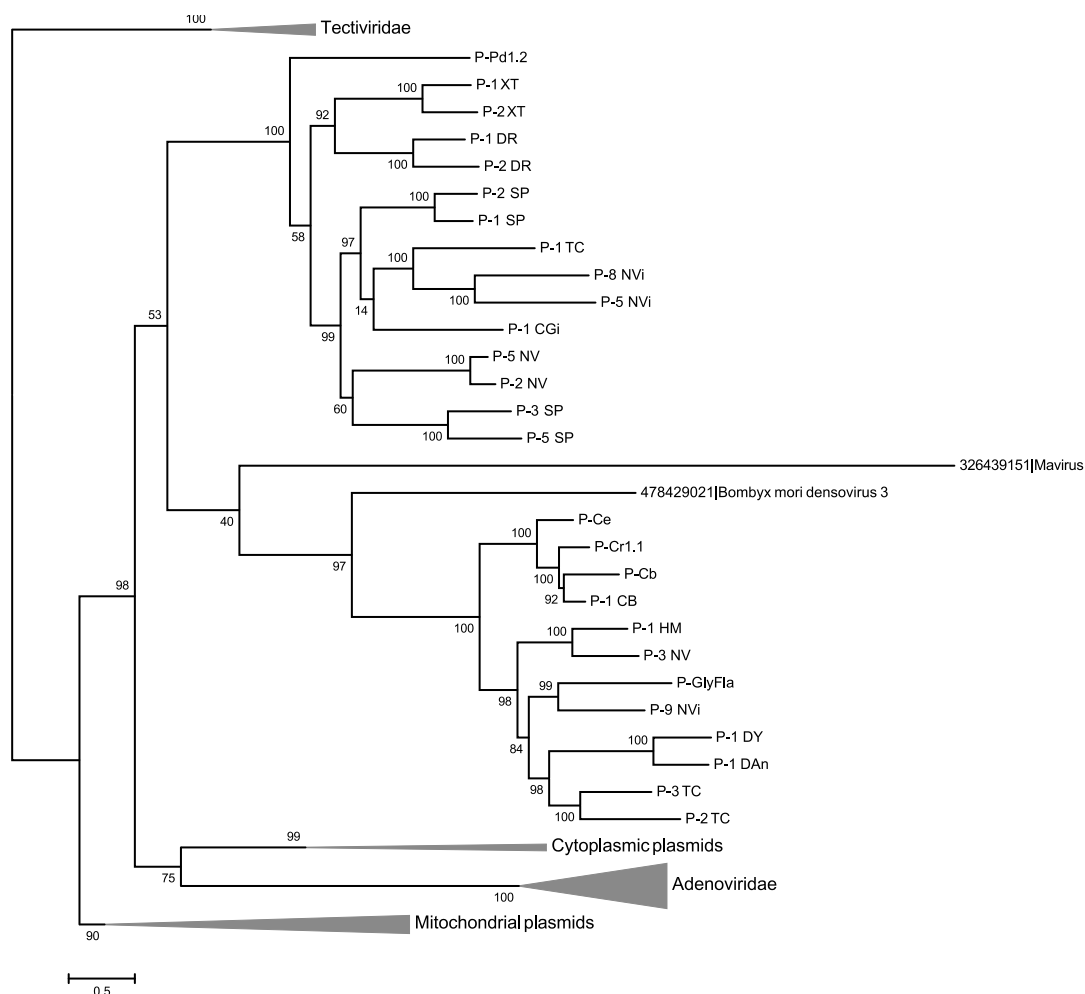


## Supplementary information S3 (figure)



Phylogenetic analysis of pPolBs from prokaryotic and eukaryotic mobile elements. The maximum likelihood tree was calculated using PhyML, with the WAG model of amino acid substitution, including a gamma law (4 categories) and an estimated proportion of invariable sites. Numbers at the branch points represent SH-like local support values. The tree is rooted with bacterial tectiviruses.