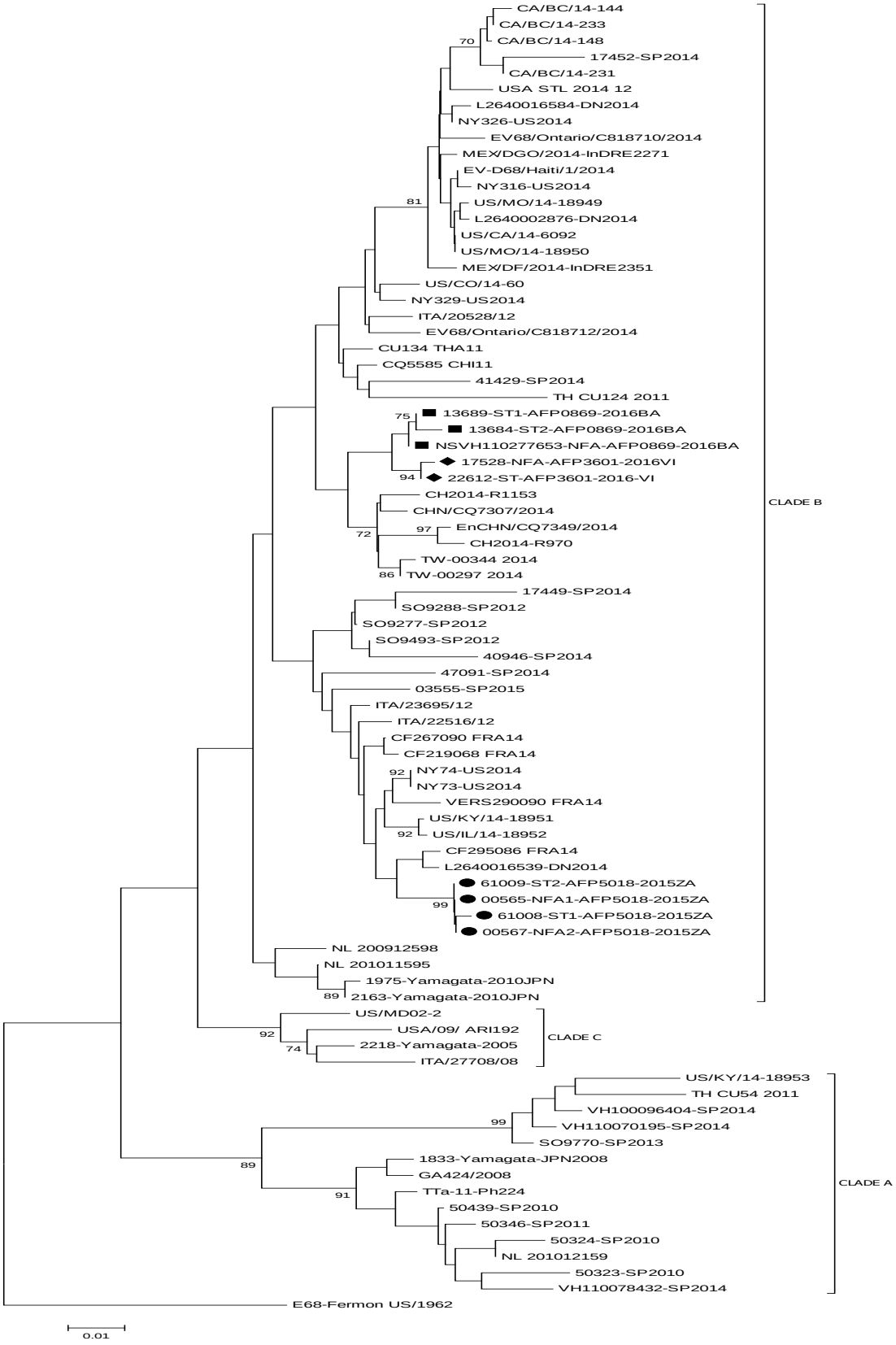
SDC 1. The phylogenetic tree was constructed by the neighbor-joining method and evaluated with 1000 bootstrap pseudoreplicates using MEGA vs 6. Only bootstrap values >70% are indicated. Genetic distances were calculated with maximum composite likelihood model of evolution. 3'-VP1 sequences (400 bp) from case 1, 2 and 3 are marked with ♦, ■, and ●, respectively. ST, stool sample; NFA, nasopharyngeal aspirate; AFP, acute flaccid paralysis; BA, Barcelona; VI, Vigo; ZA, Zaragoza.


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EnCHN/CQ7349/2014
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