

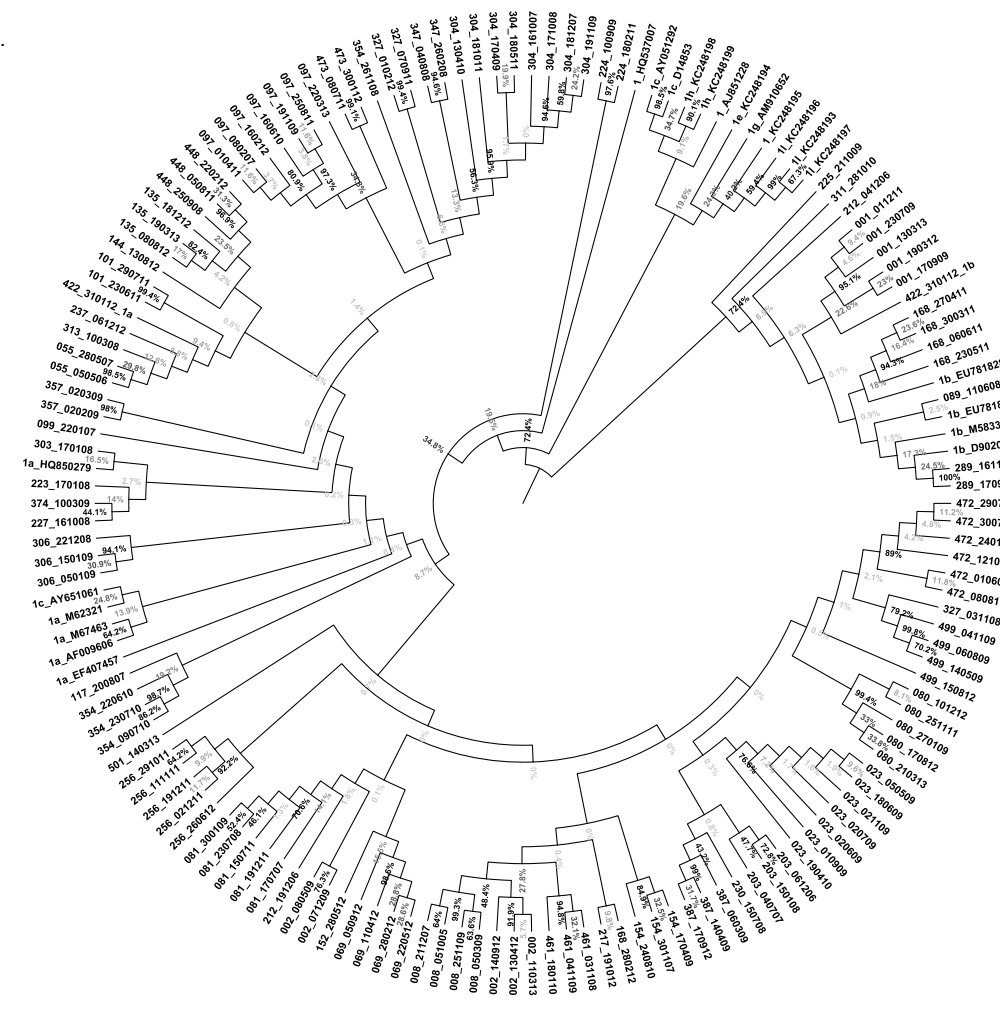
## Supplementary Data

**Supplementary Figure 1. Maximum likelihood cladograms, including all time points from each subject and reference strains from each subtype.** HCV strains sequenced from HITS-p subjects designated by subject identifier followed by sampling date. *Super-infections* with the same genotype are distinguished with determined subtype. Reference sequences are designated by subtype followed by GenBank accession number (1) A. Core region, genotype 1. B. Core region, genotype 2. C. Core region, genotype 3. D. Core region, genotype 6. E. E1/HVR1 region, genotype 1. F. E1/HVR1 region, genotype 2. G. E1/HVR1 region, genotype 3. H. E1/HVR1 region, genotype 6. I. 5'UTR region, genotype 1. J. 5'UTR region, genotype 2. K. 5'UTR region, genotype 3.

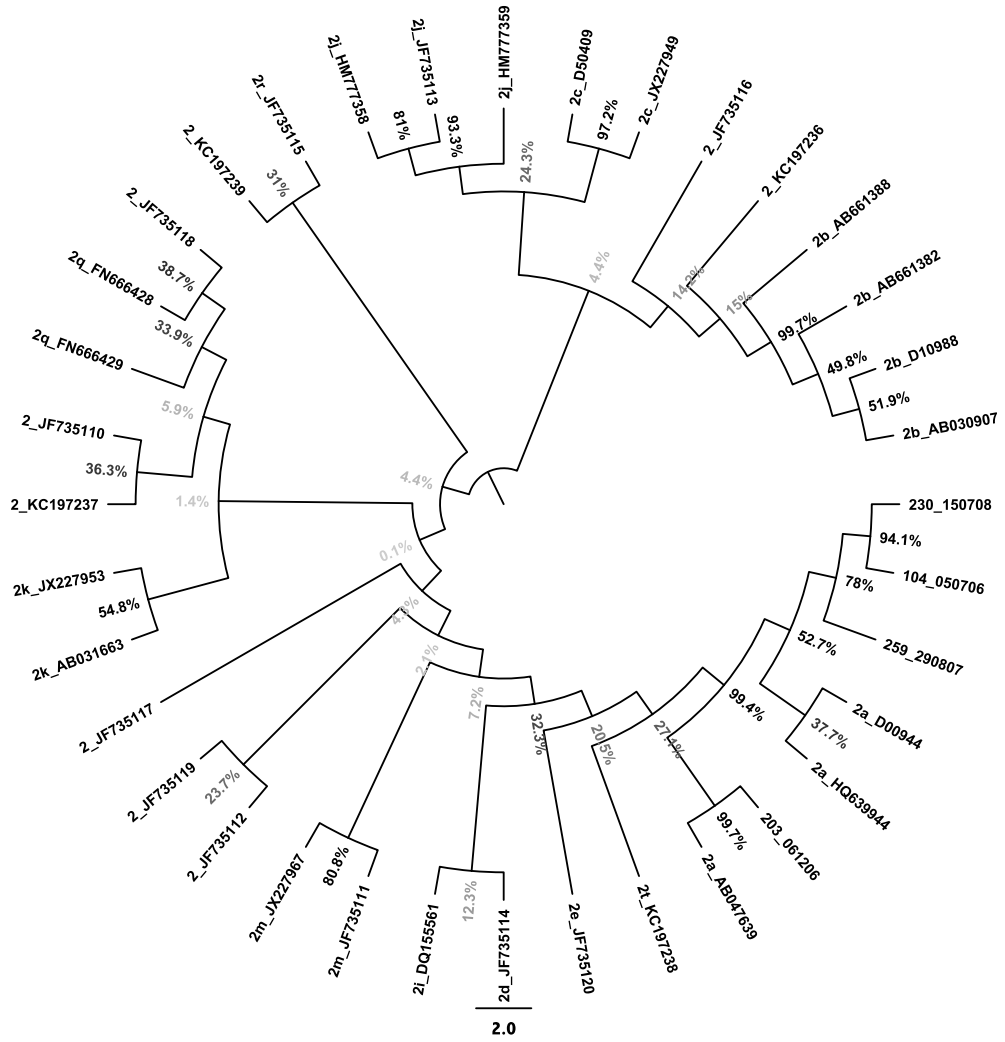
## Reference

1. **Smith DB BJ, Kuiken C, Muerhoff AS, Rice CM, Stapleton JT, Simmonds P.** 2014. Expanded classification of hepatitis C virus into 7 genotypes and 67 subtypes: Updated criteria and genotype assignment web resource. *Hepatology* **59**.

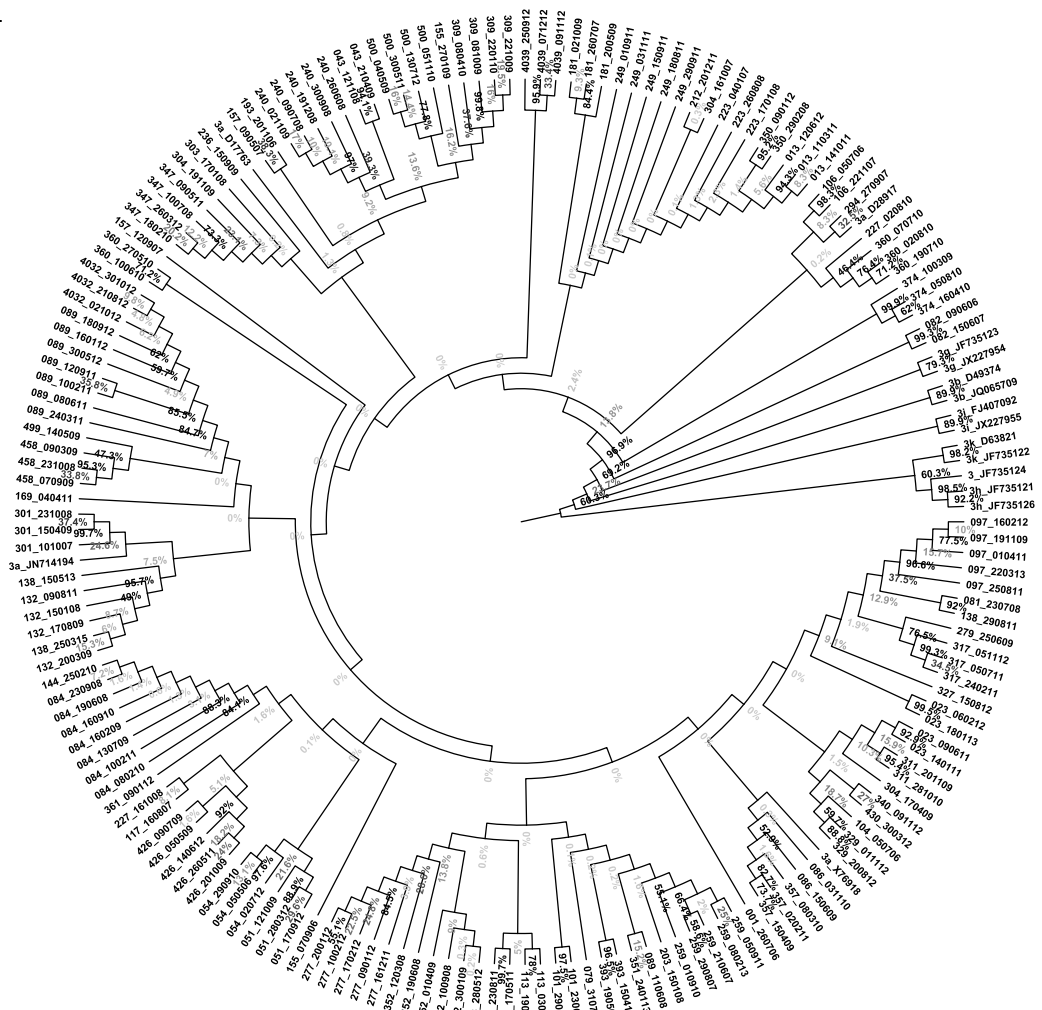
A.



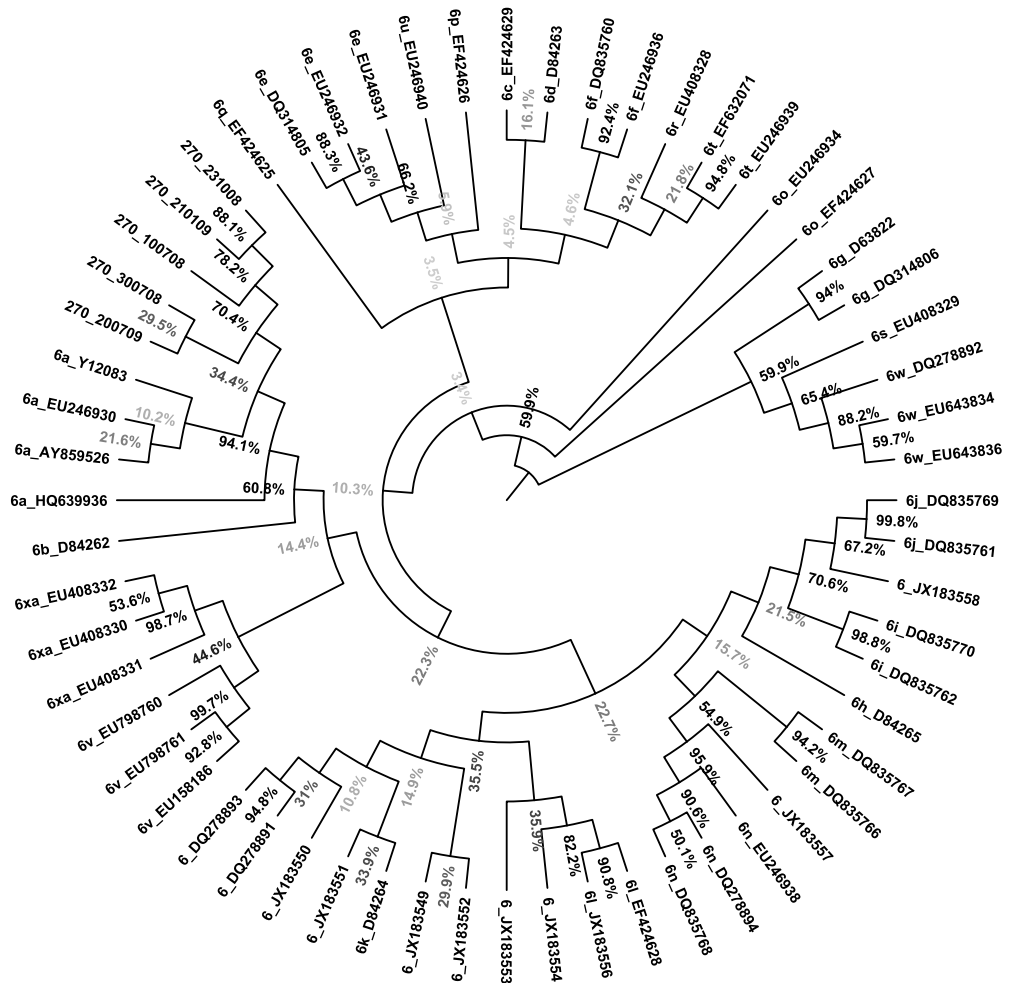
B.



C.

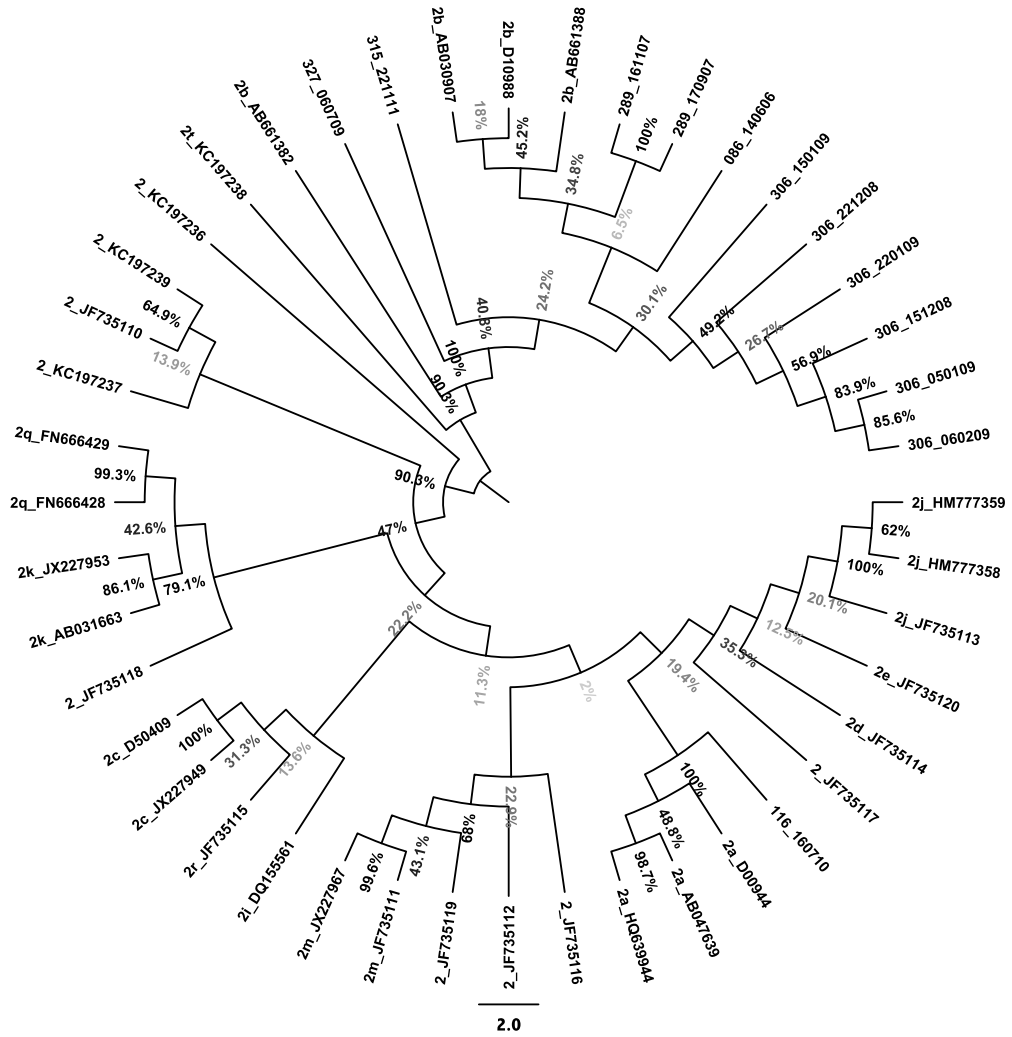


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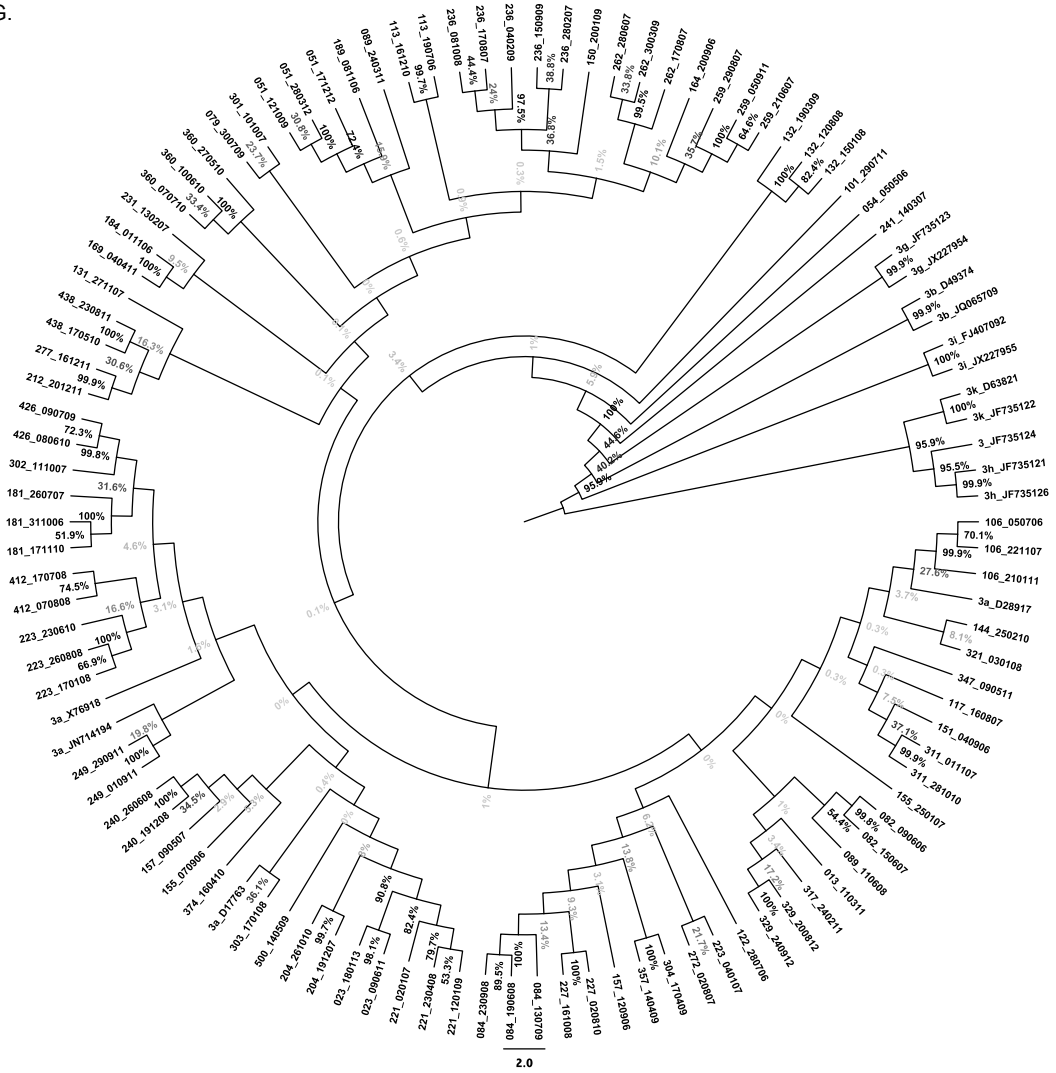


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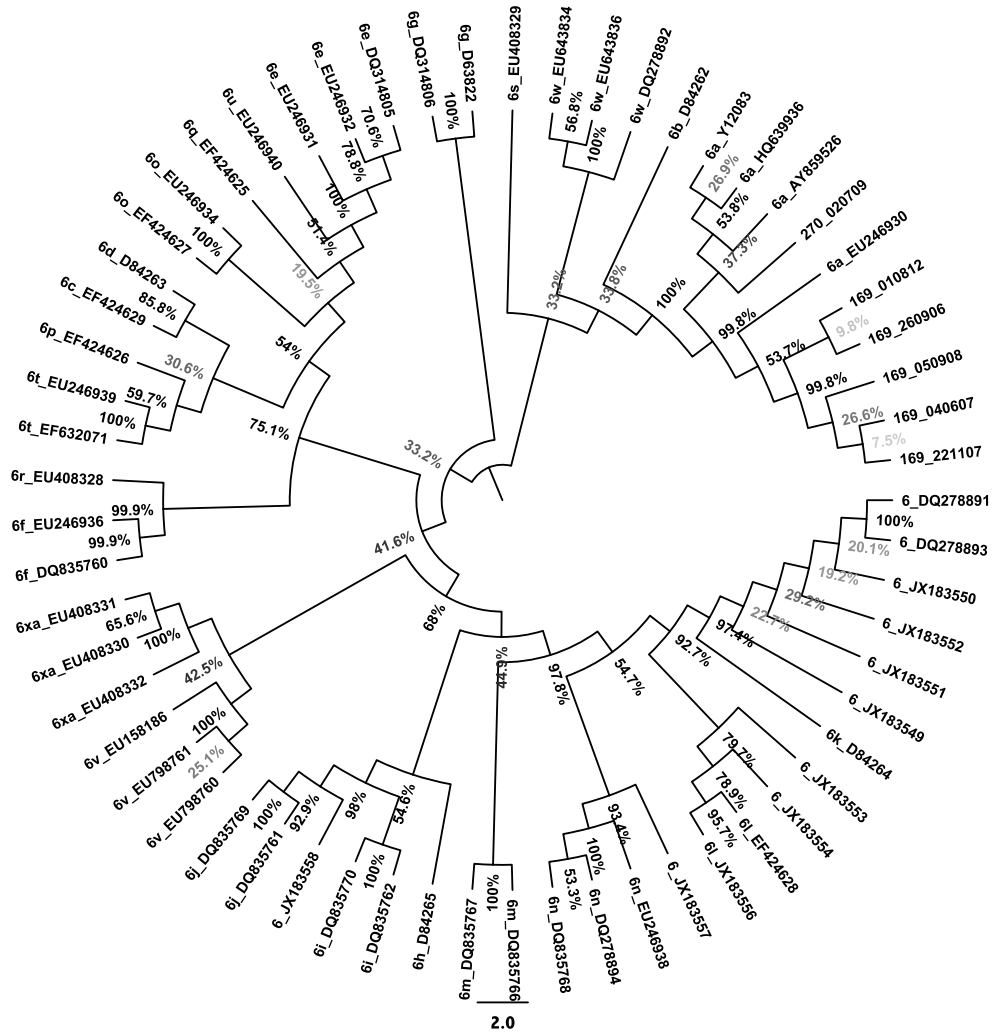
2.0

G.

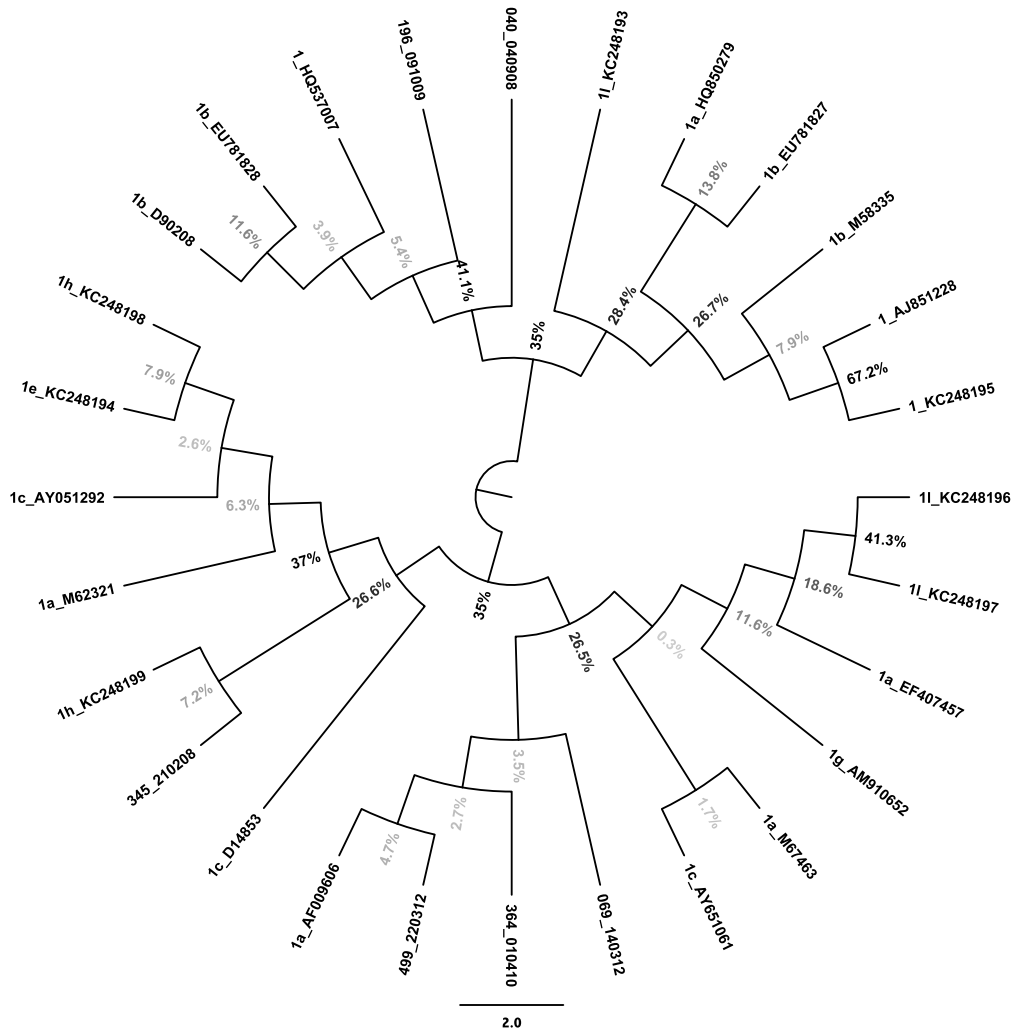




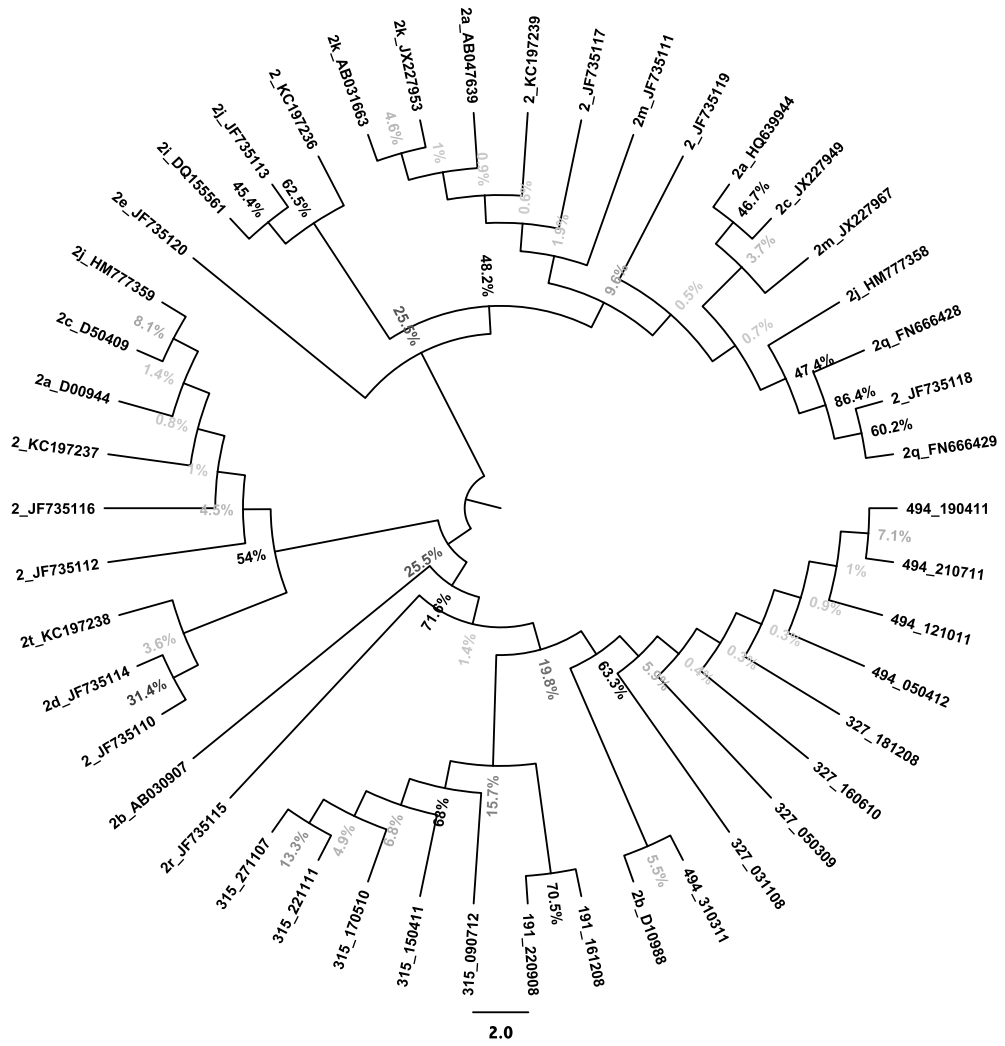
H.



I.



J.



K.

