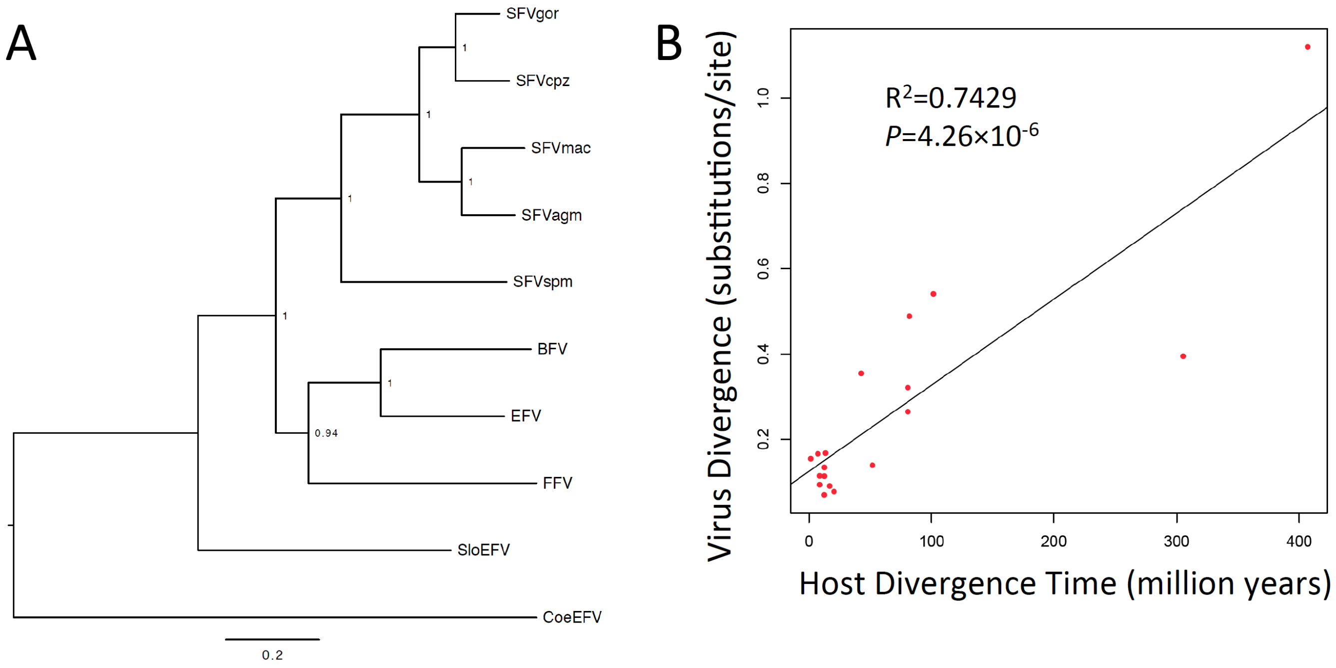

Figure S6. A) Midpoint rooted phylogenetic tree of foamy viruses. The phylogeny is the 50% majority-rule consensus tree inferred from conserved region of foamy virus Env protein alignment with MrBayes 3.1.2. Posterior probabilities are shown at the nodes. Branch lengths are in expected amino acid changes per site. B) A plot of the correlation between foamy virus divergence and their vertebrate hosts' divergence times. The virus branch lengths are derived from the virus tree in A.