



**SUPPLEMENTAL FIG. 1.** The relative variability at each position in the V3 loop. Data are based on 6010 sequences, selected as described in Materials and Methods from the Los Alamos Database. The *y*-axis denotes the relative variability (calculated as described in Materials and Methods), with 100% equal to the most variable of the 35 amino acid positions of the V3 loop (*x*-axis). Residues shown along the *x*-axis represent the consensus sequence of the 6010 sequences used in this study. Residues in the crown region are color coded according to the regions outlined in Fig. 3: stem, orange; turn, green; hydrophilic, red; hydrophobic, blue.