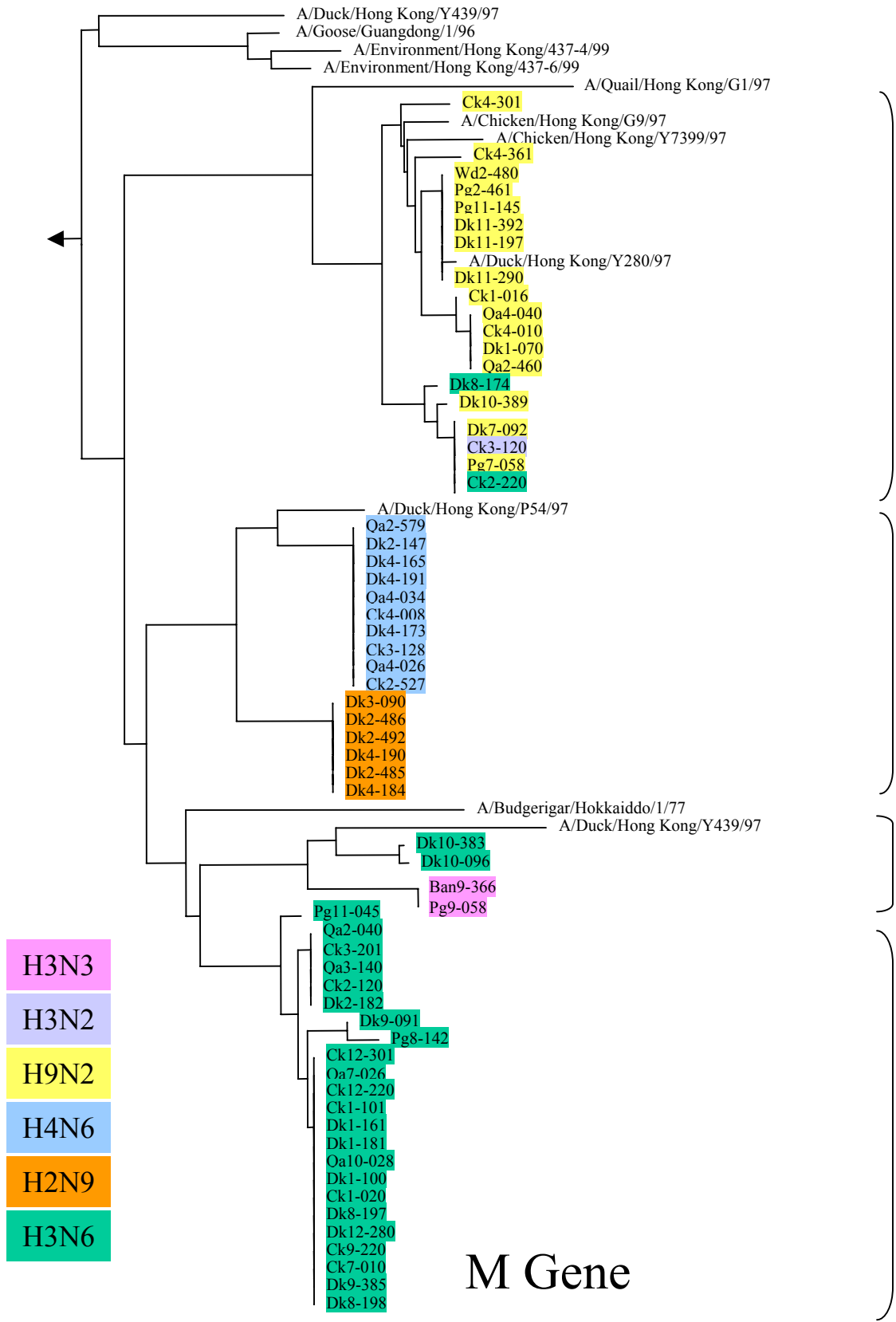
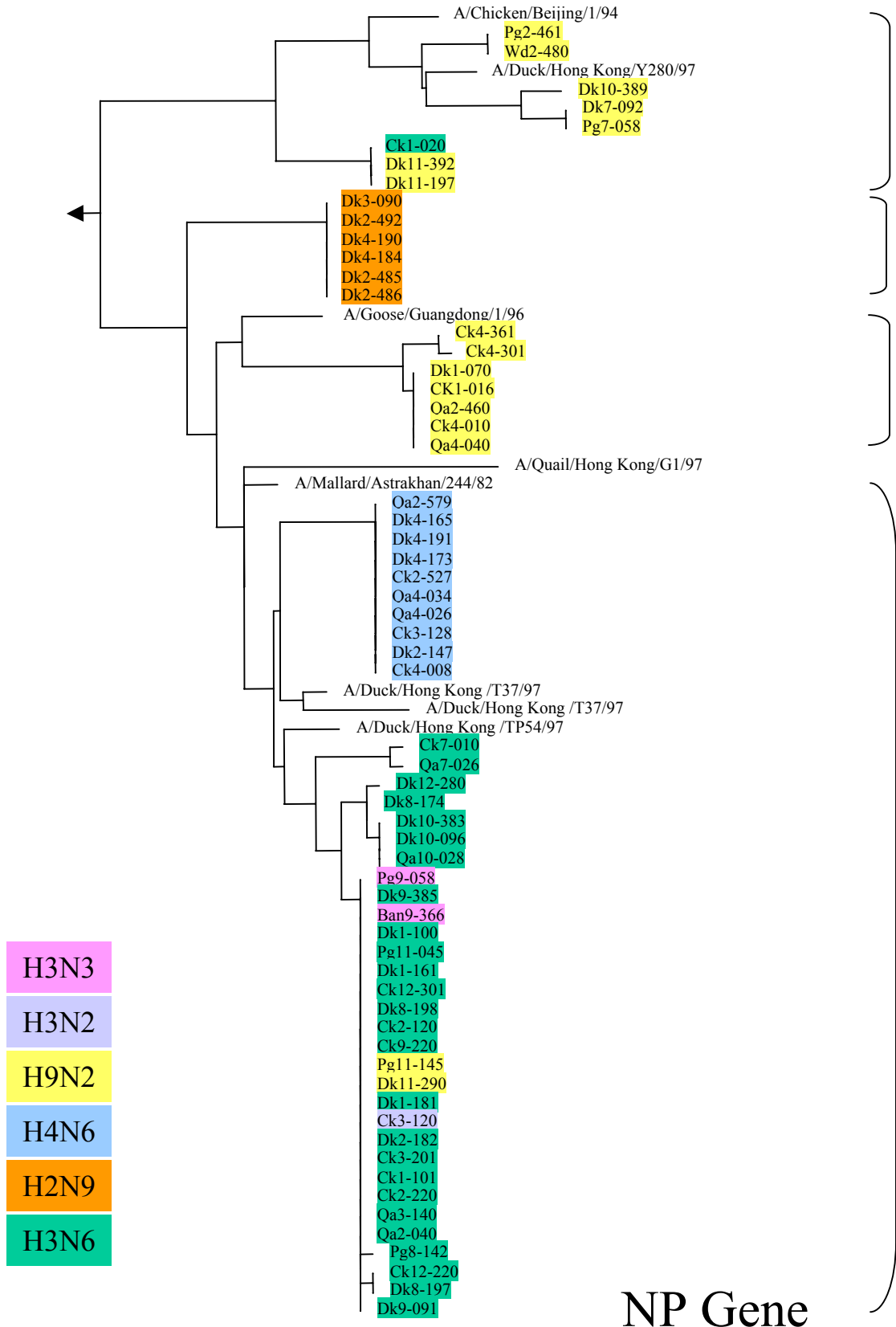


Appendix 1. List of virus abbreviations.

Appendix 2. Phylogenetic trees produced from the partial nucleotide sequences of the M, NS, NP, PA, PB1, and PB2 genes. Multiple sequence alignments were made by using CLUSTAL W , and phylogenetic trees were generated by using the neighbor-joining algorithm in the PHYLIP version 3.57C software package . The following regions of the gene segments were used for phylogenetic analysis: PB2, nucleotide positions 65 to 603; PB1, 45 to 634; PA, 47 to 525; NP, 41 to 631; M, 40 to 668; and NS, 101 to 621. All trees are rooted to A/Quail/Nanchang/12-340/2000 except that for the NS gene which is rooted to A/equine/Prague/1/56. The open brackets at the right of the trees indicate the phylogenetic groups used in our analysis (see text for more detail).

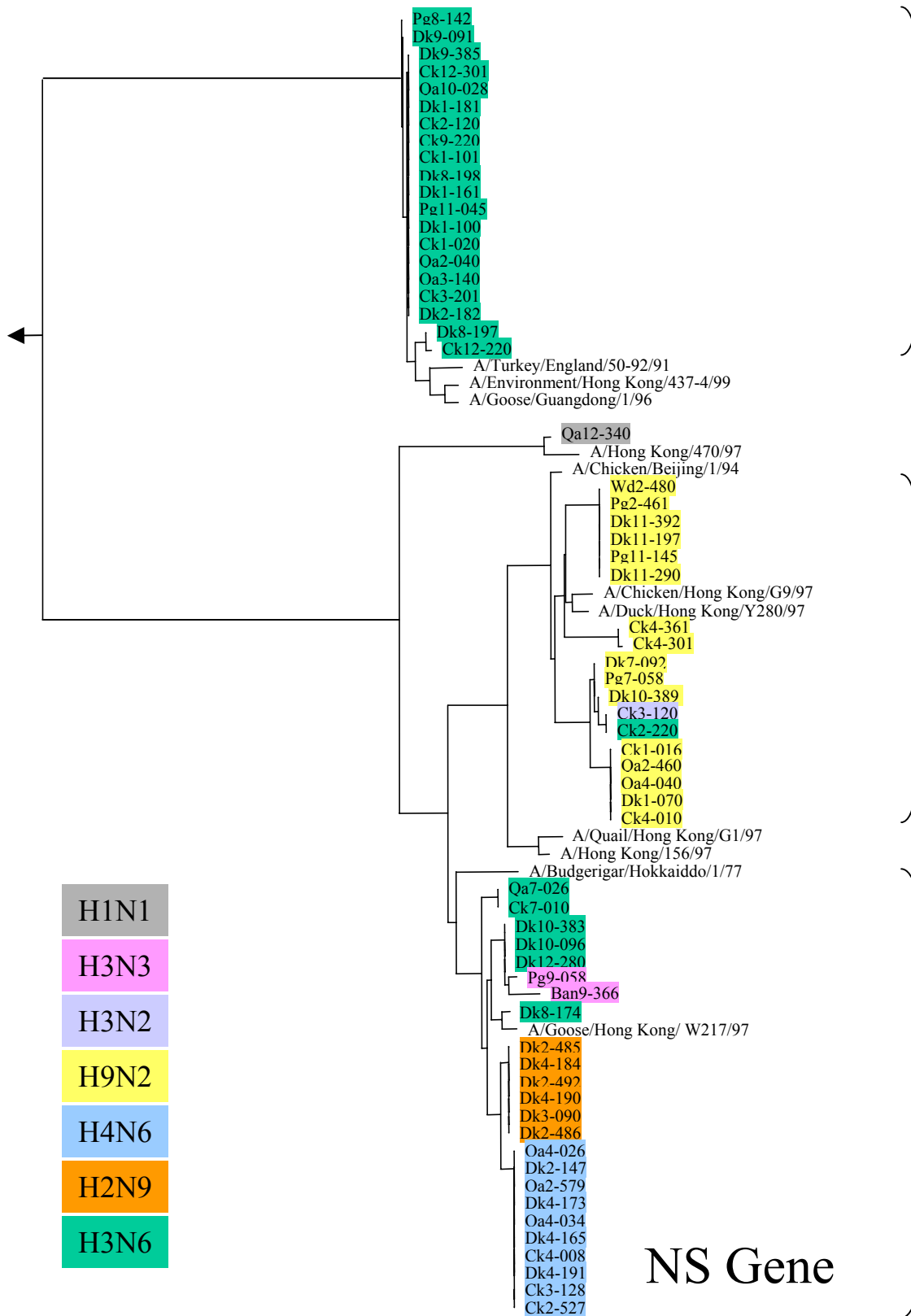


M Gene



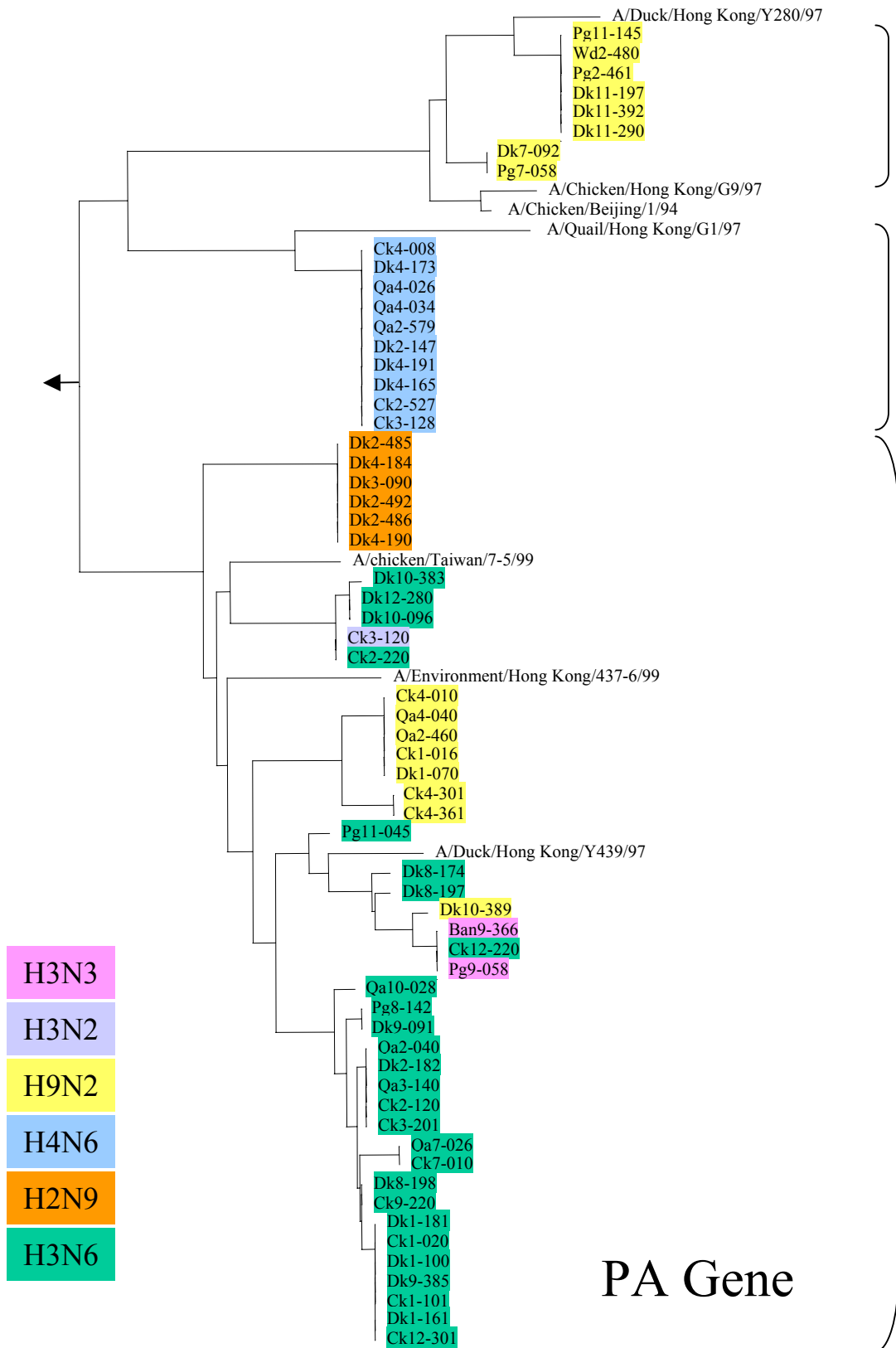
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NP Gene

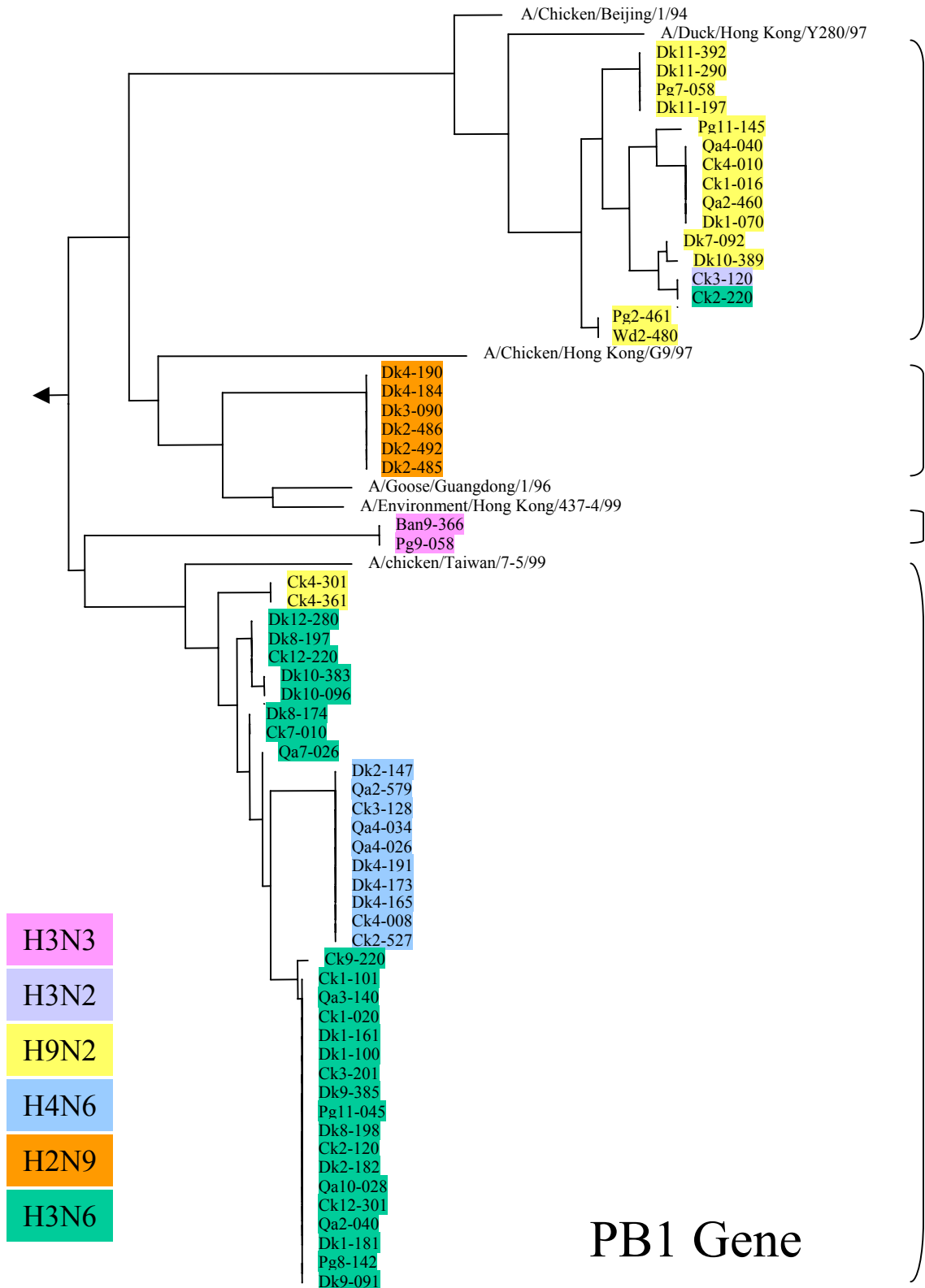


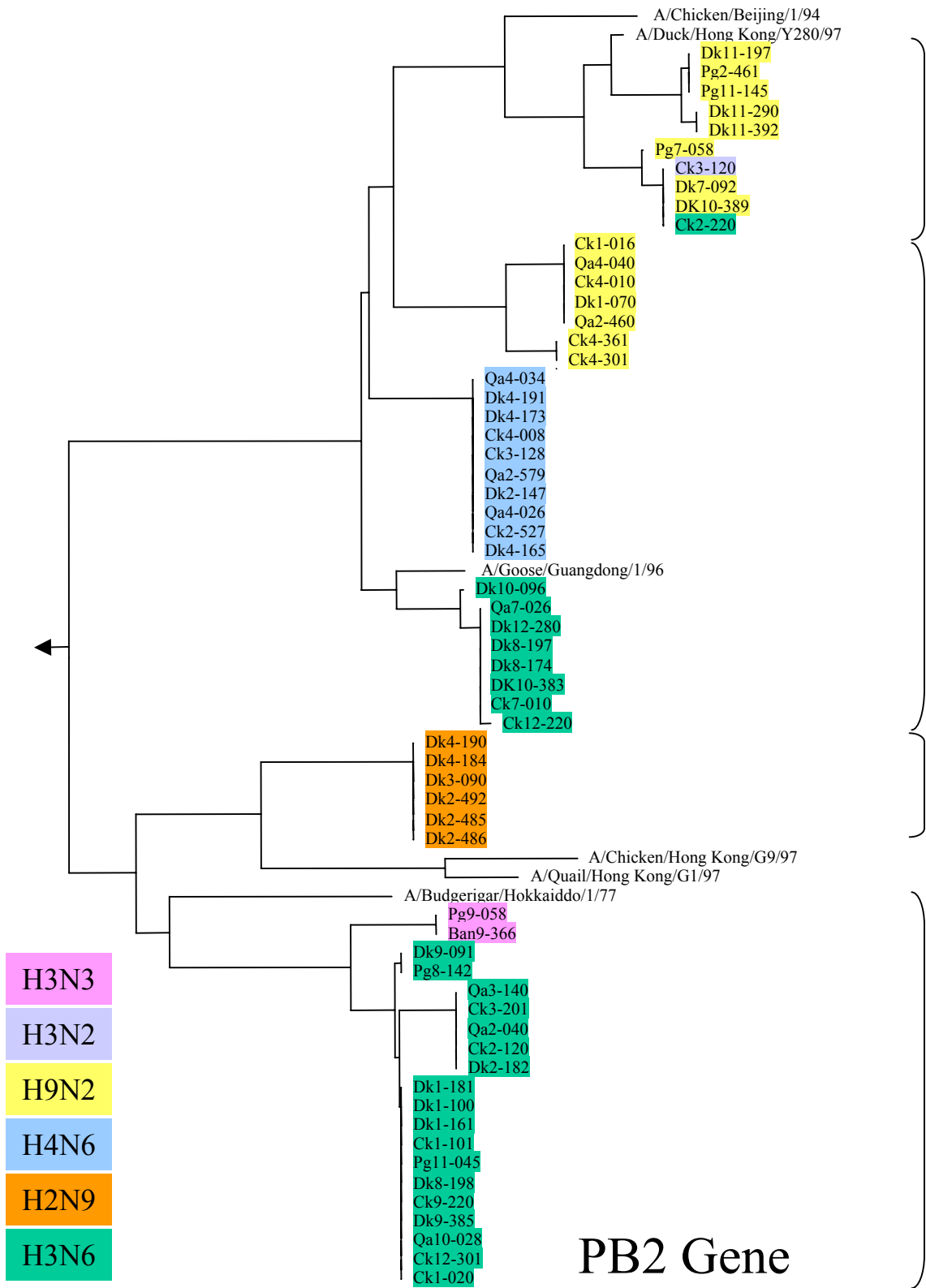
0.1

NS Gene



0.1





0.1

PB2 Gene