ELM: Enhanced lowest common ancestor based method for detecting a pathogenic virus from a large sequence dataset

Keisuke Ueno[1], Akihiro Ishii[2], Kimihito Ito[1]*

[1]Division of Bioinformatics, Research Center for Zoonosis Control, Hokkaido University, Sapporo, Hokkaido, 001-0020, Japan
[2]Hokudai Center for Zoonosis Control in Zambia, Research Center for Zoonosis Control, Hokkaido University, Sapporo, Hokkaido, 001-0020, Japan

*Corresponding author

Supplementary data

This file contains Supplementary Figures S1 and S2 with legends.

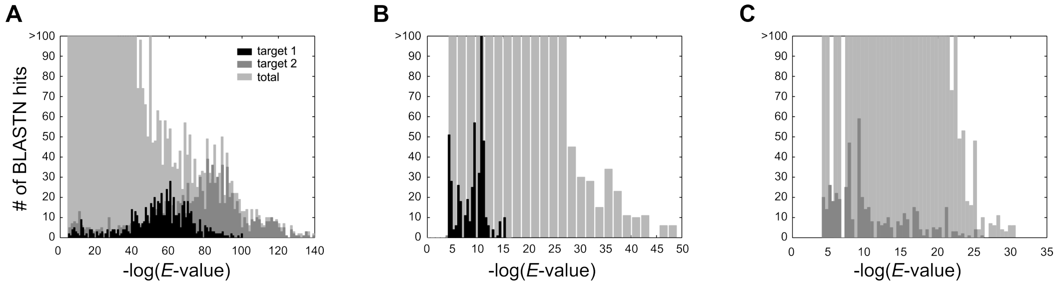

Figure S1. Distribution of *E*-values in BLASTN viruses for (A) rodent, (B) reptile and (C) simian samples.

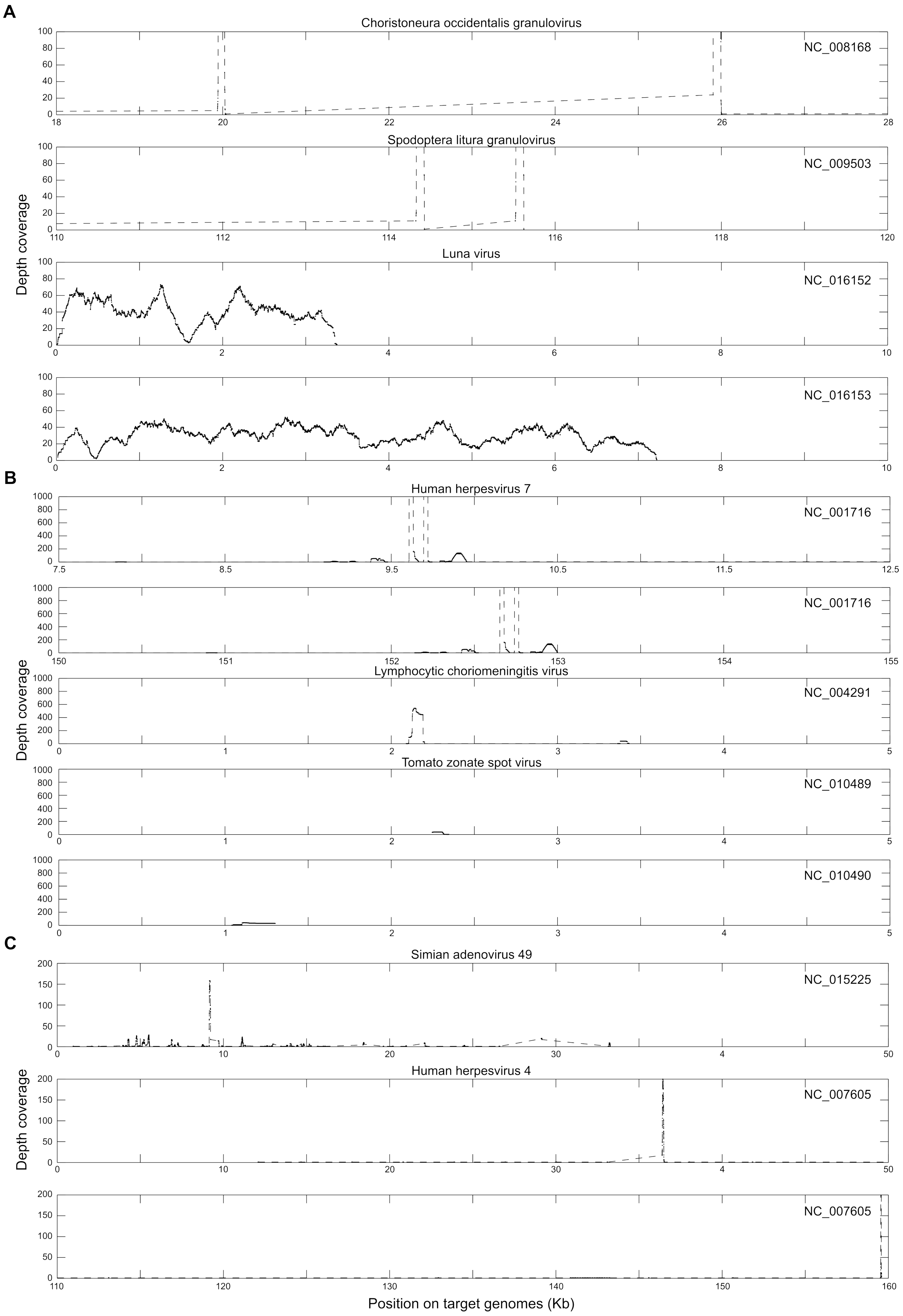

Figure S2. Read coverage on the position of target genomes for (A) rodent, (B) reptile and (C) simian samples.