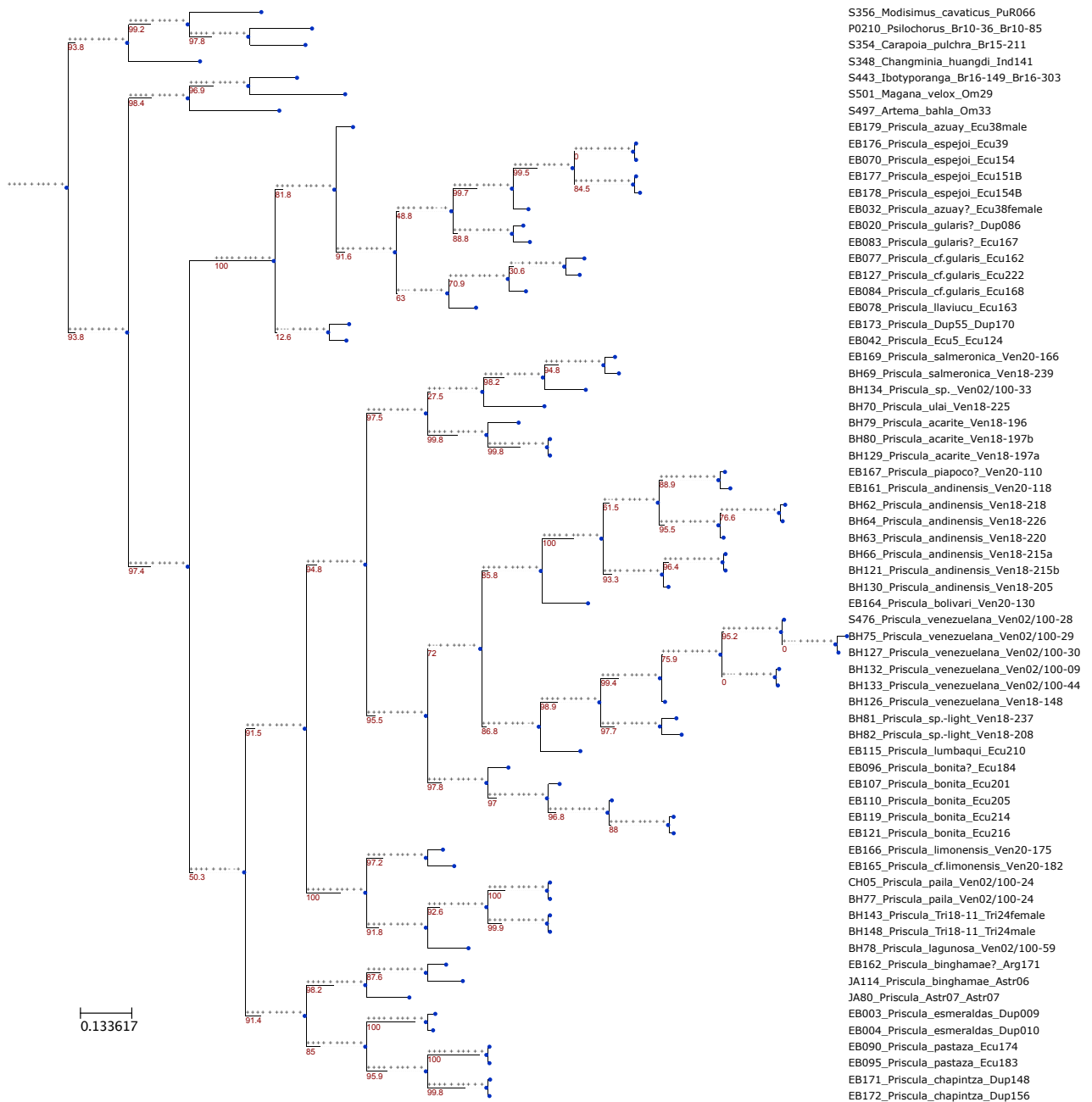


Query tree supports (+/-) from left to right:  
 ClipKIT\_gappy, ClipKIT\_kpi-gappy, ClipKIT\_kpi-smart-gap, ClipKIT\_kpi, ClipKIT\_kpic-gappy, ClipKIT\_kpic, ClipKIT\_smart-gap, Gblocks, TrimAl, untrimmed



**Figure S2.** Summary tree of all trees constructed from unpartitioned analyses. All trees were constructed from the same gene set but with different multiple-sequence-alignment (MSA) trimming strategies or from the untrimmed MSA using IQ-TREE. The ClipKIT\_kpic-smart-gap tree was used as the reference tree. The trees (query trees) from other MSA-trimming strategies were compared to the reference tree, with ‘+’ or ‘-’ indicating that the query trees agree or disagree, respectively with the branching events of the reference tree. Numbers on the branches are SH-aLRT support (%). Best-fit model according to BIC for the reference tree: SYM+I+G4.

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