

Electronic Supplementary Material

Application of Human Adenovirus Genotyping by Phylogenetic Analysis in an Outbreak to Identify Nosocomial Infection

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Fig. S1: Phylogenetic trees of the *penton base* (left), *hexon* (middle), and *fiber* (right) genes constructed using MEGA X software to identify the genotypes of HAdV-positive specimens. Sequences from the study were named as No. of specimens–date of admission–date of discharging–No. of ward and bed–typing of HAdV. Sequences from GenBank were labelled with their GenBank number- typing of HAdV.

