

Supporting Information

Alayyoubi et al. 10.1073/pnas.1503941112

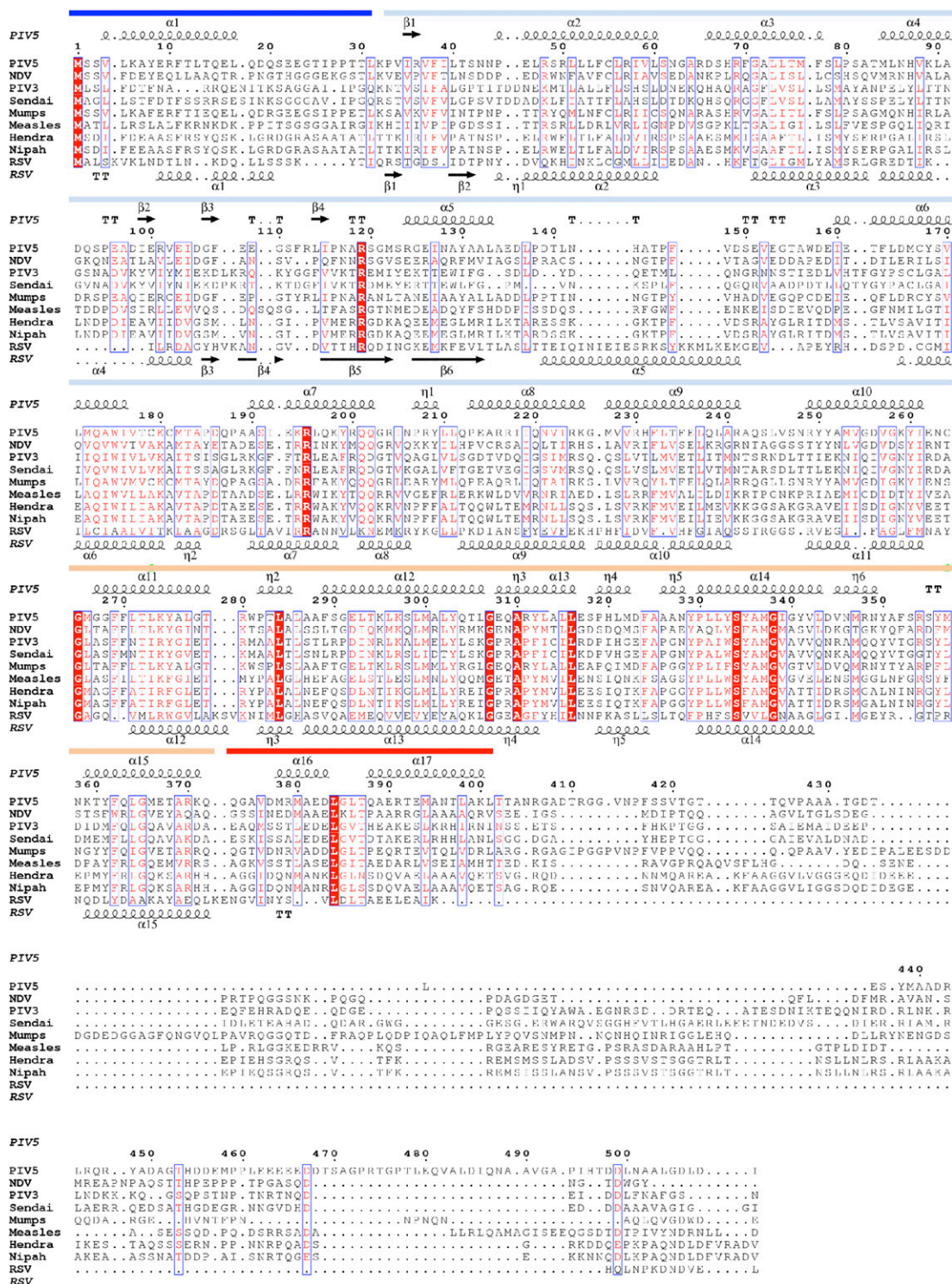


Fig. S1. Amino acid sequence alignment of PIV5-N with sequences of N from NDV, PIV3 (parainfluenza virus 3), Sendai virus, mumps virus, measles virus, Hendra/Nipah viruses (*Paramyxovirinae* subfamily), and RSV-N (*Pneumovirinae* subfamily). Secondary structures for PIV5-N (Upper) and RSV-N (Lower) are mapped by Esprict. Domains are colored according to Fig. 2. PIV5-N sequence numbering is shown on top. The structure of PIV5-N is missing residues 401–509, due to self-proteolysis of the PIV5-N during protein preparation. RSV-N is almost 100 residues shorter than the N-sequences from the *Paramyxovirinae* subfamily.