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Original Article

A Novel Complex Recombinant Form of Type 48-Related Human Adenovirus Species D Isolated in Japan

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Volume 67, no. 4, p. 282–287, 2014. Page 282, footnote *Corresponding author: Mailing address: “Department of Ophthalmology, Hokkaido University Graduate School of Medicine, Sapporo 060-8638, Japan” should read “Graduate School of Information Science and Technology, Hokkaido University, Sapporo 060-0814, Japan.”

Volume 67, no. 4, p. 282–287, 2014. Page 284, Figure 1 should appear as shown below.

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### Figure 1

The recombination signals that were supported by >3 different algorithms in the RDP analysis. The putative recombined regions identified by the RDP analysis of the MGA (see the Materials and Methods) are shown in the table and schematically represented beneath the table. Regions 1 to 8, corresponding to the 8 bars in the schematic representation, are the putative recombined regions that were supported by >3 algorithms in the RDP analysis. Region 0 is a set of 4 divided regions that were not included in any of the putative recombined regions. The breakpoint positions are shown in the base position in the HAdV-Chiba_E086/2012 genome. The p-values calculated by 7 different algorithms are shown for each region. NS means not significant (p ≥ 0.001). The region numbers are shown with “#” in the schematic representation followed by the counterpart type in parentheses. The coding exon regions and protein product names are shown under the scale bar that represents the physical position in base pair in the HAdV-Chiba_E086/2012 genome. The gray lines represent the intron regions between coding exons. The positions and the transcription orientations of the genes in the genome are shown in blue.

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