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.