

Fig. S1 Legend

Maximum likelihood tree based on partial RdRp and VP1 genes (526 bp) of GII.3[P12] NoV. (Evolutionary distances were computed using the K2+G model in MEGA X. Bootstrap values (>70%) from 1,000 replicates are shown at the nodes. Scale bars indicate nucleotide substitutions per site. Reference sequences are marked with red triangles. CHN: China, JP: Japan, ESP: Spain, RUS: Russia, USA: The United States of America, ID: India, CAN: Canada, AUS: Australia, SKO: South Korea).

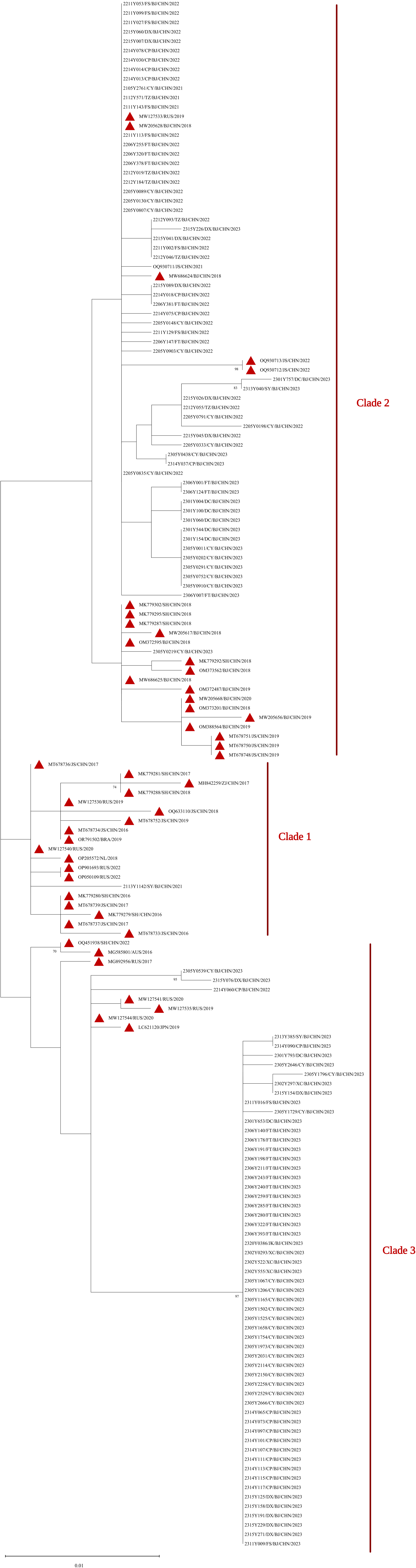


Fig. S2 Legend

Maximum likelihood tree based on whole-genome sequences of GIL.3[P12] NoV.

(Evolutionary distances were computed using the GTR+G model in MEGA X. Bootstrap values (>70%) from 1,000 replicates are shown at the nodes. Scale bars indicate nucleotide substitutions per site. Reference sequences are marked with red triangles. CHN: China, JP: Japan, ESP: Spain, RUS: Russia, USA: The United States of America, ID: India, CAN: Canada, AUS: Australia, SKO: South Korea)

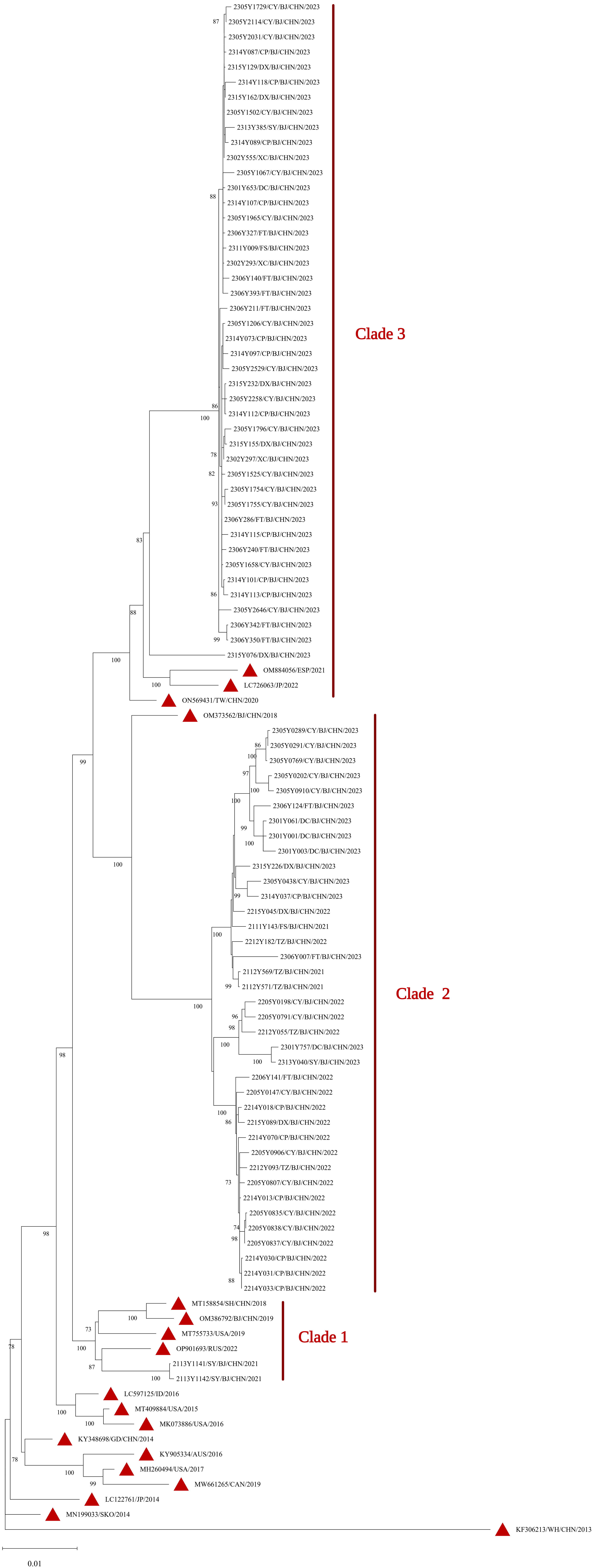


Fig. S3 Legend

Maximum likelihood tree based on VP1 genes (1647 bp) of GII.3[P12] NoV. (Evolutionary distances were computed using the K2+G model in MEGA X. Bootstrap values (>70%) from 1,000 replicates are shown at the nodes. Scale bars indicate nucleotide substitutions per site. Reference sequences are marked with red triangles. CHN: China, JP: Japan, ESP: Spain, RUS: Russia, USA: The United States of America, ID: India, CAN: Canada, AUS: Australia, SKO: South Korea).

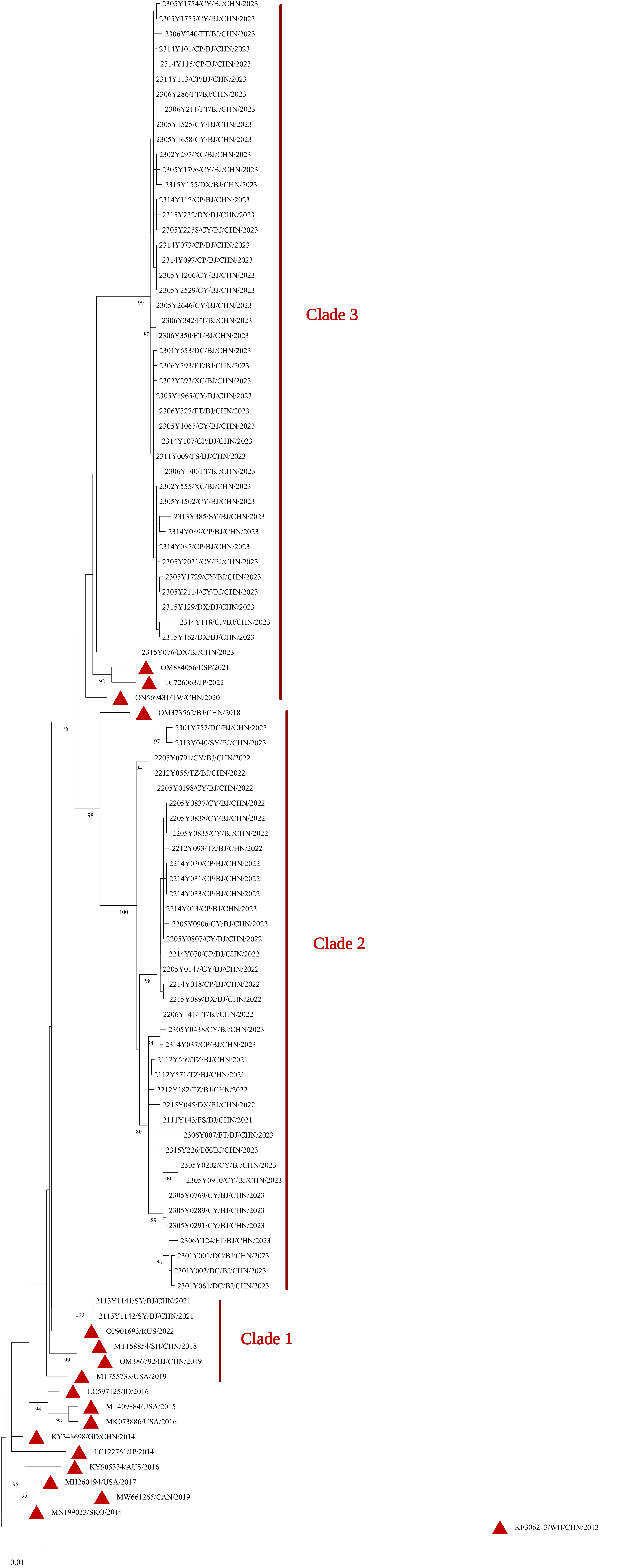


Fig. S4 Legend

Maximum likelihood tree based on RdRp genes (1530 bp) of GII.3[P12] NoV. (Evolutionary distances were computed using the K2+G model in MEGA X. Bootstrap values (>70%) from 1,000 replicates are shown at the nodes. Scale bars indicate nucleotide substitutions per site. Reference sequences are marked with red triangles. CHN: China, JP: Japan, ESP: Spain, RUS: Russia, USA: The United States of America, ID: India, CAN: Canada, AUS: Australia, SKO: South Korea)

