

## Erratum to: Genomic characterization of the first class I Newcastle disease virus isolated from the mainland of China

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Some of the information provided in Figure 2 of the online published article is not pertinent to the subject matter. The correct version of Figure 2 is shown overleaf.

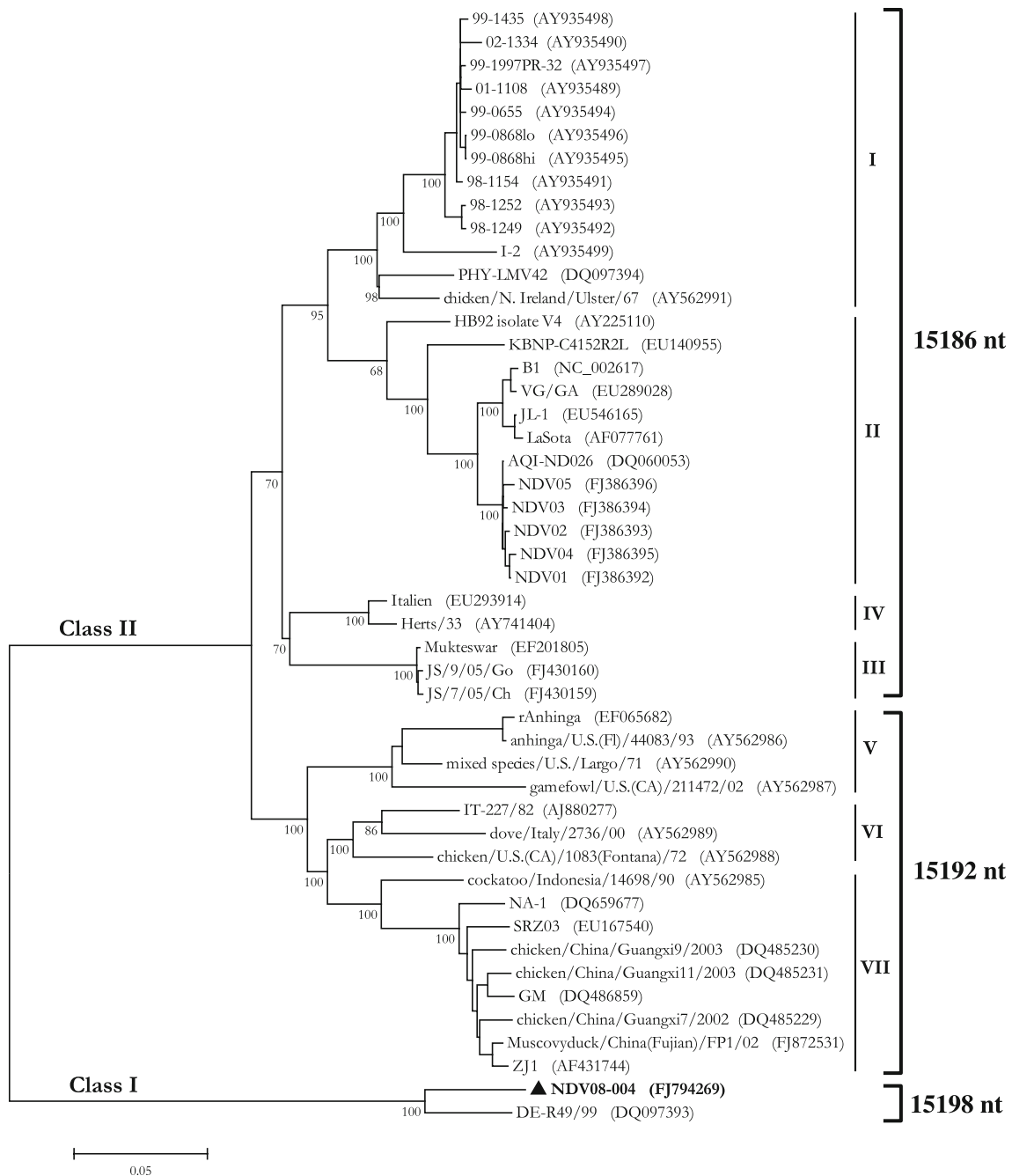
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**Fig. 2** Phylogenetic tree of 48 NDV strains based on the complete genomic sequence. The sequence determined in this study is in **bold**. The GenBank accession numbers of the NDV isolates are shown in *brackets*. The genomic length for different strains is indicated on the

*right*. The tree was constructed using the neighbor-joining algorithm of MEGA 3.1, with a 1000 bootstrap trial to assign confidence to groupings