



Supplement Figure S2. Root-mean square fluctuation (RMSF) of residues in HIV proteins during the molecular dynamics (MD) simulations. Panel A-L represent CA, GP41, MA, NC, P6, PR, REV, RT, TAT, VIF, VPR, and VPU respectively. For each protein, X axis is the sequence of the protein structure in Table 2 while Y axis is the average RMSF during the 10 ns molecular dynamic simulations.