Table 9: Significantly overrepresented network motifs in HIV-host protein interaction network. Black nodes are HIV proteins and white nodes are human proteins. Interactions can either be activations, suppressions, inhibitions, downregulations, and signaling regulations or both (arrow without sign in the diagram).

N_{real} is the number of specific motifs found. N_{rand} ± SD is the average number and standard deviation of the motif found in one thousand randomized networks. P-value is the probability that N_{real} or more motifs are found in the randomized networks. Z-score is the number of standard deviations N_{rand} differs from N_{real}.

Network motifs were classified as significant when P-value < 0.05 and Z-score > 1.