Supp Fig.1

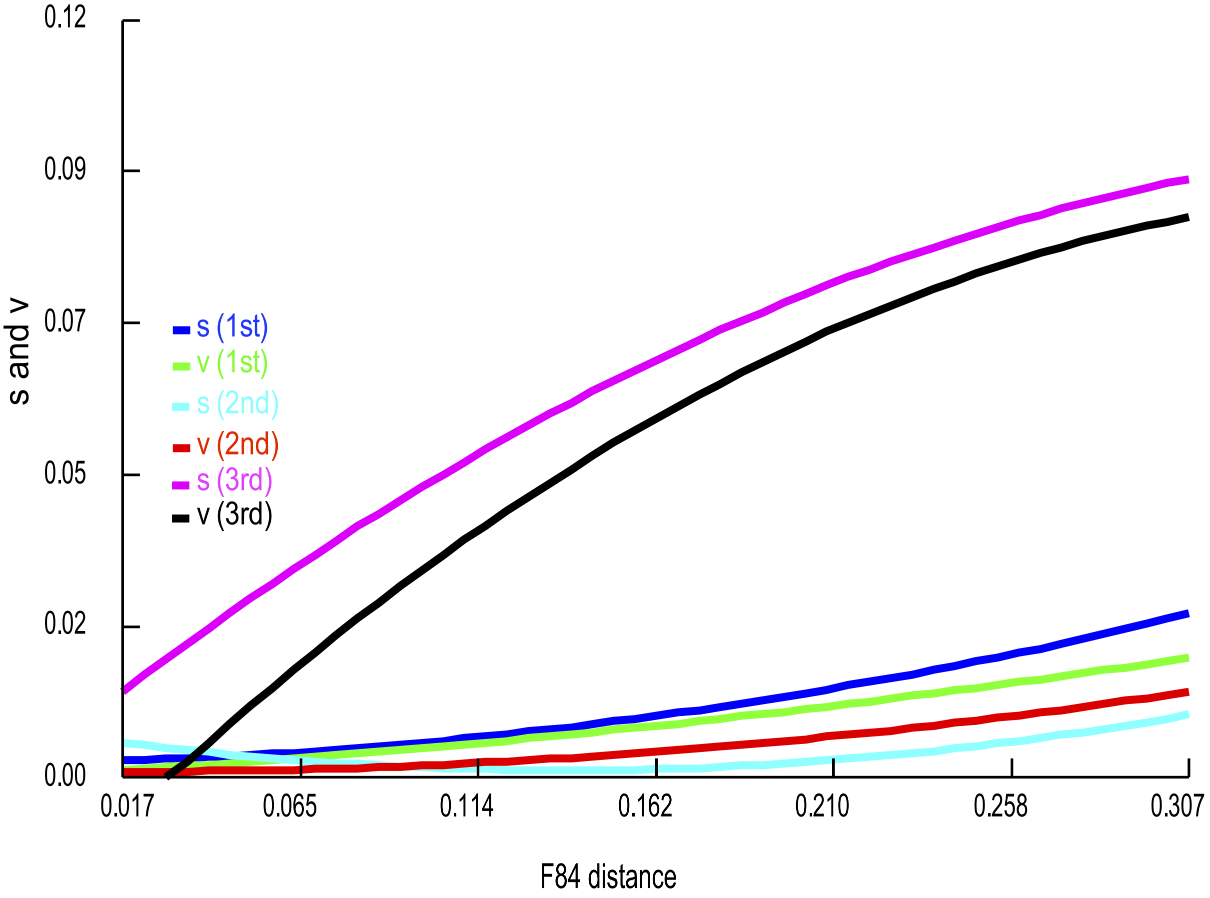

Fig. S1. Saturation plot for each codon position with transversions (v) and transitions (s) plotted against F84 distance.

Supp. Fig. 2

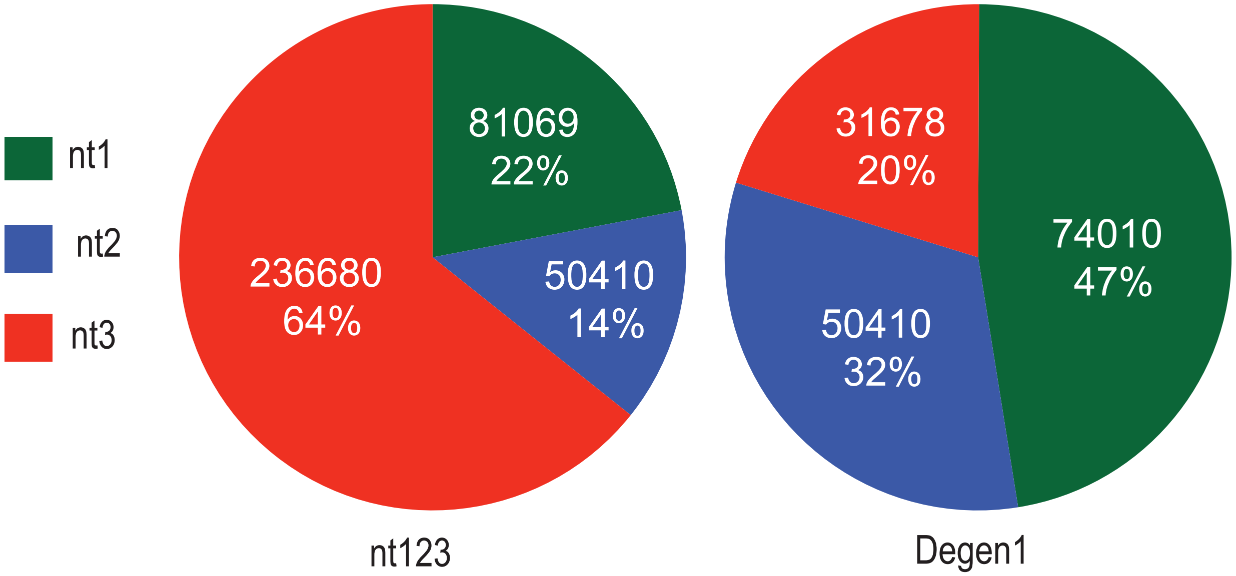

Fig. S2. Pie charts showing the number of variable sites and percent of total variable sites by codon position from nt123 and degen1 matrices.

Supp. Fig. 3

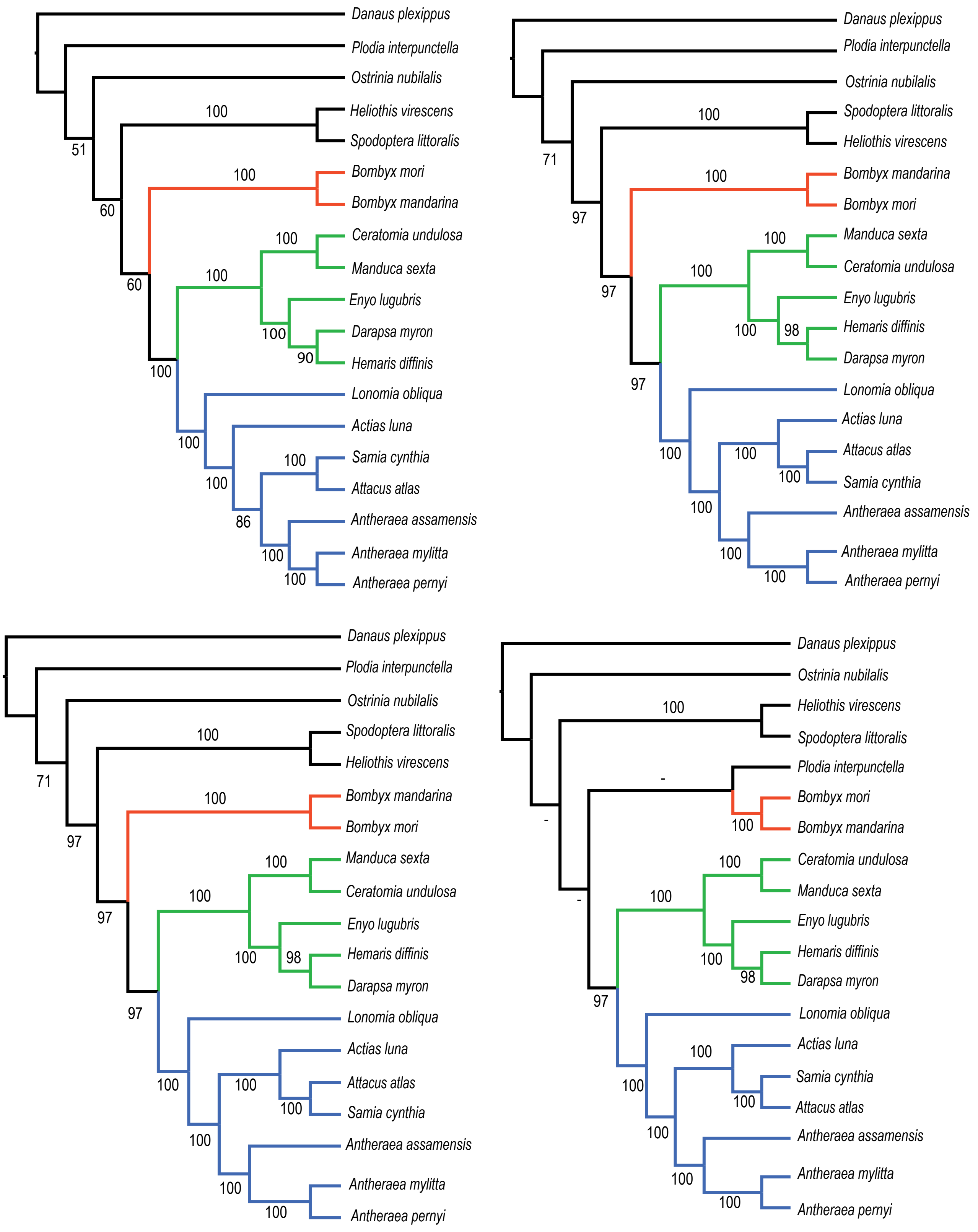

Fig. S3. Phylogenetic trees estimated using parsimony and gene-tree parsimony in TNT and iGTP, respectively. Bootstrap supports from 100 pseudoreplicates are placed on branches leading to each node. A) Most parsimonious tree resulting from nt123; B) Gene tree parsimony, “minimize duplication and losses”; C) Gene tree parsimony, “minimize duplications”; D) Gene tree parsimony, “minimizing deep coalescence”. iGTP trees (B through D) were built from 938 gene trees.

Supp. Fig. 4

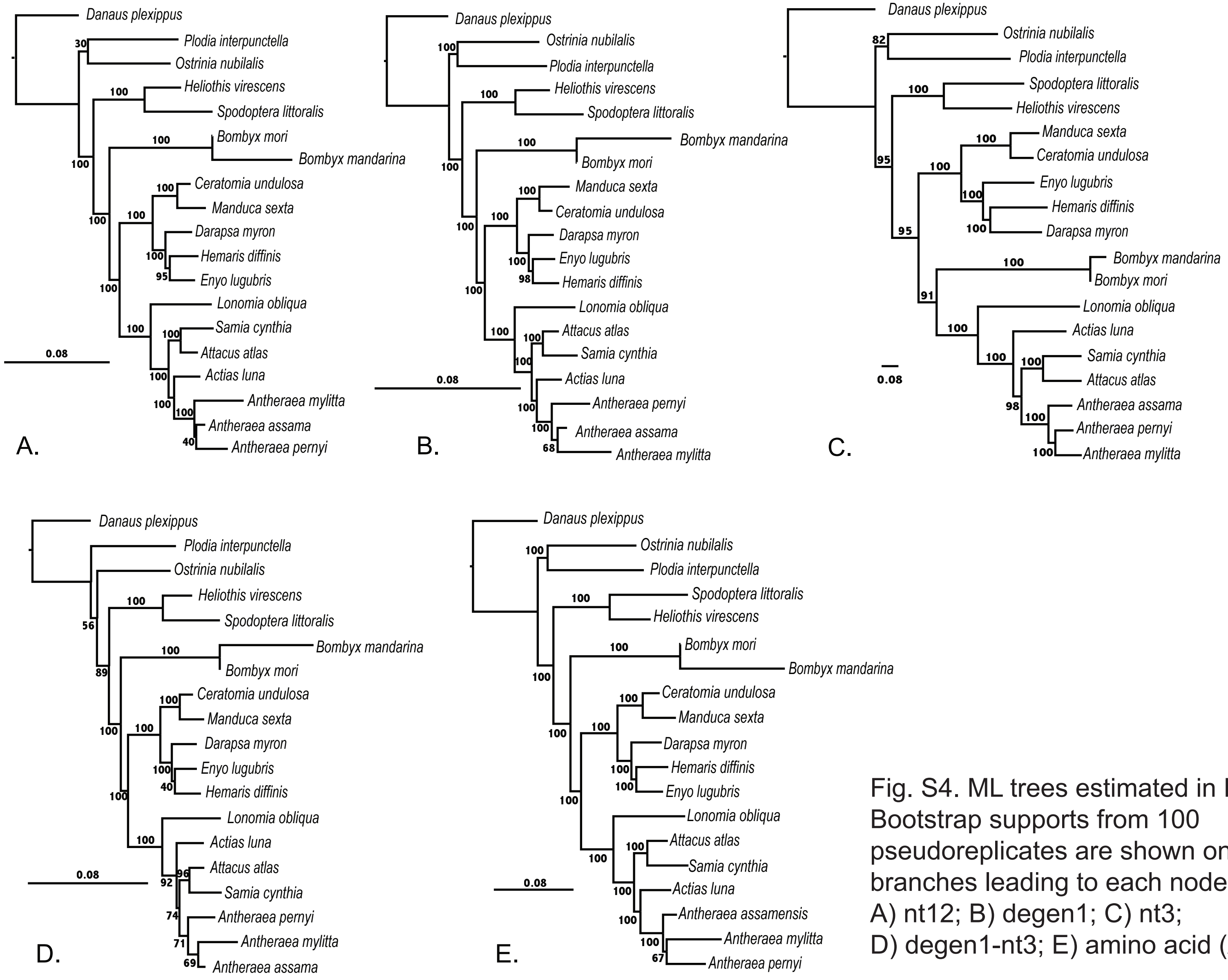

Fig. S4. ML trees estimated in RAxML. Bootstrap supports from 100 pseudoreplicates are shown on branches leading to each node. A) nt12; B) degen1; C) nt3; D) degen1-nt3; E) amino acid (AA).