Methods

Results

Sample assembly details

One sample (*C. soui poliocephalus* ANSP 187533) had relatively low coverage (mean coverage = 10.42x, standard deviation = 76.95x) and thus read-mapping resulted in a highly incomplete genome (Table S1). This sample was dropped from all subsequent analyses.

Introgression analyses

Our breakpoint analysis revealed that m=2 was the optimal m-value for our PhyloNet analysis (Figure S8), with diminishing gains or reduced likelihood for successively larger m-values. Specifically, the slope of the segmented model was significant and tightly fitting (Breakpoint = 2.43, Adj. R^2 = 0.932, β = 10424, P = 0.0017).

Supplemental Tables and Figures:

| Dataset	Model	Adj. R-squared	slope	P	AIC
BUSCOs	linear (#PIS)	0.04086	-0.0062133	0	22306
	logarithmic (#PIS)	**0.04872**	**-6.7871**	**0**	**22286**
	linear (%PIS)	**0.01448**	**24.903**	**0**	**22374**
	logarithmic (%PIS)	0.0101	7.169	0	22385
UCE100Flank	linear (#PIS)	0.04058	-21.7212	0	25321
	logarithmic (#PIS)	**0.04609**	**-21.7212**	**0**	**25304**
	linear (%PIS)	0.03632	-46.4612	0	25334
	logarithmic (%PIS)	**0.04608**	**-6.0591**	**0**	**25304**
UCE300Flank	linear (#PIS)	0.5104	-0.148854	0	22890
	logarithmic (#PIS)	**0.6474**	**-29.2997**	**0**	**21945**
	linear (%PIS)	0.5568	-130.995	0	22604
	logarithmic (%PIS)	**0.6651**	**-31.2986**	**0**	**21797**
UCE1000Flank	linear (#PIS)	0.01031	-0.0034907	0	19828
	logarithmic (#PIS)	**0.02537**	**-5.033**	**0**	**19785**
	linear (%PIS)	0.03698	-19.8045	0	19752
	logarithmic (%PIS)	**0.05108**	**-8.5341**	**0**	**19710**
UCE Combined	linear (#PIS)	0.5769	-0.0590176	0	77987
	logarithmic (#PIS)	**0.7858**	**-21.7212**	**0**	**72165**
	linear (%PIS)	**0.6499**	**-195.5041**	**0**	**76369**

	logarithmic (%PIS)	0.6043	-36.9592	0	77413

Table S2: Model tests of log versus linear fits for all generalized linear models. This model test was done twice for each dataset, once using the number of parsimony informative sites per locus (#PIS) and once using the percentage of parsimony informative sites per locus (%PIS). Rows with bold text indicate the best model for each paired model test.
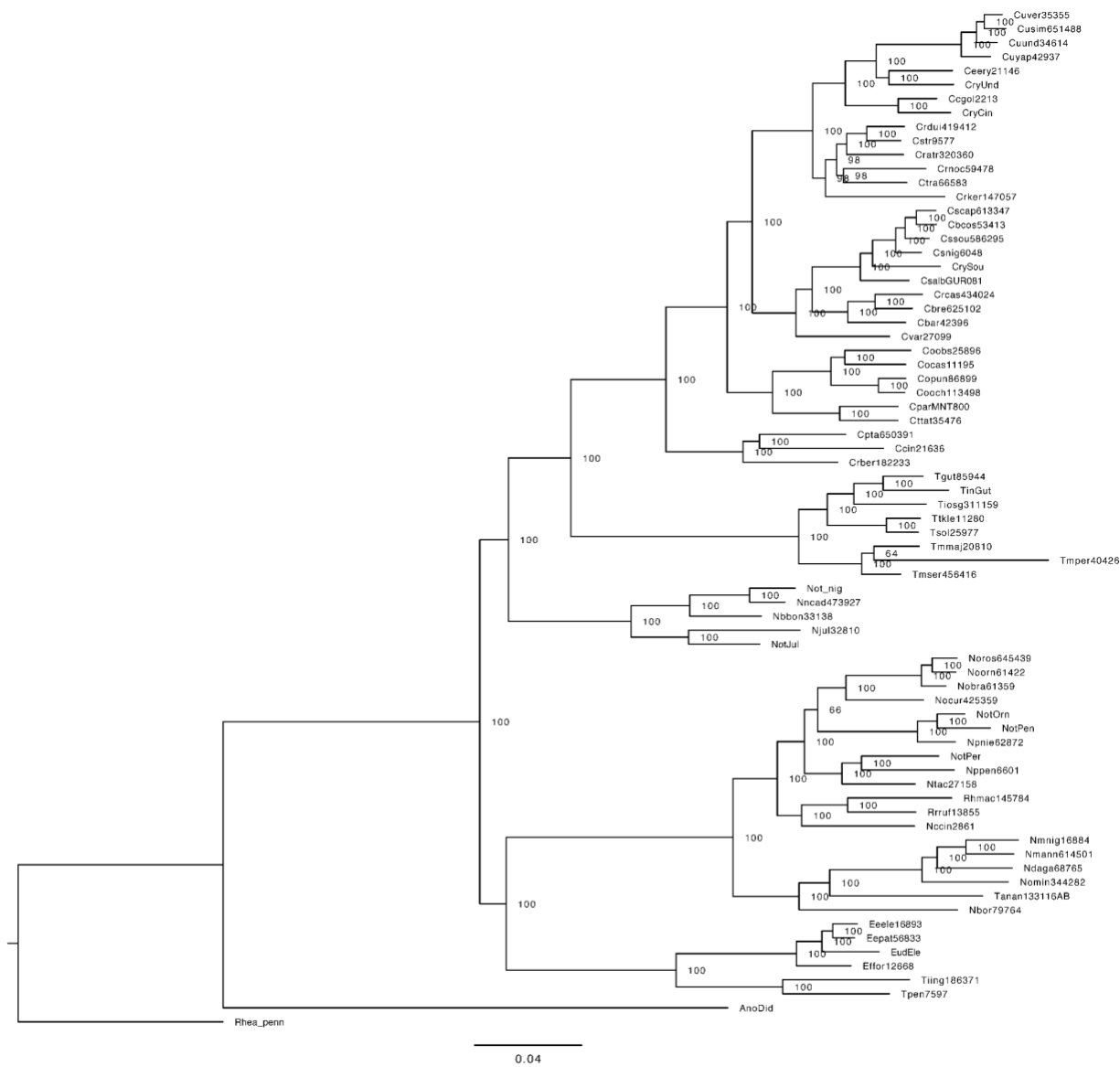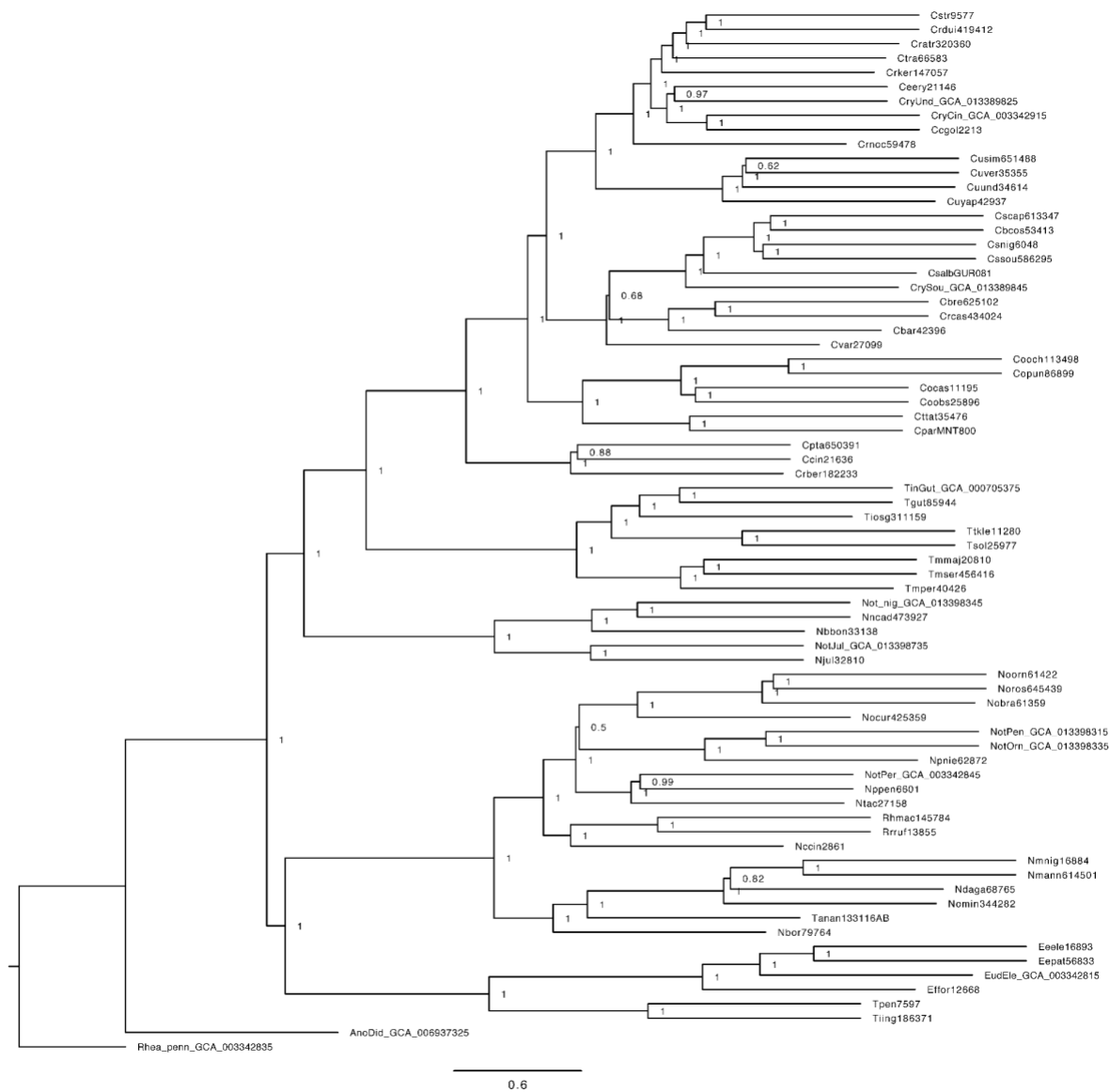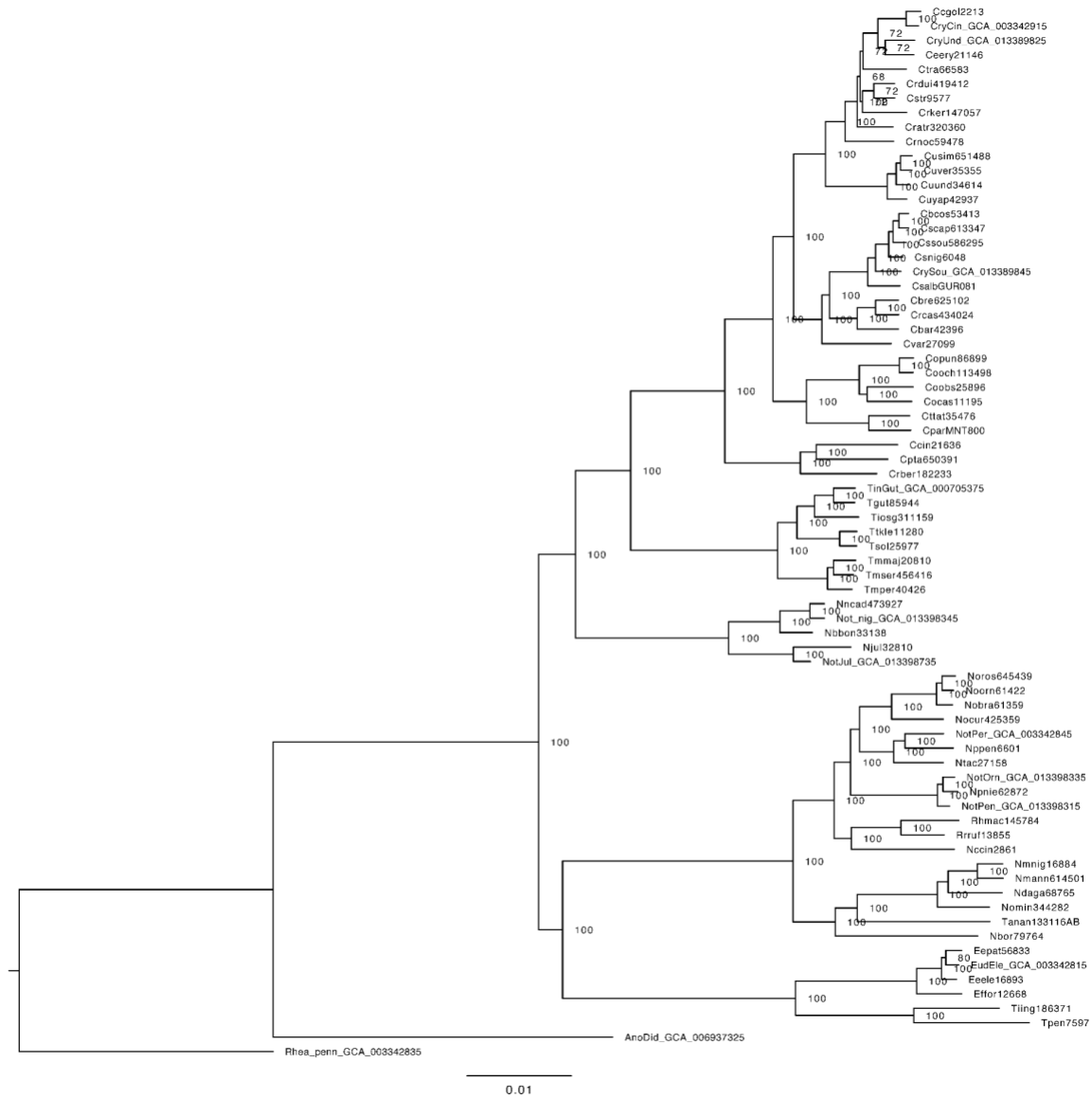

Figure S1: CDS Concatenated phylogeny
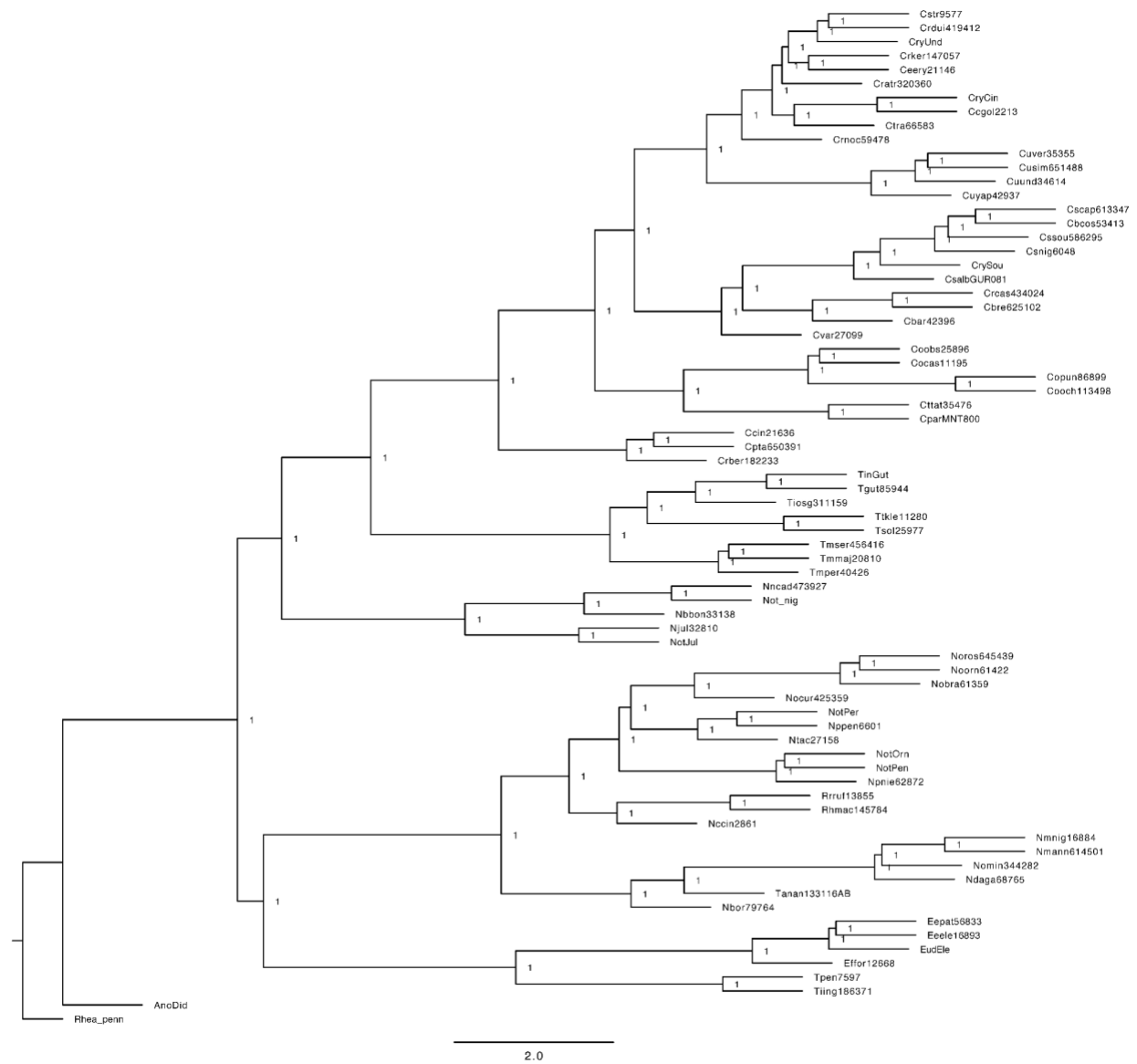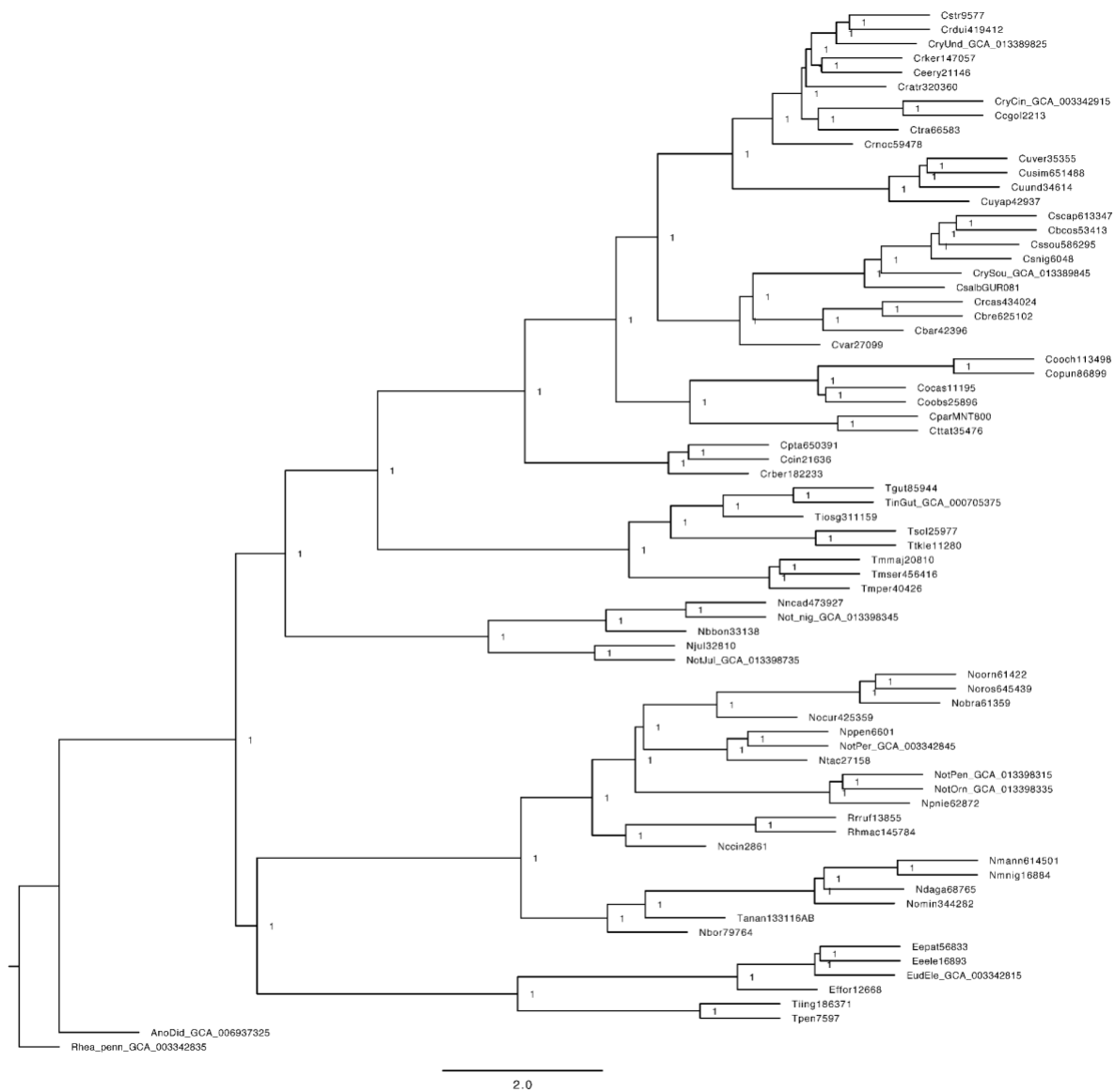
Figure S2: CDS MSC phylogeny

Figure S3: UCE100Flank Concatenated phylogeny

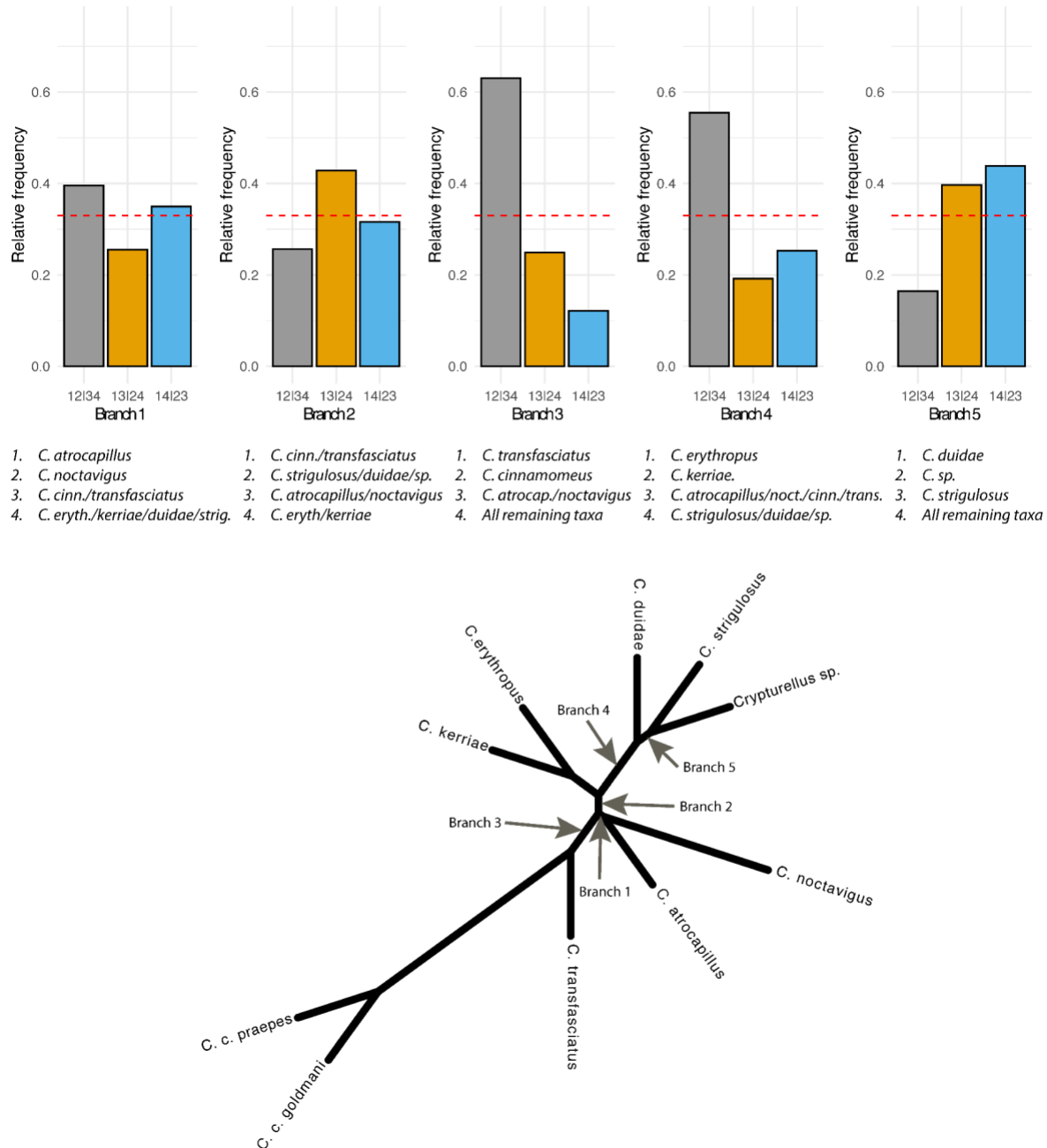**Figure S4: UCE100Flank MSC phylogeny**

Figure S5: UCE300Flank Concatenated phylogeny

Figure S6: UCE300Flank MSC phylogeny

Figure S7: Relative quartet frequencies for five short internodal branches in Clade A based on the UCE1000Flank dataset. Bars depict the relative frequencies of each of three alternative unrooted quartet topologies. The stippled lines indicate the ⅓ threshold for the frequency of gene trees given a multispecies coalescent model, which predicts a single majority quartet topology consistent with the true species tree, and two minority topologies of equivalent frequency below the ⅓ threshold. As quartet frequencies approach the ⅓ threshold, they indicate stronger ILS. Major deviations from the expectations of the MSC model indicate violations of the model may be present, such as gene tree estimation bias or introgression. Branch numbers correspond to Figures 2 and 7.
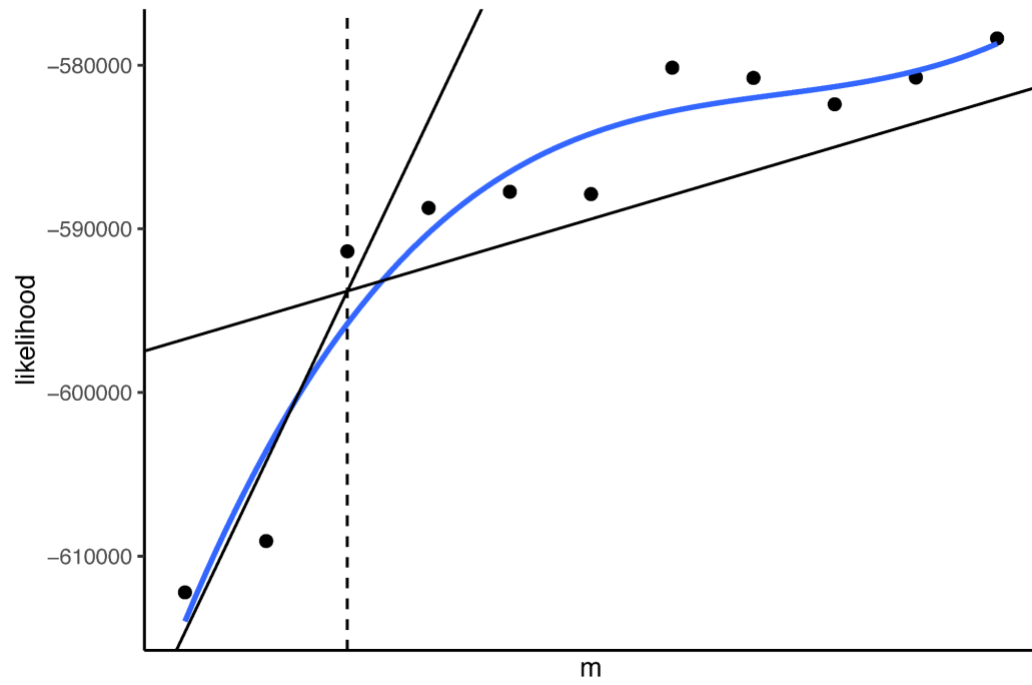
Figure S8: Breakpoint analysis for the best-fit m-value for the introgression analysis.