S2 Figure

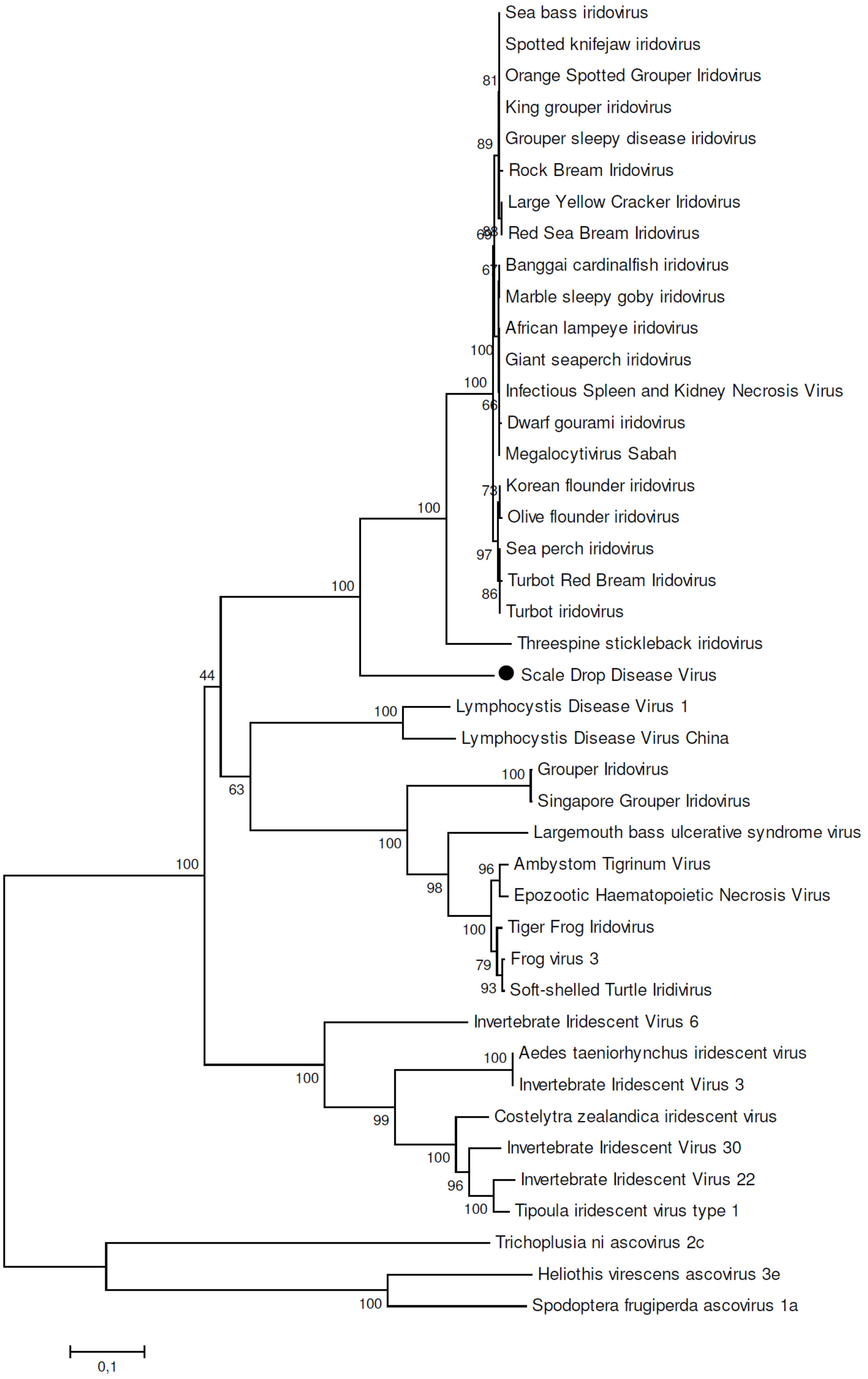

Figure S2: The deduced amino acid sequences of the major capsid protein encoding gene was aligned with the corresponding gene of all iridoviruses of which this gene has been sequenced. The neighbor-joining method with pairwise deletion within the MEGA-5 package was used, bootstrap values (for 500 replications) are provided at the root of the clusters and the scale bar is a measure of the proportion of divergence. A • indicates SDDV.