Fig. S1. Latency genes-LTNP state network. The network was inferred for 212 HIV latency over-expressed genes from all LTNP samples. Standard Banjo parameters were adopted with a q6 discretization policy. The consensus graph depicted here was obtained from the concensus of the best 100 nets (after searching through $3 \times 10^8$ networks). The node size was proportional to the betweenness centrality and visually reinforced.