SUPPLEMENTARY TABLES AND FIGURES

Table S1 PCR amplification primers.			Annealing Temp.
Cyt *b*	CytBa	GATATGAAAAACCATCGTTG	50C
	CytBj	CTGCAGTCATCTCCGGTTTACAAGAC	
Anon	Anon1F	CTGCGCAGCCCTGACATATGG	53C
	Anon2R	GAAGATGGGATCCAGCTCCAGC	
ACR	ACR11F	TATGGTRGAGATGCTGCCAACTG	53C
	ACR15R	GCAGTGAGCAGCTGTAAGCACC	
ZAN	ZAN19F	CCGCTTCTCAGGGAAATGCACC	52C
	ZAN20R	AGGAGGACCCCAAGACTCC	
Zp2	ZP23F	GATCAATGCAGAAGCAGCAAATGG	51C
	ZP24R	GTGACTCACAGAGACACTCAGG	

Internal sequencing primers for long fragments available upon request

Table S2 Models of sequence evolution

Cyt *b*	
All	HKY+I+G
Position 1	TrN+G
Position 2	TrNef+I+G
Positions 1/2	HKY+I+G
Position 3	TIM+I
Nuclear	
Anon	K2P+I+G
ACR	HKY+G
ZAN	K2P+G
Zp2	TrN+I+G
concatenated	K2P+I+G
gaps	MrBayes Mk

(Selected by DT ModSel)

Table S3. Maximum Likelihood estimates of θ

Species	min	MLE	max
cinereicollis	0.002334	0.003358	0.005028
minimus	0.009737	0.012119	0.015207
quadrivitattus	0.000363	0.000796	0.001482
ruficaudus	0.000625	0.001156	0.001844

Produced using LAMARC. Min and max are 95% confidence
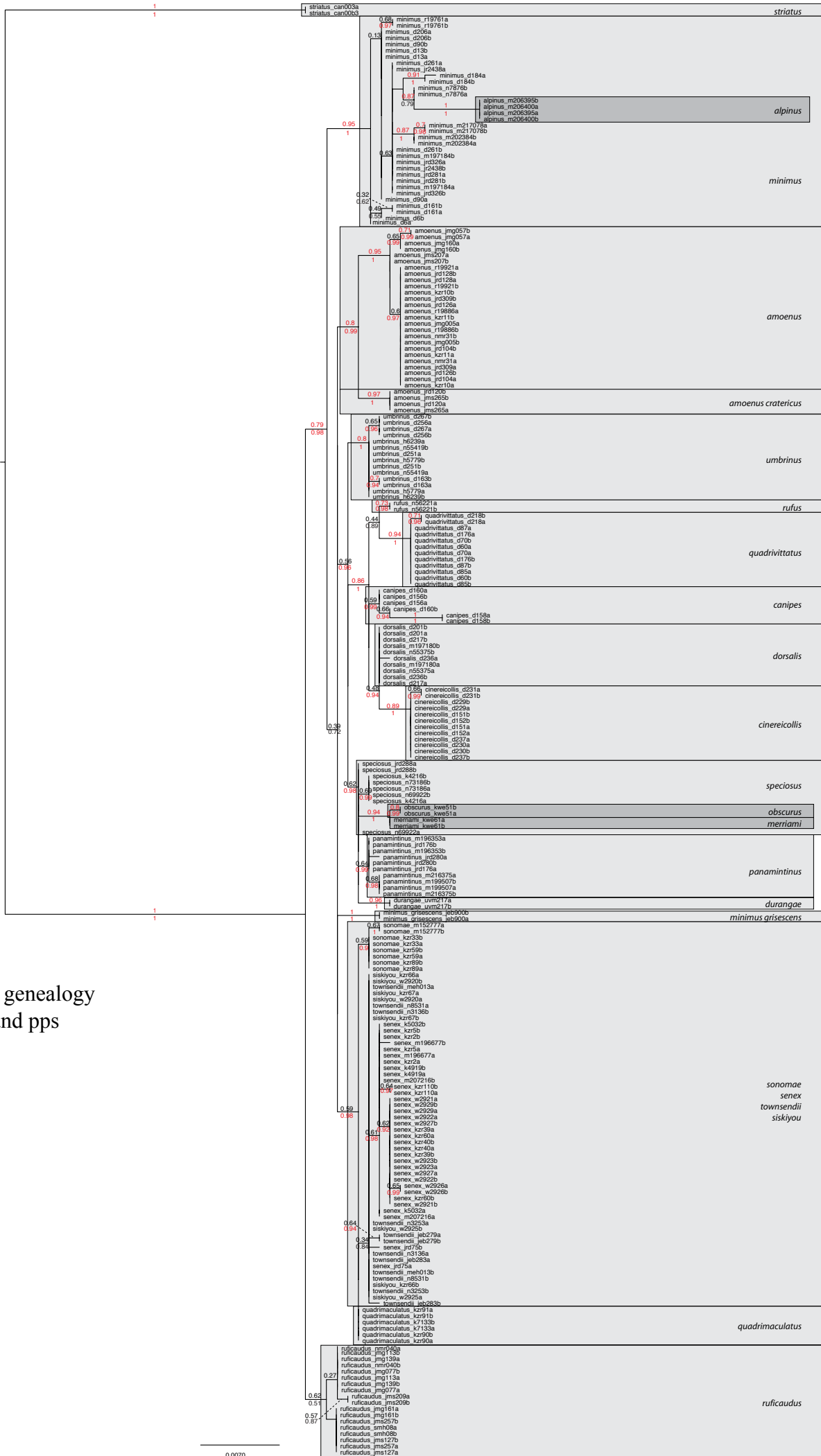bounds. MLE is the maximum likelihood estimate.

Figure S1. ACR ML genealogy
with ML bootstraps and pps

Figure S2. ANON ML genealogy with ML bootstraps and pps

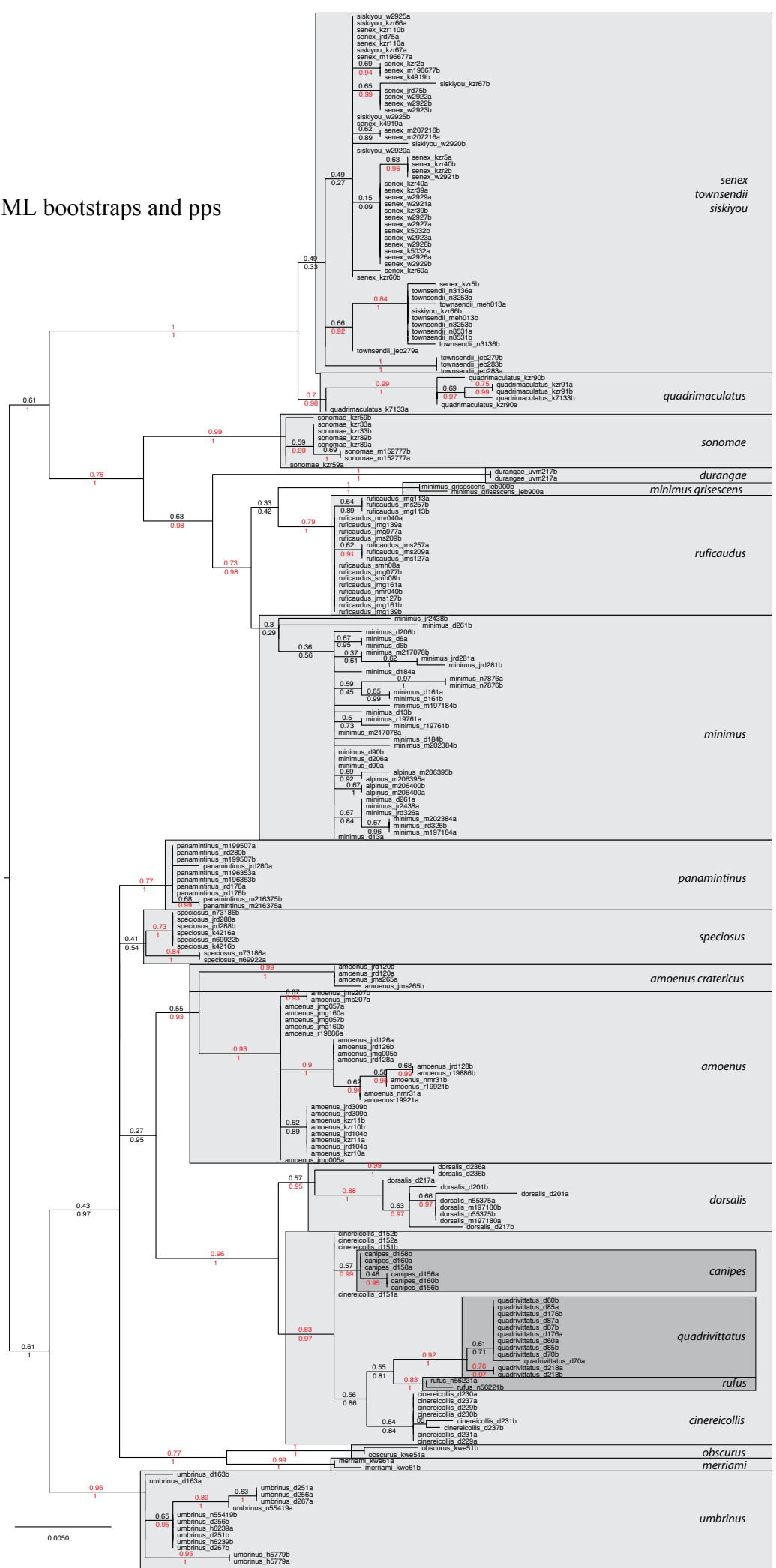Figure S3. ZAN ML genealogy
with ML bootstraps and pps

Figure S4. ZP2 ML genealogy with
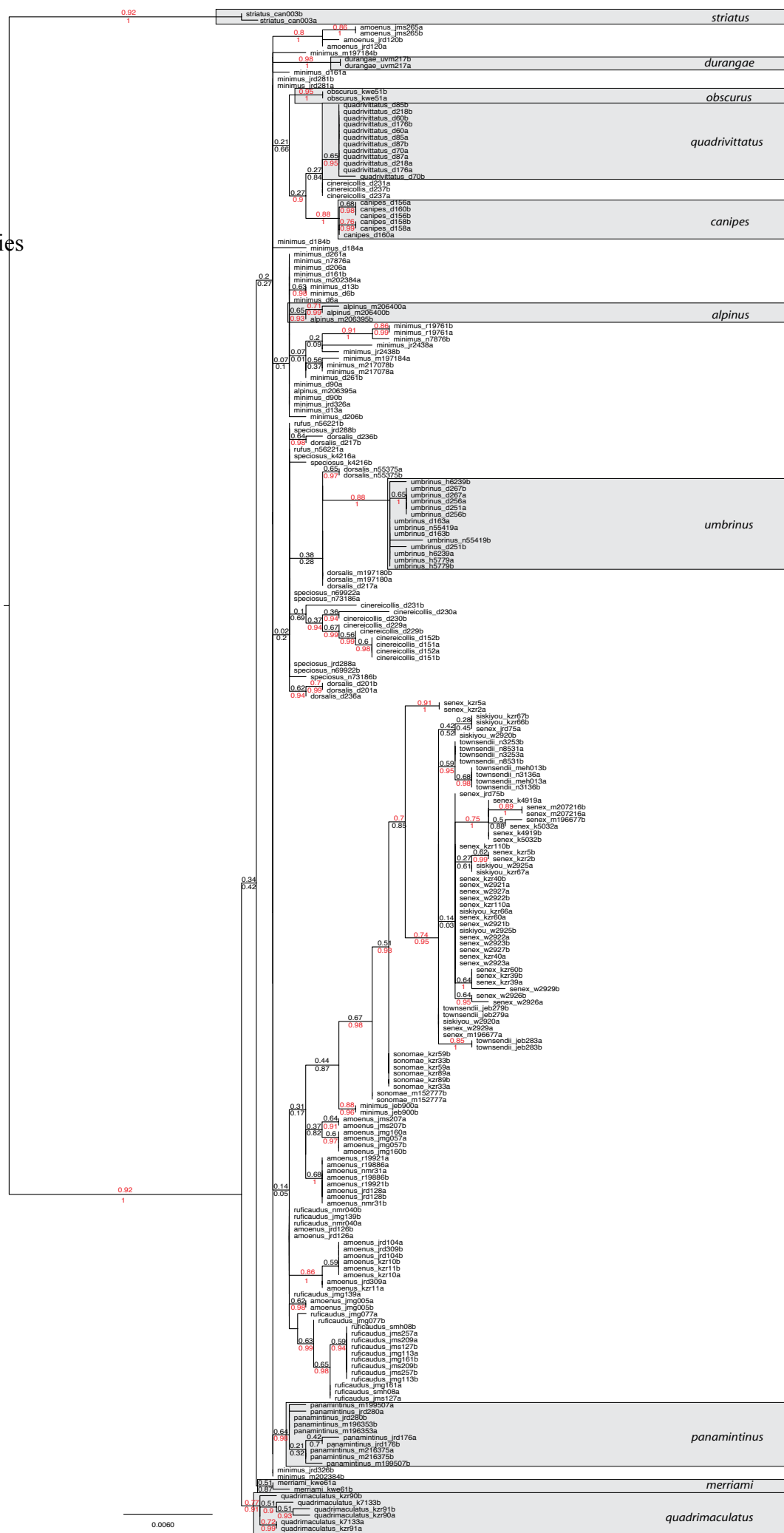ML bootstraps and posterior probabilities

Figure S5. ML tree with bootstrap support of concatenated nuclear data with outgroup *T. striatus*
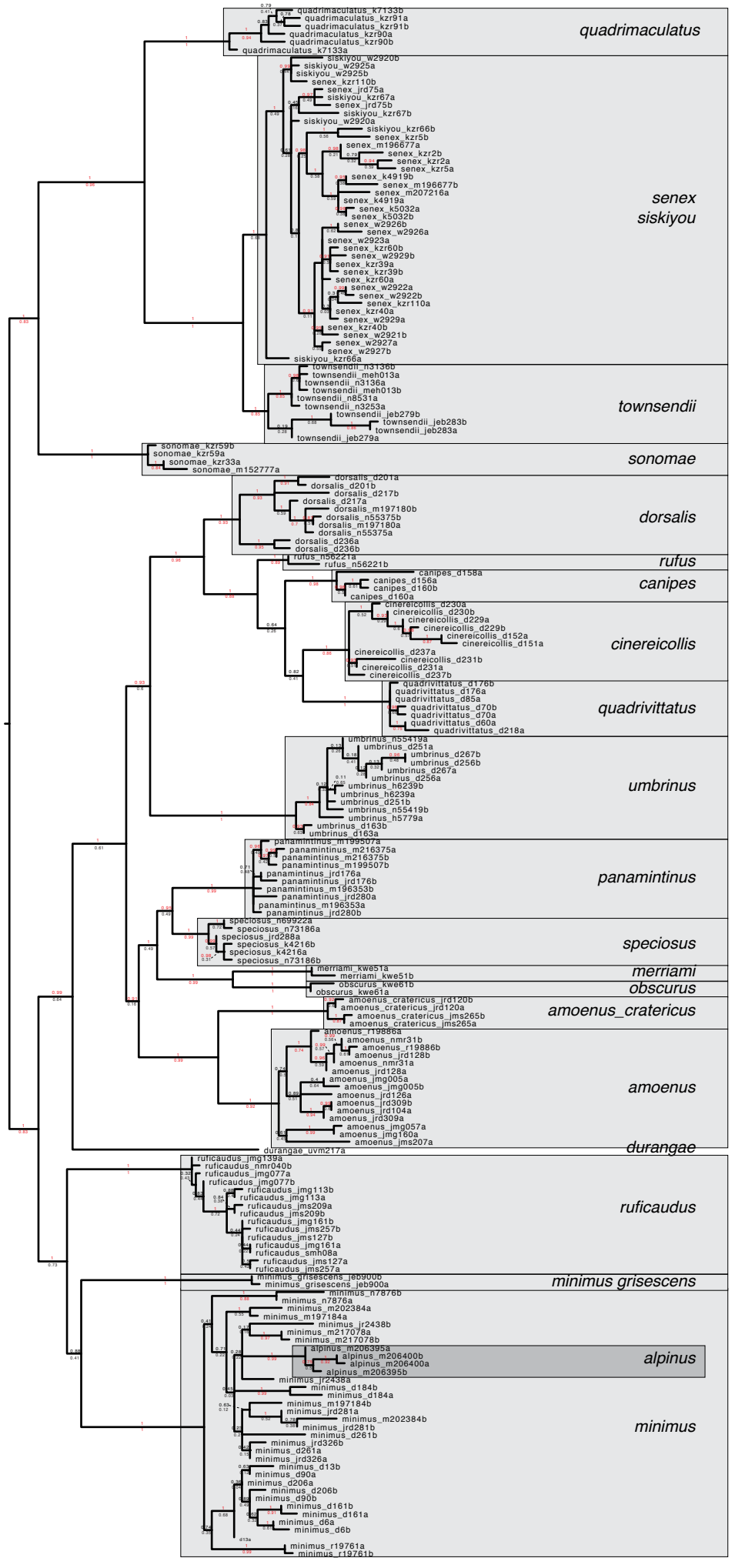
Figure S6. Maximum clade credibility tree from a *BEAST run with all four nuclear loci.
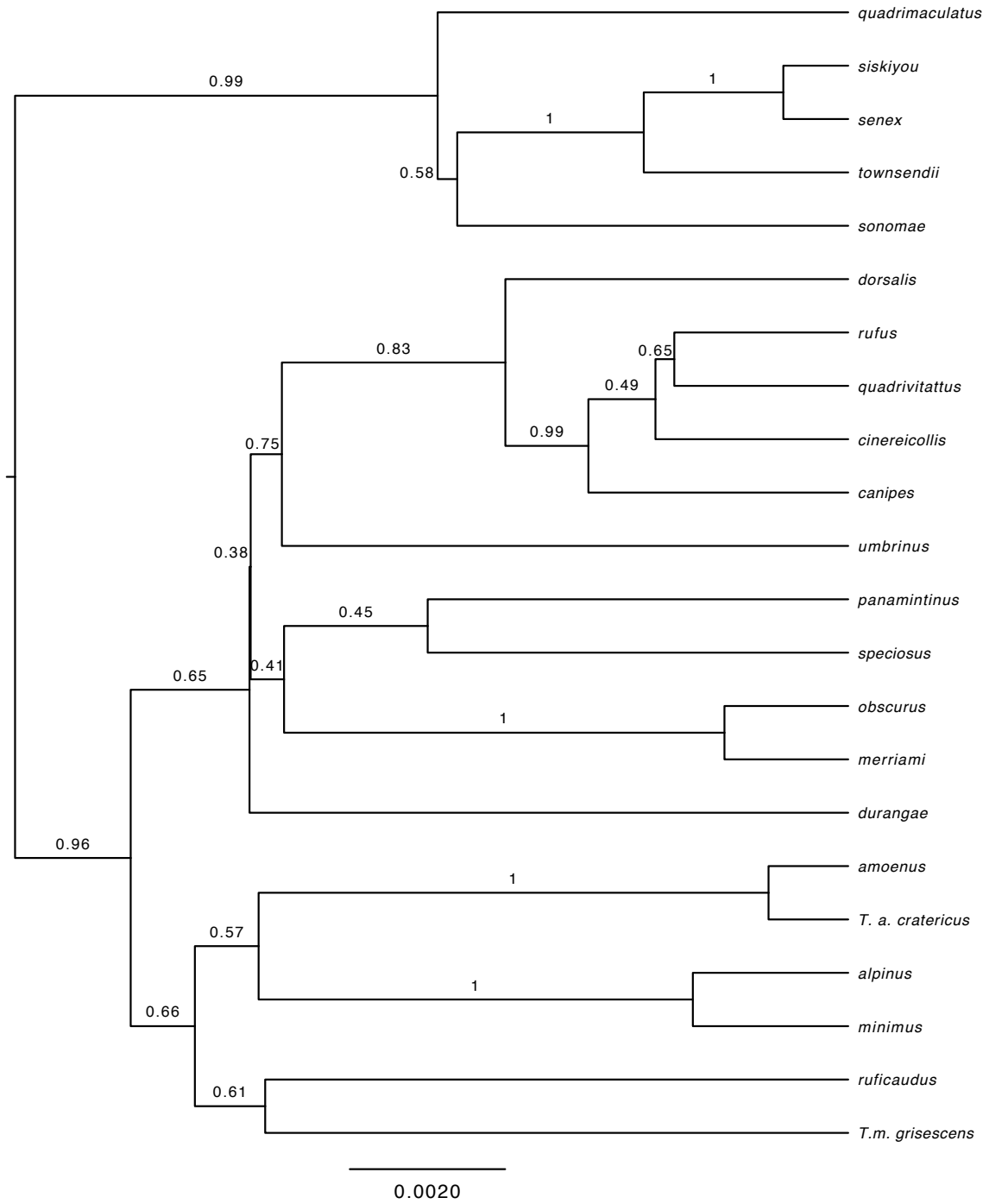
Figure S7. Maximum clade credibility tree from *BEAST including mitochondrial Cytochrome *b* as well as the four nuclear loci. Numbers on branches are nodal posterior probabilities.

9.0E−4