



**Figure S11**

**Phylogenetic relationships of polyomaviruses based on conserved amino acid blocks of the LTA<sub>g</sub> sequences with highlighted host orders.** Polyomavirus naming follow the recommendations of the ICTV Polyomaviridae study group using Latin binomials of their hosts and a serial number; accession numbers and vernacular names of the host are also given. This maximum clade credibility tree was generated using Bayesian Markov chain Monte Carlo analyses; a maximum likelihood analysis recovered a very similar topology (not shown). Grey branches are relatively weakly supported with posterior probability values < 0.95. Names of viruses are given in black or white font. The names of the novel polyomaviruses are given in bold and light brown font.