



Supporting Figure 1 - Phylogenetic analysis of amino acid sequences derived from partial *L* gene fragments

A 439 bp segment of *L* gene of IFBPV01/2010, IFBPV32/2011, IFBPV39/2011 and IFBPV46/2011 was obtained by using the degenerate primer set for the *Respirovirus-Morbillivirus-Henipavirus* subgroup. Phylogenetic tree was constructed by using the deduced amino acid sequence (146 amino acids) and homologous sequences from known paramyxoviruses. The bootstrap values obtained after 1000 replicates are indicated at each branch. Scale bars indicate amino acid substitutions per site.