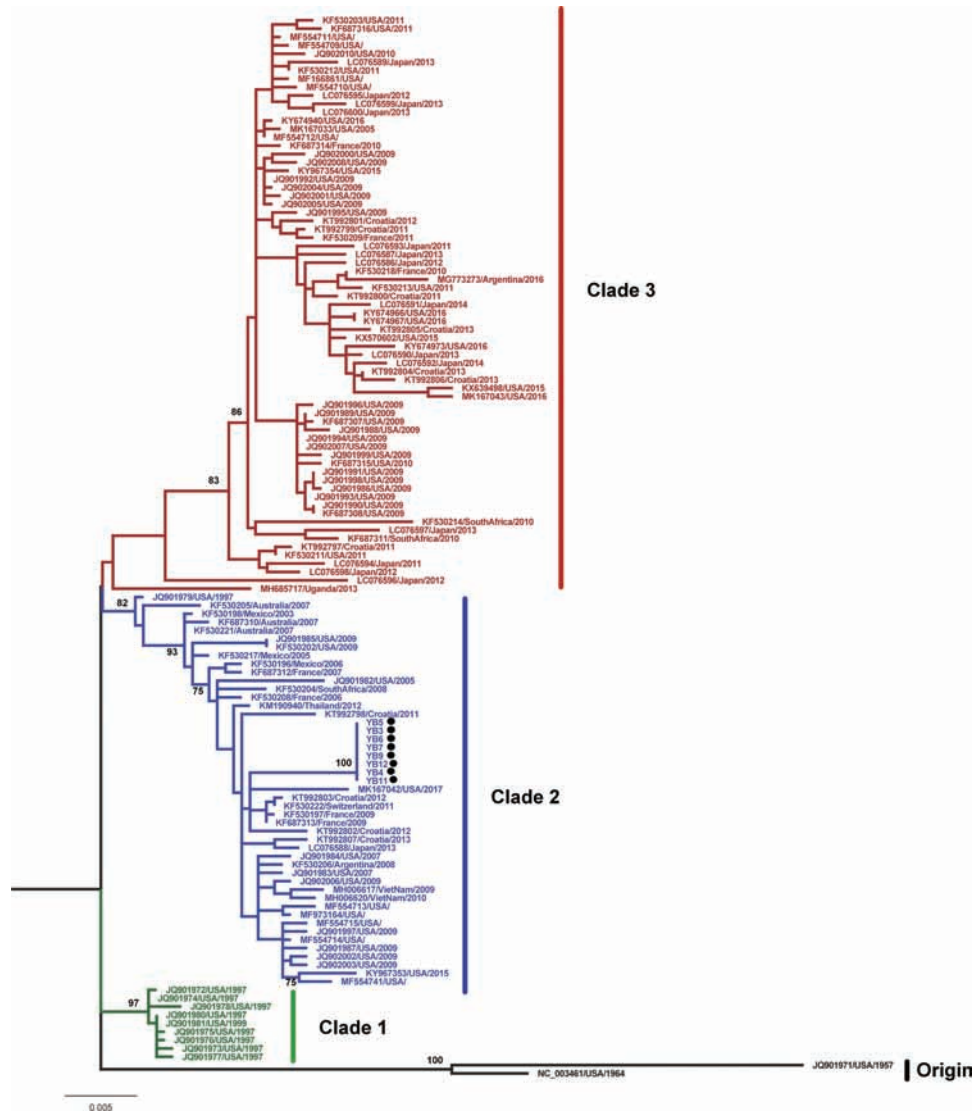
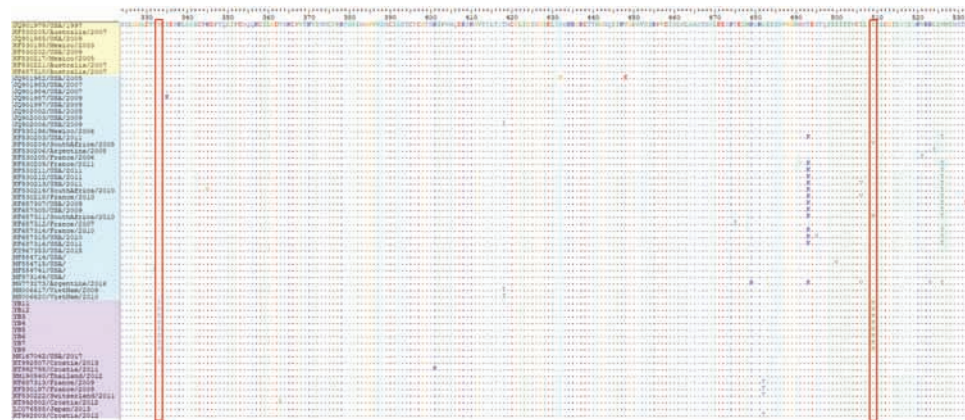


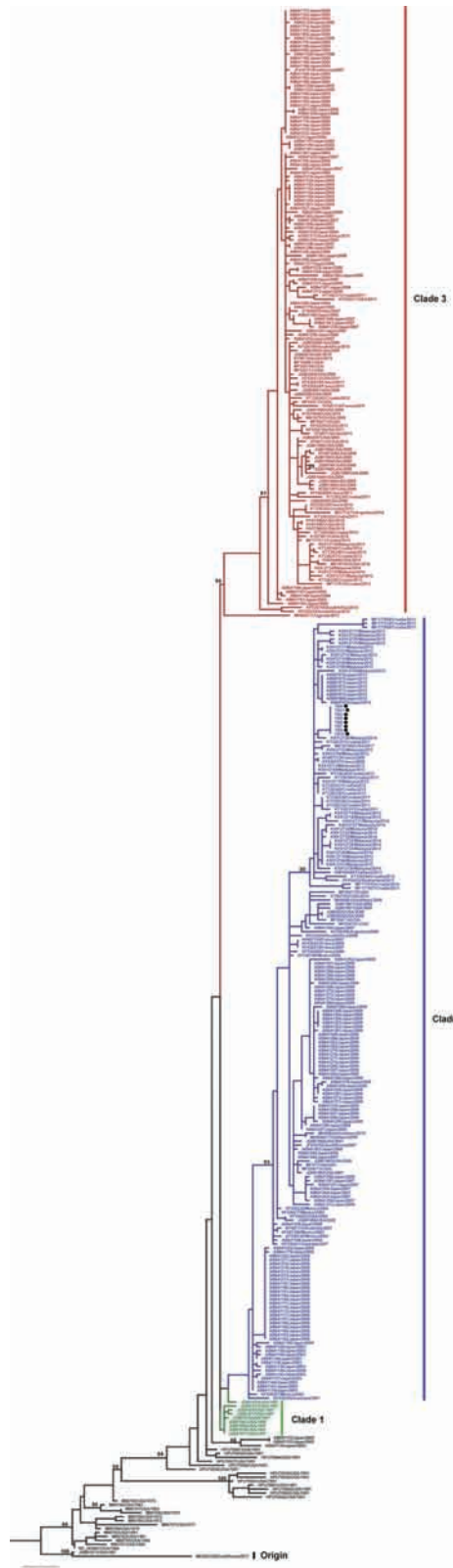
Supplementary Fig. S1 The disease onset times for the pediatric patients in the study. CDC, centers for disease control and prevention.



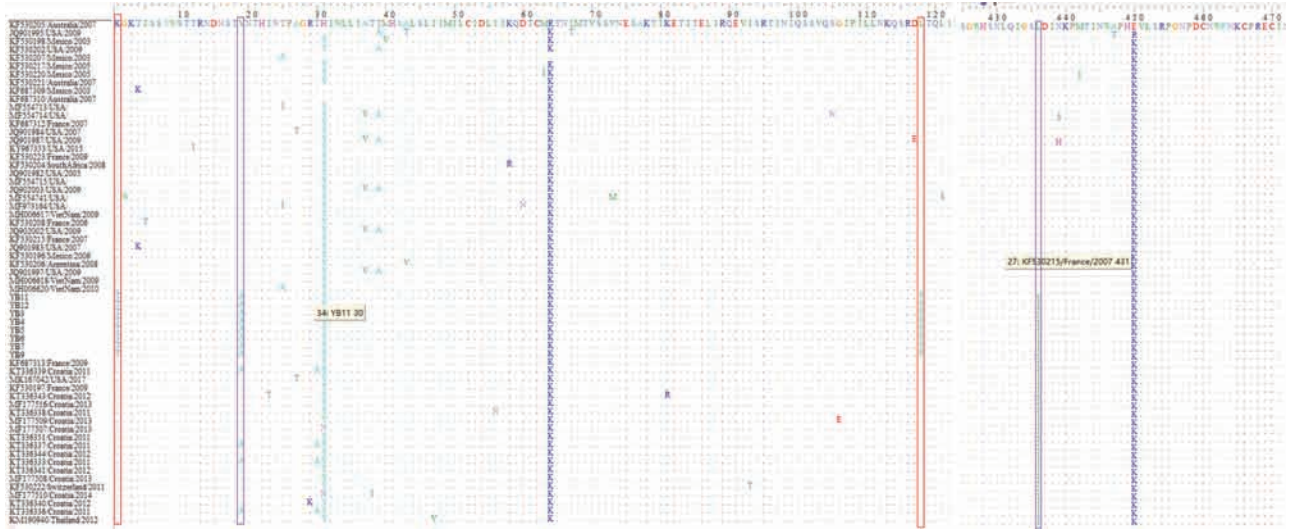
Supplementary Fig. S2 Phylogenetic analysis of HPIV1 based on F gene constructed using a 1755 nucleotide sequence corresponding to nucleotide 5088–6842 in the Washington_1964 strain from the USA (GenBank accession no: NC_003461). A tree with 1,000 bootstrap replicates was reconstructed using maximum likelihood method with the MEGA 7.0 based on nucleotide sequences. The location and year of collection are shown. The strains detected in this study are in black solid circle.



Supplementary Fig. S3 Two specific substitutions (N333S and I509M), in the amino acids of the F protein, which was different from other strains in the clade 2.



Supplementary Fig. S4 Phylogenetic analysis of HPIV1 based on HN gene constructed using a 7245 nucleotide sequence corresponding to nucleotide 7245–8477 in the Washington_1964 strain from the USA (GenBank accession no: NC_003461). A tree with 1,000 bootstrap replicates was reconstructed using maximum likelihood method with the MEGA 7.0 based on nucleotide sequences. The location and year of collection are shown. The strains detected in this study are in black solid circle.



Supplementary Fig. S5 Specific substitutions in the amino acids of the HN protein, which was different from other strains in the clade 2. Two specific substitutions (V19A and L436I) in the amino acids of clade 2.3. Two specific substitutions (K1T and L108F) were only detected in our strains.