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**Supplementary Data**

**Diversity and independent evolutionary profiling of rodent-borne viruses in Hainan, a tropical island of China**

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**Supplementary Table S1.xlsx** The locations and species of rodent sampled on Hainan Island.

**Supplementary Table S2.xlsx** Primers used in this study.

**Supplementary Table S3.xlsx** Overview of virus-associated contigs.

**Supplementary Table S4.xlsx** Overview of sequence contigs from mammal related viral families.

**Supplementary Table S5.xlsx** Virus origin and accession number identified in this study.

**Supplementary Table S6.xlsx** Amino acid sequence identity in the L regions of novel rodent arenaviruses and known arenaviruses (AreV).

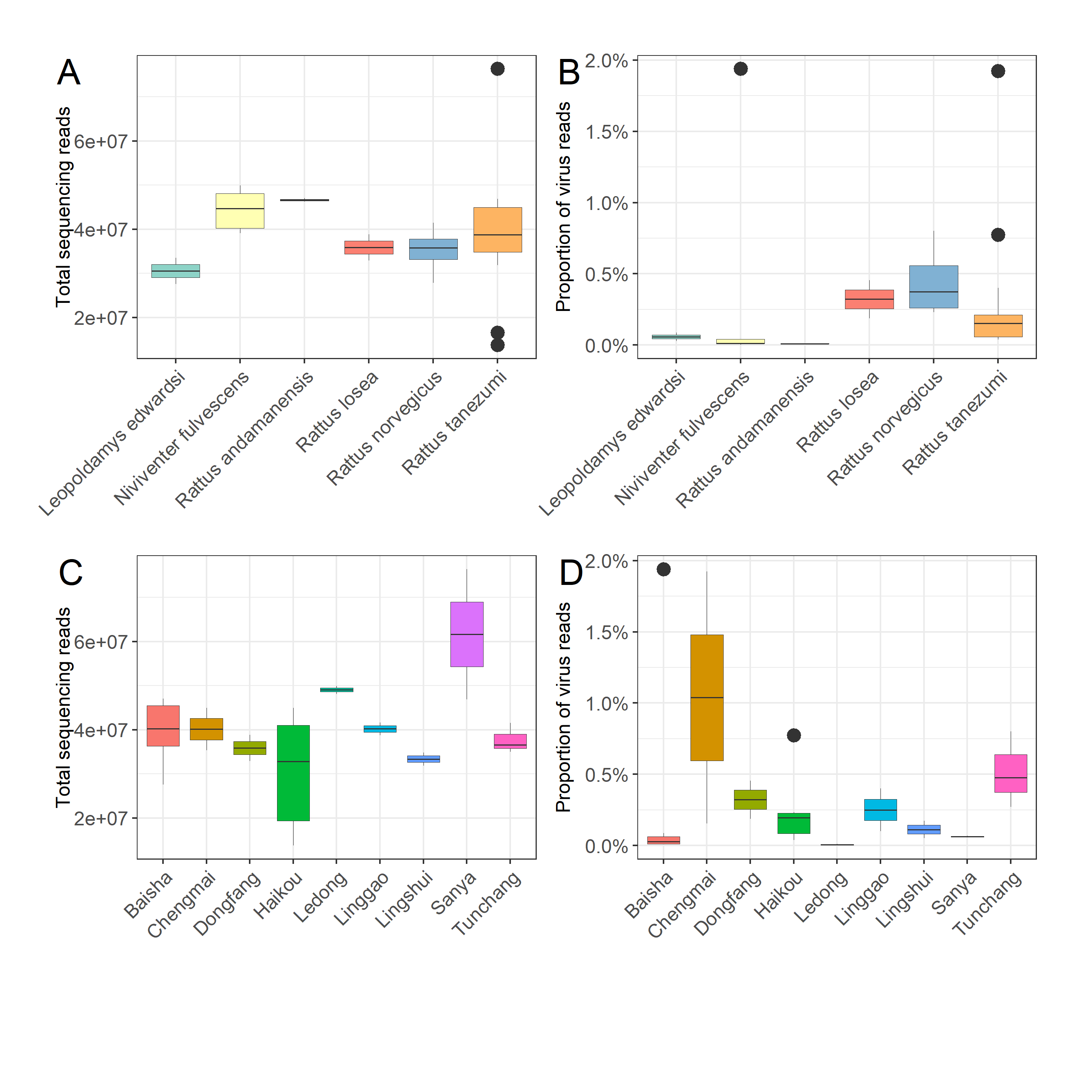
**Supplementary Table S7.xlsx** Amino acid sequence identity of novel rodent and well-known coronaviruses (CoVs) in the RdRp.

**Supplementary Table S8.xlsx** Amino acid sequence identity of novel rodent pestviruses and known pestviruses (PestV).

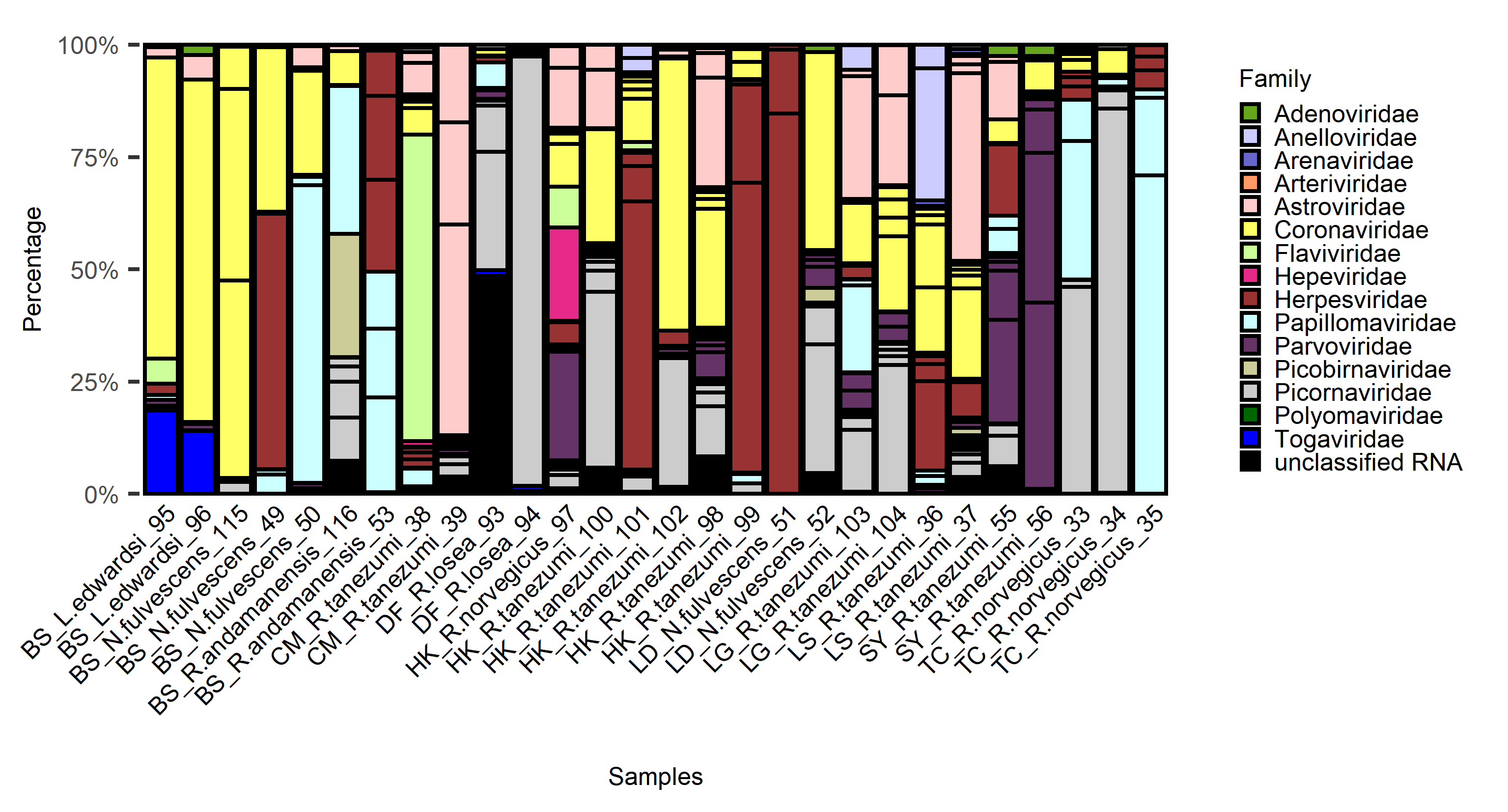
**Supplementary Table S9.xlsx** Amino acid sequence identity of novel rodent astroviruses (AstroVs) in the RdRp region.

**Supplementary Table S10.xlsx** NS1 region amino acid sequence identity of novel rodent parvoviruses and known parvoviruses (ParVs).

**Supplementary Table S11.xlsx** Amino acid sequence identity in the L regions of novel rodent papillomaviruses and known papillomaviruses (PVs).

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**Supplementary** **Fig. S1** **A, B** Comparison of the number of total reads and proportions of viral reads from the six rodent species. **C, D** Comparison of the numbers of total reads and proportions of viral reads from the fifteen sampling locations.

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**Supplementary** **Fig. S2.** The proportions of the number of reads assigned to each viral family in each of the 28 pools are shown in the bar graph.