**A Proposal for the Classification and Nomenclature of Hand, Foot and Mouth Disease-Related Enteroviruses**

**Supplementary materials**



**Supplementary Figure S1. Bootscan analysis of EVA71 subtypes D (A) and F (B), and CVA10 subtype B (C).** The used reference strains of EVA71 were genotypes A (U22521), B (JF738001), C (JQ742002), D (MG672478) and G (HQ647172). The used reference strains of CVA10 were genotypes A (AY421767), C (HQ728262), D (MF678312), G (MH118054) and H (MH118051). The analyses were performed using a sliding 600-bp window with 20-bp steps.



**Supplementary Figure S2.** Separate phylogenetic analyses of EVA71 RF01\_CG. According to the plausible recombination breakpoints identified in bootscan analyses (Figure 2A), the EVA71 genomic sequences were divided into seven segments (I-VII). Each segment was then subjected to separate ML tree analysis to confirm its subtype origin. The RF01\_CG sequence is highlighted by a red circle.



**Supplementary Figure S3.** Separate phylogenetic analyses of EVA71 RF02\_CG. According to the plausible recombination breakpoints identified in bootscan analyses (Figure 2B), the EVA71 genomic sequences were divided into seven segments (I-VI). Each segment was then subjected to separate ML tree analysis to confirm its subtype origin. The RF02\_CG sequence is highlighted by a red circle.

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