Figure 1 Phylogenetic analysis of SIVcpzUS. **a**, Phylogenetic relationship of SIVcpzUS to other primate lentiviruses. The tree was derived by neighbour-joining analysis[27] of full-length Pol sequences (trees derived by maximum-likelihood methods[28] yielded very similar topologies). Horizontal branch lengths are drawn to scale with the bar indicating 0.1 amino-acid replacements per site. Numbers at each node indicate the percentage of bootstrap samples (out of 1,000) in which the cluster to the right is supported (only values >80% are shown). Other SIVcpz strains closely or more distantly related to SIVcpzUS are shown in red and blue, respectively. **b**, Diversity plots of concatenated SIVcpz protein sequences depicting the proportion of amino-acid sequence differences between SIVcpzUS and SIVcpzGAB1 (red), SIVcpzUS and SIVcpzANT (blue), and SIVcpzGAB1 and SIVcpzANT (black), calculated for a window of 200 amino acids moved in steps of 10 amino acids along the alignment (available as Supplementary Information). The x-axis shows the amino-acid positions along the alignment. The positions of Gag, Pol, Vif, Env and Nef regions are shown. The y-axis denotes the distance between the viral proteins compared ($0.1 = 10\%$ difference). **c**, Unrooted neighbour-joining tree of partial Pol protein sequences (distances are drawn to scale).