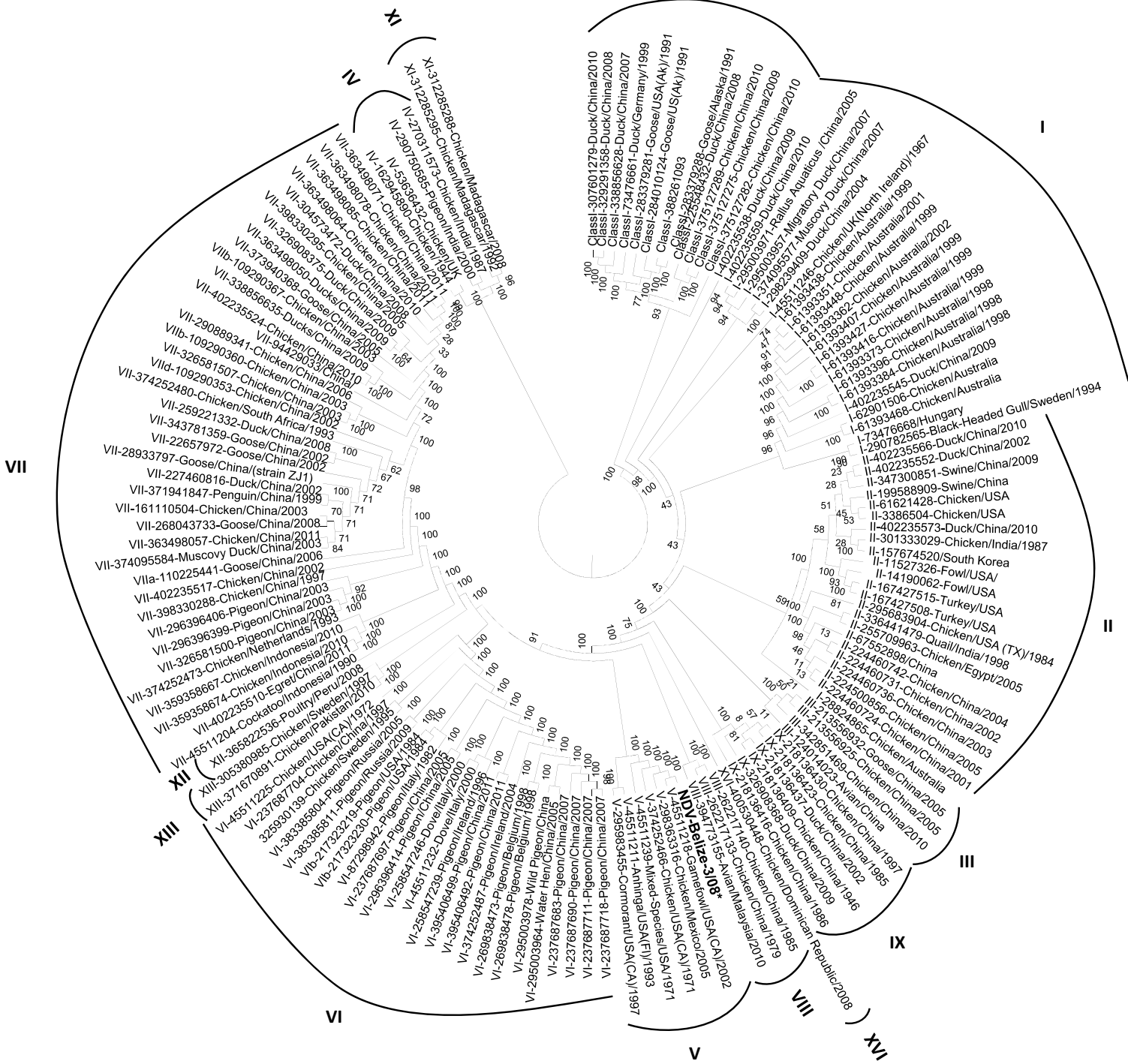


Class I



Supplementary figure 1. Molecular Phylogenetic analysis by Maximum Likelihood method using the concatenated full coding sequences of all six structural proteins of NDV-Belize- 3/08 among 149 NDV strains representative of different NDV genotypes. The evolutionary history was inferred by using the Maximum Likelihood method based on the General Time Reversible model (1). The tree with the highest log likelihood (-278572.2698) is shown. The percentage of trees in which the associated taxa clustered together in the bootstrap test is shown next to the branches (number of replicates = 100). Initial tree(s) for the heuristic search were obtained automatically by applying the Maximum Parsimony method. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 150 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated. There were a total of 15022 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 (2).

Supplementary reference list.

- 1) **Nei M, Kumar S.** 2000. Molecular Evolution and Phylogenetics. Oxford University Press, New York.
- 2) **Tamura K, Stecher G, Peterson D, Filipski A, Kumar S.** 2013. MEGA6: Molecular Evolutionary Genetics Analysis Version 6.0. Mol Biol Evol. **30**:2725-9.