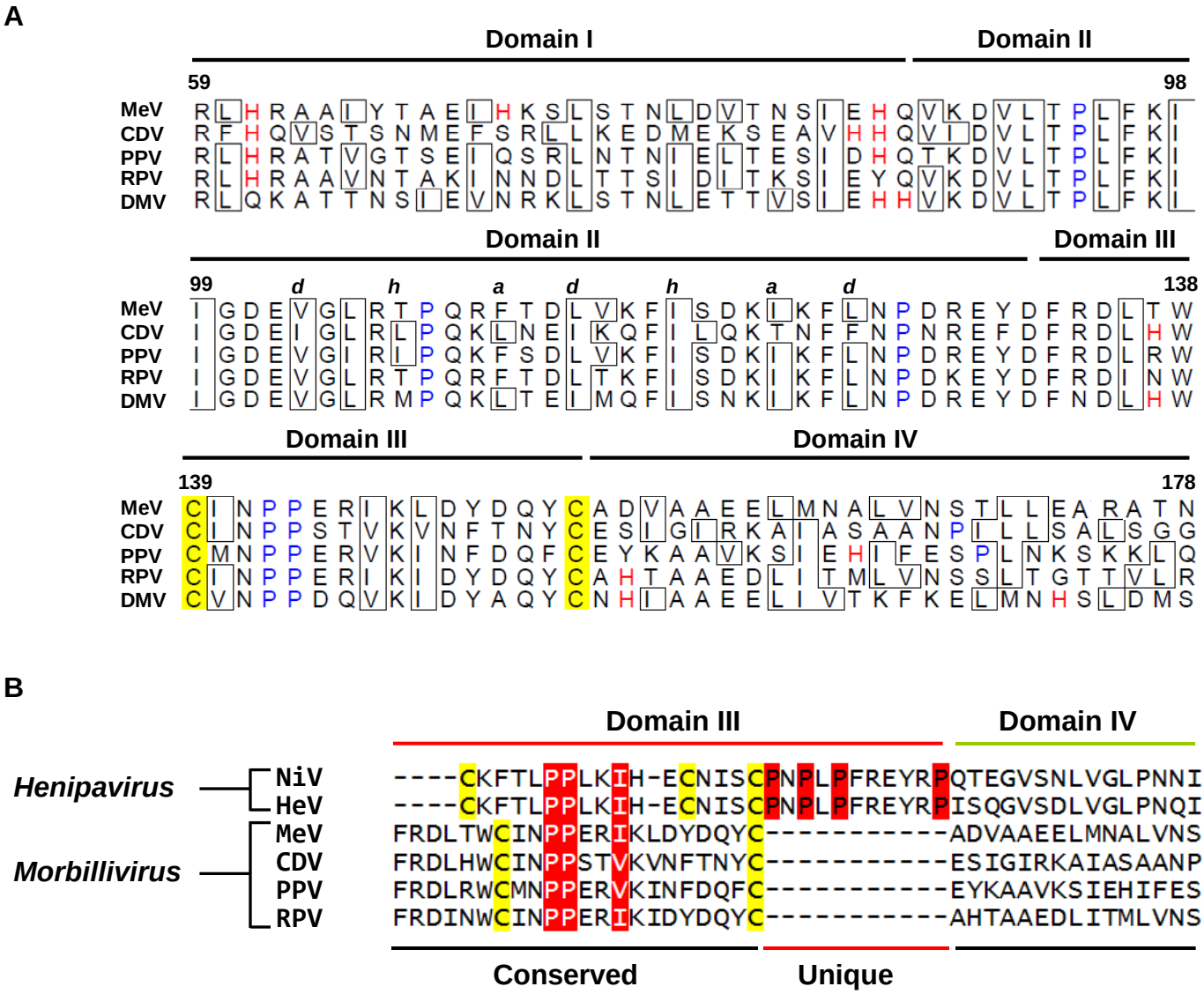

Figure S1. Location of predicted subdomains in the stalk regions of *Morbillivirus* H attachment proteins and the unique *Henipavirus* G proline-rich stalk microdomain. (A) The amino acid residues 59-178 from the H protein reference sequences of Measles virus (MeV) (NC_001498.1), Canine distemper virus (CDV) (NC_001921.1), Peste-des-petits-ruminants virus (PPV) (NC_006383.2), Rinderpest virus (RPV) (NC_006296.2) and Dolphin morbillivirus (DMV) (NC_005283.1) were aligned to hydrophobic residues (boxed) by the online Jpred server (http://www.compbio.dundee.ac.uk/~www-jpred/; University of Dundee, UK). The subdomains within the *morbillivirus* H stalks were partitioned in a similar fashion as NiV-G and HeV-G were in Figure 9A, where domains I and IV contain increase variability between virus species, domain II contains the 11-mer hydrophobic residue repeat pattern ('a', 'd', and 'h') of the NDV and PIV5 HN 4HB structures and domain III contains conserved cysteine residues (highlighted in yellow) that mediate intersubunit H disulfide bonds. (B) The stalk residues 146-188 (domain III, IV) of *Henipavirus* G proteins were aligned to *Morbillivirus* H proteins through a conserved PP-XX-I/V motif highlighted in red with white lettering. The unique region between the last cysteine in G and H proteins and the variable domain in IV is shown in red underline.