



Supplementary Fig. 1 Phylogenetic tree based on the C-terminal end of the *p72* protein comparing the Kenyan and Eastern Uganda ASFV isolates collected in this study (●) between 2011 and 2013 with other African swine fever virus isolates belonging to ASFV genotypes IX and X. A total of 91 distinct taxa were used to infer a Minimum Evolution tree and the percentage of replicate trees in which the associated taxa clustered together in a bootstrap analysis (1000 replicates) are shown adjacent to the branches. The tree is drawn to scale; with branch lengths represented using the same units as the evolutionary distances used to infer the phylogenetic tree.