

Figure 1. TEM micrograph of typical IBV-particles showing the characteristic depression and a “crown” of projections forming a corona (crown) at the periphery of each particle (source: Putterill, 2014).



Figure 1. The morphological characteristics of a normal embryo (source: Deltamune, 2023).



Figure 2. An embryo displaying morphological characteristics of IBV – curling, stunting growth retardation, and feather club-down (source: Deltamune, 2023).

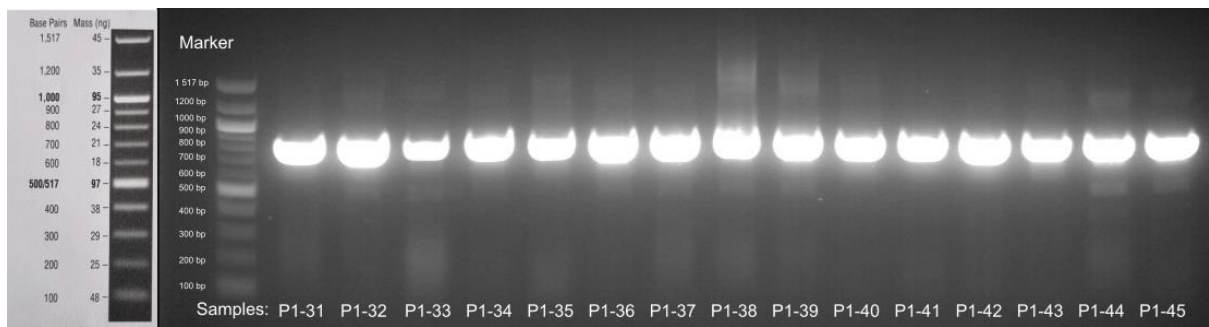


Figure 3. 1% Agarose gel of partial S1 gene bands of 745 bp.

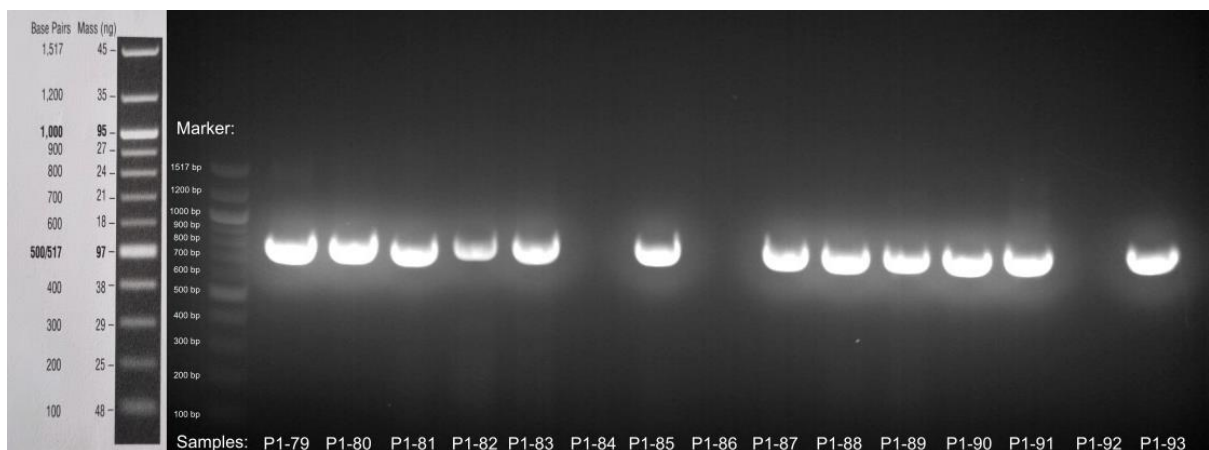


Figure 4. 1% Agarose gel of partial S1 gene bands 745 bp.

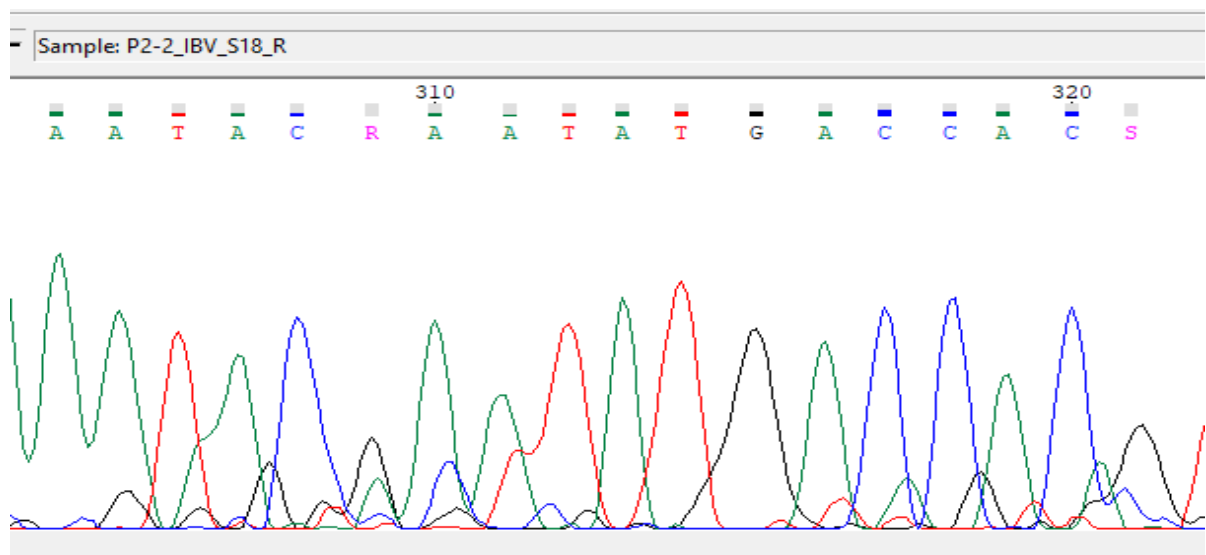


Figure 5. Sample number P2-2 showed as an example of where the letter “R” and “S” would have been changed to a “G” according to the IUPAC nucleotide guidelines.

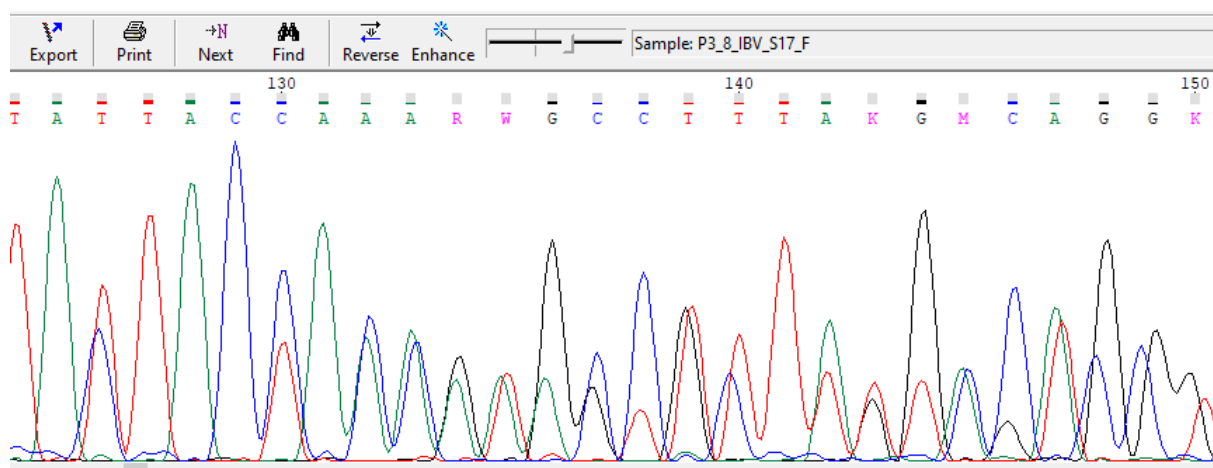


Figure 6. Sample P3-8 displayed as an example of overlapping sequences that indicate a possible mixed sequence.

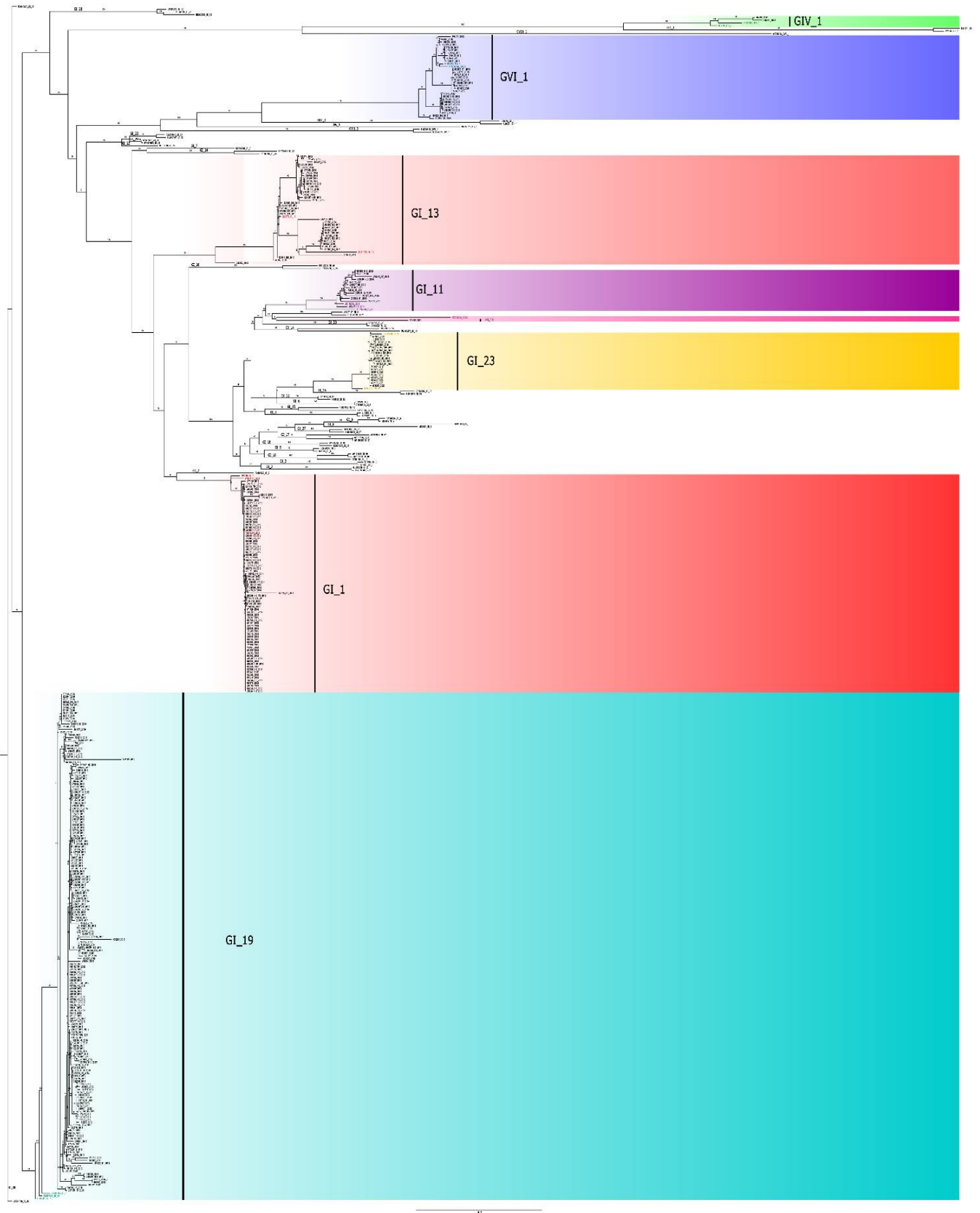


Figure 7. Maximum-likelihood phylogenetic tree based on a partial sequence of the S1 gene that includes all reference and isolate sequences.

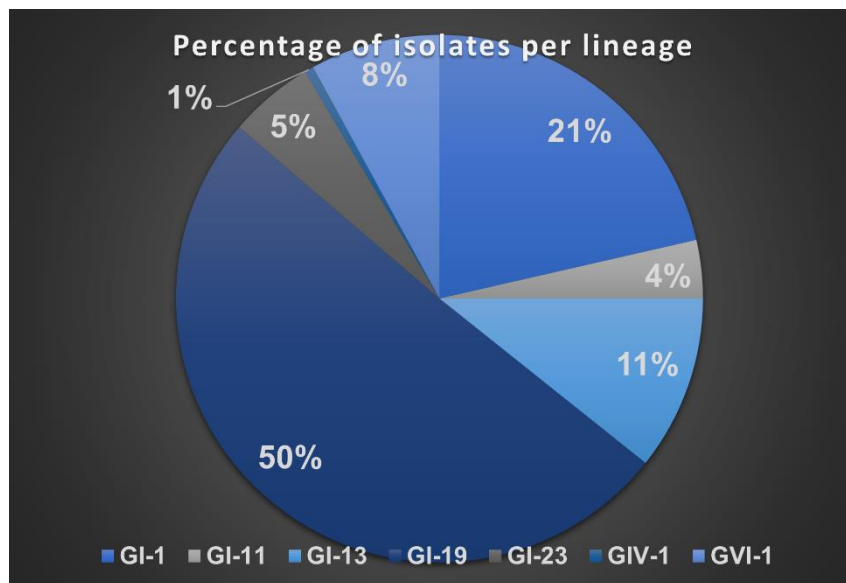


Figure 8. The percentage of IBV isolates identified per lineage during the study period of 2011-2020.

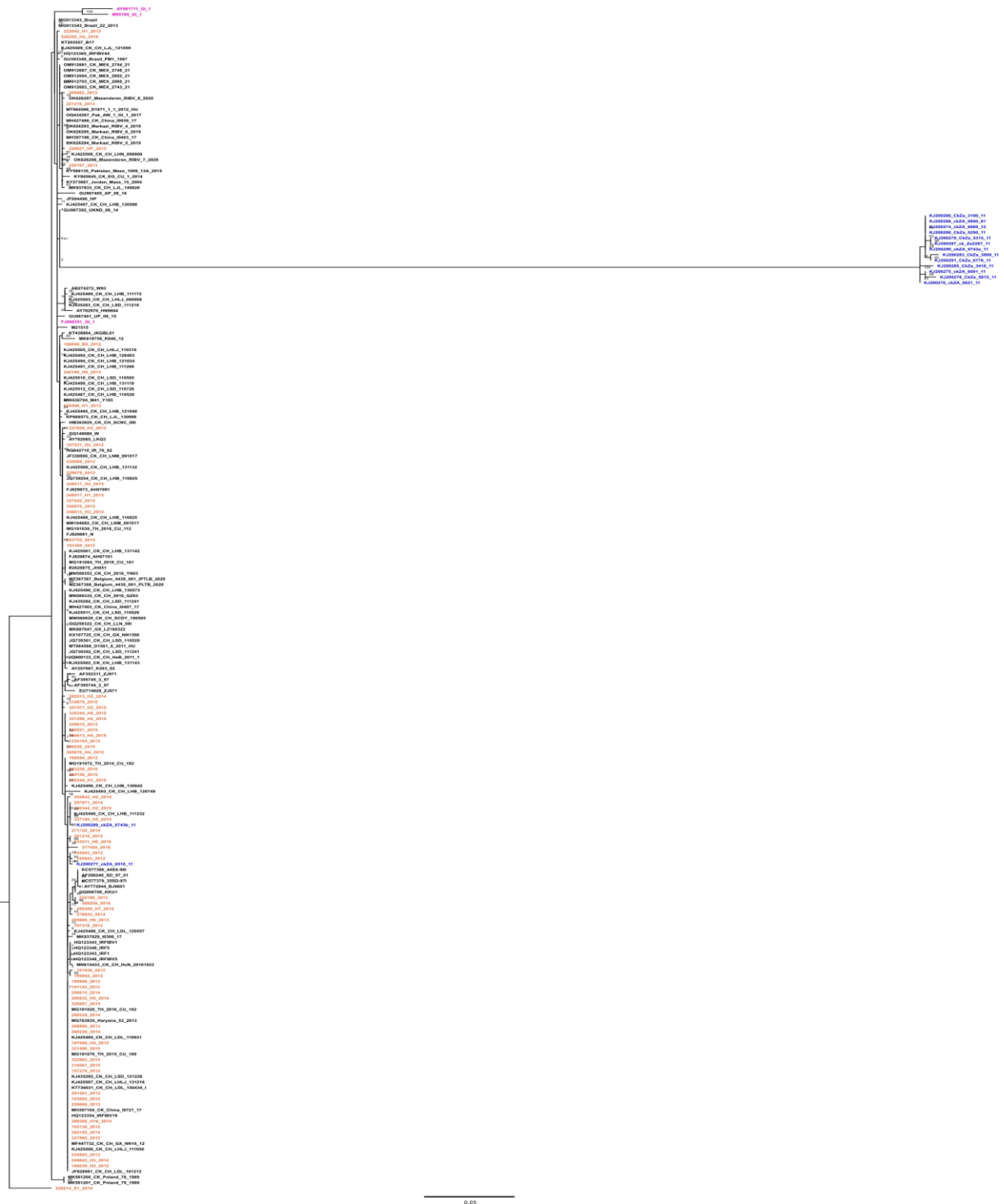


Figure 13(b). Maximum-likelihood phylogenetic tree of lineage GI-1 that includes previously identified ZA H120-like strains from Knoetze et al., 2014 (KJ200286, KJ200283, KJ200280, KJ200279, KJ200278, KJ200291, KJ200275, KJ200276, KJ200277, KJ200290, KJ200289, KJ200274, KJ200288, KJ200287, KJ200285) that were retrieved from Genbank. Study isolates are in orange font, ZA strains are in blue font, genome classification reference samples are in magenta, field viruses retrieved from Genbank are in black.

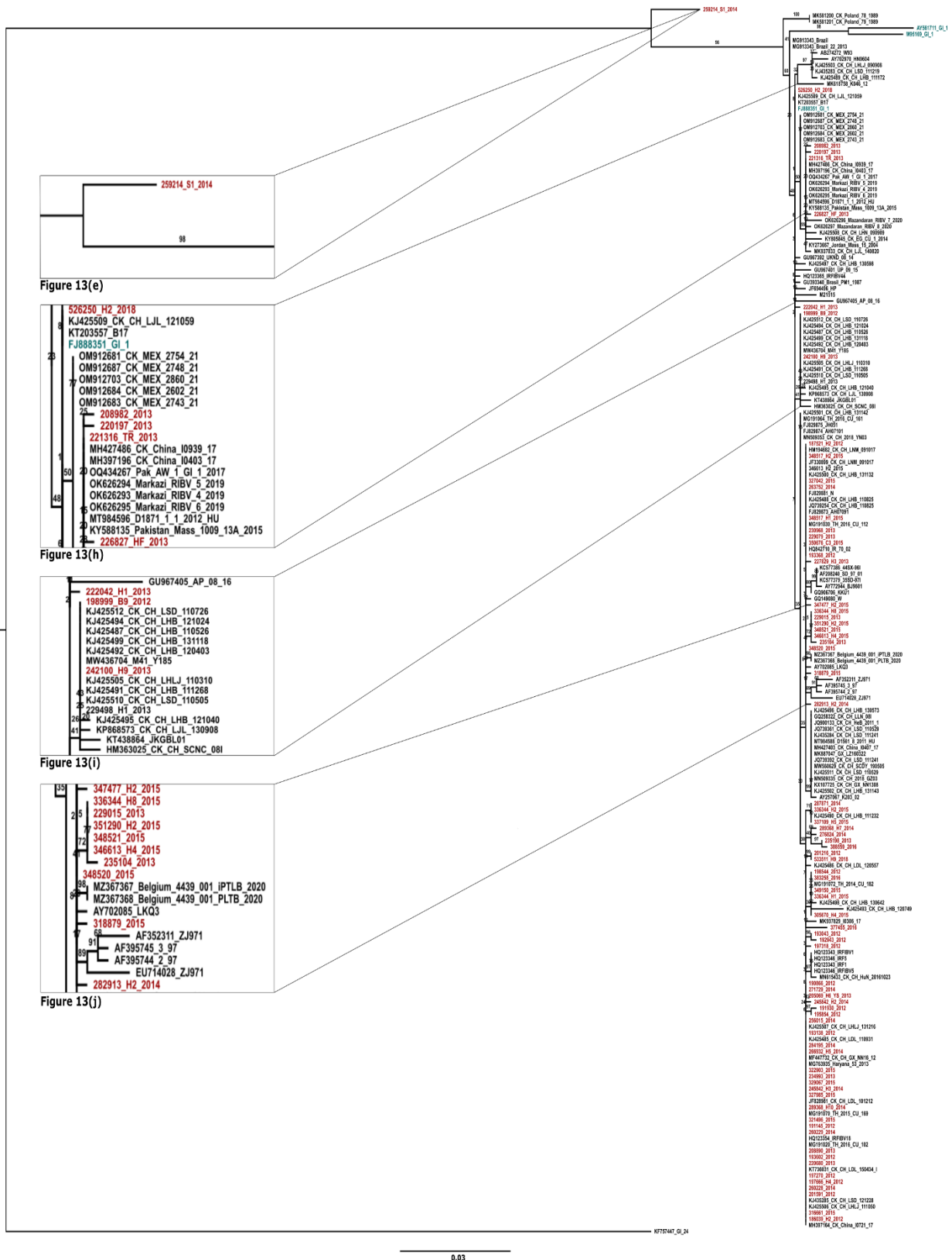


Figure 13(d). Maximum-likelihood phylogenetic tree of lineage GI-1 highlighting sub-set-based trees in Figs 13 (e to j) that follow for a better visualization and discussion. Study isolates are in red font, genome classification reference samples are in light blue font, field viruses retrieved from Genbank are in black font.

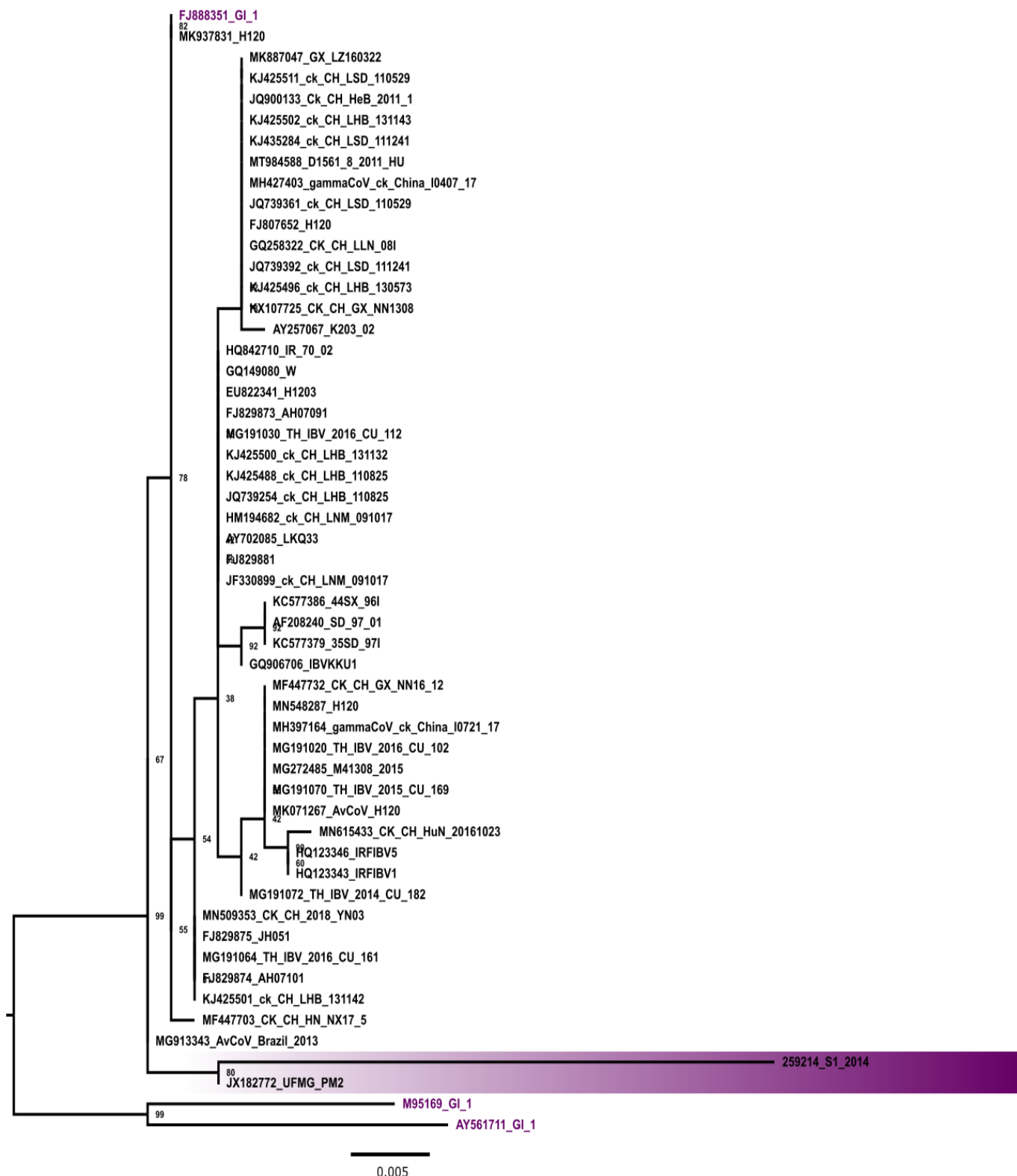


Figure 13(e). Maximum-likelihood phylogenetic tree of the GI-1 lineage re-rooted for an enlarged view of isolate 259214_S1_2014(shaded in purple). Genome classification reference samples are in purple font and field viruses retrieved from Genbank are in black font.



Figure 13(f). Maximum-likelihood phylogenetic tree of the GI-1 lineage, re-rooted for an enlarged view of isolates 259214_S1_2014, 289368_H7_2014 and 276824_2014. Study isolates are highlighted in purple, genome classification reference samples are highlighted in magenta and field viruses retrieved from Genbank are in black.



Figure 13(h). Maximum-likelihood phylogenetic tree of the GI-1 lineage, re-rooted for an enlarged view of isolates 226827_HF_2013, 220197_2013, 221316_2013, 222042_2013, and 526250_H2_2018. Study isolates are highlighted in gold, genome classification reference samples are highlighted in purple and field viruses retrieved from Genbank are in black.



Figure 13(i). Maximum-likelihood phylogenetic tree GI-1, re-rooted for an enlarged view of isolates 198999_B9_2012, 229498_H1_2013, and 242100_H9_2013. Study isolates are highlighted in orange, genome classification reference samples are highlighted in green and field viruses retrieved from Genbank are in black.



Figure 13(j). Maximum-likelihood phylogenetic tree re-rooted for an enlarged view of isolates 347477_H2_2015, 336344_H8_2015, 346613_H4_2015, 351290_H2_2015, 229015_2013, 235104_2013, 348520_2015, 318879_2015, and 282913_H2_2014 in the GI-1 lineage. Study isolates are highlighted in red; genome classification reference samples are highlighted in blue and field viruses retrieved from Genbank are in black.

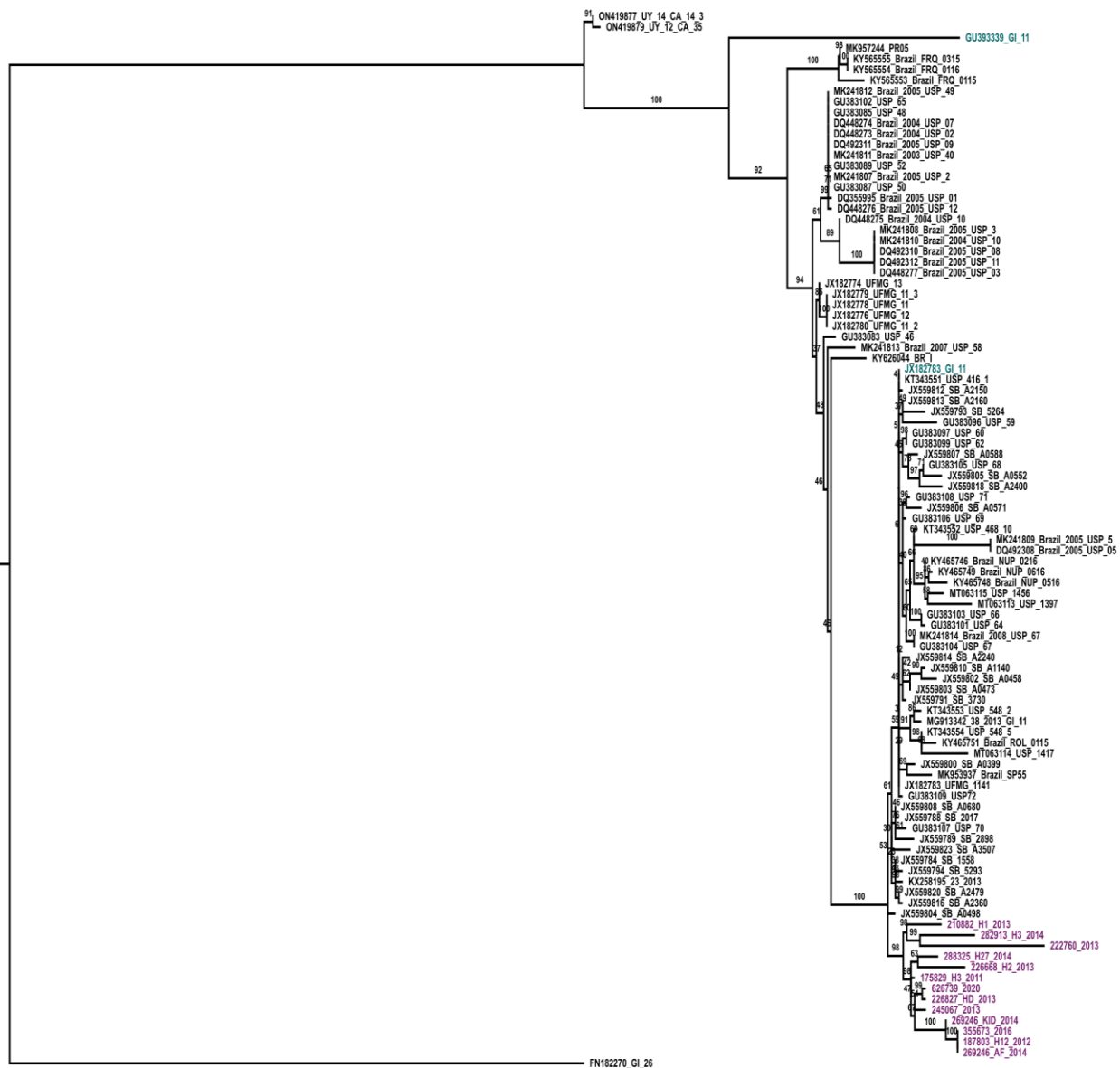


Figure 14. Maximum-likelihood phylogenetic tree of lineage GI-11 IBV. Study isolates are highlighted in purple, genome classification reference samples are in light blue, field viruses retrieved from Genbank are in black.

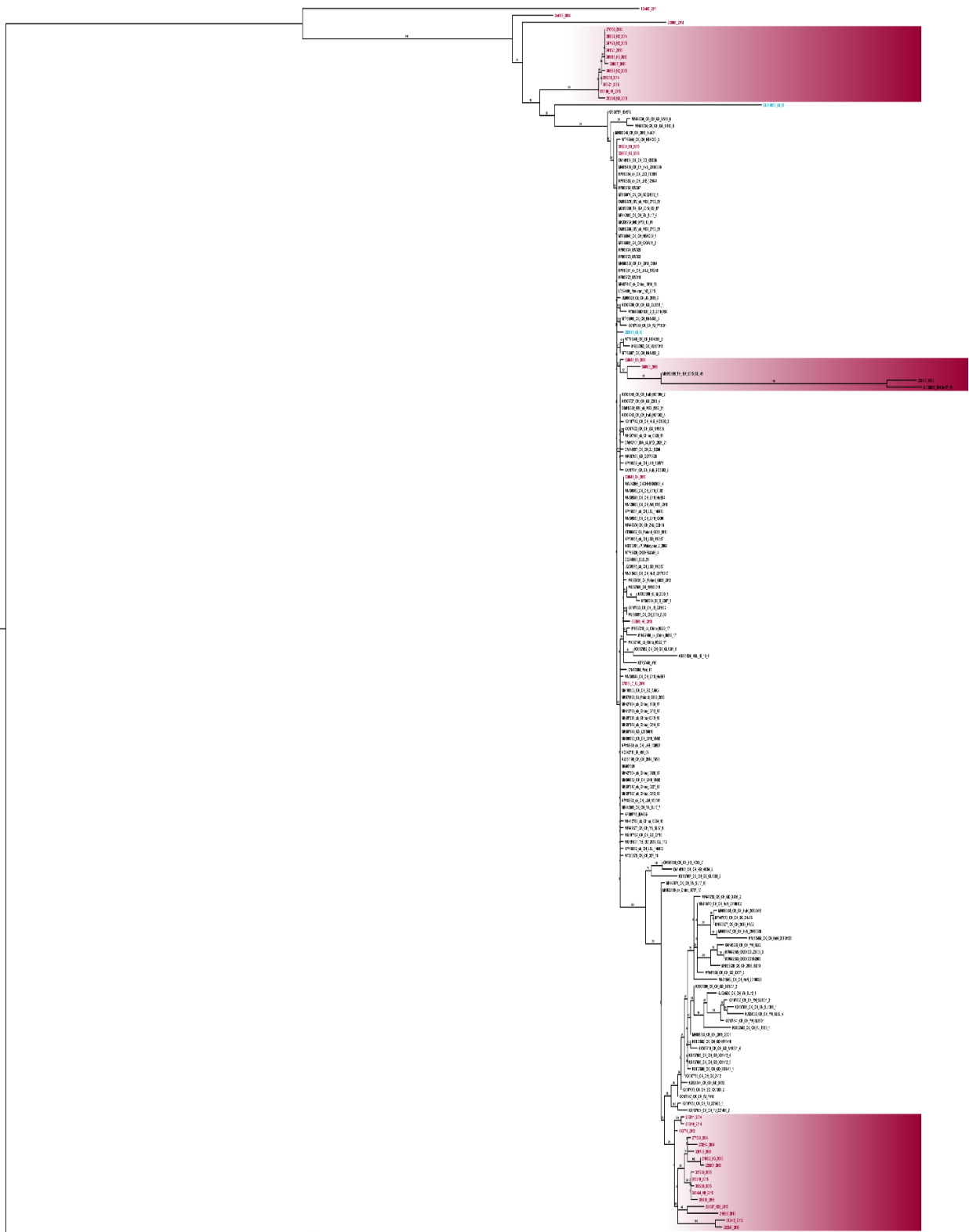
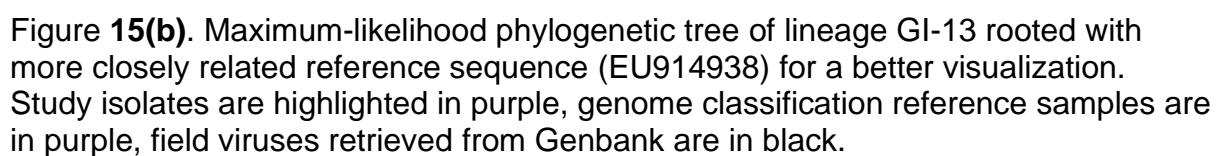


Figure 15(a). Maximum-likelihood phylogenetic tree of lineage GI-13 IBV. Study isolates are highlighted in red, genome classification reference samples are in light blue, field viruses retrieved from Genbank are in black.



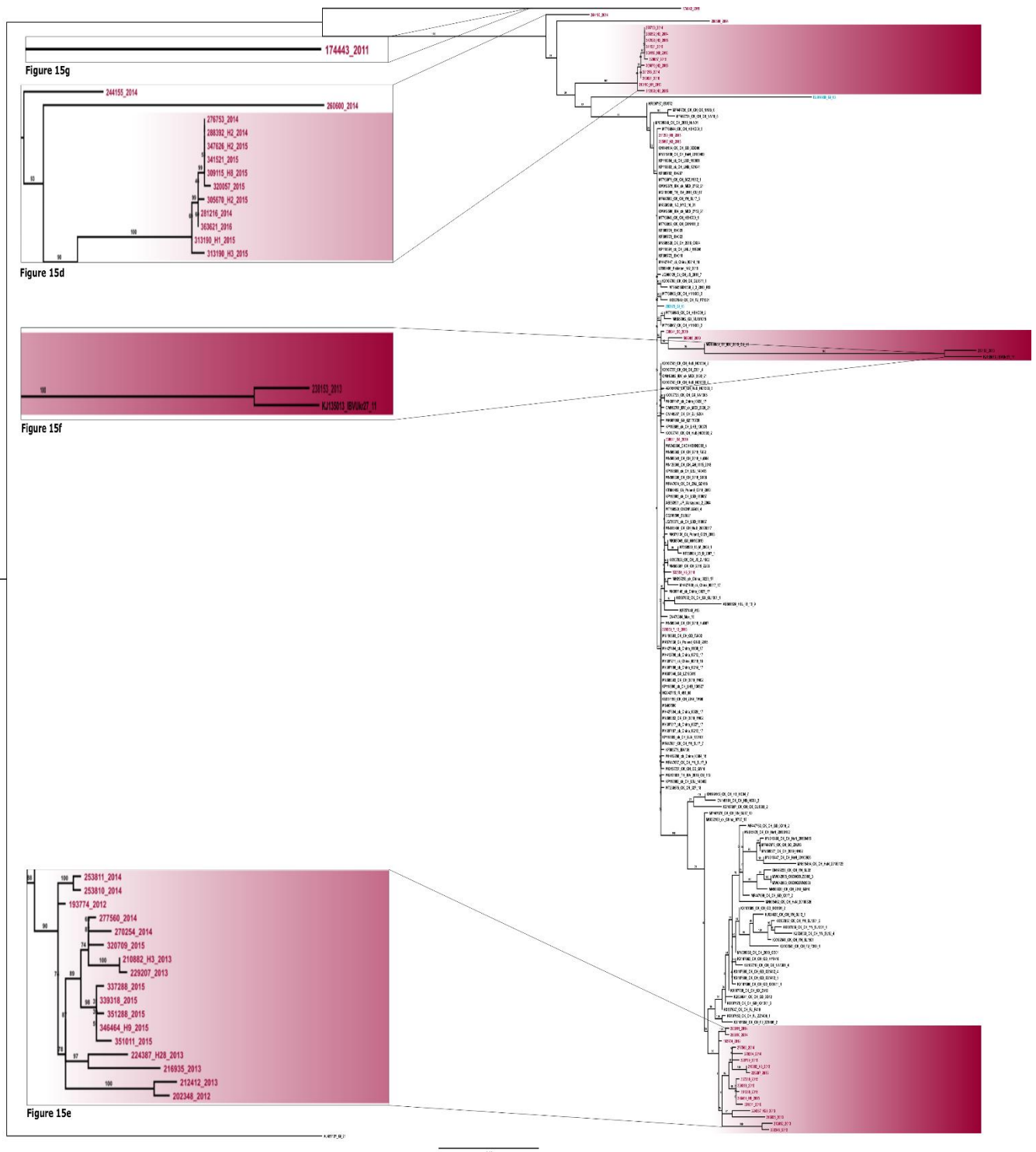


Figure 15(c). Maximum-likelihood phylogenetic tree of lineage GI-13, highlighting isolates in the trees to follow (Figure 15d, 15e, and 15g), with more closely related reference sequences for a better visualization. Study isolates are highlighted in red, genome classification reference samples are in light blue, field viruses retrieved from Genbank are in black.

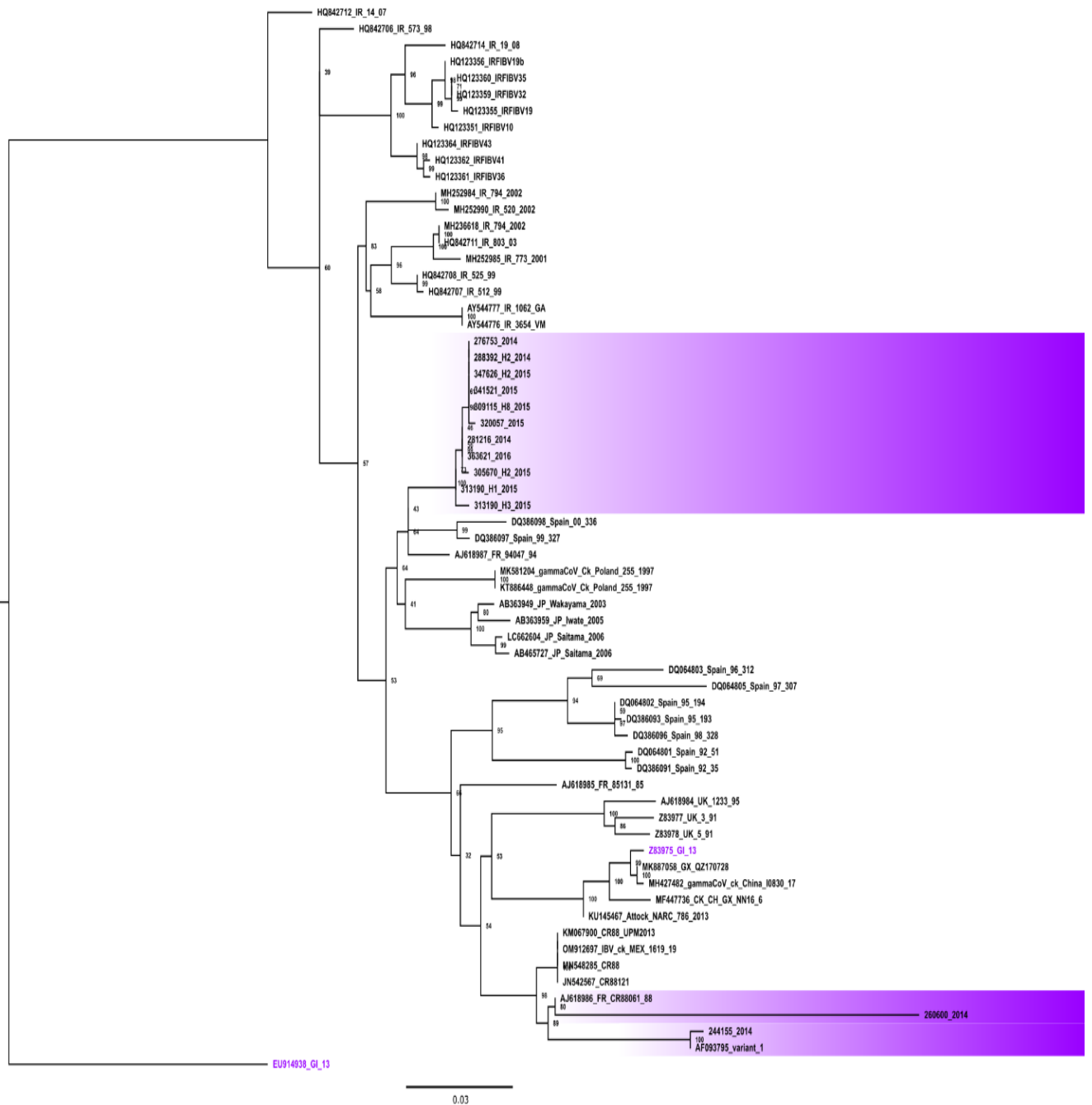


Figure 15(d). Maximum-likelihood phylogenetic tree of the lineage GI-13, re-rooted for an enlarged view of isolates 244155_2014, 260600_2014, 27753_2014, 288392_H2_2014, 347626_H2_2015, 341521_2015, 309115_H8_2015, 320057_2015, 305670_H2_2015, 281216_2014, 363621_2016, 313190_H1_2015, 313190_H3_2015. Isolates are shaded in purple; genome classification reference samples are highlighted in purple font and field viruses retrieved from Genbank are in black font.



Figure 15(e). Maximum-likelihood phylogenetic tree of the GI-13 lineage re-rooted for an enlarged view of isolates 253811_2014, 253810_2014, 193774_2012, 277560_2014, 270254_2014, 320709_2015, 210882_H3_2013, 229207_2013, 337288_2015, 351288_2015, 346464_H9_2015, 351011_2015, 224387_H28_2013, 216935_2013, 21241_2013, and 202348_2012. Isolates are shaded in pink; genome classification reference samples are highlighted in pink and field viruses retrieved from Genbank are in black.

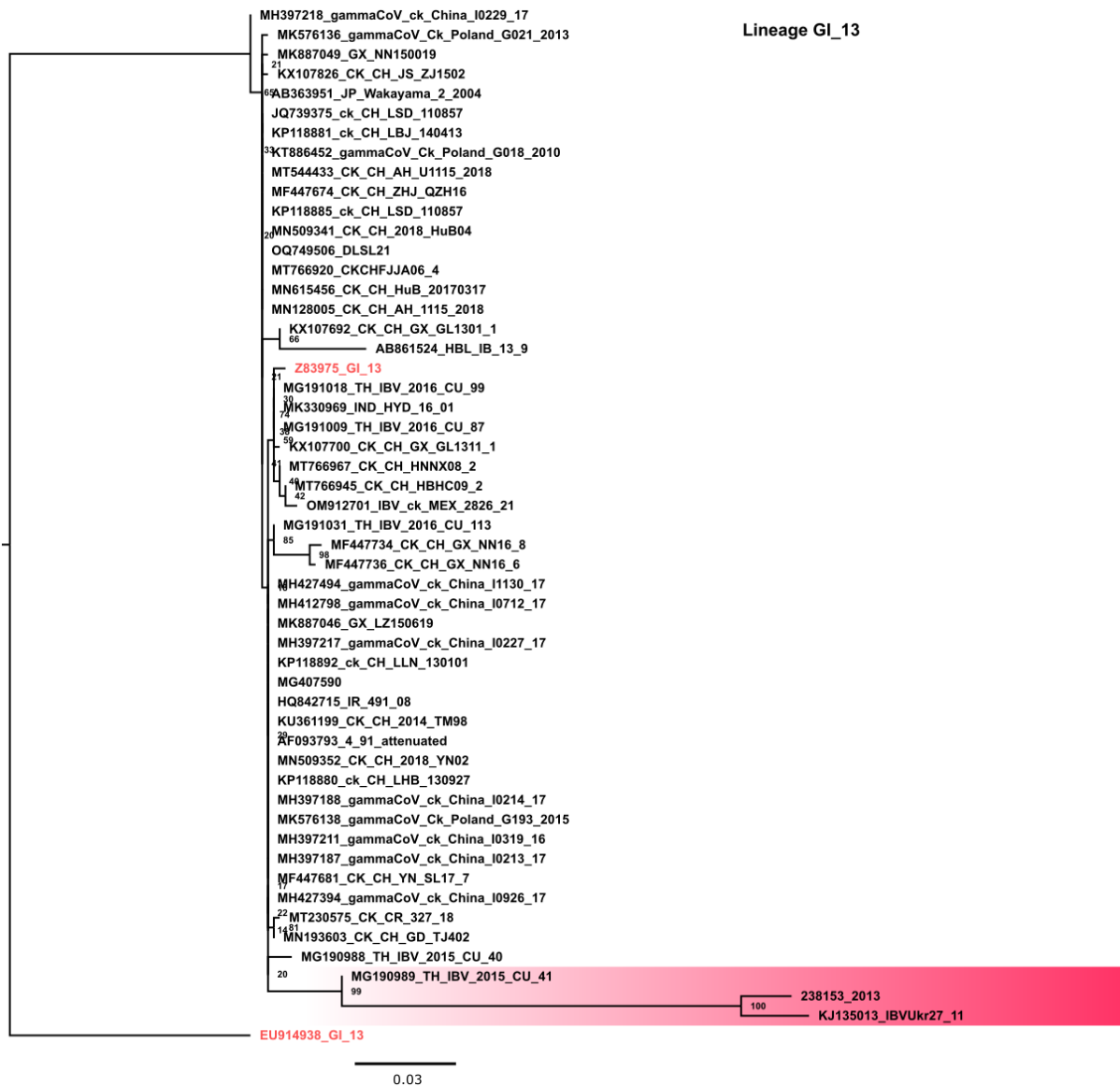


Figure 15(f). Maximum-likelihood phylogenetic tree re-rooted for an enlarged view of isolate 238153_2013 in the GI-13 lineage. Isolates are shaded in red; genome classification reference samples are highlighted in red and field viruses retrieved from Genbank are in black.

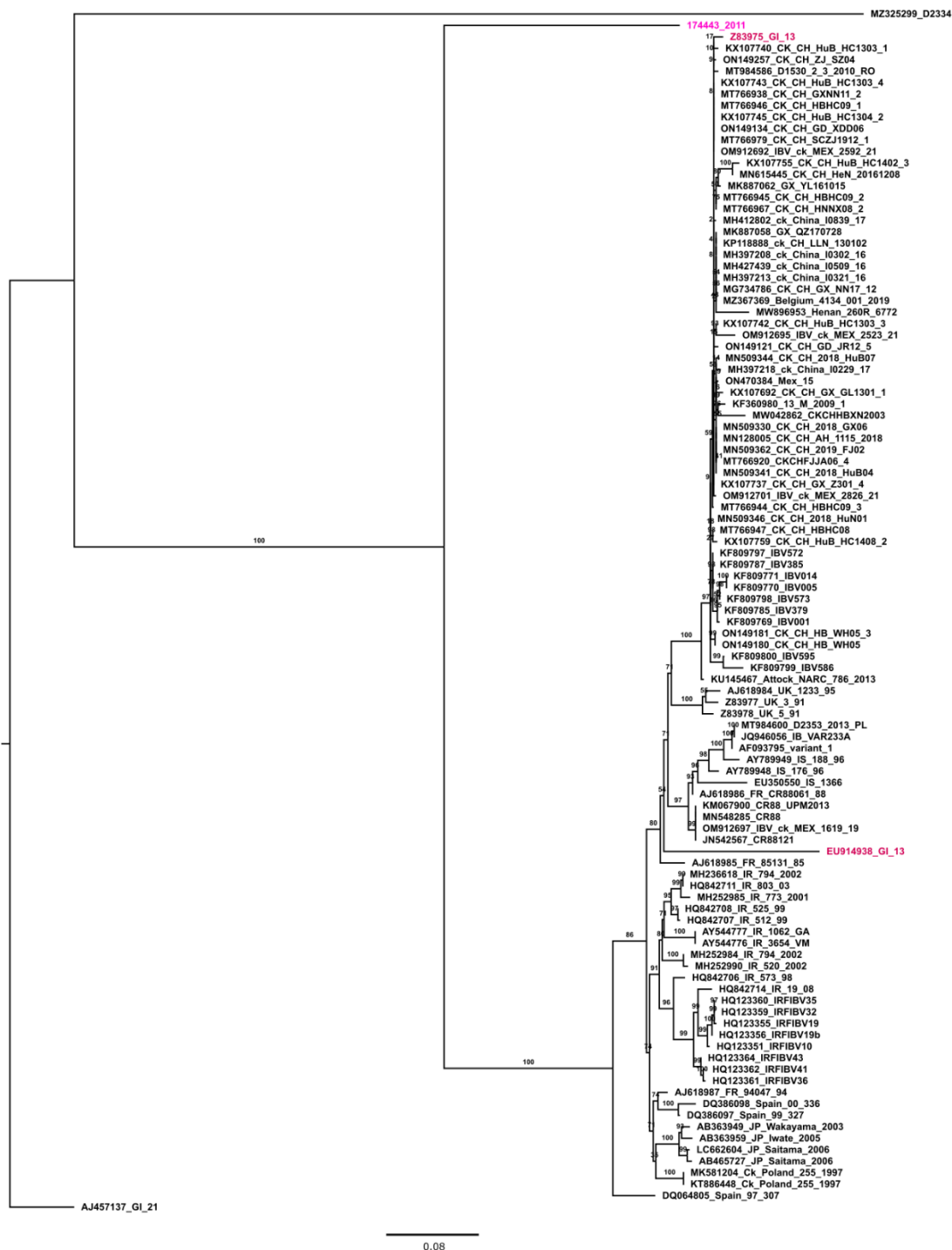


Figure 15(g). Maximum-likelihood phylogenetic tree re-rooted for an enlarged view of isolate 174443_2011 in the GI-13 lineage. Isolates are highlighted in bright pink; genome classification reference samples are highlighted in dark pink and field viruses retrieved from Genbank are in black.

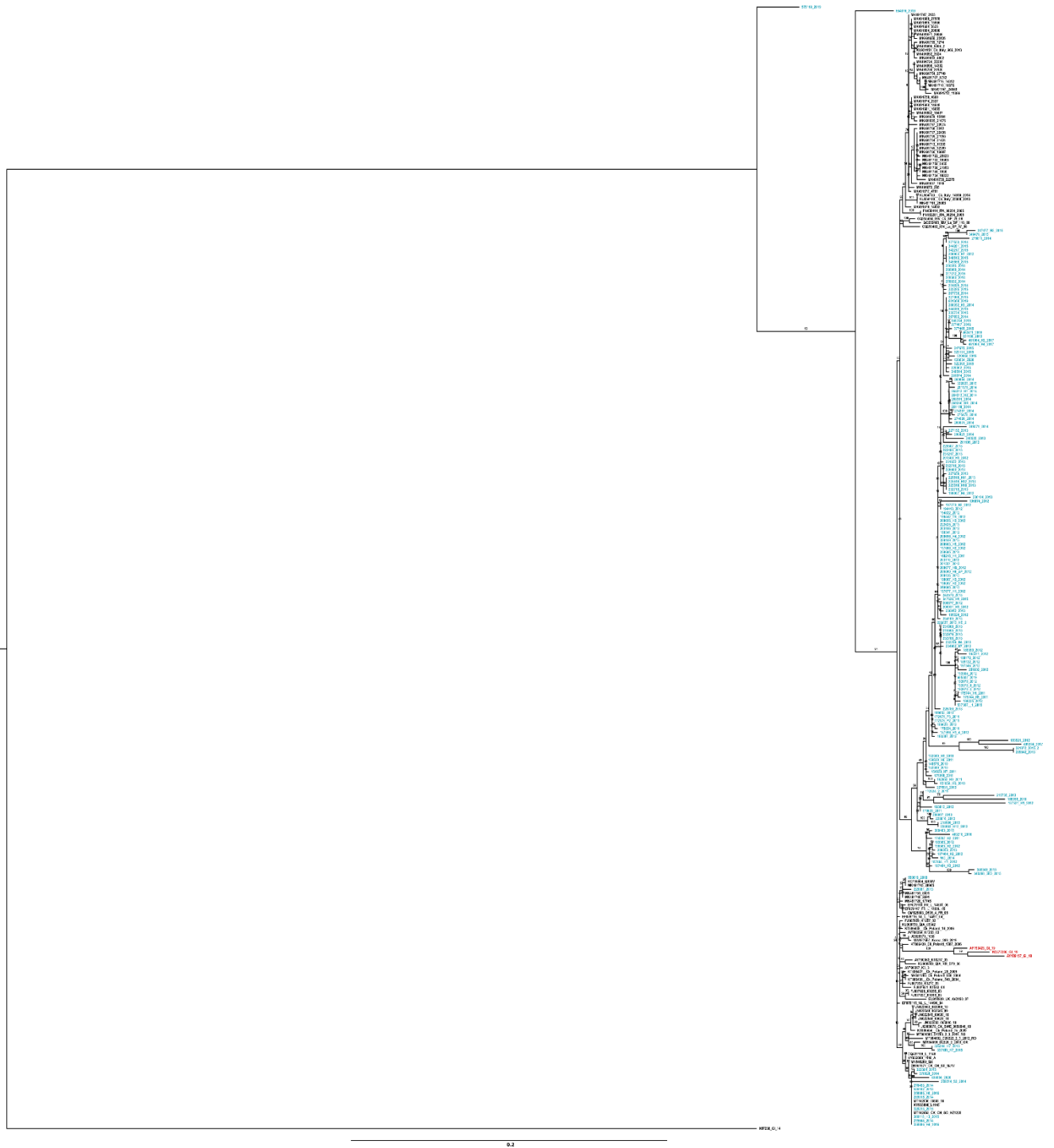


Figure 16(a). Maximum-likelihood phylogenetic tree of lineage GI-19 IBV. Study isolates are highlighted in light blue, genome classification reference samples are in red, field viruses retrieved from Genbank are in black.

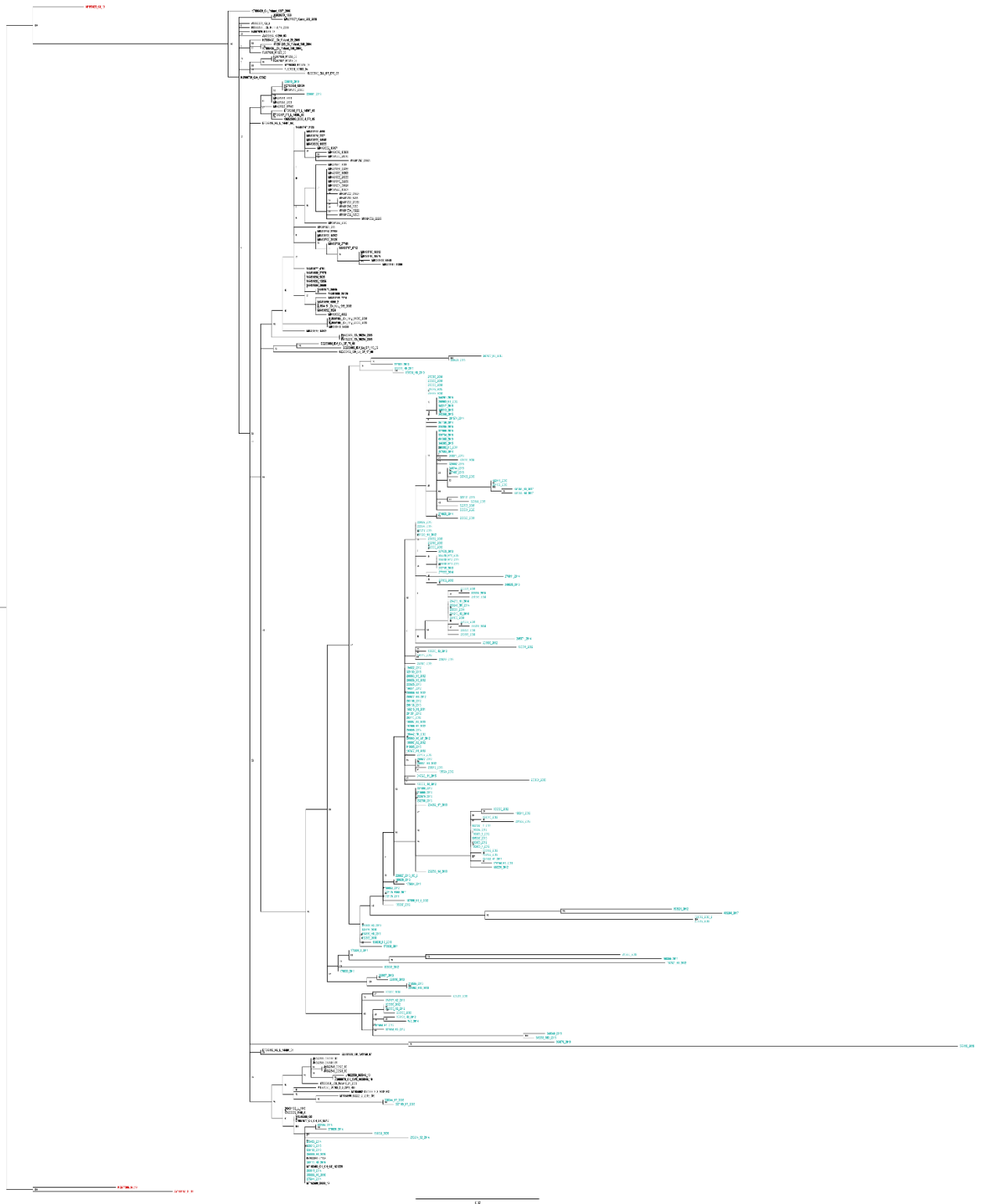


Figure 16(b). Maximum-likelihood phylogenetic tree of GI-19 lineage rooted with more closely related reference sequences (KC577395 and AY189157) for a better visualization. Study isolates are highlighted in light blue, genome classification reference samples are in red, field viruses retrieved from Genbank are in black.

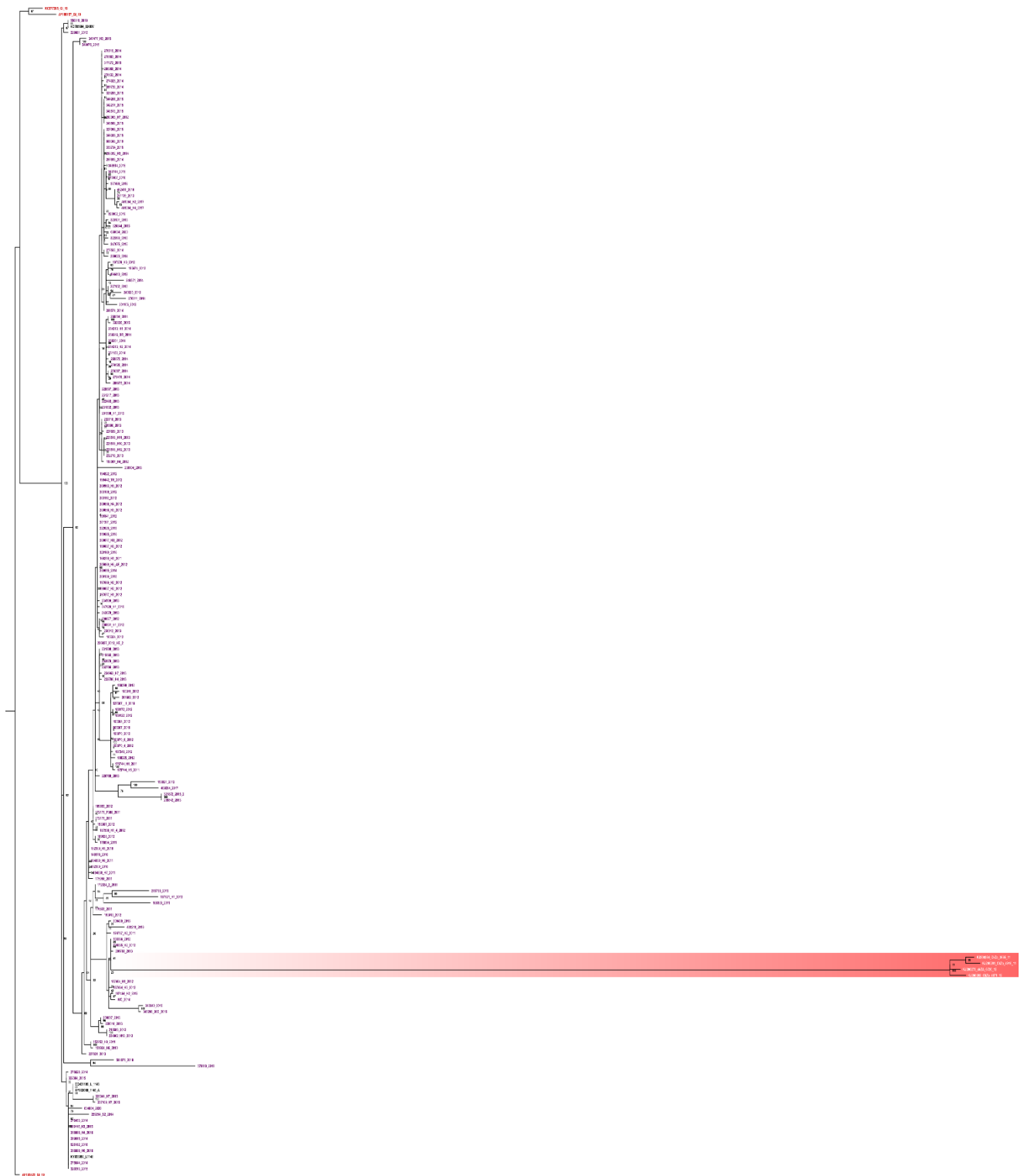


Figure 16(c). Maximum-likelihood phylogenetic tree of lineage GI-19 that includes previously identified ZA QX-like strains from Knoetze et al., 2014 (KJ200284, KJ200281, KJ200282, and KJ200273) shaded in red. Study isolates are highlighted in purple font, genome classification reference samples are in red font, field viruses retrieved from Genbank are in black font.

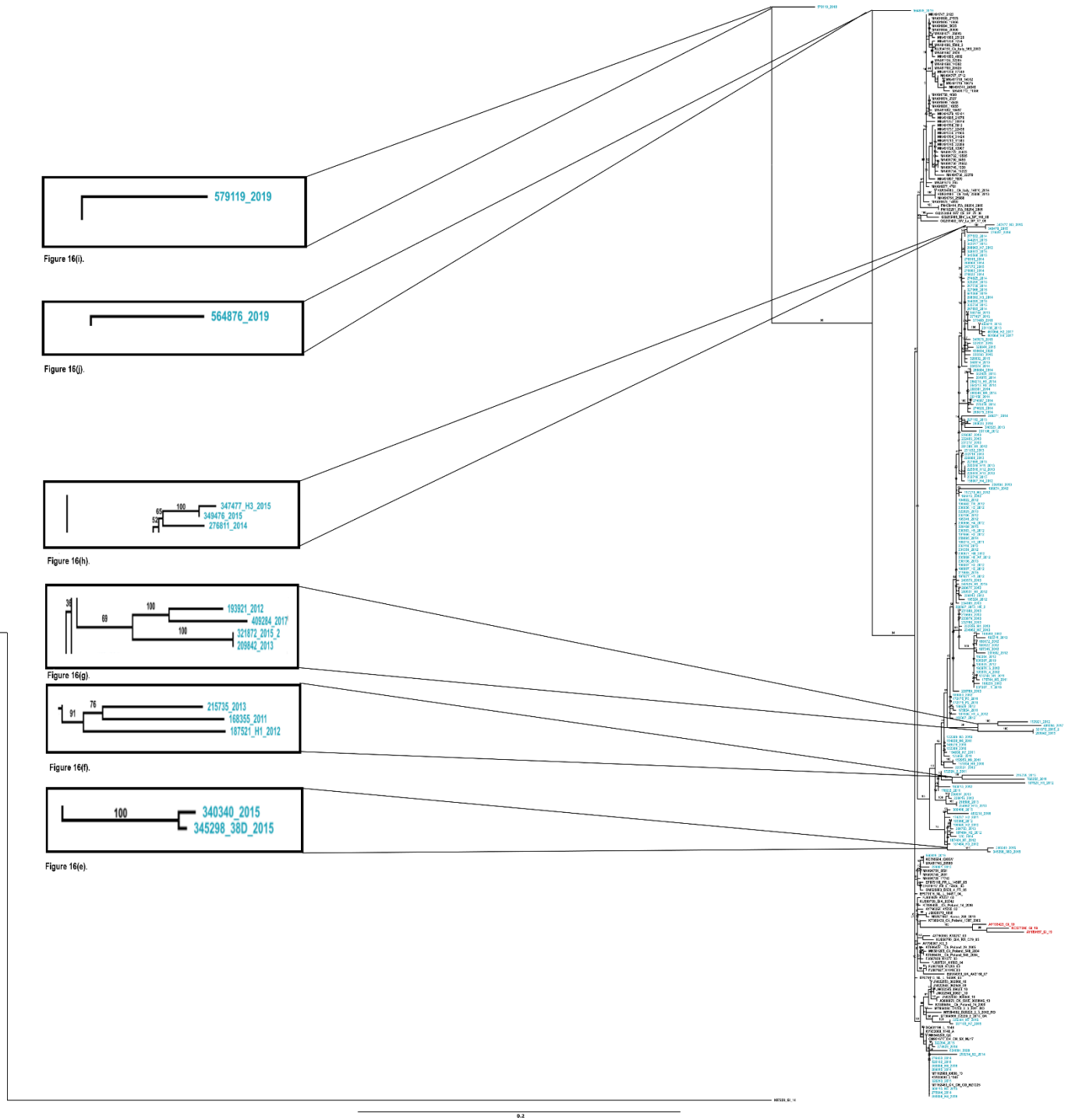


Figure 16(d). Maximum-likelihood phylogenetic tree of GI-19 lineage highlighting isolates in the trees to follow (Figure 16(e), 16(f), 16(g), 16(h), 16(i), 16(j)), with more closely related reference sequences for a better visualization. Study isolates are highlighted in light blue, genome classification reference samples are in red, field viruses retrieved from Genbank are in black.



Figure 16(e). Maximum-likelihood phylogenetic tree of GI-19 lineage re-rooted for an enlarged view of isolates 340340_2015 and 345298_38D_2015. Isolates are shaded in purple; genome classification reference samples are highlighted in purple and field viruses retrieved from Genbank are in black.

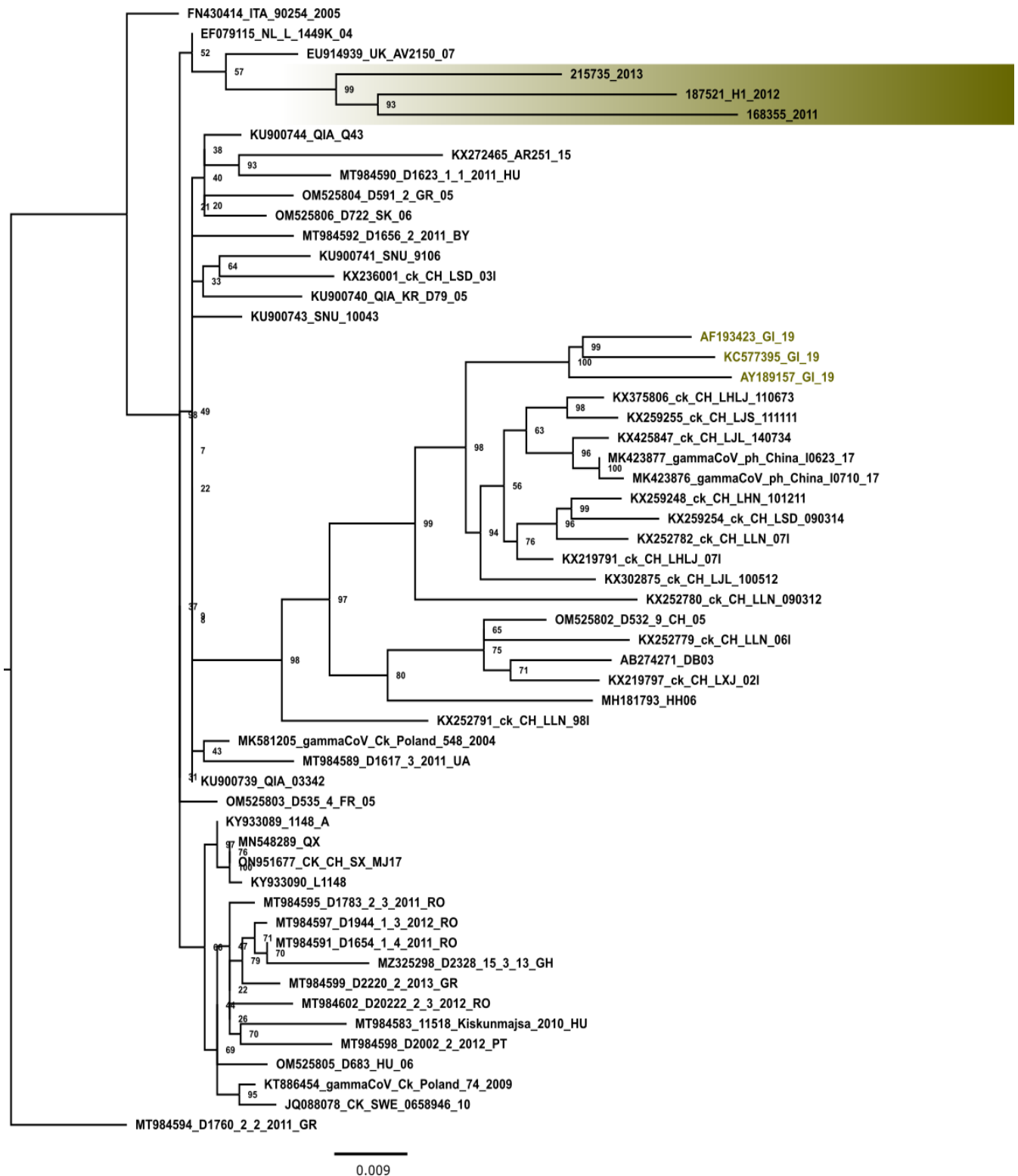


Figure 16(f). Maximum-likelihood phylogenetic tree of the GI-19 lineage, re-rooted for an enlarged view of isolates 166355_2011, 187521_H1_2012, and 215735_2013 in the GI-19 lineage. Isolates are shaded in green; genome classification reference samples are highlighted in green and field viruses retrieved from Genbank are in black.

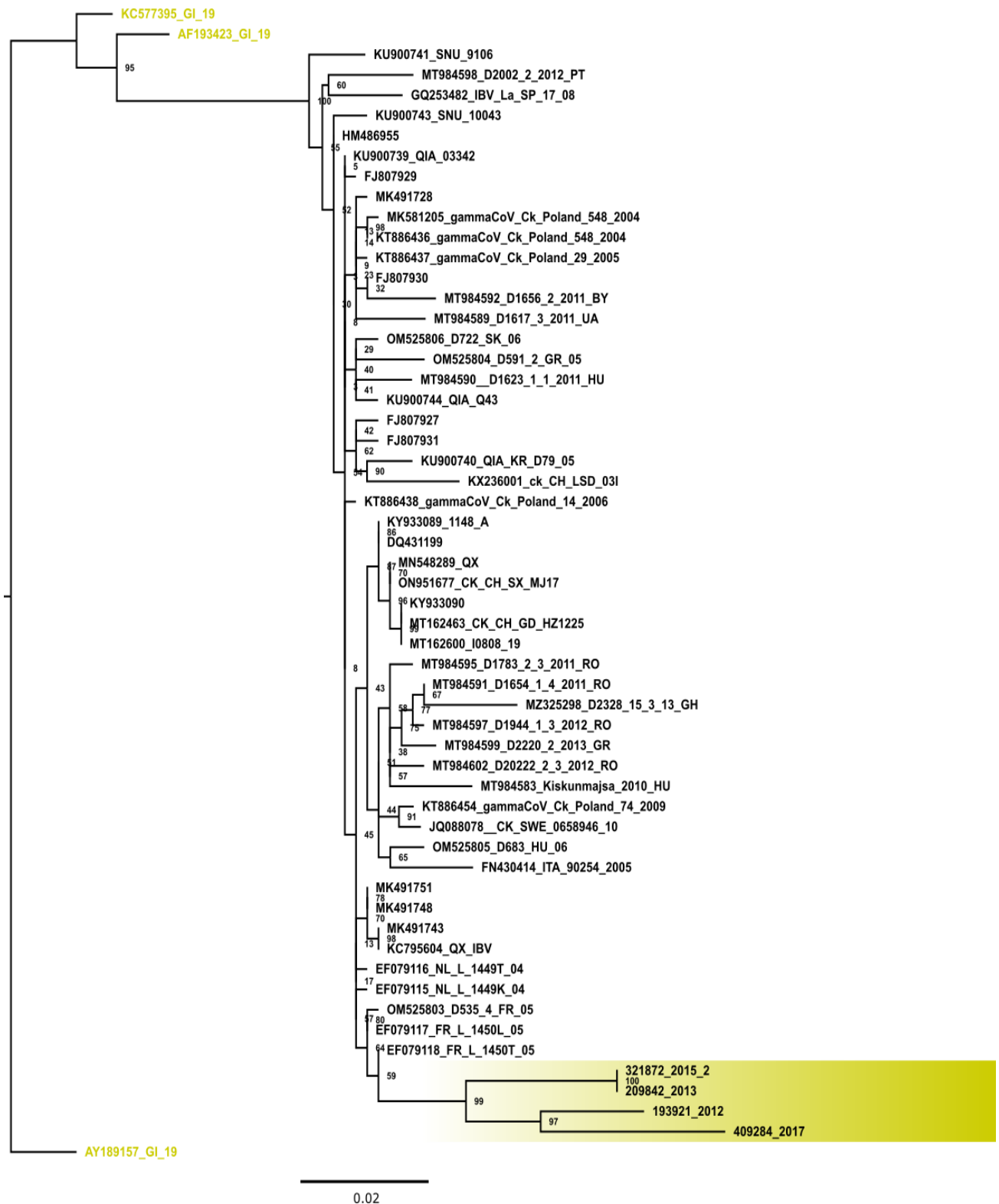


Figure16(g). Maximum-likelihood phylogenetic tree of the GI-19 lineage, re-rooted for an enlarged view of isolates 321872_2015_2, 209842_2013, 193921_2012 and 409284_2017. Isolates are shaded in yellow; genome classification reference samples are highlighted in yellow and field viruses retrieved from Genbank are in black.

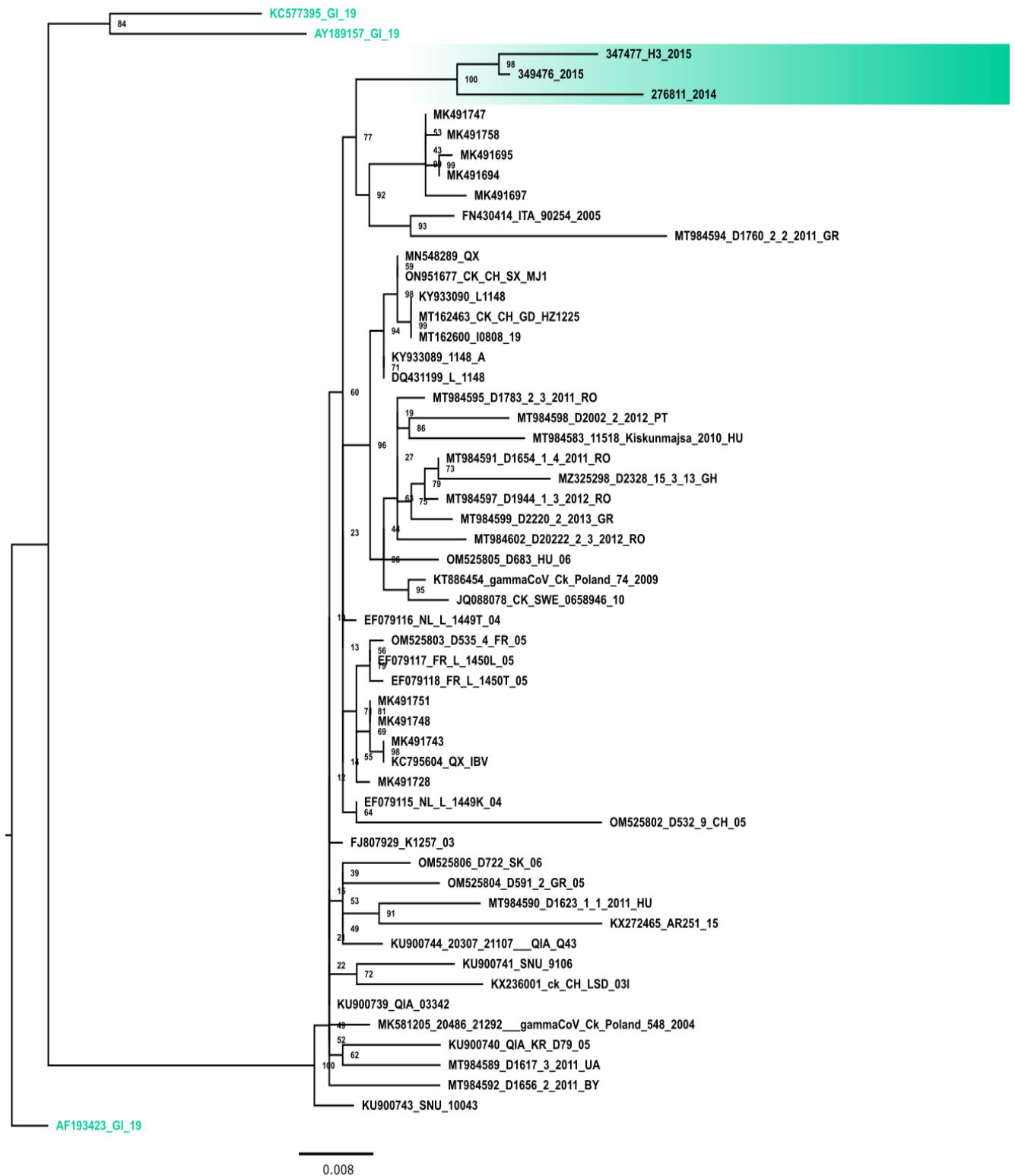


Figure 16(h). Maximum-likelihood phylogenetic tree of the GI-19 lineage re-rooted for an enlarged view of isolates 276811_2014, 347477_H3_2015, and 349476_2015. Isolates are shaded in light blue; genome classification reference samples are highlighted in light blue and field viruses retrieved from Genbank are in black.

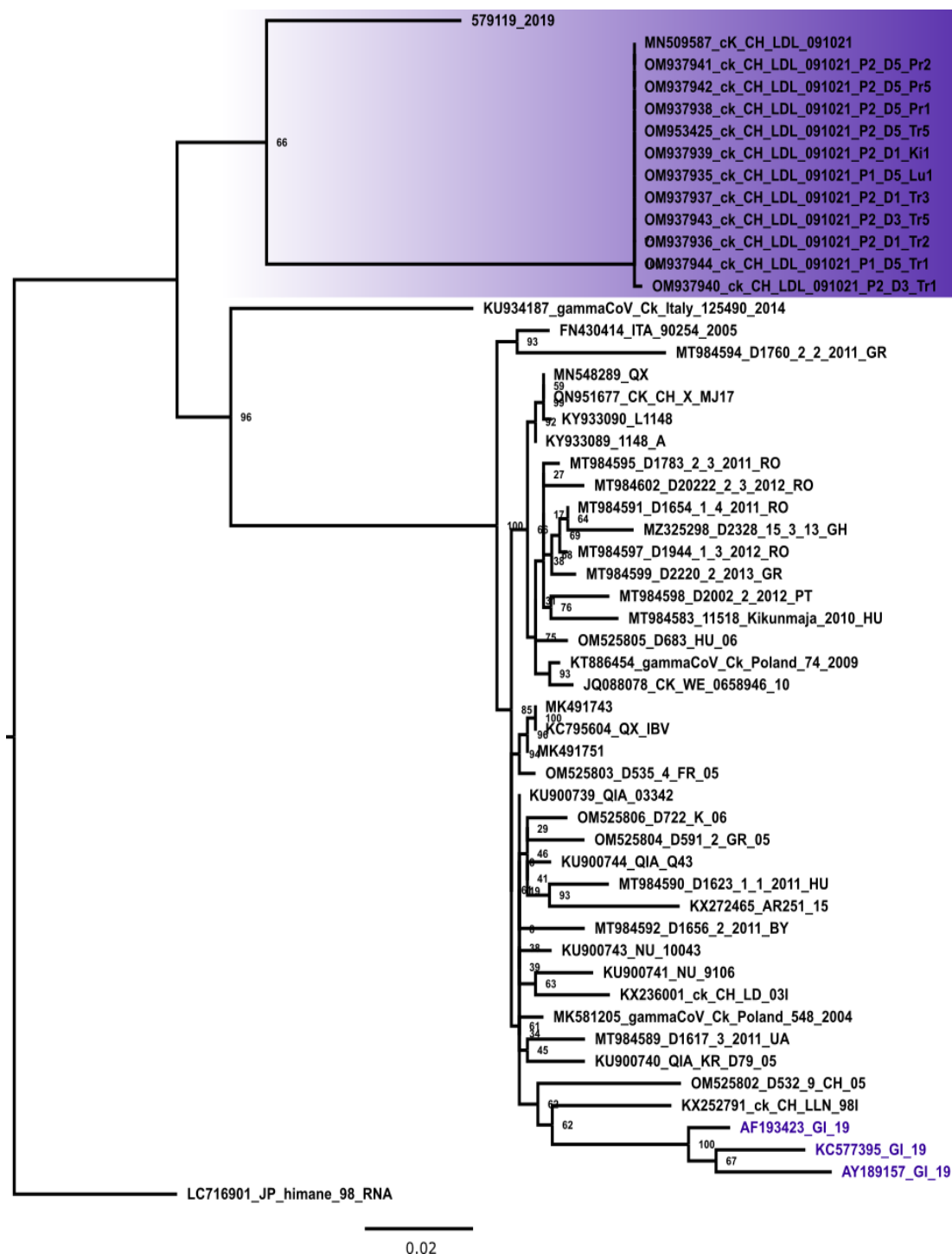


Figure 16(i). Maximum-likelihood phylogenetic tree of the GI-19 lineage re-rooted for an enlarged view of isolates 579119_2019. Isolate is shaded in blue with closest related field viruses retrieved from Genbank in black; genome classification reference samples are highlighted in dark blue. All other field viruses retrieved from Genbank are in black.



Figure 16(j). Maximum-likelihood phylogenetic tree of the GI-19 lineage re-rooted for an enlarged view of isolates 564876_2019. Isolate is shaded in light green with closest relating field virus retrieved from Genbank in black; genome classification reference samples are highlighted in light green and field viruses retrieved from Genbank are in black.

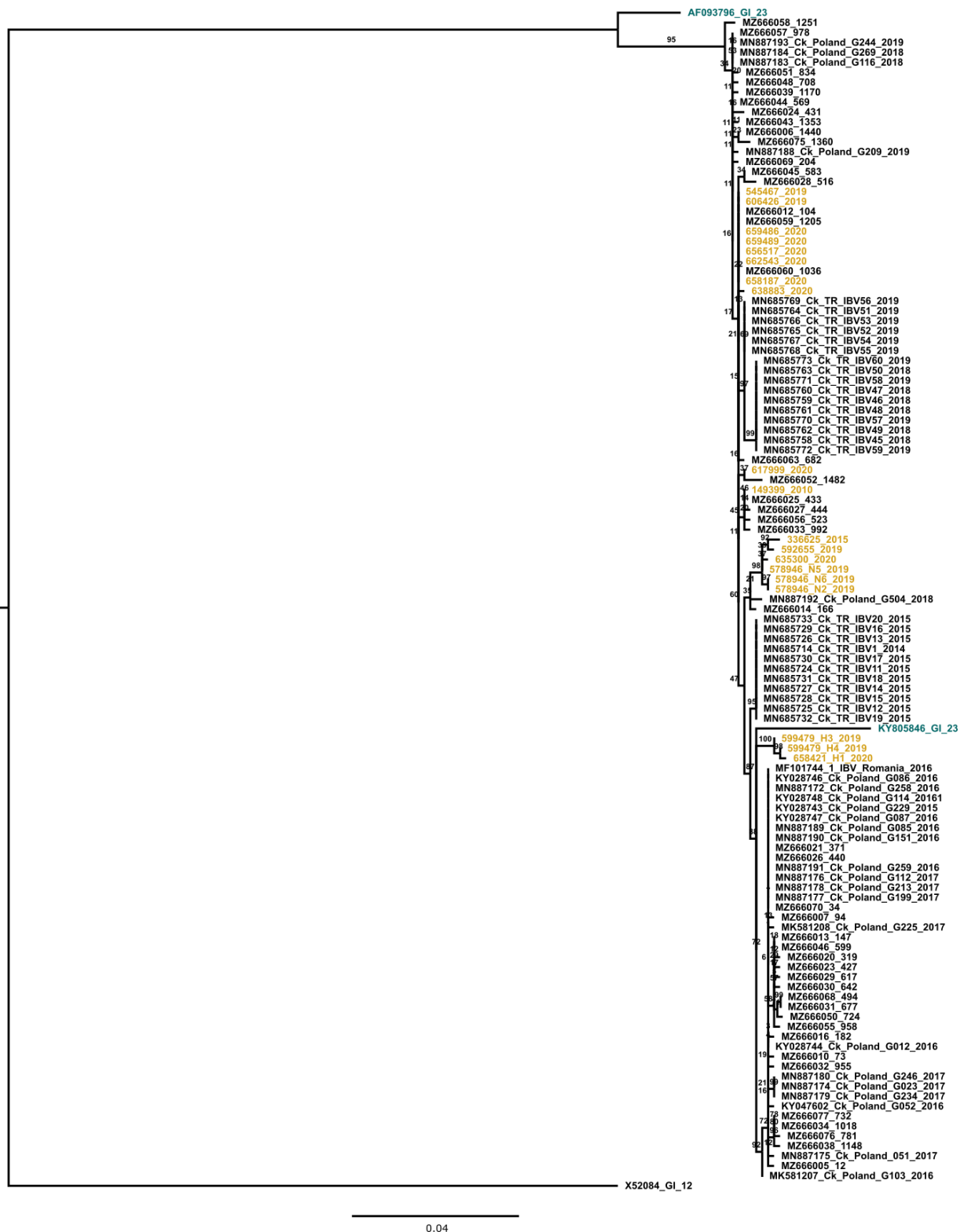


Figure 17(a). Maximum-likelihood phylogenetic tree of lineage GI-23 IBV. Study isolates are highlighted in green, genome classification reference samples are in yellow, field viruses retrieved from Genbank are in black.

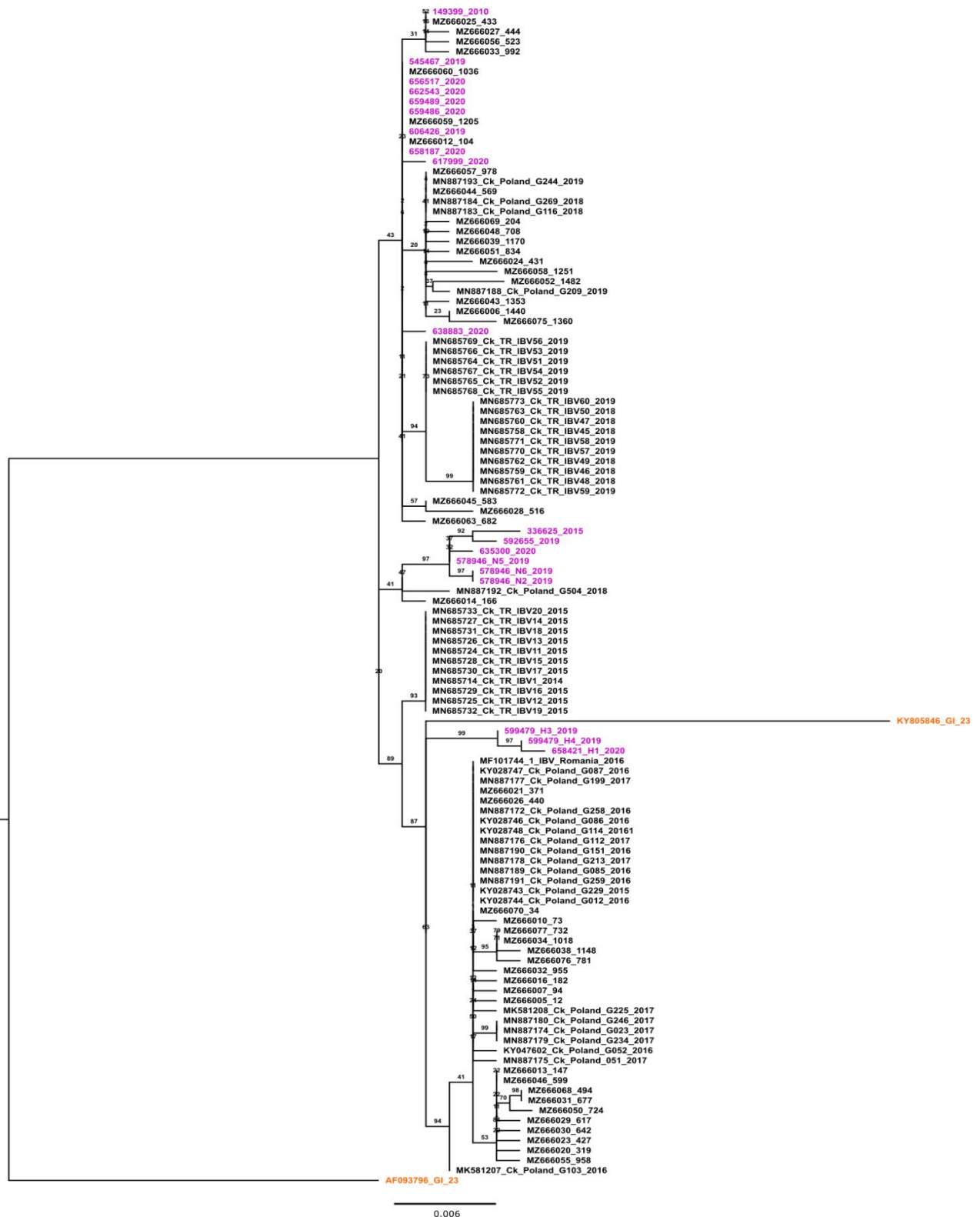


Figure 17(b). Maximum-likelihood phylogenetic tree rooted with more closely related reference sequence (AF093796) for a better visualization of lineage GI-23. Study isolates are highlighted in pink, genome classification reference samples are in orange, field viruses retrieved from Genbank are in black.

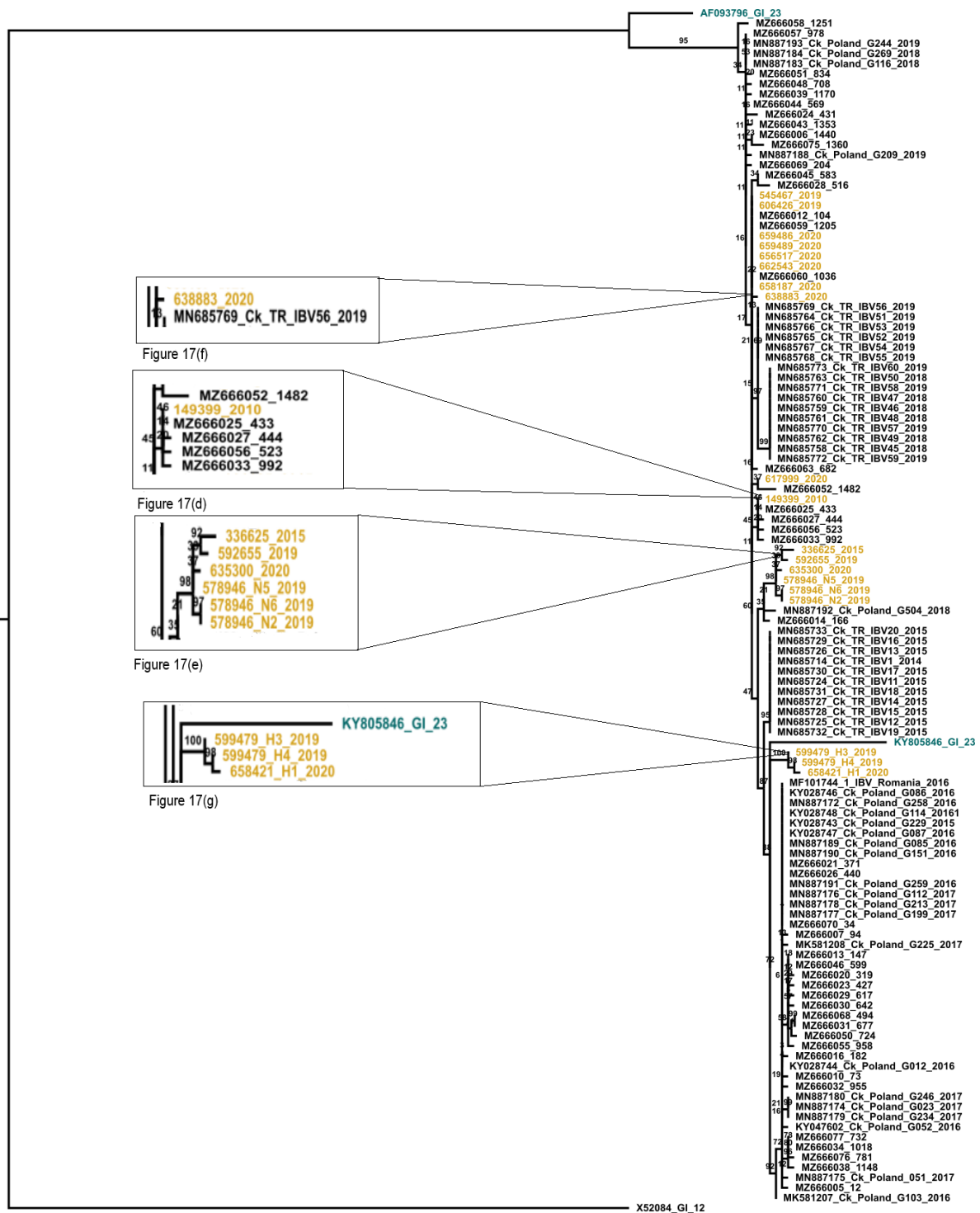


Figure 17(c). Maximum-likelihood phylogenetic tree of the GI-23 lineage highlighting isolates in the trees to follow (Figure 17(d), 17(e), 17(f), 17(g)), with more closely related reference sequences for a better visualization. Study isolates are highlighted in light blue, genome classification reference samples are in red, field viruses retrieved from Genbank are in black.

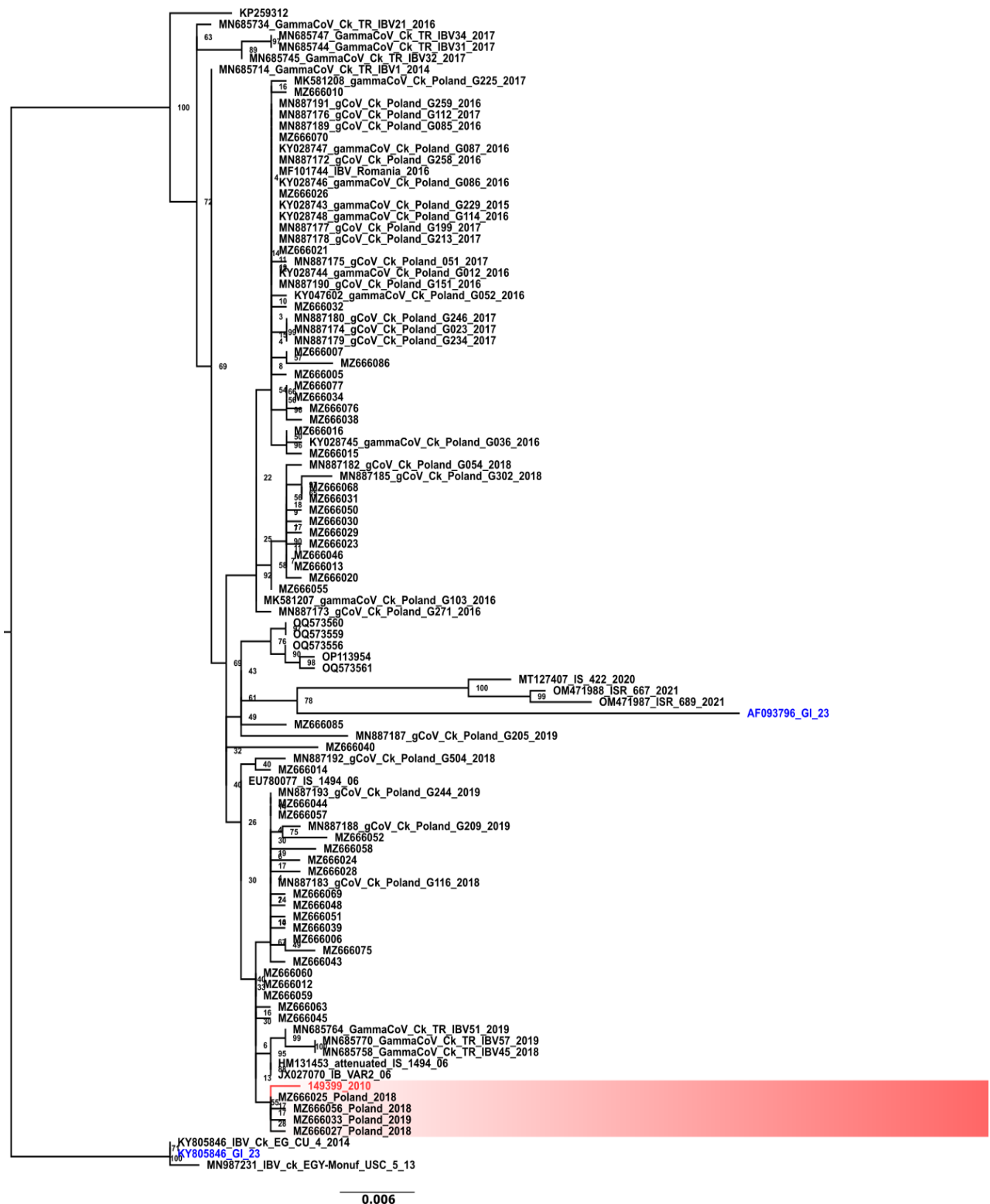


Figure 17(d). Maximum-likelihood phylogenetic tree of the GI-23 lineage re-rooted for an enlarged view of isolates 149399_2010. Isolates are shaded in red; genome classification reference samples are highlighted in blue and field viruses retrieved from Genbank are in black.



Figure 17(e). Maximum-likelihood phylogenetic tree of the GI-23 lineage re-rooted for an enlarged view of isolates 635300_2020, 578946_N5_2019, 578946_N6_2019, 578946_N2_2019, 336625_2015 and 592655_2019. Isolates are shaded in yellow; genome classification reference samples are highlighted in gold and field viruses retrieved from Genbank are in black.

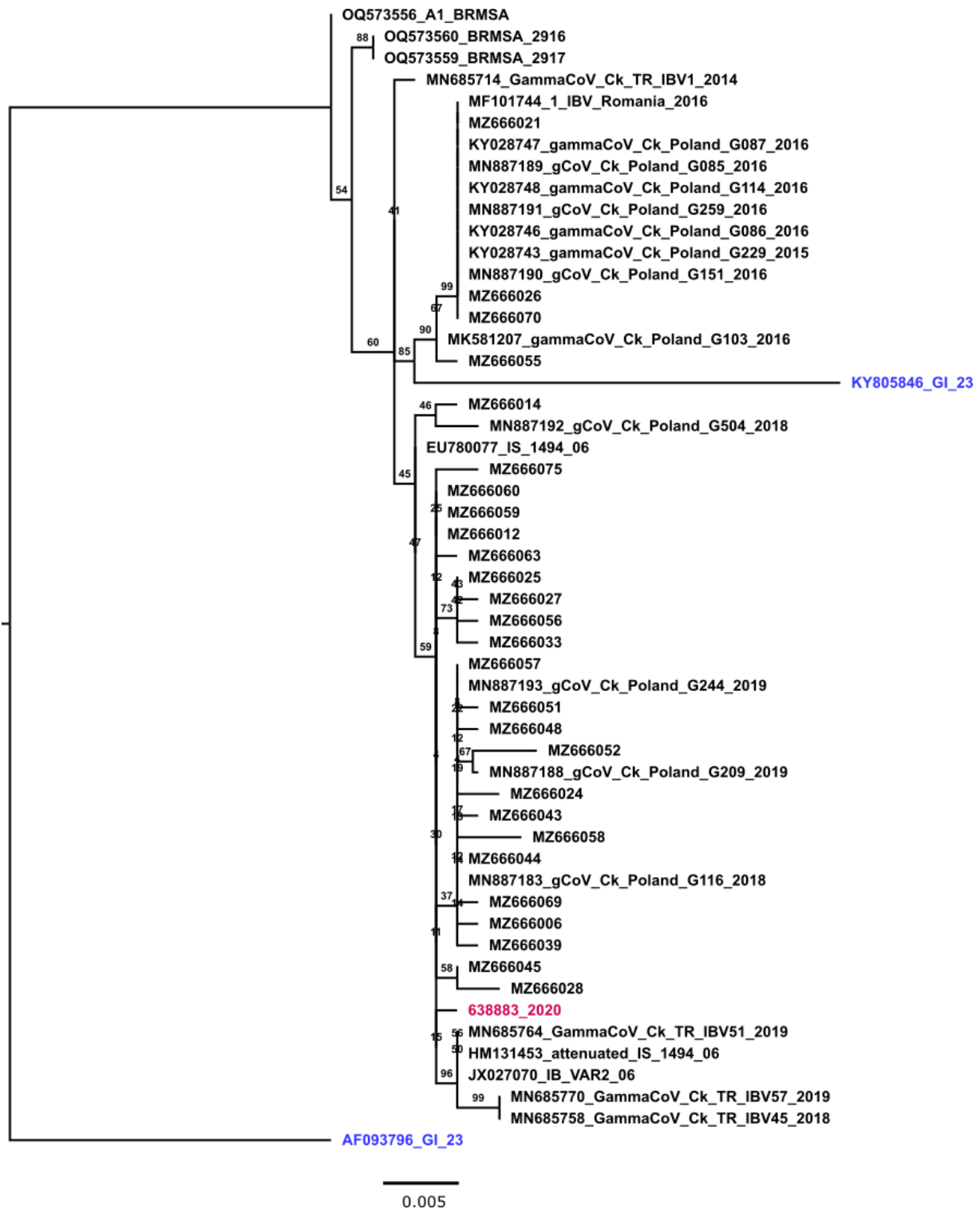


Figure 17(f). Maximum-likelihood phylogenetic tree of the GI-23 lineage re-rooted for an enlarged view of isolates 638883_2020. Isolates are highlighted in pink; genome classification reference samples are highlighted in blue and field viruses retrieved from Genbank are in black.

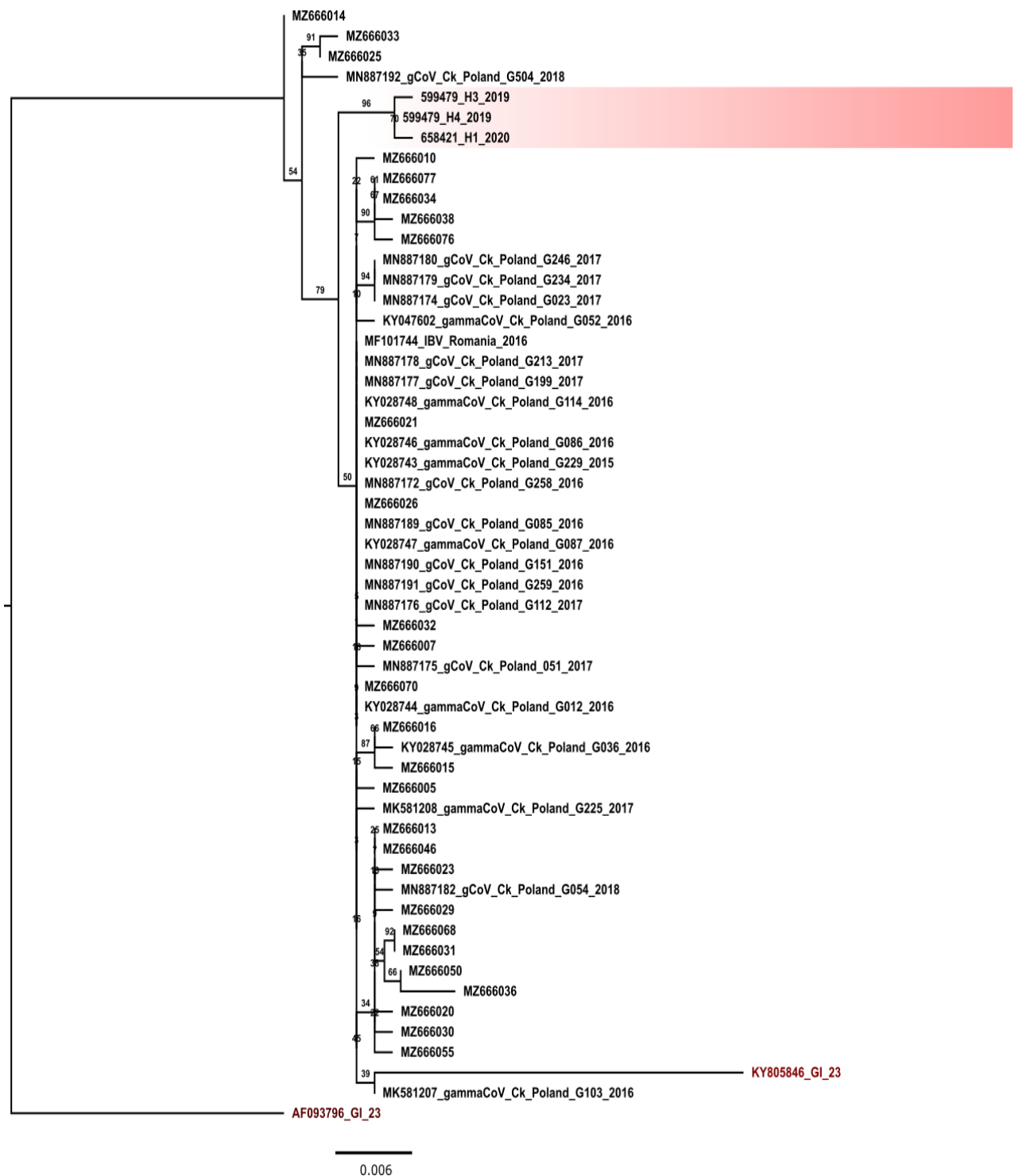


Figure 17(g). Maximum-likelihood phylogenetic tree of the GI-23 lineage re-rooted for an enlarged view of isolates 599479_H3_2019, 599479_H4_2019, 658421_H1_2020. Isolates are shaded in red; genome classification reference samples are highlighted in maroon and field viruses retrieved from Genbank are in black.

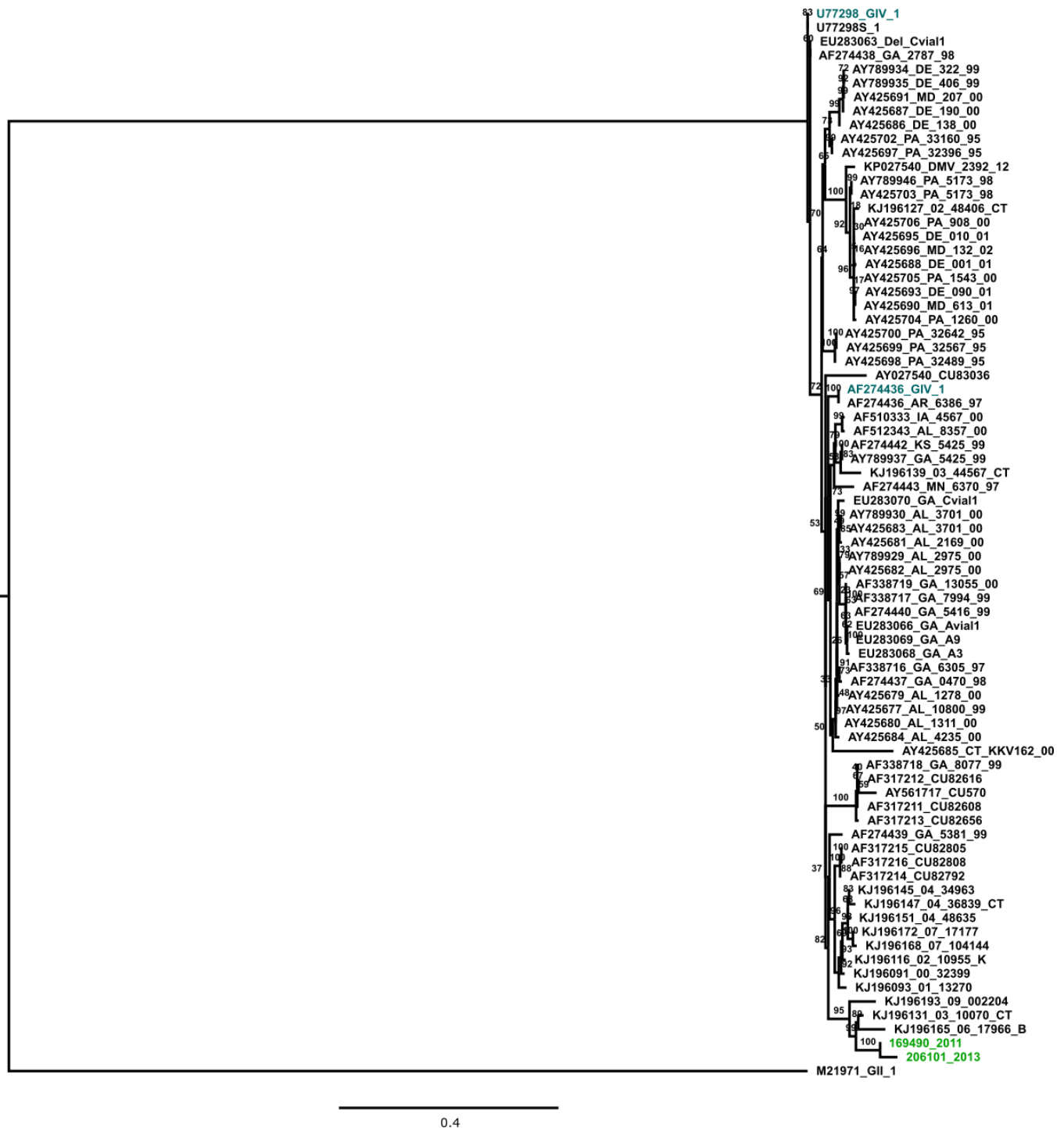


Figure 18(a). Maximum-likelihood phylogenetic tree of lineage GIV-1 IBV. Study isolates are highlighted in green, genome classification reference samples are in blue, field viruses retrieved from Genbank are in black.

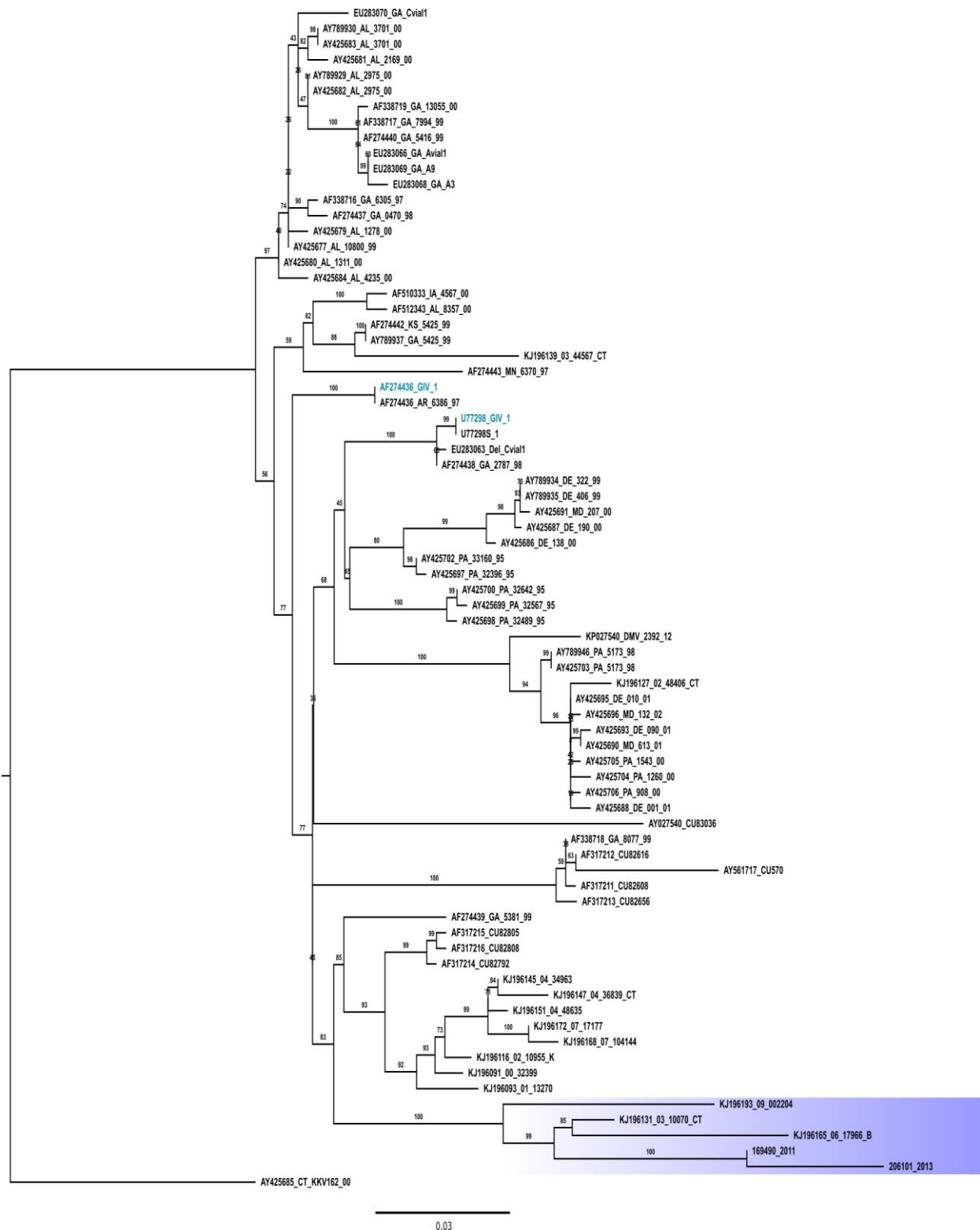


Figure 18(b). Maximum-likelihood phylogenetic tree of the lineage GIV-1, rooted with more closely related sequence (AY425685) for a better visualization. Study isolates are shaded blue, genome classification reference samples are blue, field viruses retrieved from Genbank are in black.

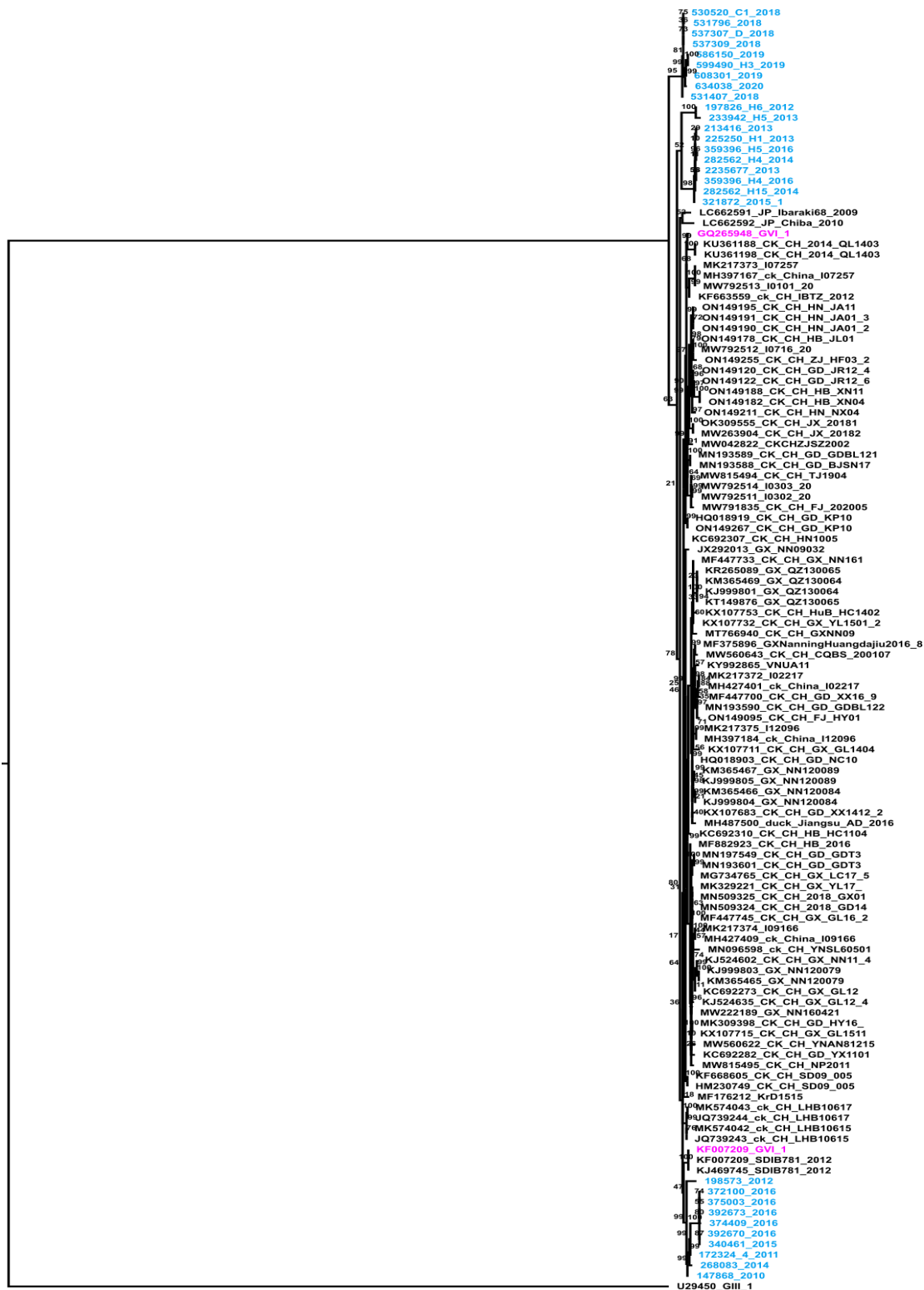


Figure 19(a). Maximum-likelihood phylogenetic tree of lineage GVI-1 IBV. Study isolates are highlighted in light blue, genome classification reference samples are in pink, field viruses retrieved from Genbank are in black.

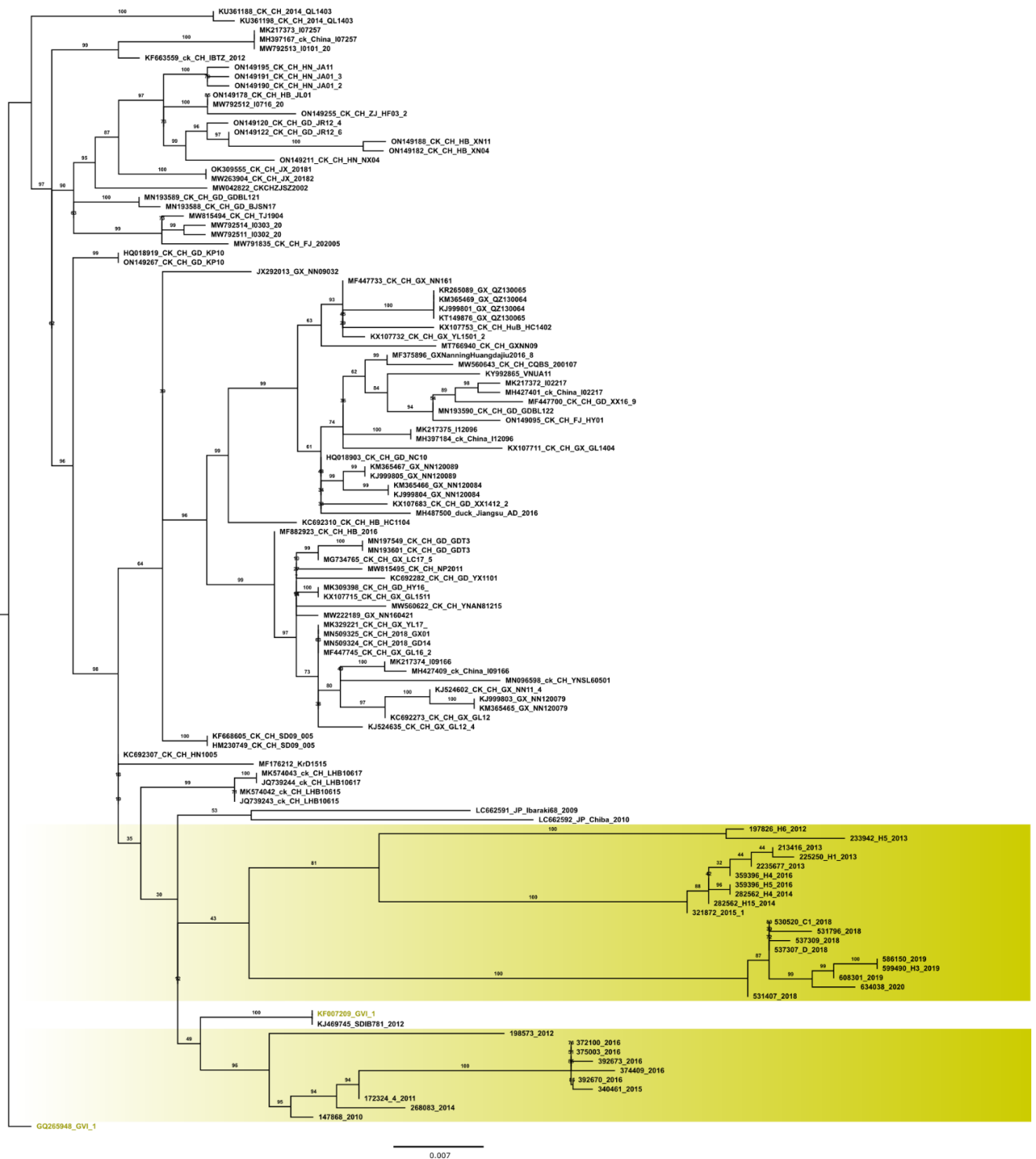


Figure 19(b). Maximum-likelihood phylogenetic tree of the lineage GVI-1, rooted with more closely related reference sequence for a better visualization. Study isolates are shaded yellow, genome classification reference samples are in yellow font, field viruses retrieved from Genbank are in black font.