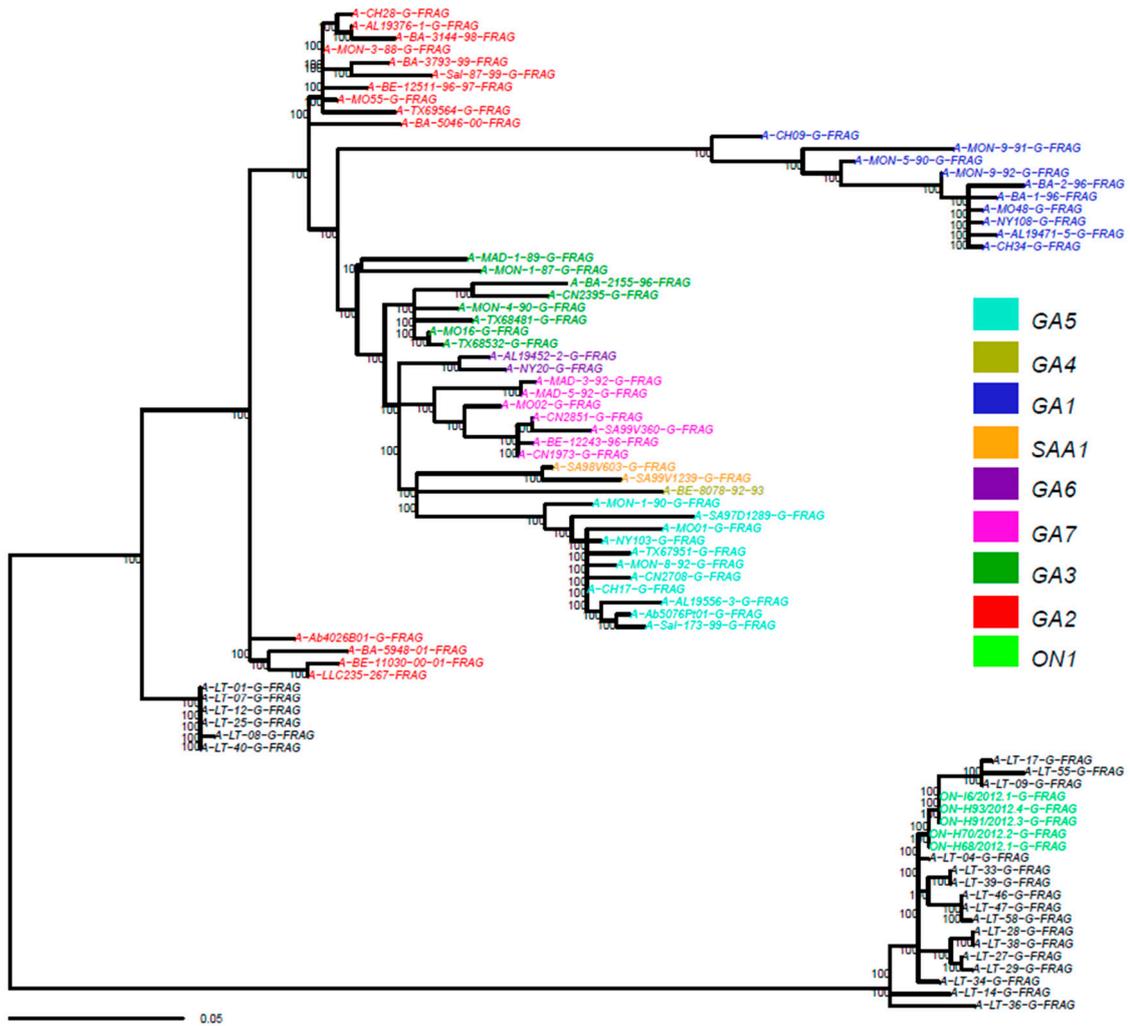
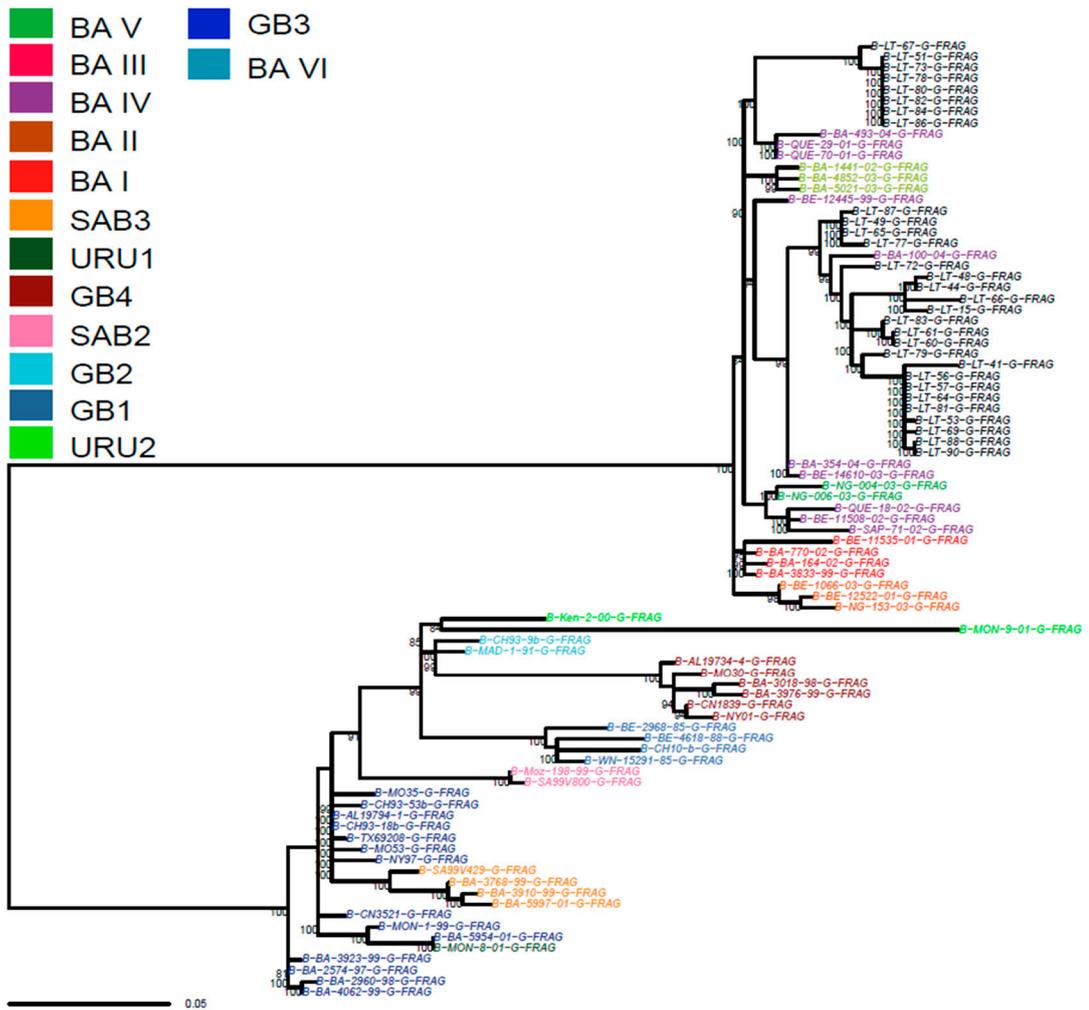


Supplementary Material



**Figure S1.** RSV Phylogenetic trees of RSV strains group A, based on the second hypervariable region of G-gene as described by Peret et al [9]. Selected worldwide previously described sequences (color), were retrieved from GenBank and compared to local strains from Santiago, Chile (black). Phylogenetic tree construction was performed by maximum likelihood analysis, and bootstrap values were calculated to support clustering. Only bootstrap values greater than 75% are shown.



**Figure S2.** RSV Phylogenetic trees of RSV strains group B, based on the second hypervariable region of G-gene as described by Peret et al [9]. Selected worldwide previously described sequences (color), were retrieved from GenBank and compared to local strains from Santiago, Chile (black). Phylogenetic tree construction was performed by maximum likelihood analysis, and bootstrap values were calculated to support clustering. Only bootstrap values greater than 75% are shown.