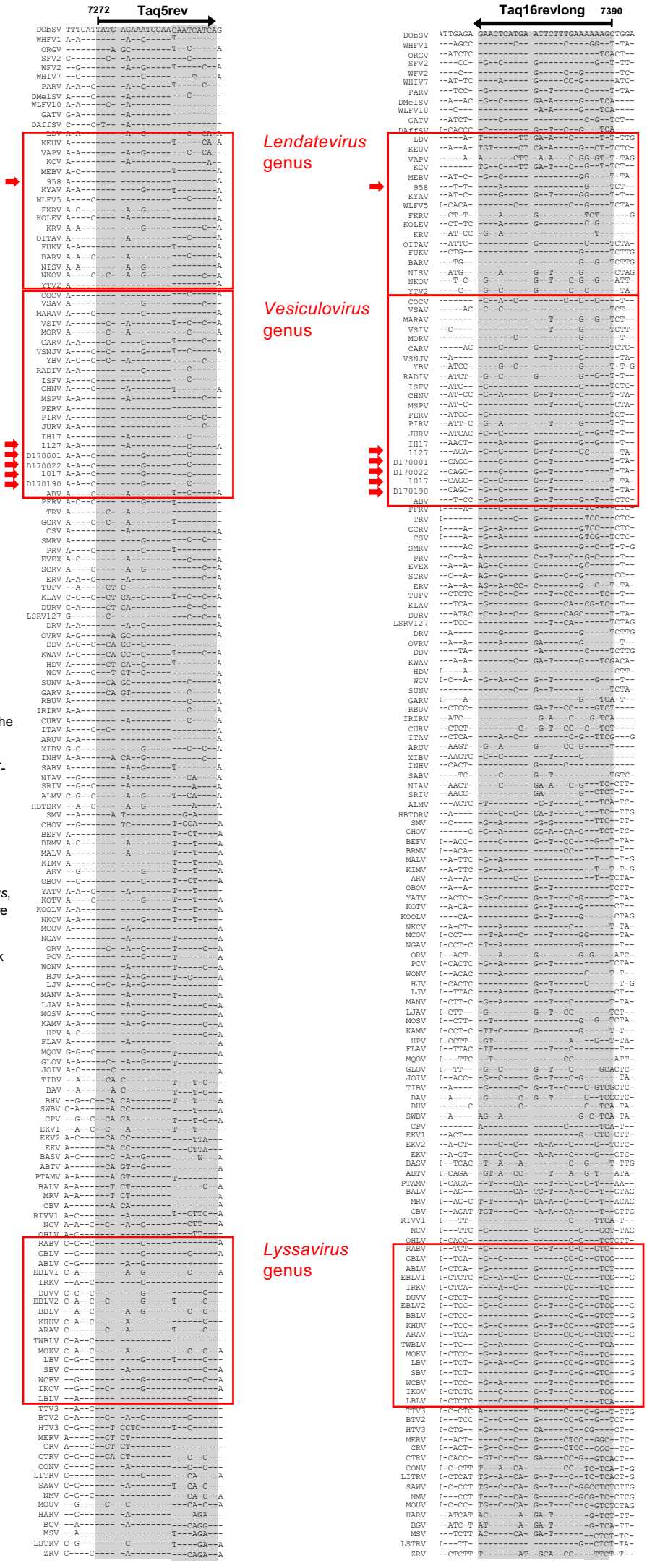
Figure S2



Legend:
Alignement of a dataset of 161 nucleotide sequences of rhabdoviruses, corresponding to the regions (in grey) targeted by the primers Taq5long and Taq16revlong of the pan-lyssa RT-qPCR [50]. This dataset of sequences is the same used for Figure 3, and the list of the rhabdoviruses is detailed in Table S5. The 6 Chinese bat rhabdoviruses are indicated by a red arrow, and the viruses belonging to the genera *Lyssavirus*, *Vesiculovirus* and *Ledantevirus* are grouped in red square. Positions are indicated according to the reference sequence PV (GenBank accession number M13215).