

Fig. S1. Phylogenetic analysis of Israeli CVA6 isolates. CVA6 partial VP1 sequences (214 nt) from 5 viruses isolated from 5 Israeli toddlers (red) and 5 Israeli adults (blue) are mapped into a phylogenetic tree and aligned with 39 representative sequences. Strains isolated from 4 toddlers were similar to those isolated from 2 Israeli adults and distinct from the sequence of a fifth toddler. Phylogenetic comparable sequences were downloaded from the DDBJ/EMBL/Genbank and an unrooted neighbor-joining tree with Kimura 2-parmeter correction was constructed after 1000 bootstrap replications using ClustalX v1.83. The tree was visualized using the NJplot program. Numbers correspond to the numbers of bootstrap replicates for the branch. Scale bars indicate nucleotide substitutions per site. The CDC prototype AY421764 was set as outgroup for comparison. Each isolate is identified by an accession number, a 3-letter country code, and 2 digits to indicate the year of isolation.