

## Supplementary figure 1

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2 **FIG S1** Phylogenetic tree based on the alignment of the complete genome sequence  
3 of worldwide Coxsackievirus A6 strains (7.4 kb). The maximum likelihood (ML)  
4 method was used to construct the phylogenetic tree with 1000 bootstrap replicates.  
5 Only bootstrap values >70% were shown.

6 ■ Indicates the WF057R strain used to establish a neonatal mouse model of CVA6  
7 infection.

8 ▲ Indicates four clinical isolates of CVA6 from different regions of Shandong:  
9 DY003R, DY005R, LW03R and WH15066.

10 ● Indicates the strains associated with the Finnish HFMD outbreaks in 2008.

11 CHN: China; JPN: Japan; FIN: Finland; UK: United Kingdom; TW: Taiwan; VNM:  
12 Vietnam.

