



Figure S1. Mutation of the N-terminal aa does not affect the predicted secondary structure of p6. Structure alignment of p6 derived from HIV-1NL4-3 wt (green) and L1P (light blue) (**A**) or SG3 wt (purple blue) and P1L (magenta) (**B**) as predicted using the Phyre2 protein folding recognition server. A close up of the first six aa residues is shown as an inset.