**Supplementary Fig. 1.** Phylogenetic analysis of partial HEV ORF2 sequences (98 nt) from 5 study samples and 14 reference sequences from GenBank. Nucleotide sequences were aligned by Clustal W method (MegAlign™, DNASTAR®) and analysed in Mega (version 4.1) using the neighbour-joining method. Bootstrap values (from 1000 replicates) over 70% are indicated accordingly. Distance measure of 0.02 indicates nucleotide substitutions per site.