Figure 4 (on line only). Phylogenetic analysis of HRV isolates. A 394 bp fragment of the 5’ untranslated region of the HRV genome was amplified for sequence analysis. The phylogenetic tree was constructed using sequence data from New Haven isolates in conjunction with reference sequences obtained from GenBank (reference strains denoted by an asterisk, *) Reference strains are identified by GenBank accession number and strain name. New Haven isolates are designated by the prefix NH. Number of nucleotide substitutions per 100 basepairs is designated along the x-axis. All New Haven HRV isolates whose sequence differed by less than 2% are represented by one reference isolate. Black arrows denote three prototype isolates, NH3285, NH3328 and NH357 (representing five New Haven isolates), which were distinct from reference strains included in this figure. However, a region of these amplicons had up to 97% identity to shorter sequences available in GenBank and, therefore, these strains are likely related to other HRV genotypes which have not yet been fully characterized (GenBank accession numbers EU126764, EU126783, EU126781). HRV clade A strains are contained within the red box; HRV clade B strains are contained within the blue box and; HRV clade C strains are contained within the yellow box.