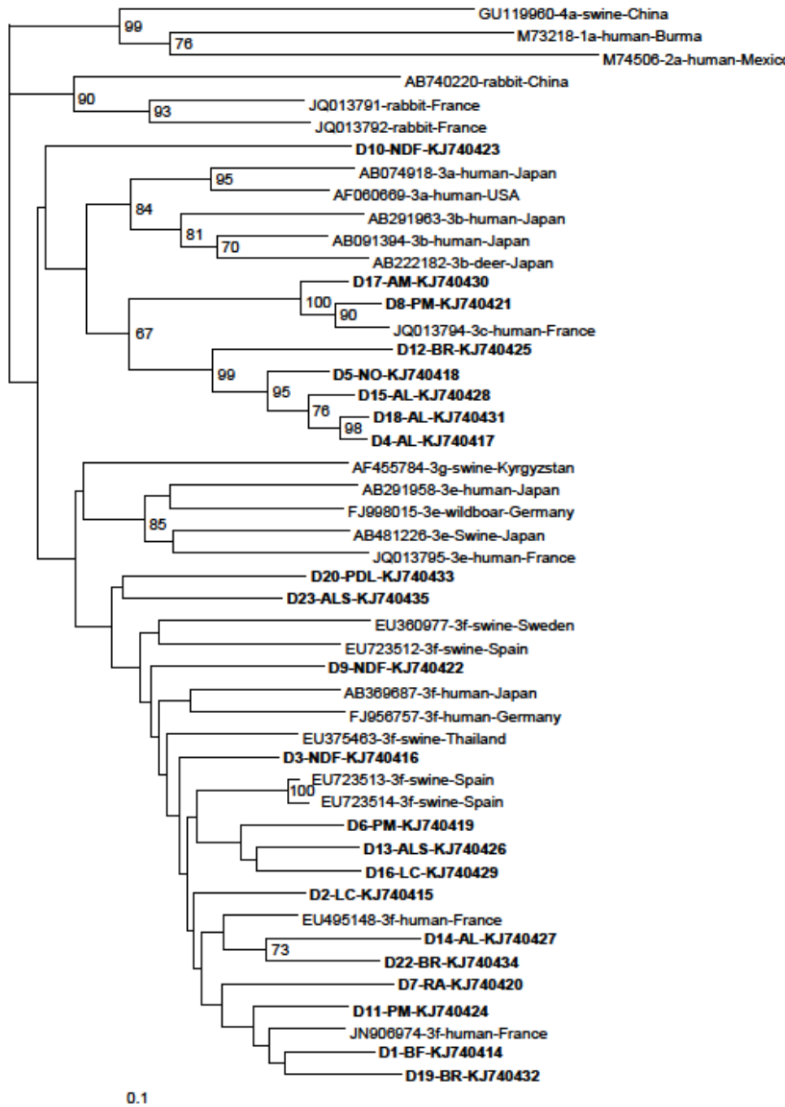


Hepatitis E Virus Infections in Blood Donors, France

Technical Appendix



Technical Appendix Figure. Phylogenetic analysis of hepatitis E virus RNA sequences by using the neighbor-joining method and a Kimura 2-parameter distance matrix based on a 305-nt fragment of open reading frame 2. GenBank accession nos. for isolates from this study (in bold) are KJ740414–KJ740435. Values along the branches are bootstrap values, which are indicated as a percentage of the data obtained from 1,000 resamplings. Scale bar indicates nucleotide substitutions per site.