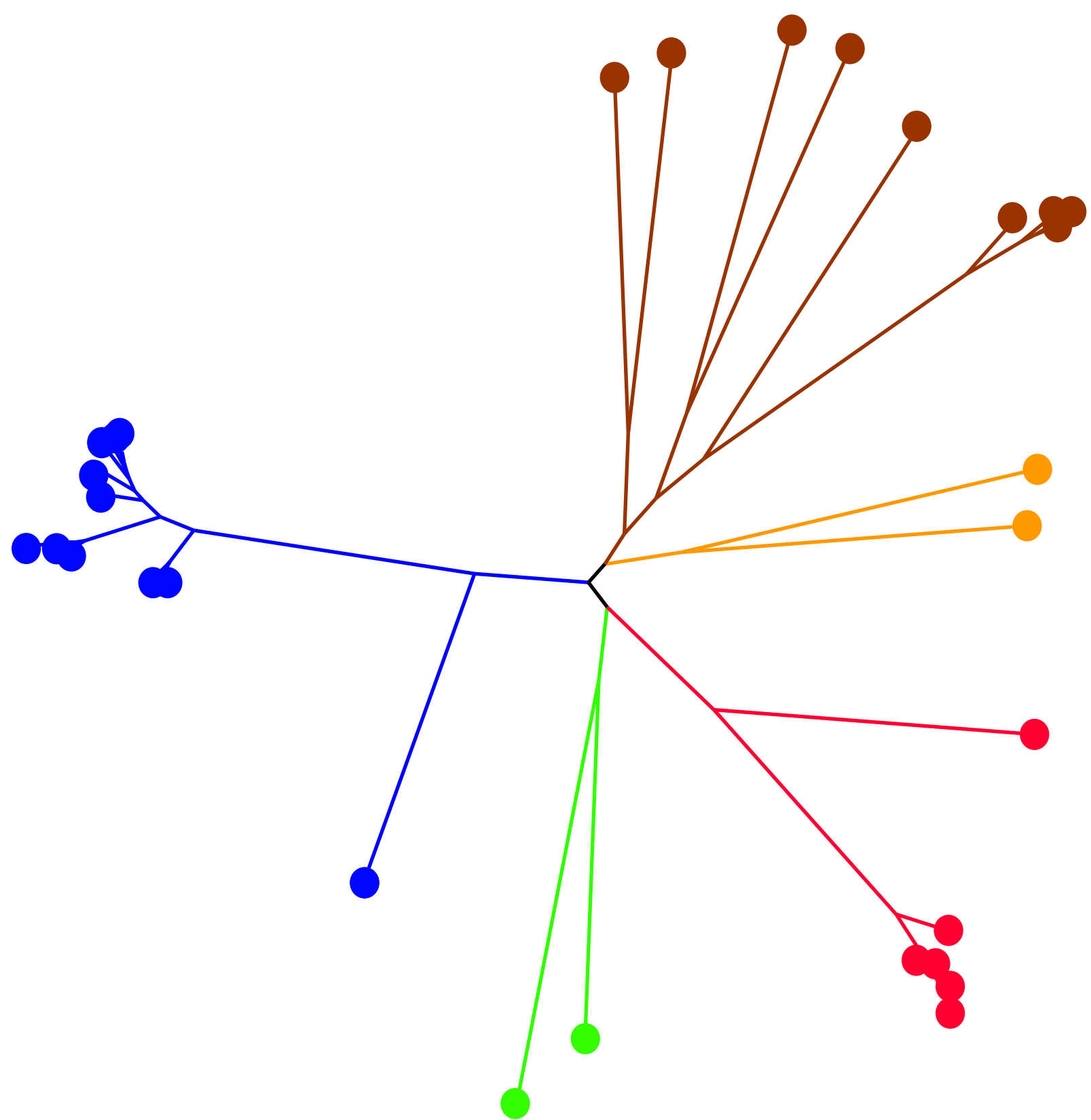
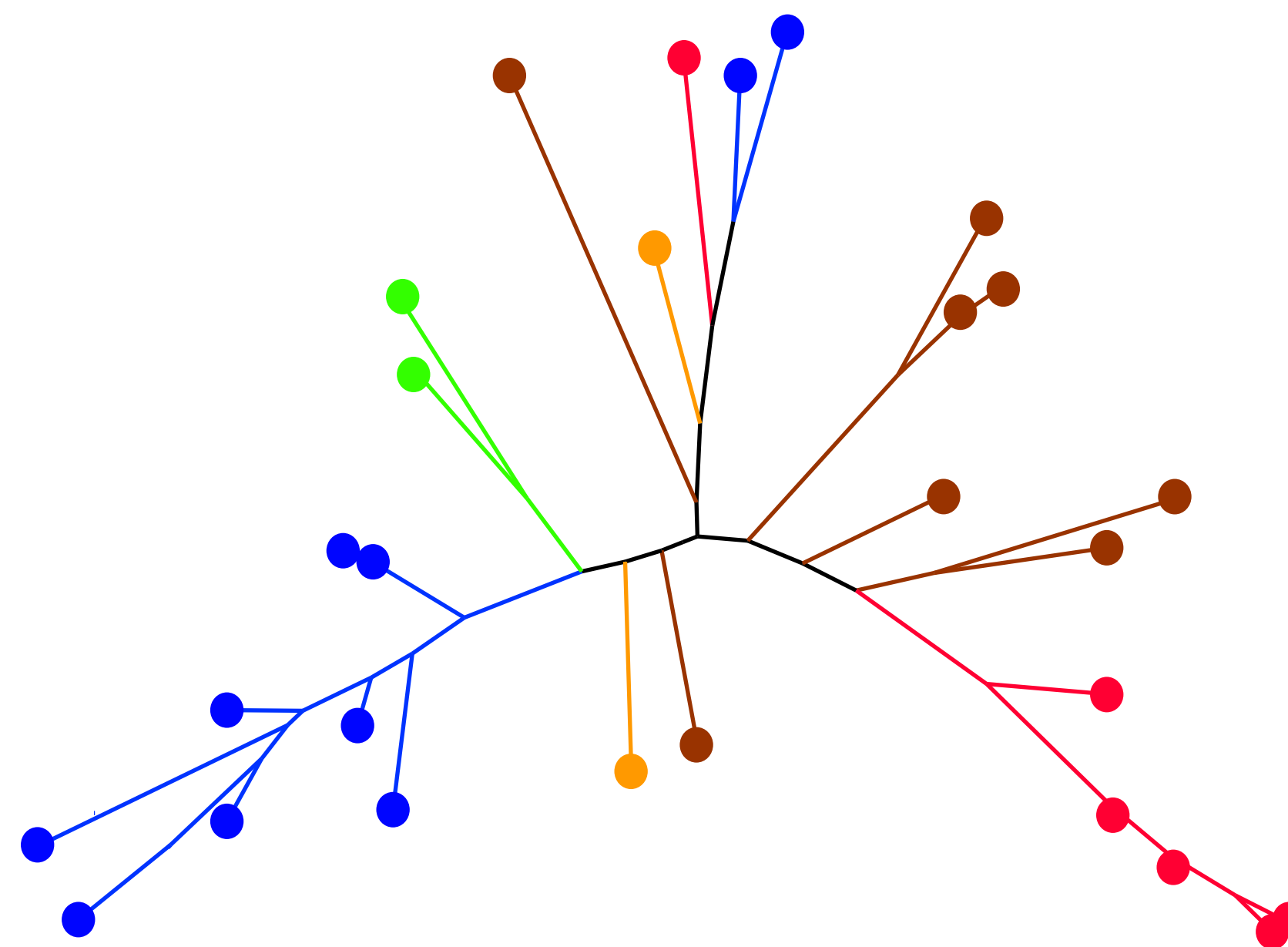


Comparison of WGA, pubMLST, and GIG-3 markers on a set of 42 *Acinetobacter baumannii* genomes. GIG markers were identified by Phylomark using a fragment length of 800 and a step size of 10. Colors are associated with 5 monophyletic lineages identified in the WGA phylogeny. All trees were inferred with FastTree2.

WGA



GIG-system (RF=22)



pubMLST (RF=29)

