

Fig. S2. Unrooted Maximum Likelihood trees (General Time Reversible model, uniform rates) of sequenced viral clones. Percent bootstrap support is indicated at relevant nodes (500 replicates). Coloured tip labels are cloned sequences from individual hosts, with each colour representing a different species. Clone number (c1-5) and site information are also given. (a) SBPV: (b) BQCV