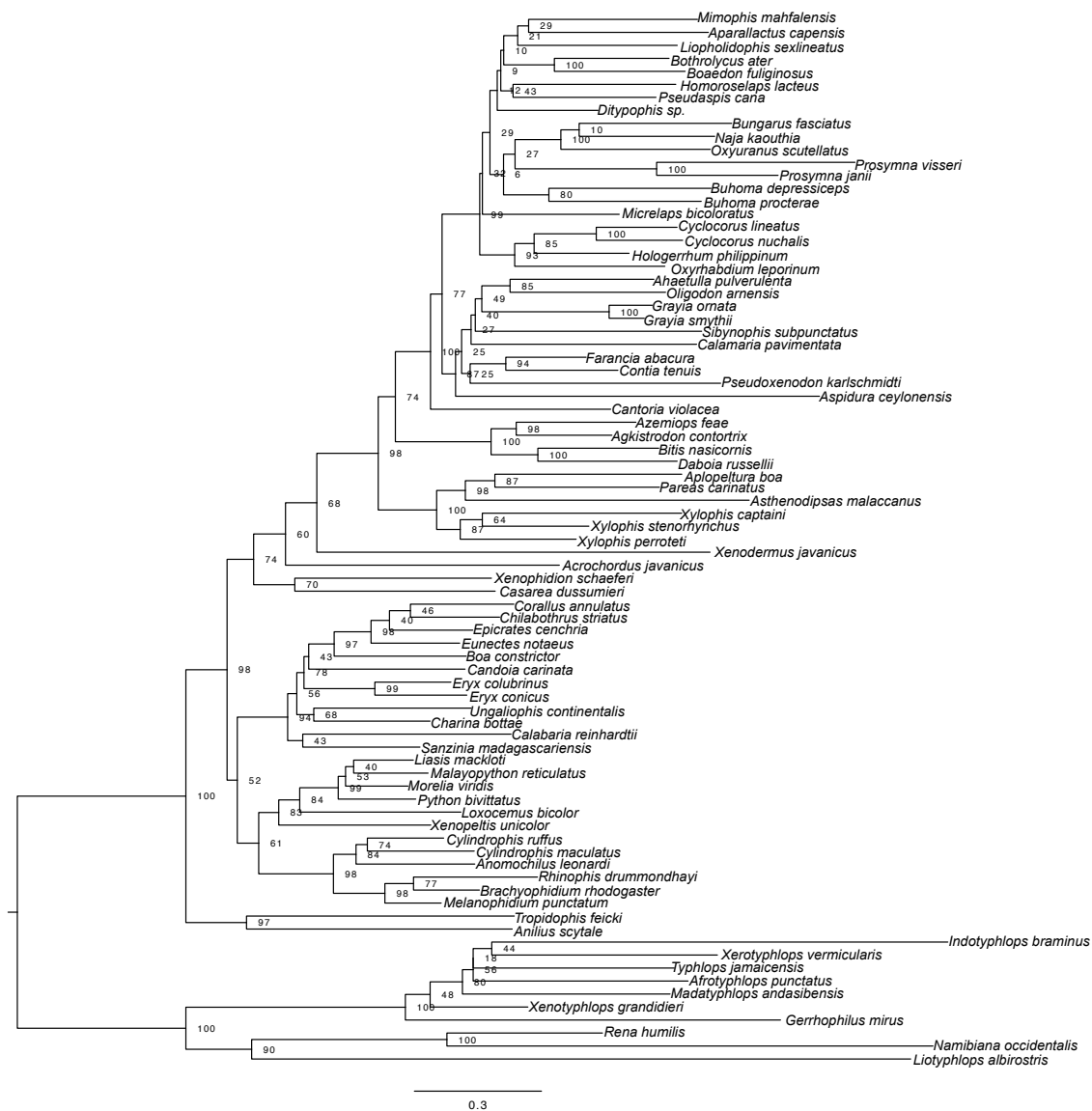
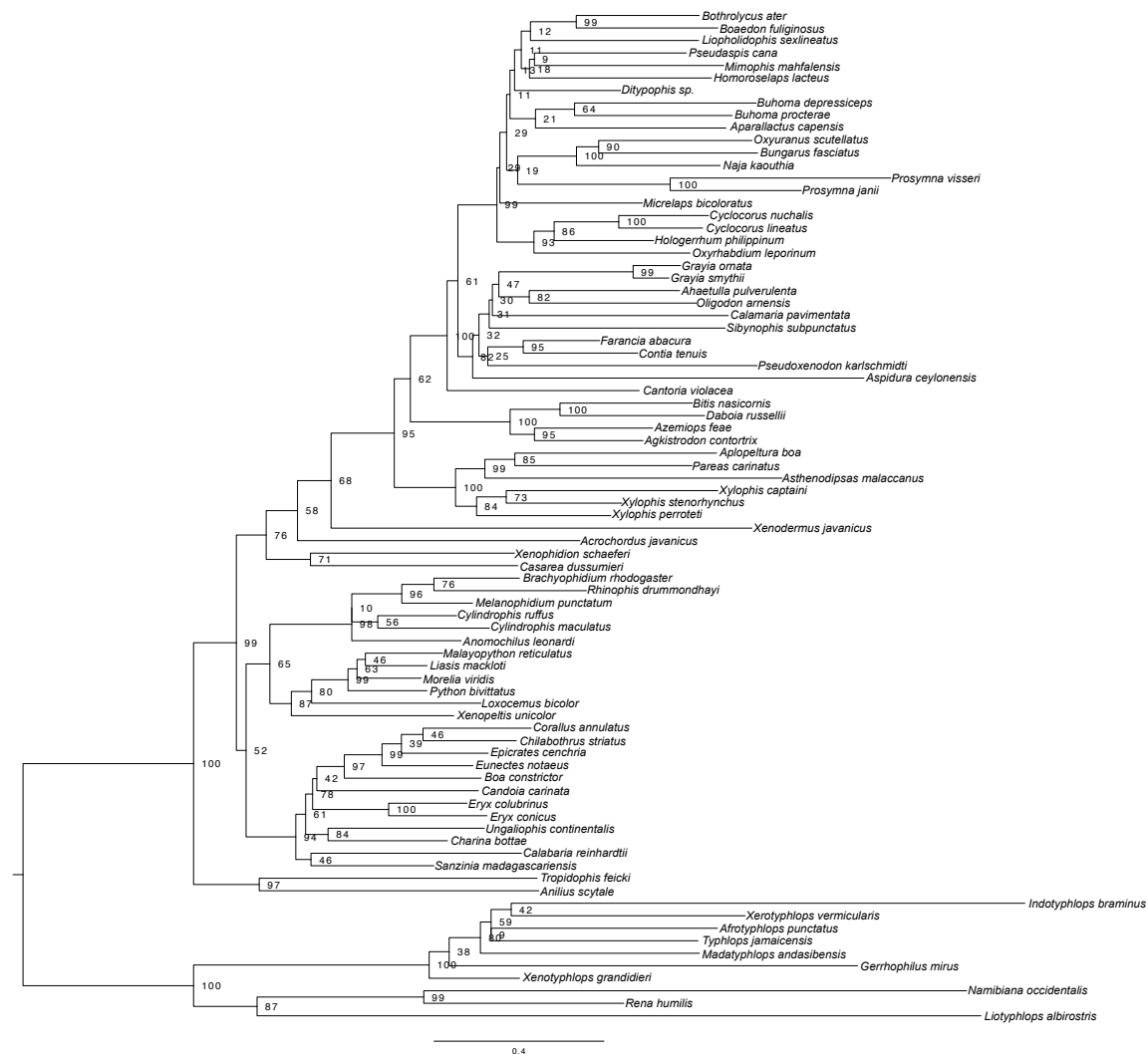


Figure S1. RAxML trees for concatenated data for 81 taxa, with three different alignment treatments for *16s*.

A) ML tree for concatenated data including *16s* aligned by ClustalW, with all sites included. Numbers on tree are bootstrap values (based on 1,000 replicates). Scale bar indicates substitutions per site.



B) ML tree for concatenated data including 16s aligned by MUSCLE, with all sites included. Numbers on tree are bootstrap values (based on 1,000 replicates). Scale bar indicates substitutions per site.



C) ML tree for concatenated data including 16s aligned by ClustalW, with ambiguously aligned sites removed under 'less stringent' option in Gblocks. Numbers on tree are bootstrap values (based on 1,000 replicates). Scale bar indicates substitutions per site.

