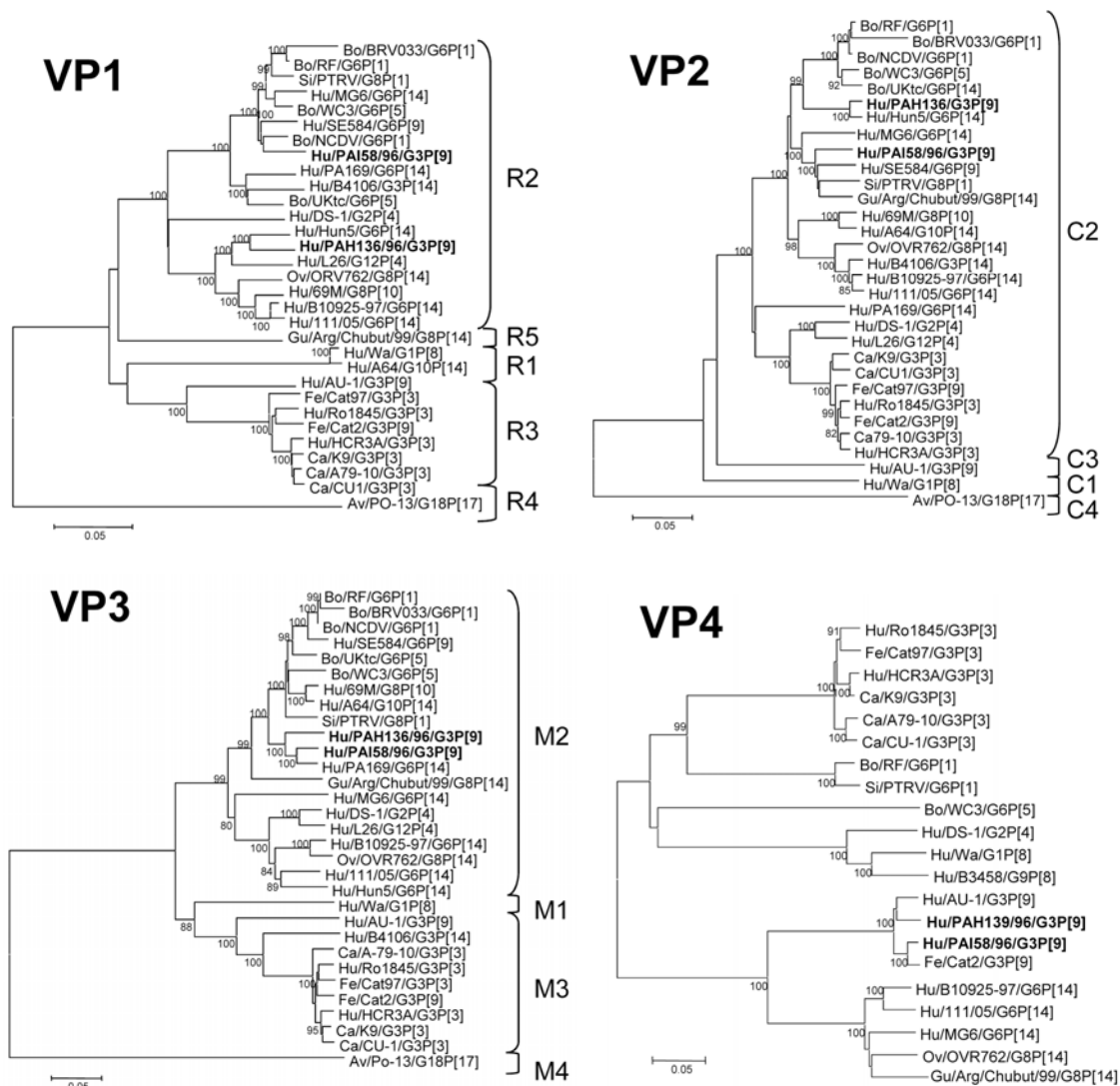


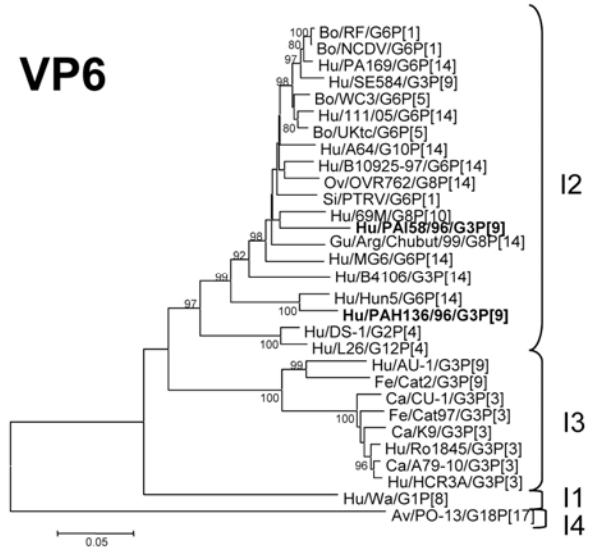
Unusual Assortment of Segments in 2 Rare Human Rotavirus Genomes

Technical Appendix

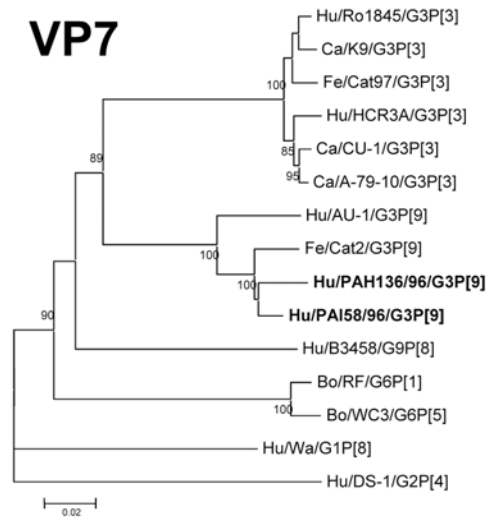
Phylogenetic trees based on the full-length nucleotide sequences of 11 rotavirus genes: viral proteins (VP) 1–5, 6, and 7, and nonstructural proteins (NSP) 1–5. The trees were generated by using the neighbor-joining method and Kimura 2-parameter model. Bootstrap values (500 replicates) >80 are shown. The various genotypes are bo, bovine; hu, human; fe, feline; ca, canine; gu, guanacos; si, simian; ov, ovine; av, avian. The Italian G3P[9] viruses are in **boldface**. Scale bars indicate genetic distance between sequences of segments analyzed.



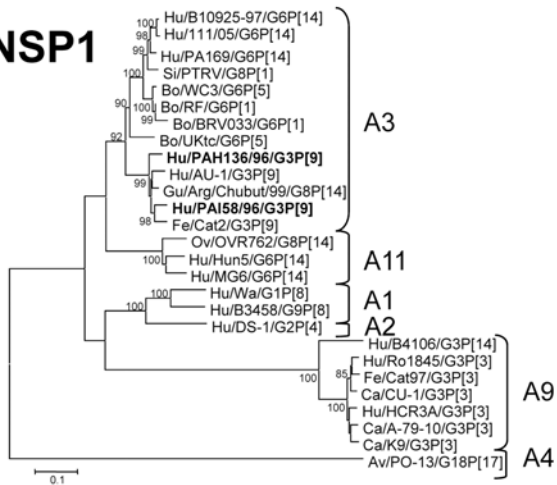
VP6



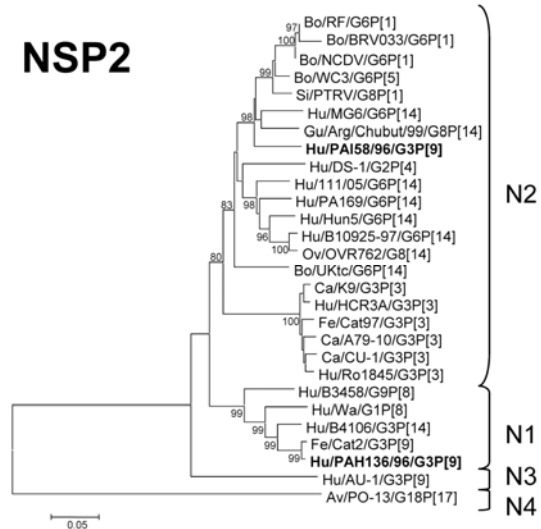
VP7



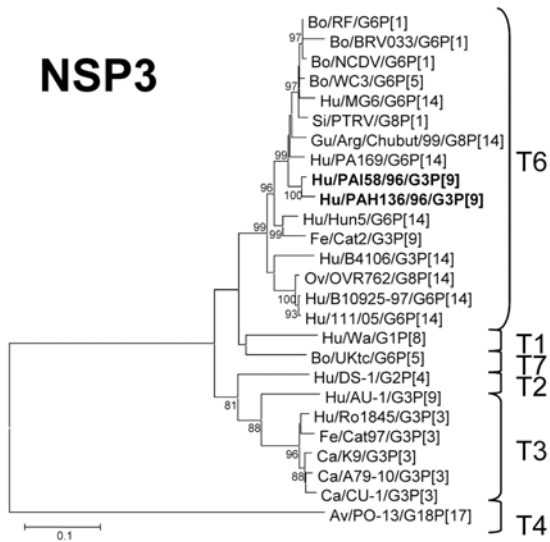
NSP1



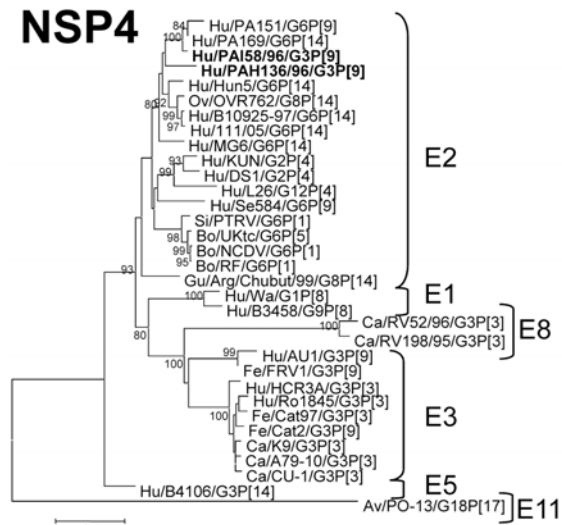
NSP2



NSP3



NSP4



NSP5

