

Fig. S1. DensiTree plot of the post-burnin species trees from the StarBEAST2 analyses. Posterior probabilities are shown at each node.

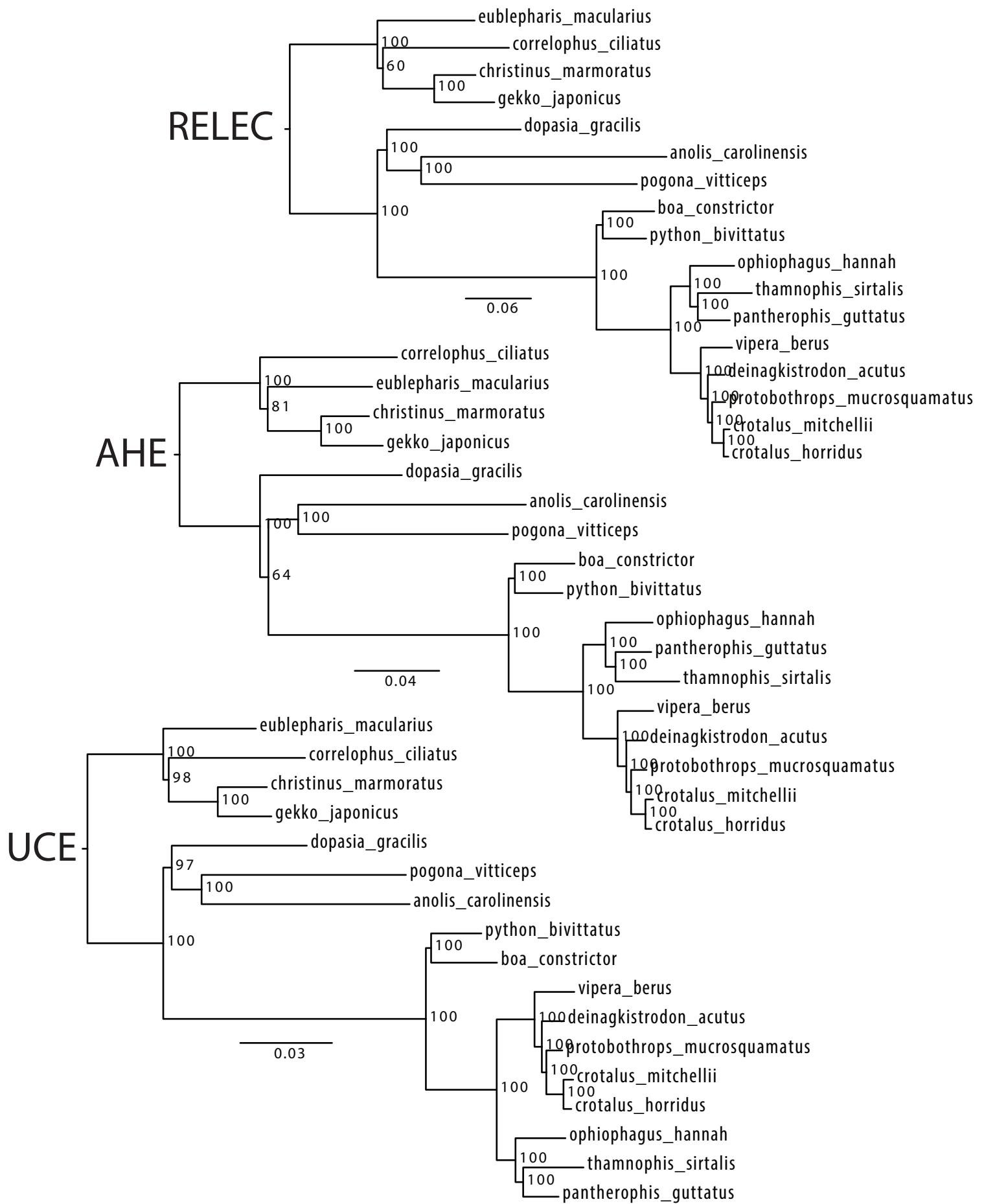
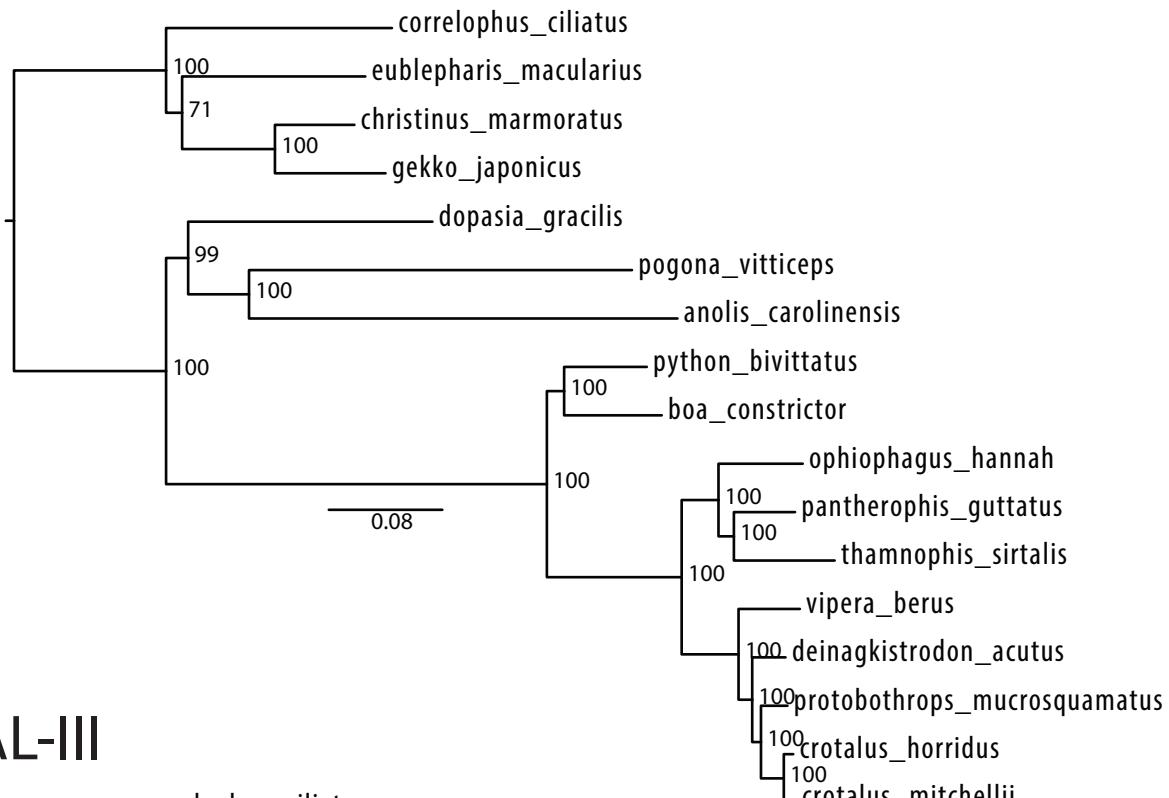


Fig. S2. Concatenated and ASTRAL species tree of RELEC translated amino acid dataset.

RAxML Concatenated - partitioned by locus



ASTRAL-III

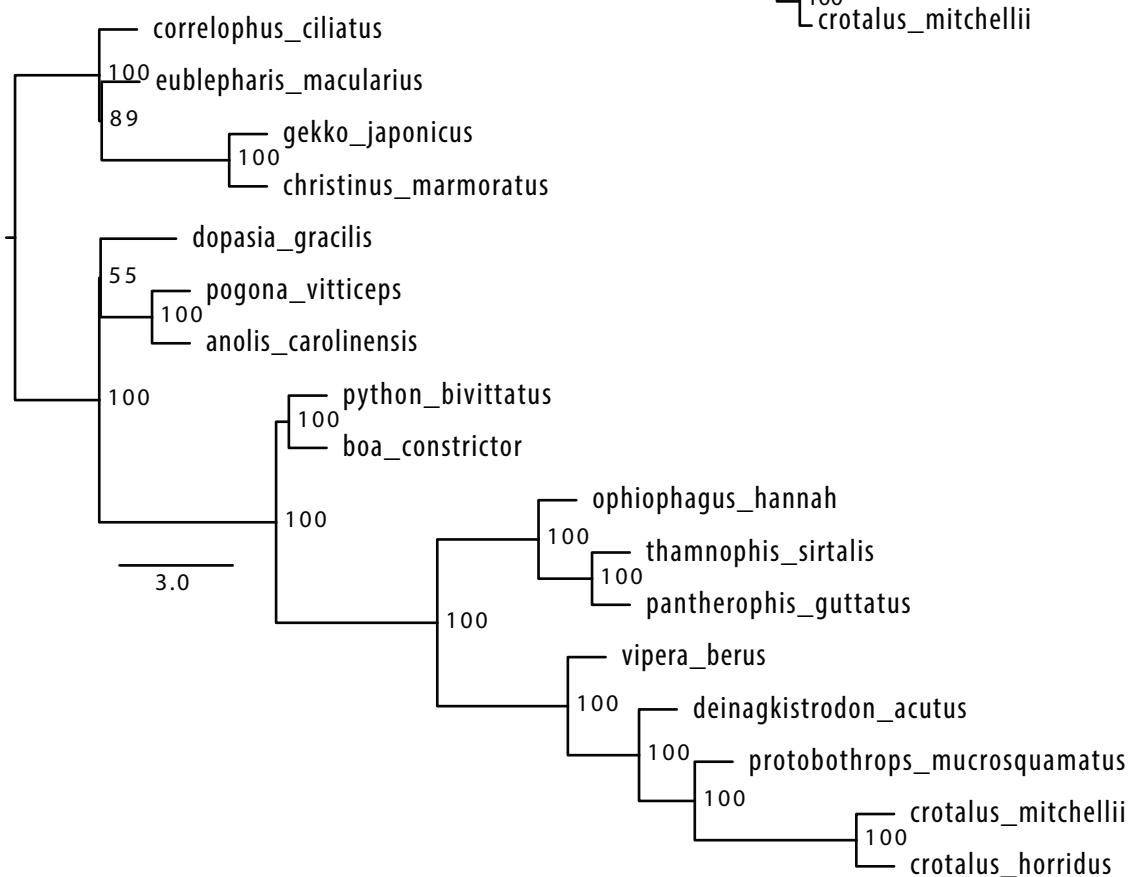


Fig. S3. Concatenated and ASTRAL species tree of RELEC translated amino acid dataset.

Separate File

Fig. S4. Saturation Plots of all loci. Divergence time (Ma) is the x-axis, and raw pairwise distance is the y-axis.

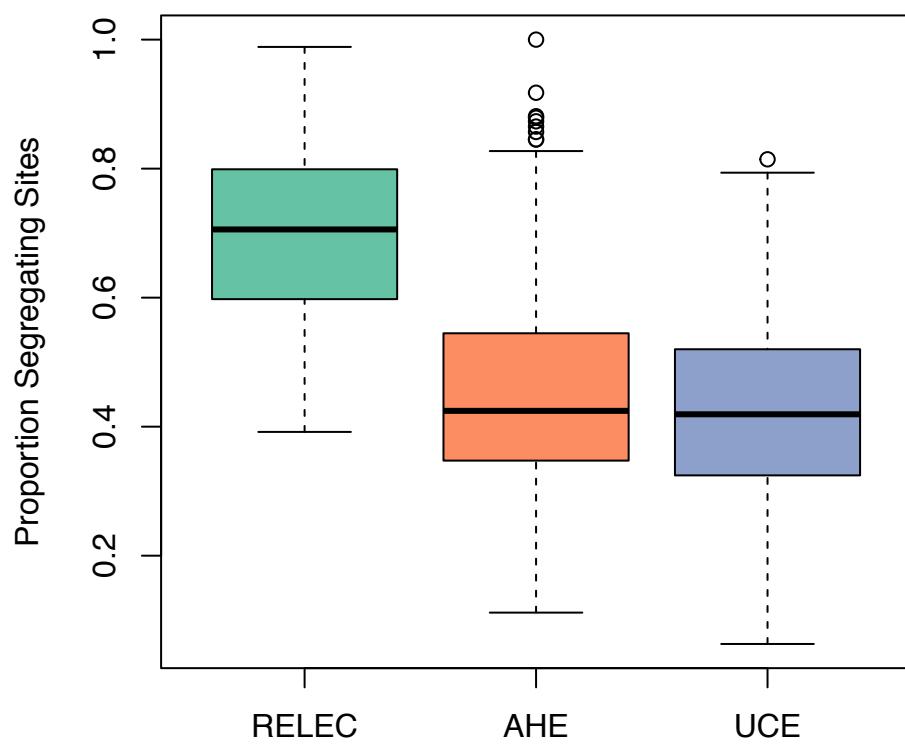


Fig. S5. Proportion of segregating sites within RELEC, AHE, and UCE alignments.

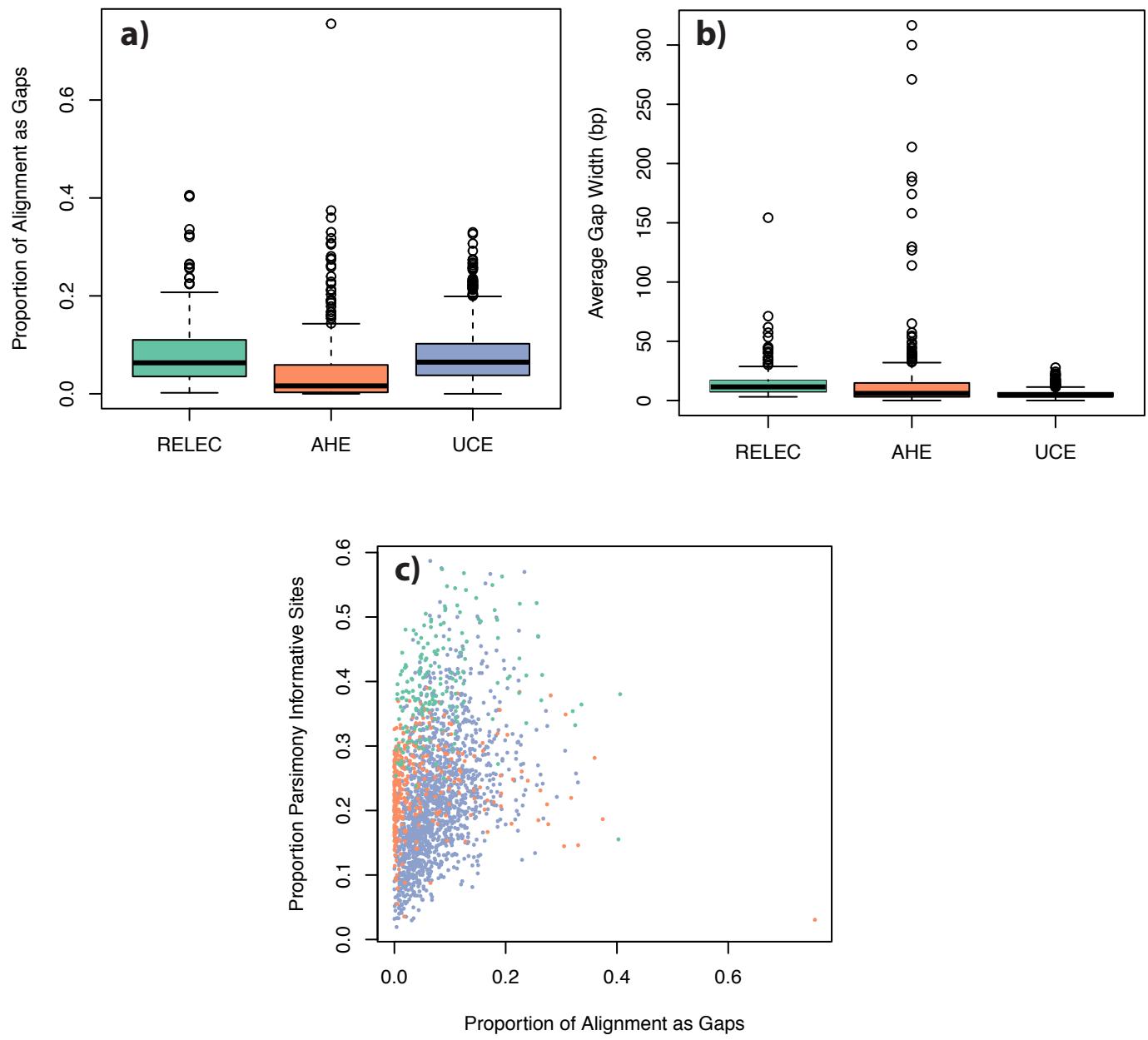


Fig. S6. Comparison of RELEC, AHE and UCE alignments for: a) the proportion of the alignment as gaps; b) the average gap width within locus alignments; and c) the relationship between the proportion of gaps and the proportion of parsimony informative sites in each alignment. RELEC loci show more PIS relative to the proportion of gaps, suggesting that they may provide more information content with less alignment issues. Color coding of (c) matches boxplots.

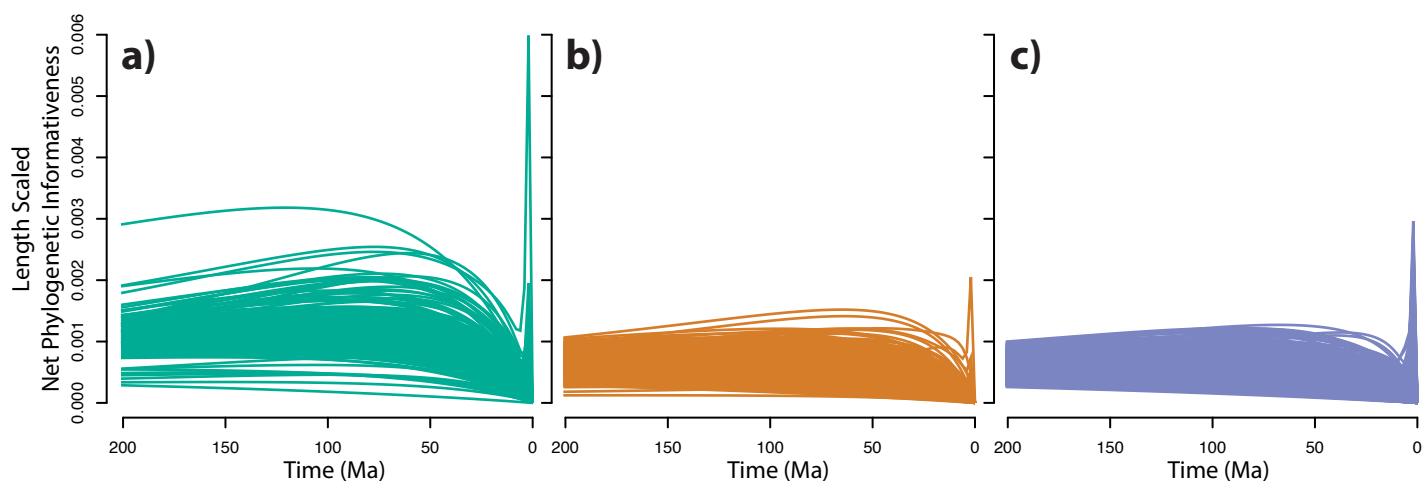


Fig. S7. Phylogenetic informativeness for (a) RELEC, (b) AHE, and (c) UCE loci, scaled by alignment length.

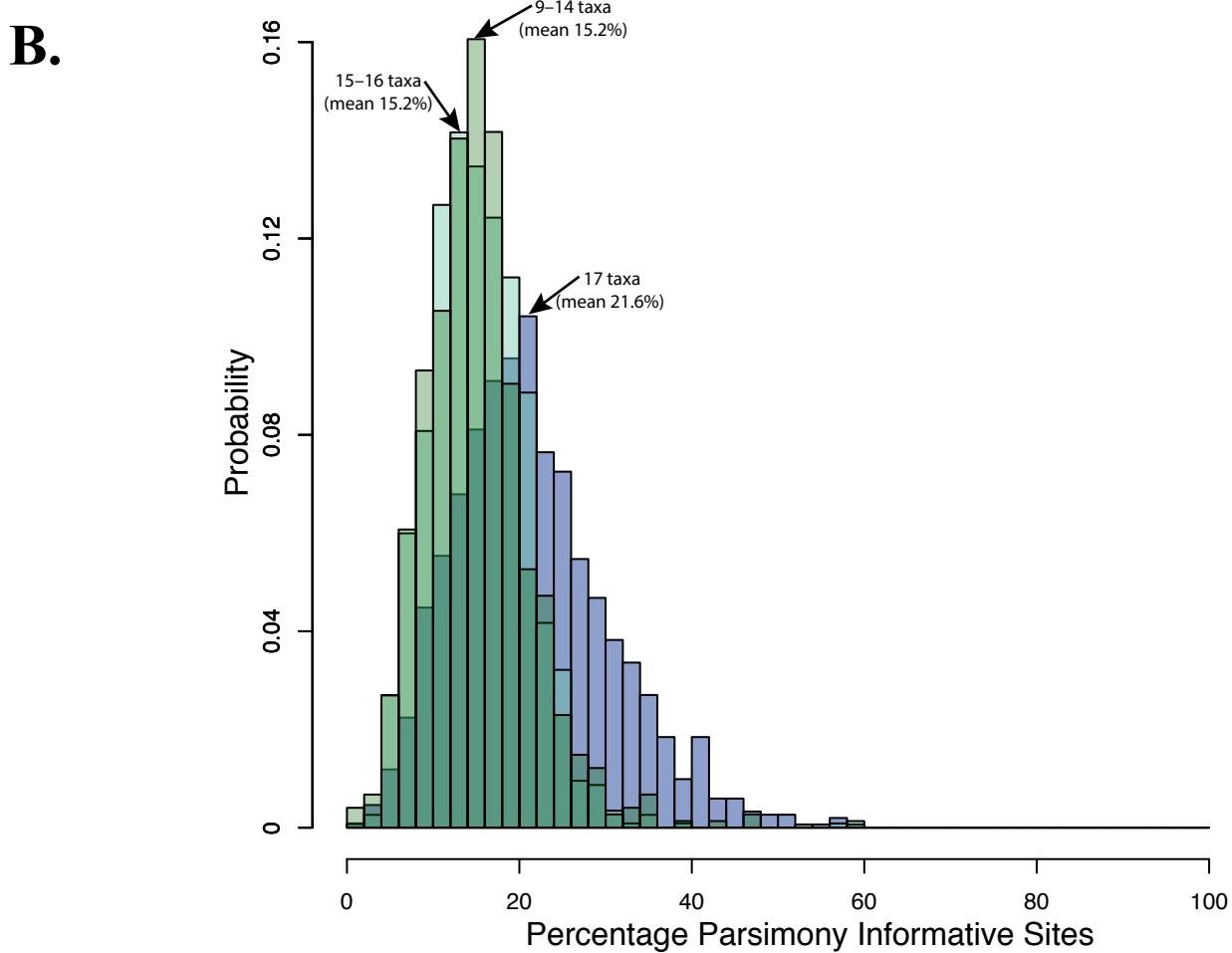
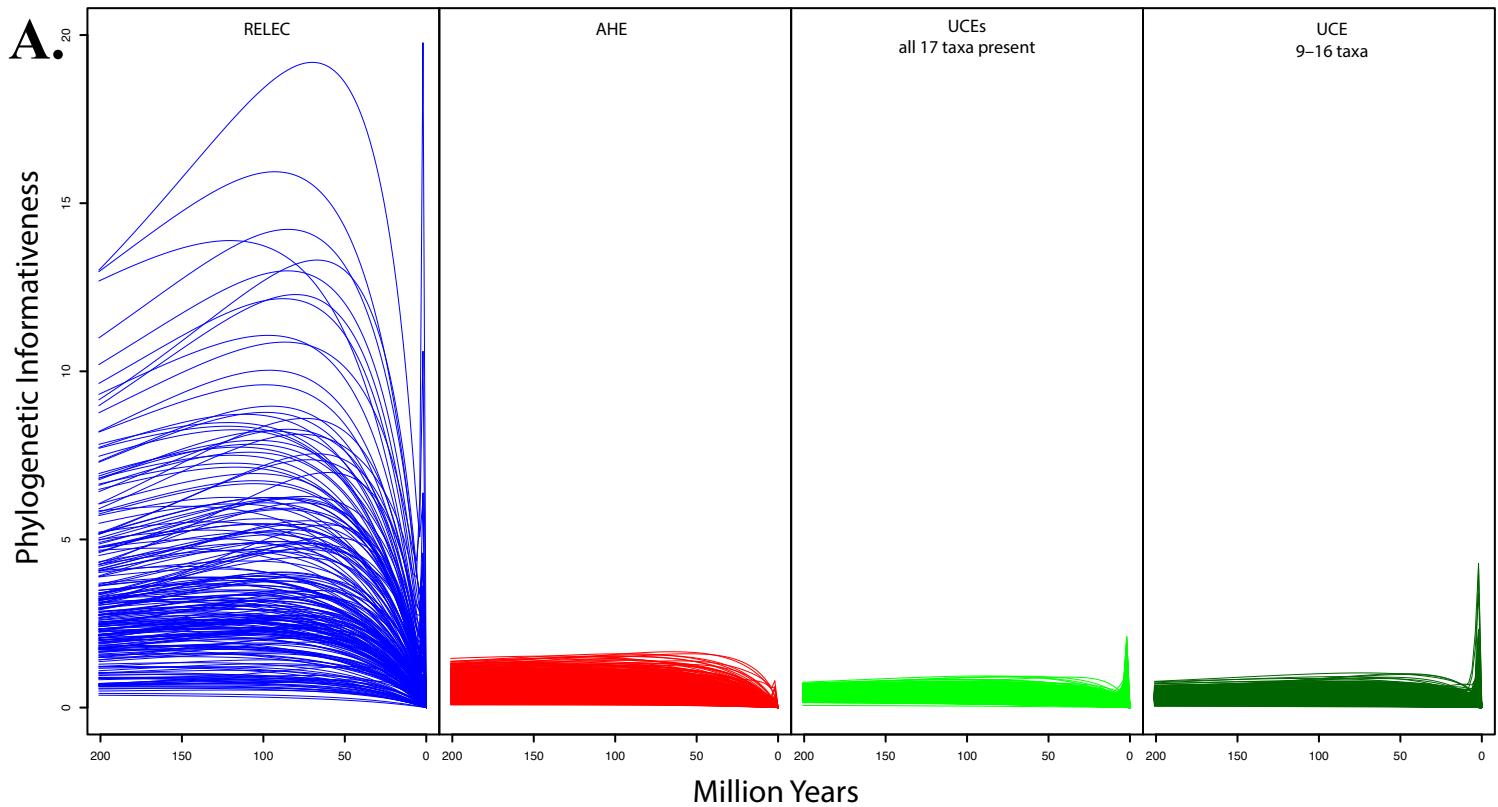


Fig. S8. Comparison of phylogenetic informativeness (A) and the percentage of parsimony informative sites (B) in UCE datasets that are complete with 17 taxa to those with differing amounts of missing data.