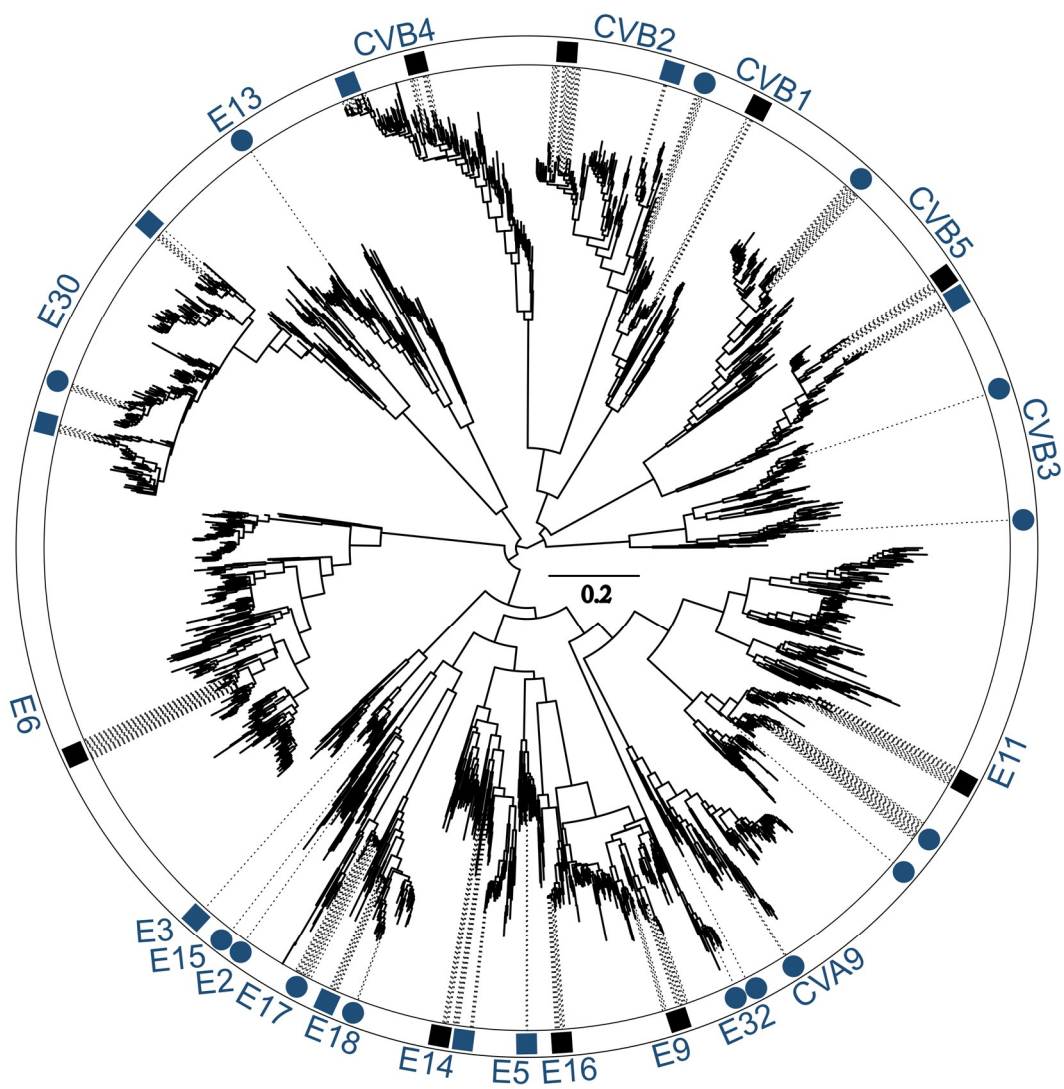
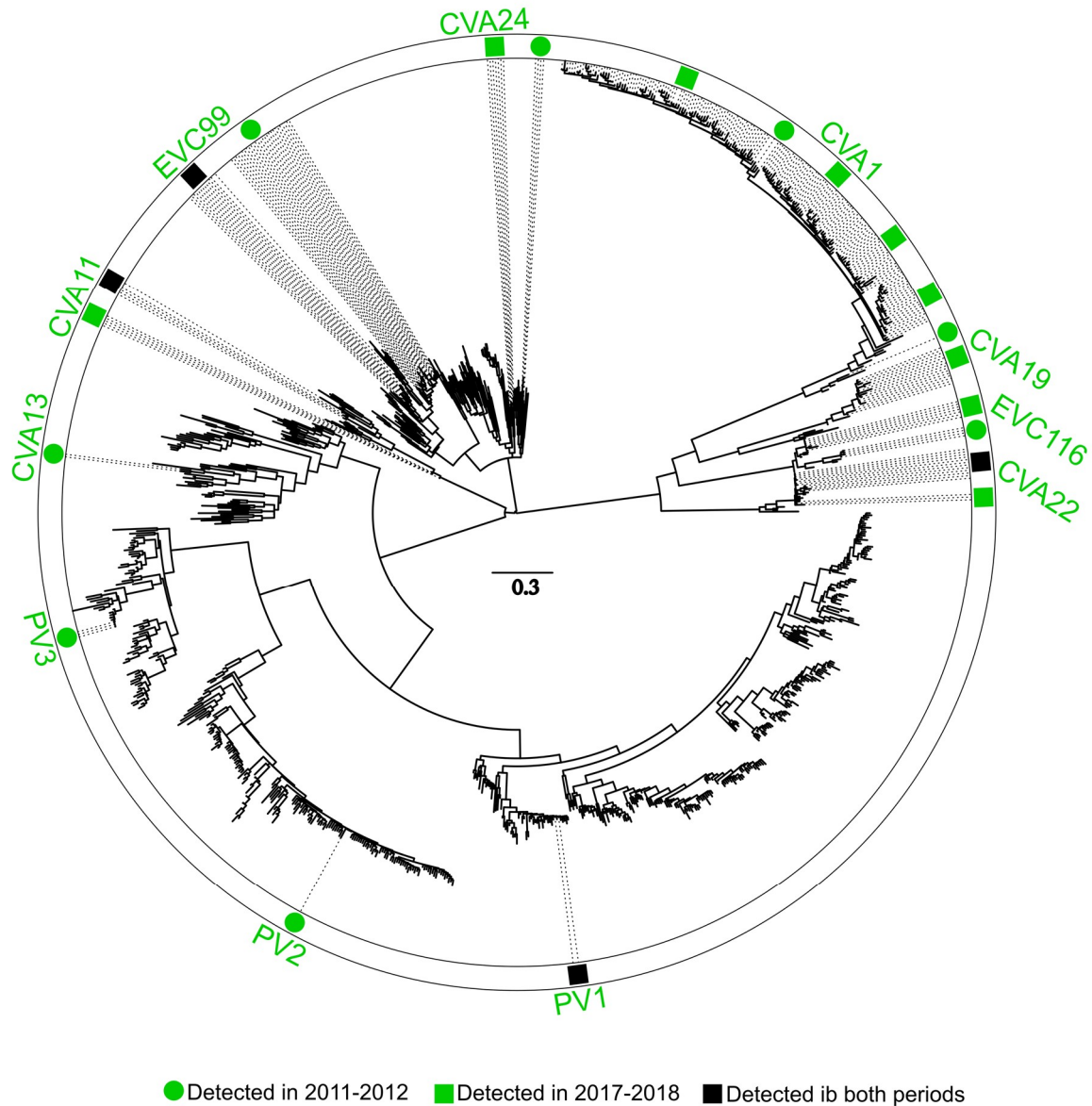


(A)



● Detected in 2011-2012 ■ Detected in 2017-2018 ■ Detected in both periods

(B)



(C)

**Figure S1.** Maximum likelihood phylogenetic trees of Human Enterovirus species A (A), B (B), and C (C). Each tree was constructed with centroid sequences detected in wastewater samples from Córdoba City (Argentina) during this study and representative sequences of different Human Enteroviruses types reported elsewhere. Dotted lines projecting outward from branches represent centroid sequences. Colored circles and squares indicate the period(s) in which different phylogenetic clusters of this study were detected. aLRT-SH values at type-definition node levels were  $>0.7$  for all types. The bar at the center of each phylogenetic tree denotes genetic distance. CVA: coxsackievirus type A; CVB: coxsackievirus type B; E: echovirus; EVA: enterovirus type A; EVB: enterovirus type B; EVC: enterovirus type C; PV: poliovirus.