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, signalings, or combinations thereof. 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.