



**Figure S1. Coverage and read depth of Seoul virus (SEOV) tripartite genomes from SEOV 80-39 RNA by amplicon-based nanopore sequencing.** Whole-genome sequencing of SEOV was performed by amplicon-based MinION sequencing within 6 h. The genome coverage and read depth of SEOV are shown. The raw data was analyzed for SEOV 80-39 genomes generated by Sanger sequencing using a reference mapping tool in CLC Genomics Workbench v.22.0.2. (A) 10<sup>4</sup> to 10<sup>5</sup> viral copies/μL of SEOV 80-39 RNA, (B) 10<sup>3</sup> to 10<sup>4</sup> viral copies/μL of SEOV 80-39 RNA, (C) 10<sup>2</sup> to 10<sup>3</sup> viral copies/μL of SEOV 80-39 RNA, (D) 10 to 10<sup>2</sup> viral copies/μL of SEOV 80-39 RNA, (E) 1 to 10 viral copies/μL of SEOV 80-39 RNA, (F) 0 to 1 viral copies/μL of SEOV 80-39 RNA.