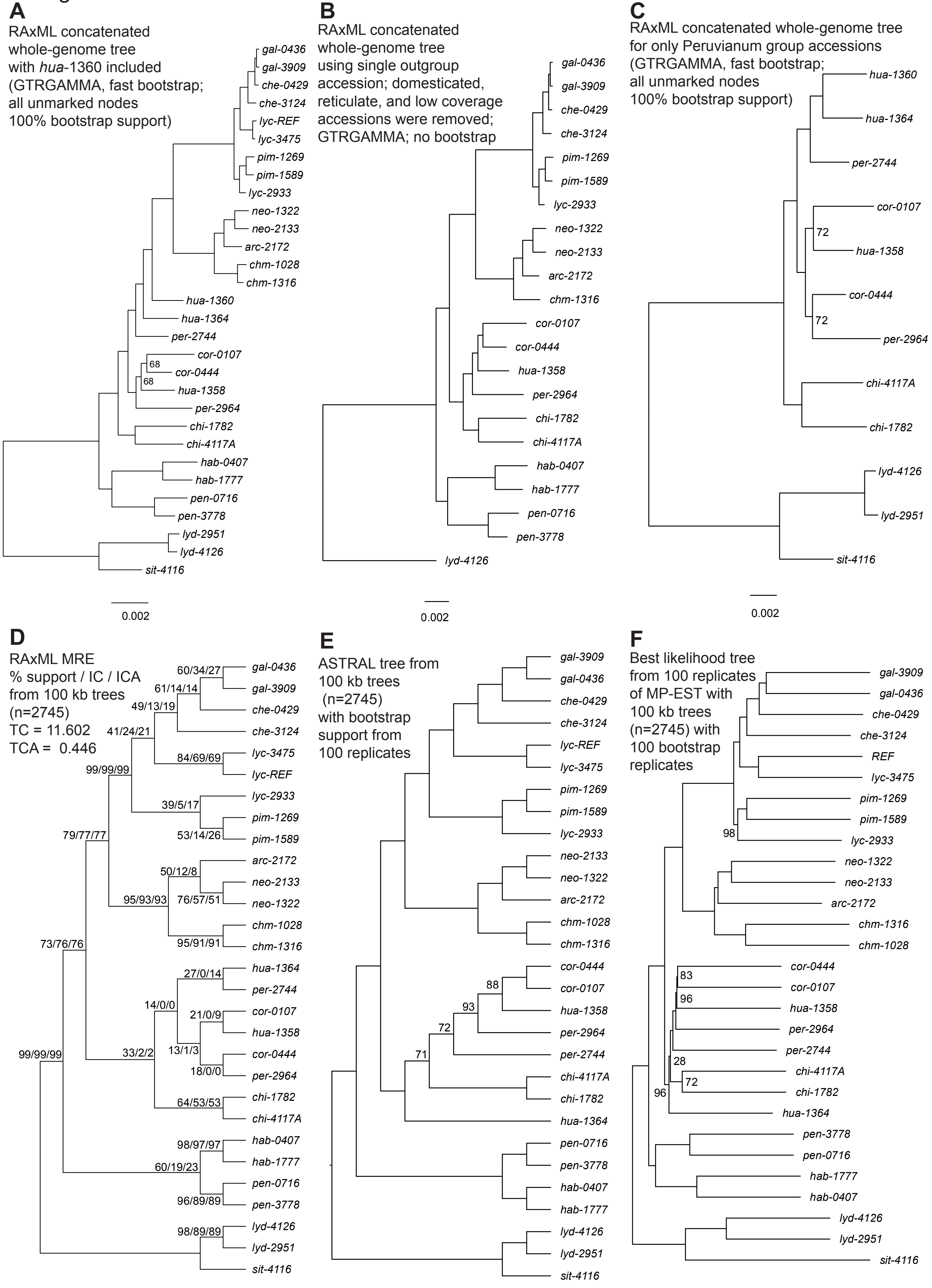
Figure S2



A RAxML concatenated whole-genome tree with *hua*-1360 included (GTRGAMMA, fast bootstrap; all unmarked nodes 100% bootstrap support)

B RAxML concatenated whole-genome tree using single outgroup accession; domesticated, reticulate, and low coverage accessions were removed; GTRGAMMA; no bootstrap

C RAxML concatenated whole-genome tree for only Peruvianum group accessions (GTRGAMMA, fast bootstrap; all unmarked nodes 100% bootstrap support)

D RAxML MRE % support / IC / ICA from 100 kb trees (n=2745) TC = 11.602 TCA = 0.446

E ASTRAL tree from 100 kb trees (n=2745) with bootstrap support from 100 replicates

F Best likelihood tree from 100 replicates of MP-EST with 100 kb trees (n=2745) with 100 bootstrap replicates