

Fig. S1 Primer map for new (*KEA1* introns 11 and 17, *TEB* exon 17) and redesigned (*ETS*, *matK*) molecular markers.

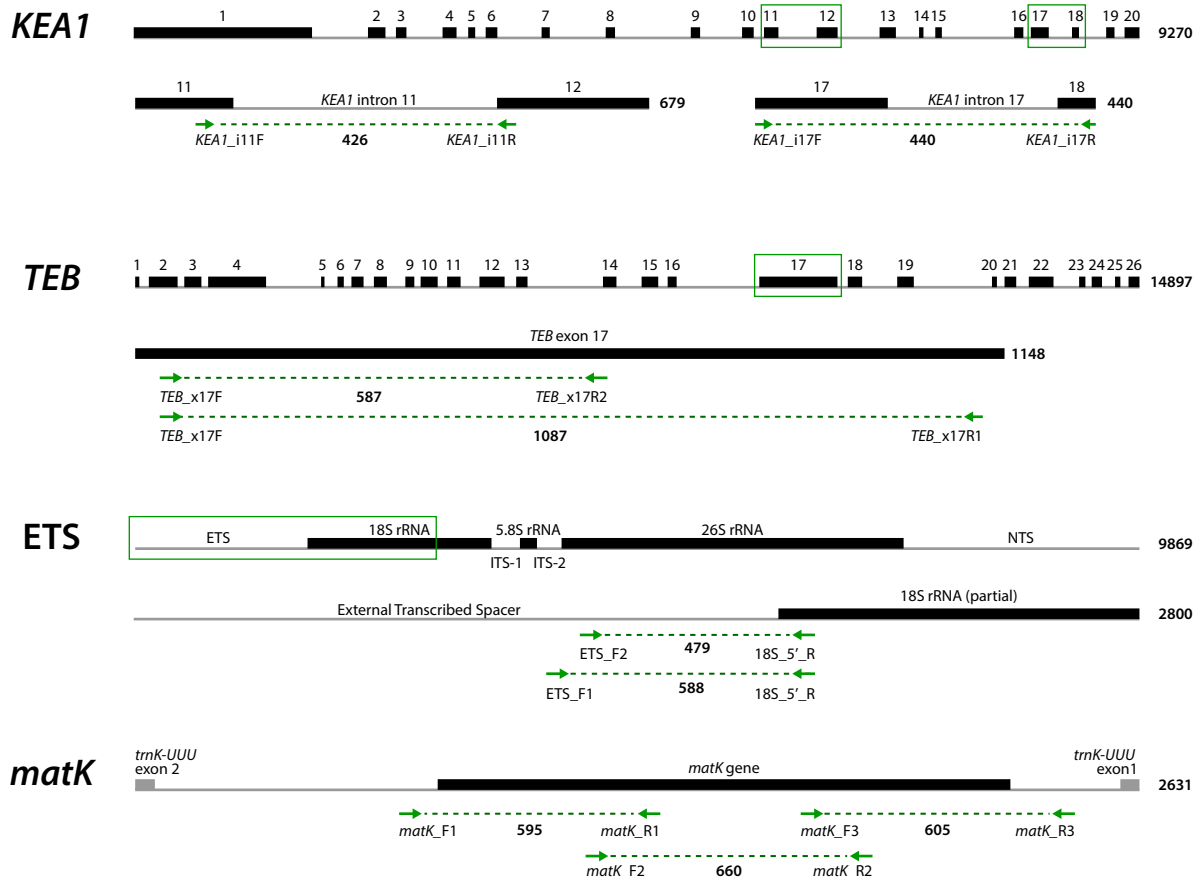


Fig. S2 a
nrDNA ETS

HKY+G

500 ML Bootstrap Replicates

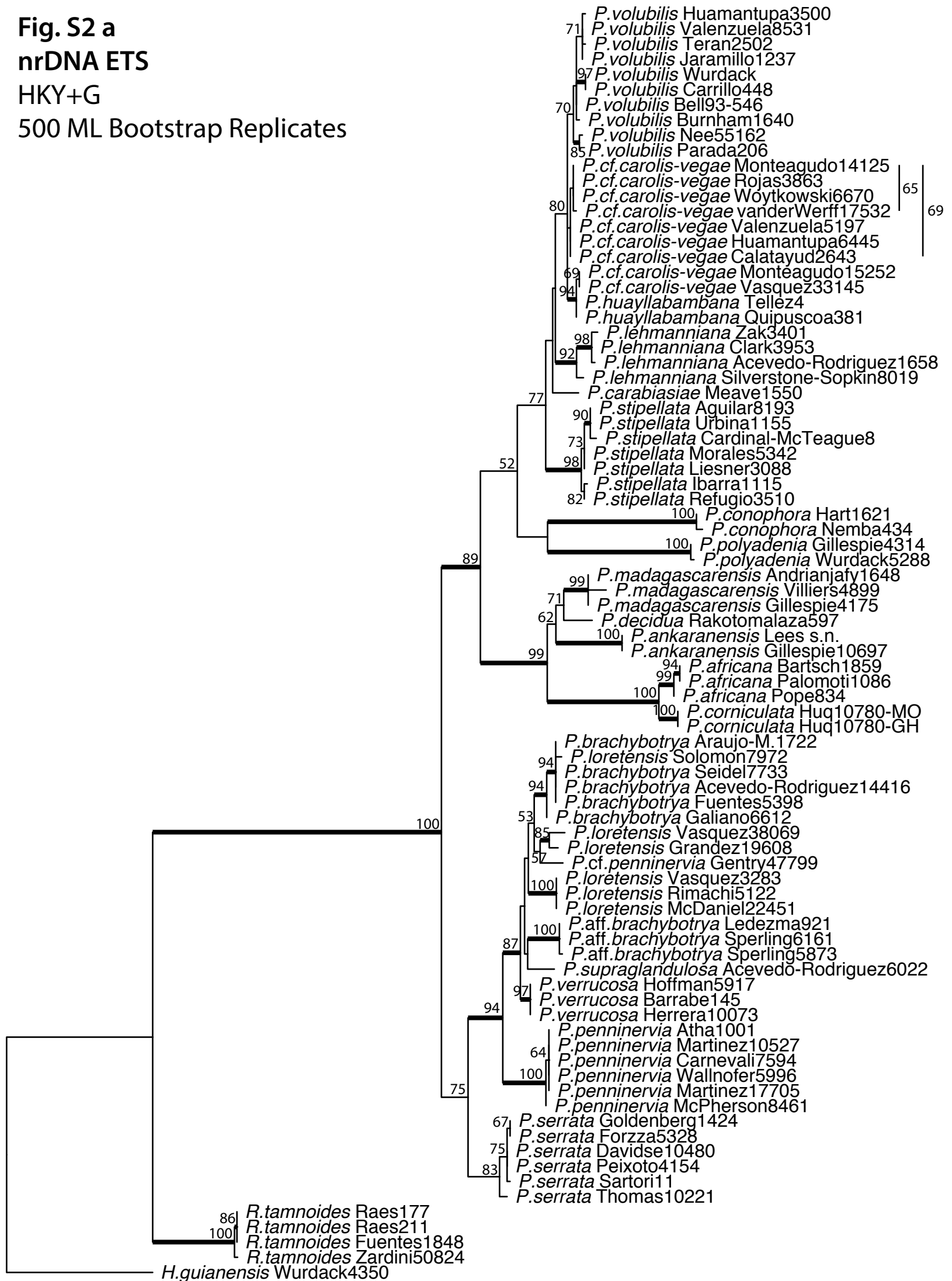


Fig. S2 b
nrDNA ITS

GTR+I+G

500 ML Bootstrap Replicates

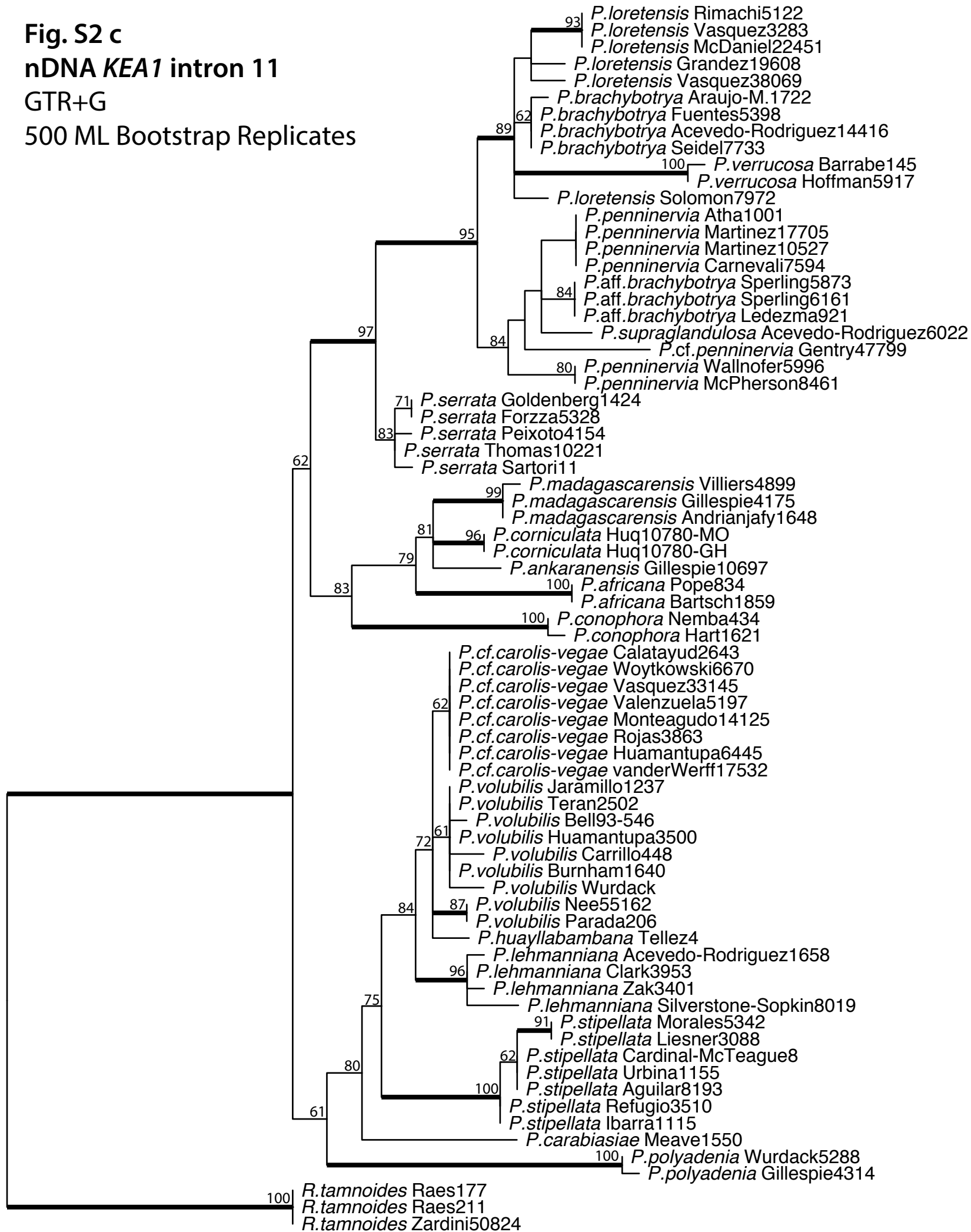


Fig. S2 c

nDNA KEA1 intron 11

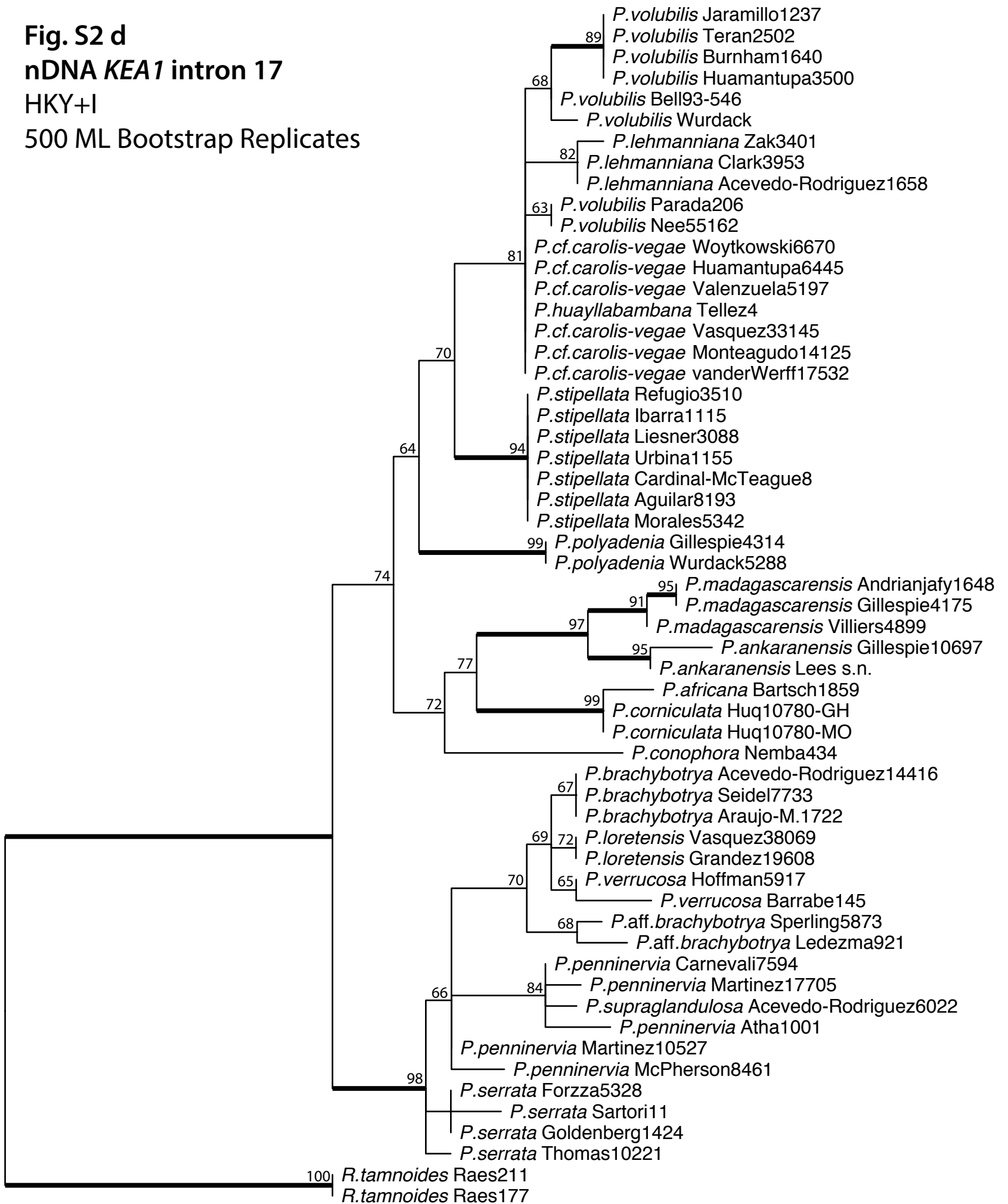
GTR+G

500 ML Bootstrap Replicates



0.02

Fig. S2 d
nDNA KEA1 intron 17
 HKY+I
 500 ML Bootstrap Replicates



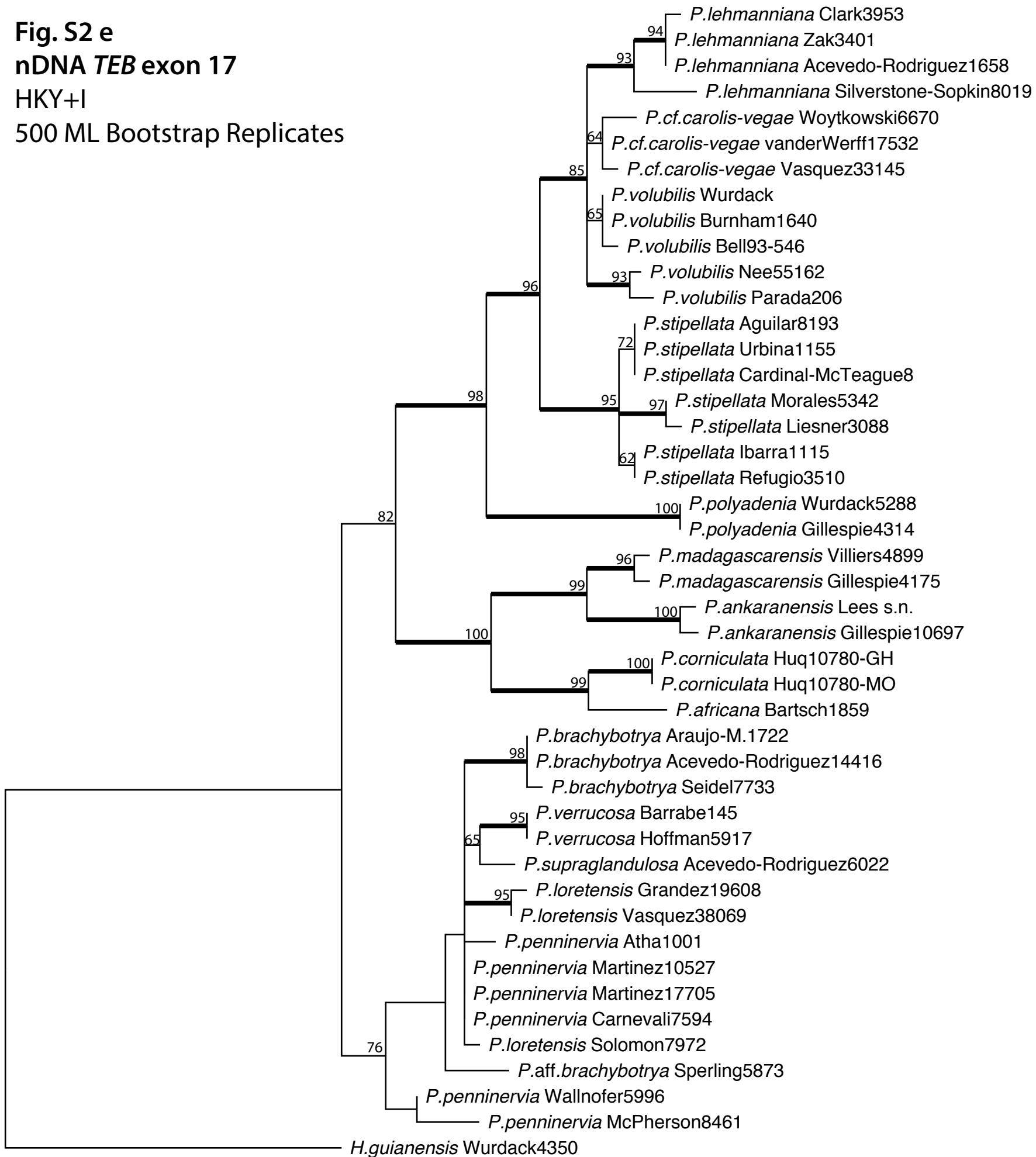
0.01

Fig. S2 e

nDNA *TEB* exon 17

HKY+I

500 ML Bootstrap Replicates



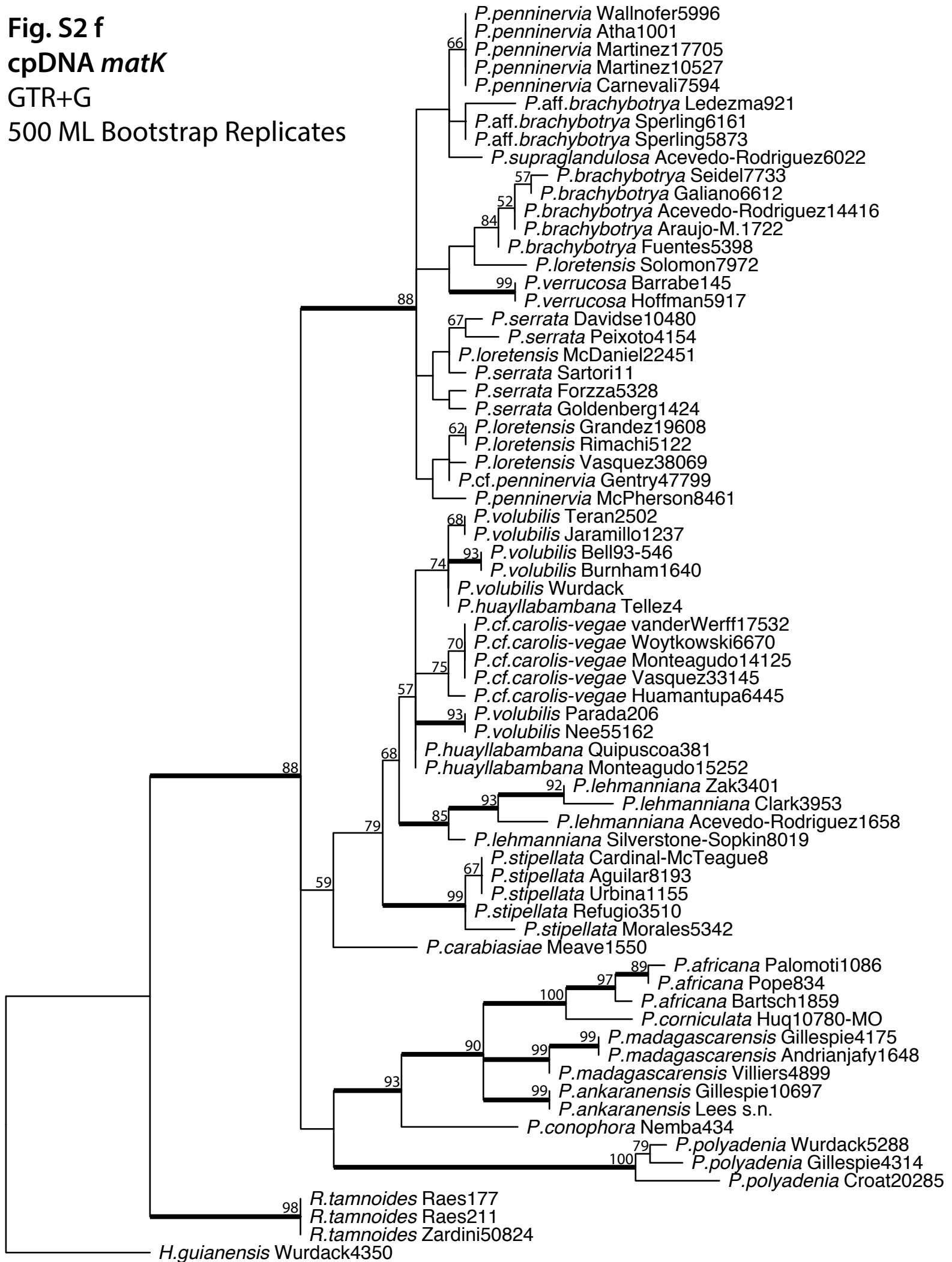
0.0080

Fig. S2 f

cpDNA *matK*

GTR+G

500 ML Bootstrap Replicates

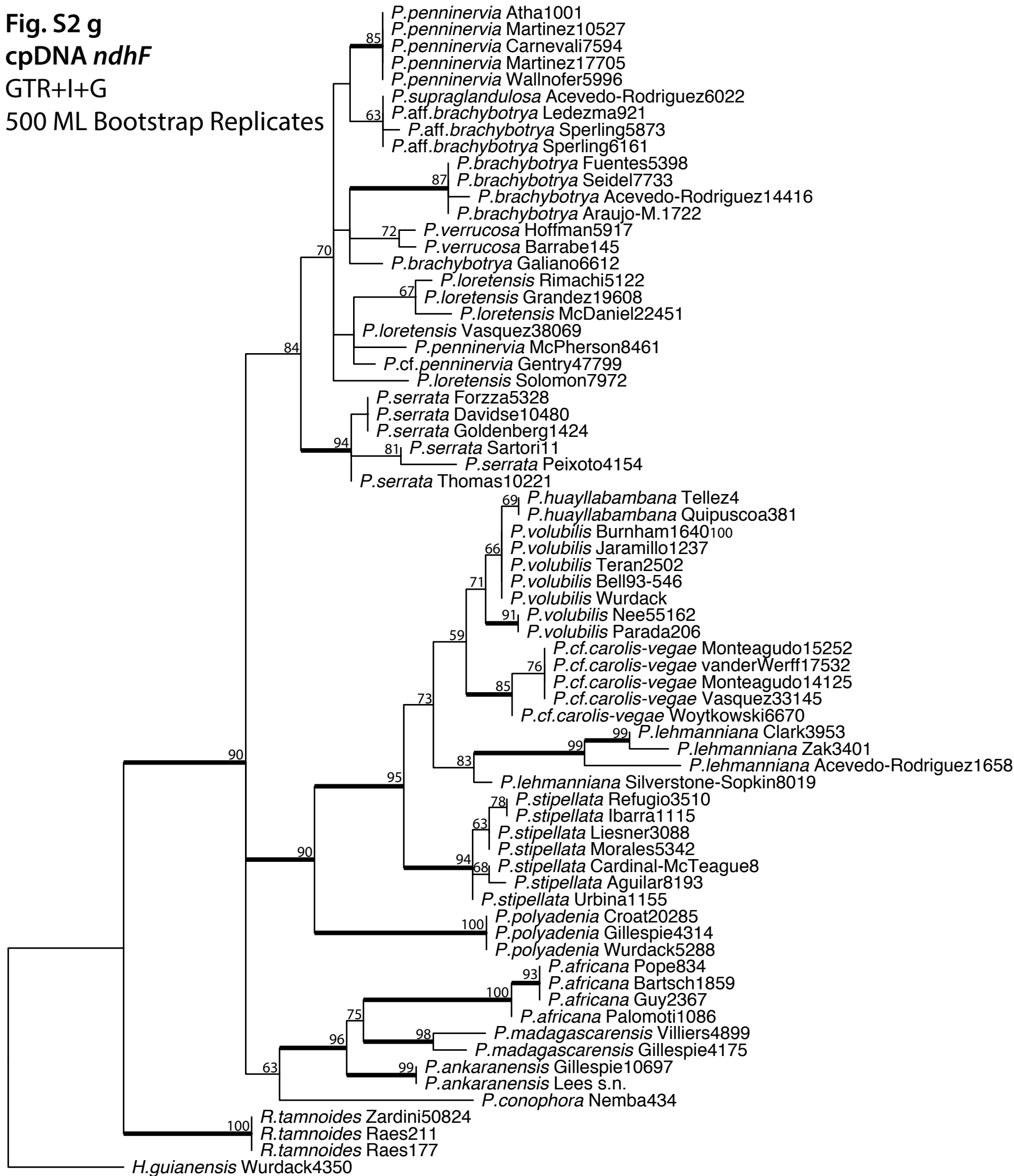


0.0030

Fig. S2 g
cpDNA *ndhF*

GTR+I+G

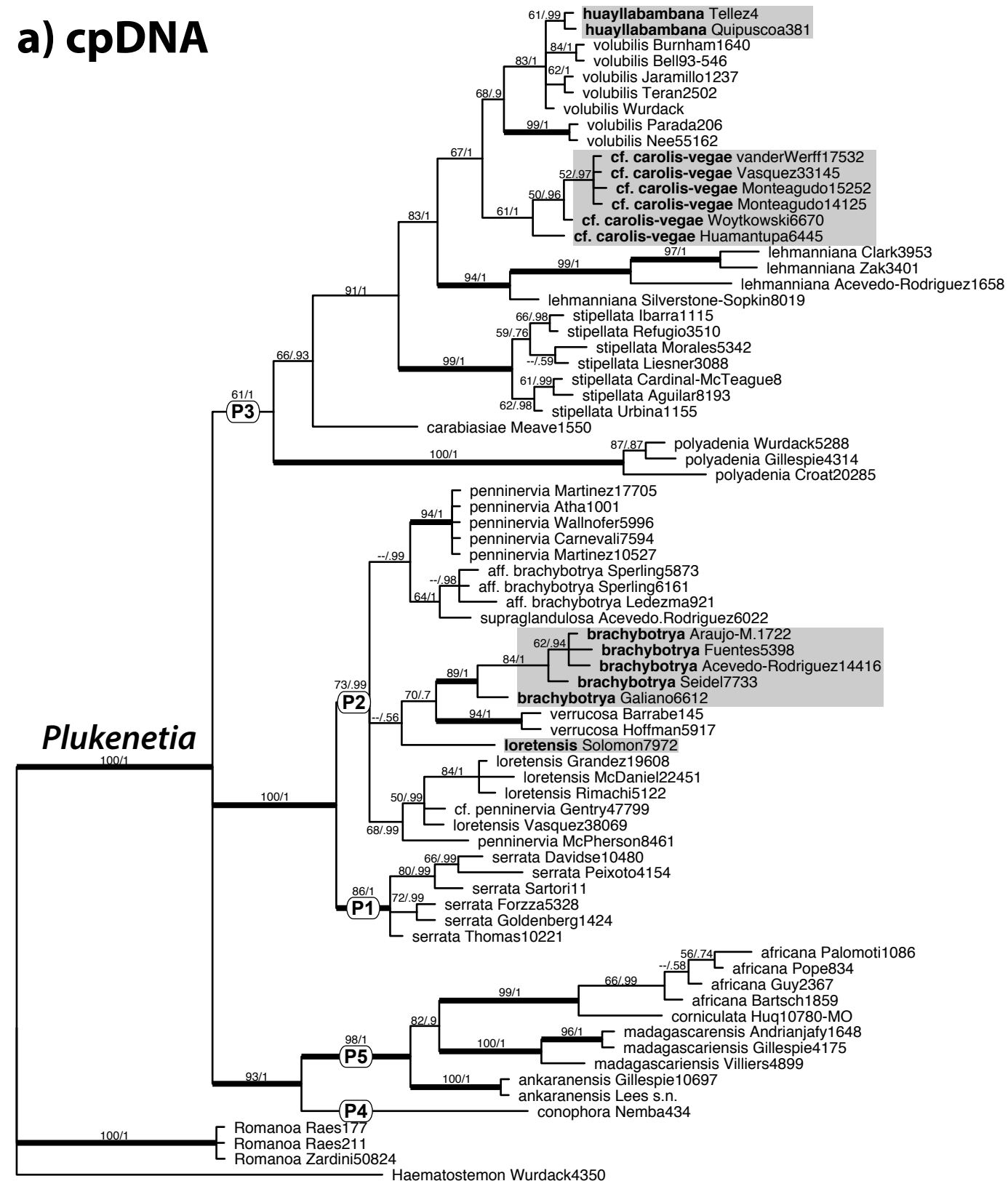
500 ML Bootstrap Replicates



0.0050

Fig. S3 Bayesian maximum clade credibility tree based on (a) plastid DNA (cpDNA) two marker, 74 accession dataset, and (b) nuclear DNA (nDNA) five marker, 86 accession dataset, for *Plukenetia* and Plukenetiinae outgroups. Maximum parsimony bootstrap percentage (MPBP) and Bayesian posterior probability (PP) support values > 50% are indicated on each branch. Branches in bold indicate strong support (≥ 85 MPBP and ≥ 0.95 PP). Grey boxes highlight strongly supported topological incongruences.

a) cpDNA



b) nDNA

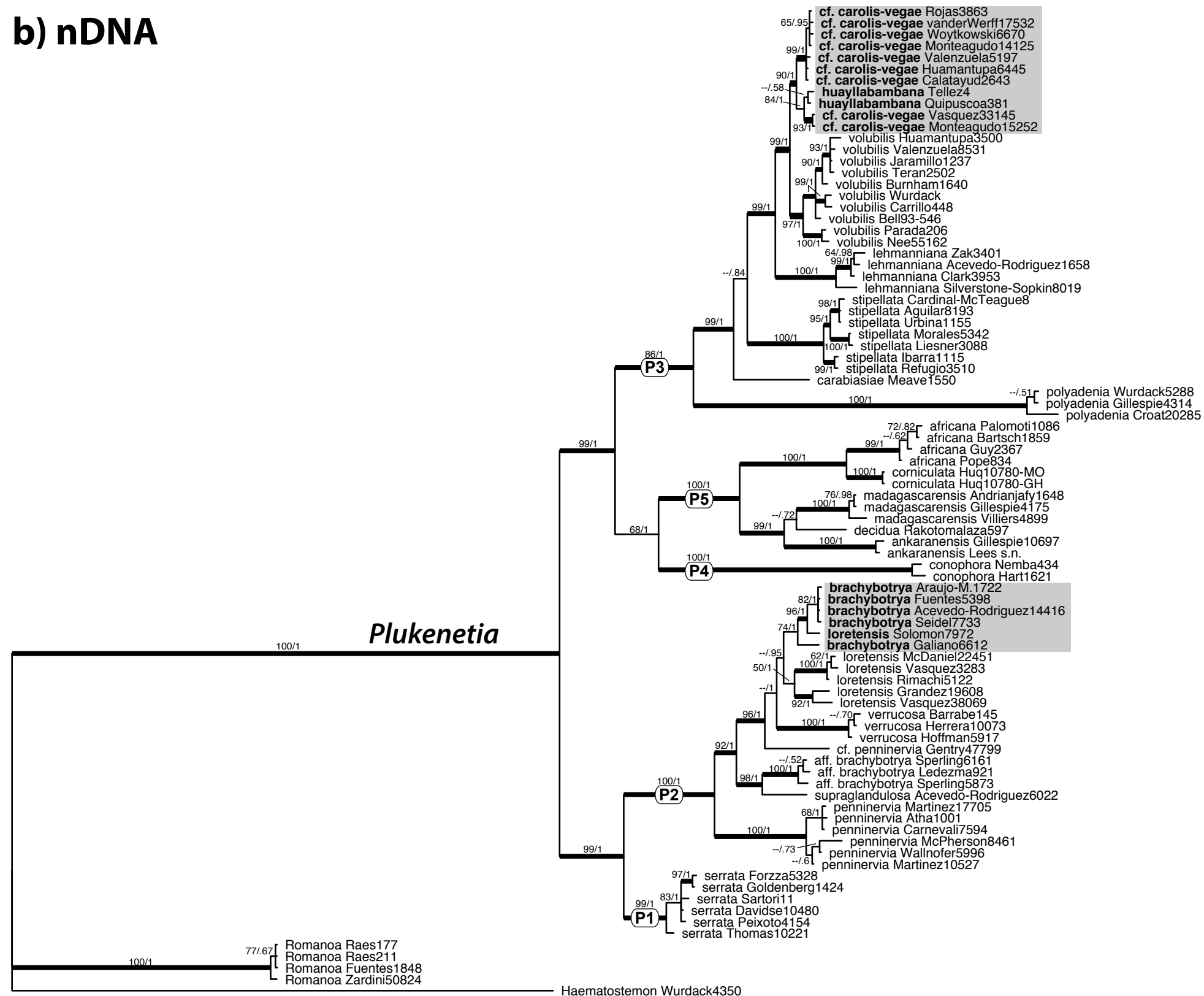


Fig. S4 BEAST chronogram of *Plukenetia* and Plukenetiinae outgroups inferred from the combined seven marker (cpDNA and nDNA), 83 accession dataset and two normal-distribution priors (indicated in red) based on previous subfamily Acalyphoideae estimates using three fossil calibrations. Numbers at each node indicate mean age estimates, and blue bars the 95% highest posterior density confidence interval.

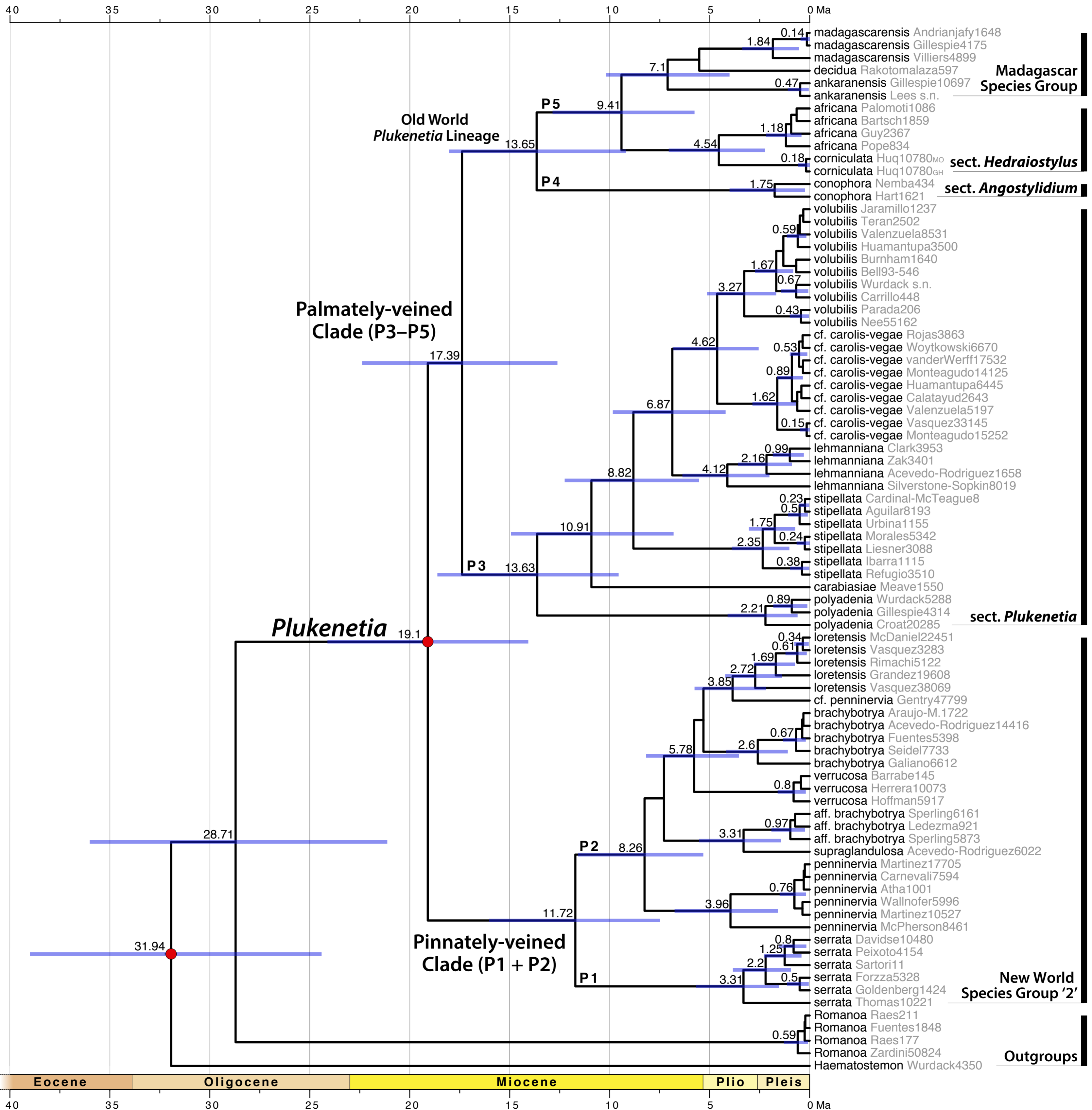


Fig. S5 a BioGeoBEARS DEC+J on *Plukenetia*
 ancstates: global optim, 2 areas max. d=0; e=0; j=0.3997; LnL=-27.26

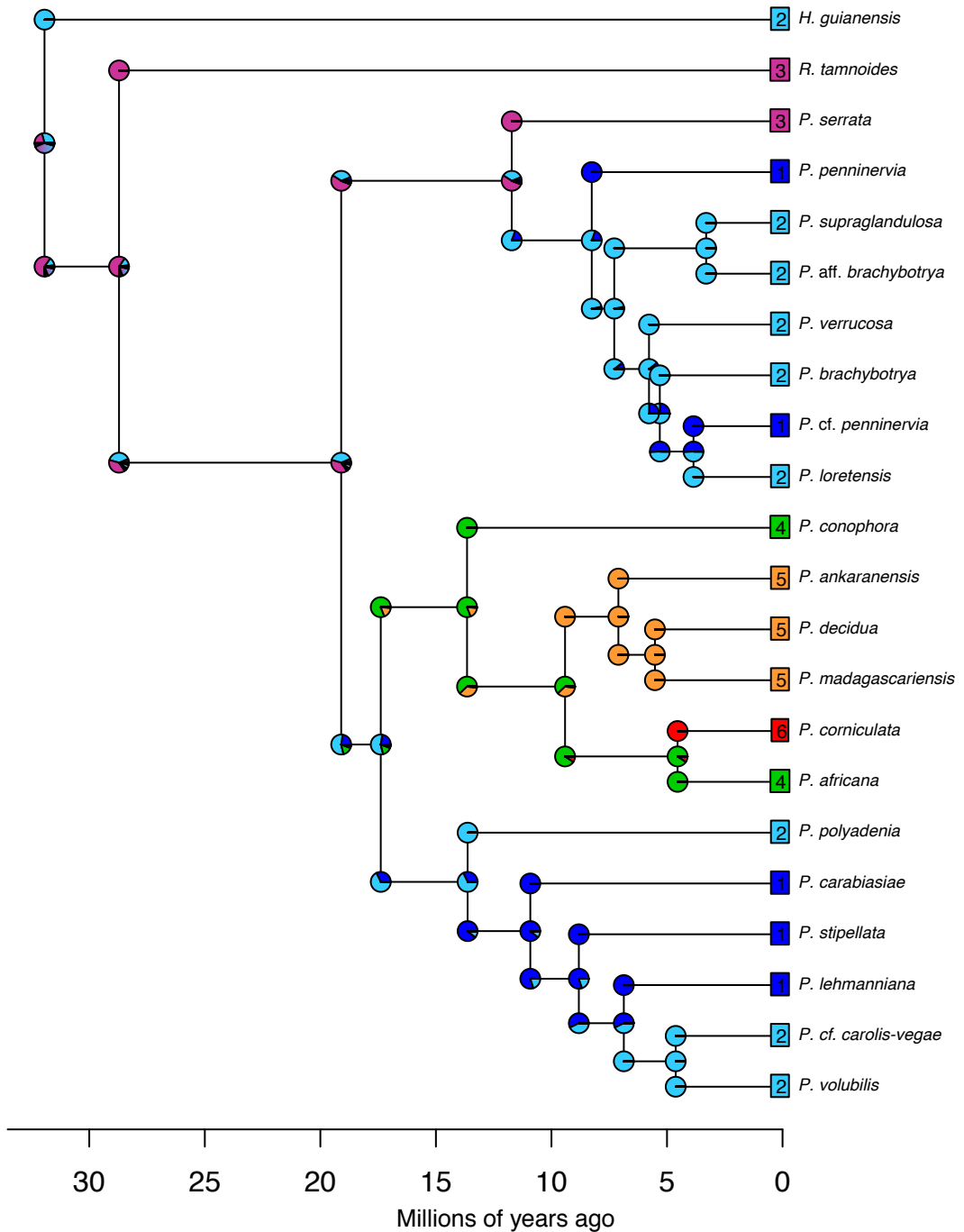


Fig. S5 b BioGeoBEARS DEC on *Plukenetia*
 ancstates: global optim, 2 areas max. d=0.034; e=0.0163; j=0; LnL=-46.67

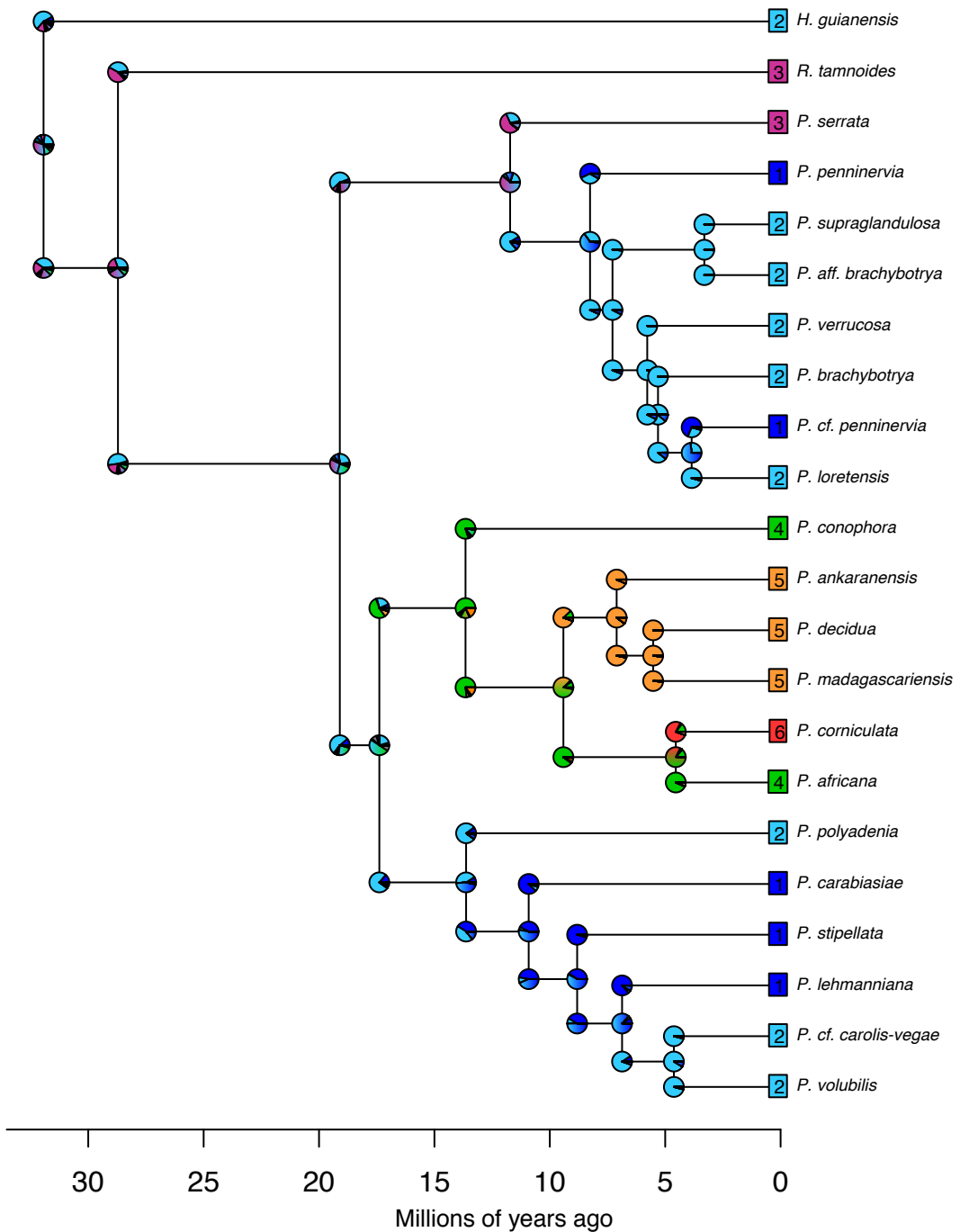


Fig. S6 UPGMA clustering analysis of log10 transformed seed dimensions (length, width, thickness) for 190 accessions of *Plukenetia*.

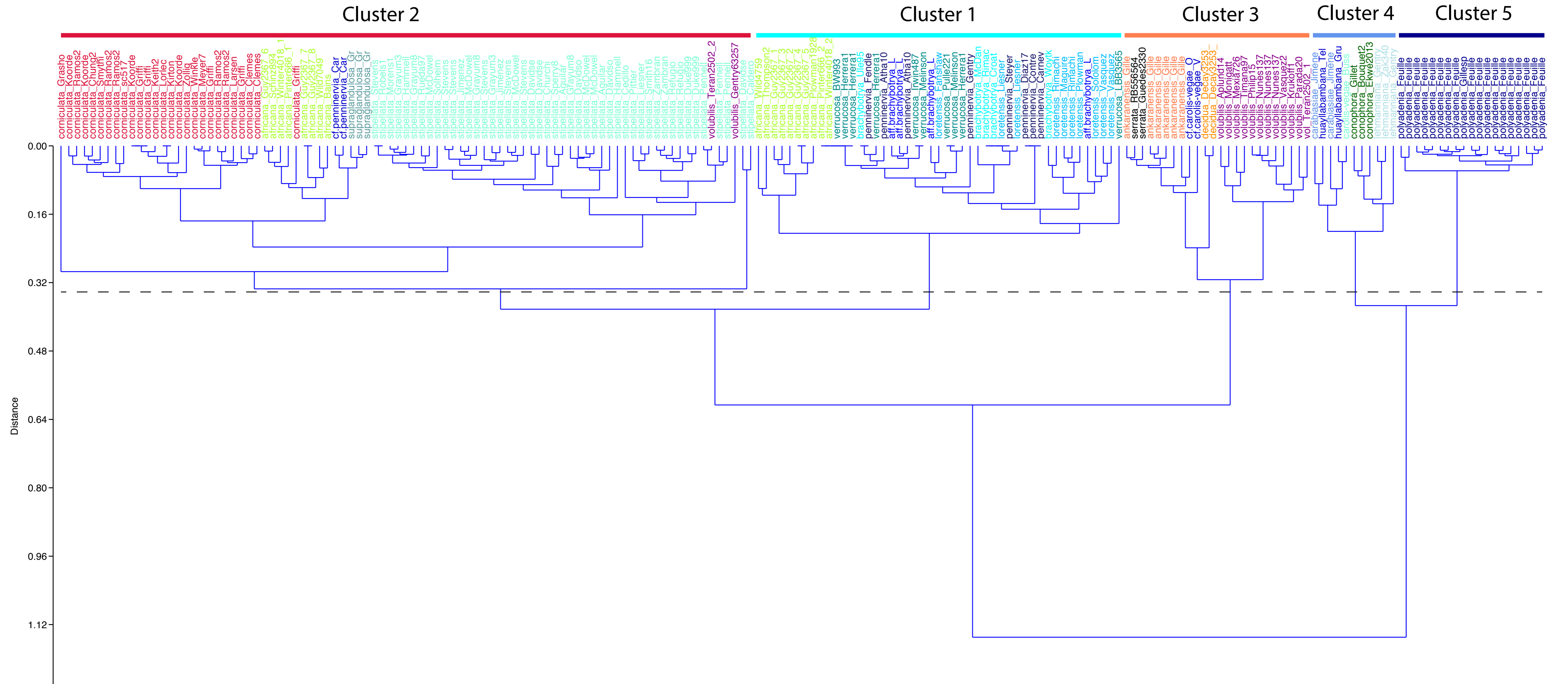


Fig. S7 Principal components analysis of log10 transformed seed dimensions (length, width, thickness) for 190 accessions of *Plukenetia*.

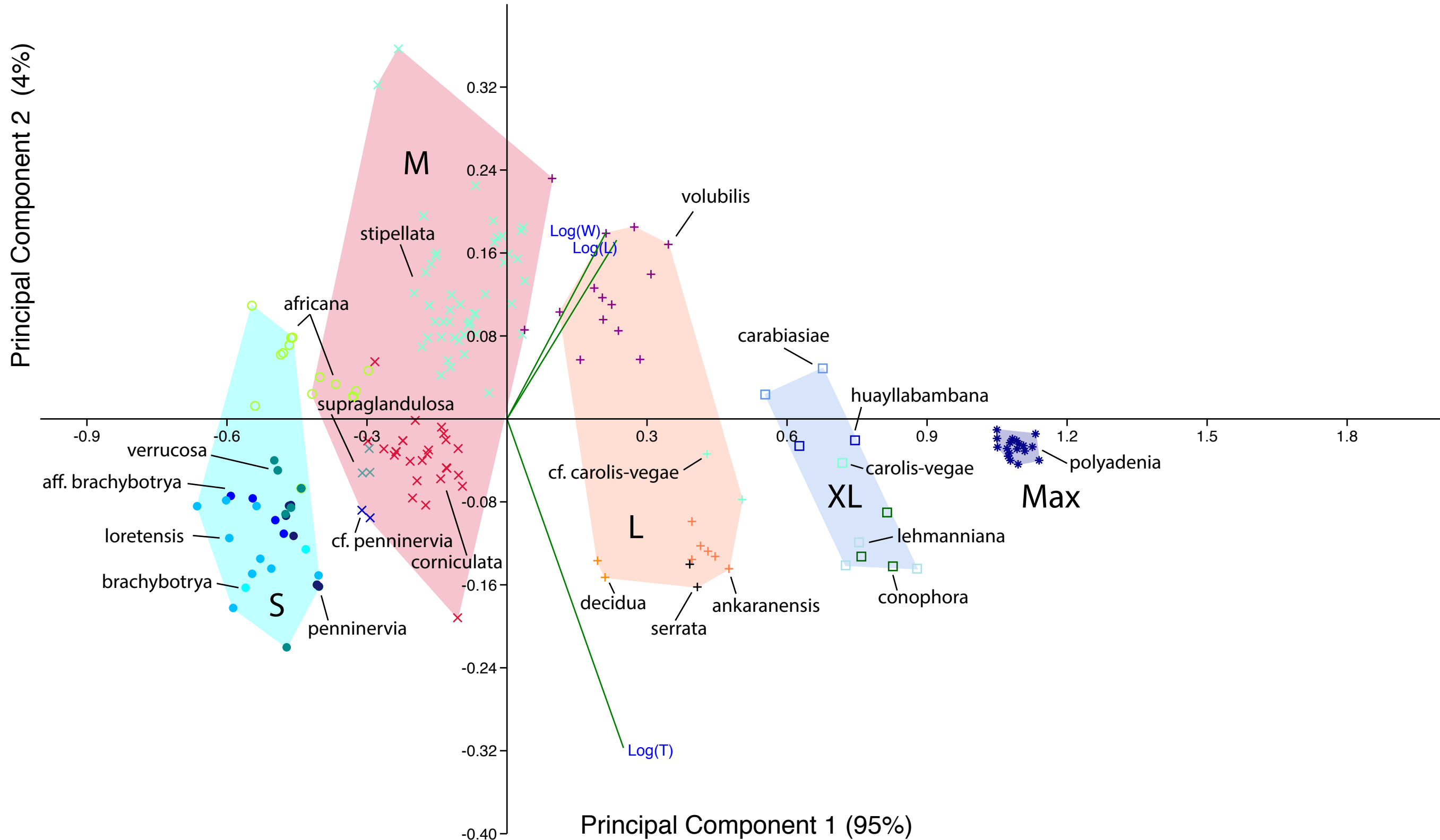


Fig. S8 Posterior distributions of the correlation coefficients (r) between the liabilities of seed size and (a) plant size, (b) fruit type, (c) seedling ecology, (d) fire tolerance, and (e) biome type, under the threshold model.

