

VP7-G2

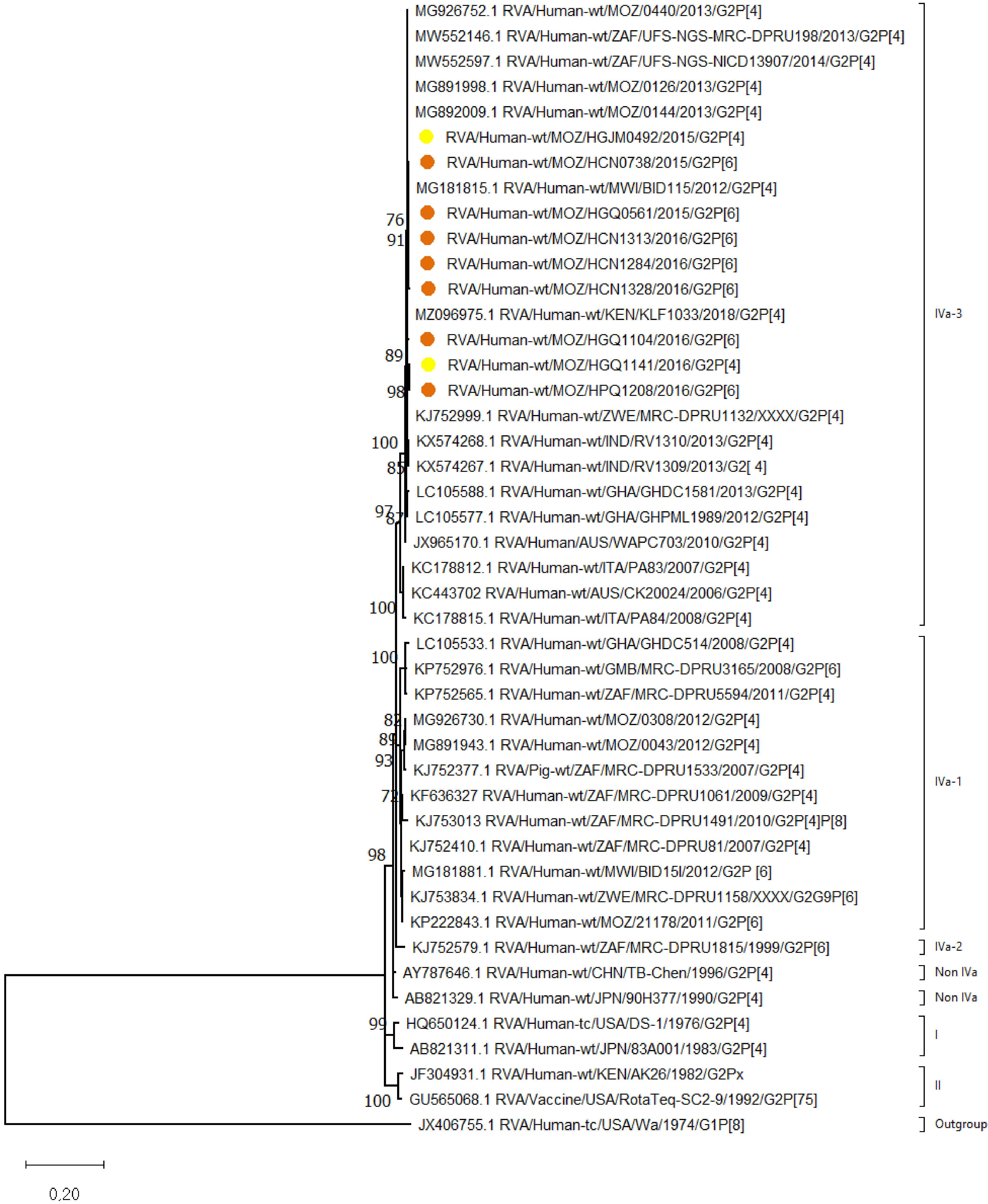
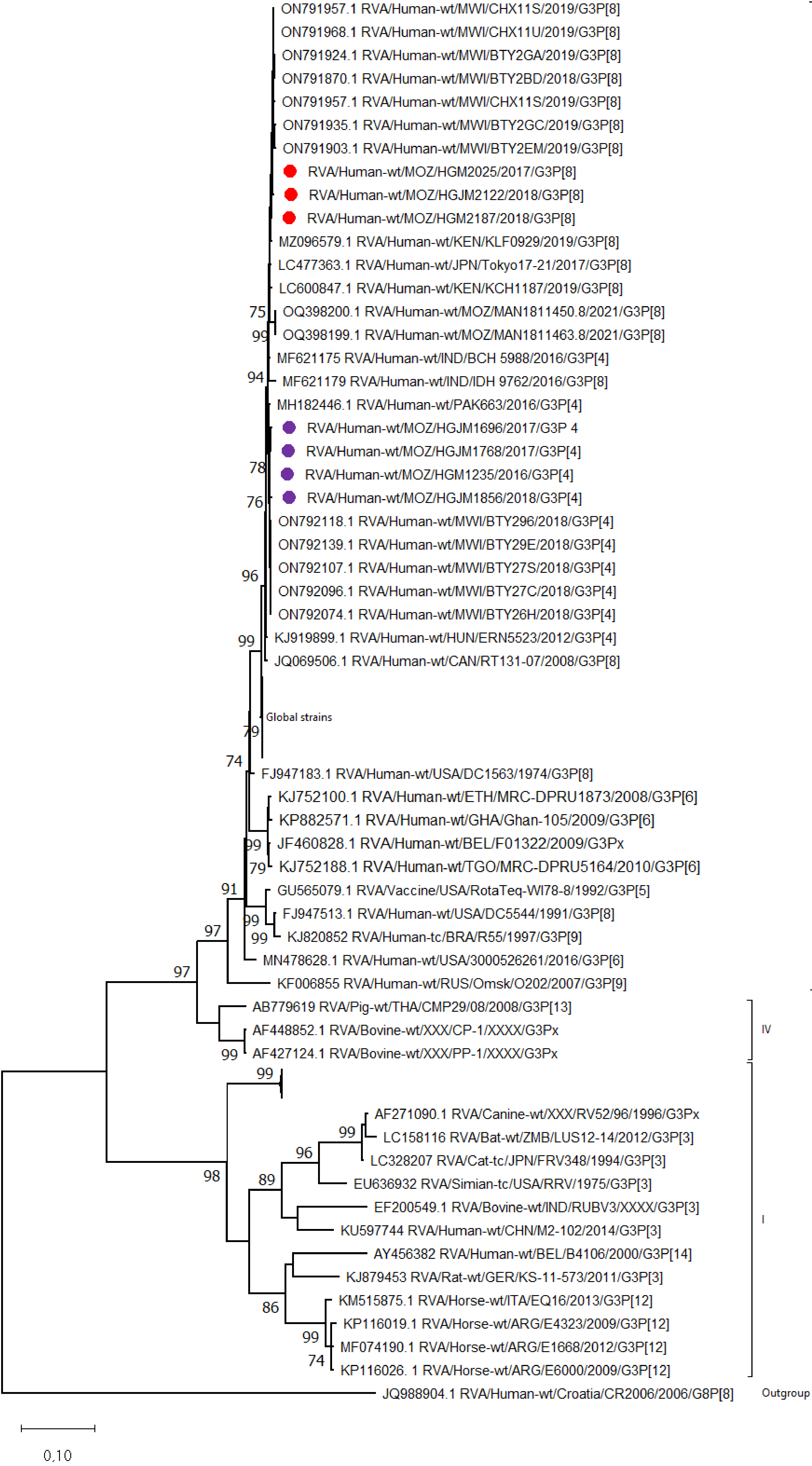
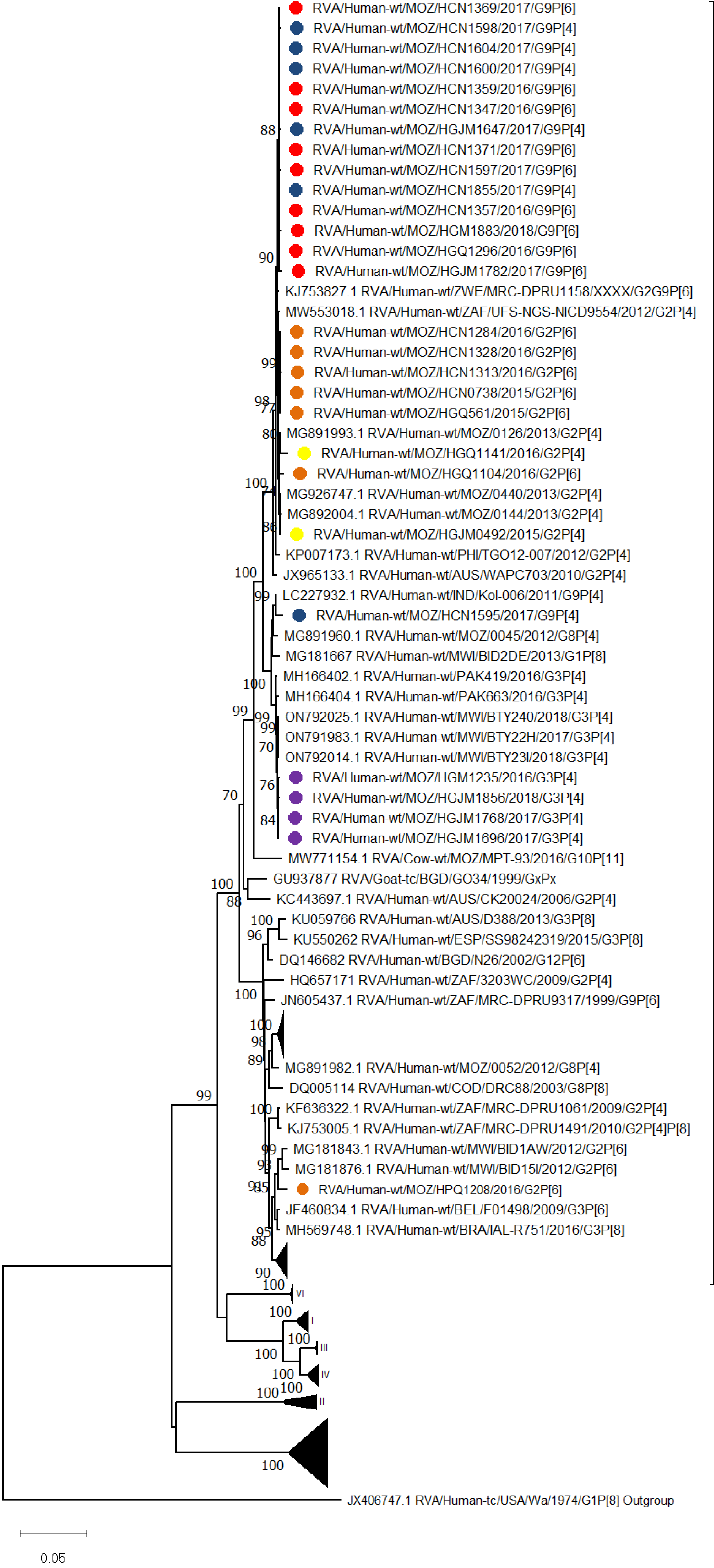


Figure S1: Phylogenetic trees based on the ORF nucleotide sequences of the DS1-S (VP7-G2, VP7-G3, VP1-R2, VP2-C2, VP3-M2, NSP1-A2, NSP2-N2, NSP3-T2, NSP4-E2 and NSP5/6-H2) and (VP7-G1, VP6-I1, VP1-R1, VP2-C1, VP3-M1, NSP1-A1, NSP2-N1, NSP3-T1, NSP4-E1, and NSP5/6-H1) genes of circulating Mozambican and global strains obtained from GenBank. The trees were constructed based on the maximum likelihood method implemented in MEGA X [29], using the best-fit nucleotide substitution model Tamura-3-parameter (T92+G+I) for VP6-I2, VP3- M2, VP7-G1 and VP2-C1, T92+G for VP7-G3, VP7-G2, NSP1-A2 and NSP3-T2, T92+I for , NSP4-E2 and NSP4-E1, T92 for NSP4-E6, NSP1-A1 and NSP2-N1, General Time Reversible (GTR+G+I) for VP1-R2, NSP2-N2 and VP3-M1, GTR+G for VP2-C1 and NSP5/6-H2, GTR+I for VP1-R1 and NSP5/6-H1. Bootstrap values (1000 replicates) 70%. Scale bar indicates genetic distance expressed as the number of nucleotide substitutions per site. G9P[4] strains are indicated by blue, G9P[6] by red, G3P[4] by purple, G3P[8] by red, G2P[4] by yellow, G2P[6] by brown and G1P[8] by black circles.

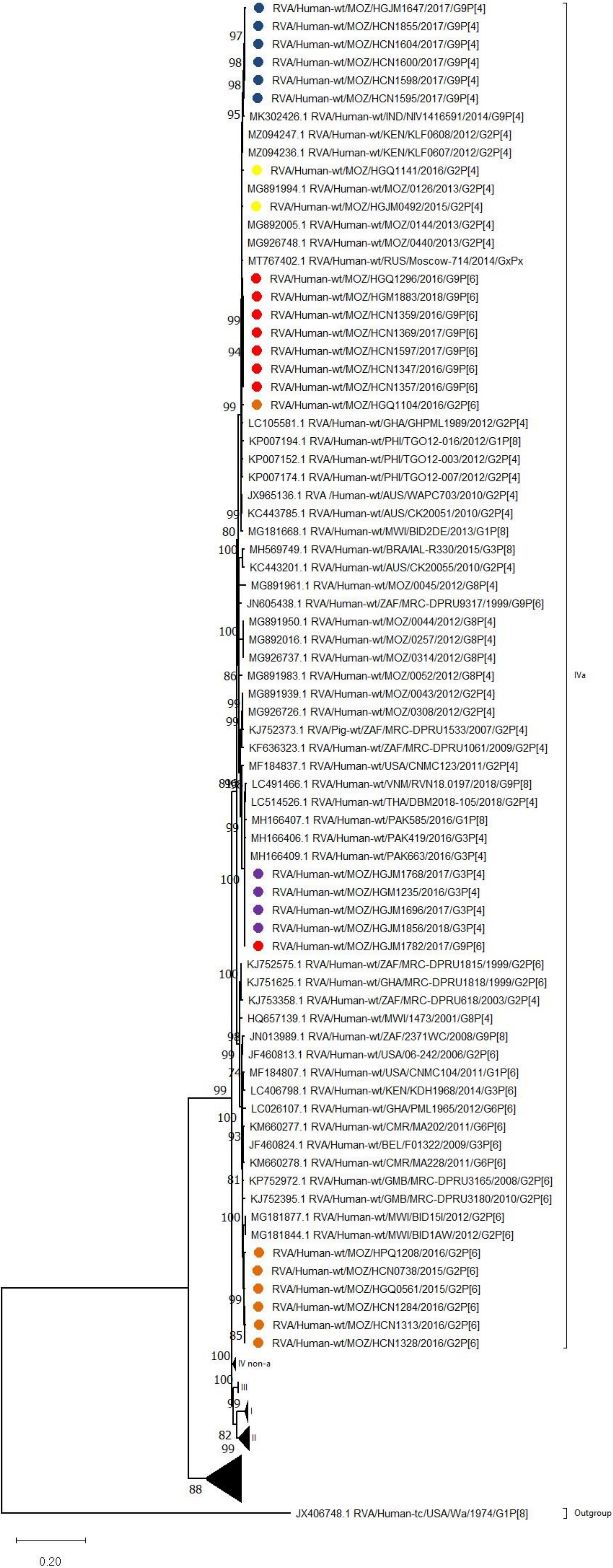
VP7-G3



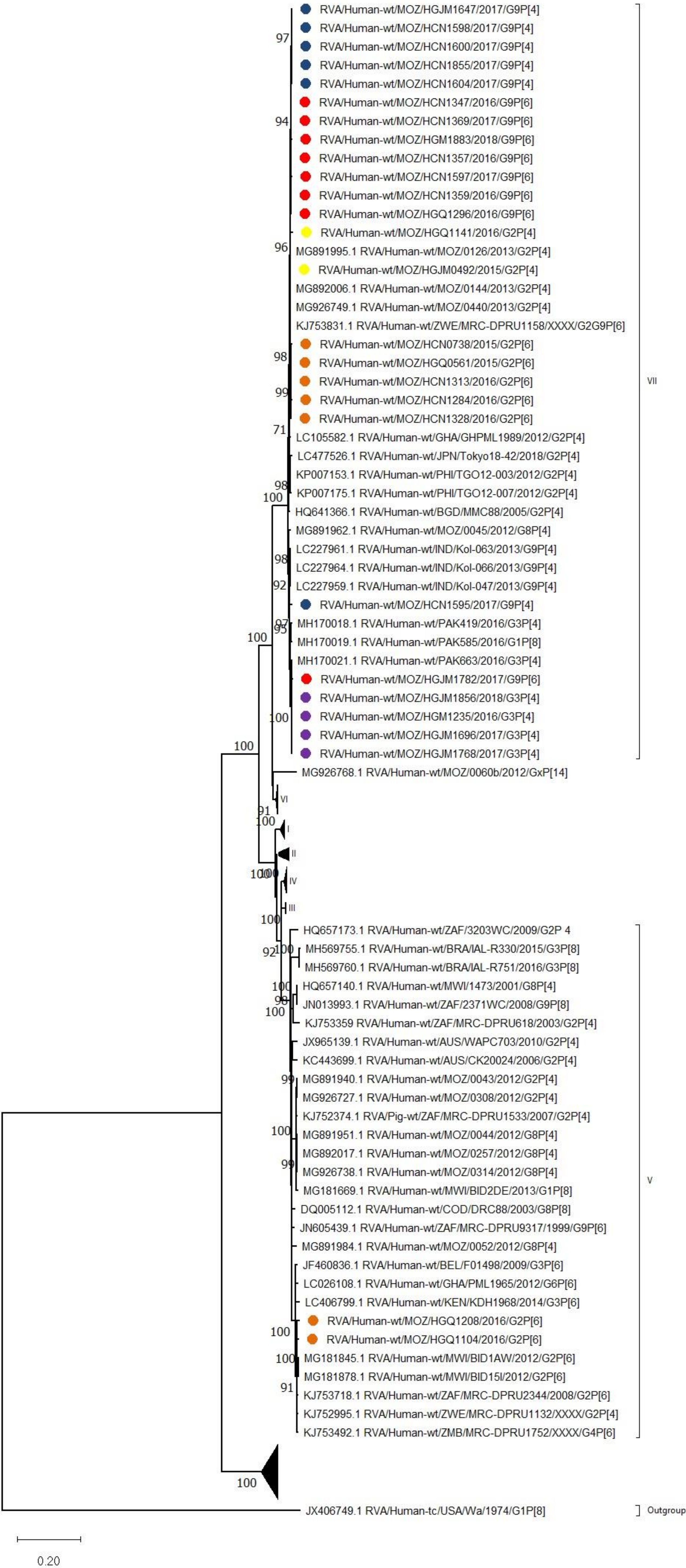
VP1-R2



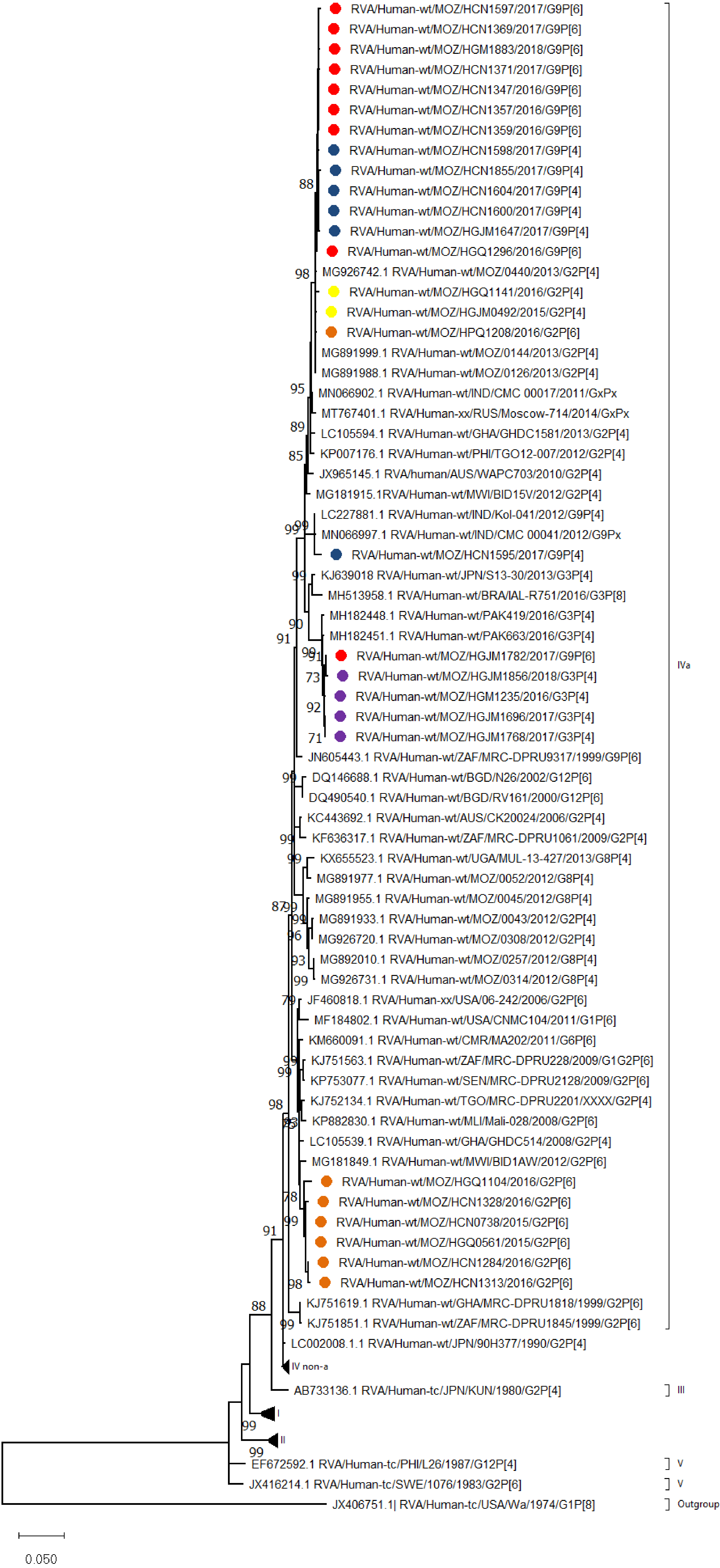
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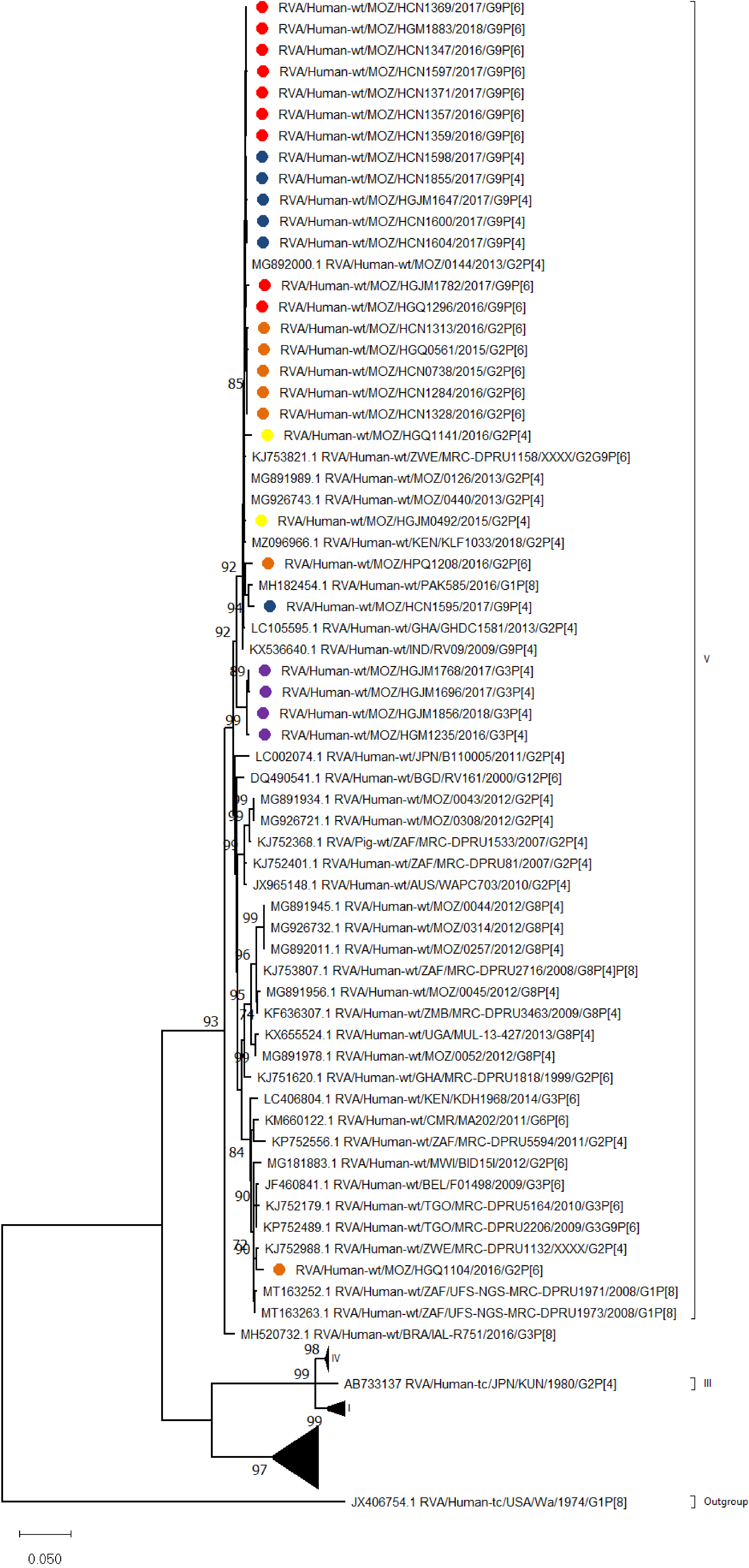
VP3-M2



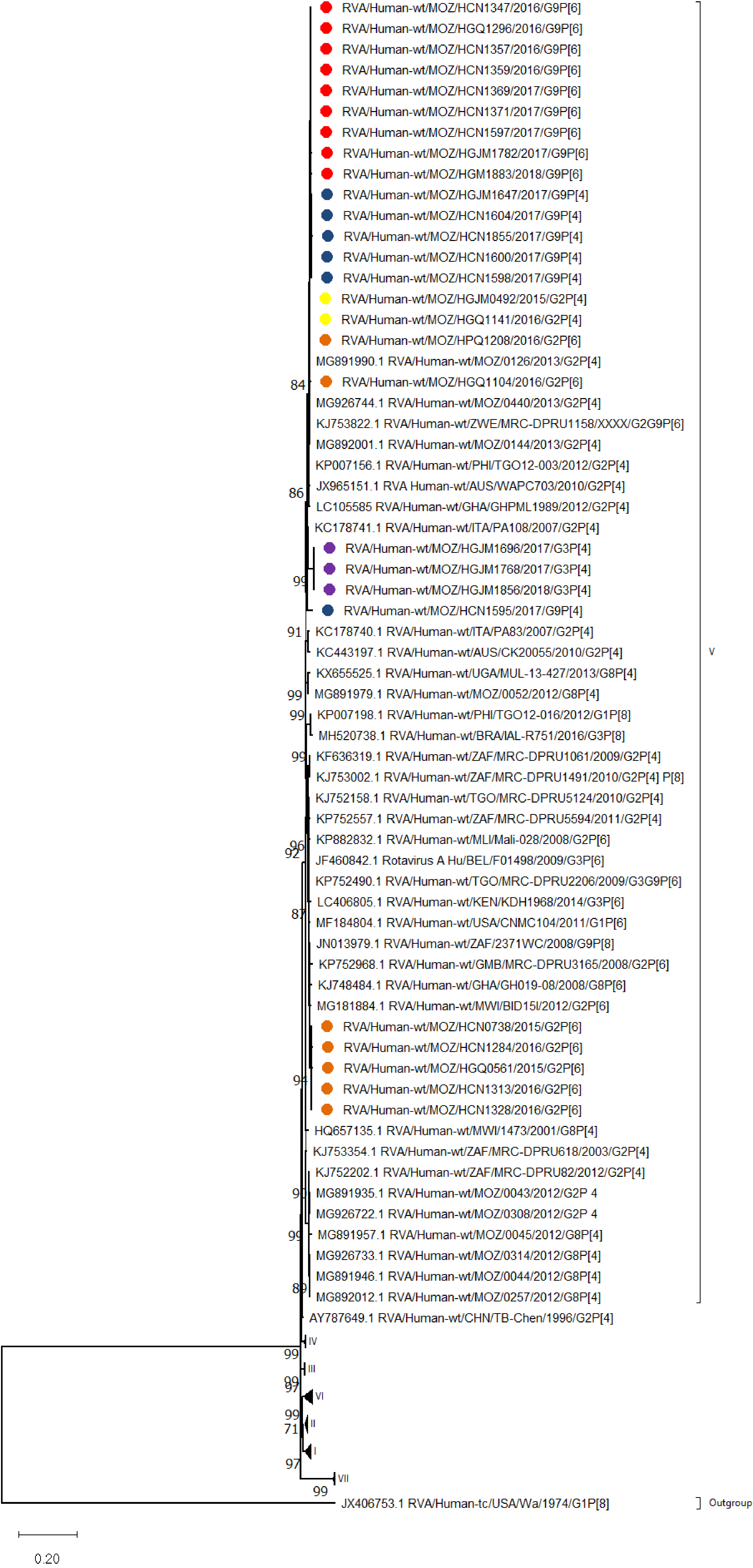
NSP1-A2



NSP2-N2



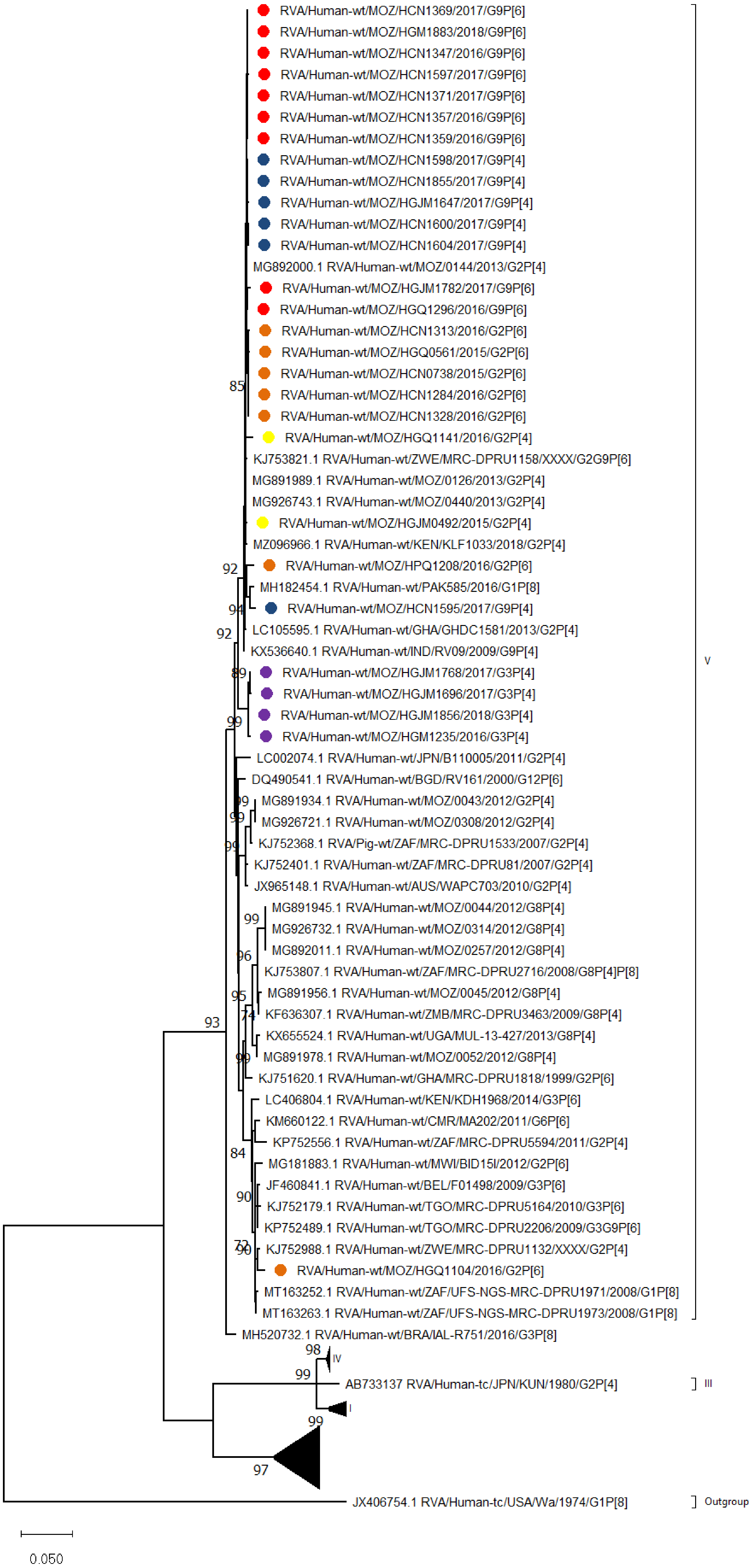
NSP3-T2



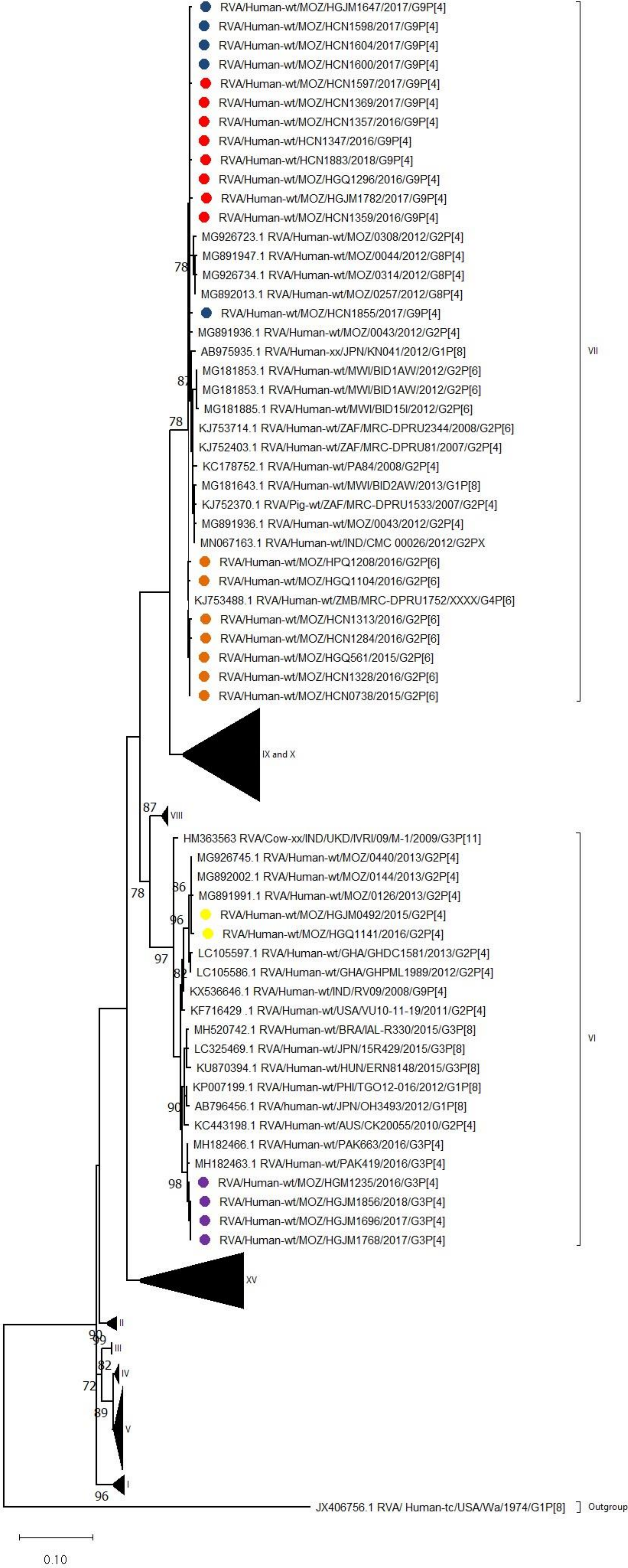
NSP4-E6



NSP4-E2



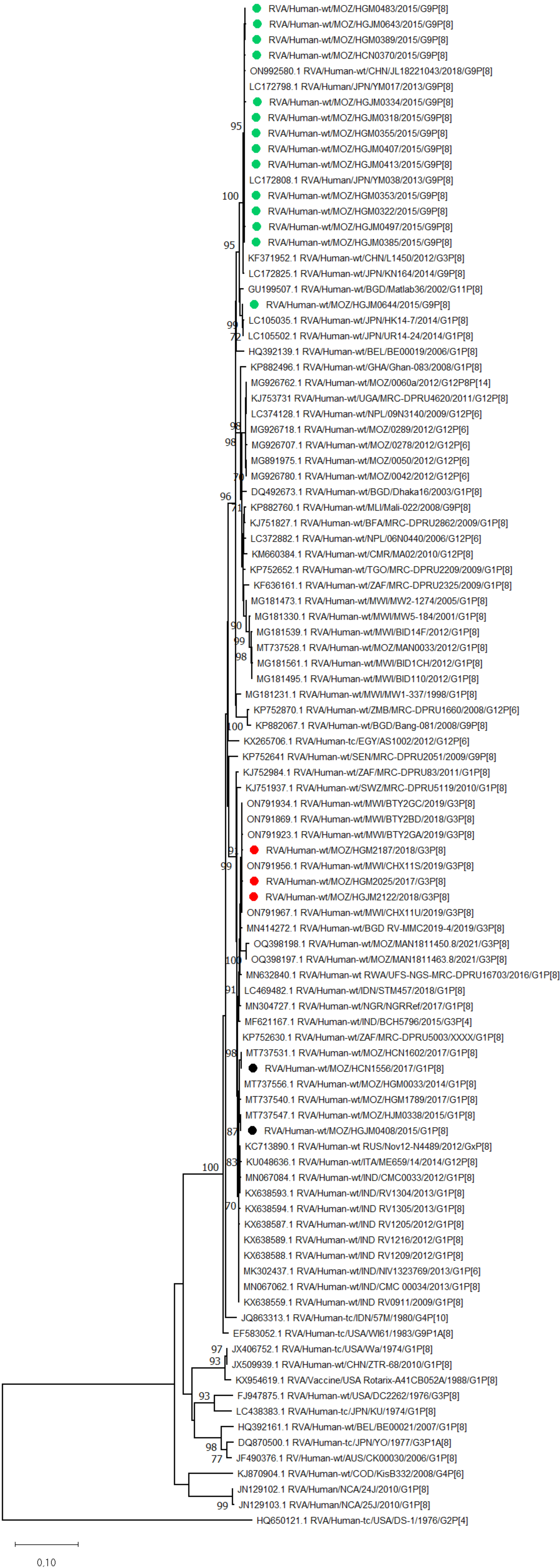
NSP5/6-H2



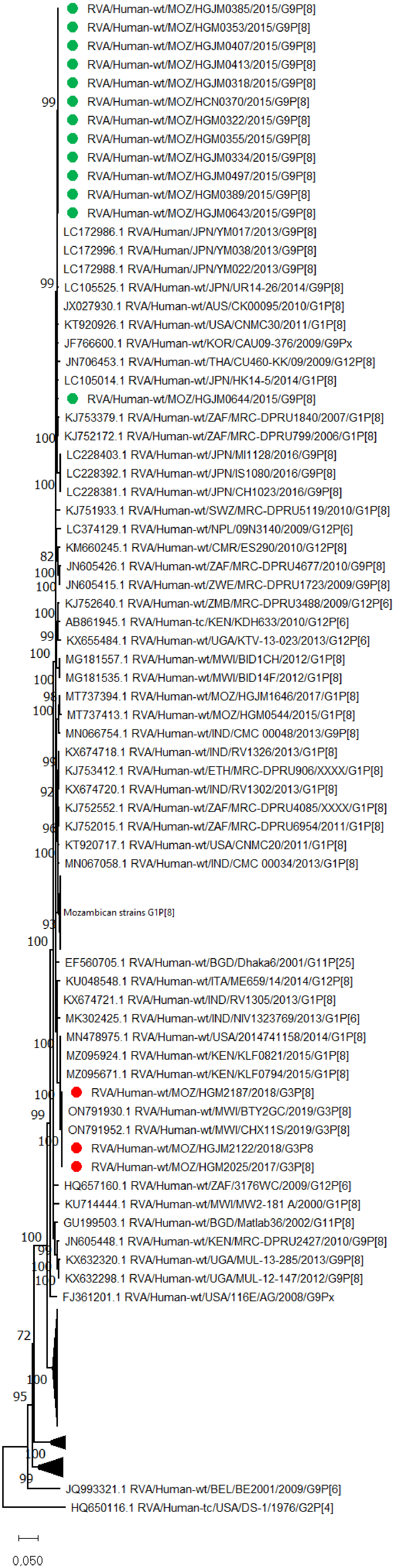
VP7-G1



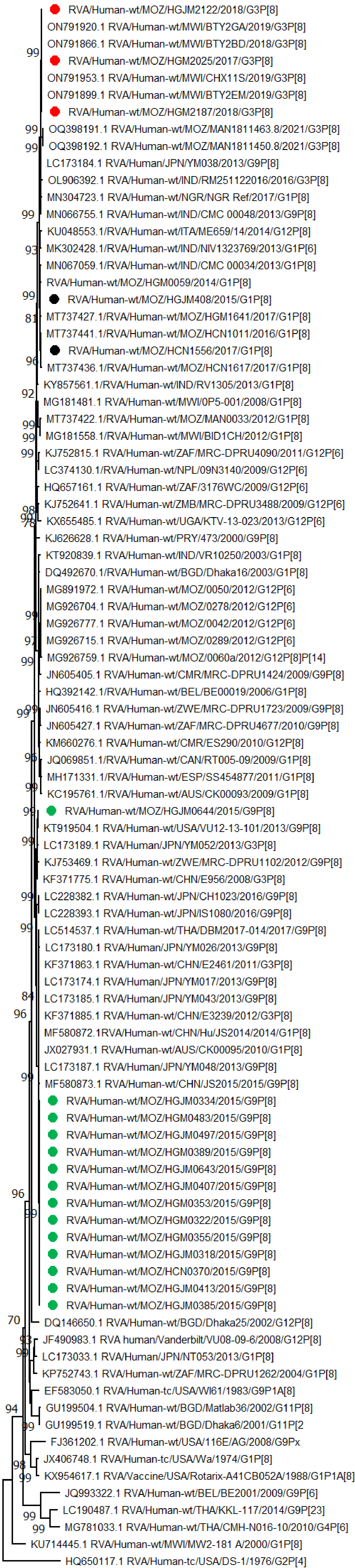
VP6-I1



VP1-R1



VP2-C1

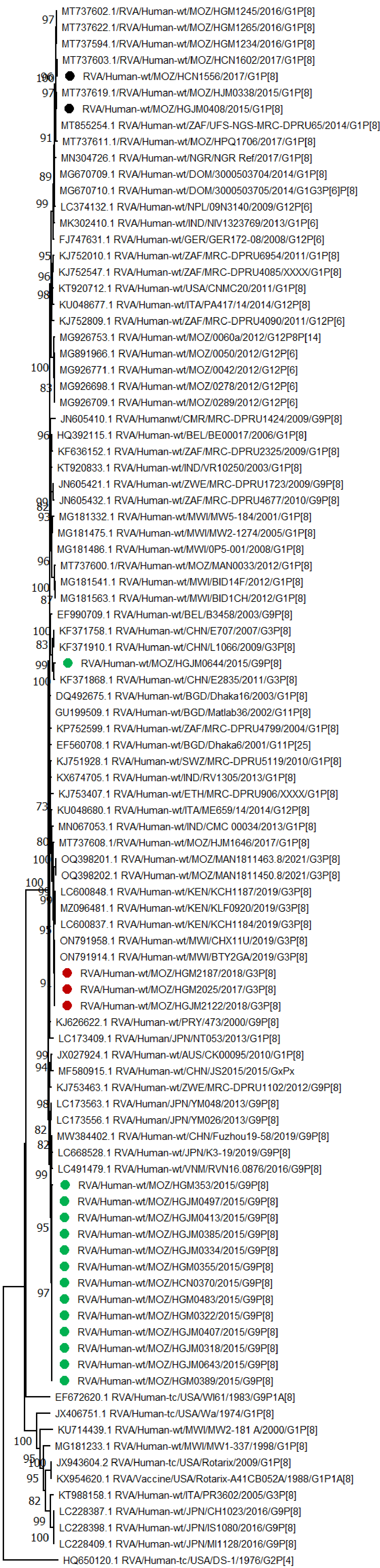


0.050

VP3-M1

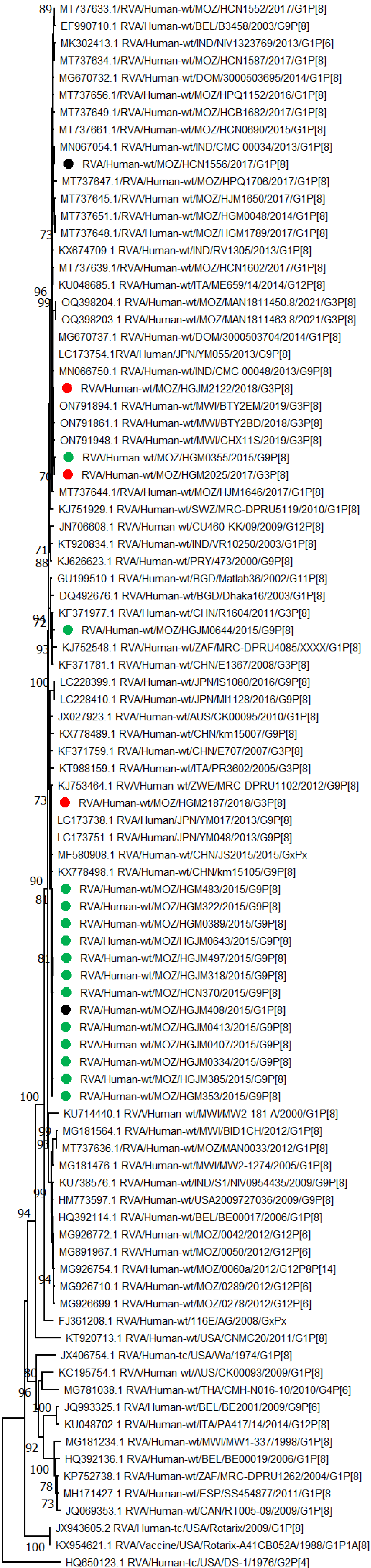


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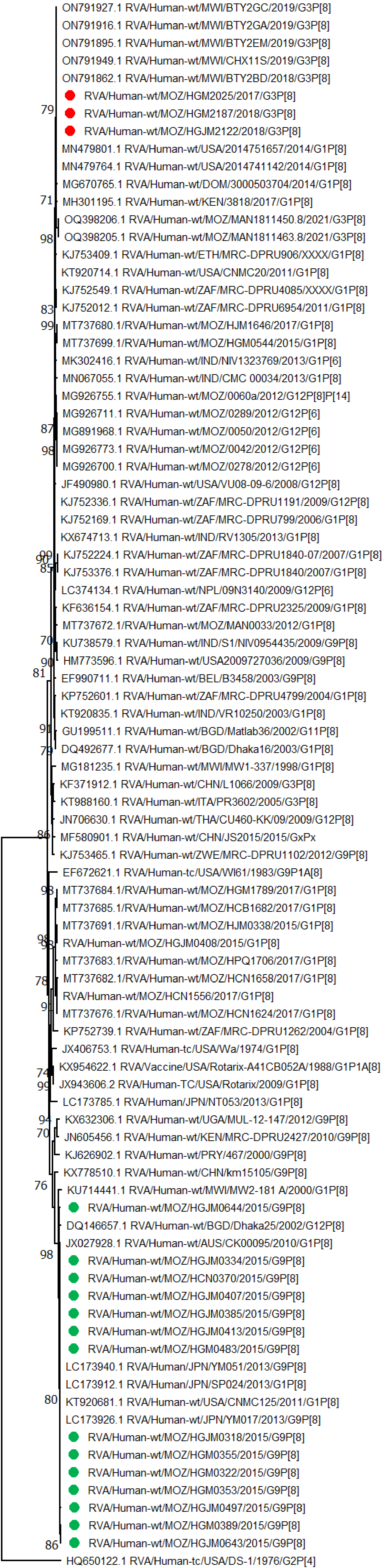
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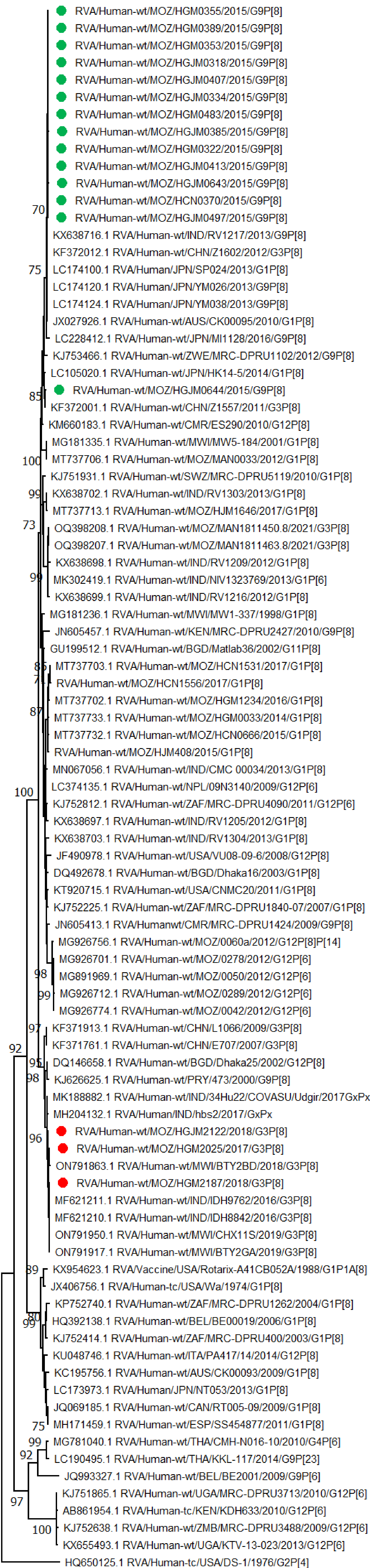
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NSP3-T1



0.050

NSP4-E1



H

0.01

NSP5/6-H1



0.02