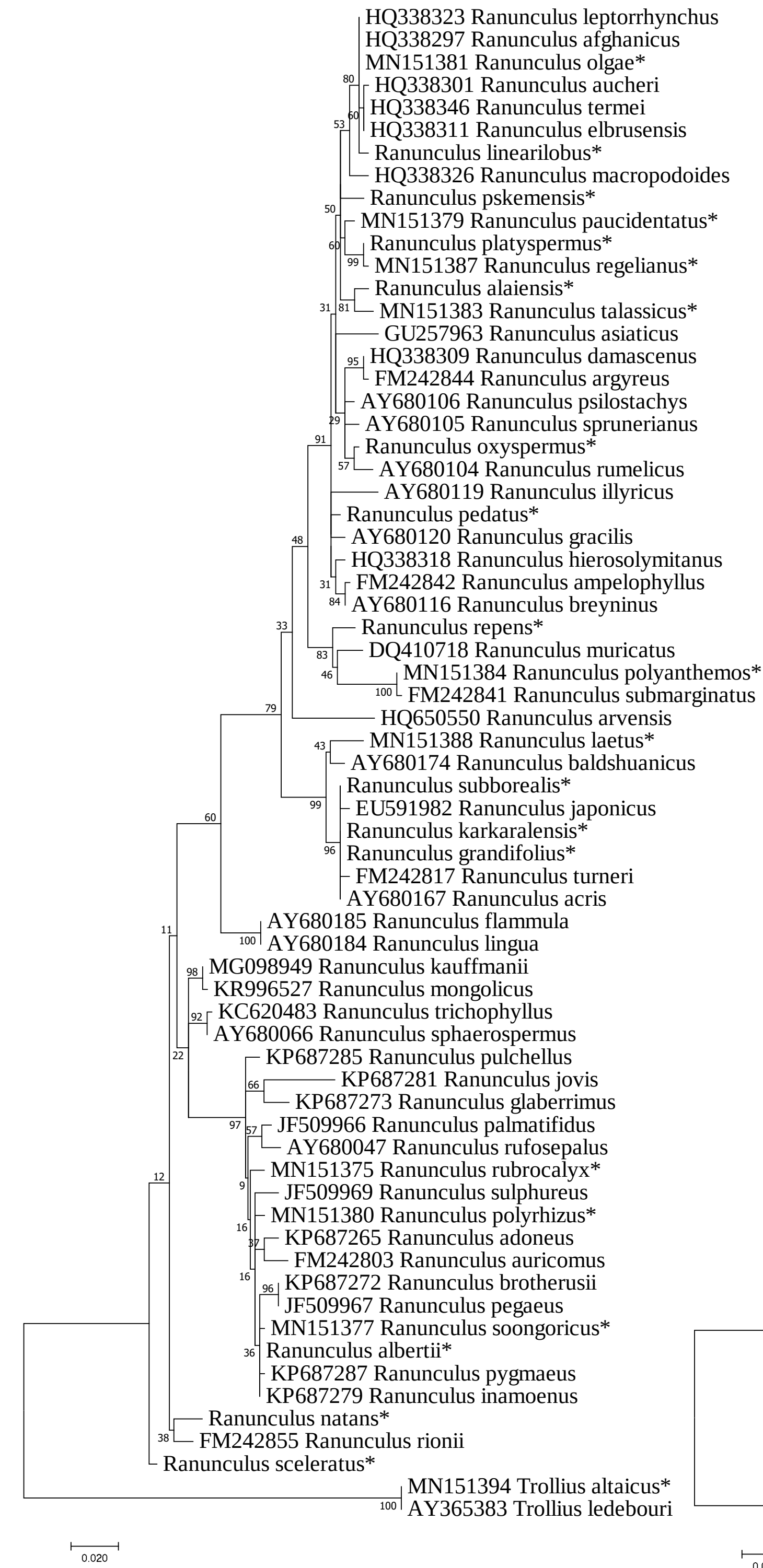
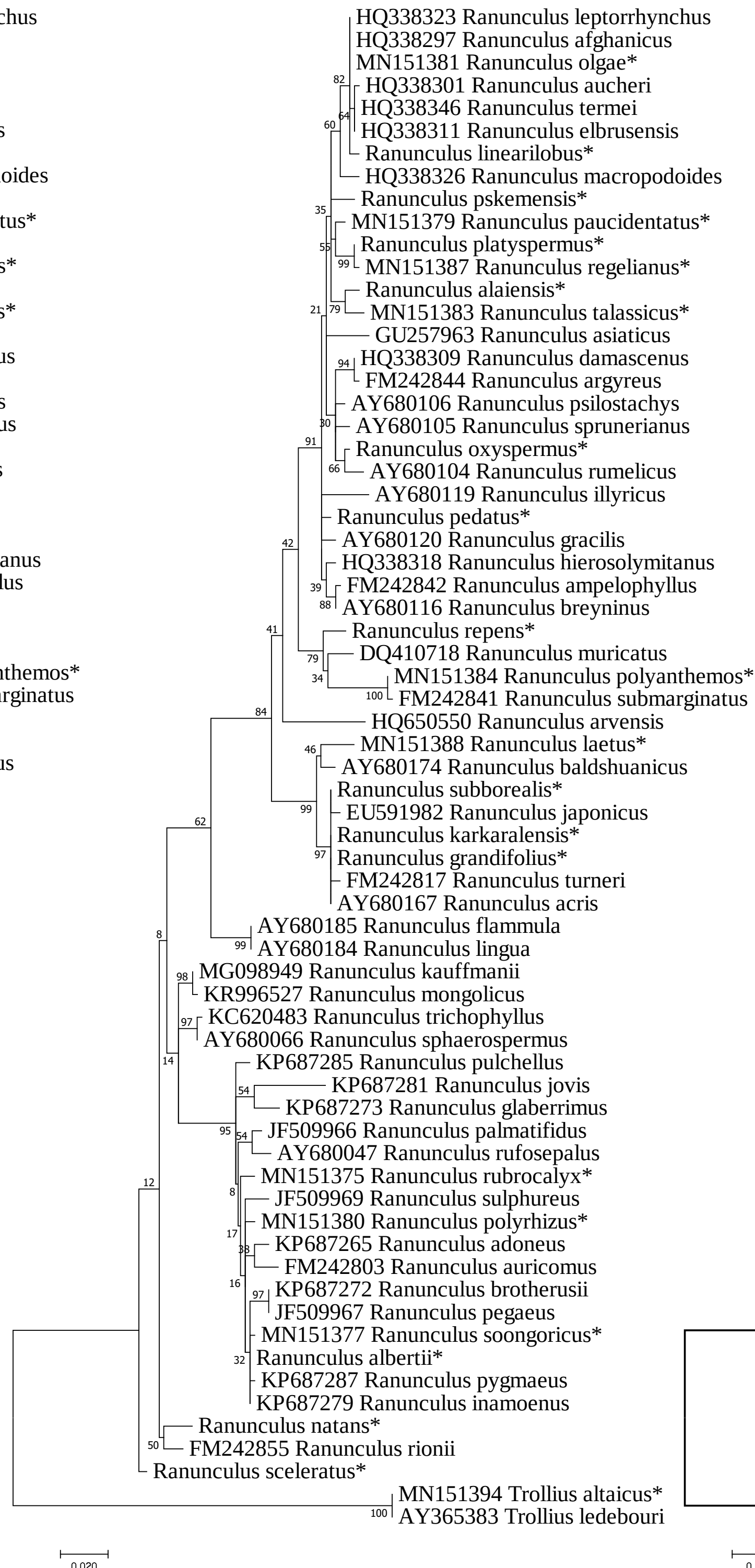


**S2 Appendix. Phylogenetic trees generated by using
Neighbour Joining (NJ), Maximum Likelihood (ML),
and Maximum Parsimony (MP) methods,
with bootstrap 100, 500, 1000, 5000, 10000 replicates**

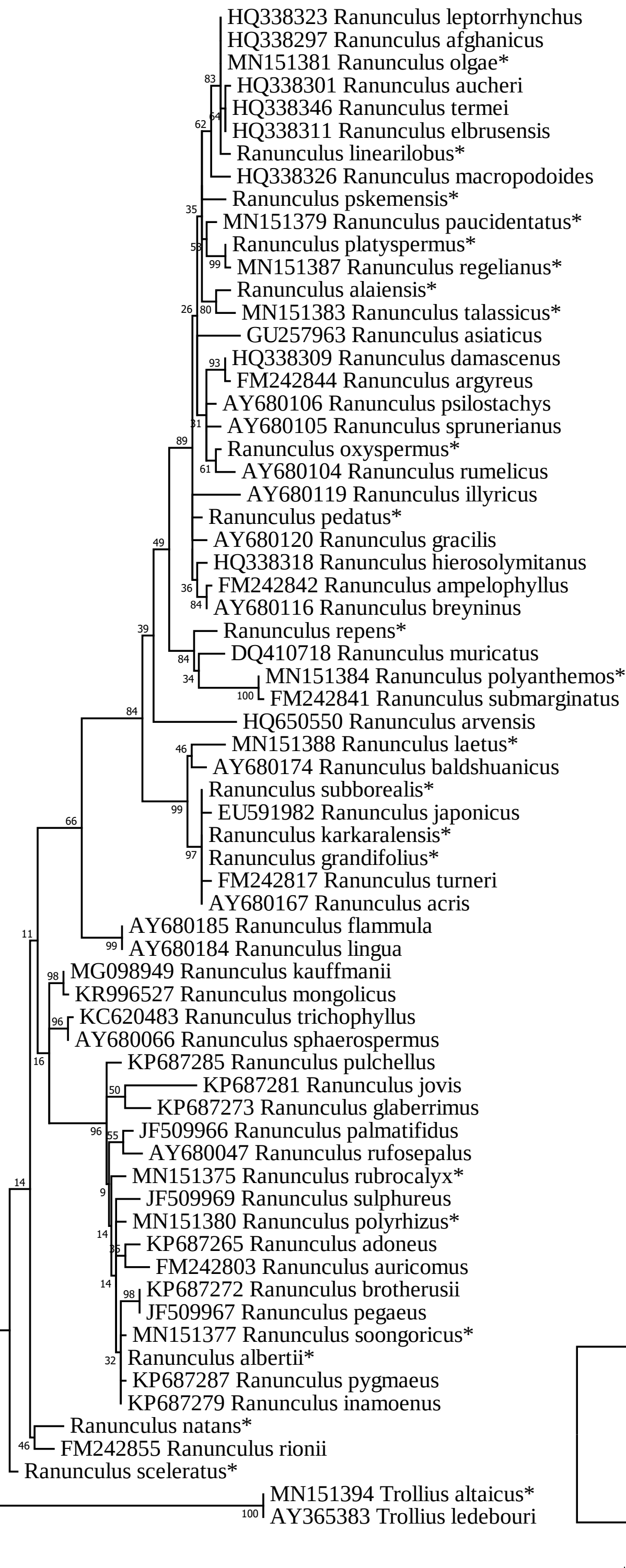
ML tree, 100 replicates



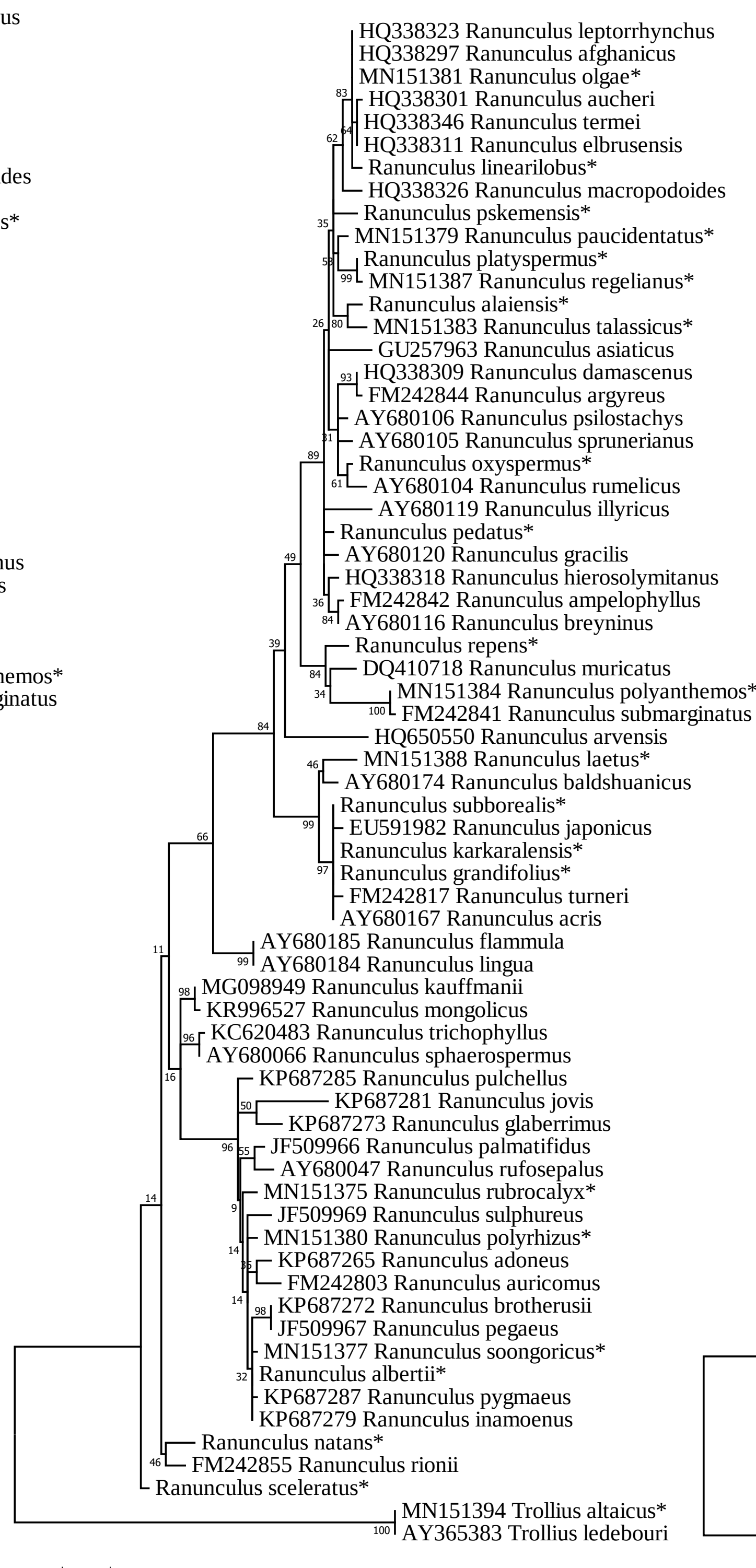
ML tree, 500 replicates



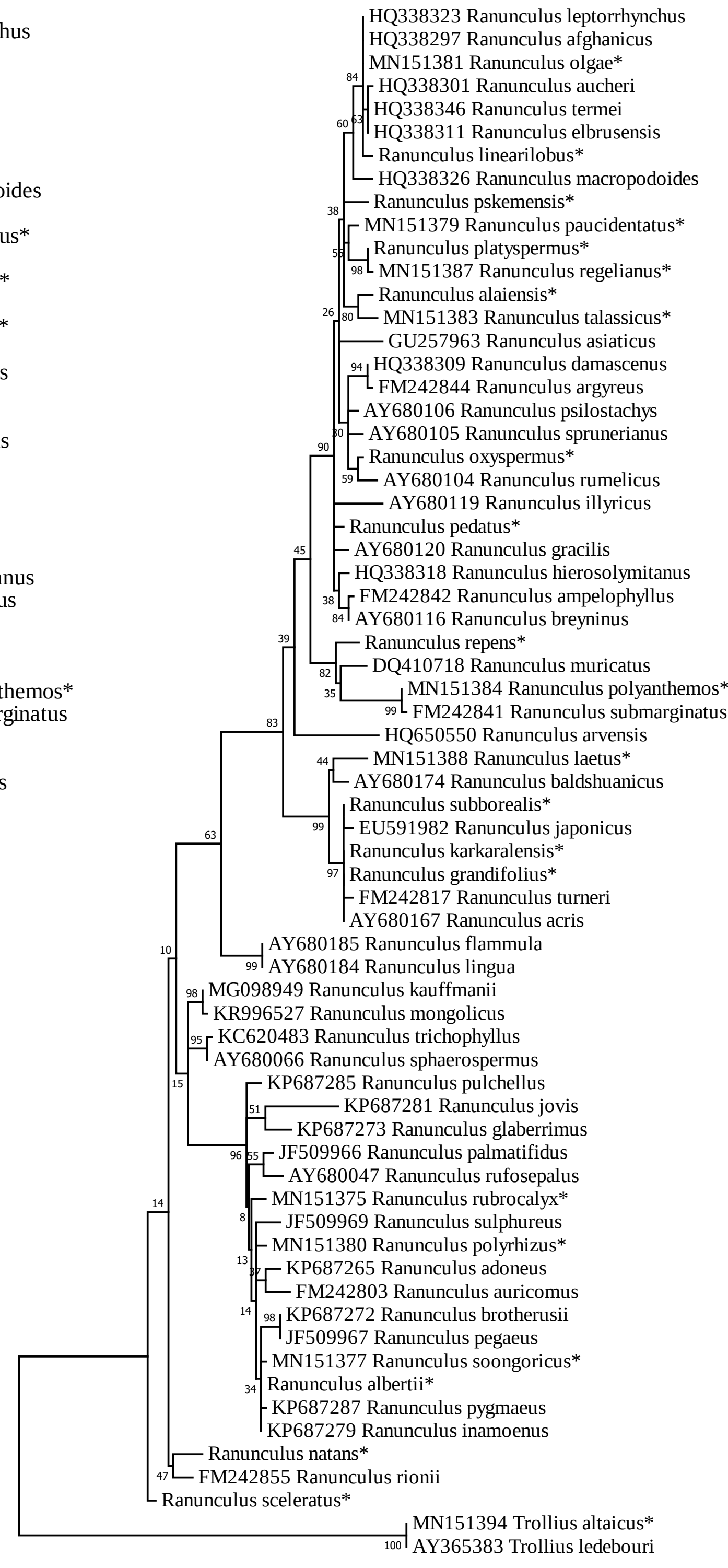
ML tree, 1000 replicates



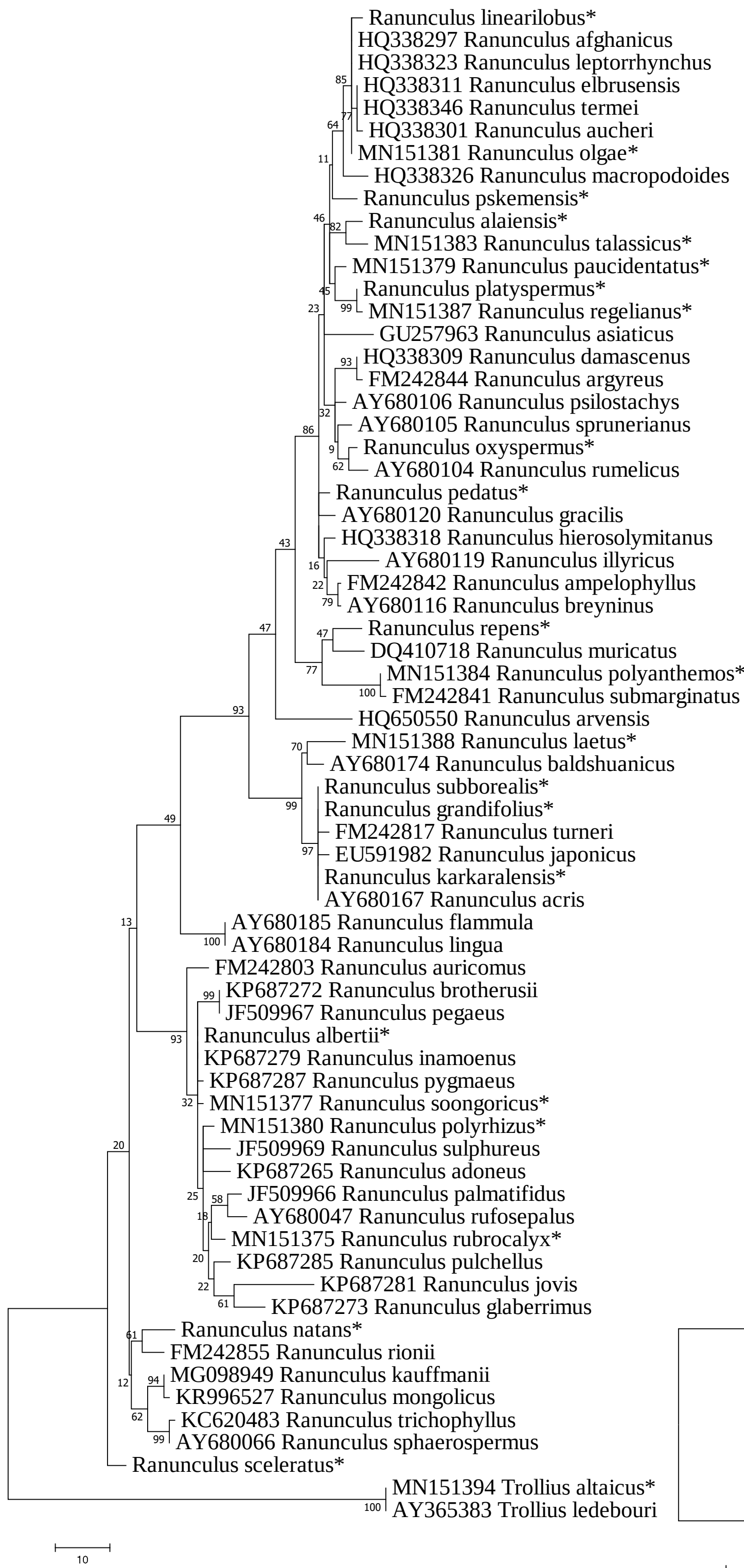
ML tree, 5000 replicates



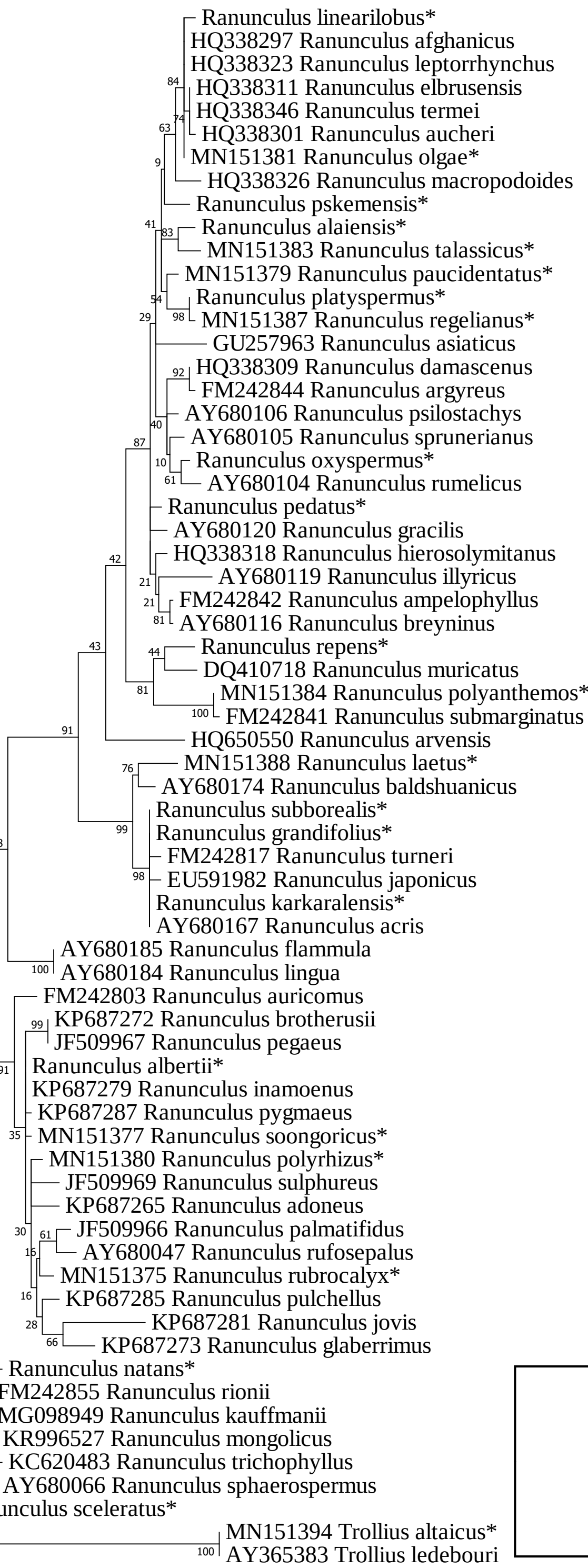
ML tree, 10 000 replicates



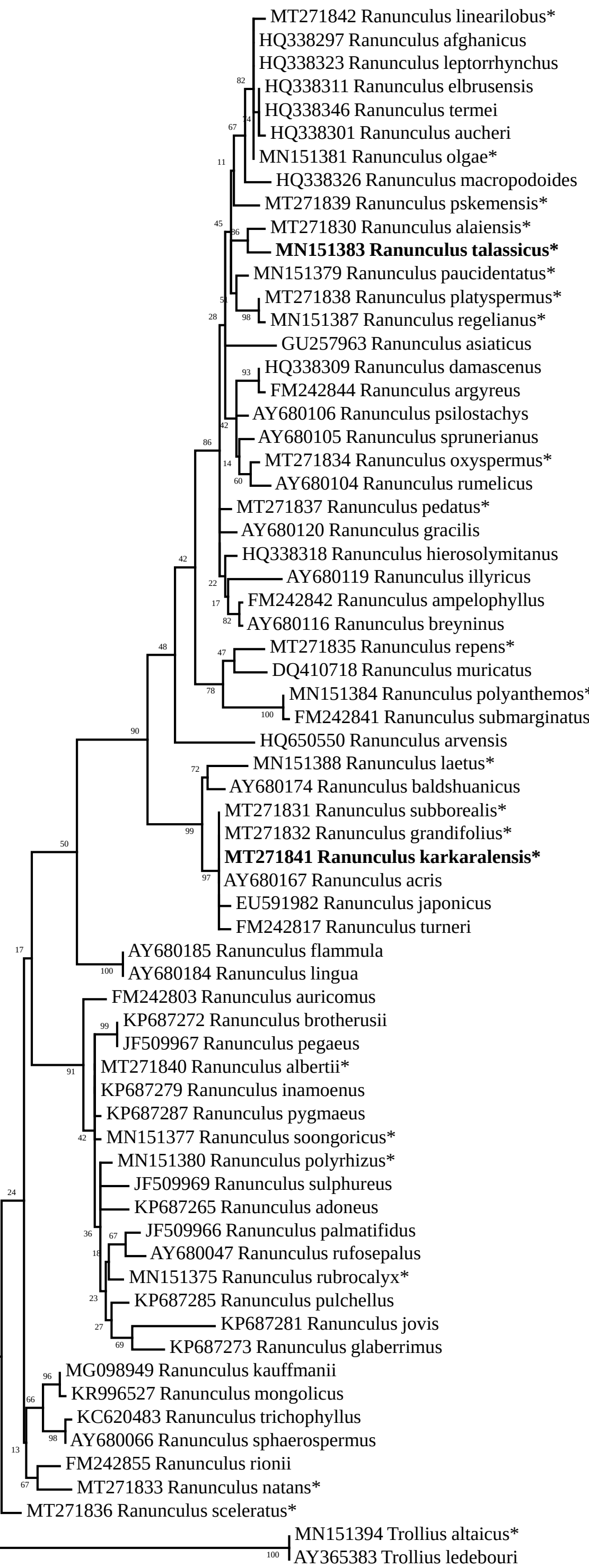
MP tree, 100 replicates



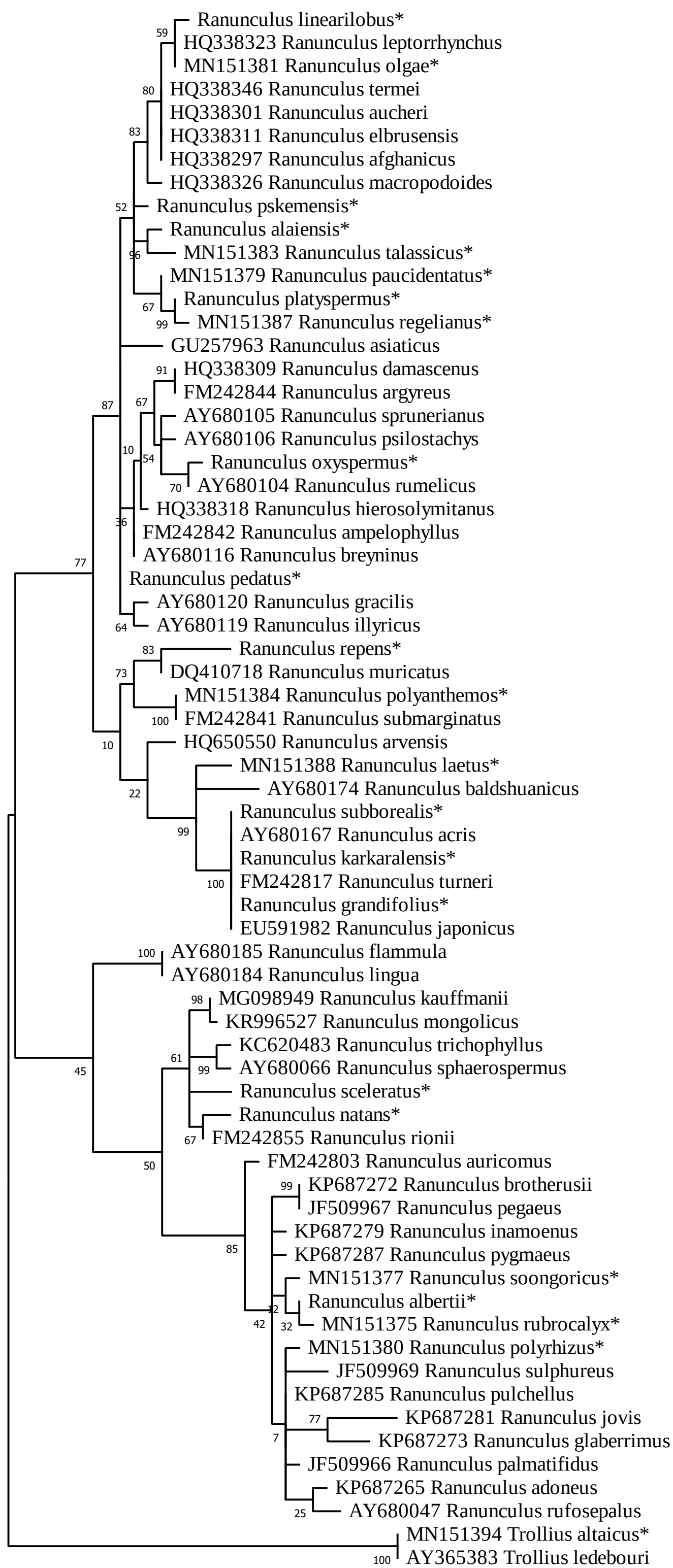
MP tree, 500 replicates



MP tree, 1000 replicates



MP tree, 5000 replicates



MP tree, 10 000 replicates

