

Figure S1. Phylogenetic analysis of ECHO30 lineage h based on entire *VP1* gene nucleotide sequence. All ECHO30 viral sequences were downloaded from GenBank (as on 15 April 2014), the strains belong to lineage E30_h were shown. The ECHO30 viral strains isolated from clinical samples in this study were marked with solid dots. The strains isolated from Luoding and Guangzhou sewage were marked with solid triangle and open triangle respectively. Bar, nucleotide distance as substitutions per site. Only bootstrap values of over 60% are shown.

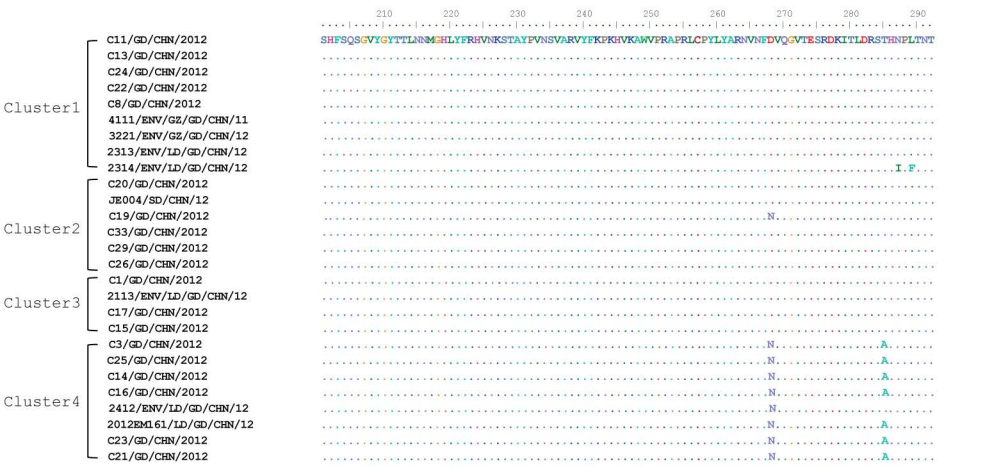


Figure S2. Comparison of the deduced amino acid sequences of E30 strains in the cluster 1-4.