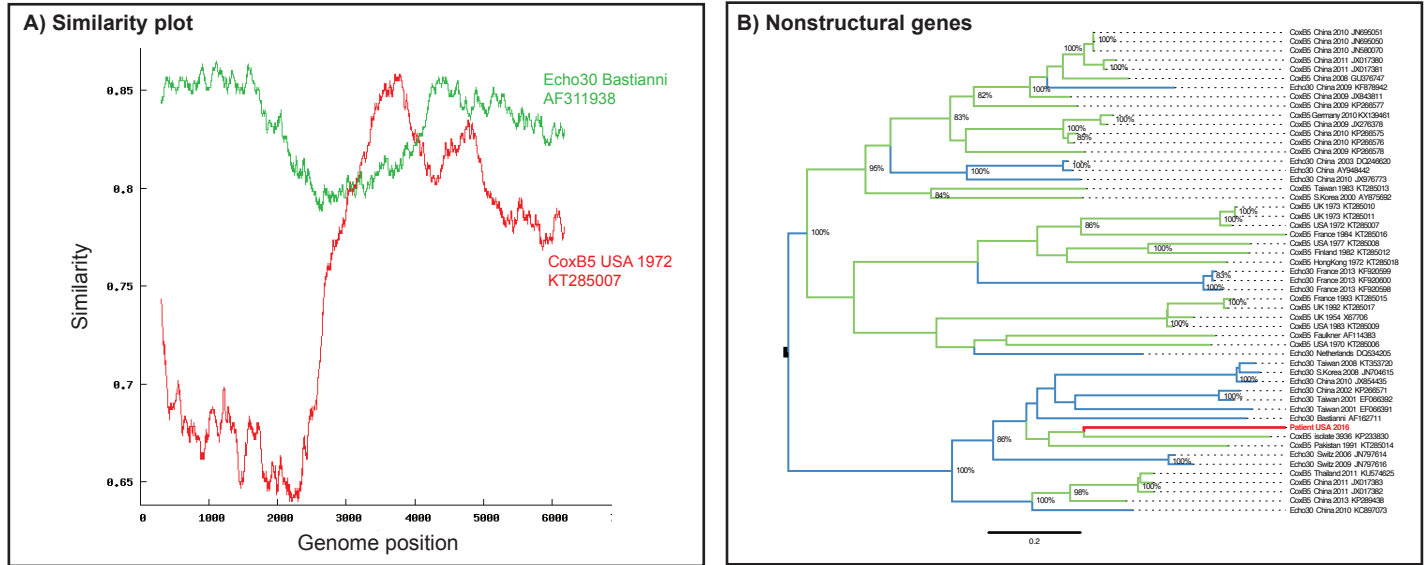


Supplementary Figure 1



Supplementary Figure 1. A) Similarity plot comparing this genome against reference sequences of echovirus 30 (green) and coxsackievirus B5 (red). In the 5-prime half of the genome (approximately 3kb), the sequence from this patient more closely resembles echovirus 30, whereas in the 3-prime half of the genome (approximately 4kb), it is fairly similar to both echovirus 30 and coxsackievirus B5. B) Phylogenetic tree of nonstructural genes, comprised of 4kb at the 3-prime end of the genome. The sequence identified in this study ("Patient USA 2016", labeled in red) clusters with sequences belonging to the coxsackie B5 subgroup (labeled in light green) with low bootstrap support. Throughout the tree, coxsackie B5 genomes interdigitate with echovirus 30 genomes (labeled in light blue), indicating that in this region of the genome there is overall similarity between these groups. Because these groups are phylogenetically distinct in the VP1 gene (Figure 1B), there has likely been a history of recombination between these classes in this region. Branches are named with the enterovirus subtype and location and date of sequence acquisition (clinical samples) or name of reference strain (viral isolates), as well as Genbank accession number. Trees were constructed with 1,000 bootstrap replicates, and nodes with at least 80% support are labeled with percent bootstrap support.