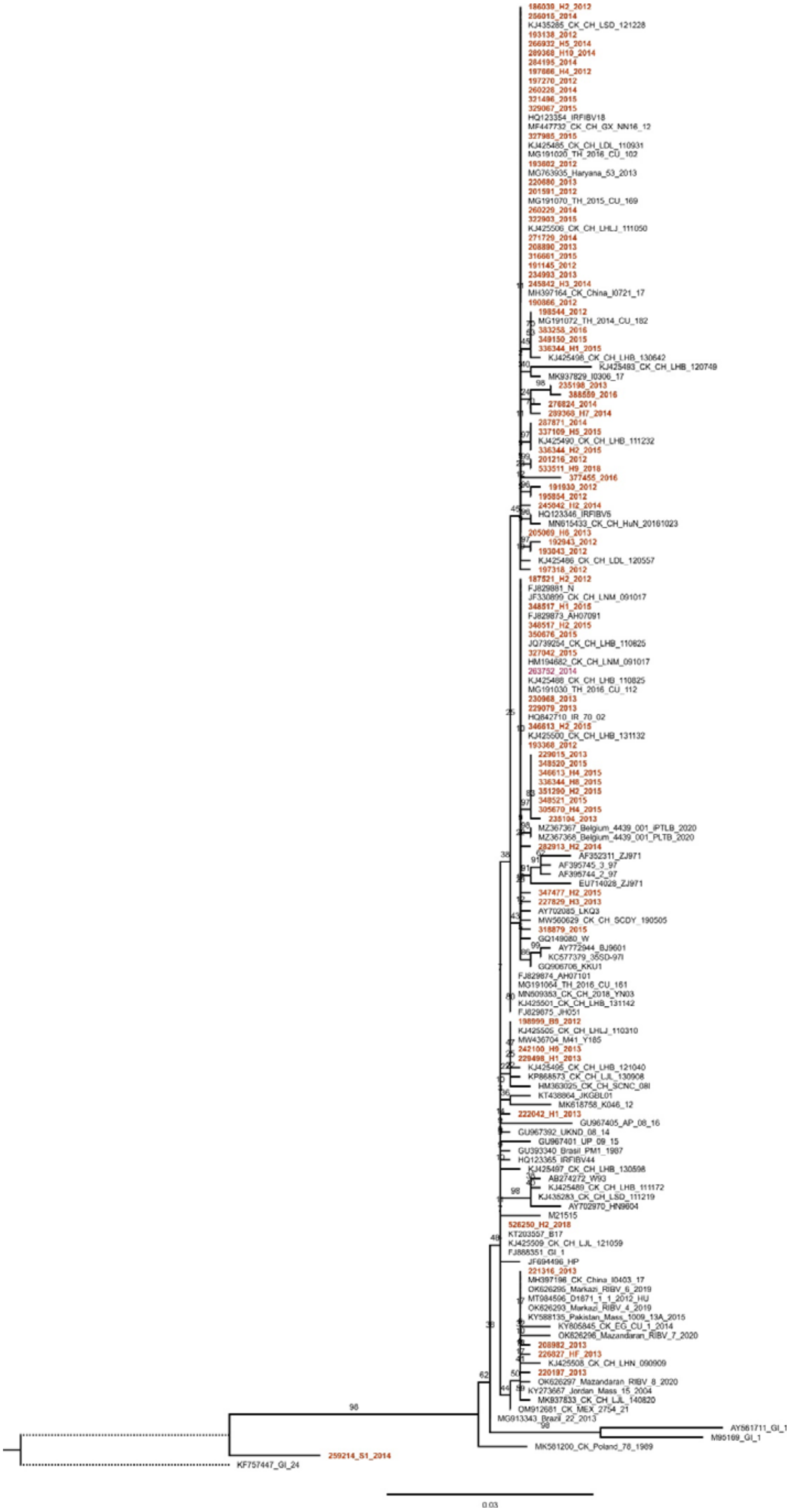


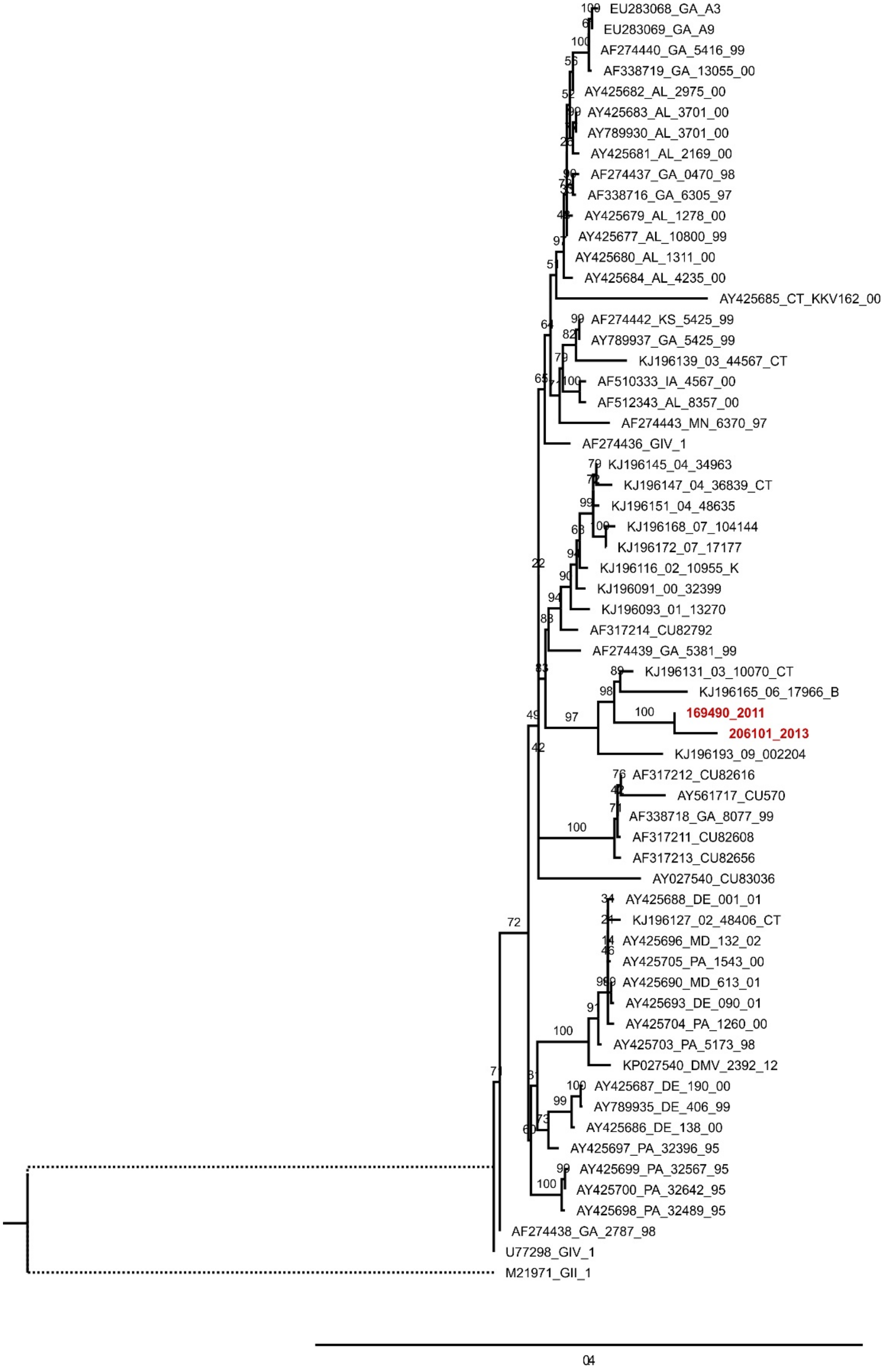
Supplementary Figure 1. Infectious bronchitis virus **genotype G1-1** Maximum Likelihood phylogenetic tree reconstructed from 700 nucleotides of the S1 gene. Isolates sequenced in this study are highlighted, the tree is rooted with a GI-24 strain; branches shortened for scaling purposes are indicated by dotted lines.

Supplementary Figure 2. Infectious bronchitis virus genotype **GI-11** Maximum Likelihood phylogenetic tree reconstructed from 501 nucleotides of the S1 gene. Isolates sequenced in this study are highlighted, the tree is rooted with a GI-26 strain; branches shortened for scaling purposes are indicated by dotted lines.

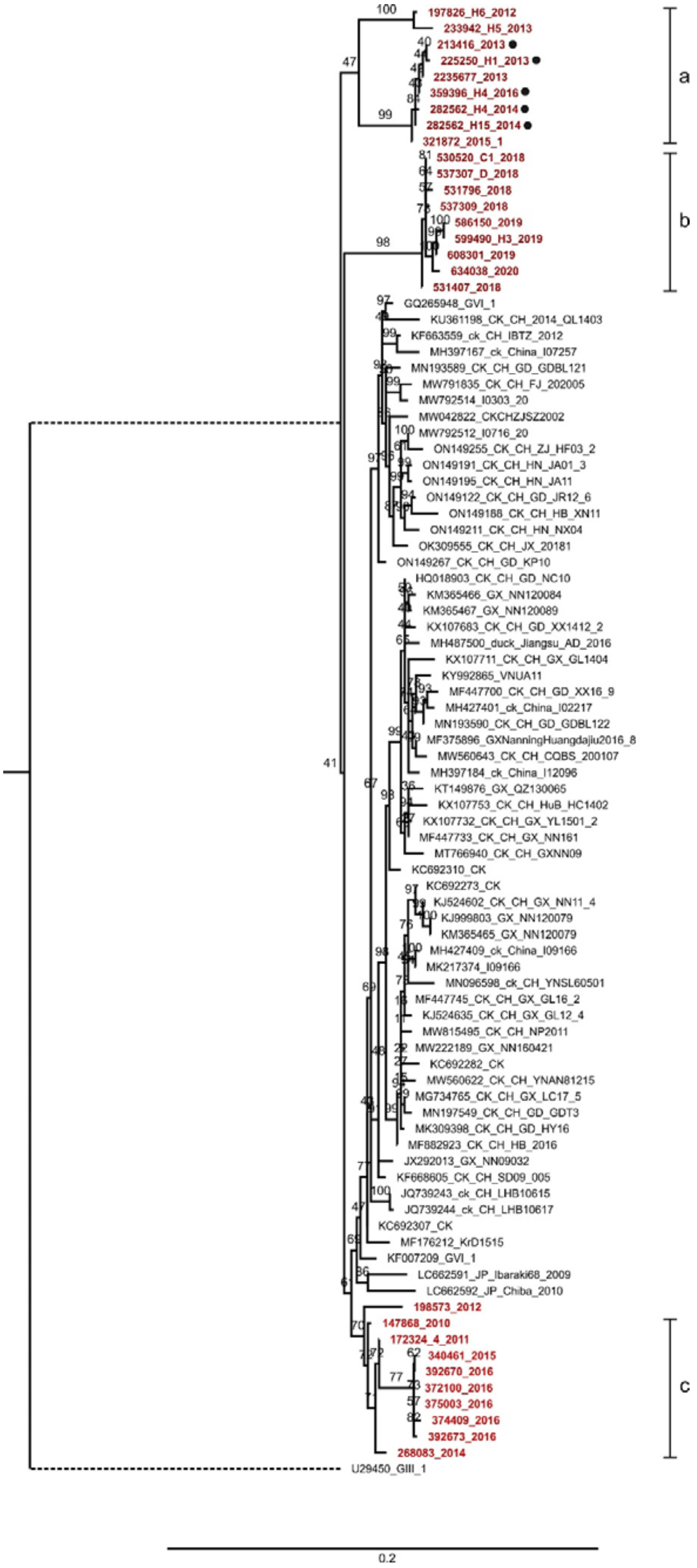
Supplementary Figure 3. Infectious bronchitis virus genotype **GI-13** Maximum Likelihood phylogenetic tree reconstructed from 588 nucleotides of the S1 gene. Isolates sequenced in this study are highlighted, with sub-clades denoted by letters. The tree is rooted with a GI-21 strain, branches shortened for scaling purposes are indicated by dotted lines, isolates selected for full genome sequencing are indicated by a black dot, and isolates from Namibia are indicated by a red dot.

Supplementary Figure 4 Infectious bronchitis virus genotype **GI-19** Maximum Likelihood phylogenetic tree reconstructed from 662 nucleotides of the S1 gene. Isolates sequenced in this study are highlighted, the tree is rooted with a GI-14 strain; branches shortened for scaling purposes are indicated by dotted lines, isolates selected for full genome sequencing are indicated by a black dot, the isolate from Botswana by a red dot, and the isolate from Eswatini by a blue dot.

Supplementary Figure 5. Infectious bronchitis virus genotype **GI-23** Maximum Likelihood phylogenetic tree reconstructed from 709 nucleotides of the S1 gene. Isolates sequenced in this study are highlighted. The tree is rooted with a GI-12 strain; branches shortened for scaling purposes are indicated by dotted lines. The arrow indicates the IBVAR-02 vaccine strain.



Supplementary Figure 6. Infectious bronchitis virus genotype **GIV-1** Maximum Likelihood phylogenetic tree reconstructed from 509 nucleotides of the S1 gene. Isolates sequenced in this study are highlighted, the tree is rooted with a GII-1 strain; branches shortened for scaling purposes are indicated by dotted lines.



Supplementary Figure 7. Infectious bronchitis virus genotype **GVI-1** Maximum Likelihood phylogenetic tree reconstructed from 689 nucleotides of the S1 gene. Isolates sequenced in this study are highlighted, with sub-clades denoted by letters. Isolates from Namibia are indicated by the black dot. The tree is rooted with a GII-1 strain; branches shortened for scaling purposes are indicated by dotted lines.