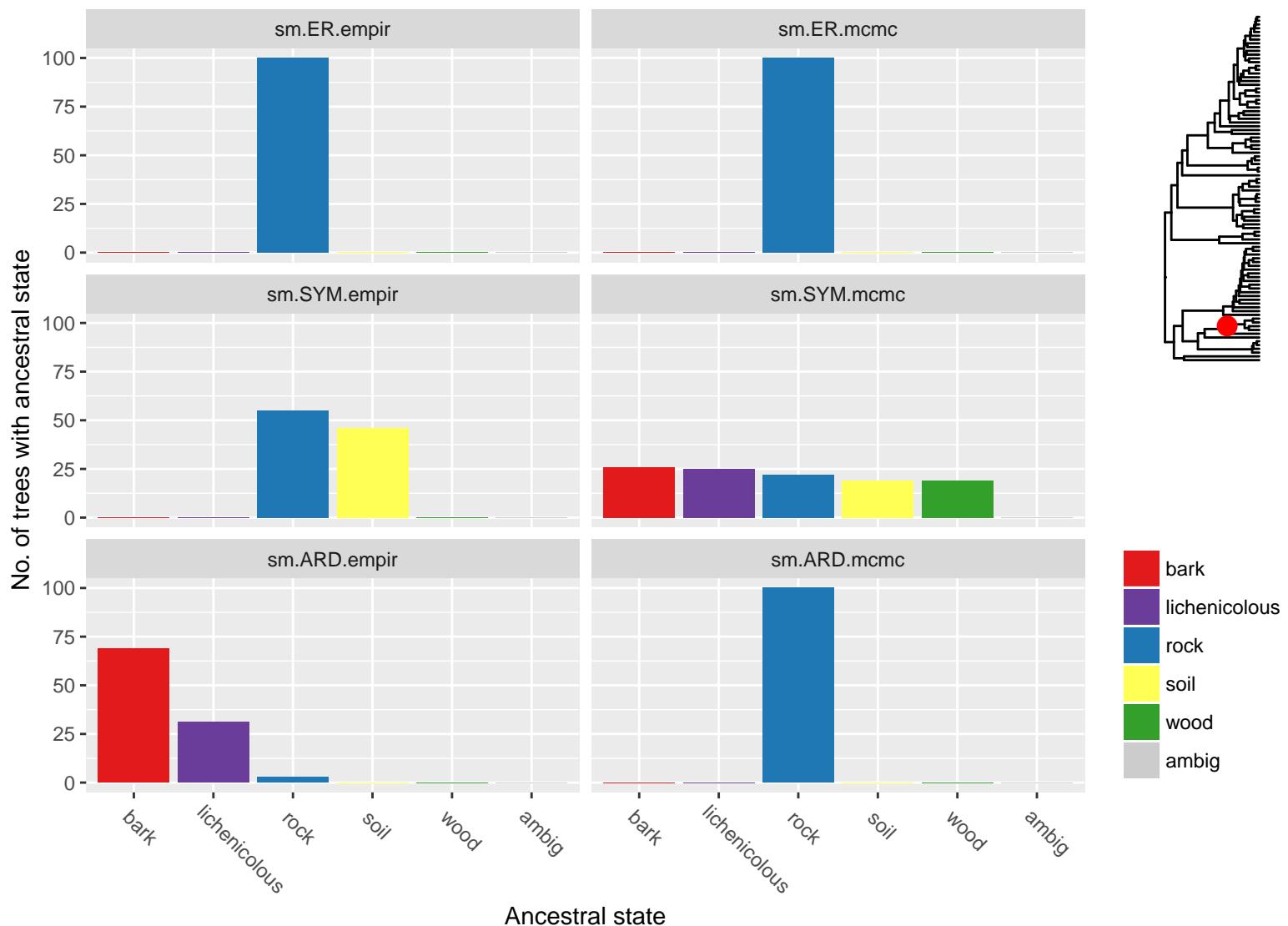


Figure S55: Ancestral states for node 14

29

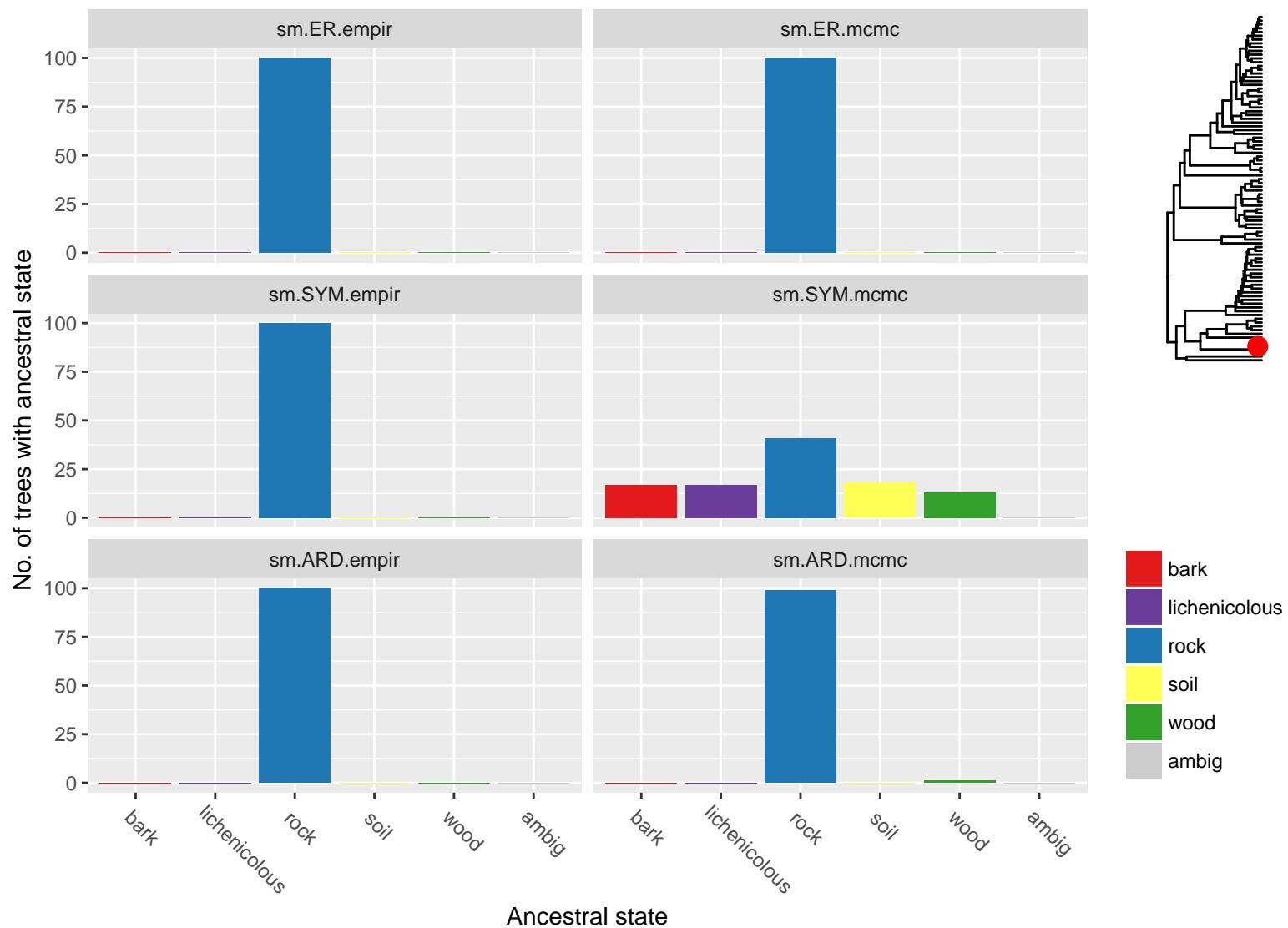


Figure S56: Ancestral states for node 15

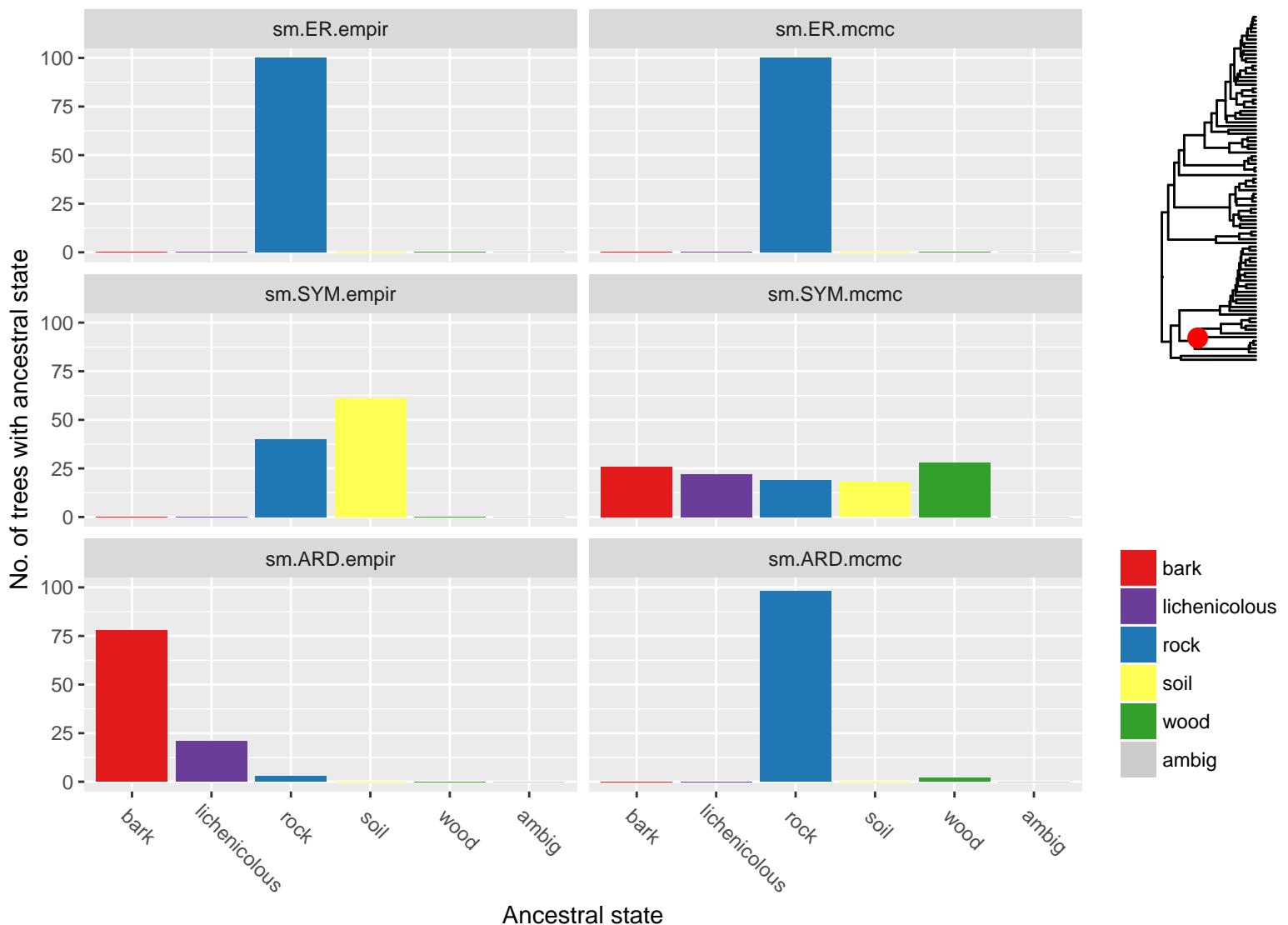


Figure S57: Ancestral states for node 16

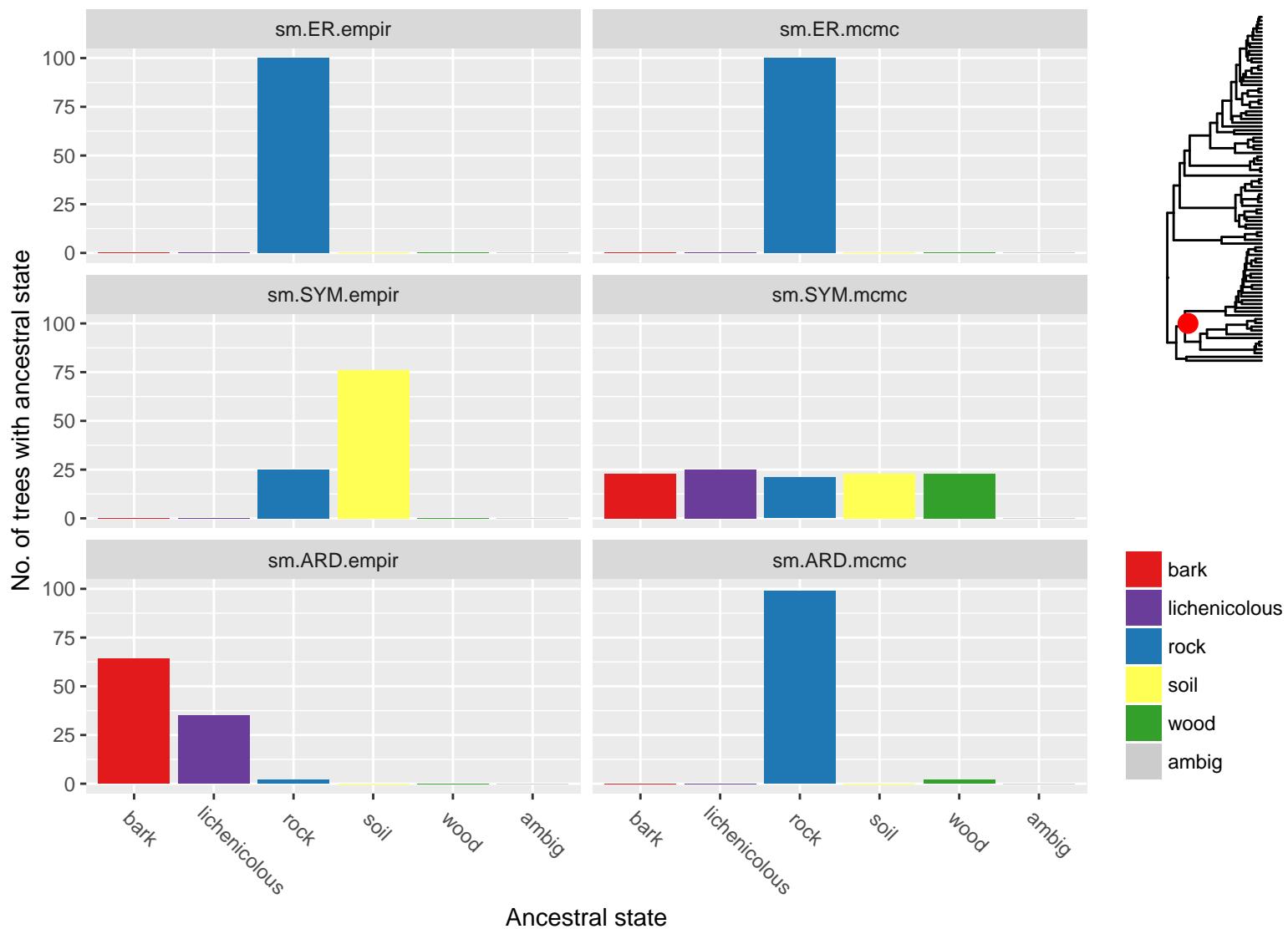


Figure S58: Ancestral states for node 17

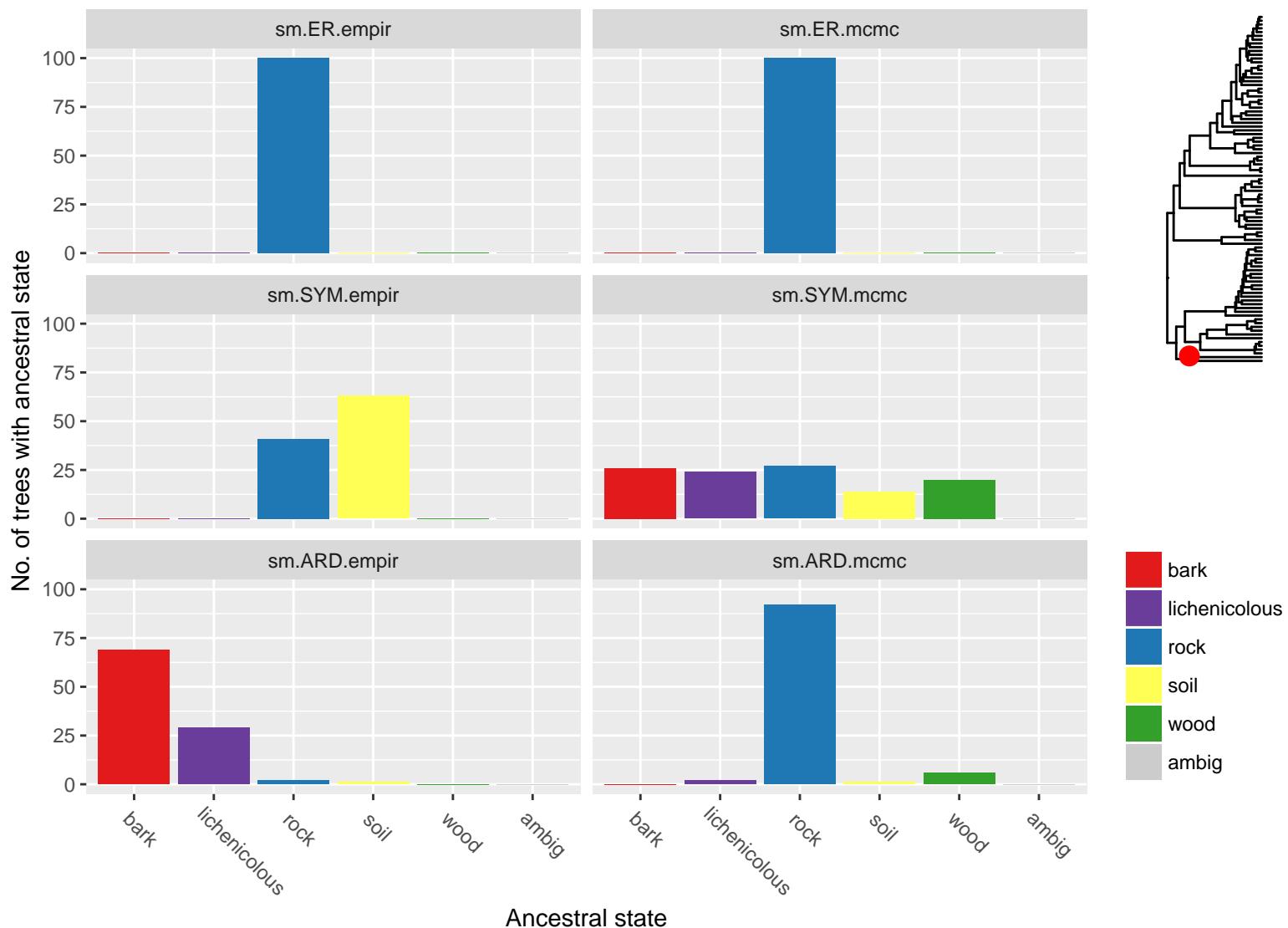


Figure S59: Ancestral states for node 18

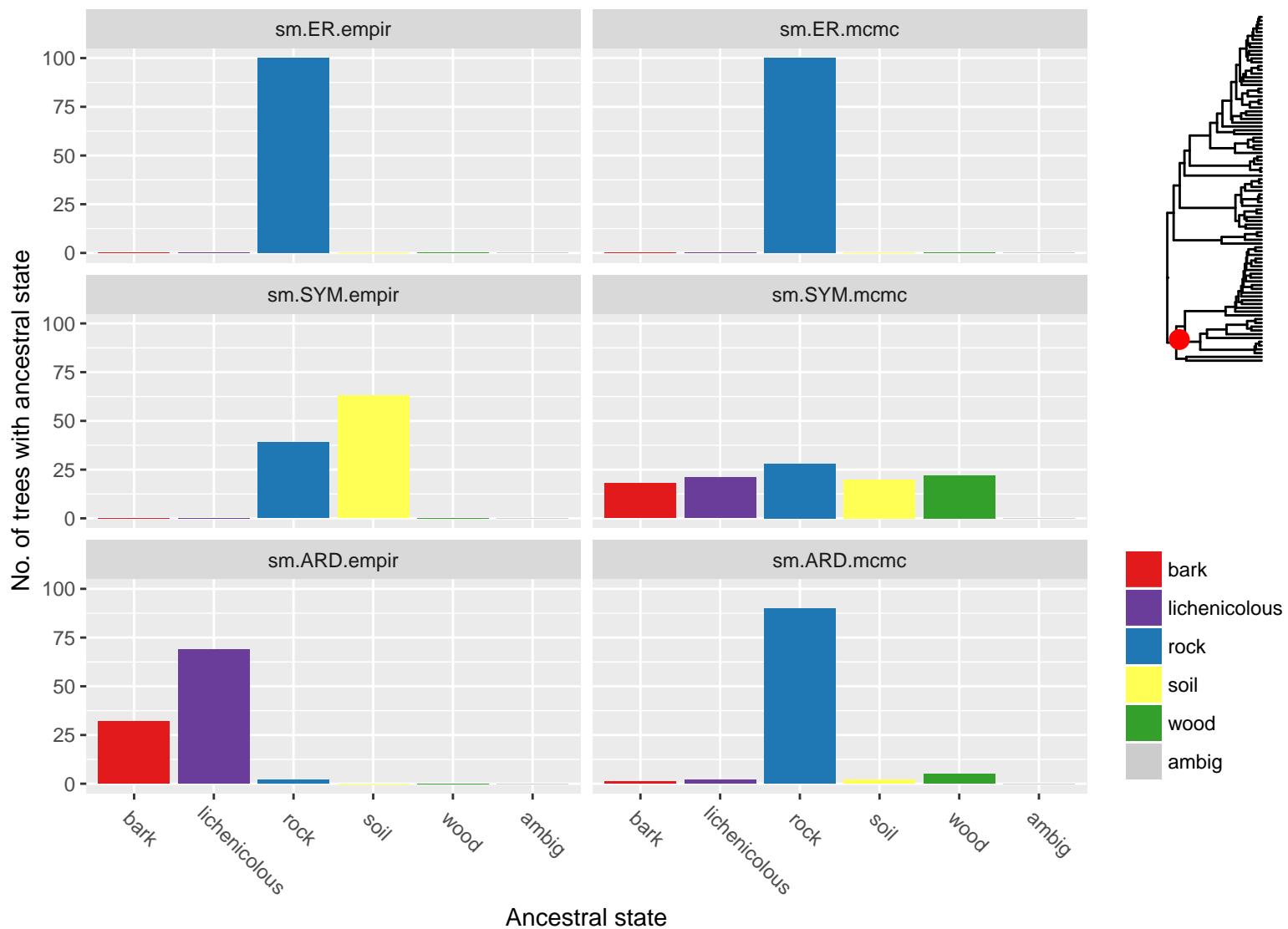


Figure S60: Ancestral states for node 19

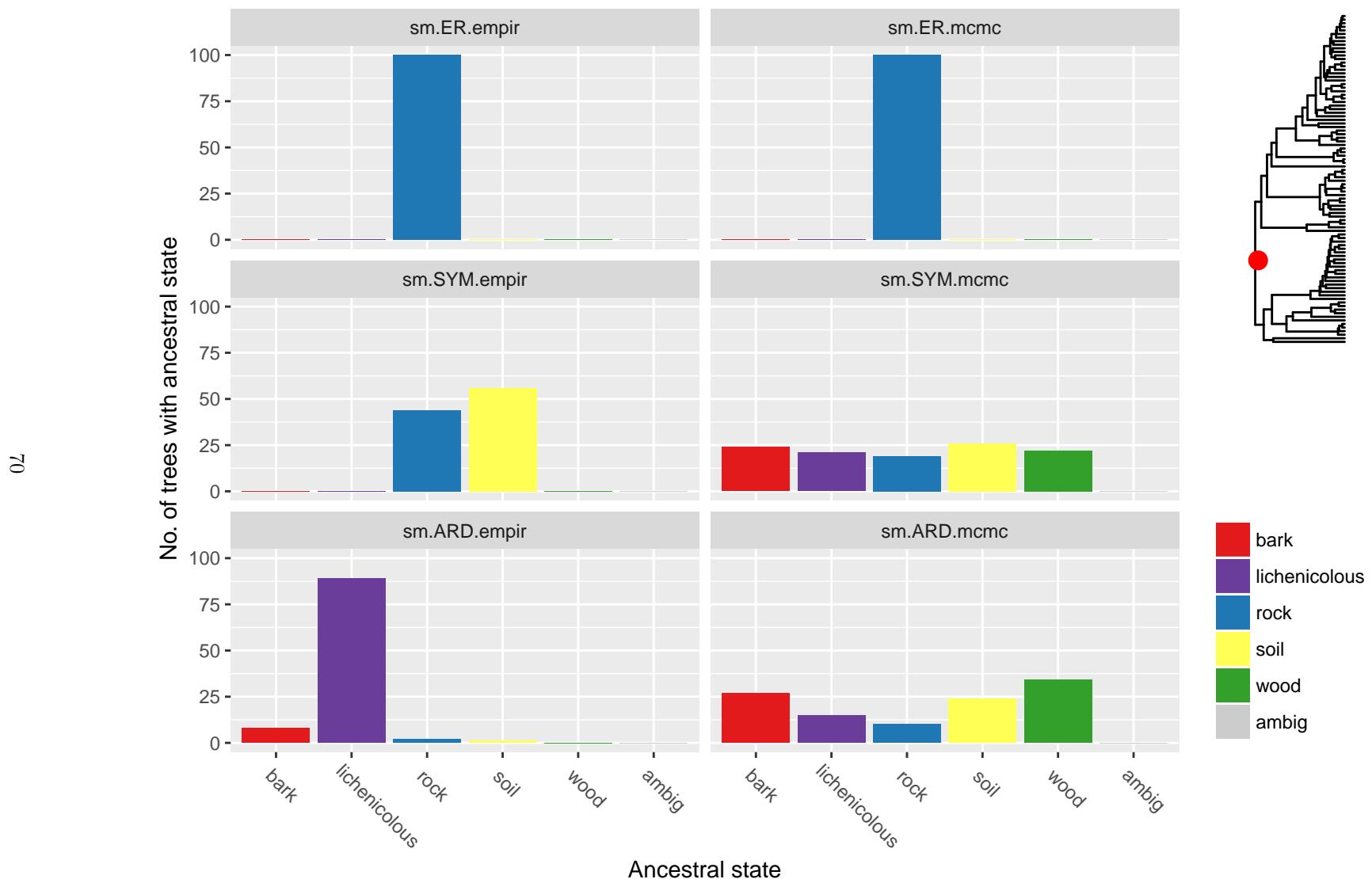


Figure S61-S79 - Results of ancestral state estimation of ecological strategy character with ace for 19 nodes of the trapezioid phylogeny

Ancestral state estimations of the ecological strategy character for 19 nodes of the trapezioid phylogeny based on the method implemented in the ace function in R package ape imposing 4 different models. Please refer to the main text for details.

Figure S61: Ancestral states for node 1

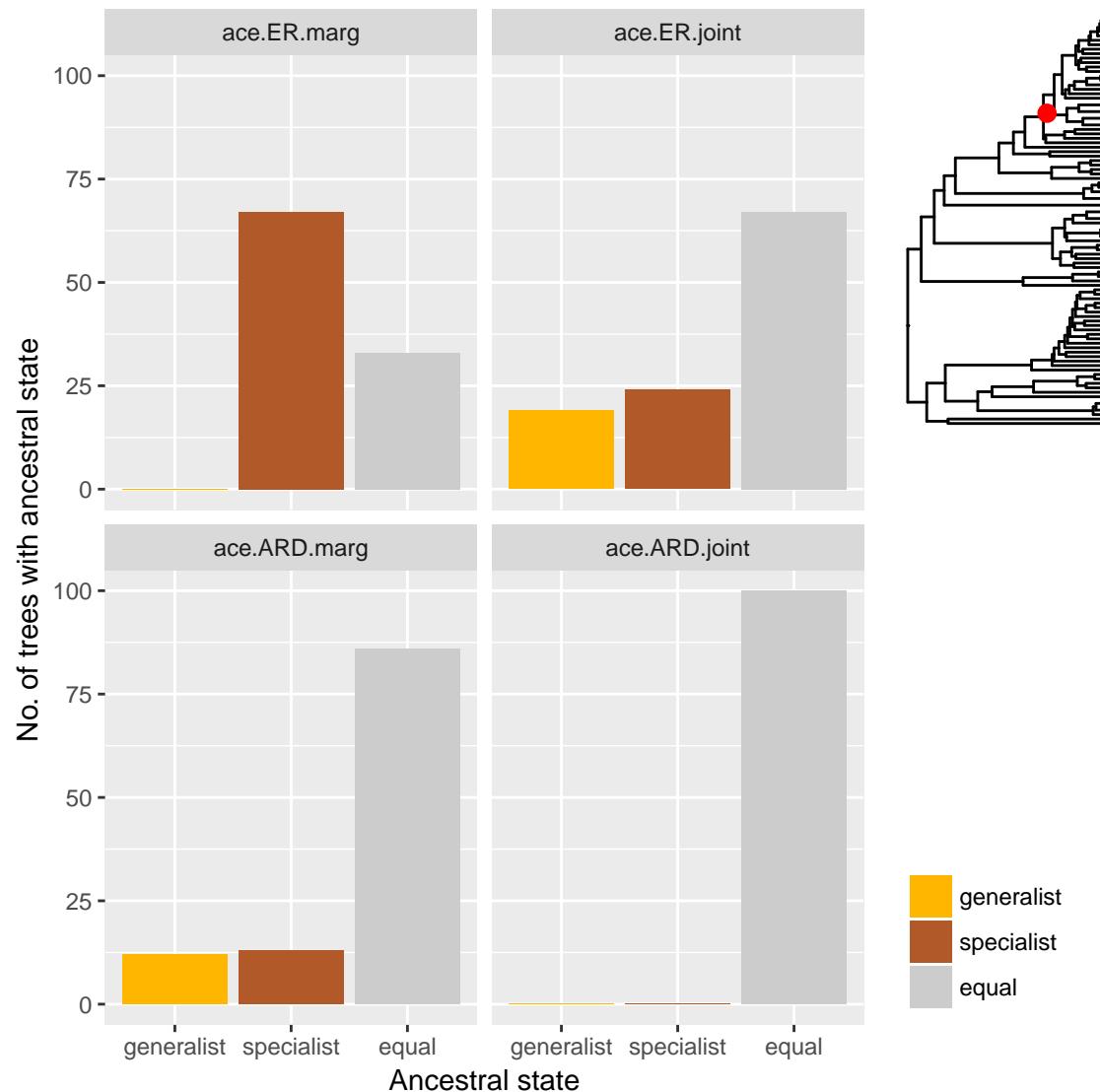


Figure S62: Ancestral states for node 2

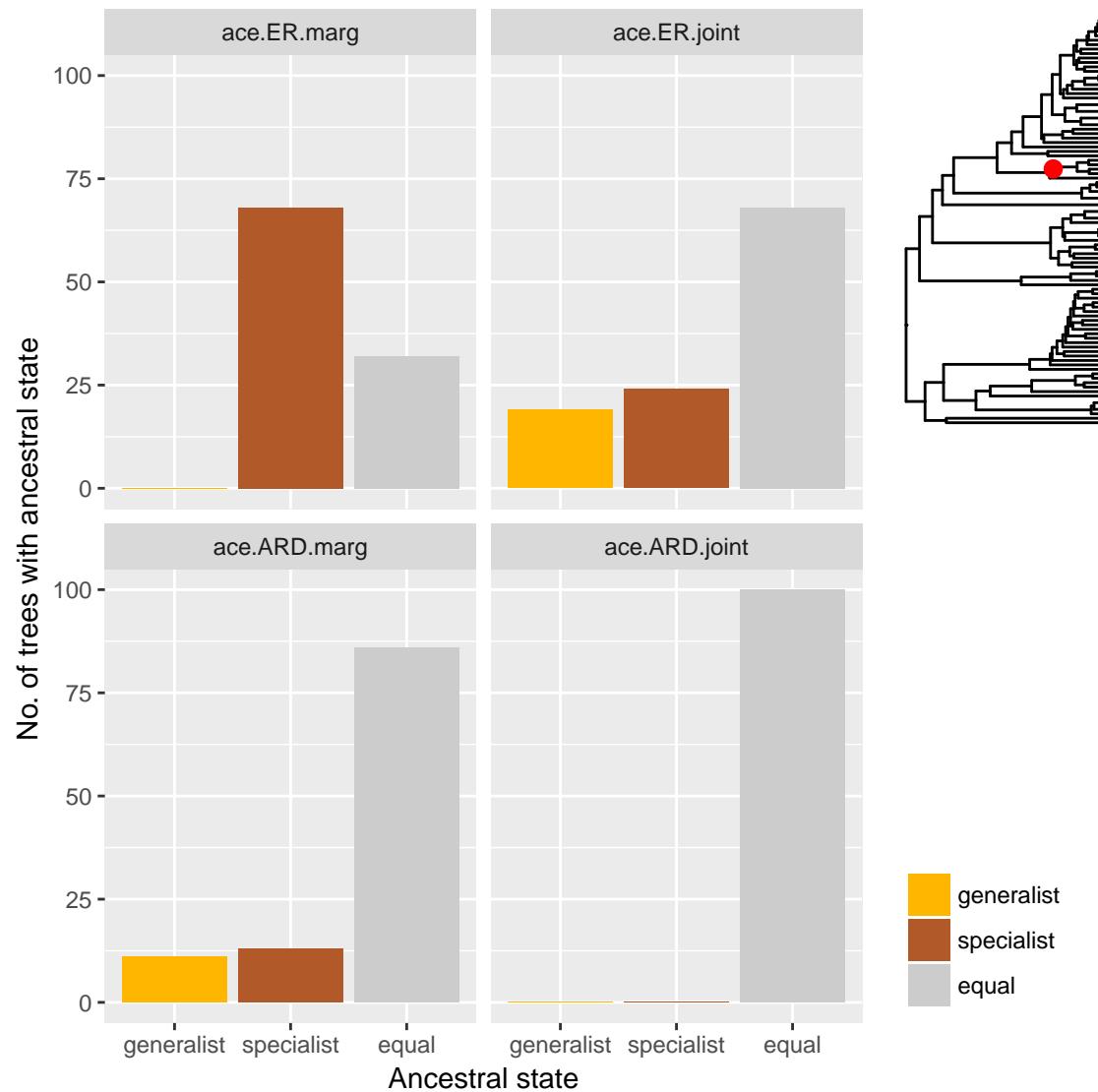


Figure S63: Ancestral states for node 3

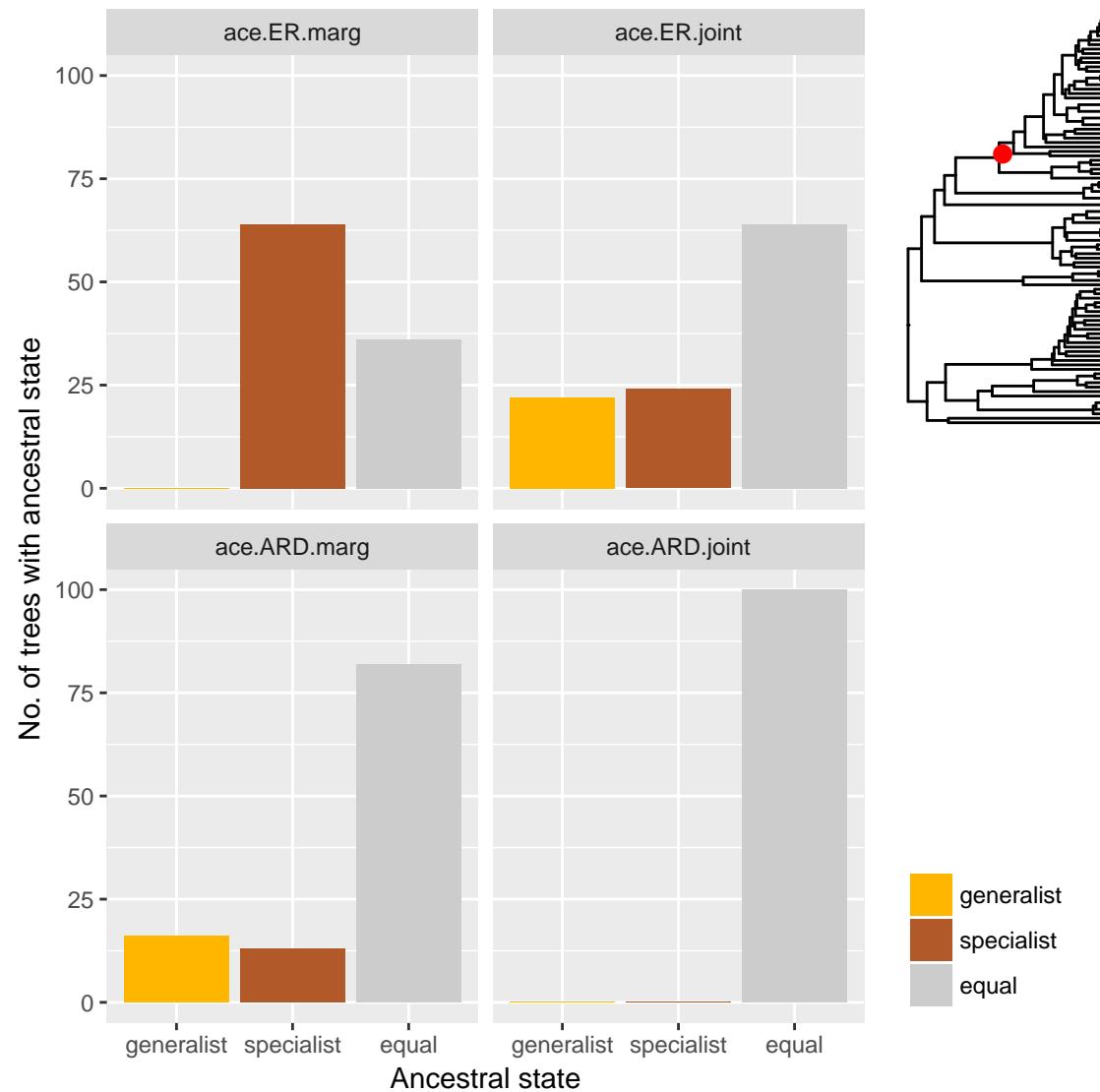


Figure S64: Ancestral states for node 4

Ω_L

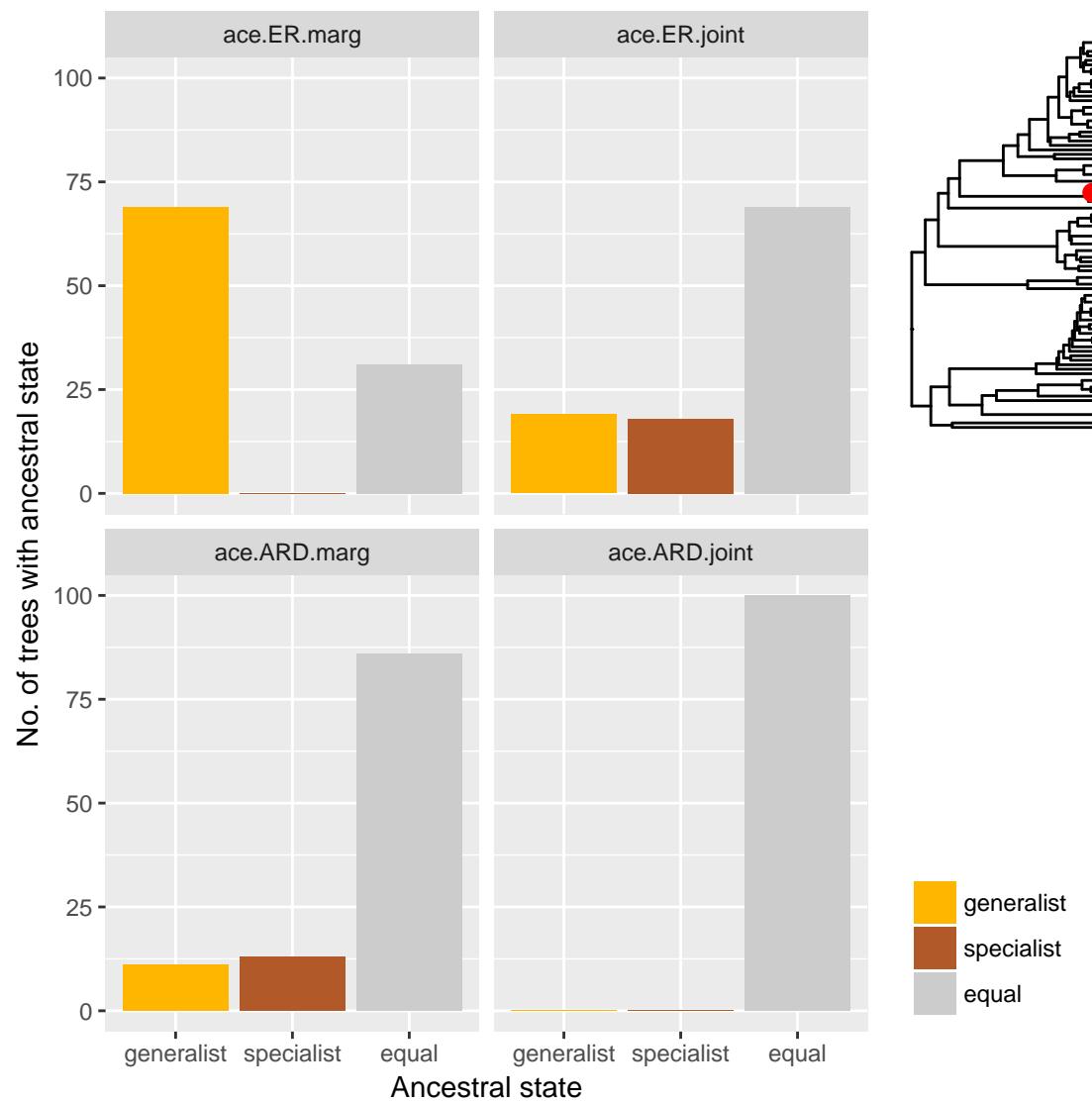


Figure S65: Ancestral states for node 5

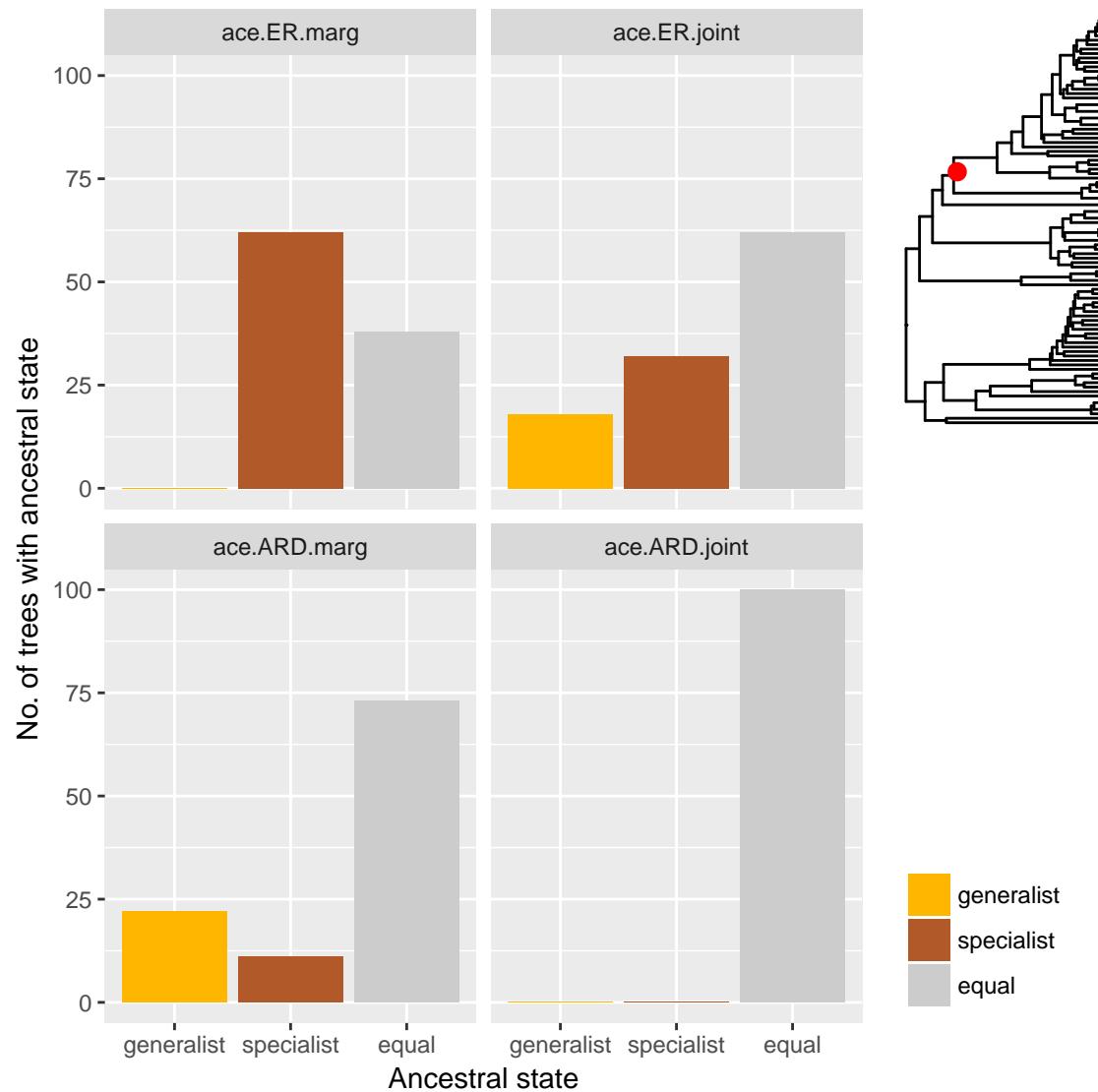


Figure S66: Ancestral states for node 6

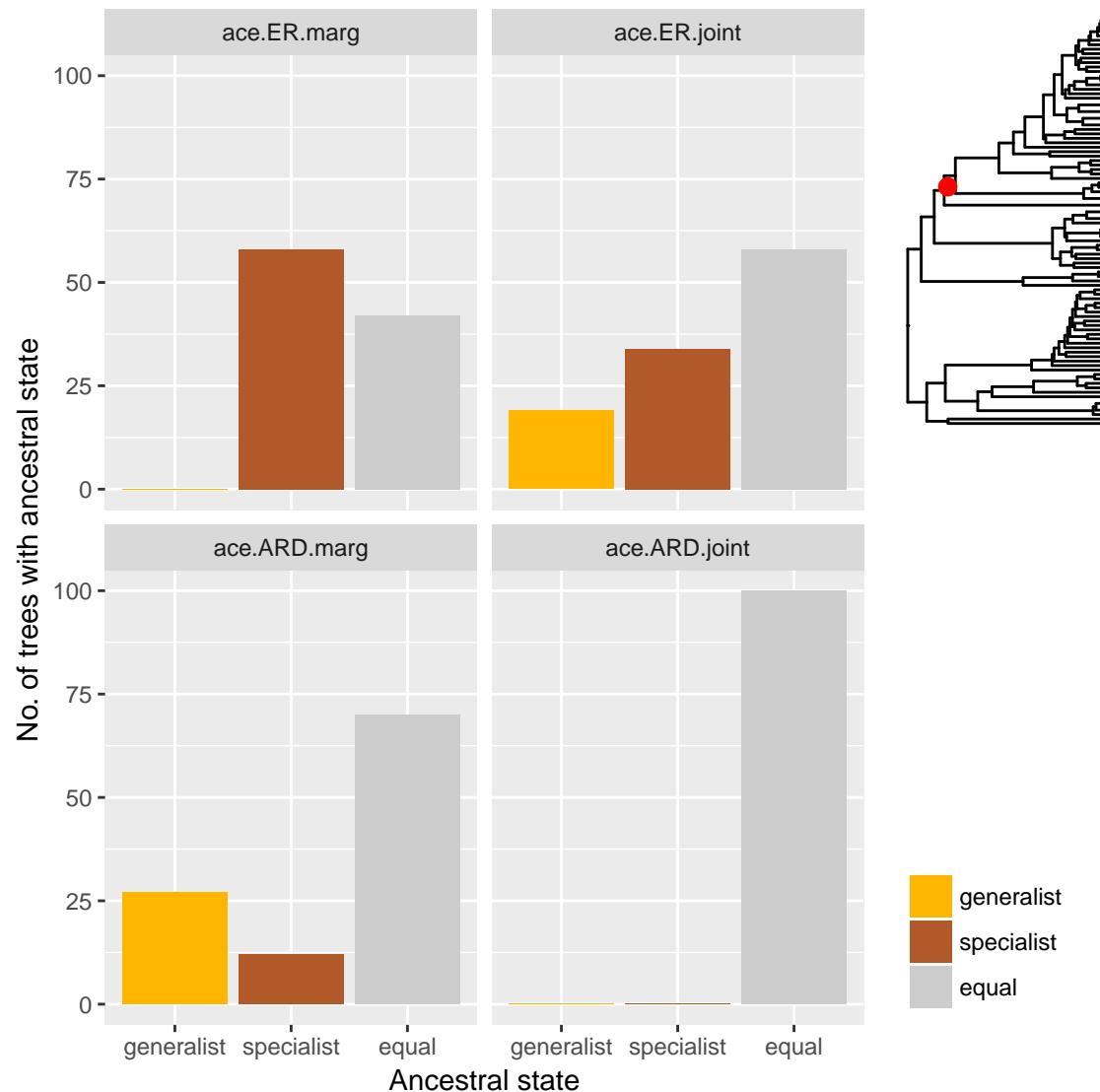


Figure S67: Ancestral states for node 7

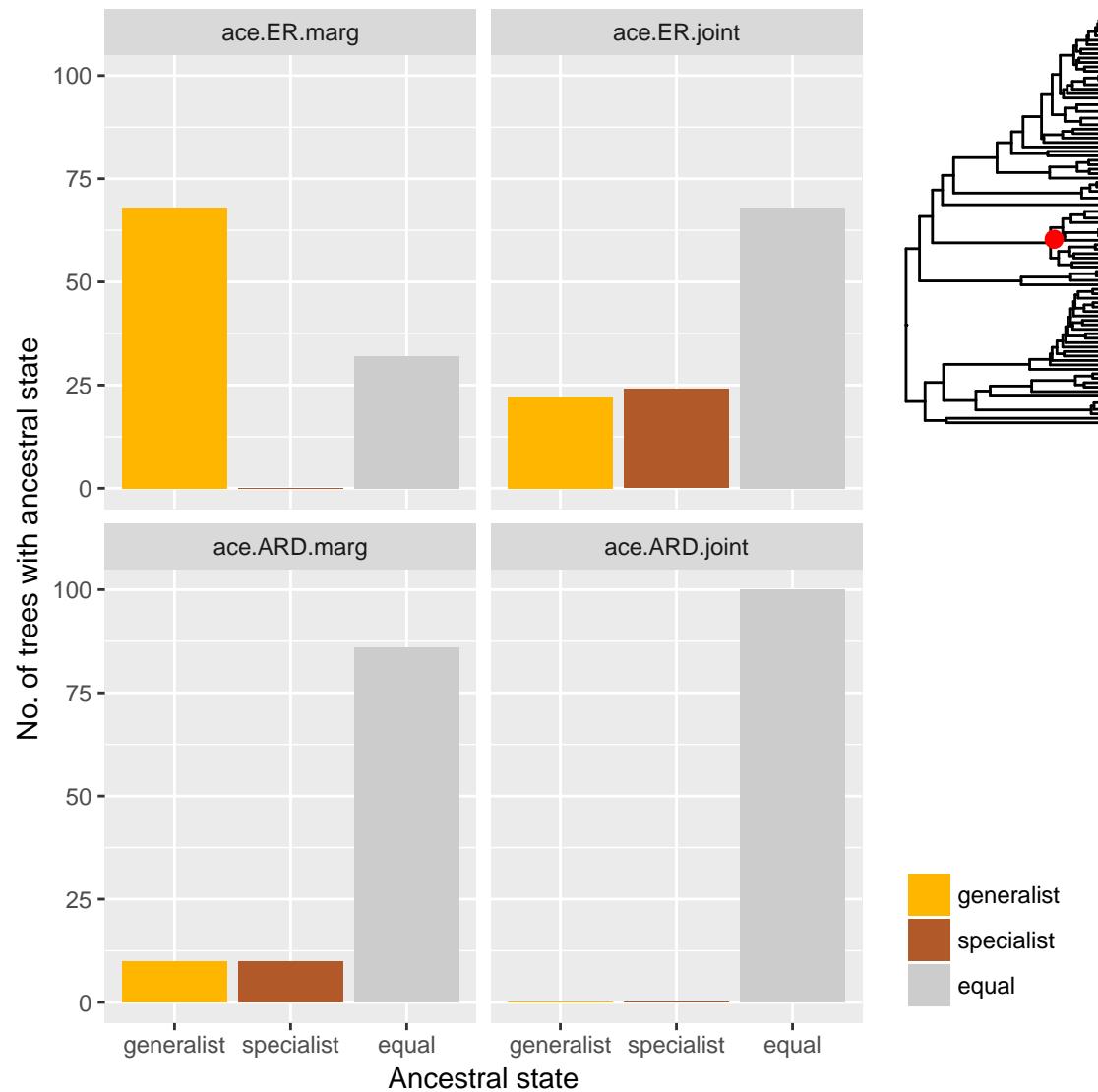


Figure S68: Ancestral states for node 8

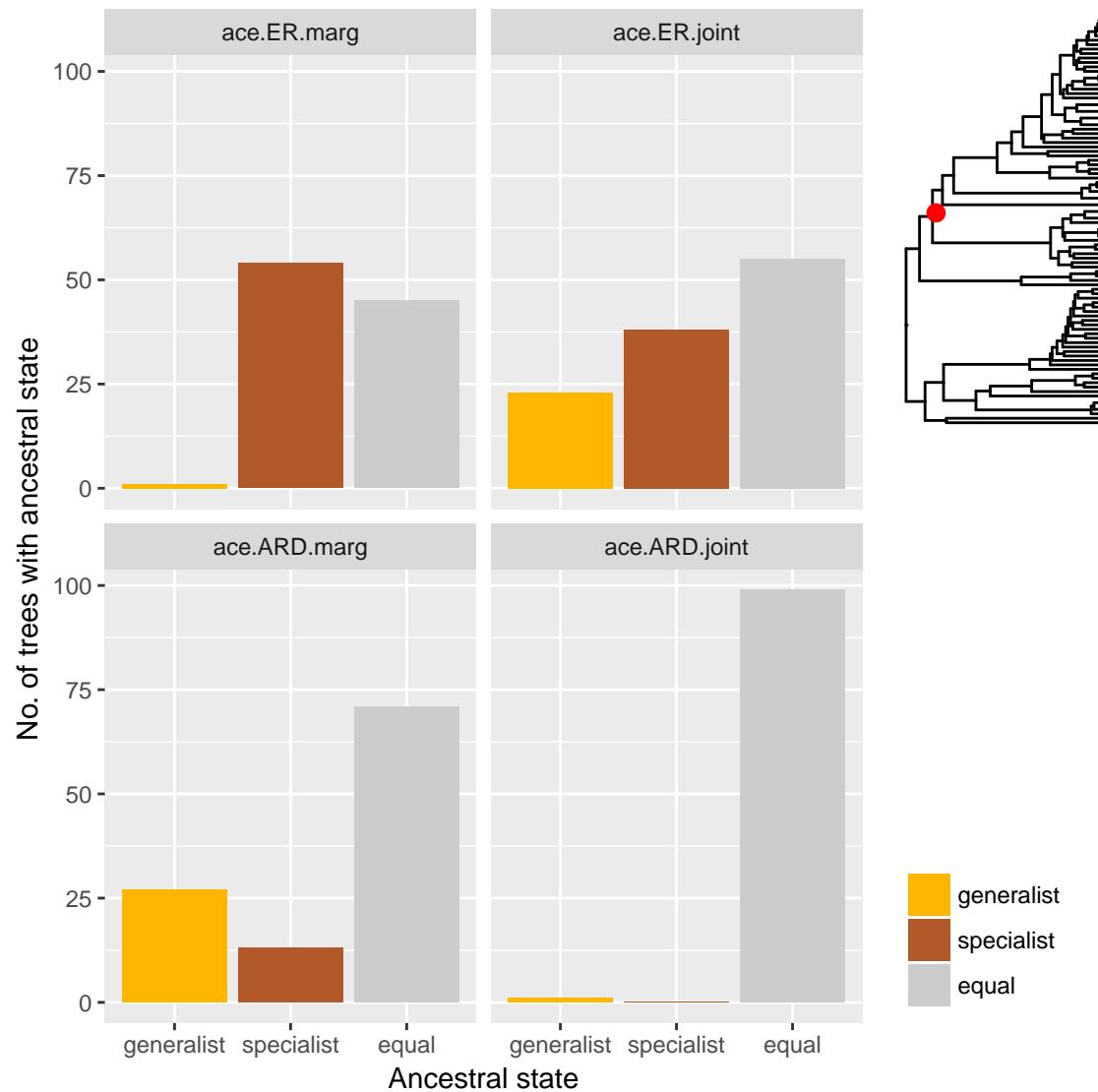


Figure S69: Ancestral states for node 9

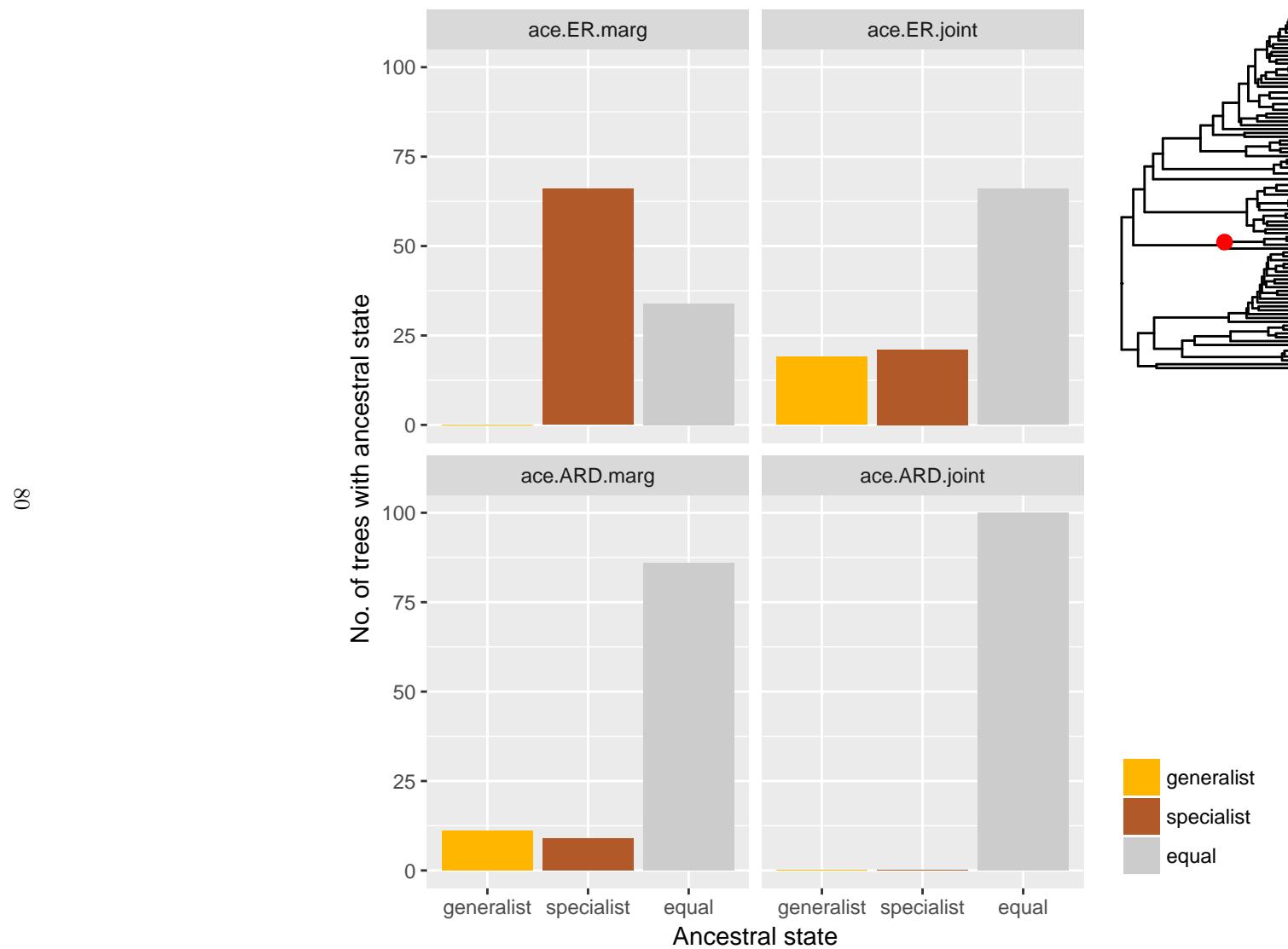


Figure S70: Ancestral states for node 10

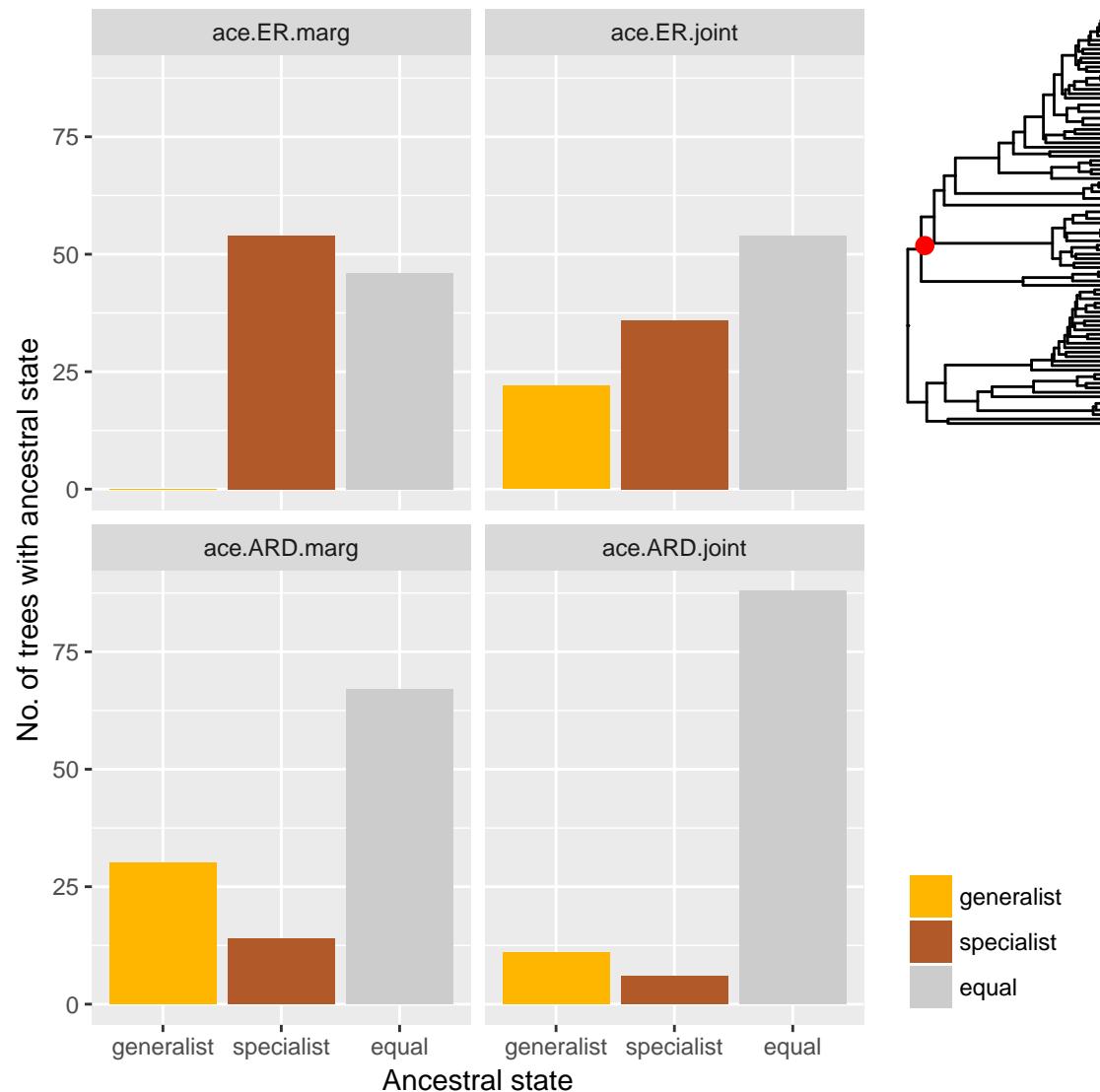


Figure S71: Ancestral states for node 11

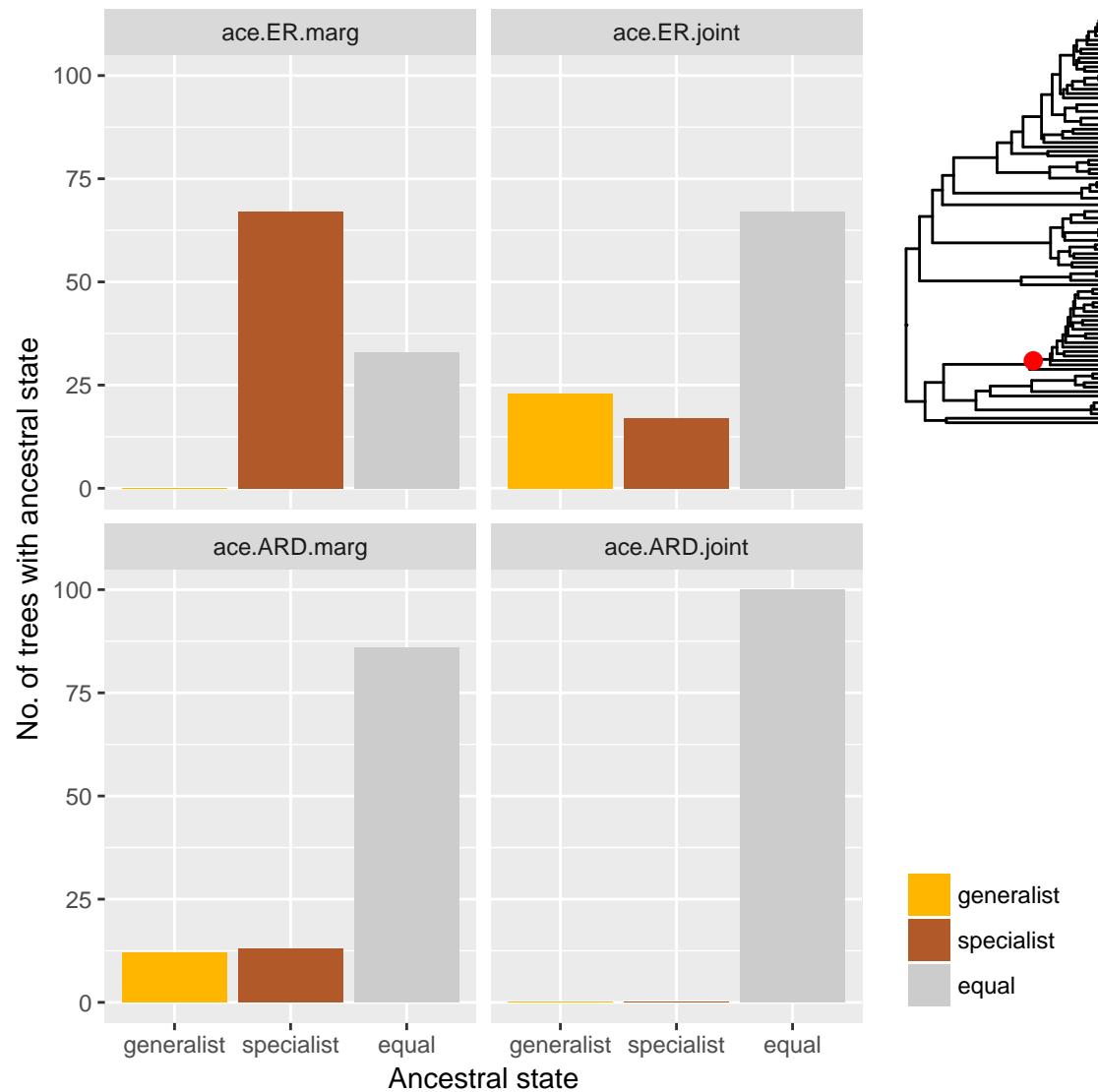


Figure S72: Ancestral states for node 12

88

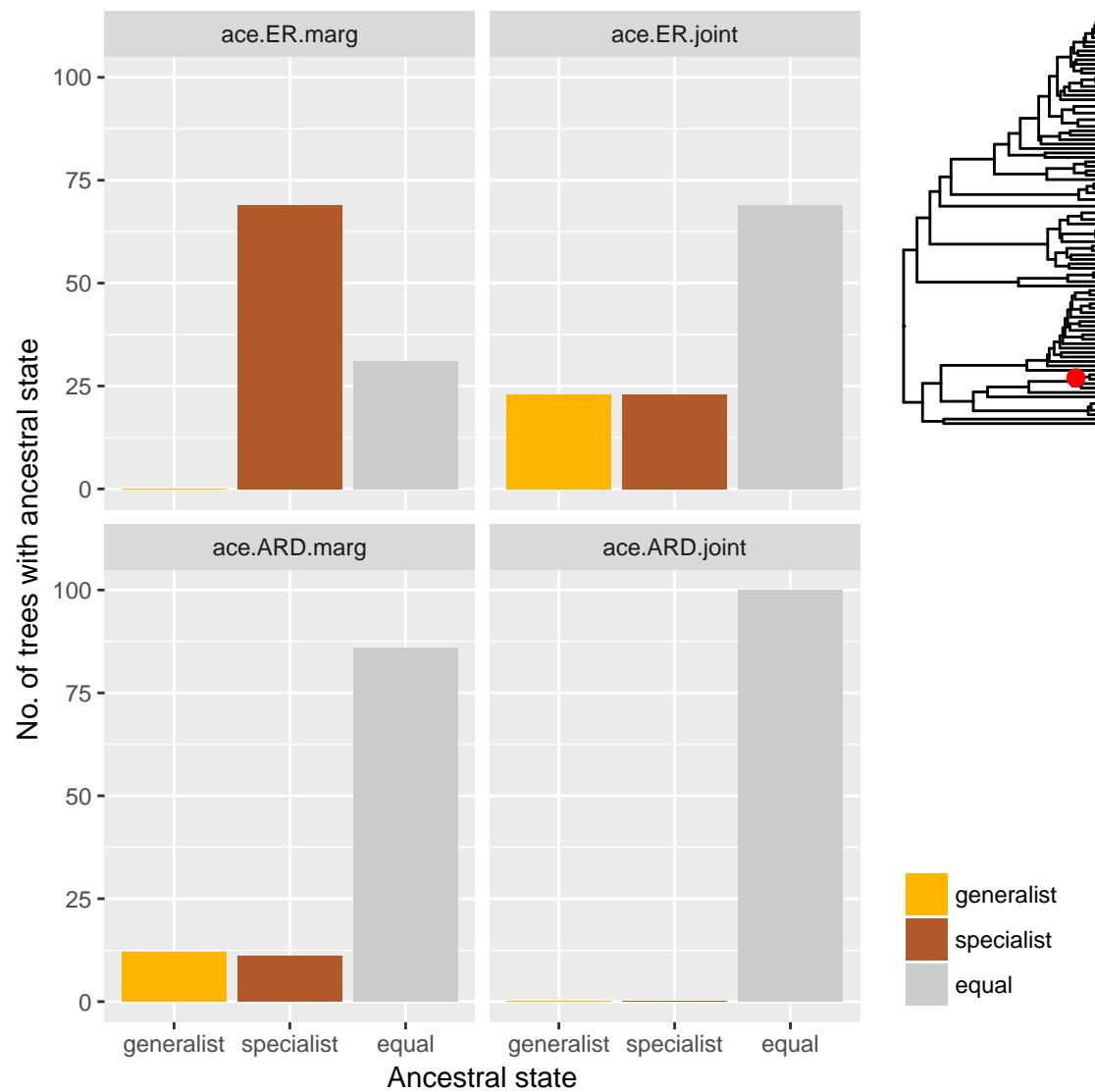


Figure S73: Ancestral states for node 13

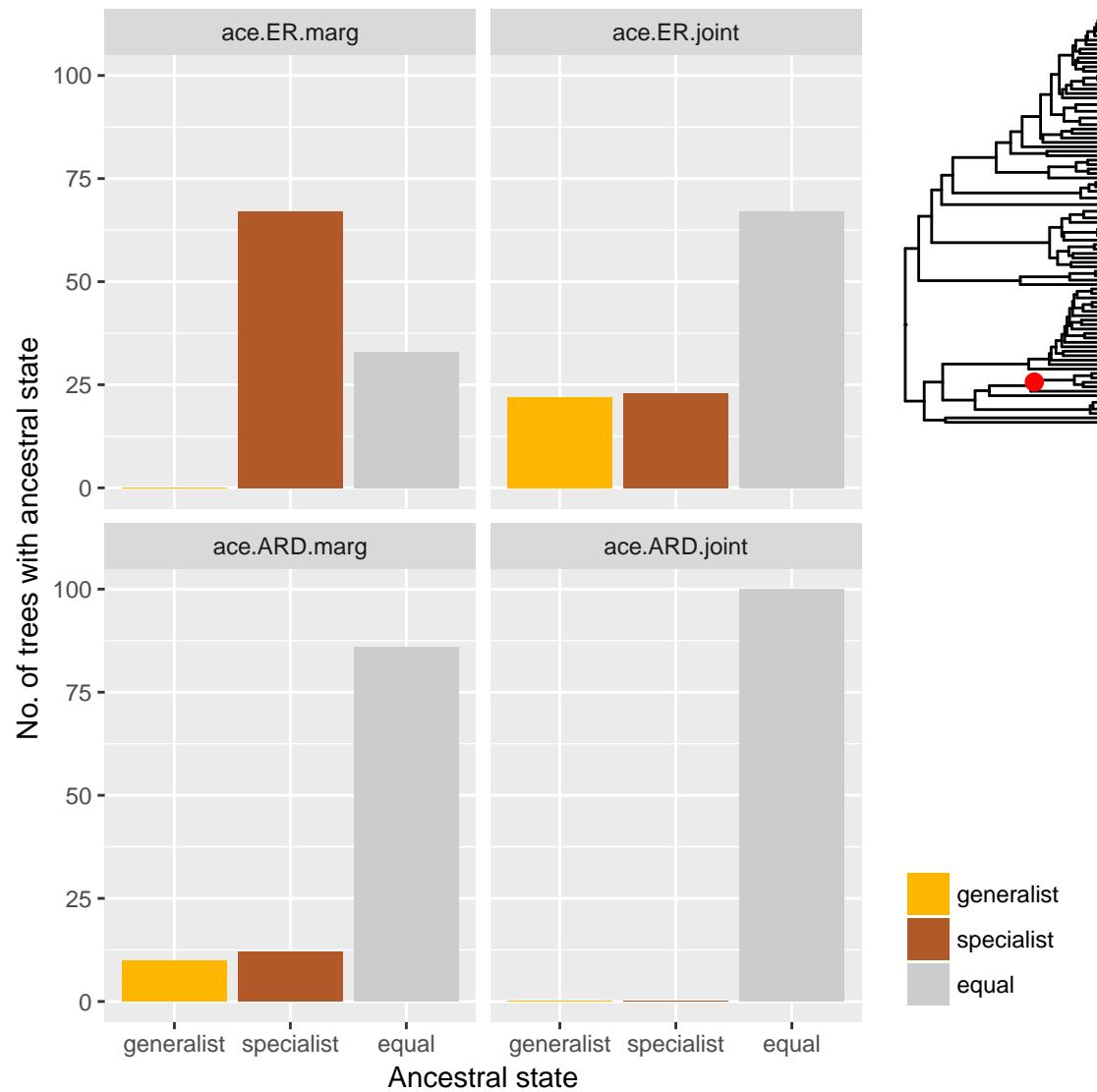


Figure S74: Ancestral states for node 14

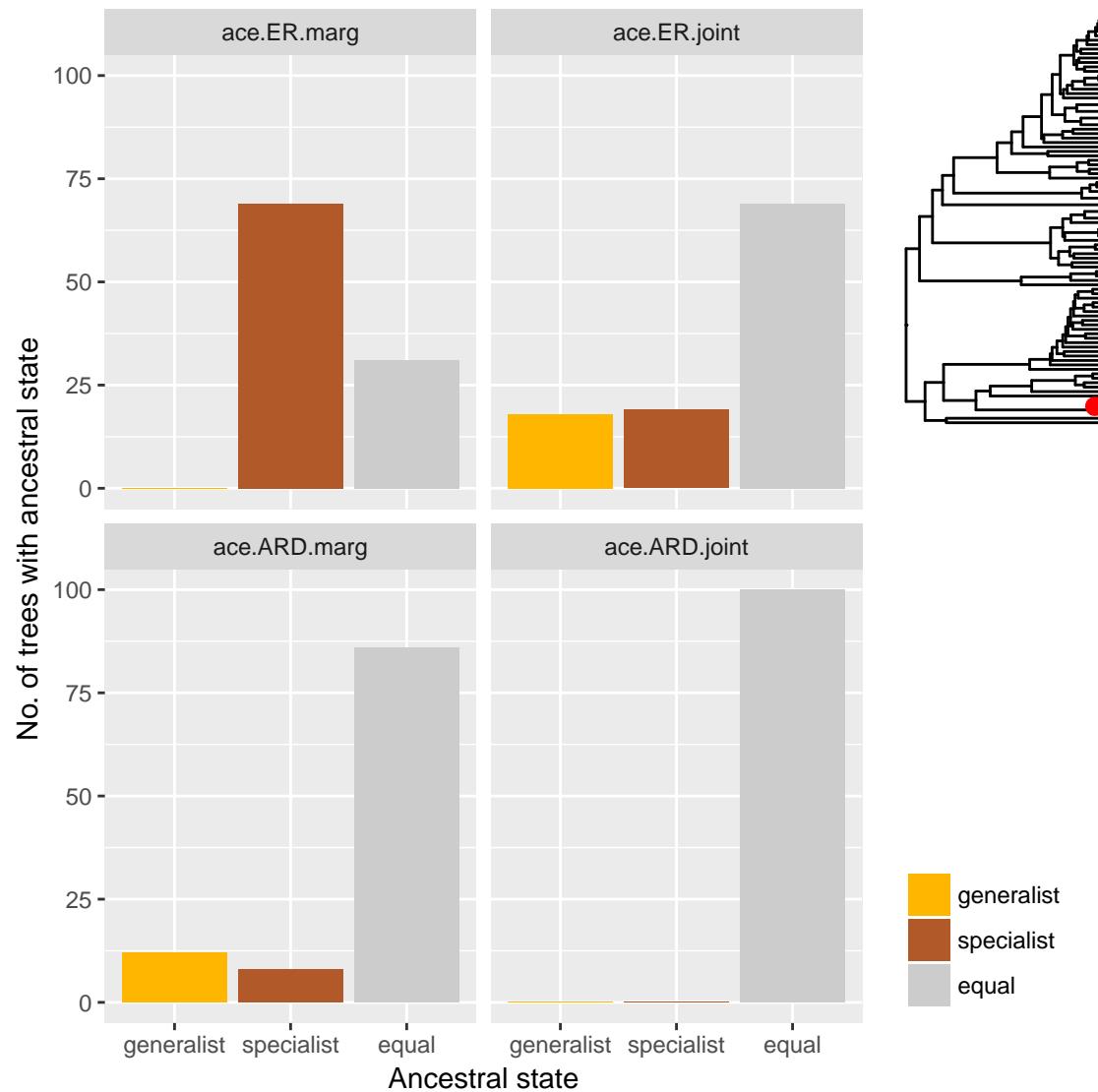


Figure S75: Ancestral states for node 15

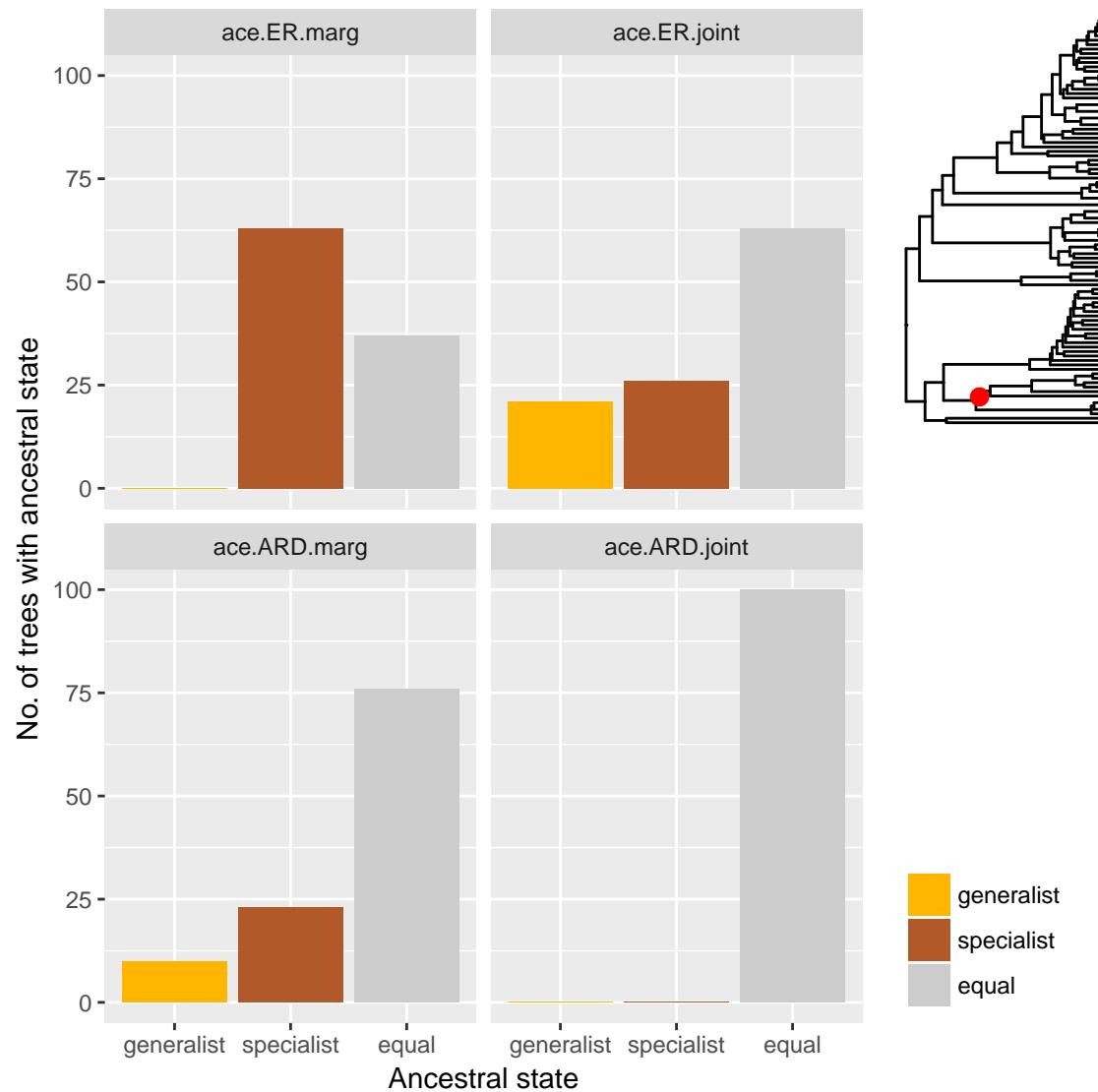


Figure S76: Ancestral states for node 16

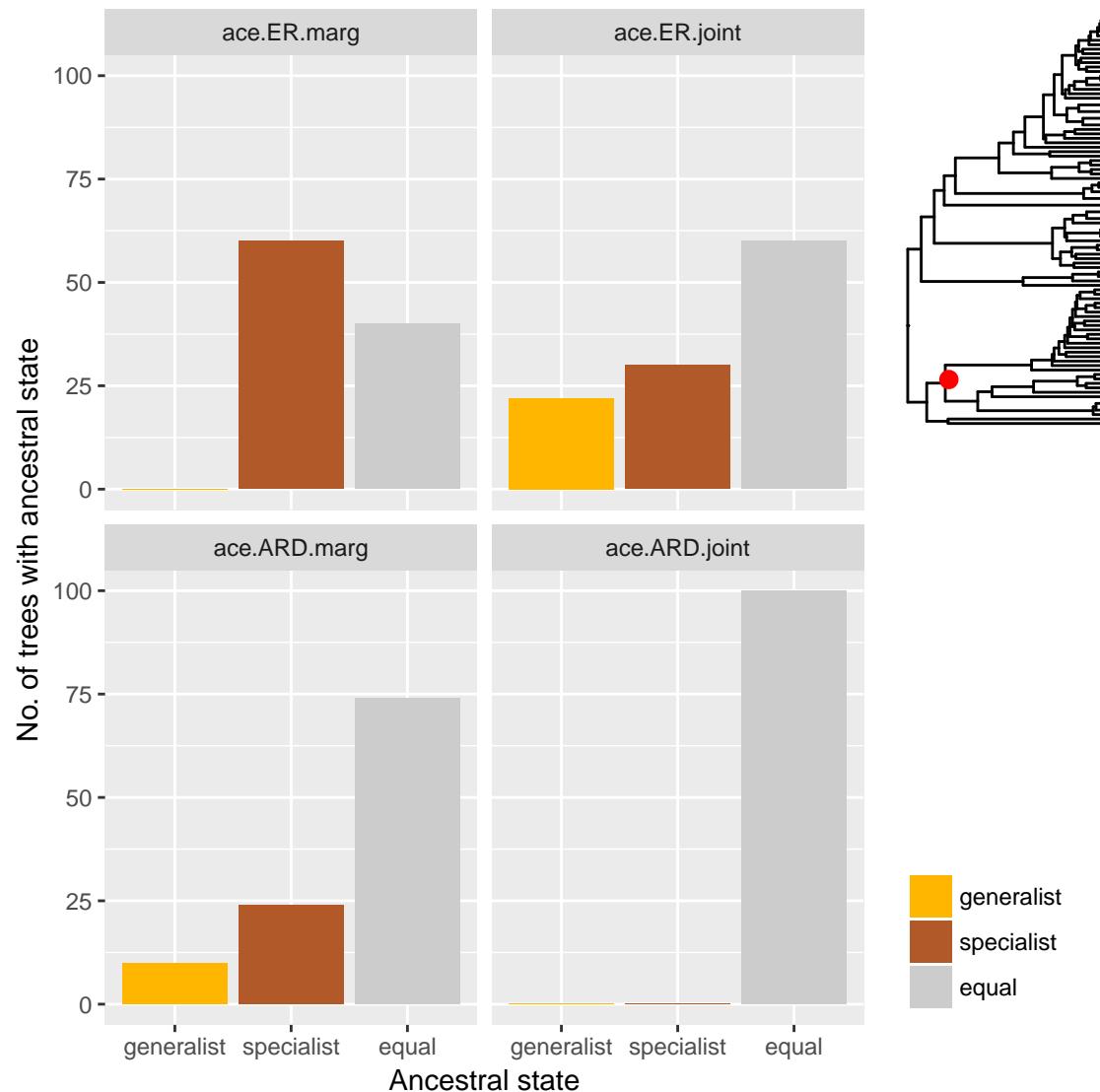


Figure S77: Ancestral states for node 17

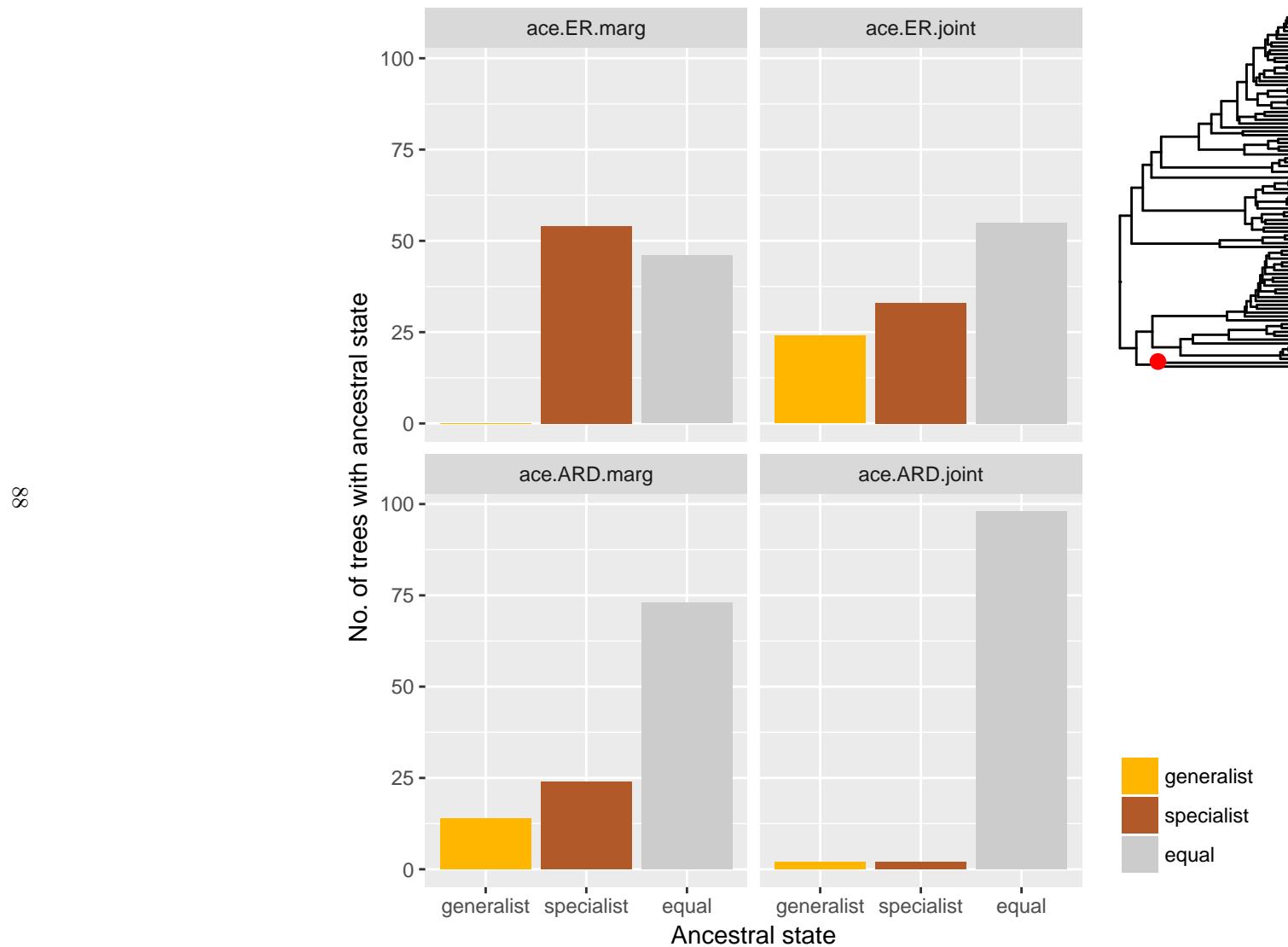


Figure S78: Ancestral states for node 18

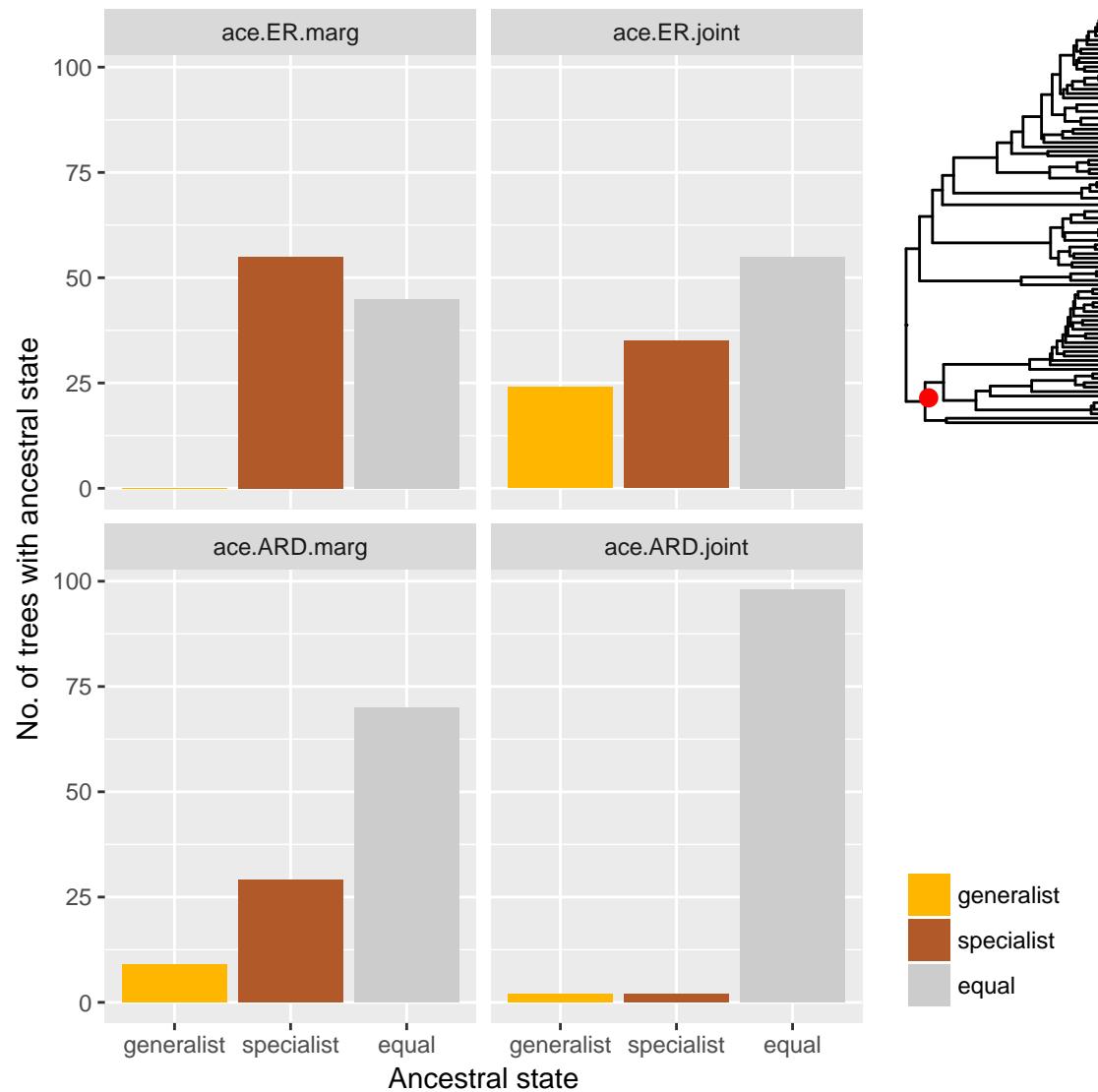


Figure S79: Ancestral states for node 19

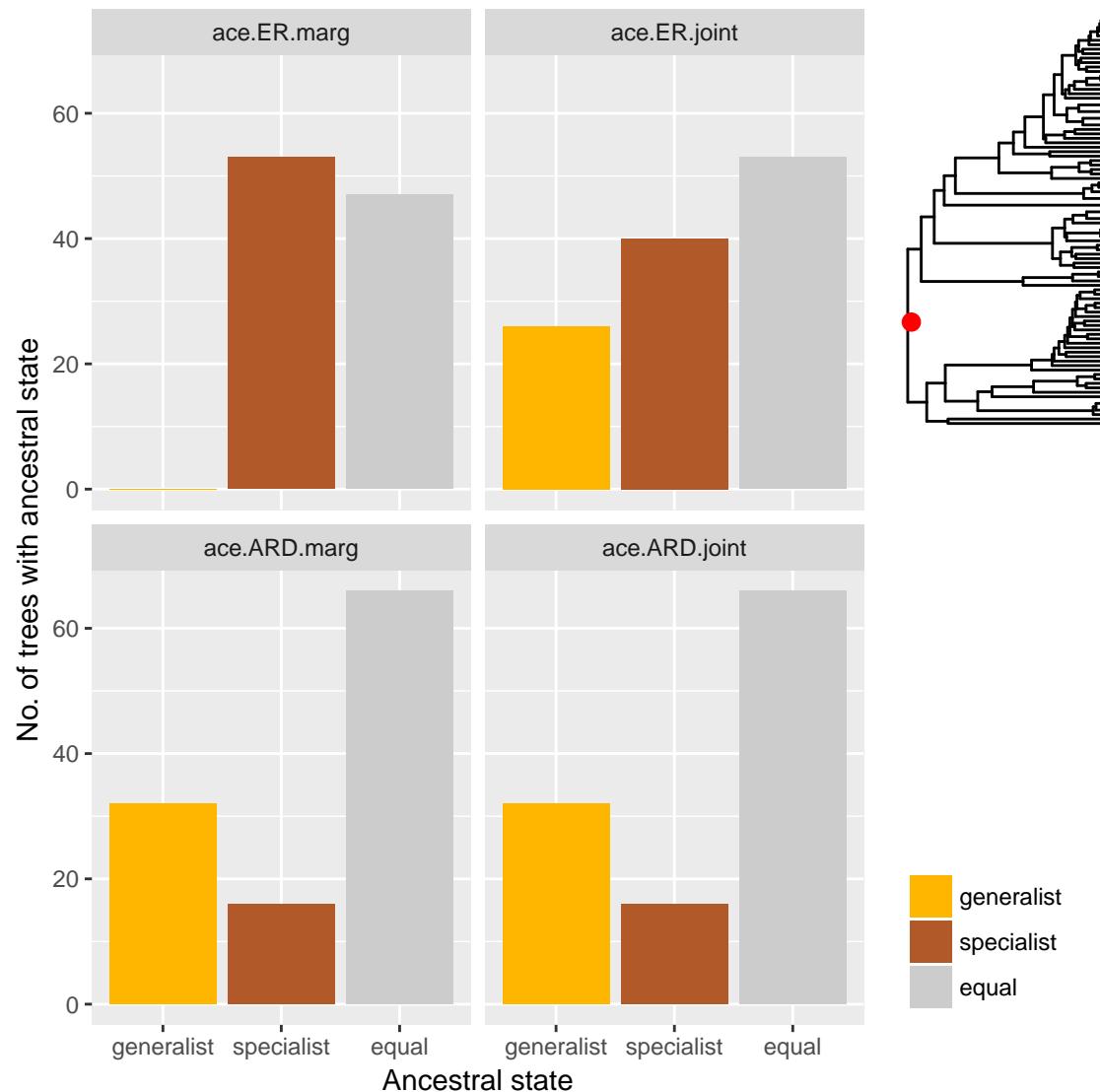
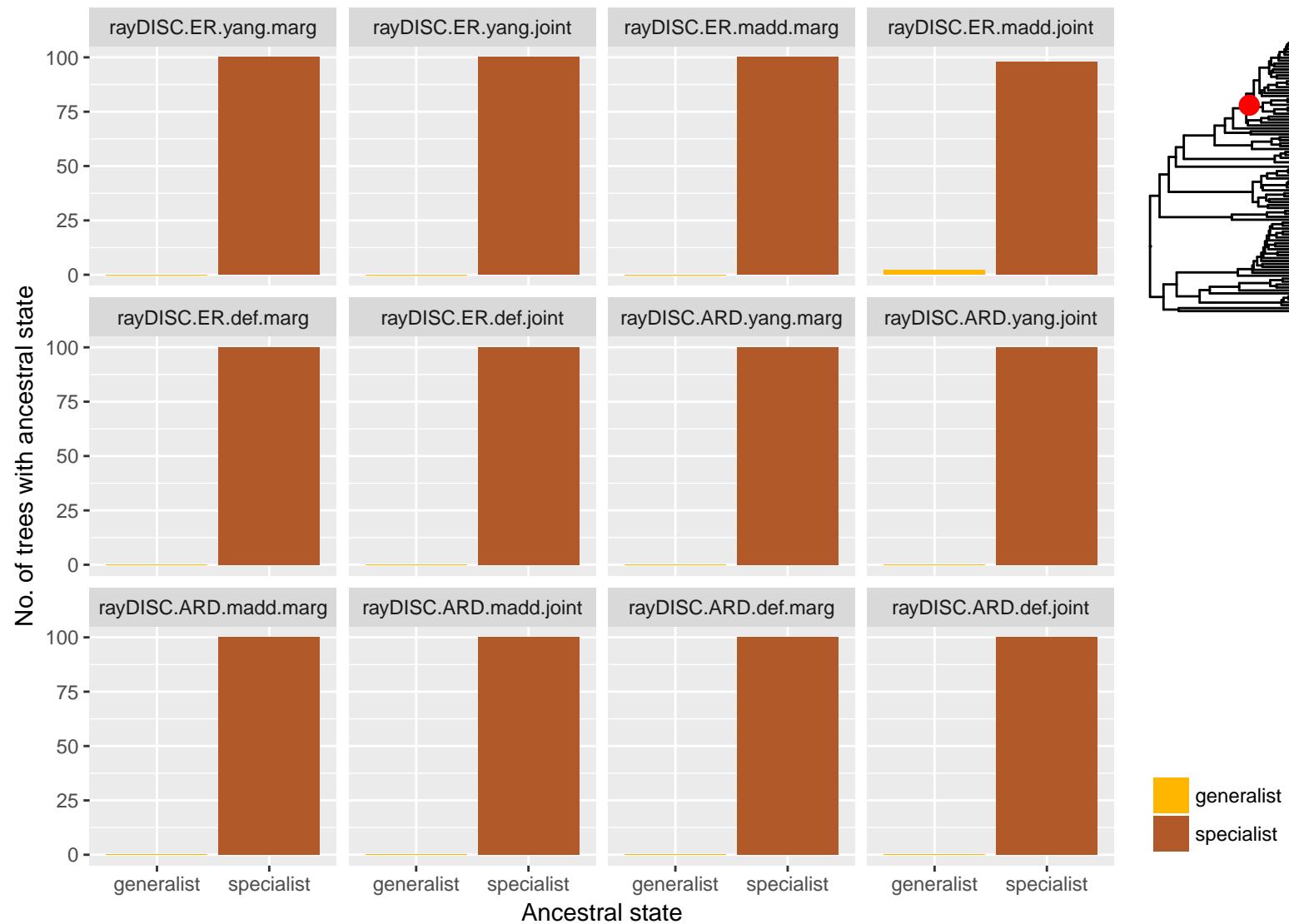


Figure S80-S98 - Results of ancestral state estimation of ecological strategy character with rayDISC for 19 nodes of the trapeloid phylogeny

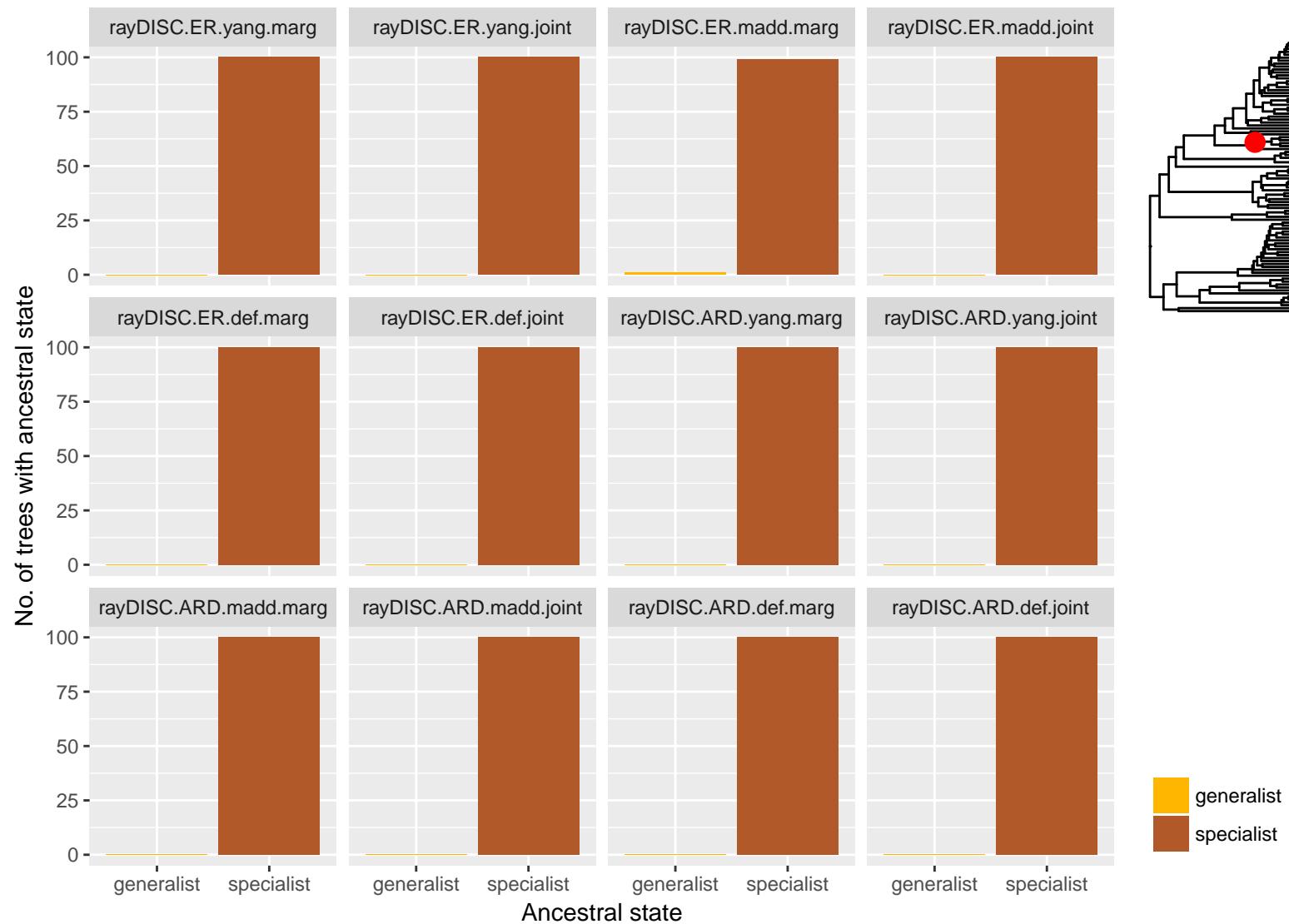
Ancestral state estimations of the preferred substrate character for 19 nodes of the trapeloid phylogeny based on the method implemented in rayDISC in the R package corHMM imposing 12 different models. Please refer to the main text for details.

FigureS 80: Ancestral states for node 1

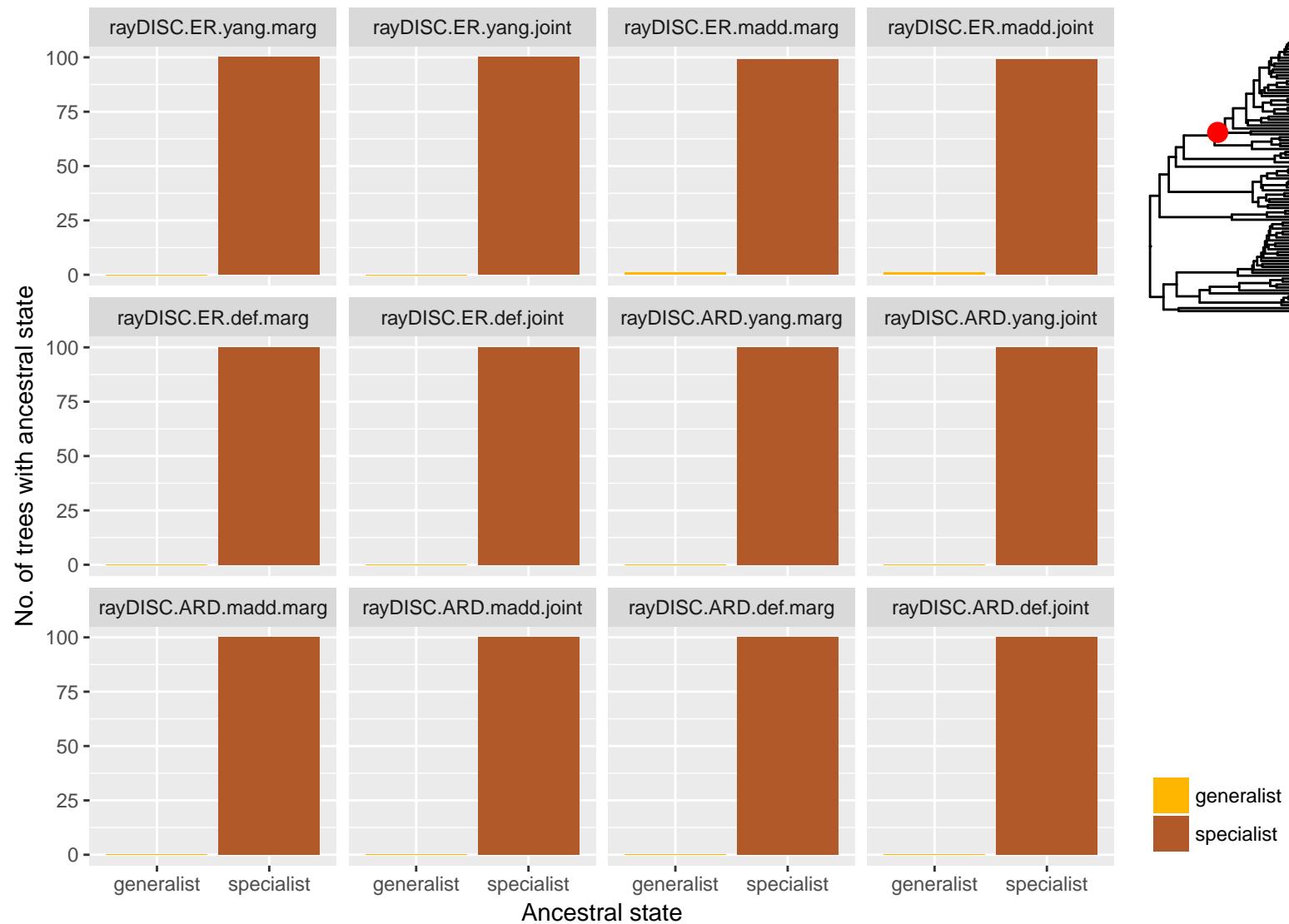


FigureS 81: Ancestral states for node 2

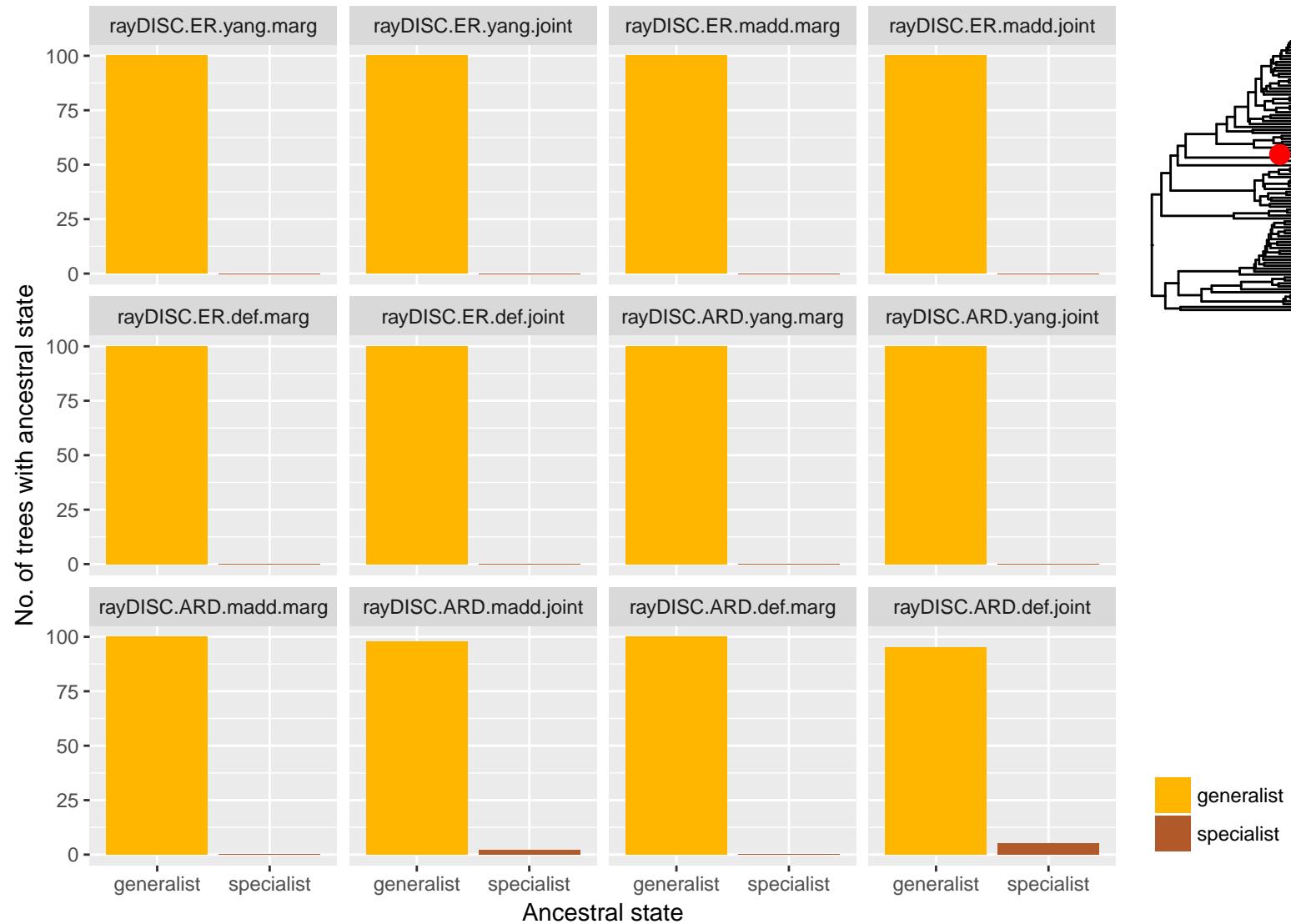
ε6



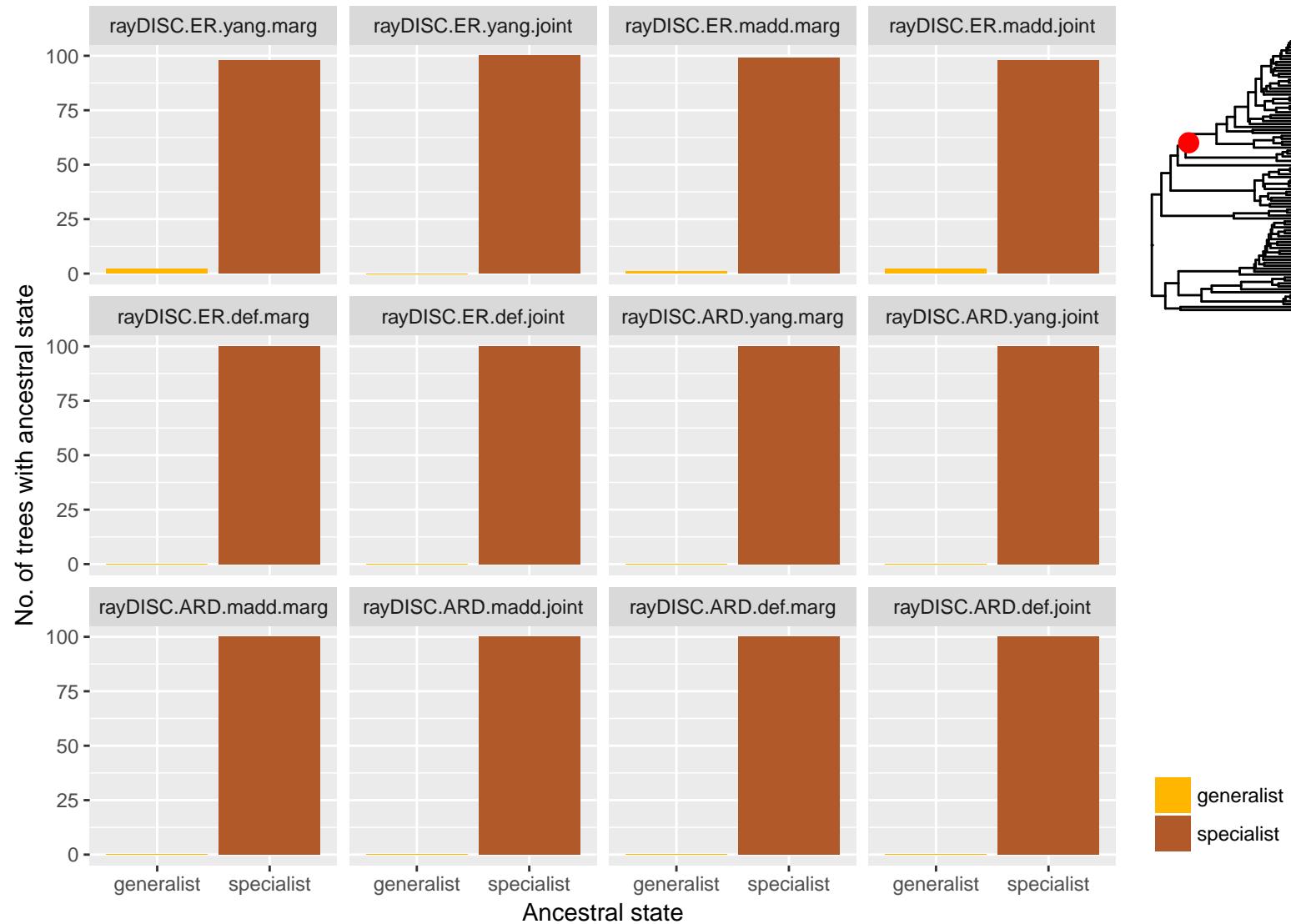
FigureS 82: Ancestral states for node 3



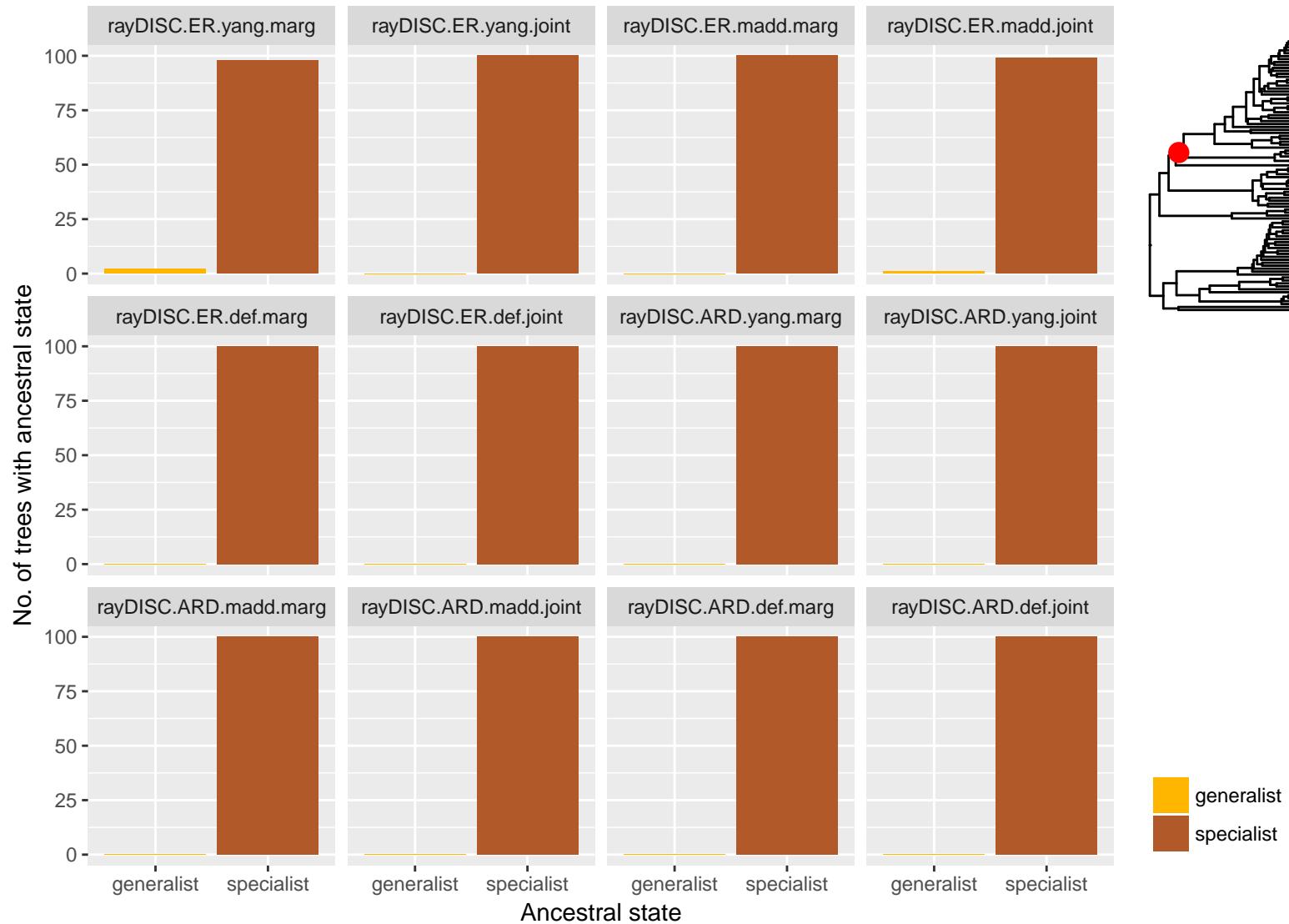
FigureS 83: Ancestral states for node 4



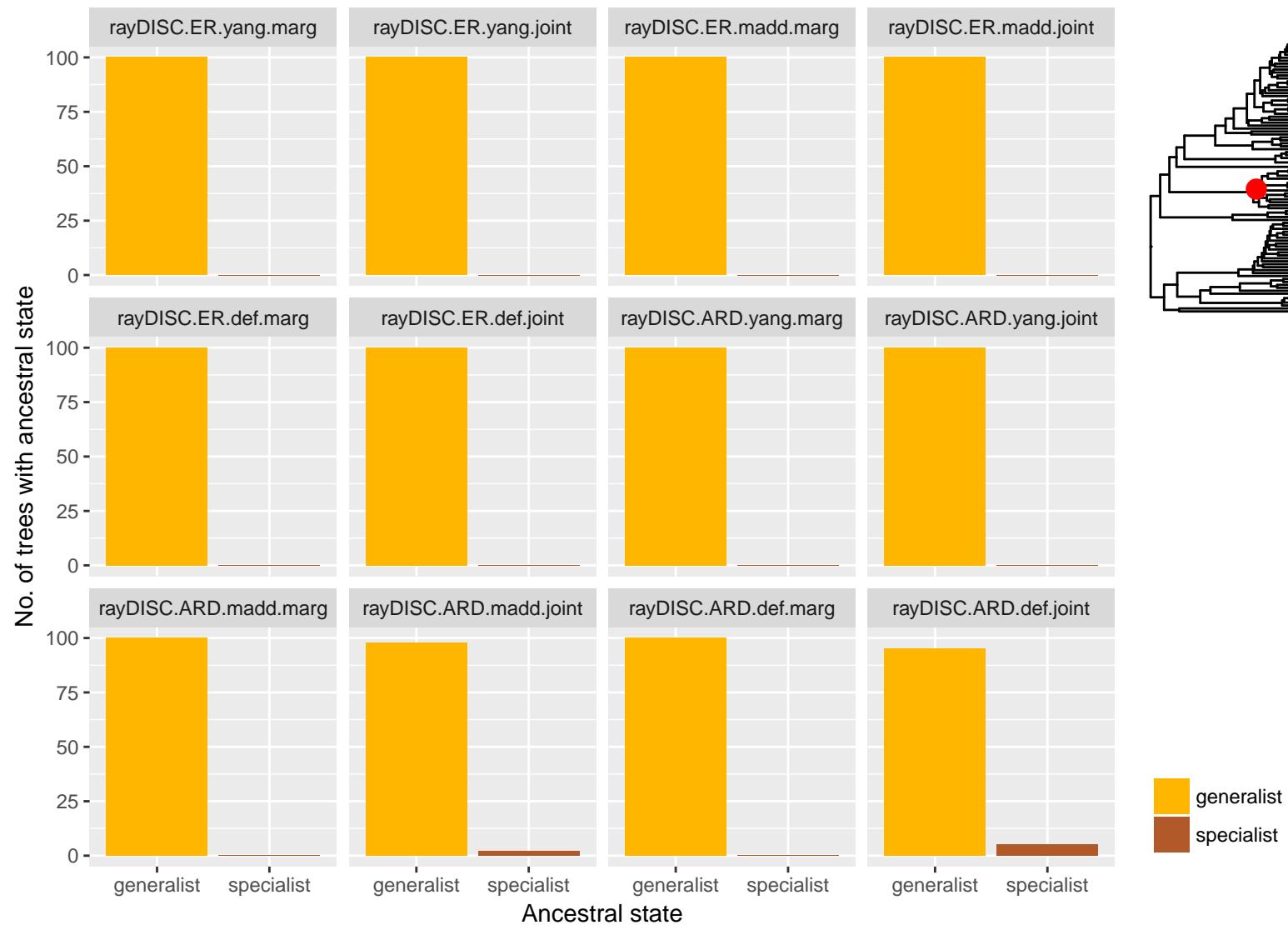
FigureS 84: Ancestral states for node 5



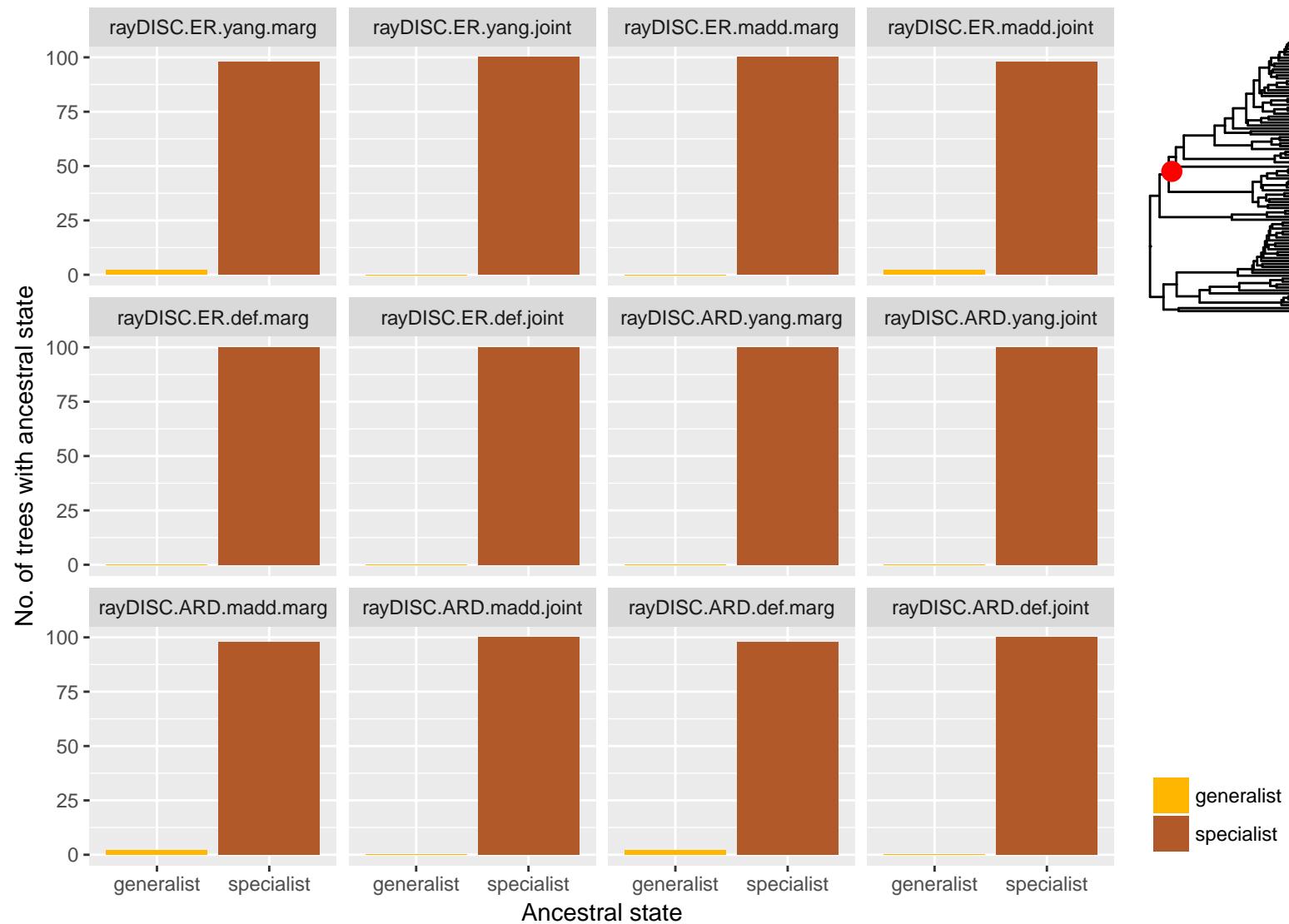
FigureS 85: Ancestral states for node 6



FigureS 86: Ancestral states for node 7

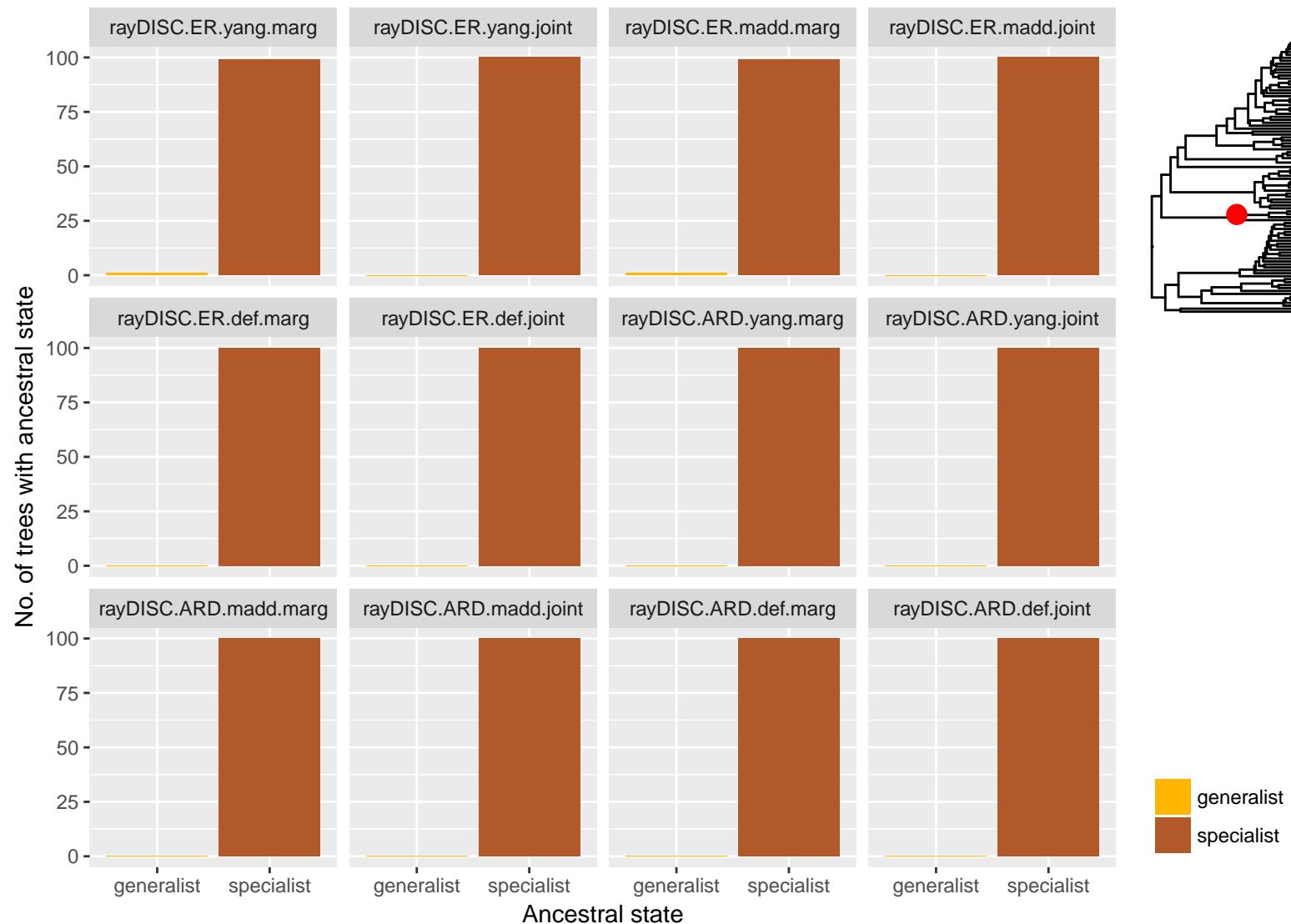


FigureS 87: Ancestral states for node 8

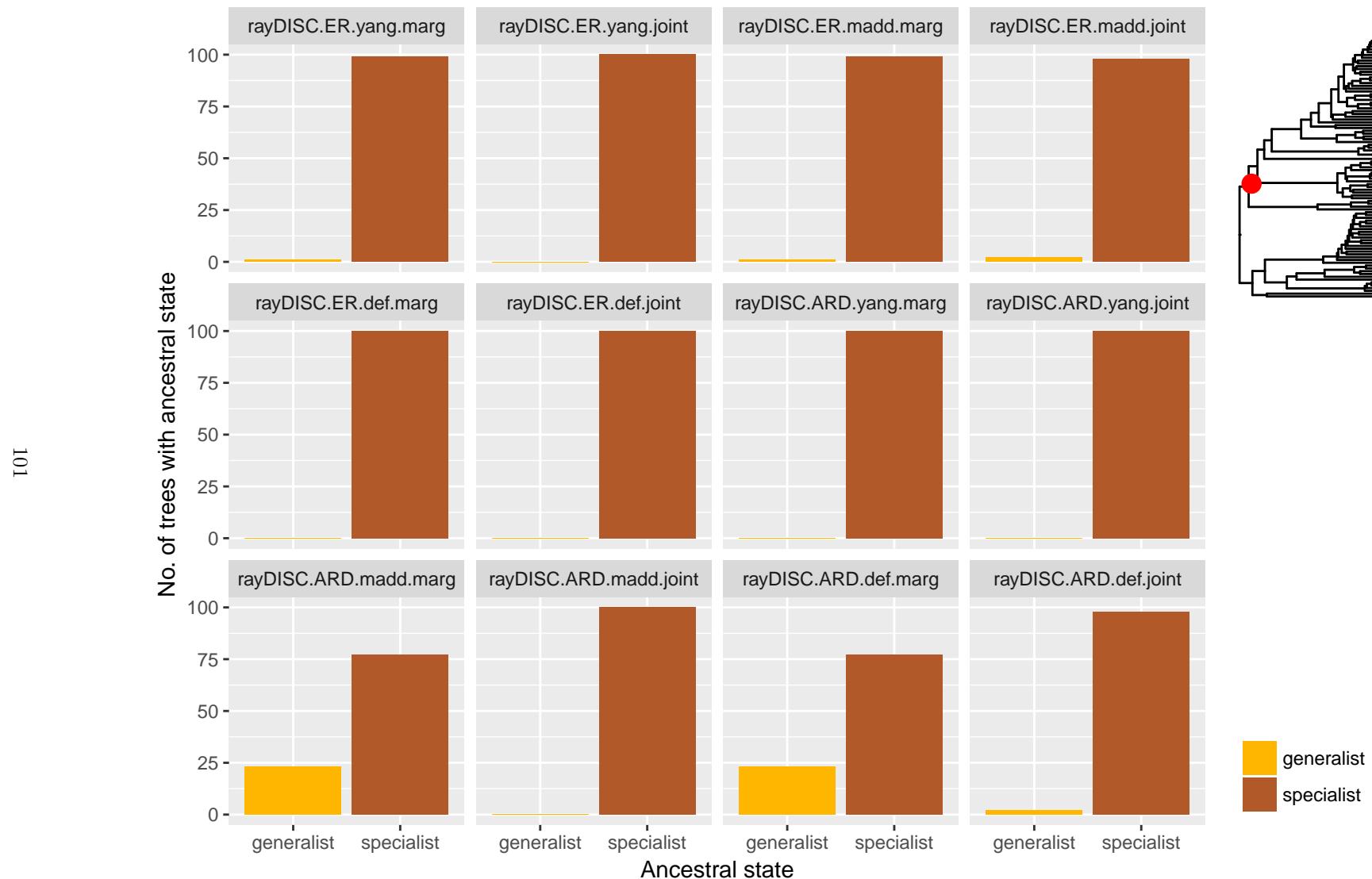


FigureS 88: Ancestral states for node 9

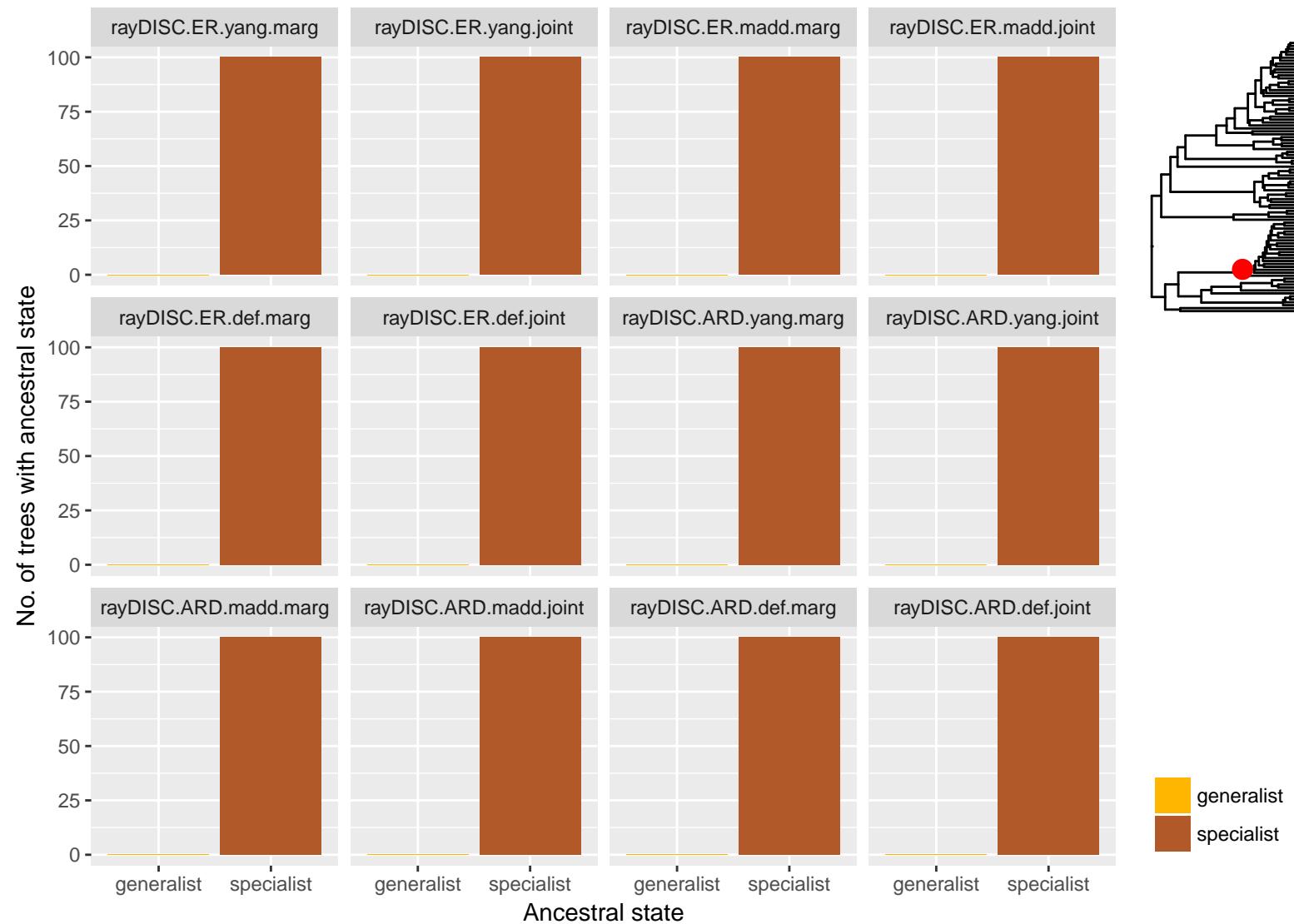
101



FigureS 89: Ancestral states for node 10

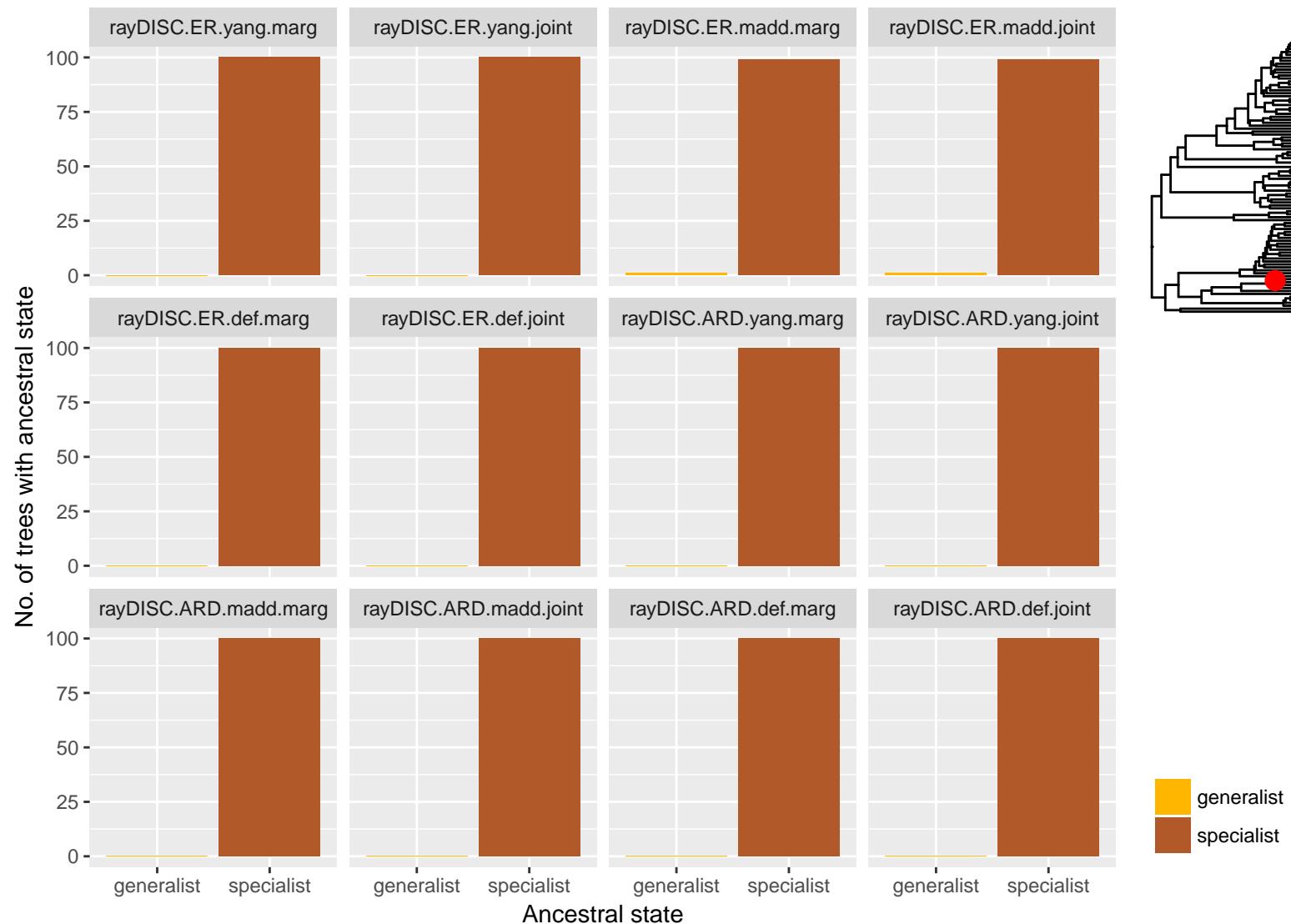


FigureS 90: Ancestral states for node 11

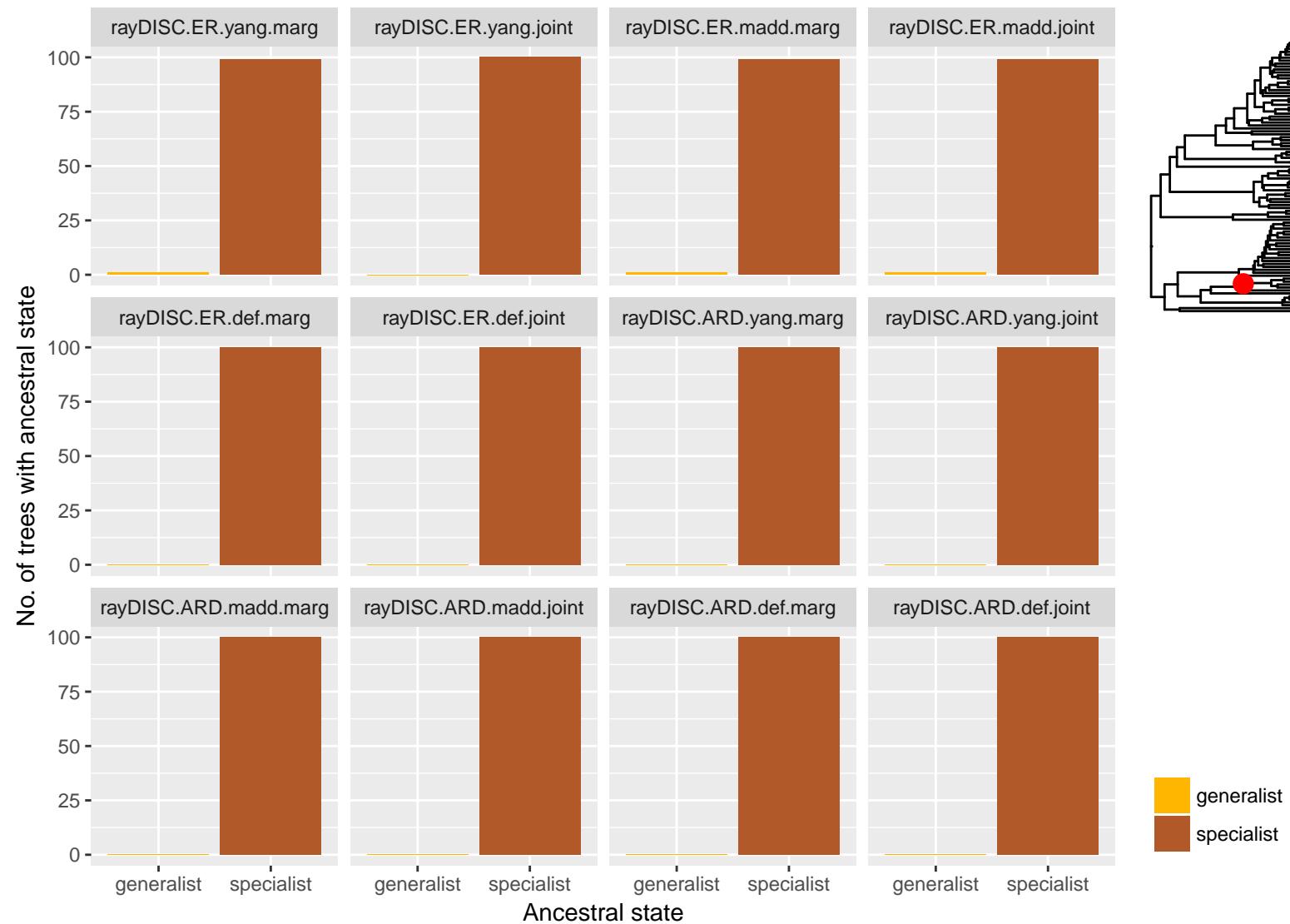


FigureS 91: Ancestral states for node 12

10³

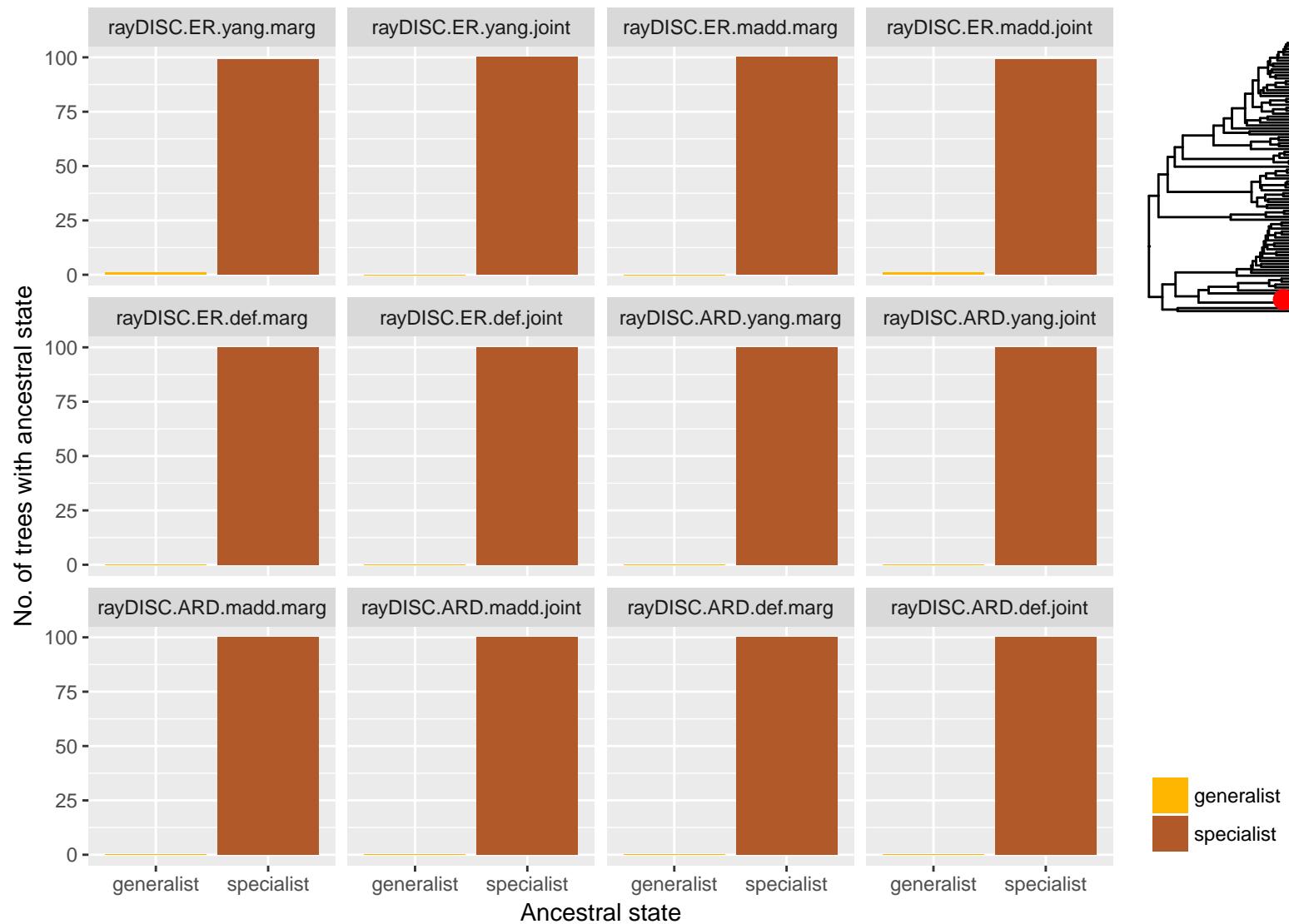


FigureS 92: Ancestral states for node 13

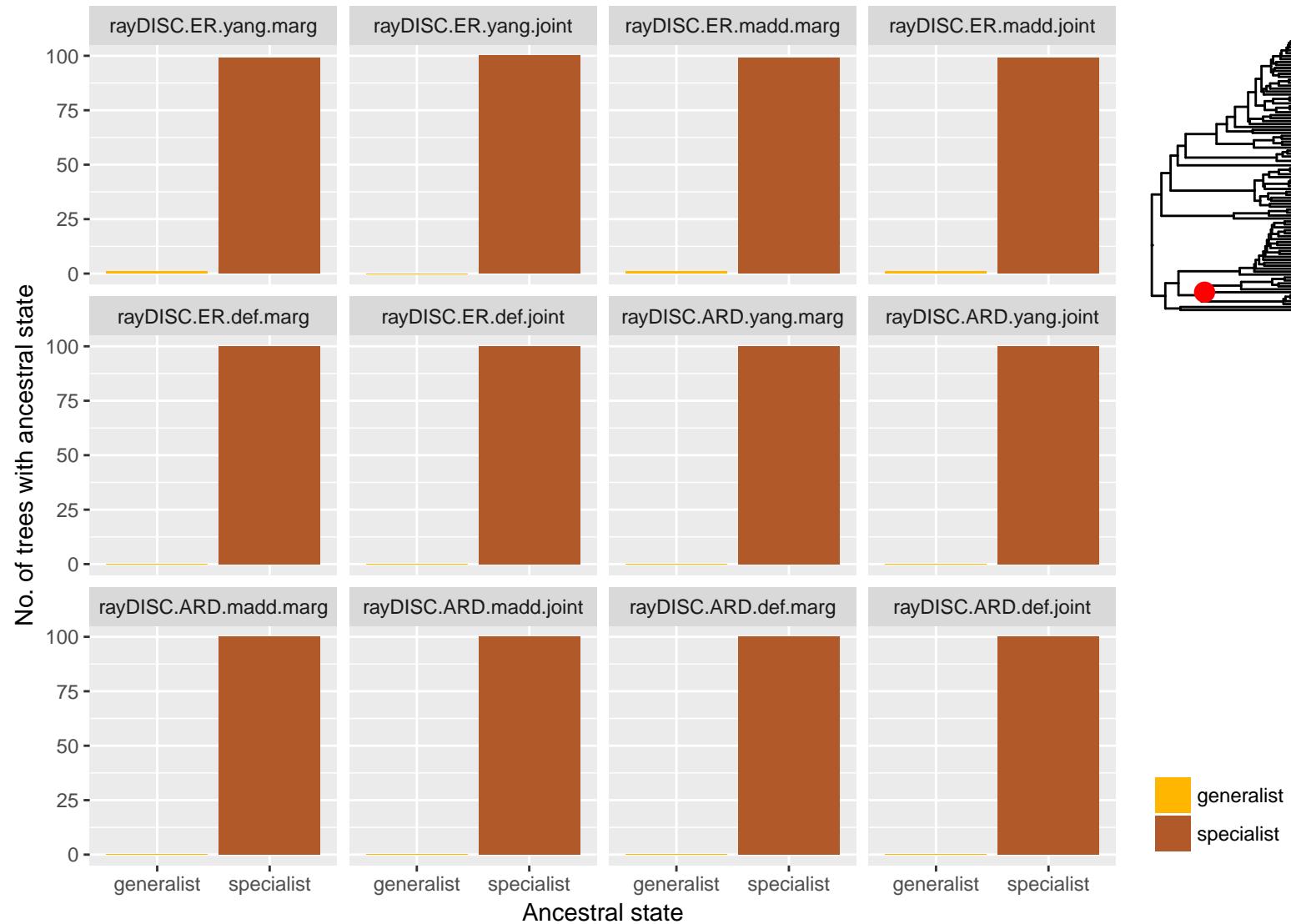


FigureS 93: Ancestral states for node 14

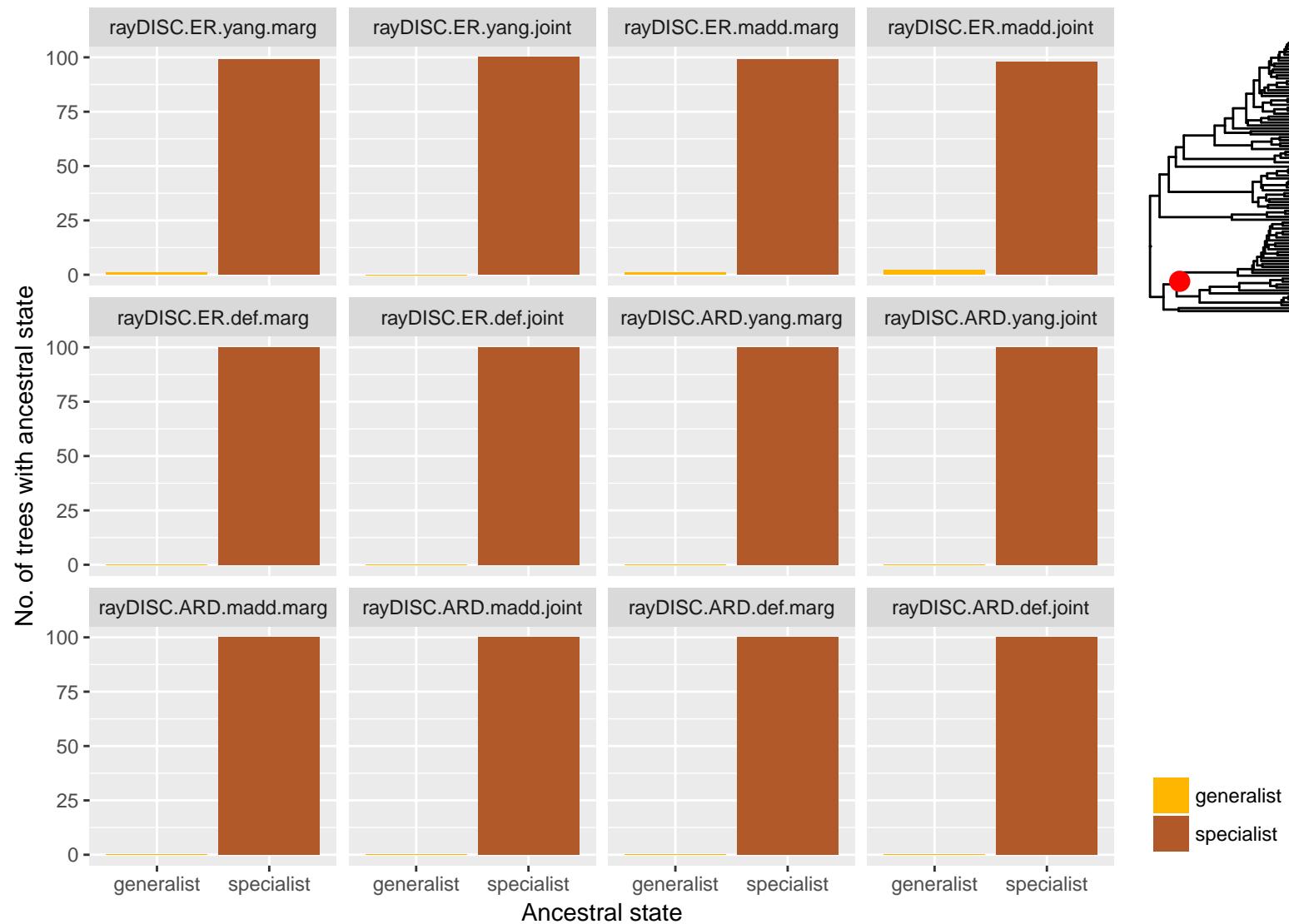
10⁵



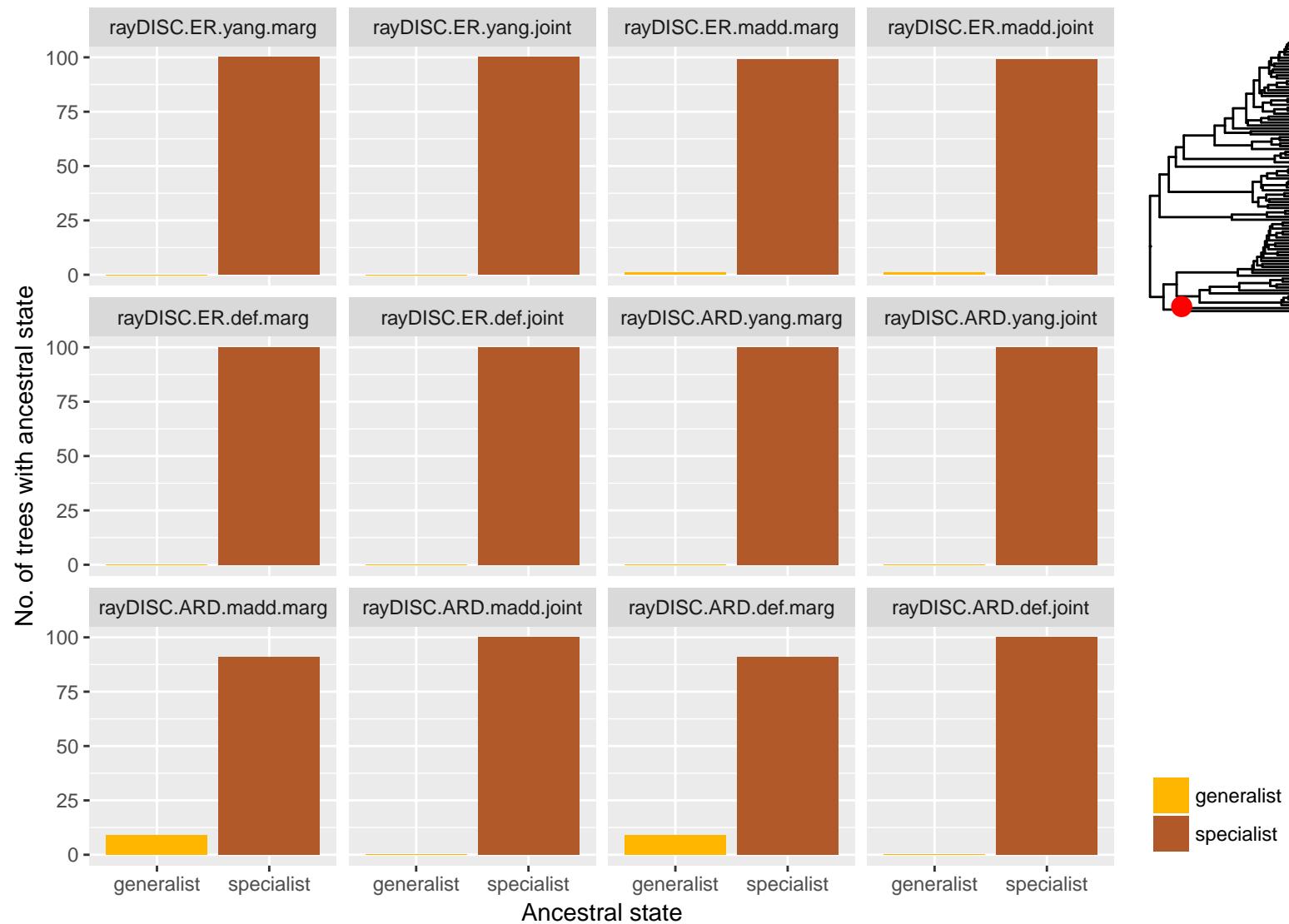
FigureS 94: Ancestral states for node 15



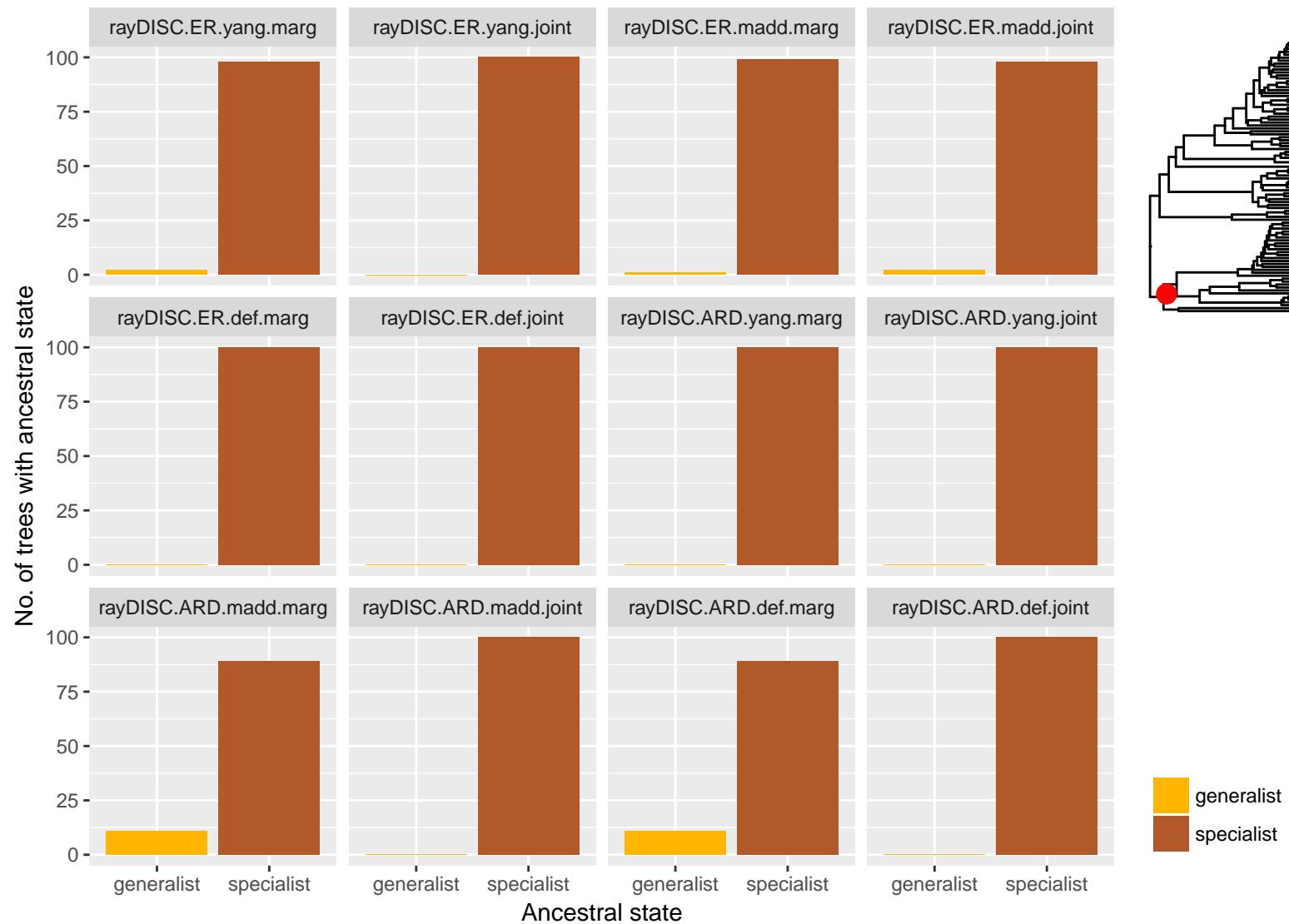
FigureS 95: Ancestral states for node 16



FigureS 96: Ancestral states for node 17



FigureS 97: Ancestral states for node 18



FigureS 98: Ancestral states for node 19

0 II

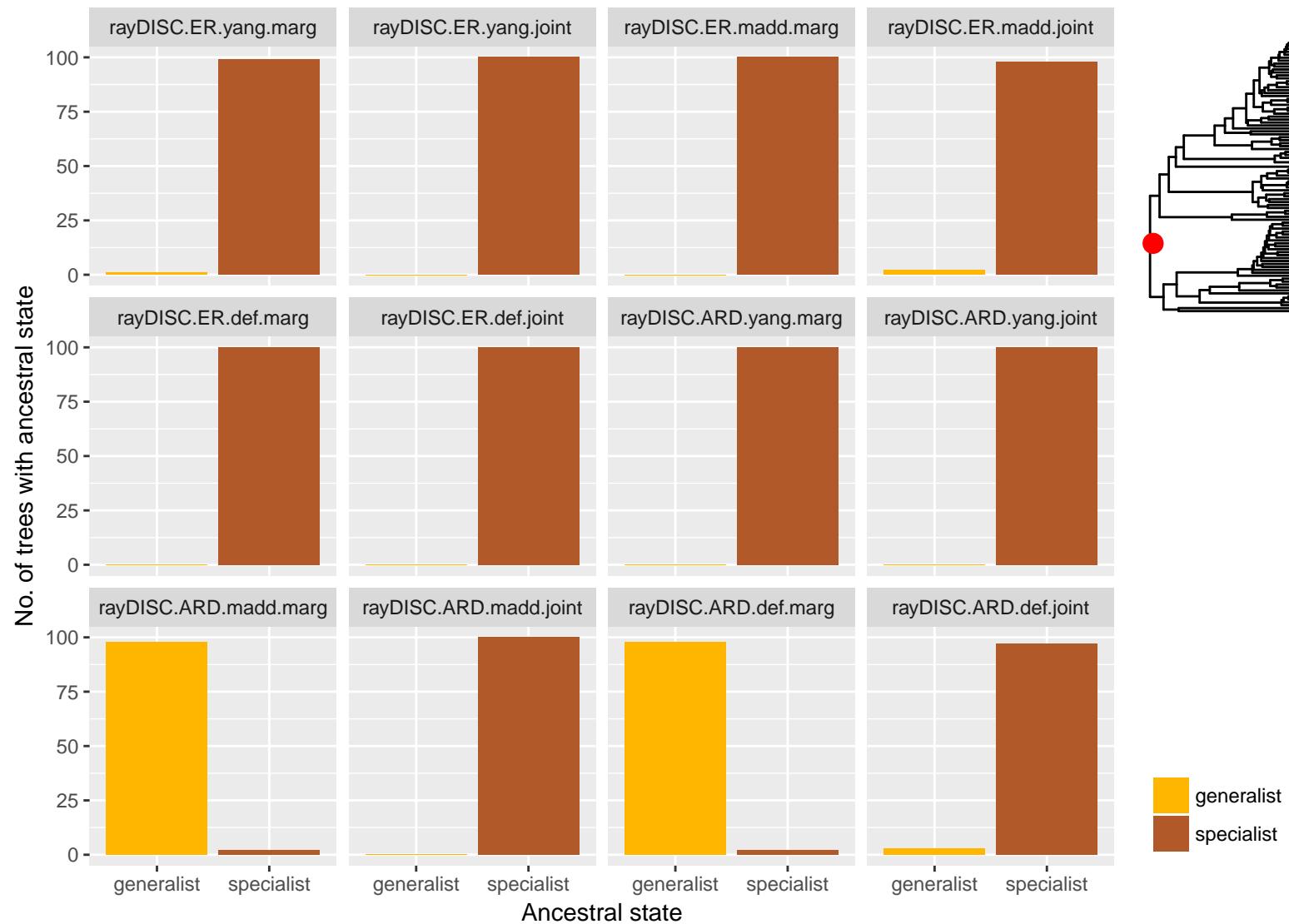
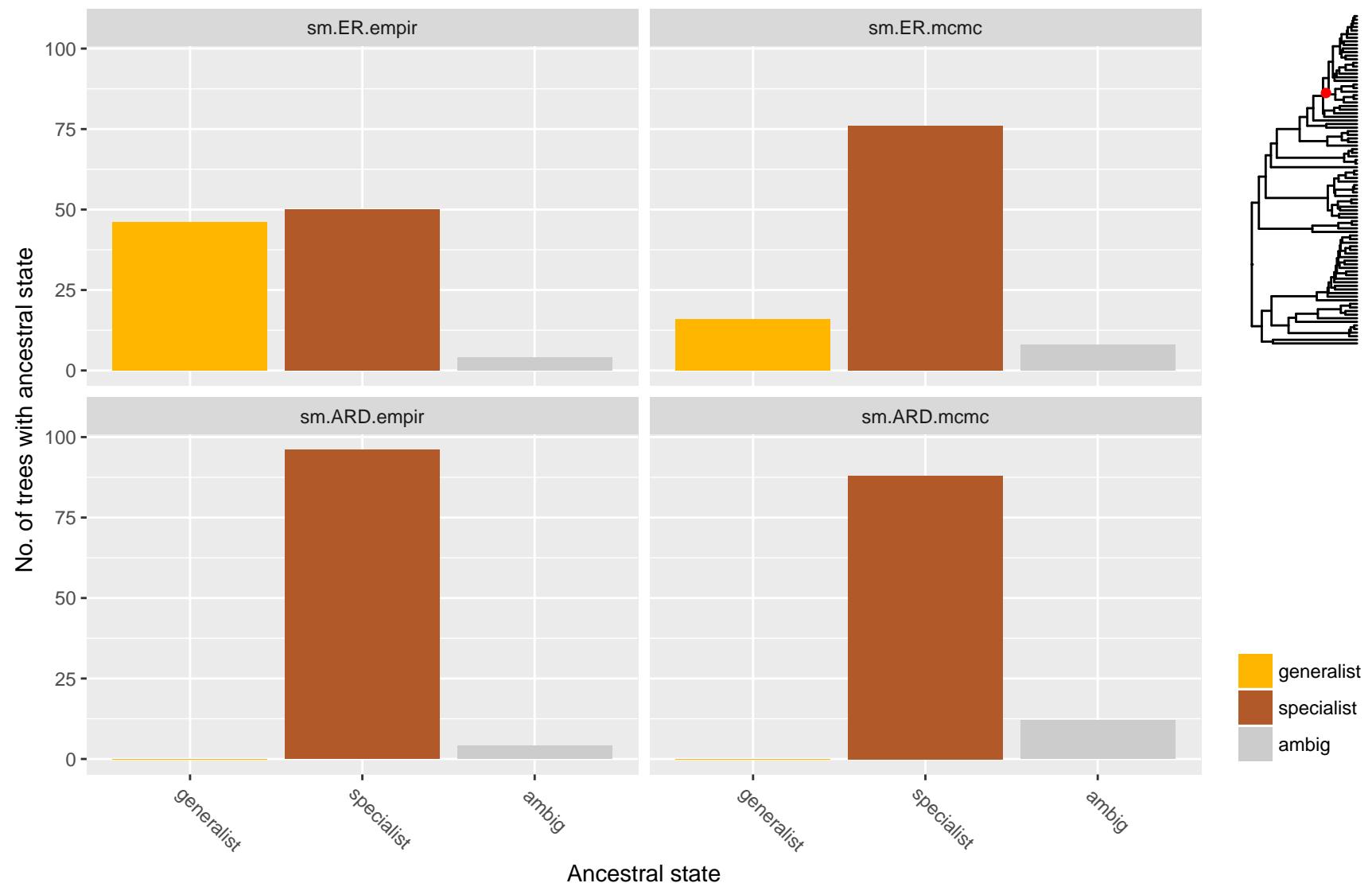


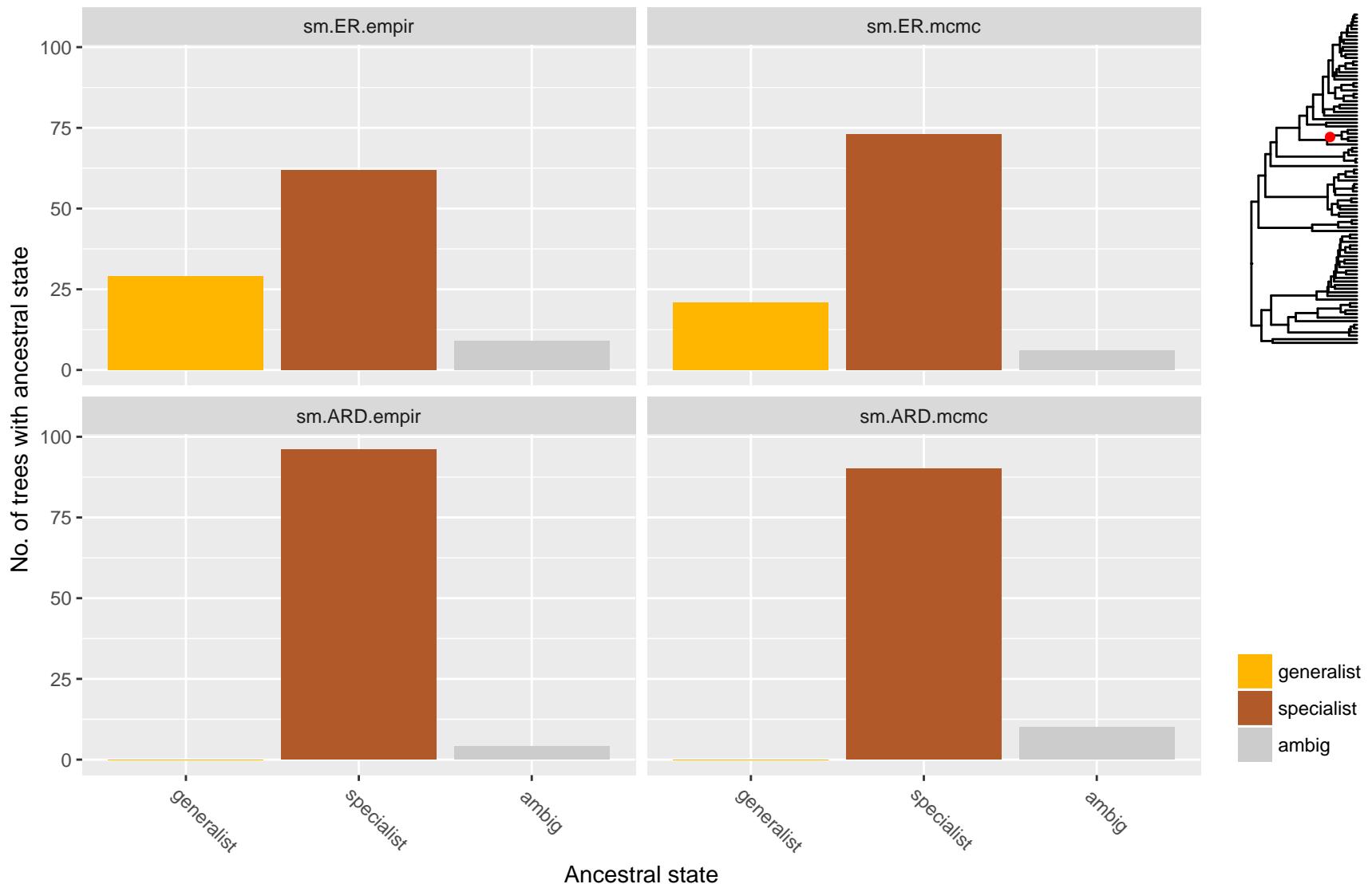
Figure S99-S117 - Results of ancestral state estimation of ecological strategy character with make-simmap for 19 nodes of the trapezioid phylogeny

Ancestral state estimations of the preferred substrate character for 19 nodes of the trapezioid phylogeny based on stochastic character mapping using the R package phytools imposing 4 different models. Please refer to the main text for details.

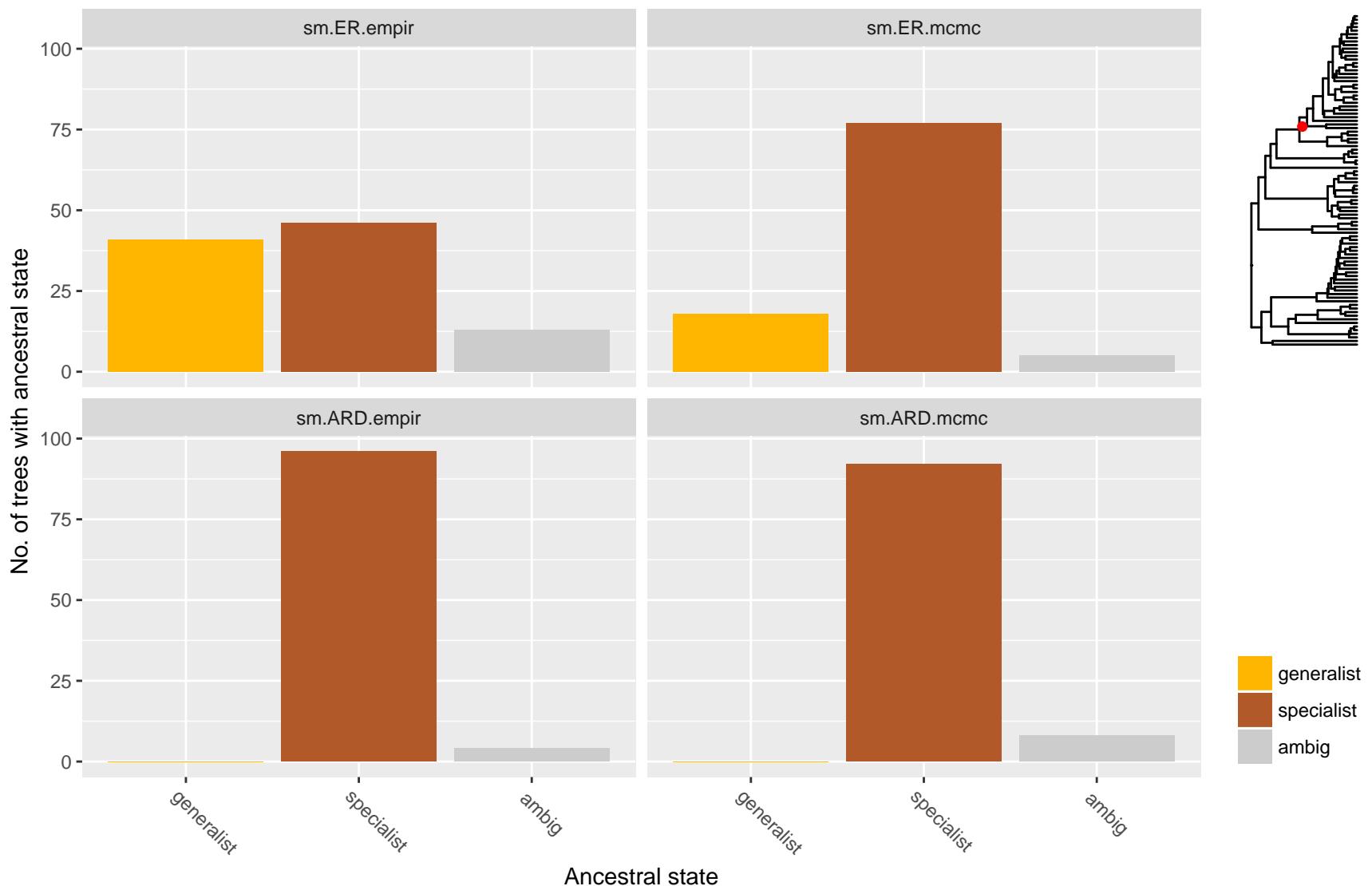
FigureS 99: Ancestral states for node 1



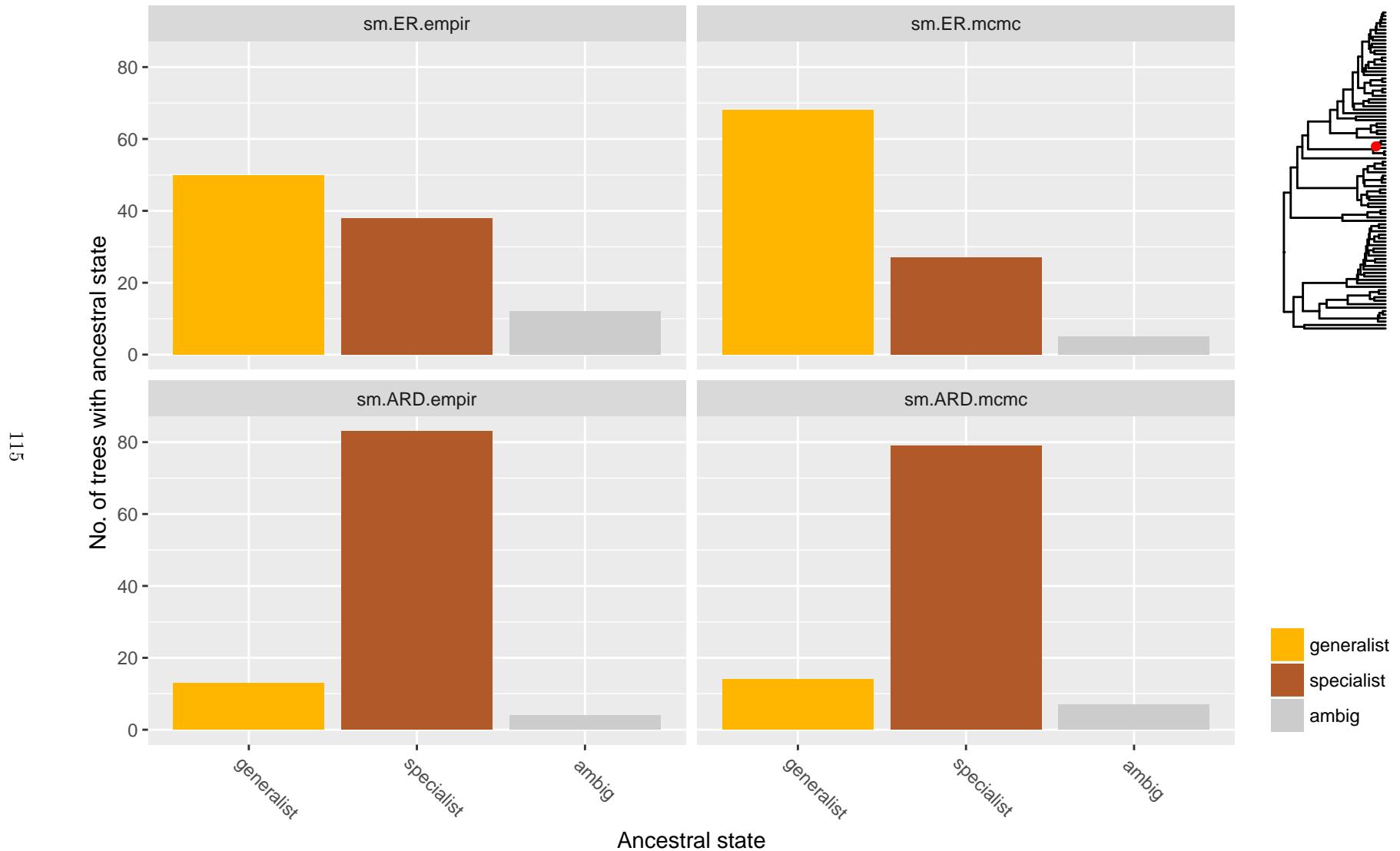
FigureS 100: Ancestral states for node 2



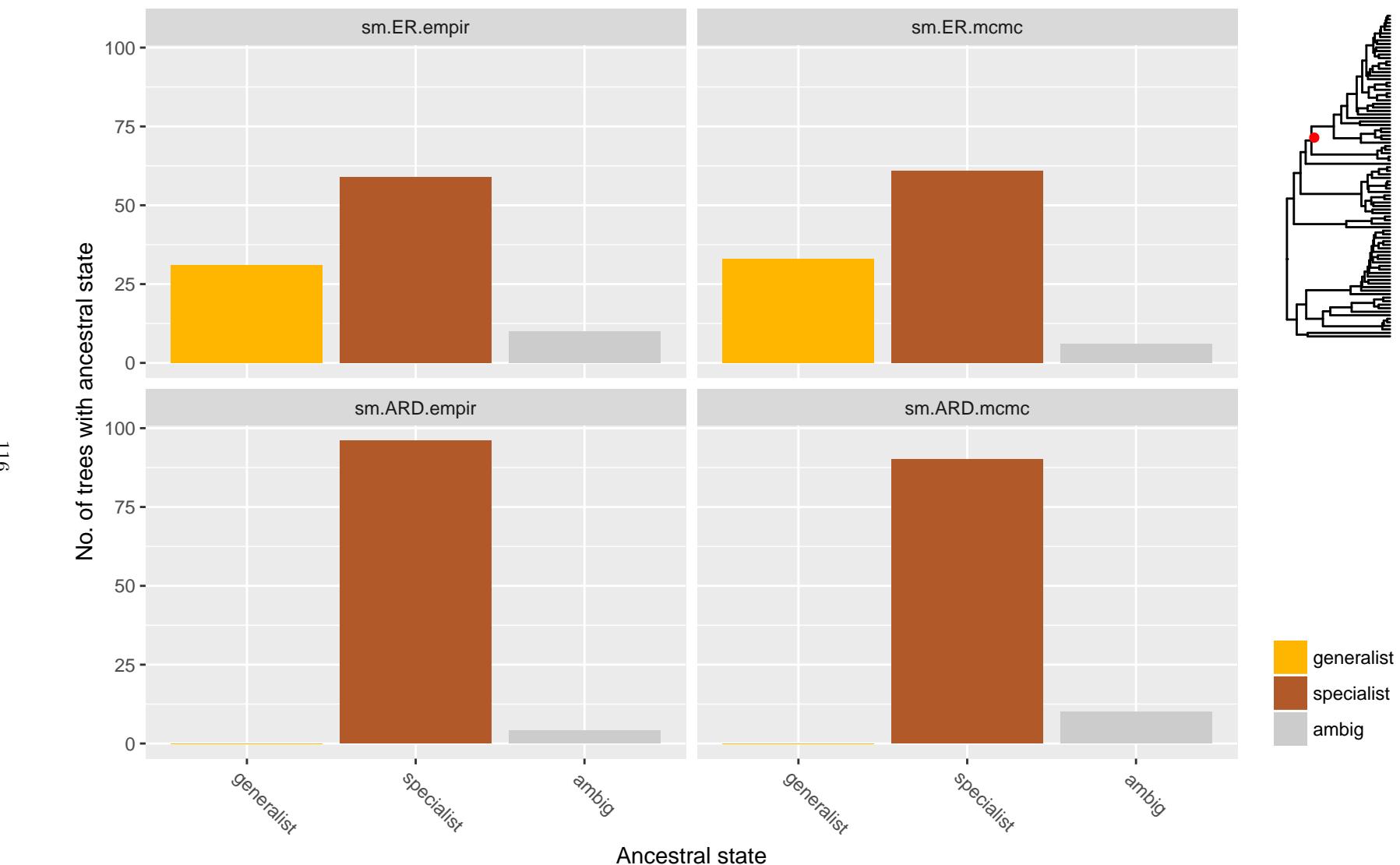
FigureS 101: Ancestral states for node 3



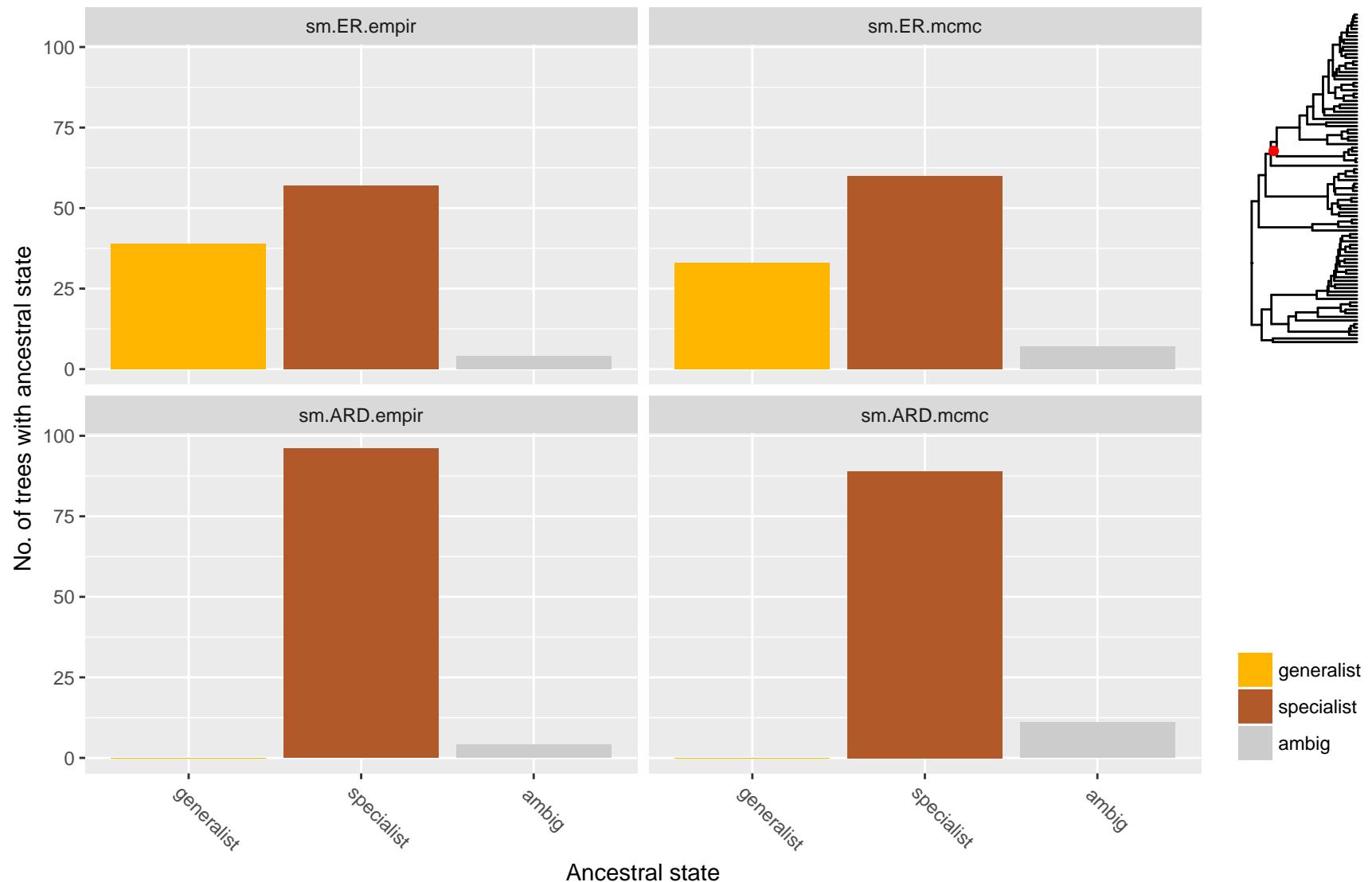
FigureS 102: Ancestral states for node 4



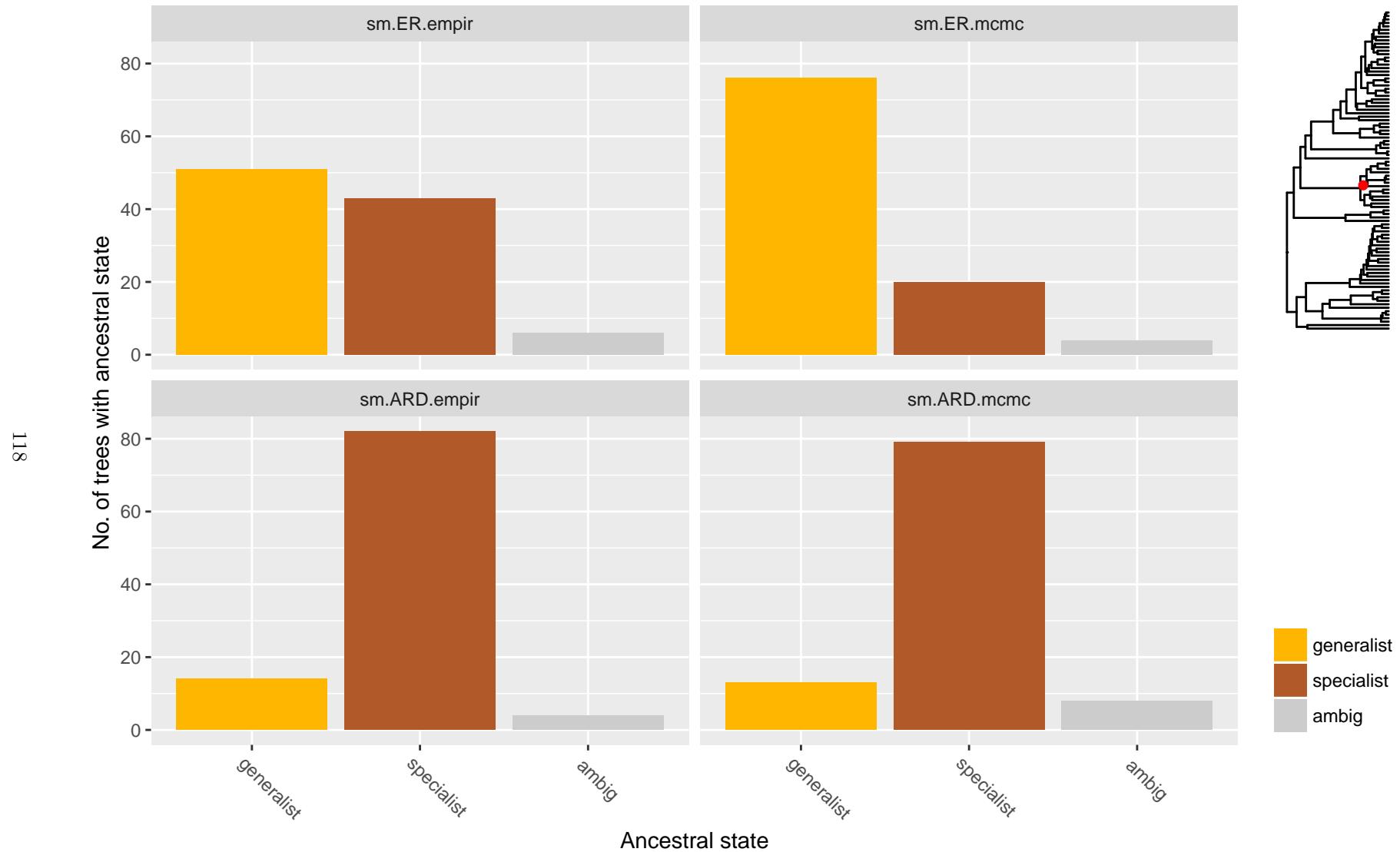
FigureS 103: Ancestral states for node 5



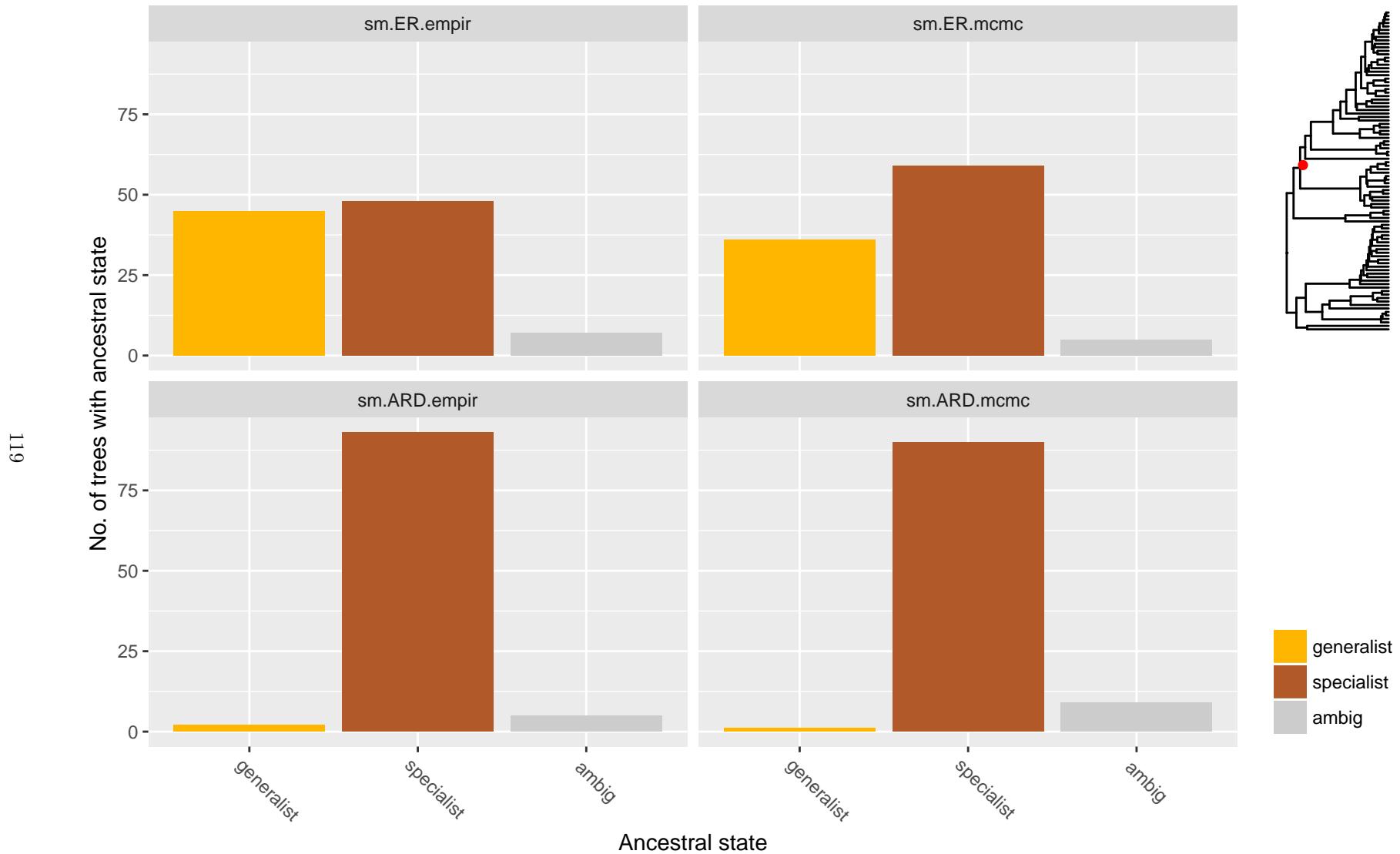
FigureS 104: Ancestral states for node 6



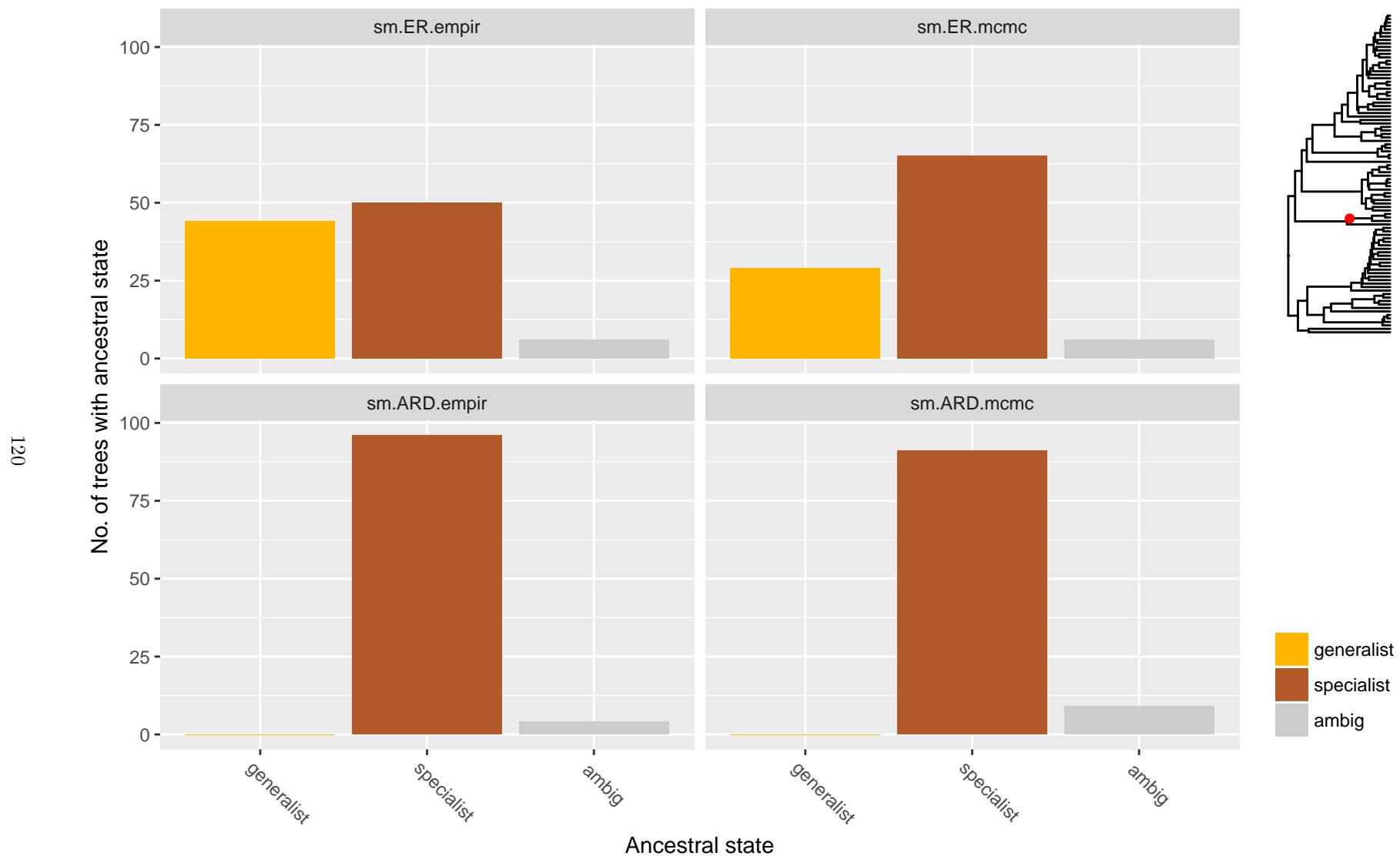
FigureS 105: Ancestral states for node 7



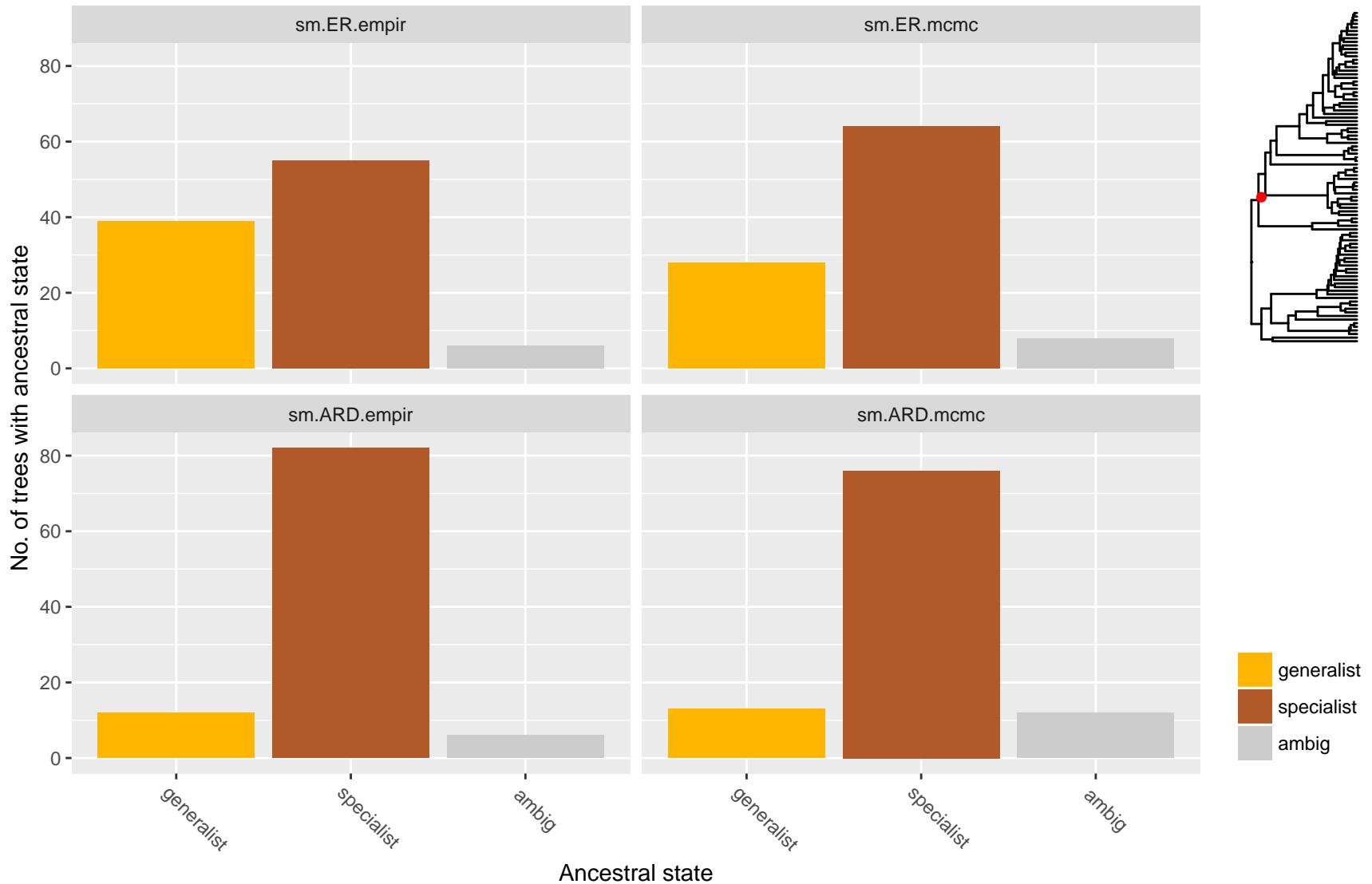
FigureS 106: Ancestral states for node 8



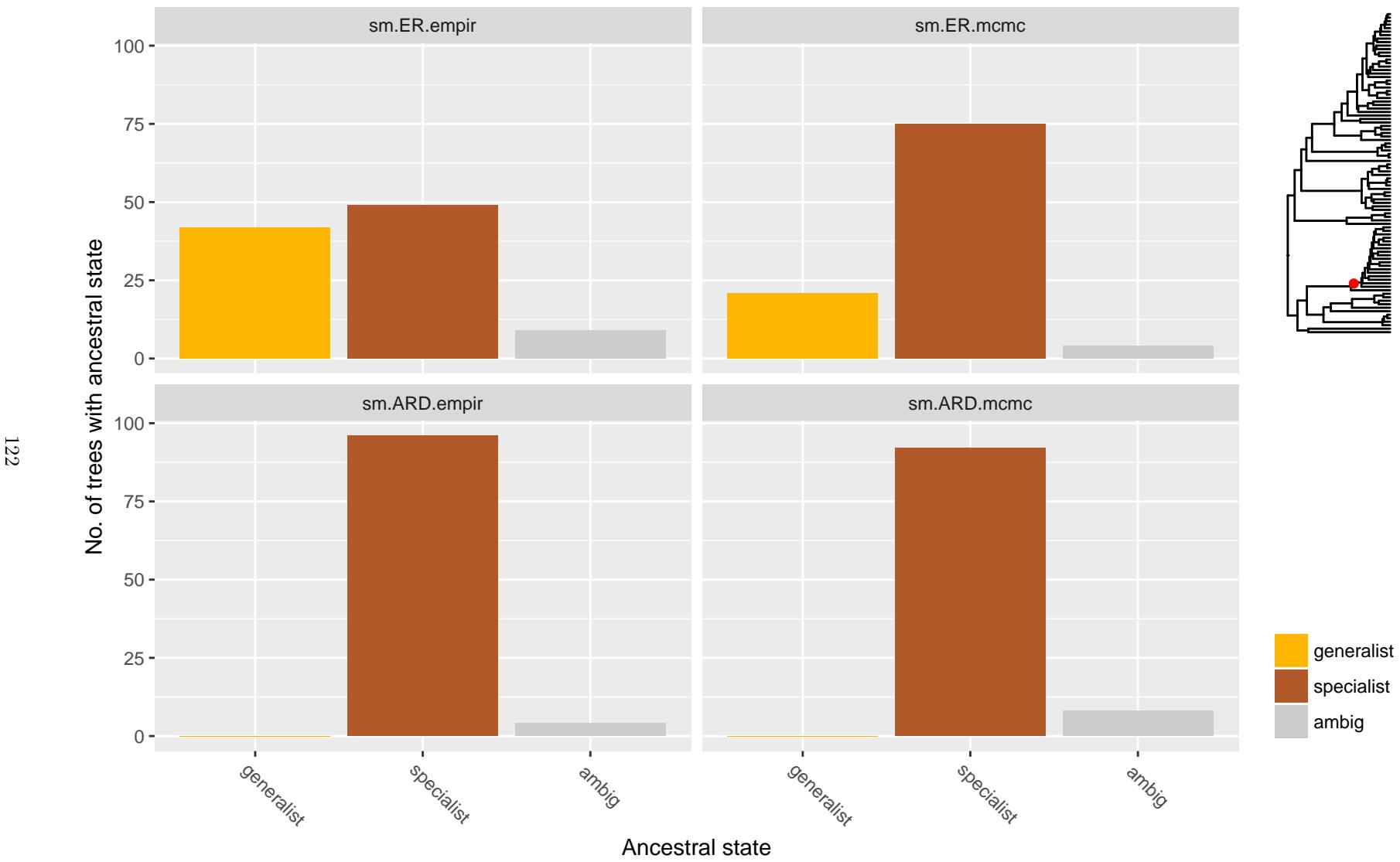
FigureS 107: Ancestral states for node 9



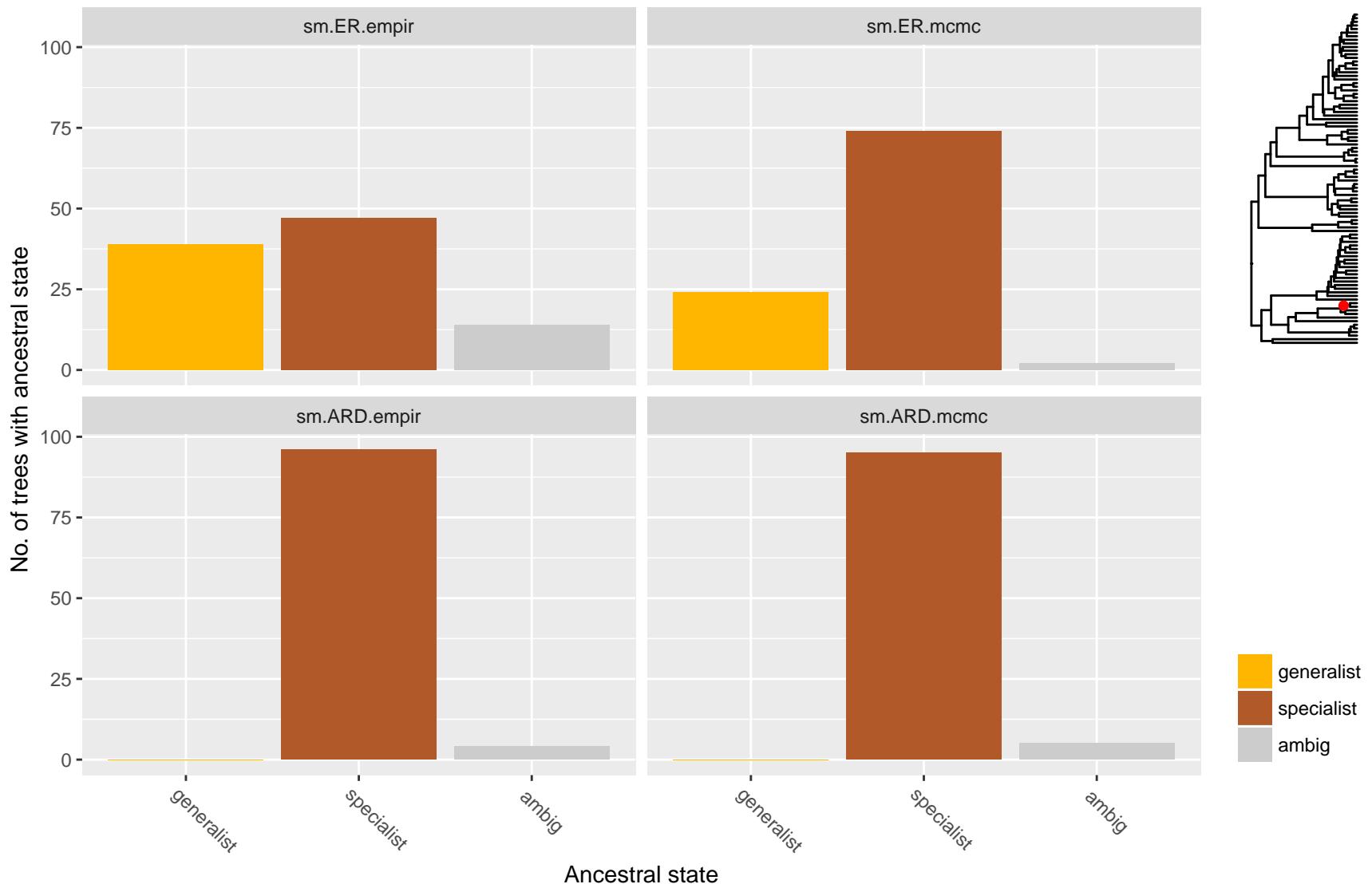
FigureS 108: Ancestral states for node 10



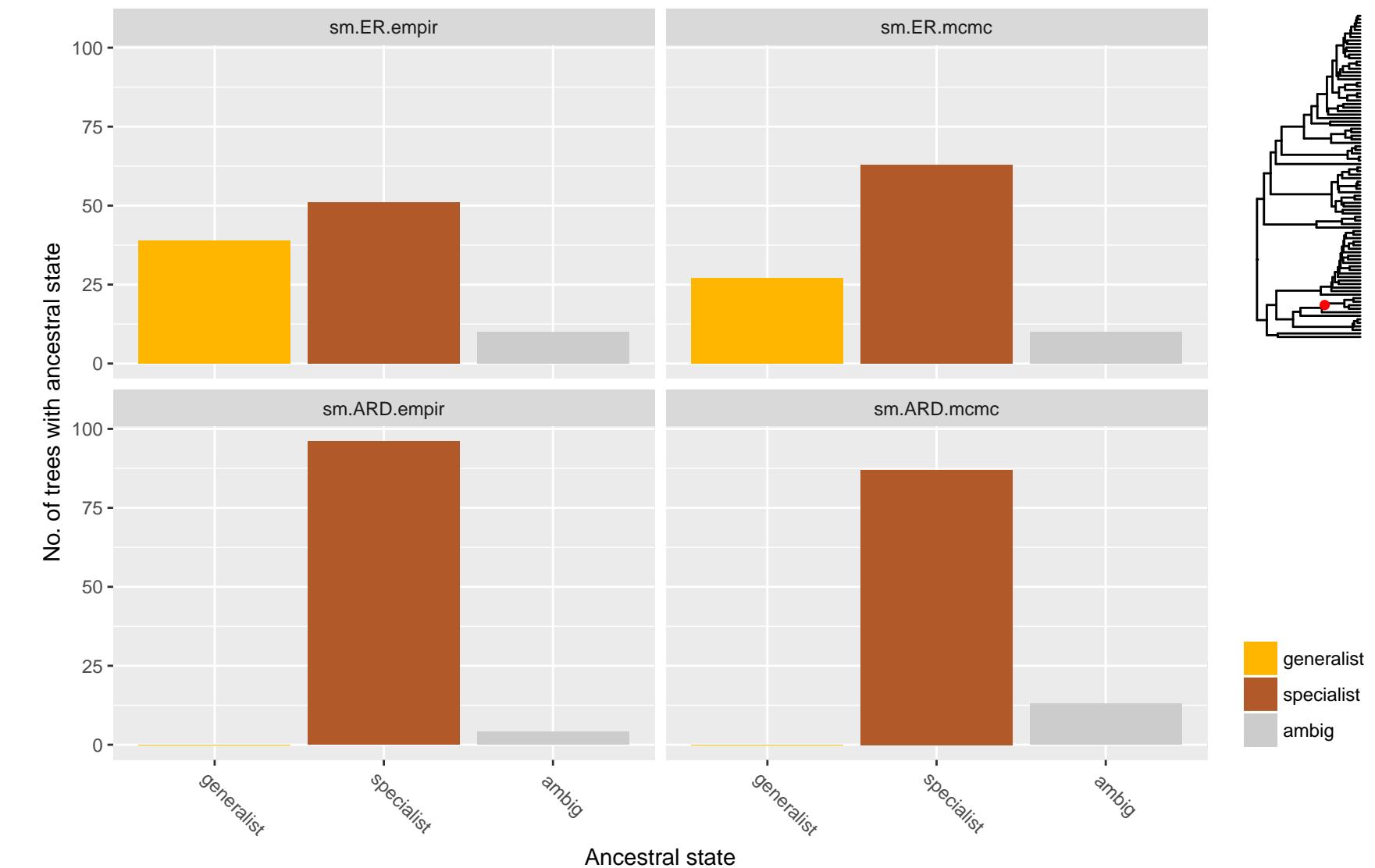
FigureS 109: Ancestral states for node 11



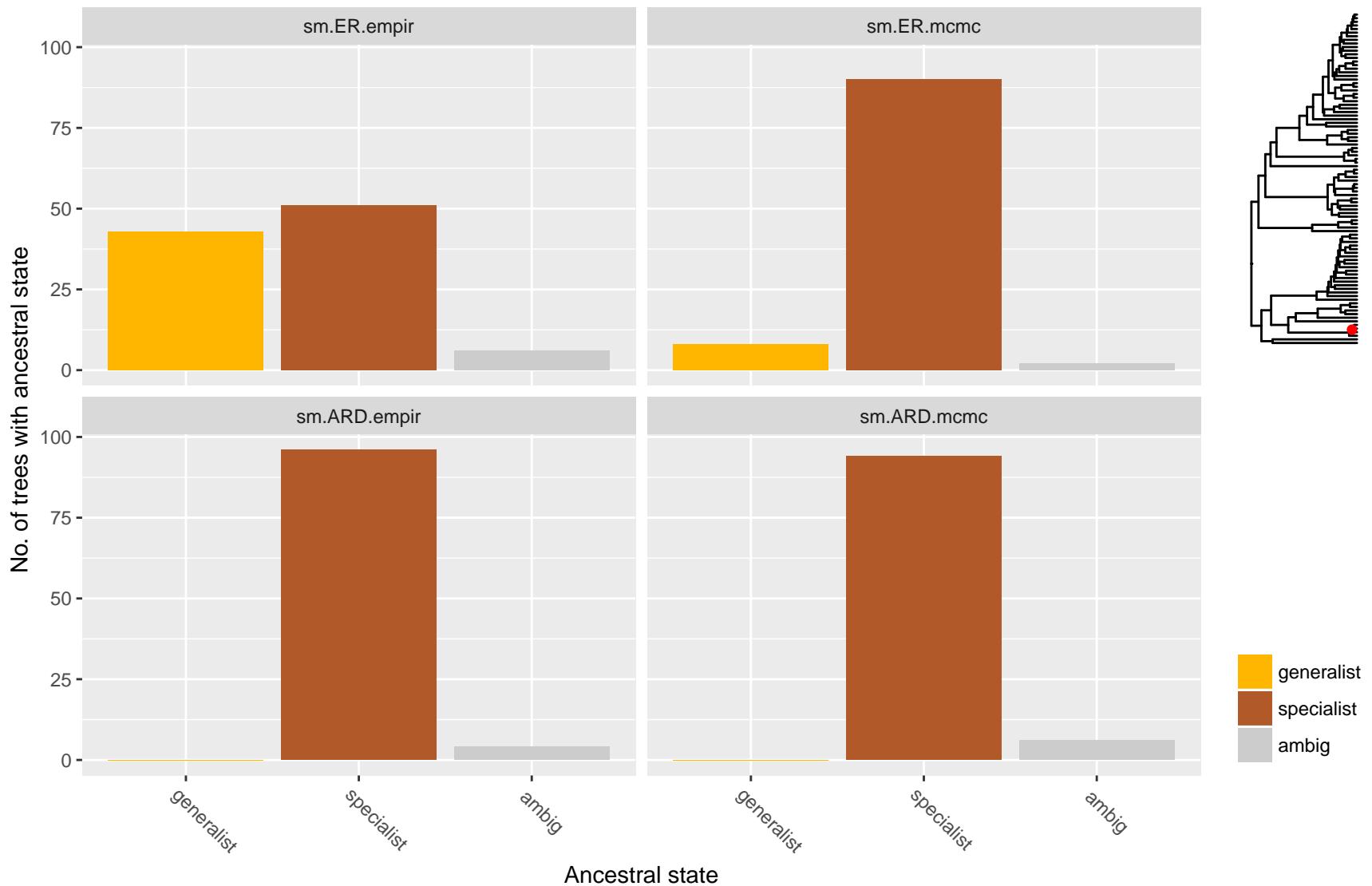
FigureS 110: Ancestral states for node 12



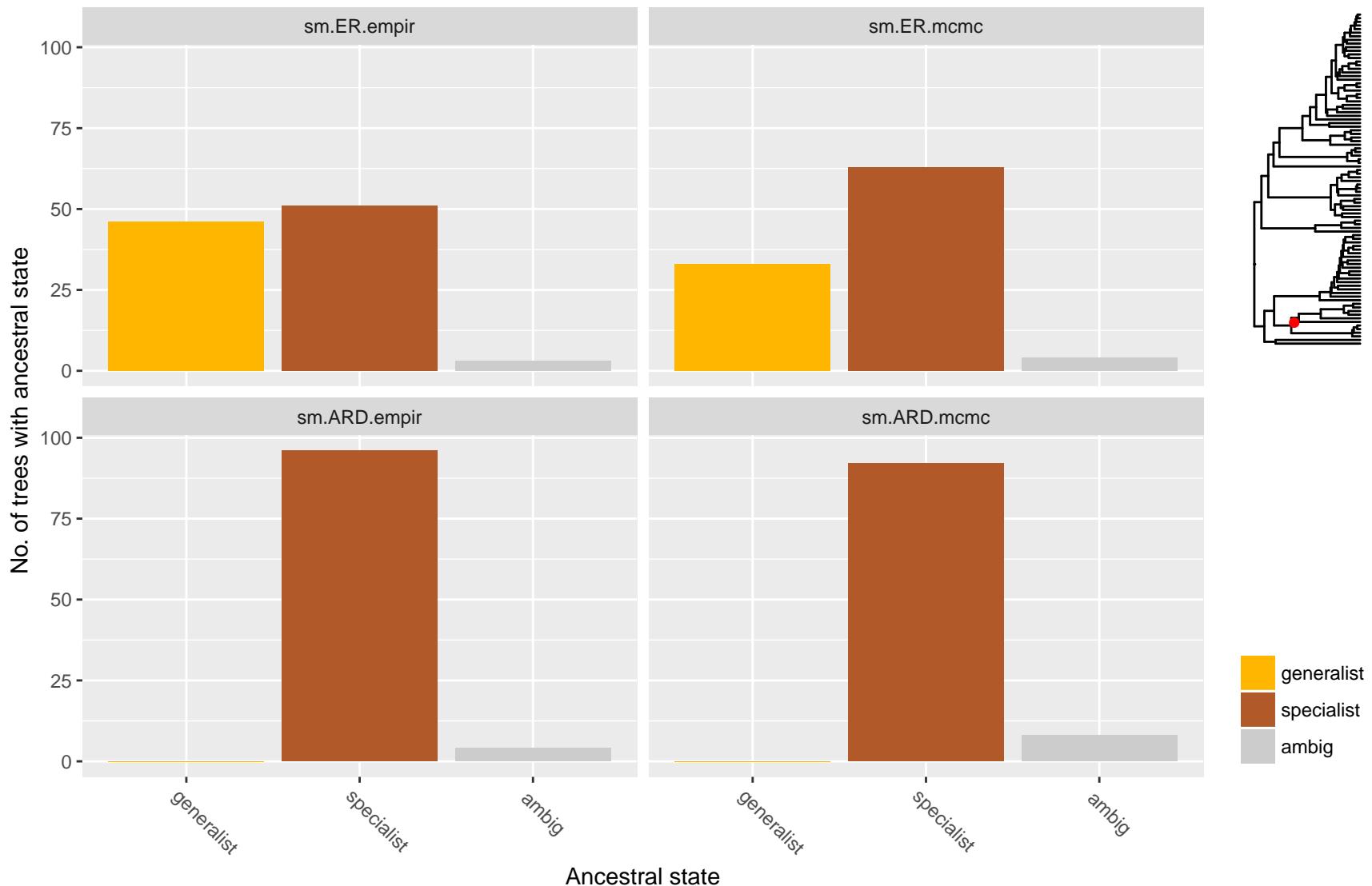
FigureS 111: Ancestral states for node 13



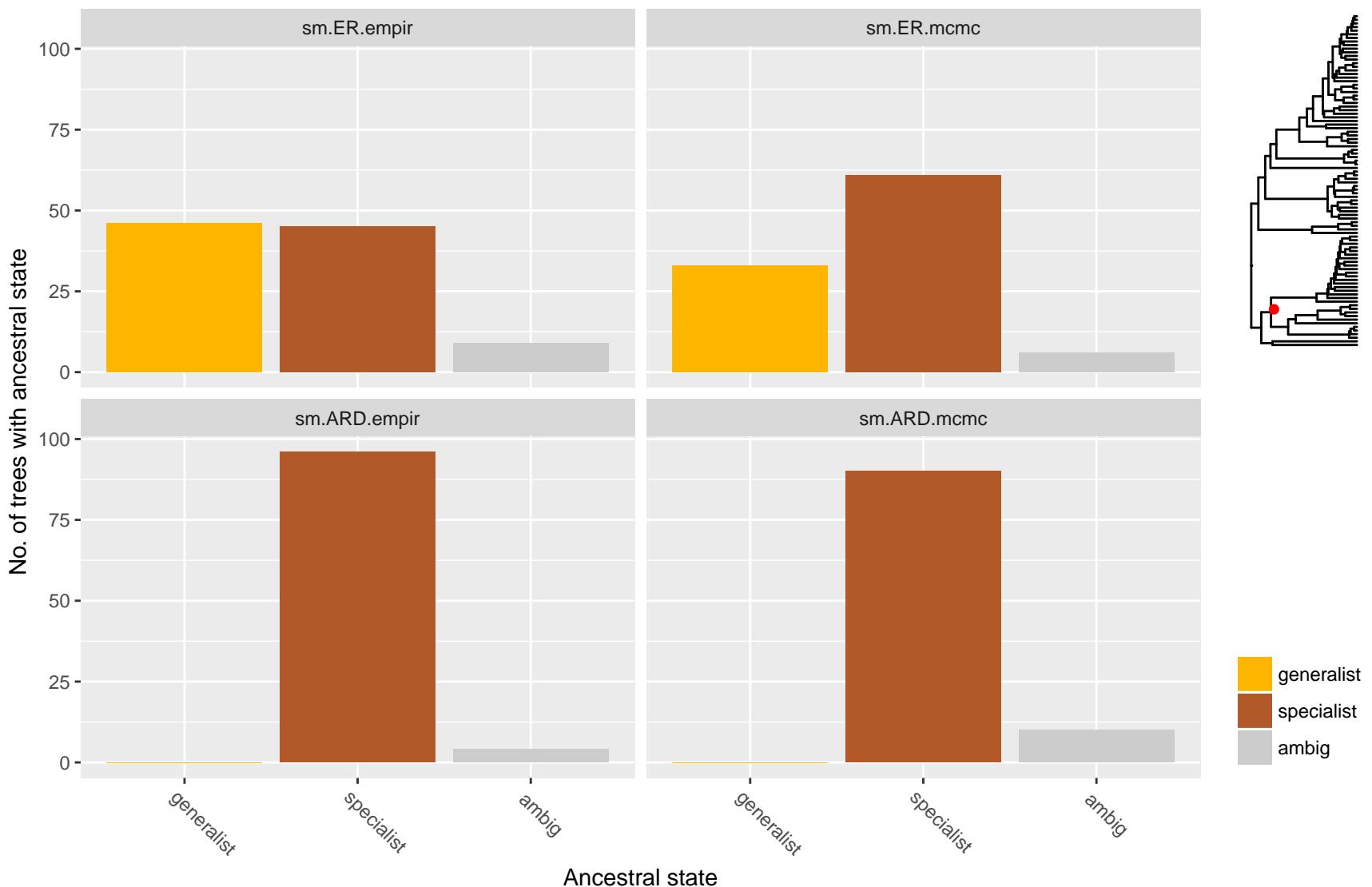
FigureS 112: Ancestral states for node 14



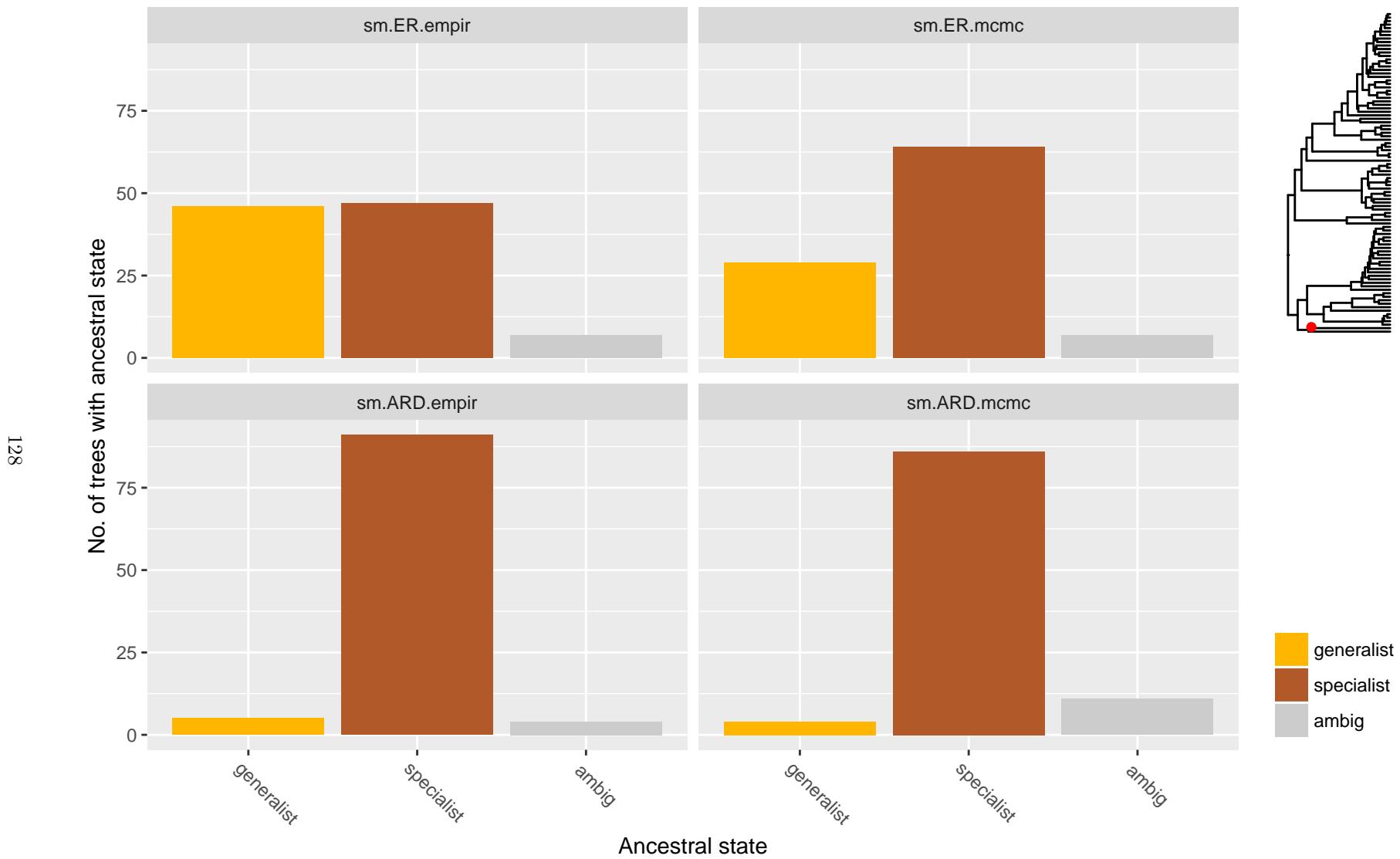
FigureS 113: Ancestral states for node 15



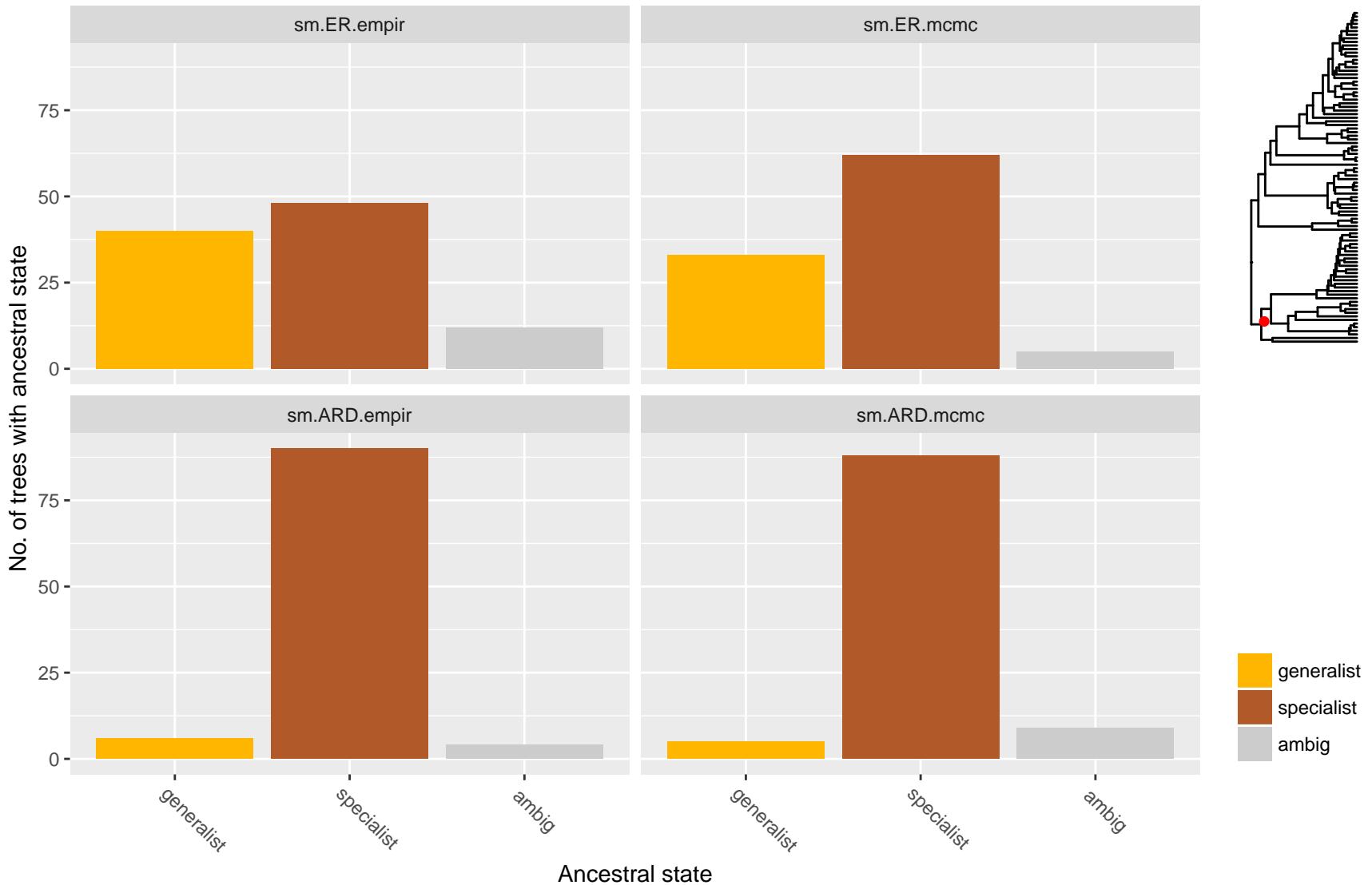
FigureS 114: Ancestral states for node 16



FigureS 115: Ancestral states for node 17



FigureS 116: Ancestral states for node 18



FigureS 117: Ancestral states for node 19

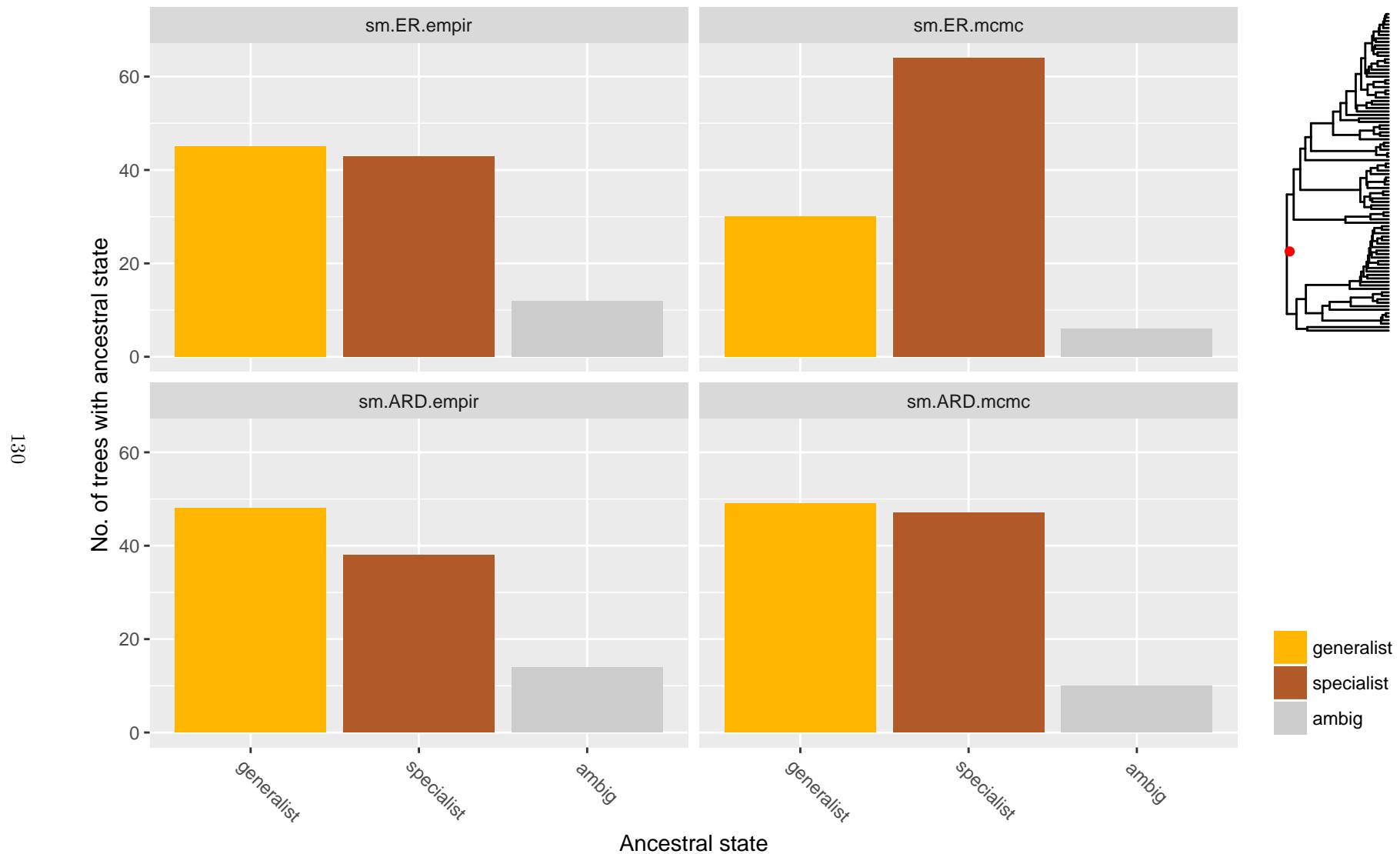


Figure S118 - Individual plots for speciation and extinction rate from MuSSE analyses

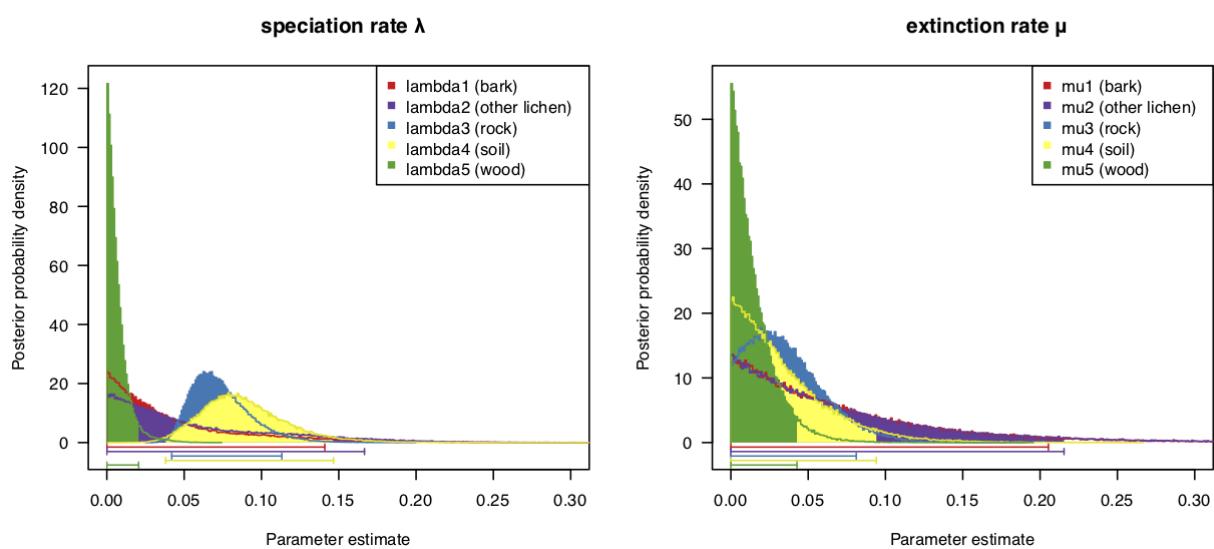
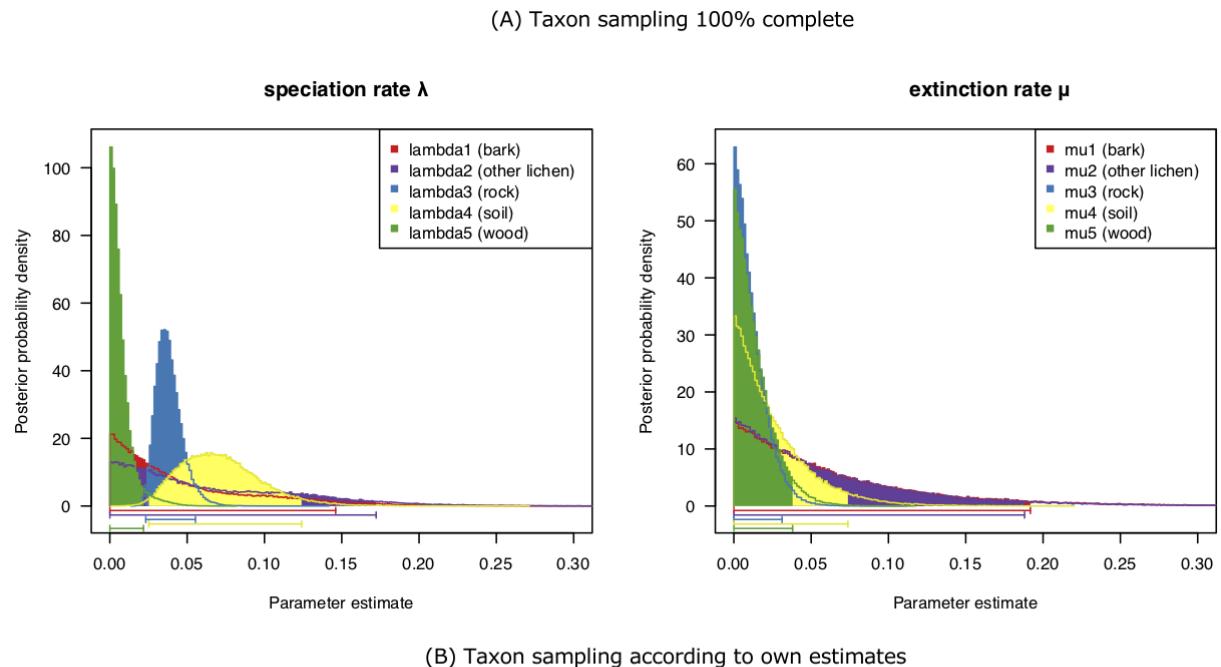


Figure S119 - MuSSE validation simulation

Simulation results to test for elevated type1 error rates in SSE analyses. For details refer to main text.

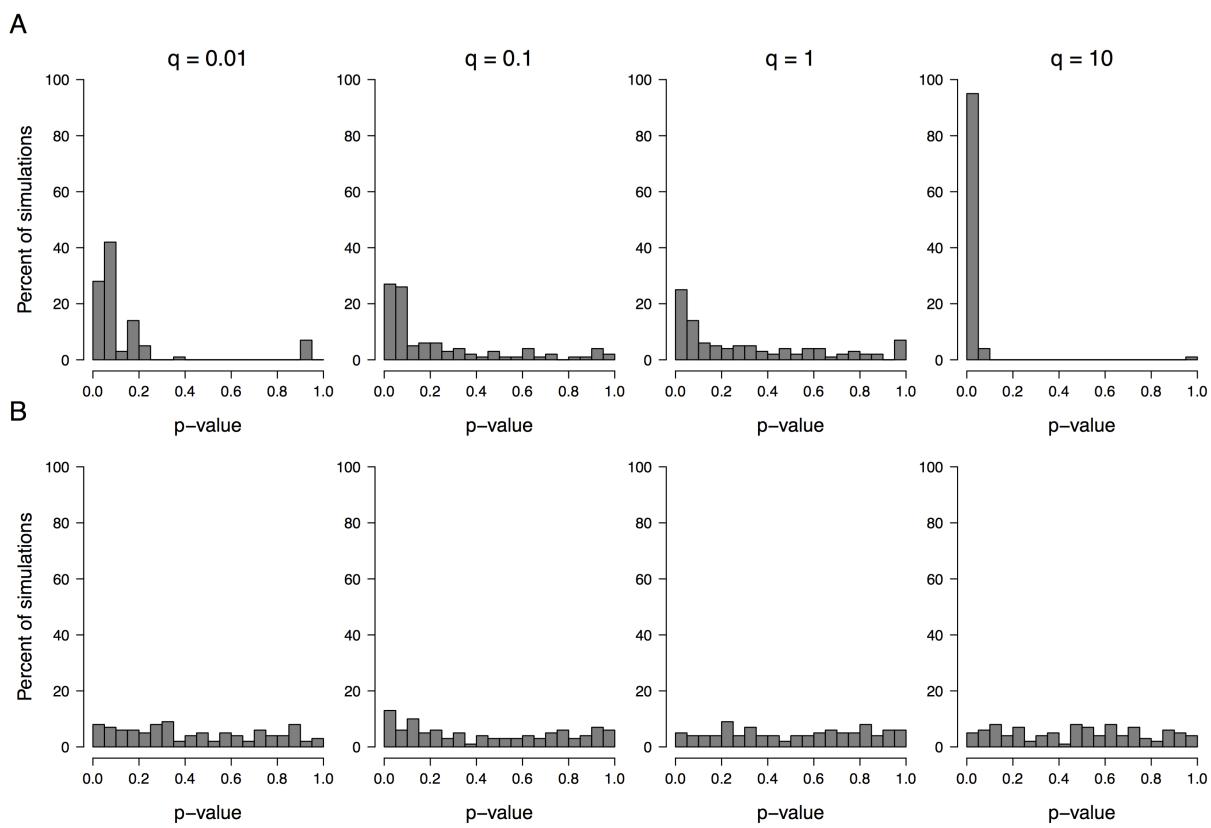


Figure S120 - BAMM rate through time plot for different trapeliod clades assuming 100% sampling completeness

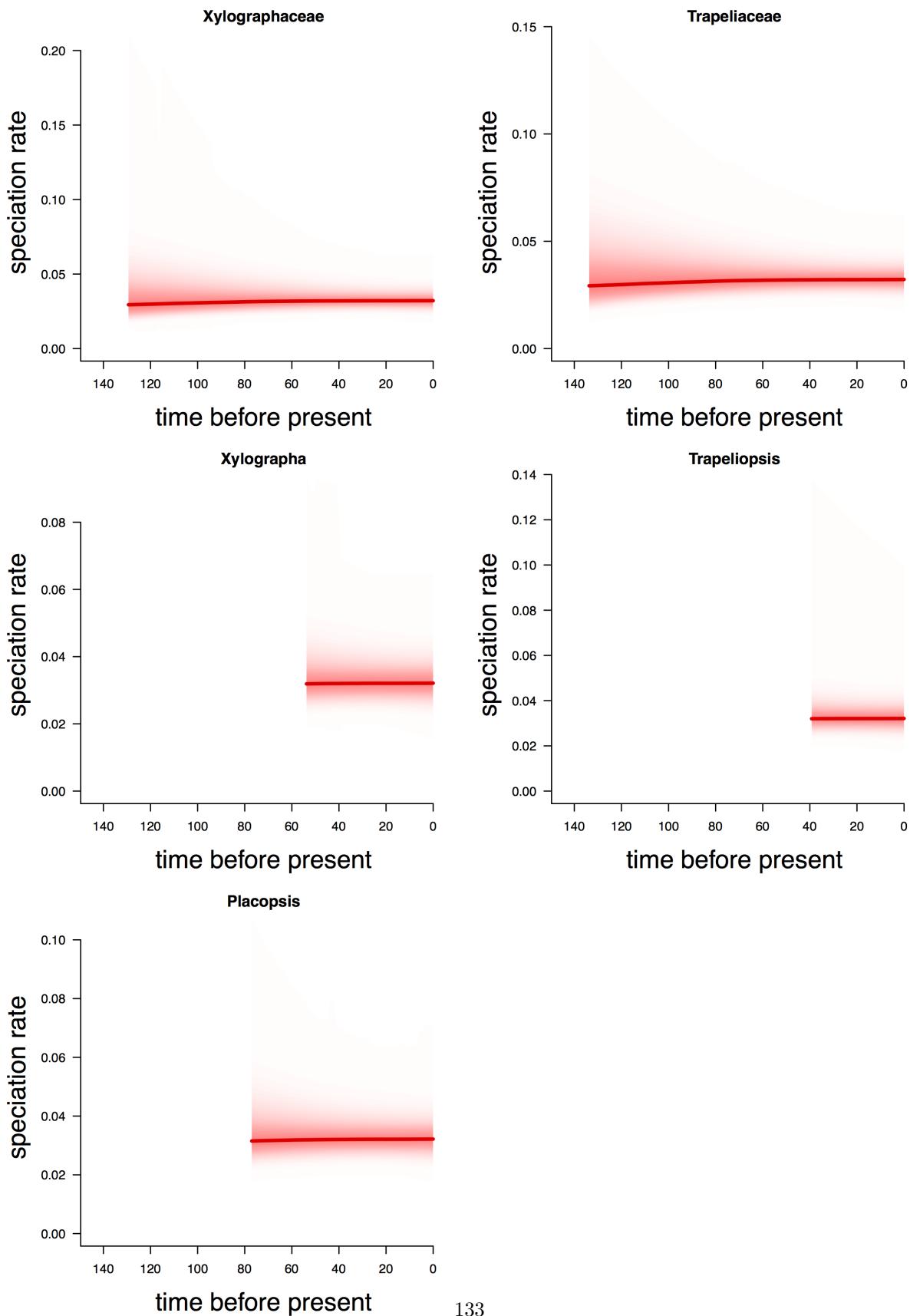


Figure S121 - BAMM rate through time plot for different trapelioid clades assuming sampling completeness according to indexfungorum.org

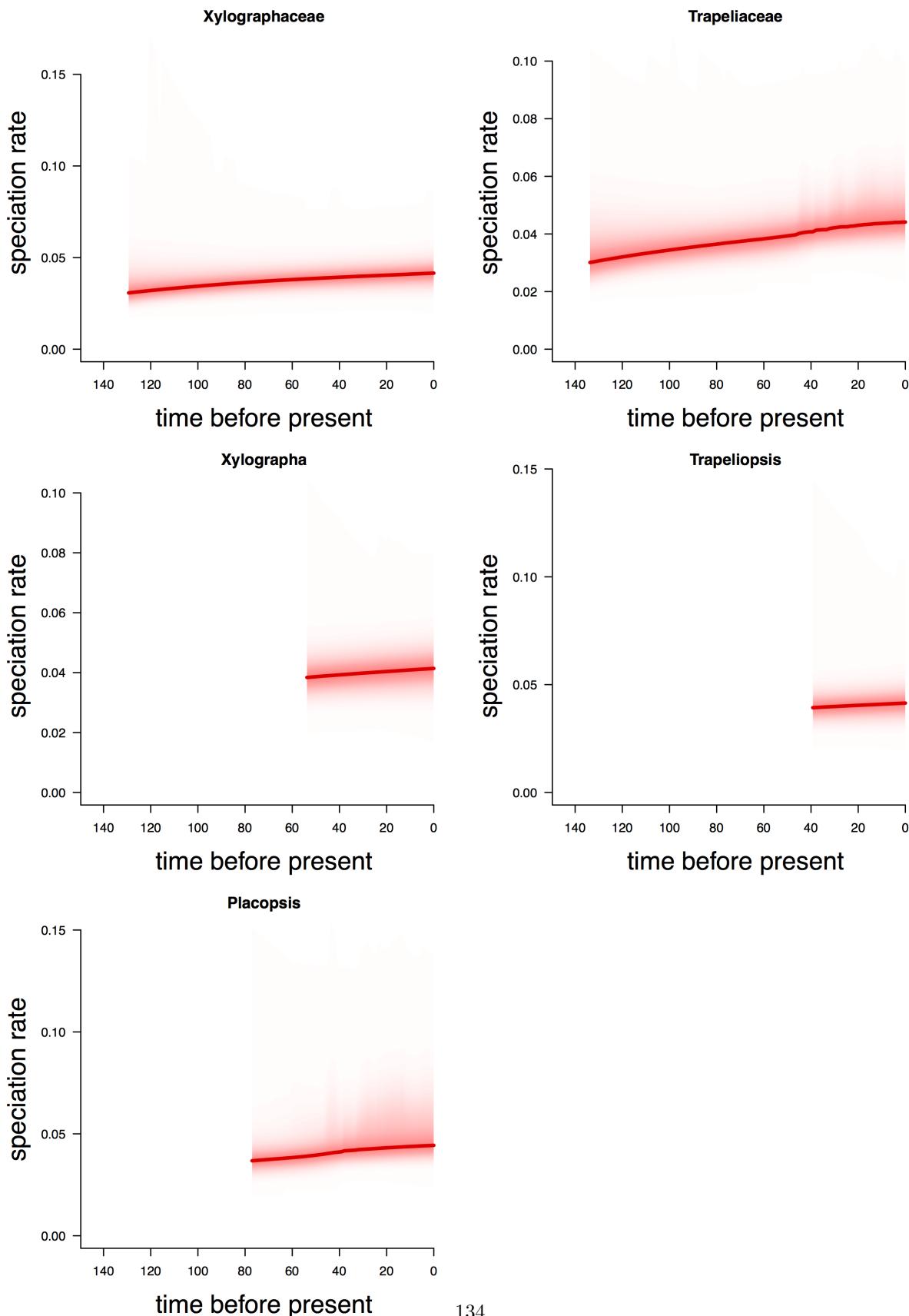


Figure S122 - BAMM rate through time plot for different trapeliod clades assuming sampling completeness according to own diversity estimates

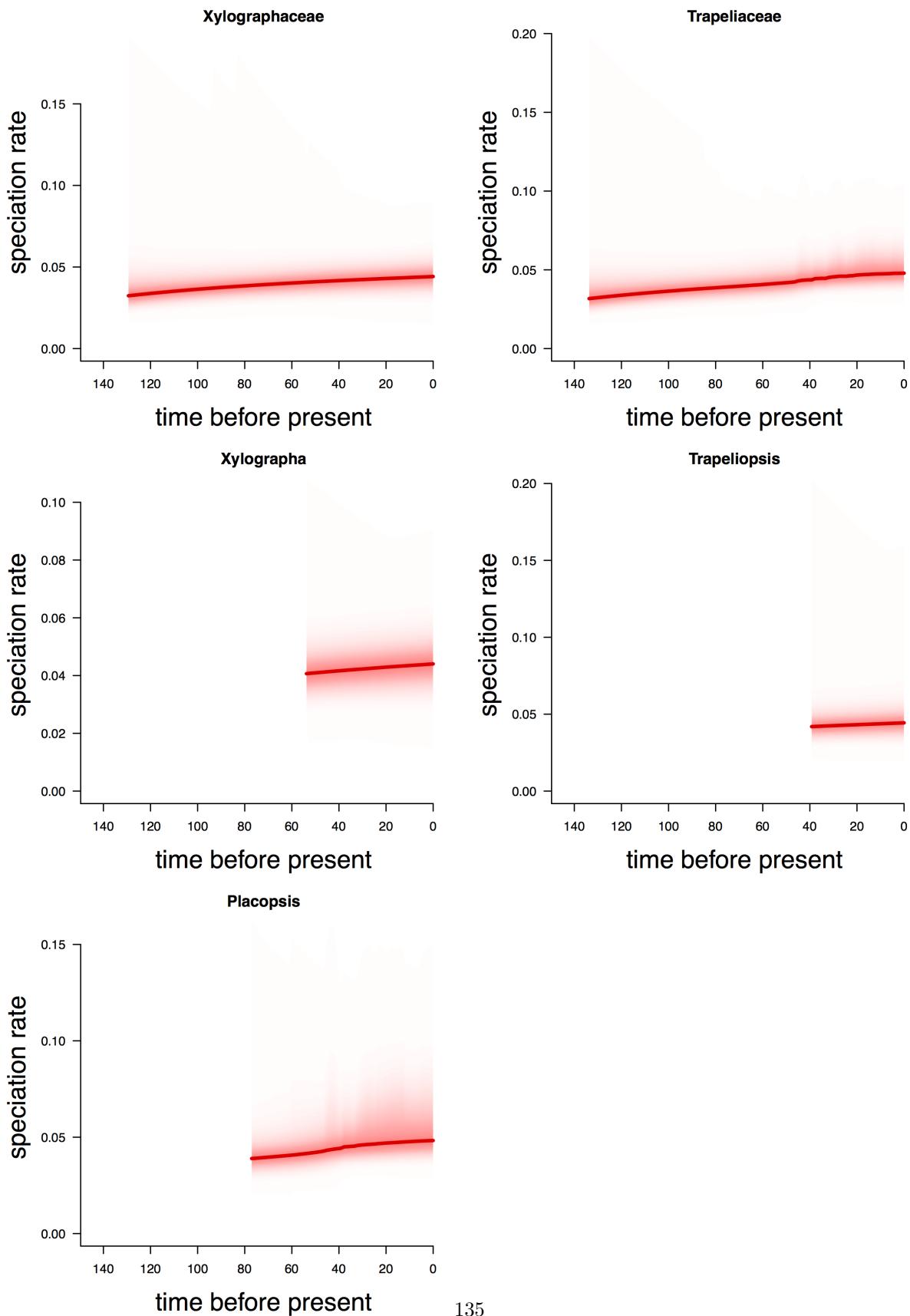


Figure S123 - Results of blocked transition model comparison with ace based on AIC score comparison of thirty models fitted to 100 trapezoidal trees

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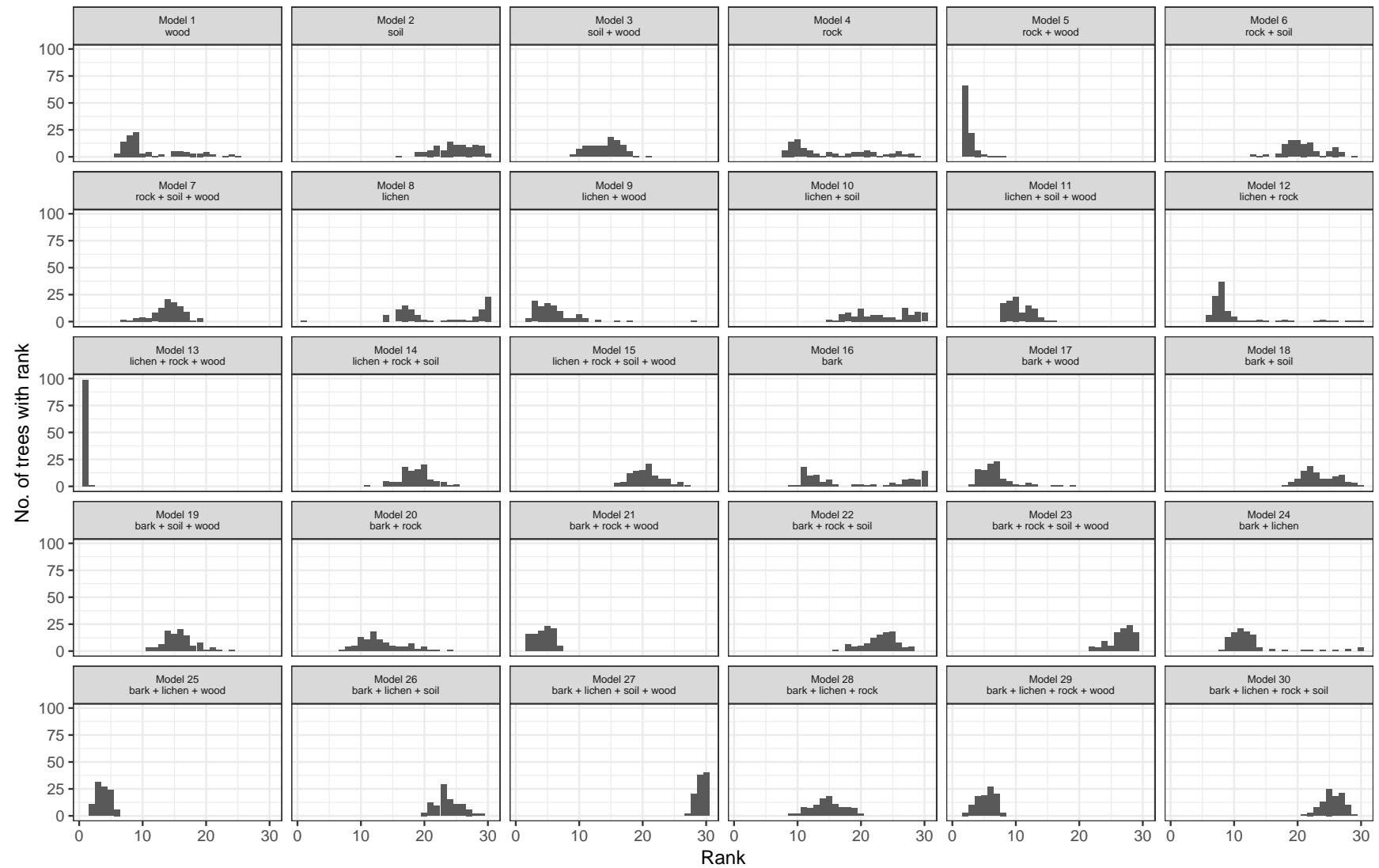


Table S1 - Specimen and sequence vouchers used in this study

For this information please refer to the separately provided spreadsheet: TableS1.xlsx

Table S2 - Mean number of character state transitions for the preferred substrate character set

Data from this table was used to create Figure 3a.

states	to	from	total
bark	3.624654	2.576534	6.201188
lichen	2.221585	1.848812	4.070397
rock	2.208812	6.941881	9.150693
soil	8.150099	9.141188	17.291287
wood	8.905446	4.602080	13.507525

Table S3 - Results from evolutionary dead end scenario analyses in tabular form.

Rank of model (based on AIC score comparison) among all models for one tree / Number of trees for which the model ranked nth place, of 100 trees, based on AIC scores. Data from this table was used to create Figure 2 and Figure S123.

Model.No.	Description	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	mean AIC*			
1	13 lichen + rock + wood	99	1																												104,5443				
2	5 rock + wood	66	22	6	2	1	1	1																						107,8556					
3	25 bark + lichen + wood	11	31	27	24	6																								109,2197					
4	21 bark + rock + wood	16	16	19	23	21	5																							109,3961					
5	29 bark + lichen + rock + wood	3	10	18	19	27	20	3																						110,1557					
6	9 lichen + wood	3	19	14	17	15	10	3	3	7	3	2					1		1										1	111,6885					
7	17 bark + wood	2	16	15	21	23	7	5	2	1	3	2				1	1		1										111,9313						
8	12 lichen + rock						6	24	37	10	5	1	1	1	2	1		1	2	1									115,9281						
9	11 lichen + soil + wood									17	19	23	8	15	12	4	1	1											117,2357						
10	1 wood									3	14	20	23	3	4	1	2	5	5	4	3	3	4	2	1	2	1		117,3383						
11	20 bark + rock										1	4	5	13	11	18	11	8	5	4	4	7	2	4	1	1			120,0705						
12	24 bark + lichen											1	13	17	21	18	15	3	2										120,676						
13	7 rock + soil + wood											2	1	3	4	3	8	13	21	18	14	9	1	3					120,8881						
14	3 soil + wood												2	7	10	10	10	18	15	11	5	1							121,0753						
15	28 bark + lichen + rock													2	2	8	7	10	16	18	11	8	8	7	2				121,6284						
16	19 bark + soil + wood														3	3	6	19	16	20	14	5	8	1	3	1			122,5742						
17	4 rock														6	14	16	8	6	3	1	4	3	4	6	4	1	2	3	5	2	3	1	122,5929	
18	14 lichen + rock + soil															1		5	4	4	18	14	16	20	6	5	4	1	2			126,3328			
19	15 lichen + rock + soil + wood																3	4	12	14	15	21	10	7	7	2	4	1				128,2759			
20	6 rock + soil																2	1	2		3	12	15	15	12	13	5	1	5	9	4	1	129,0554		
21	22 bark + rock + soil																	1		6	4	5	7	12	15	17	18	8	3	4			131,5949		
22	26 bark + lichen + soil																		3	12	9	29	15	11	11	6	2	2				132,1792			
23	18 bark + soil																		1	4	7	14	19	13	7	7	9	11	4	3	1		133,2124		
24	30 bark + lichen + rock + soil																		1	3	8	13	25	18	21	10	1				134,4323				
25	23 bark + rock + soil + wood																		4	3	9	5	17	21	24	17					136,923				
26	2 soil																		1		4	4	6	10	6	14	11	11	9	11	10	3	137,2116		
27	16 bark																		1	1	18	10	11	4	6	2	2	1	3	2	6	7	6	14	138,0049
28	10 lichen + soil																		2	1	7	8	5	12	5	6	6	4	4	2	13	6	9	8	140,5222
29	8 lichen																		6	11	15	11	6	2	1	1	2	2	2	1	5	11	23	142,6968	
30	27 bark + lichen + soil + wood		1																												2	20	38	40	152,0688

* per model for all trees

Table S4 - Individual models of dead end analyses for which ace failed to return results

model.no.	Description	tree.no.
28	bark + lichen + rock	34
9	lichen + wood	68
10	lichen + soil	71
5	rock + wood	72
25	bark + lichen + wood	84
16	bark	91
10	lichen + soil	95

Table S5a - Summary MuSSE diversification rate 100%

	bark	lichen	rock	soil	wood	mean	stddev
bark		p=1		p=1	p=1	-0.0158288	0.0791713
lichen	p<2.2e-16			p=1	p=1	0.0024461	0.0852084
rock	p<2.2e-16	p<2.2e-16			p=1	0.0265715	0.0076929
soil	p<2.2e-16	p<2.2e-16	p<2.2e-16		p<2.2e-16	0.0458740	0.0258588
wood	p<2.2e-16	p=1		p=1	p=1	-0.0067468	0.0132246

Interpretation: Can we reject the H0 that (row) is not significantly larger than (col). When p < 0.05 value in row is significantly larger than value in col.

Table S5b - Summary MuSSE diversification own diversity estimates

	bark	lichen	rock	soil	wood	mean	stddev
bark		p=1		p=1	p=1	-0.0253580	0.0809662
lichen	p<2.2e-16			p=1	p=1	p<2.2e-16	-0.0139080
rock	p<2.2e-16	p<2.2e-16			p=1	p<2.2e-16	0.0378680
soil	p<2.2e-16	p<2.2e-16	p<2.2e-16		p<2.2e-16	0.0544373	0.0236842
wood	p<2.2e-16	p=1		p=1	p=1	-0.0081949	0.0148699

Interpretation: Can we reject the H0 that (row) is not significantly larger than (col). When p < 0.05 value in row is significantly larger than value in col.

Table S6 - Overview about the number of methods which recovered the most frequent ancestral state for 10 nodes along the trapezoid tree

Node	consensus state substrate character	no. of methods recovering substrates (total = 30)	consensus state ecol. strategy	no. of methods recovering ecological amplitude (total = 20)
1	1 rock	29	specialist	17
2	2 rock	29	specialist	17
3	3 rock	29	specialist	17
4	4 soil	28	generalist	15
5	5 rock	27	specialist	17
6	6 rock	27	specialist	17
7	7 soil	22	generalist	15
8	8 rock	16	specialist	16
9	9 rock	29	specialist	17
10	10 rock	18	specialist	17
11	11 wood	28	specialist	17
12	12 bark	22	specialist	17
13	13 rock	18	specialist	17
14	14 rock	29	specialist	17
15	15 rock	18	specialist	17
16	16 rock	17	specialist	16
17	17 rock	17	specialist	17
18	18 rock	17	specialist	17
19	19 rock	16	specialist	13