I was particularly interested in the most prevalent viral subjects assigned to each contig, so I extracted the top 10. Porcine reproductive and respiratory syndrome virus (PRRSV) and PRRSV-2 were identified 987 times within the family Arteriviridae, representing approximately 91.22% of all Arteriviridae-aligned contigs, with 298 classified as novel. Notably, these two viruses and Otarine picobirnavirus were the only ones where the total number of contigs differed from those with a protein sequence identity below 90%. Among the hosts, African green monkeys (Chlorocebus sabaeus), often used in biomedical research, appeared in 981 contigs, of which 293 might be novel. Wild boars (Sus scrofa) seemed to host 4 contigs (3 of which were novel), while 2 novel contigs were identified in Bushy-tailed woodrats (Neotoma cinerea). Another rodent arterivirus was found in Old World monkeys of the genus Chlorocebus (46, Chlorocebus sabaeus) and Eastern gray squirrels (2, Sciurus carolinensis).

Of the top 10 viral subjects, half were found in the family Picobirnaviridae, comprising 279 viral contigs, with 277 having a protein sequence identity below 90%. Otarine picobirnavirus, typically associated with sea lions, was identified 90 times. In this study, the primary host appears to be domesticated pigs (Sus scrofa domesticus, 85 contigs), a finding also noted by Chauhan et al. Additionally, 4 contigs were found in donkeys (Equus asinus) and 1 in cattle (Bos taurus), suggesting that all instances of this aquatic mammal virus occurred in farm animals. Chicken picobirnavirus was detected in domesticated pigs (32), donkeys (2), and cattle (1). The dog variant was observed in pigs (44) and donkeys (2), while the variant associated with green monkeys seems to have been found in 38 pigs and 2 donkeys. Lastly, the variant primarily associated with horses (Equus caballus) was detected in pigs (60), rats (Rattus, 2), and cattle (3). Remarkably, it was also found in two Rhesus macaques (Macaca mulatta) and one Sunda pangolin (Manis javanica).

Mamastrovirus 18, typically associated with bats, was identified in three bat species (Miniopterus africanus, Rhinolophus, and Myotis tricolor). Additionally, novel contigs aligning to a hepacivirus were found in Middle East blind mole-rats (46, Nannospalax ehrenbergi), Eastern deer mice (2, Peromyscus maniculatus), and one each in muskrats (Ondatra zibethicus) and Desmarest's spiny pocket mice (Heteromys desmarestianus).

> https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3372223/