Supplementary Material

Comparative analysis of newly identified rodent arteriviruses and porcine reproductive and respiratory syndrome virus to characterize their evolutionary relationships

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**Supplementary Figure 1.** Gene-based phylogenetic analyses of arterivirus. Trees based on RNA-dependent RNA Pol (RdRp) (**A**), helicase (Hel) (**B**), 3CLpro (**C**), and nucleocapsid (N) (**D**) were constructed by using the maximum-likelihood (ML) method and bootstrap values calculated from 1,000 trees.

**Supplementary Table 1.** Comparison of nucleotide and amino acid identities and other genomic features of rodent arterivirus, PRRSV-1, PRRSV-2 and other representative arteriviruses.

**Supplementary Table 2.** Putative transcription regulatory sequences of rodent arterivirus genomes.

**Supplementary Table 3.** Basic arterivirus codon information.