



Supplementary Figure 8. Enterovirus phylogeny

Enterovirus genomes assembled from subjects in this study (red) were aligned with representative reference sequences for each subtype within the enterovirus B species (blue). This allowed classification of viral subtypes as Coxsackie B4 for M007 and echovirus 30 for M072, M108, and M126. Interestingly, viruses from M108 and M126, who were admitted approximately one month apart from one another and had no known epidemiological links, differed by only 0.6% (42 nucleotides), suggesting a common local circulating strain. Abbreviations: EV = enterovirus; Echo = echovirus; Cox = coxsackievirus.