



Figure S11**Phylogenetic relationships of polyomaviruses based on conserved amino acid****blocks of the LTA_g 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.