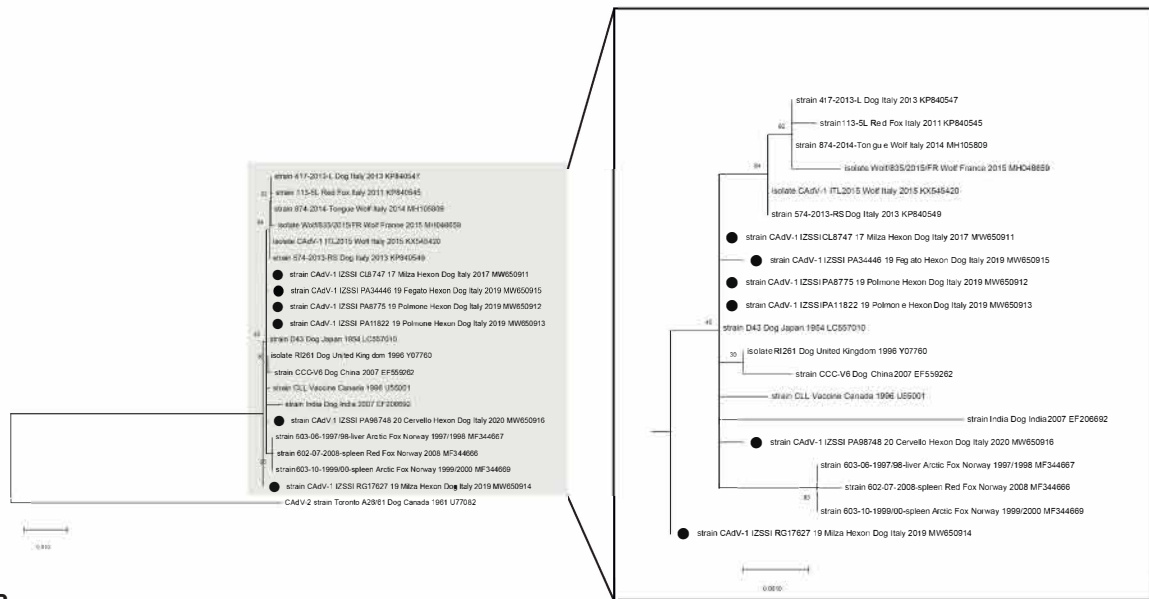
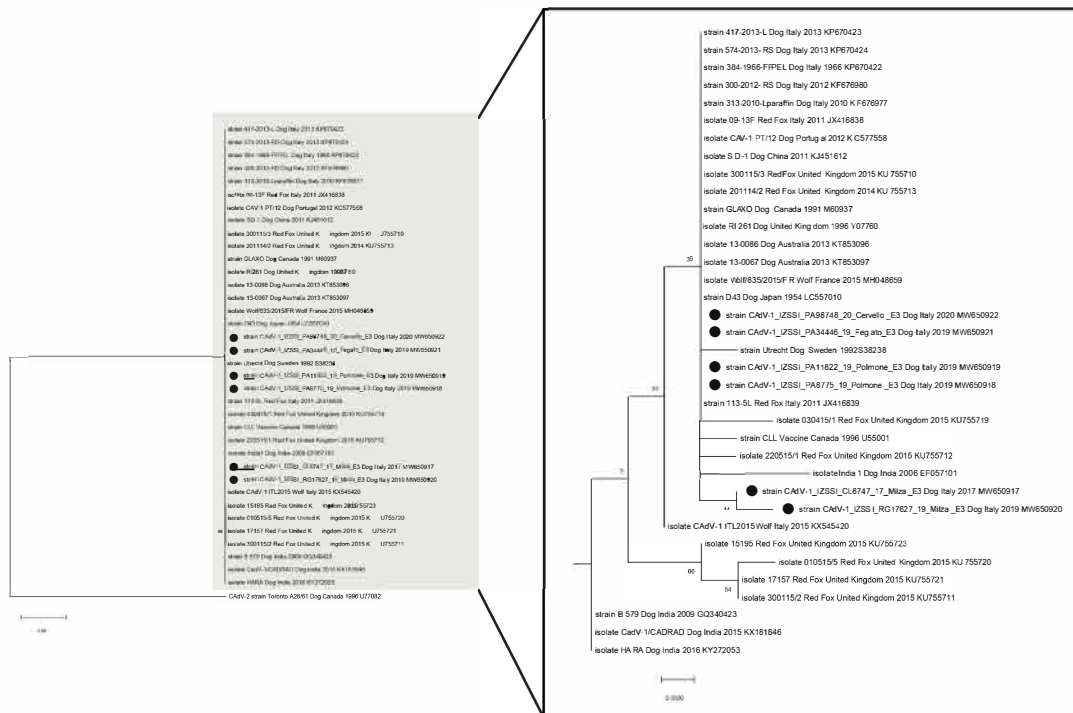


A

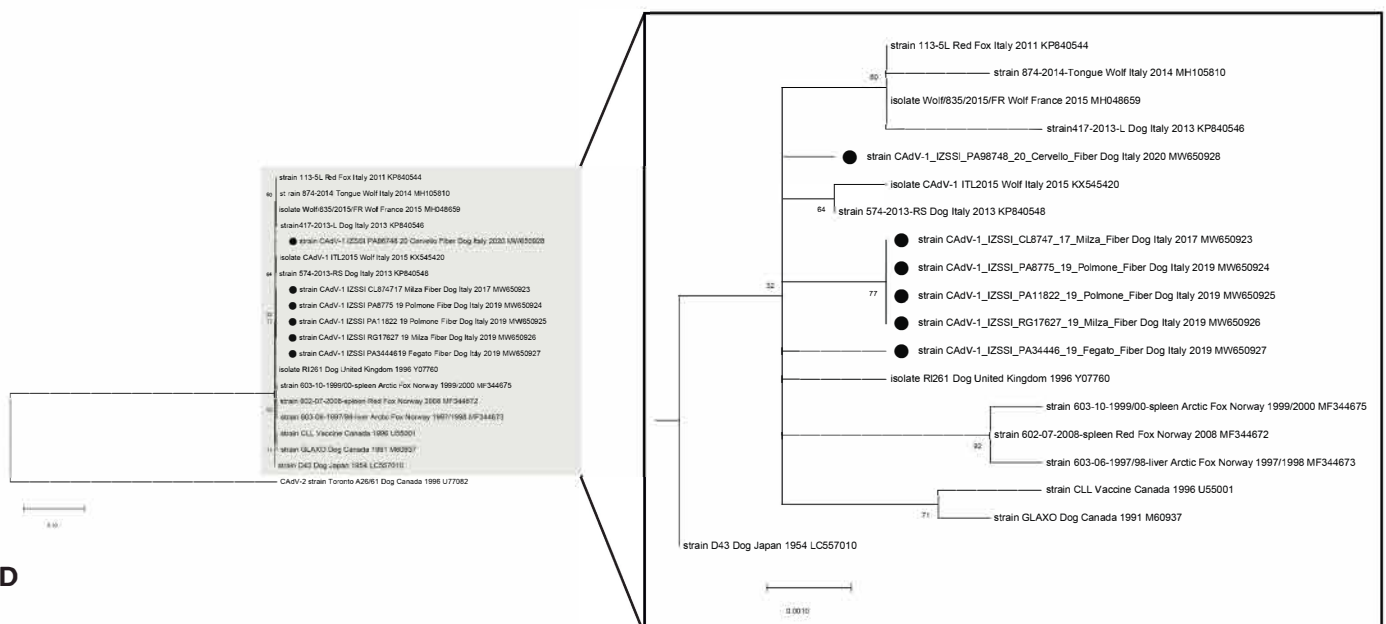


B

C



D



**Supplementary Material Figure S1.** Maximum-likelihood tree and CADV-1 clade drawn to scale based on 11 Penton (A), 20 Hexon (B), 36 E3 and flanking regions (C), and 19 Fiber (D) gene sequences, respectively, and CADV-2 strain sequence as outgroup (bootstrap 1,000 replicates). Black dots markings (●) indicate CADV-1 strains analysed in this study. Scale bar indicate the relative number of substitutions per site. Each sequence is indicated with strain/isolate name, host, country and year of collection, and accession number.