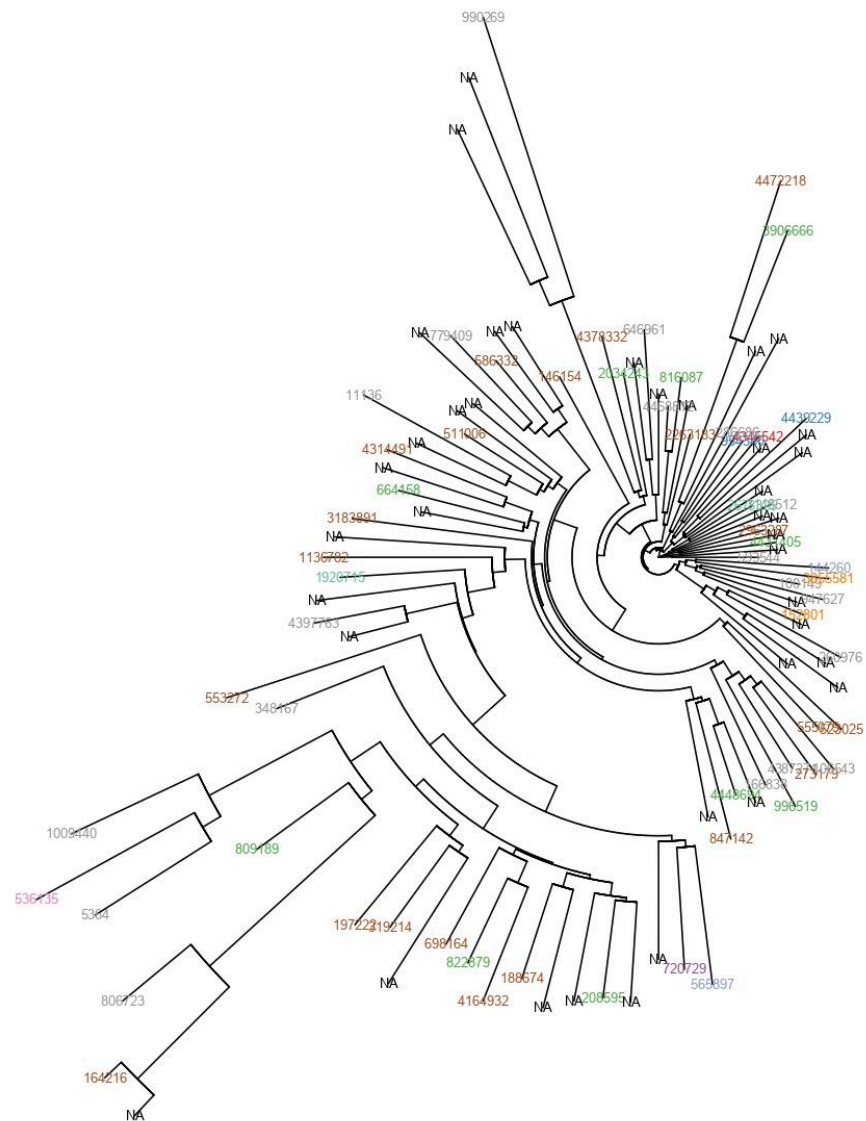
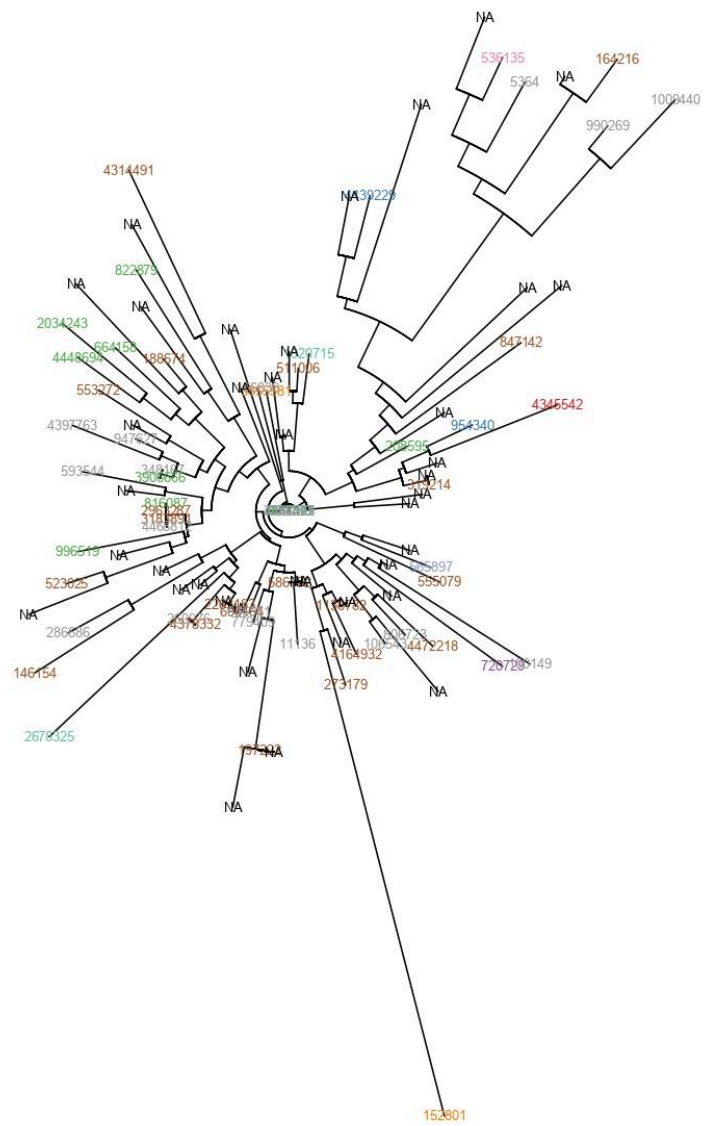


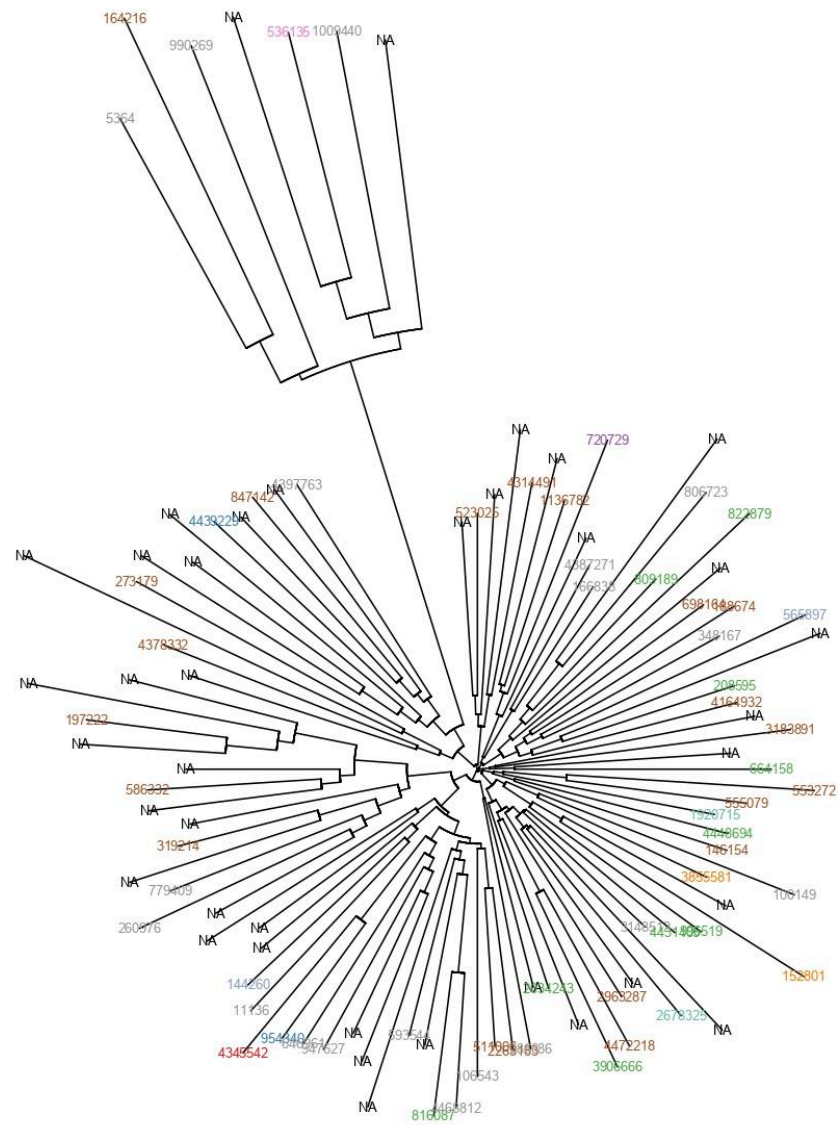
Largest variable region disordered region:



Shortest variable region



Actual tree from all nucleotides



From what I observe, both regions are about the same as the main tree. The reason I conclude this is because the real tree is fairly uniform, with 7 outliers. Both the largest variable region and shortest variable region both have these outliers. Otherwise, they both seem fairly uniform with a bit of variability. In fact, both of these regions' trees are quite similar to one another with the only difference being that the shortest region's sequences all are found to be more close to each other in general, which makes sense since there's less opportunity for potential difference in shorter sequences. Aside from these similarities to each other, the largest region is slightly more similar to the main tree, due to its generally more uniform edge lengths. This makes sense because the largest variable region contains more information than the shortest variable region, so it better identifies species and their relationships to one another.