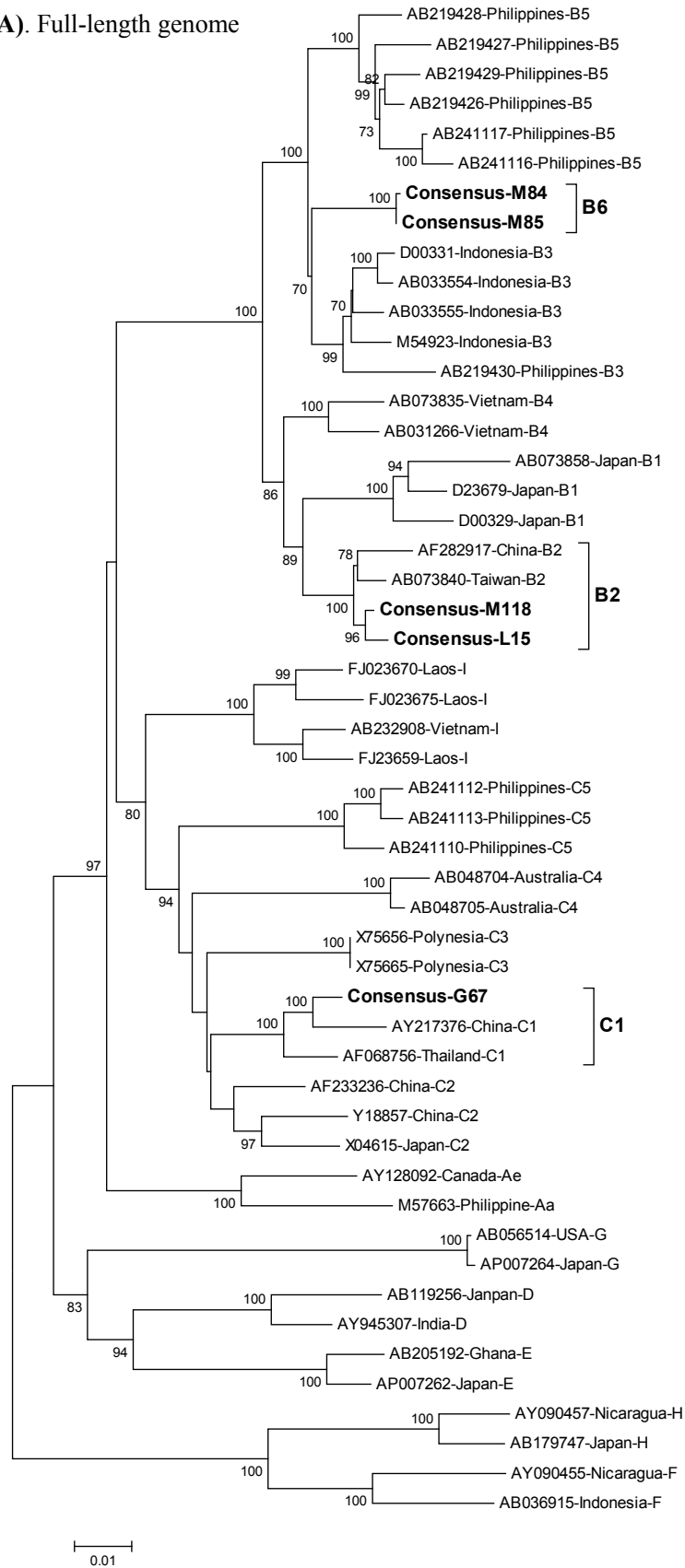
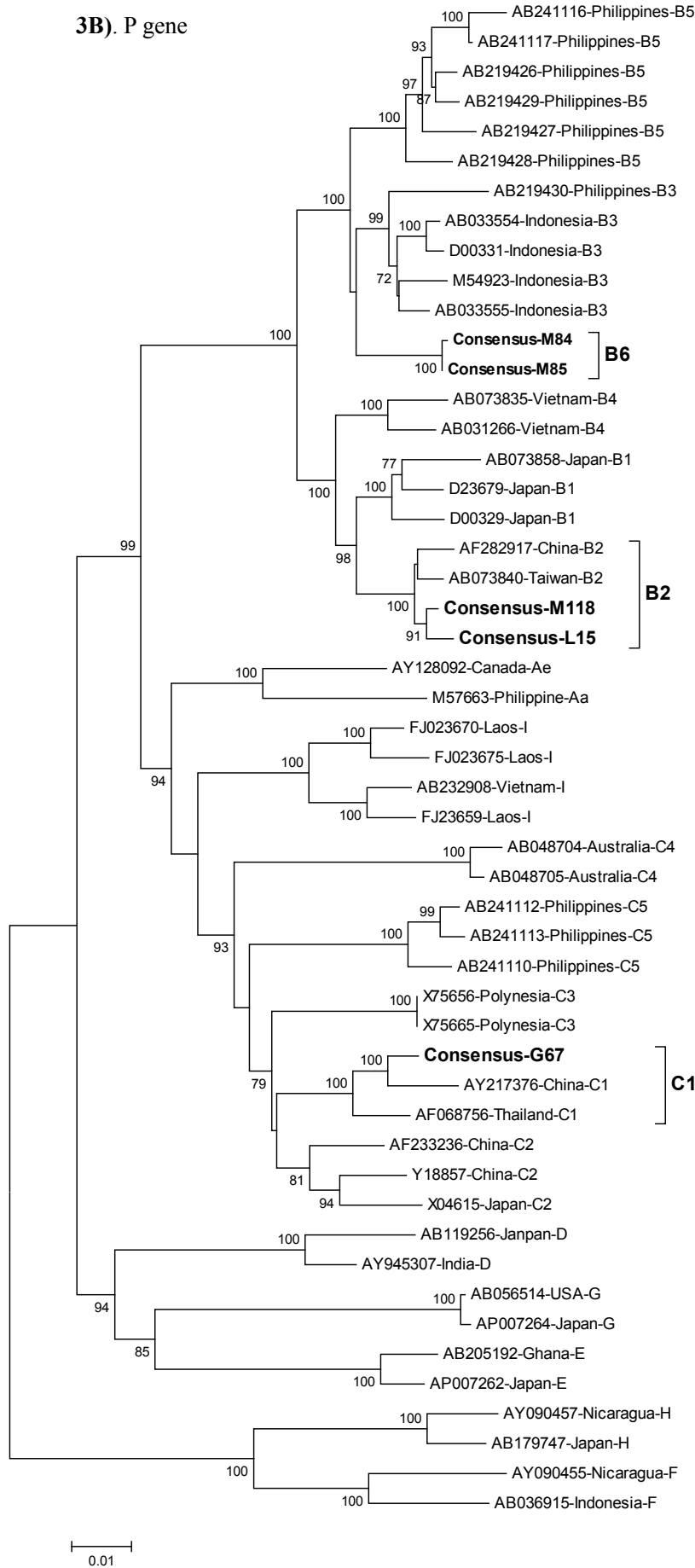


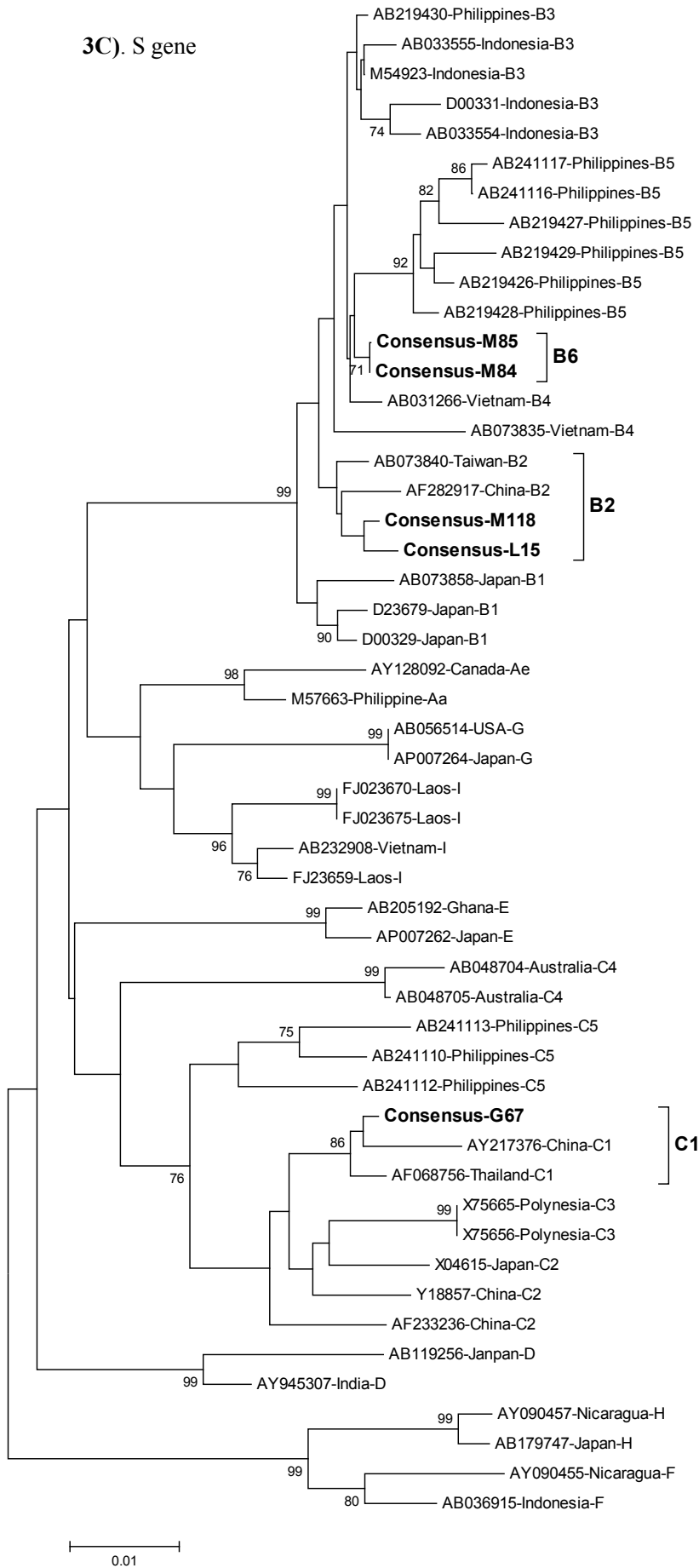
### 3A). Full-length genome



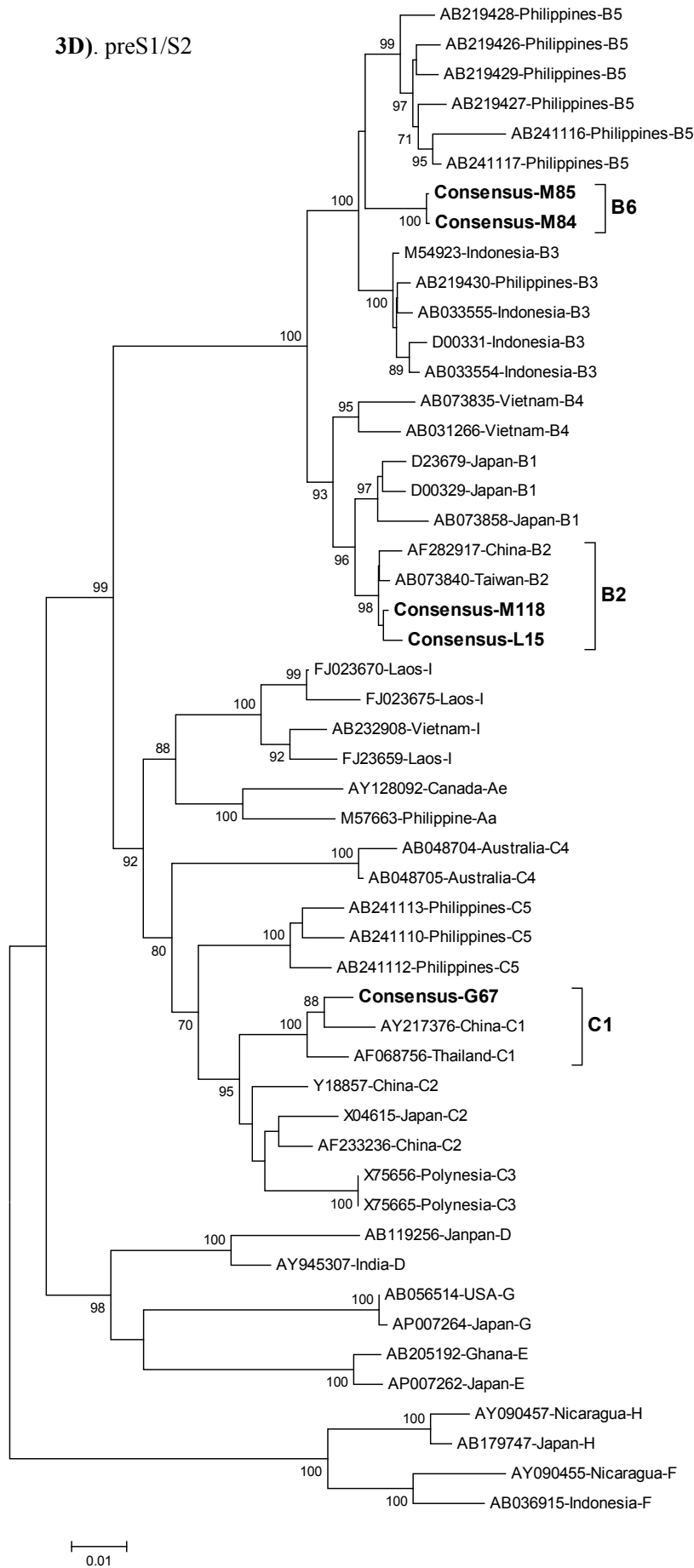
### 3B). P gene



### 3C). S gene



### 3D). preS1/S2



3E). preS1 gene

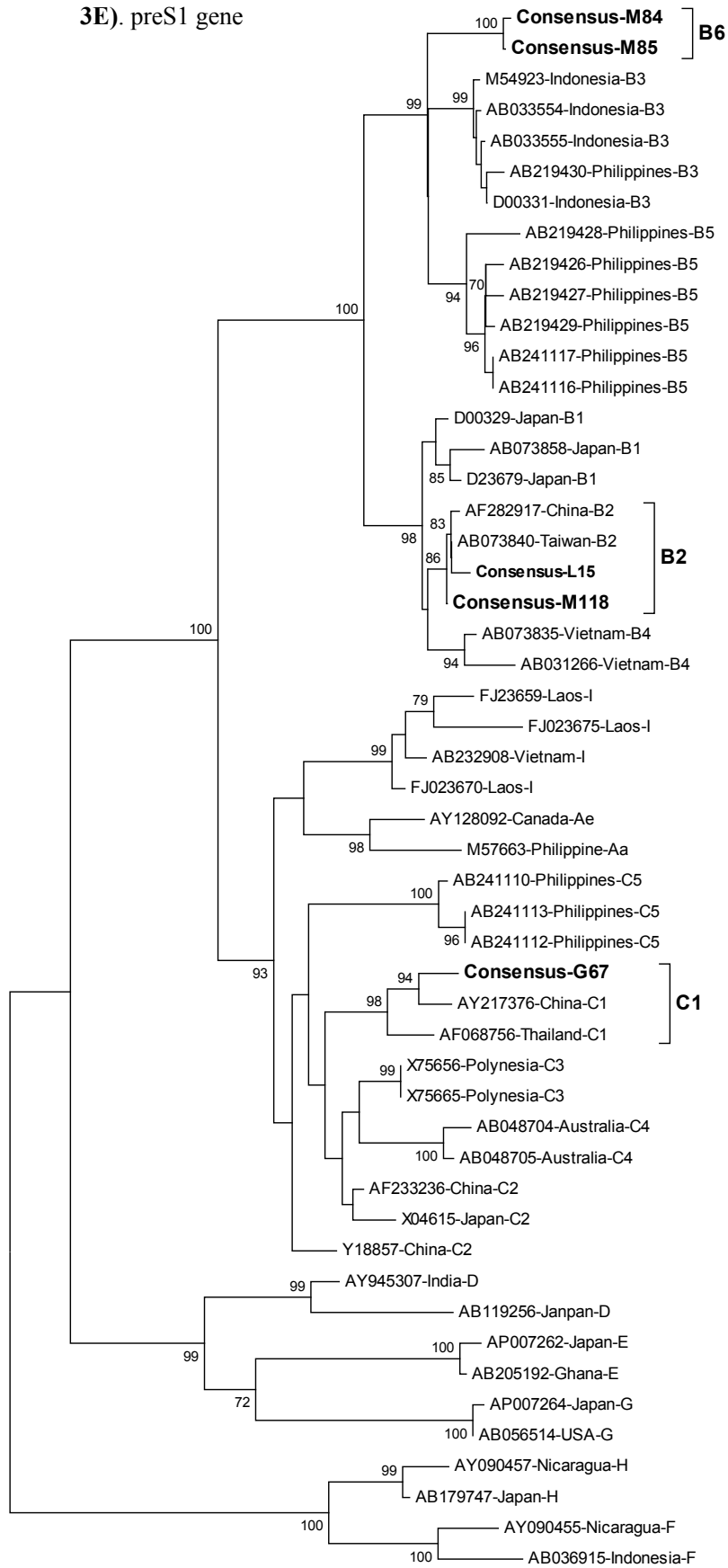


Fig 3. Phylogenetic tree of partial nucleotide constructed by the neighbor-joining method using the present five consensus sequence and other genotyp isolates retrived from DDBJ/GenBank. Bootstrap values are indicated for each group. The length of the horizontal bar indicates the number of nucleotide substitutions per site. Five consensus sequences presented in this study were shown in bold. Each consensus sequence was created by all the clones from each patient. 3A) full-length genome; 3B) region of P gene; 3C). region of HBs; 3D) region of preS1/S2 gene; 3E) region of preS1 gene