

## Complete genomic sequencing of Canine Distemper virus with Nanopore technology during an epizootic event

Zsófia Lanszki<sup>1,2</sup>, Gábor E. Tóth<sup>1,2</sup>, Éva Schütz<sup>3</sup>, Safia Zeghib<sup>1,2</sup>, Miklós Rusvai<sup>4</sup>, Ferenc Jakab<sup>1,2</sup>, Gábor Kemenesi<sup>1,2</sup>

<sup>1</sup> National Laboratory of Virology, Szentágotthai Research Centre, University of Pécs,  
7624 Pécs, Hungary

<sup>2</sup> Institute of Biology, Faculty of Sciences, University of Pécs, 7624 Pécs, Hungary

<sup>3</sup> Exo-Pet Állatgyógyászati Centrum, 1078 Budapest, Hungary

<sup>4</sup> Vet-Diagnostics Kft., 5000 Szolnok, Hungary

\* Correspondence: [kemenesi.gabor@gmail.com](mailto:kemenesi.gabor@gmail.com)

Supplementary Information: Figure 1. Visualization of sequencing coverage via the amplicon-based sequencing method for each sample. Horizontal scale represents the genomic position, whilst the vertical scale displays the coverage values of the sequencing reaction.



