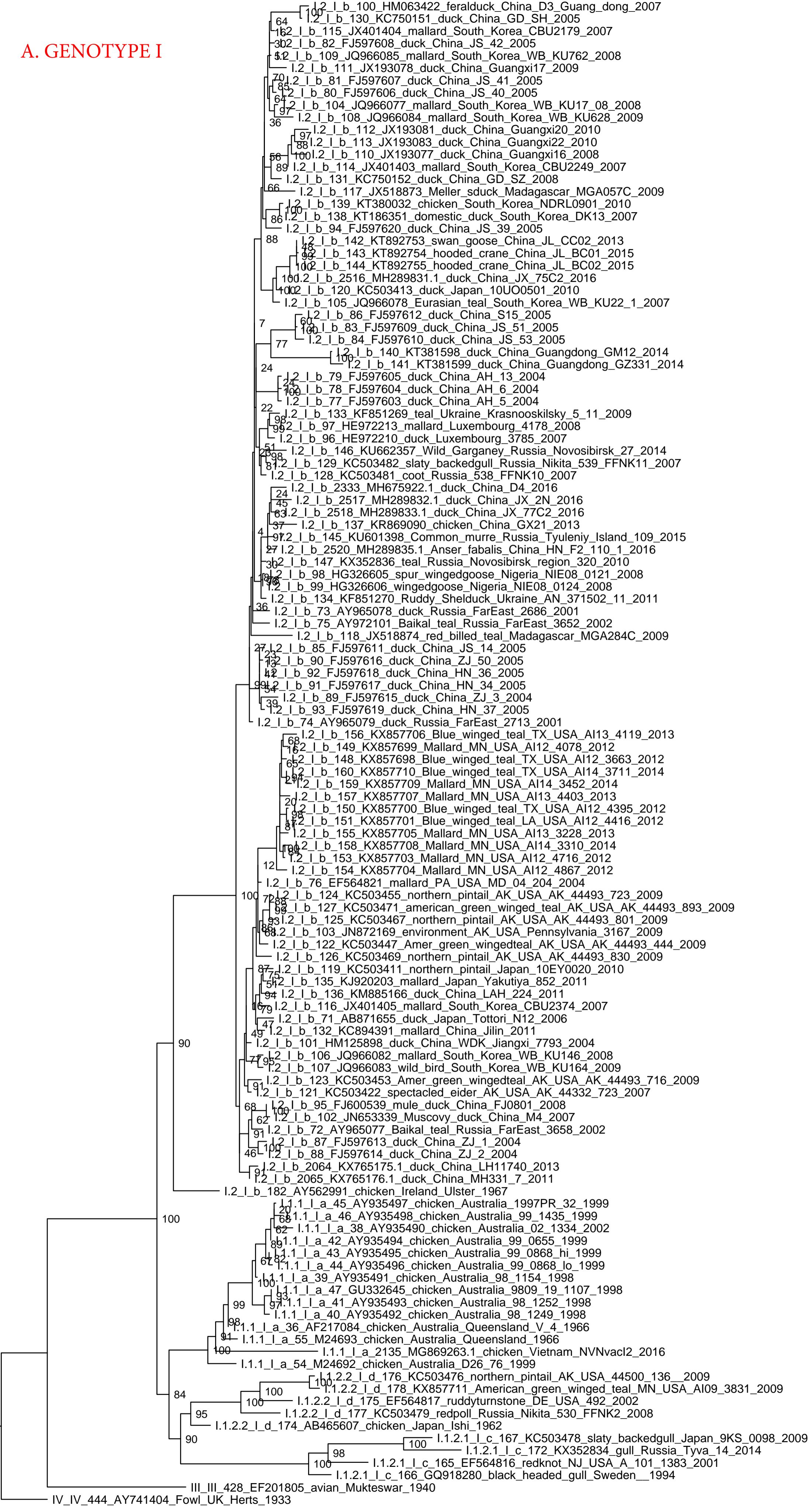
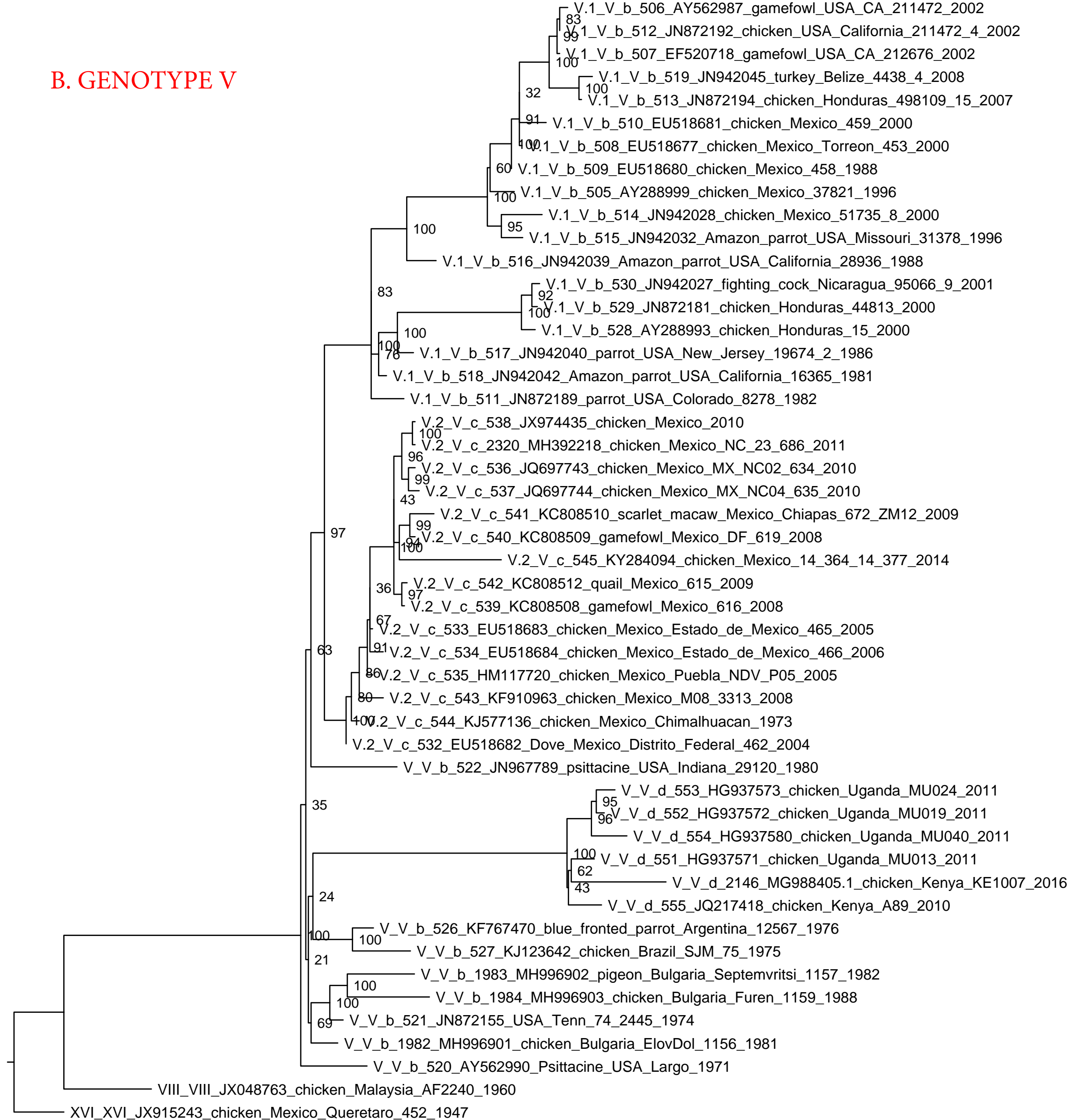


Supplemental Fig. S7. Phylogenetic sub-tree based on the complete fusion gene sequence of isolates representing Newcastle disease virus genotypes. A. Genotype I (n = 122); B. Genotype V (n = 49); C. Genotype VI (n = 267); D. Genotype VII (n = 774); E. XII. Genotype I (n = 25); F. Genotype XIII (n = 74); G. Genotype XIV (n = 79); H. Genotype XVIII (n = 19); I. Genotype XXI (n = 53). The trees were built using all sequences within each NDV genotypes and 2 to 4 additional sequences used for rooting. The sequences recommended for use for rooting are also provided in Supplemental Table S5. The evolutionary history was inferred by using the Maximum Likelihood method based on the General Time Reversible model with 1000 bootstrap replicates. The trees with the highest log likelihood are shown. A discrete gamma distribution was used to model evolutionary rate differences among sites and the rate variation model allowed for some sites to be evolutionarily invariable. The Roman numerals presented in the taxa names in the phylogenetic tree represent the respective genotype for each isolate. The new (decimal naming) and the old names (alpha-numerical) are provided for easier comparison. The taxa names also include the GenBank identification number, and when available - host name, country of isolation, strain designation, and year of isolation. The trees are drawn to scale, with branch lengths measured in the number of substitutions per site.

A. GENOTYPE I



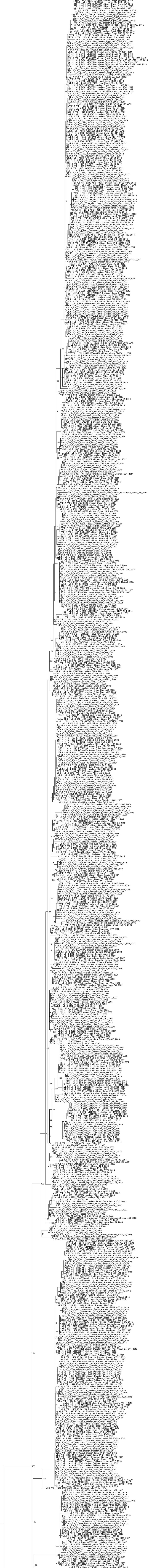
B. GENOTYPE V



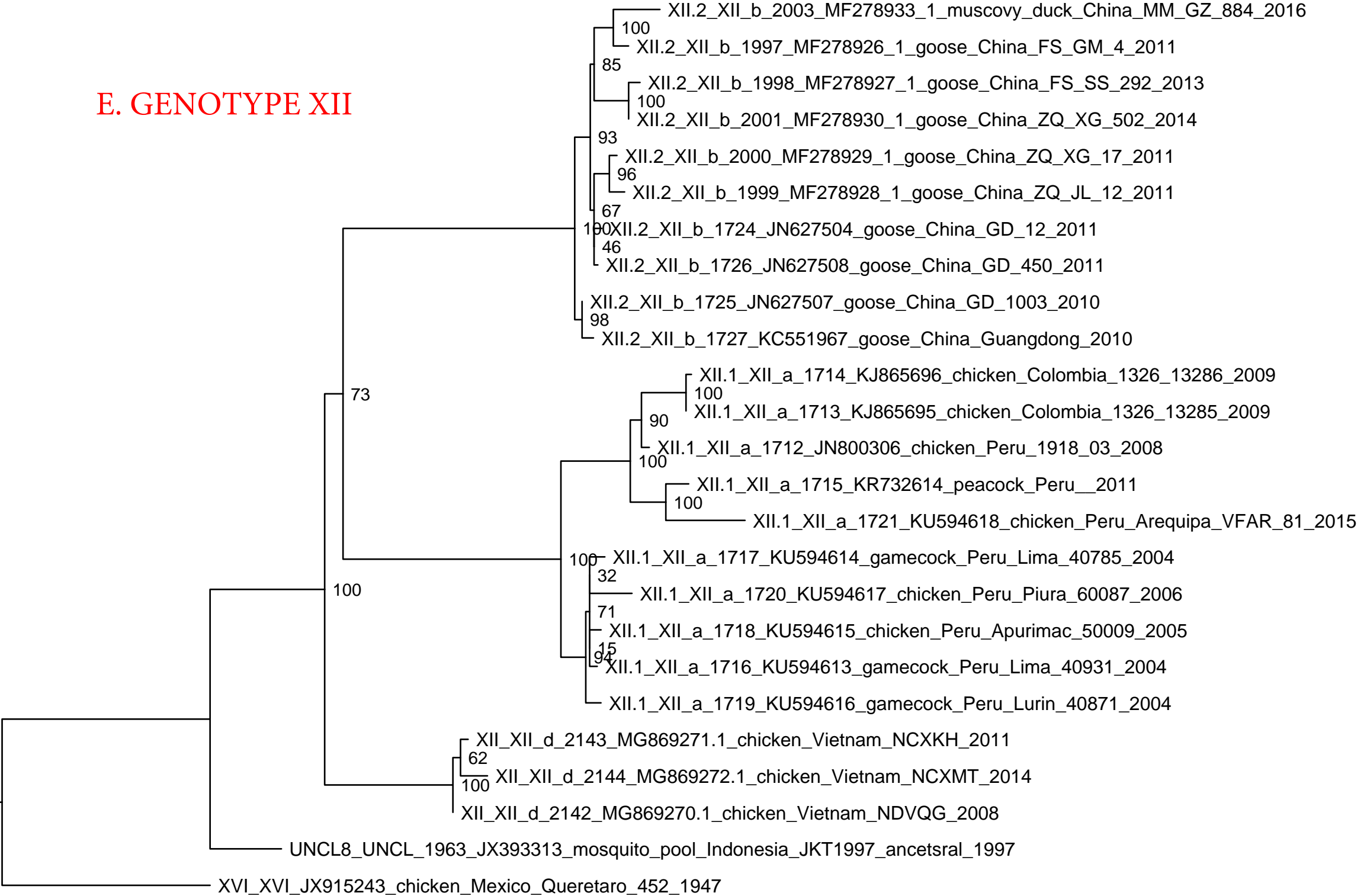
C. GENOTYPE VI



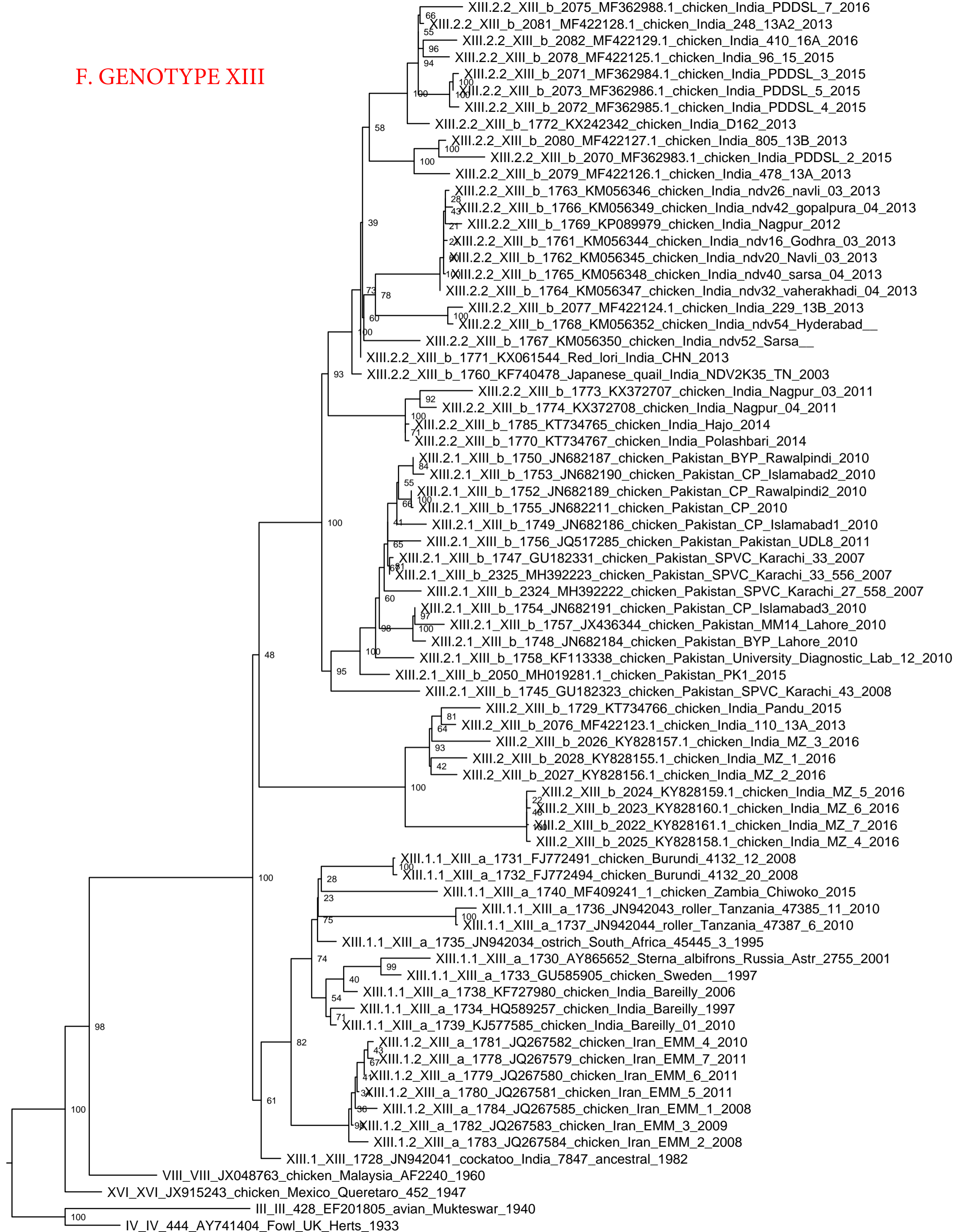
D. GENOTYPE VII



E. GENOTYPE XII



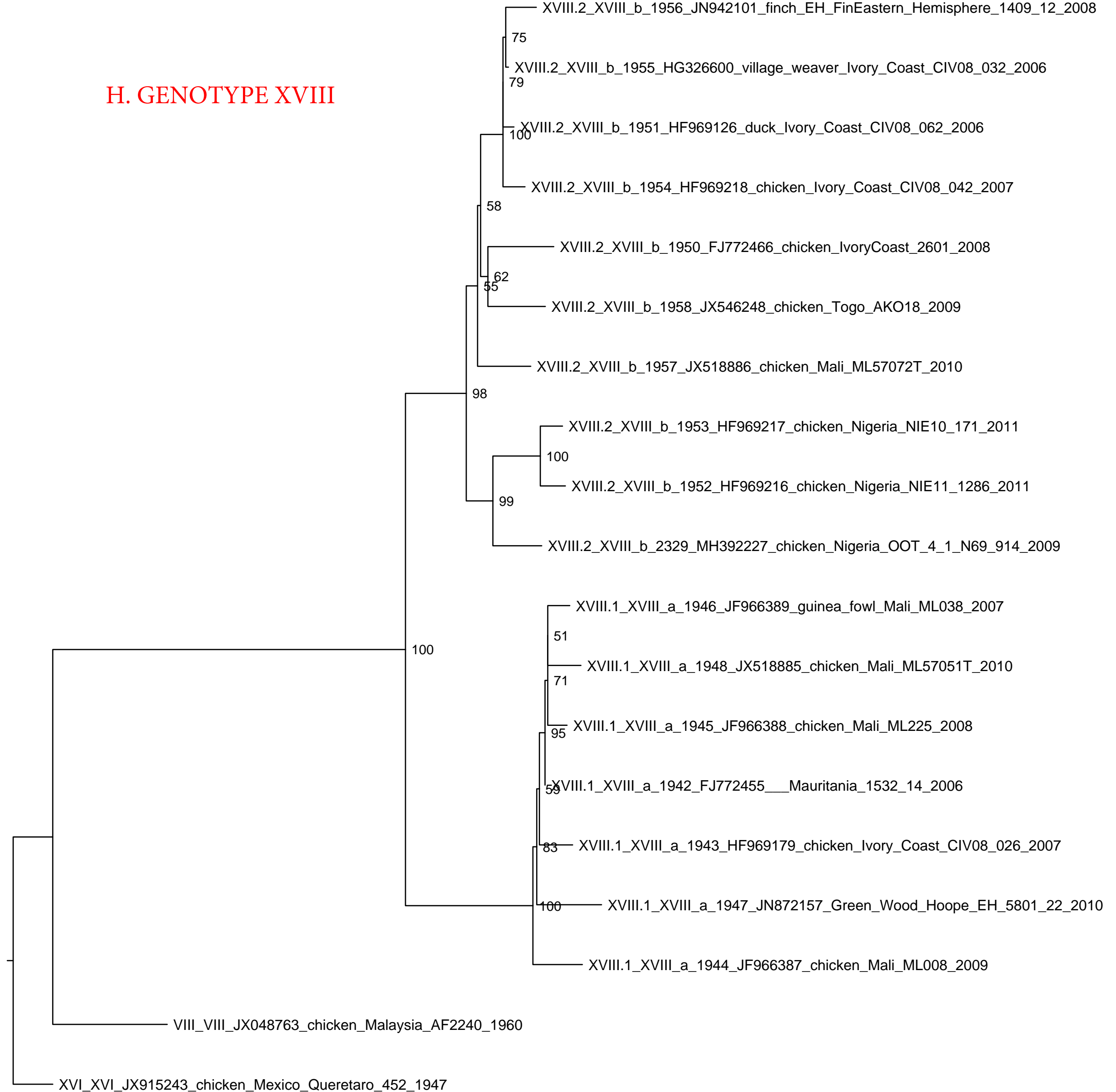
F. GENOTYPE XIII



G. GENOTYPE XIV



H. GENOTYPE XVIII



I. GENOTYPE XXI

