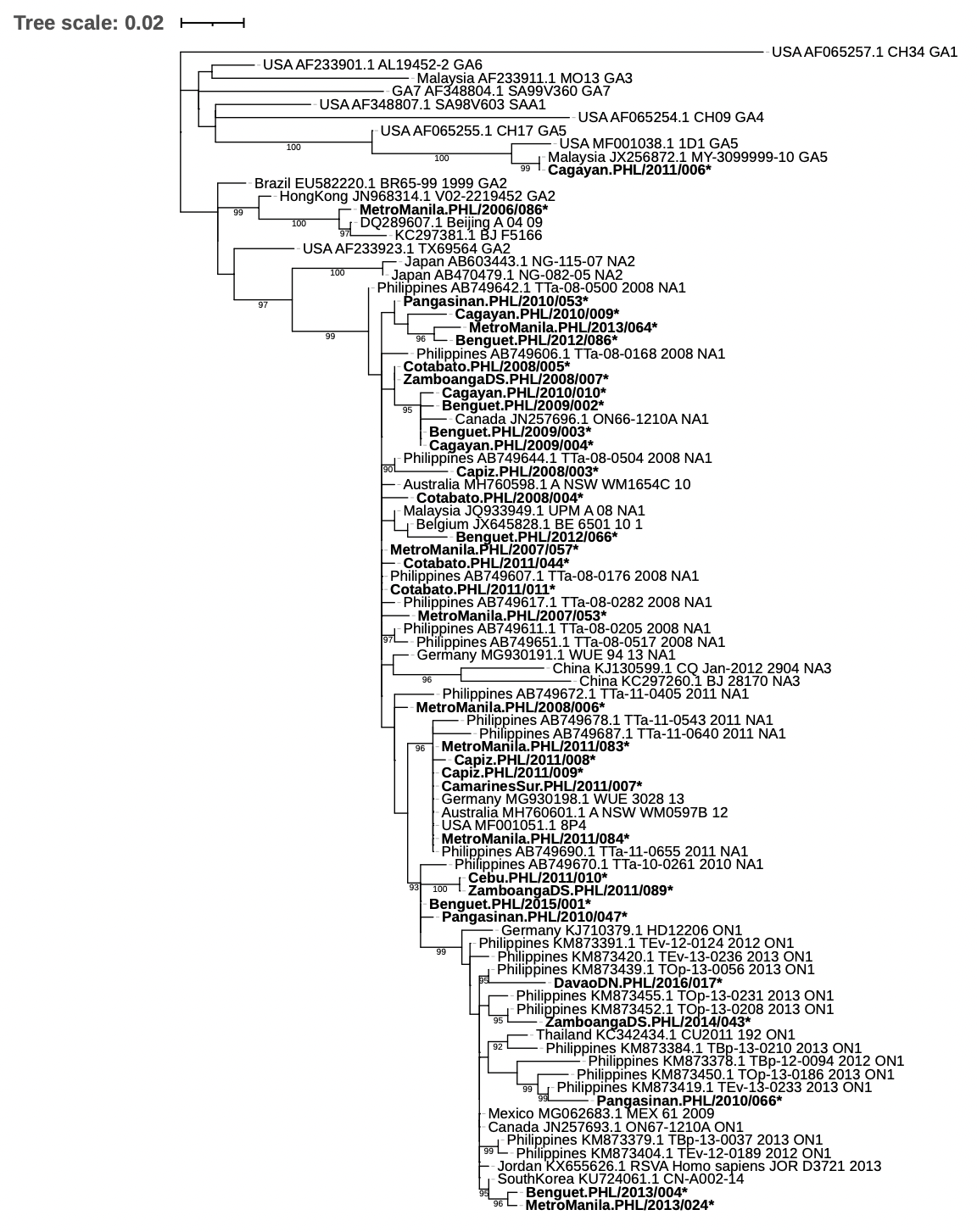
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**Figure 3A - RSV-A**

**Figure 3B**

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**Figure 3B - RSV-B**

**Figure 3.** Phylogenetic trees of (Figure 3A) RSV-A and RSV-B (Figure 3B) partial G gene region. The trees were inferred from the partial G gene regions by the maximum-likelihood method, using bootstrap values calculated from 1000 trees. Sequences about 333 bp for RSV-A, and 324 bp for RSV-B were included in the analysis. Only bootstrap values higher than 90% were shown. Strains isolated in the Philippines for this study are boldfaced and marked with asterisks.