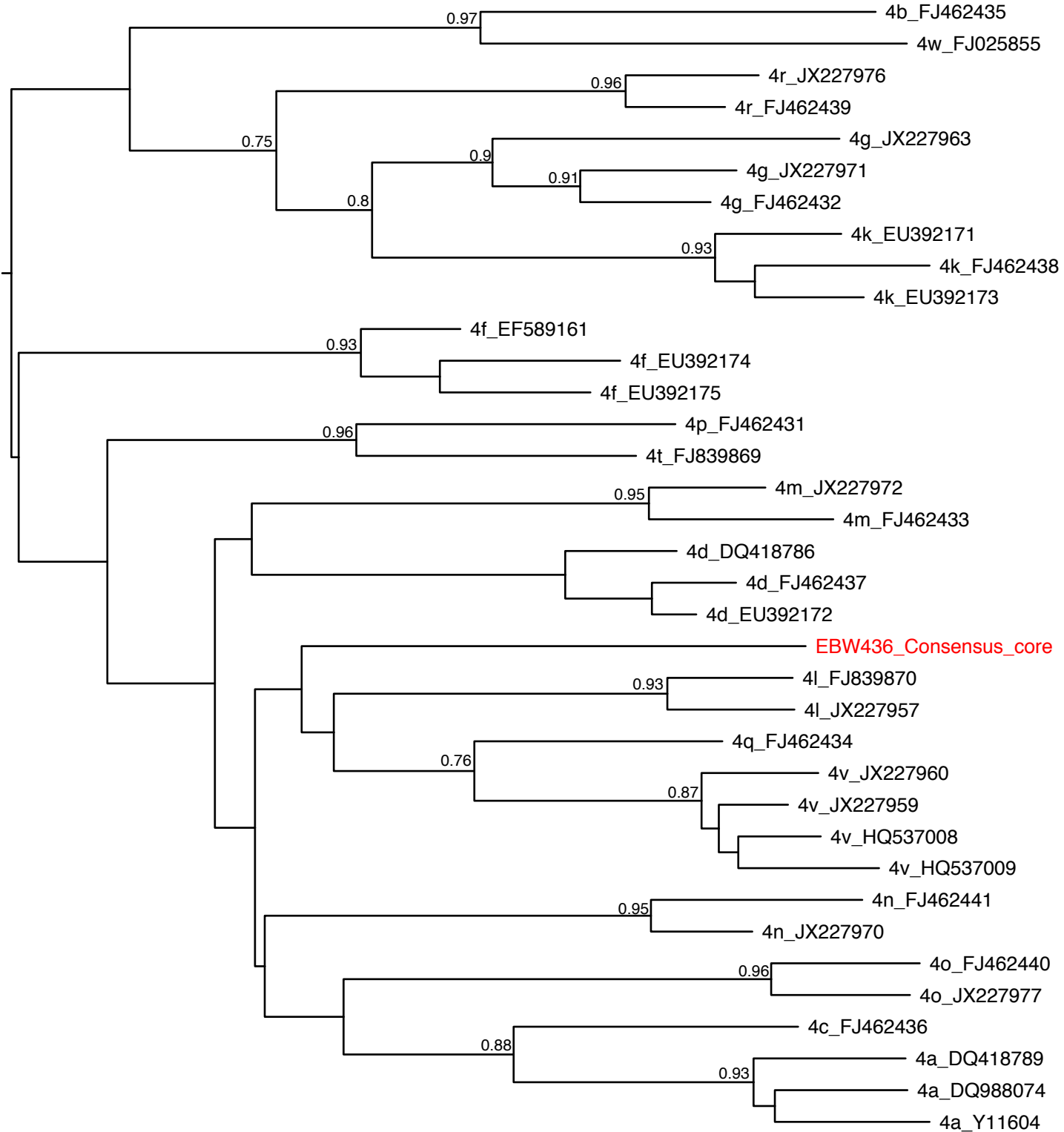


0.03

Figure S1

Estimated maximum-likelihood midpoint-rooted phylogeny of sub- genomic Core sequences. Nodes with bootstrap support >70% are labelled with their bootstrap support. Sequences generated in this study are highlighted in red. Branch lengths are in units of expected substitutions per site (see scale bar). Reference sequences are labelled with subtype and accession number. Samples EBW034_core and EBW436_core are the product of initial subtyping (see Figure 1), while samples EBW034_Genotype4Specific and EBW436_Genotype4Specific are the product of subtype-specific amplification.



0.04

Figure S2

Estimated maximum-likelihood midpoint-rooted phylogeny of the core section of the generated EBW436 consensus genome, highlighted in red, along with reference sequences. Nodes with bootstrap support $>70\%$ are labelled with their bootstrap support. Branch lengths are in units of expected substitutions per site (see scale bar). Reference sequences are labelled with subtype and accession number.