


Phylogenetic analysis of complete VP1 sequences from non-human primate (NHP) and representative human enteroviruses. For NHP EVs, the following nomenclature is used: Species-Type-Strain name-Accession number-Country-Year-Host species-Condition of life of the host. For prototype EVs, the following nomenclature is used: Species-Type-Strain name-Accession Number. Abbreviations: CAM, Cameroon; CHN, China; USA, United States of America; GAB, Gabon; NGR, Nigeria; Msph, *Mandrillus sphinx*; Mleu, *Mandrillus leucophaeus*; Ctor, *Cercocebus torquatus*; Caet, *Chlorocebus aethiops*; Ptro, *Pan troglodytes*; Ggor, *Gorilla gorilla*; Mmul, *Macaca mulatta*; W, wild; C, captive. The arrows indicate new genomes sequenced in our study (Figure 1). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site.