

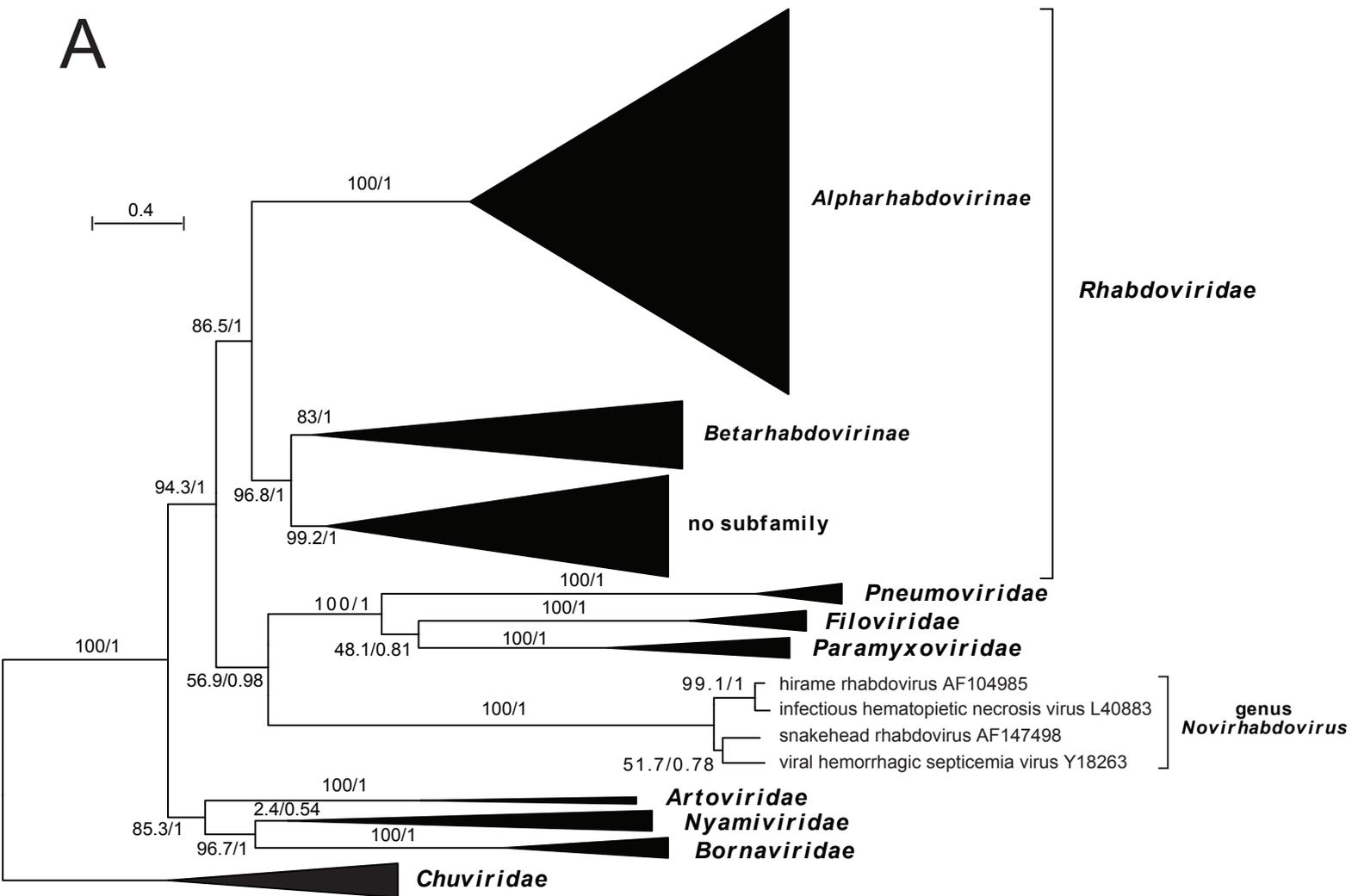
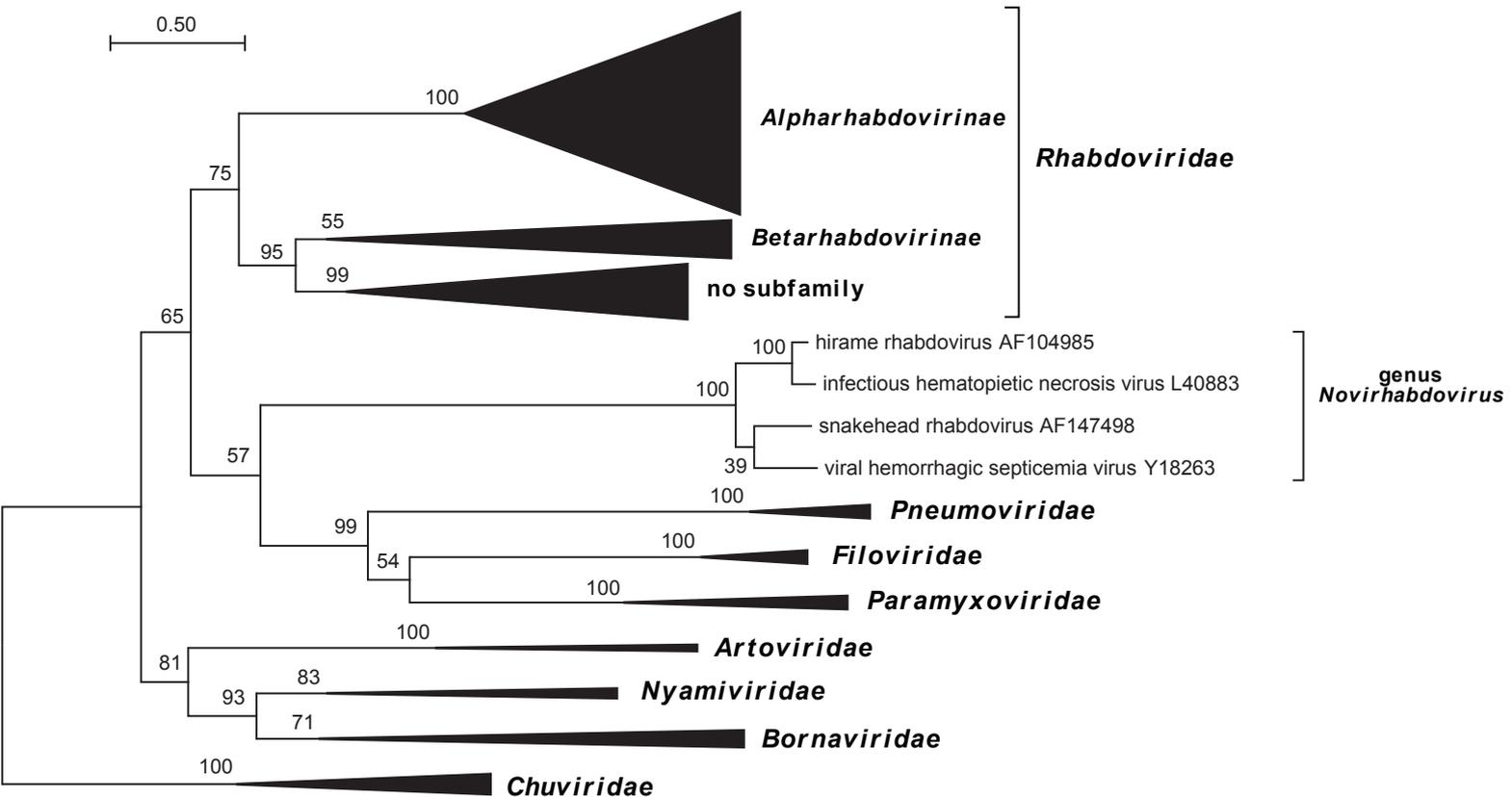
A**B**

Figure S1. Maximum-likelihood (ML) trees inferred from the same trimmed L protein sequence alignment (916 amino acids) as that used in Figure 2 but using different methods to evaluate branch support. A. ML tree inferred in PhyML using the WAG + Γ amino acid substitution model and the gamma + invariant sites model of site heterogeneity. The best model was selected automatically. The tree with the highest log likelihood (-155217.29) is shown. SH-aLRT support (%) / aBayes support are shown for each branch. B. ML tree inferred in MEGA 7 using the JTT amino acid substitution model. The tree with the highest log likelihood (-164175.08) is shown. Bootstrap support proportion values (500 iterations) are shown for each branch. The trees are rooted on the chuvirus clade and drawn to scale with branch lengths measured in the number of substitutions per site. FigTree was used to plot and annotate the trees.

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