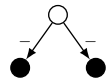
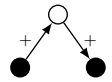
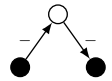
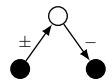
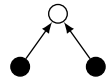
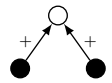
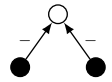
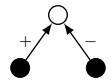
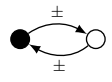
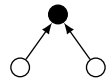
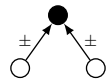
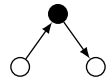
ID	motif	N_{real}	$N_{rand} \pm SD$	P_{value}	Z_{score}
1		1	0.01 ± 0.1	0	9.9
2		15	7 ± 4	0.0134	2.21
3		8	3 ± 2	0.0183	2.09
4		2	0.3 ± 0.8	0.0167	2.13
5		577	425 ± 20	$3.1 \cdot 10^{-14}$	7.50
6		200	163 ± 13	$2.5 \cdot 10^{-3}$	2.80
7		115	51 ± 10	$1.6 \cdot 10^{-10}$	6.29
8		336	278 ± 25	$9.4 \cdot 10^{-3}$	2.35
9		4	0.7 ± 0.8	$1.7 \cdot 10^{-5}$	4.14
10		2341	1569 ± 156	$3.9 \cdot 10^{-7}$	4.94
11		2155	1246 ± 128	$6.2 \cdot 10^{-13}$	7.10
12		24466	21914 ± 927	$2.9 \cdot 10^{-3}$	2.8

Table 1: Significantly over-represented network motifs in HIV-host regulatory network. Black nodes are HIV proteins and white nodes are human proteins. Interactions can either be activations/up-regulations (+), inhibitions/down-regulations (−), signaling/regulation (±), or both (arrow without sign). N_{real} is the number of specific motifs found. $N_{rand} \pm SD$ 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 $P_{value} < 0.02$ and $Z_{score} > 2$.

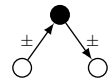
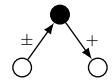
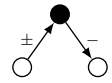
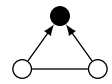
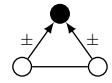
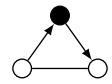
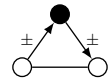
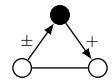
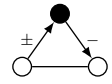
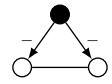
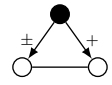
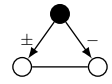
ID	motif	N_{real}	$N_{rand} \pm SD$	P_{value}	Z_{score}
13		482	374 ± 48	0.0123	2.25
14		14718	12457 ± 572	$3.9 \cdot 10^{-5}$	3.95
15		8348	6709 ± 377	$6.8 \cdot 10^{-6}$	4.35
16		74	16 ± 6	0	9.97
17		71	12 ± 5	0	11.0
18		322	218 ± 35	$1.6 \cdot 10^{-3}$	2.94
19		22	4 ± 2	$1.11 \cdot 10^{-16}$	8.28
20		181	124 ± 23	$7.7 \cdot 10^{-3}$	2.43
21		107	67 ± 15	$2.8 \cdot 10^{-3}$	2.77
22		130	90 ± 19	0.0175	2.11
23		30	16 ± 6	0.0135	2.21
24		20	10 ± 5	0.0147	2.18

Table 2: Significantly over-represented network motifs in HIV-host regulatory network. Black nodes are HIV proteins and white nodes are human proteins. Interactions can either be activations/up-regulations (+), inhibitions/down-regulations (−), signaling/regulation (±), or both (arrow without sign). N_{real} is the number of specific motifs found. $N_{rand} \pm SD$ 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 $P_{value} < 0.02$ and $Z_{score} > 2$.

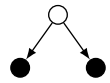
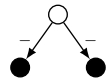
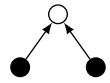
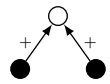
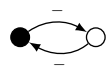
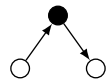
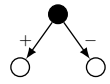
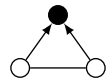
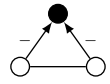
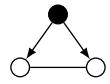
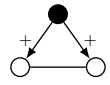
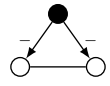
ID	motif	N_{real}	$N_{rand} \pm SD$	P_{value}	Z_{score}
25		35	23 ± 5	0.0114	2.28
26		34	21 ± 6	0.0153	2.16
27		304	240 ± 15	$6.9 \cdot 10^{-6}$	4.35
28		167	78 ± 11	$1.1 \cdot 10^{-16}$	8.19
29		22	15 ± 3	0.0140	2.20
30		42912	40680 ± 1031	0.0151	2.17
31		20912	19820 ± 511	0.0166	2.13
32		77	39 ± 11	$1.9 \cdot 10^{-4}$	3.56
33		72	36 ± 10	$1.7 \cdot 10^{-4}$	3.59
34		659	402 ± 44	$2.7 \cdot 10^{-9}$	5.84
35		324	131 ± 27	$4.5 \cdot 10^{-13}$	7.14
36		175	74 ± 17	$1.4 \cdot 10^{-9}$	5.95

Table 3: Significantly over-represented network motifs in HIV-host signaling network. Black nodes are HIV proteins and white nodes are human proteins. Interactions can either be activations/up-regulations (+), inhibitions/down-regulations (−), signaling/regulation (±), or both (arrow without sign). N_{real} is the number of specific motifs found. $N_{rand} \pm SD$ 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 $P_{value} < 0.02$ and $Z_{score} > 2$.

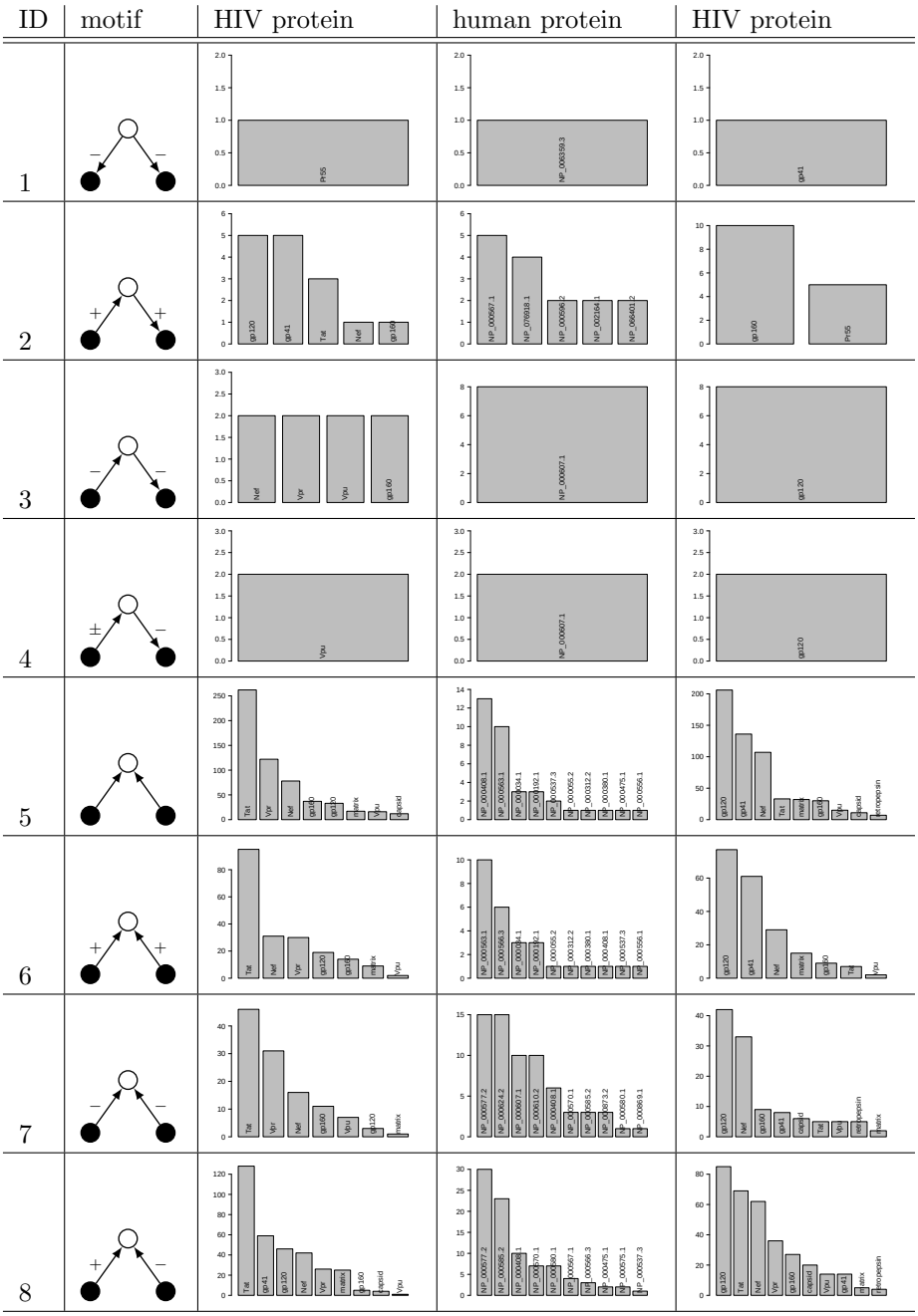


Table 4: Involvement of HIV and human proteins in network motifs of HIV-host regulatory network. HIV nodes in symmetric motifs share the same distribution. Of the human proteins at most only the 10 most frequent ones are shown. Human proteins are identified with a RefSeq protein accession number.

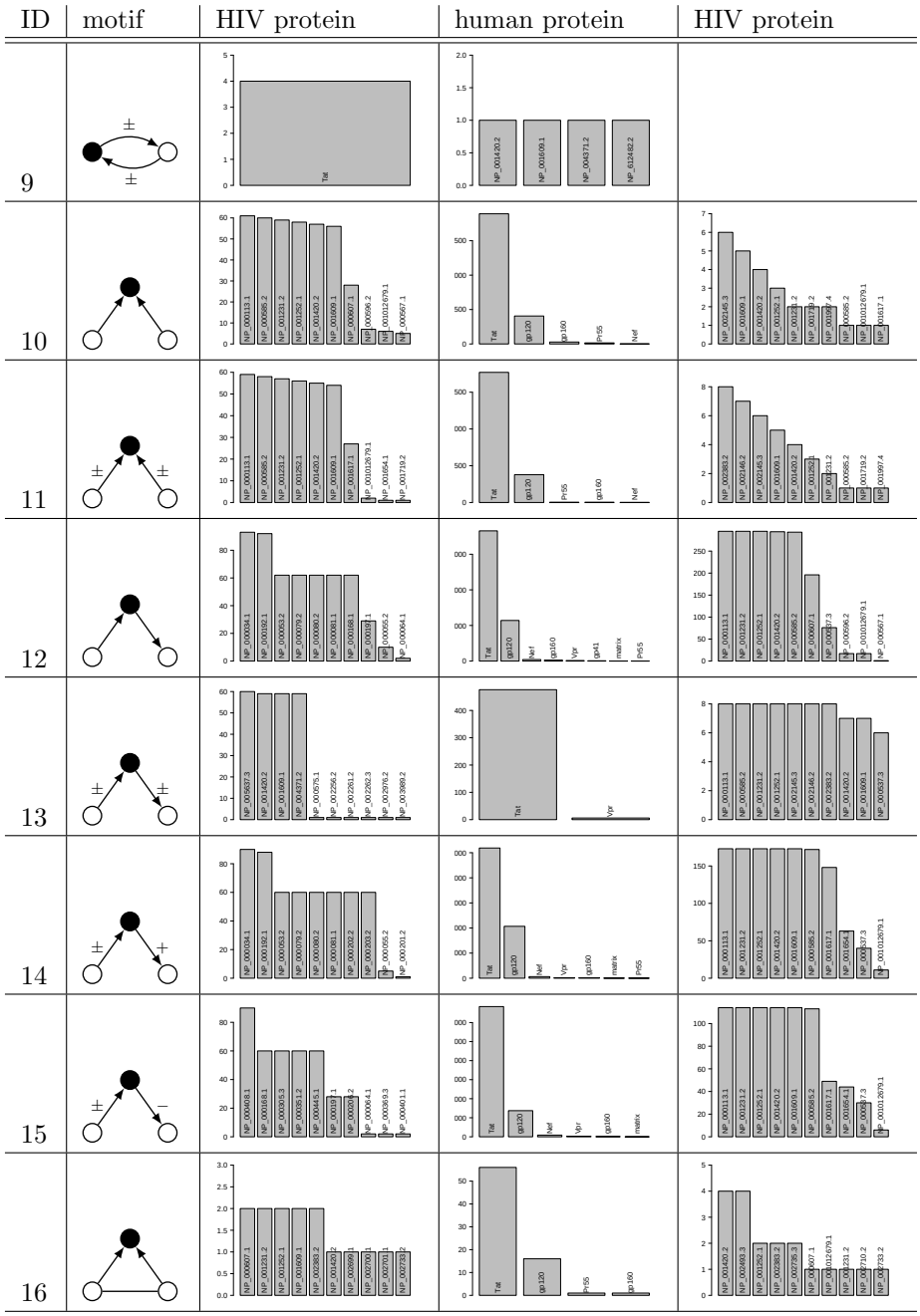


Table 5: Involvement of HIV and human proteins in network motifs of HIV-host regulatory network. HIV nodes in symmetric motifs share the same distribution. Of the human proteins at most only the 10 most frequent ones are shown. Human proteins are identified with a RefSeq protein accession number.

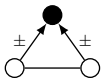
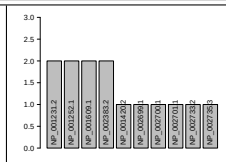
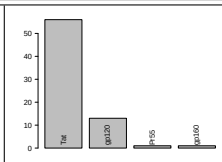
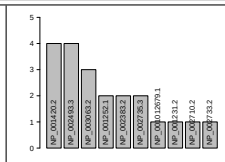
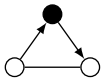
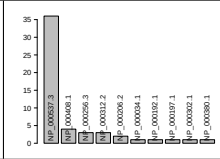
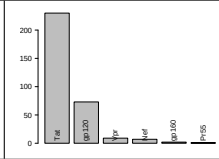
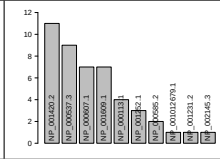
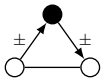
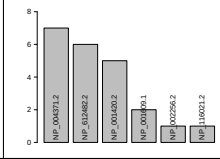
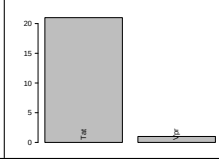
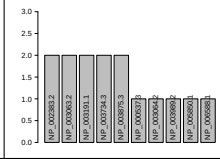
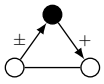
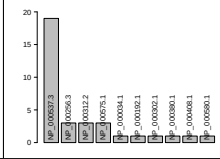
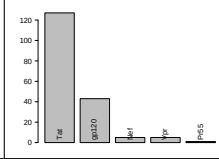
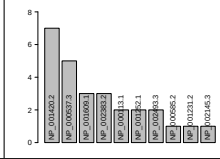
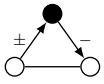
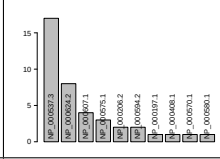
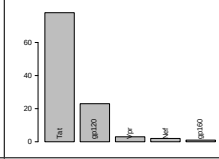
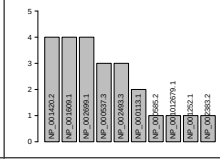
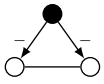
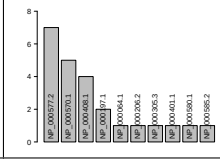
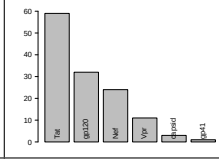
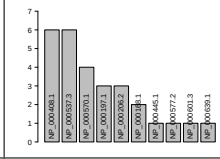
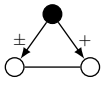
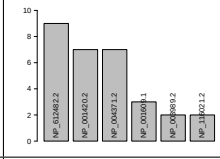
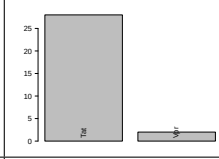
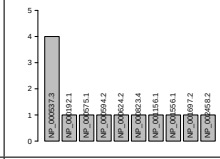
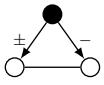
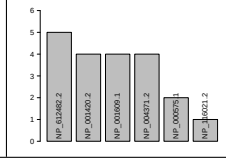
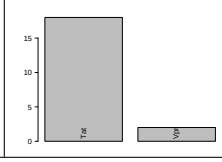
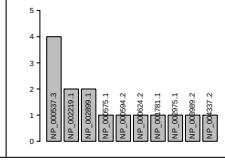
ID	motif	HIV protein	human protein	HIV protein
17				
18				
19				
20				
21				
22				
23				
24				

Table 6: Involvement of HIV and human proteins in network motifs of HIV-host regulatory network. HIV nodes in symmetric motifs share the same distribution. Of the human proteins at most only the 10 most frequent ones are shown. Human proteins are identified with a RefSeq protein accession number.

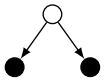
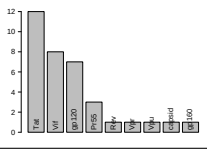
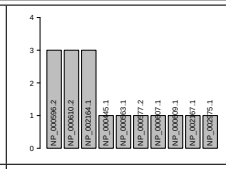
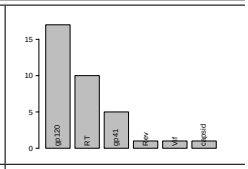
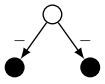
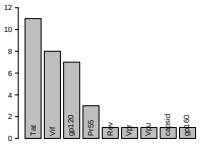
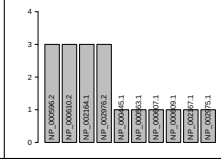
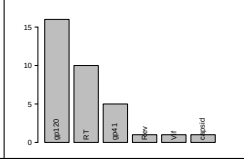
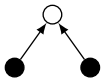
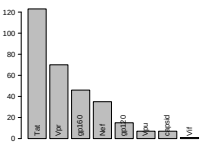
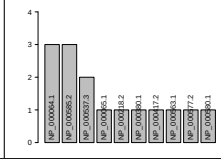
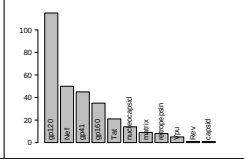
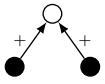
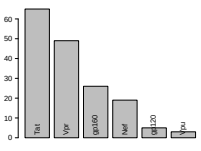
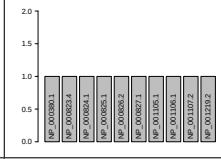
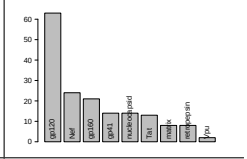
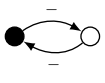
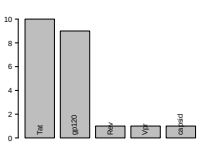
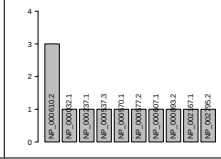
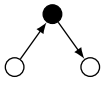
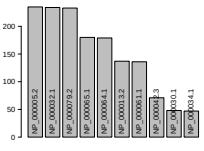
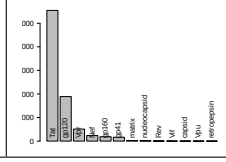
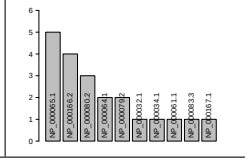
ID	motif	HIV protein	human protein	HIV protein
25				
26				
27				
28				
29				
30				

Table 7: Involvement of HIV and human proteins in network motifs of HIV-host signalling network. HIV nodes in symmetric motifs share the same distribution. Of the human proteins at most only the 10 most frequent ones are shown. Human proteins are identified with a RefSeq protein accession number.

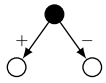
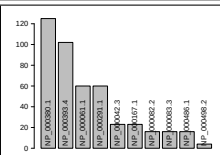
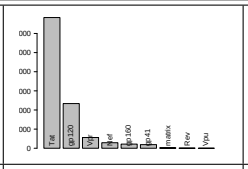
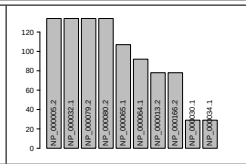
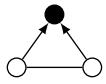
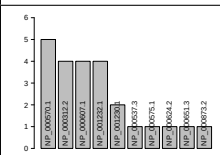
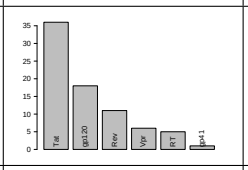
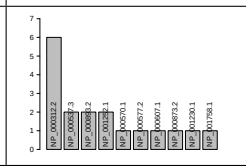
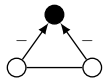
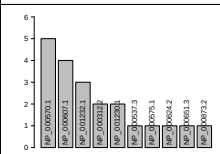
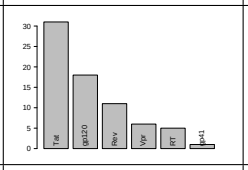
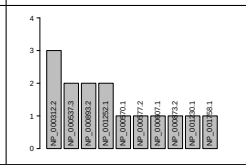
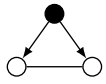
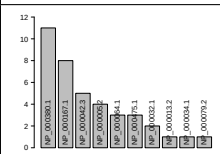
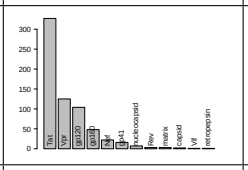
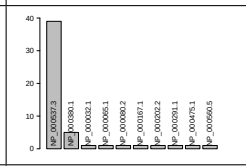
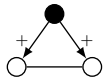
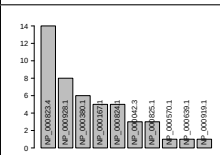
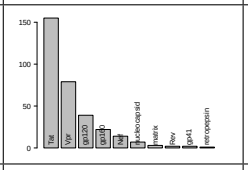
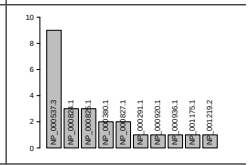
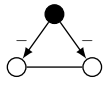
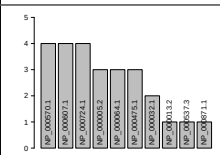
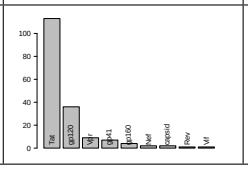
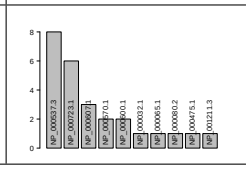
ID	motif	HIV protein	human protein	HIV protein
31				
32				
33				
34				
35				
36				

Table 8: Involvement of HIV and human proteins in network motifs of HIV-host signalling network. HIV nodes in symmetric motifs share the same distribution. Of the human proteins at most only the 10 most frequent ones are shown. Human proteins are identified with a RefSeq protein accession number.

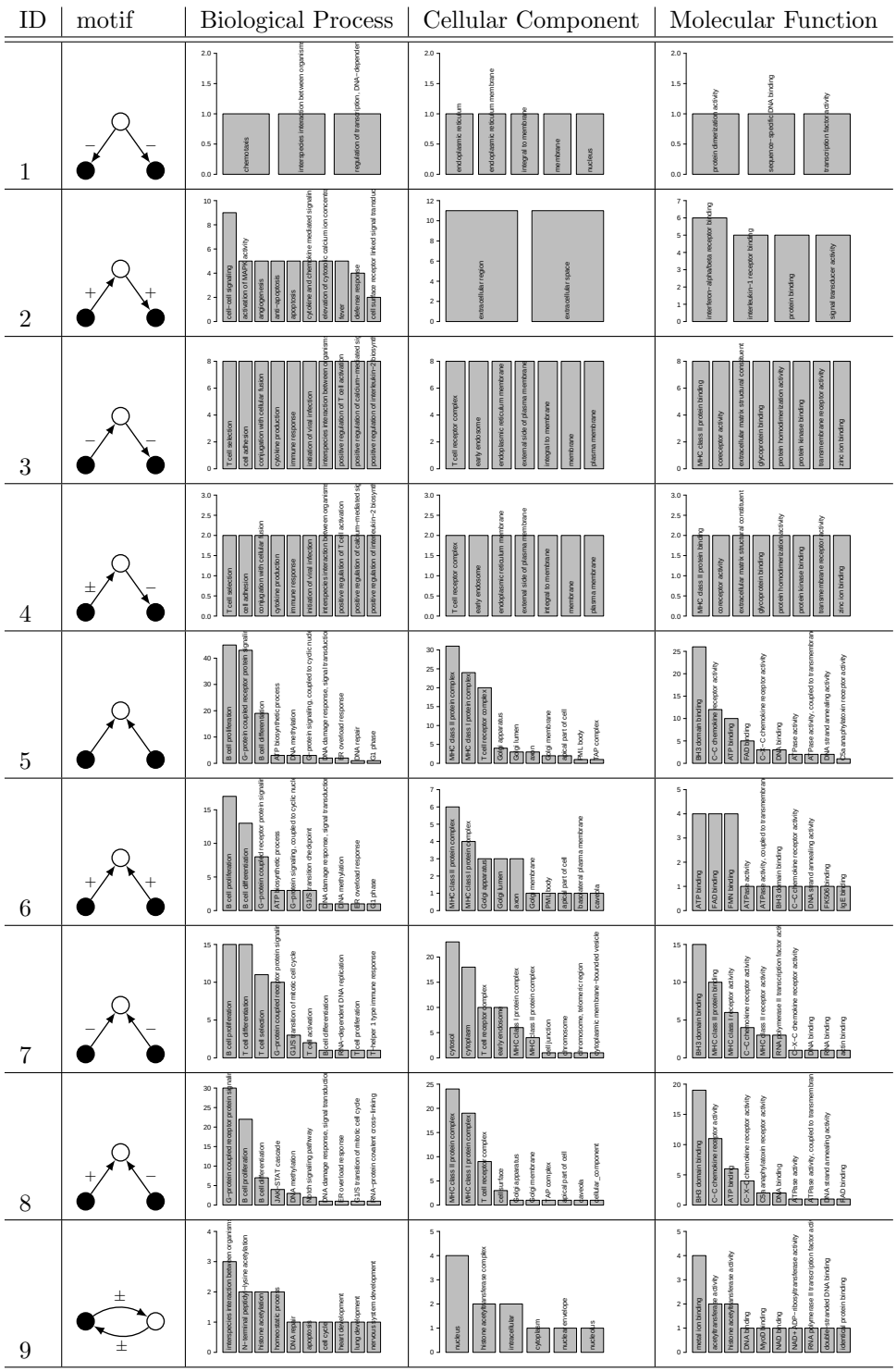


Table 9: Gene Ontology annotation of human proteins involved in network motifs of HIV-human regulatory network.

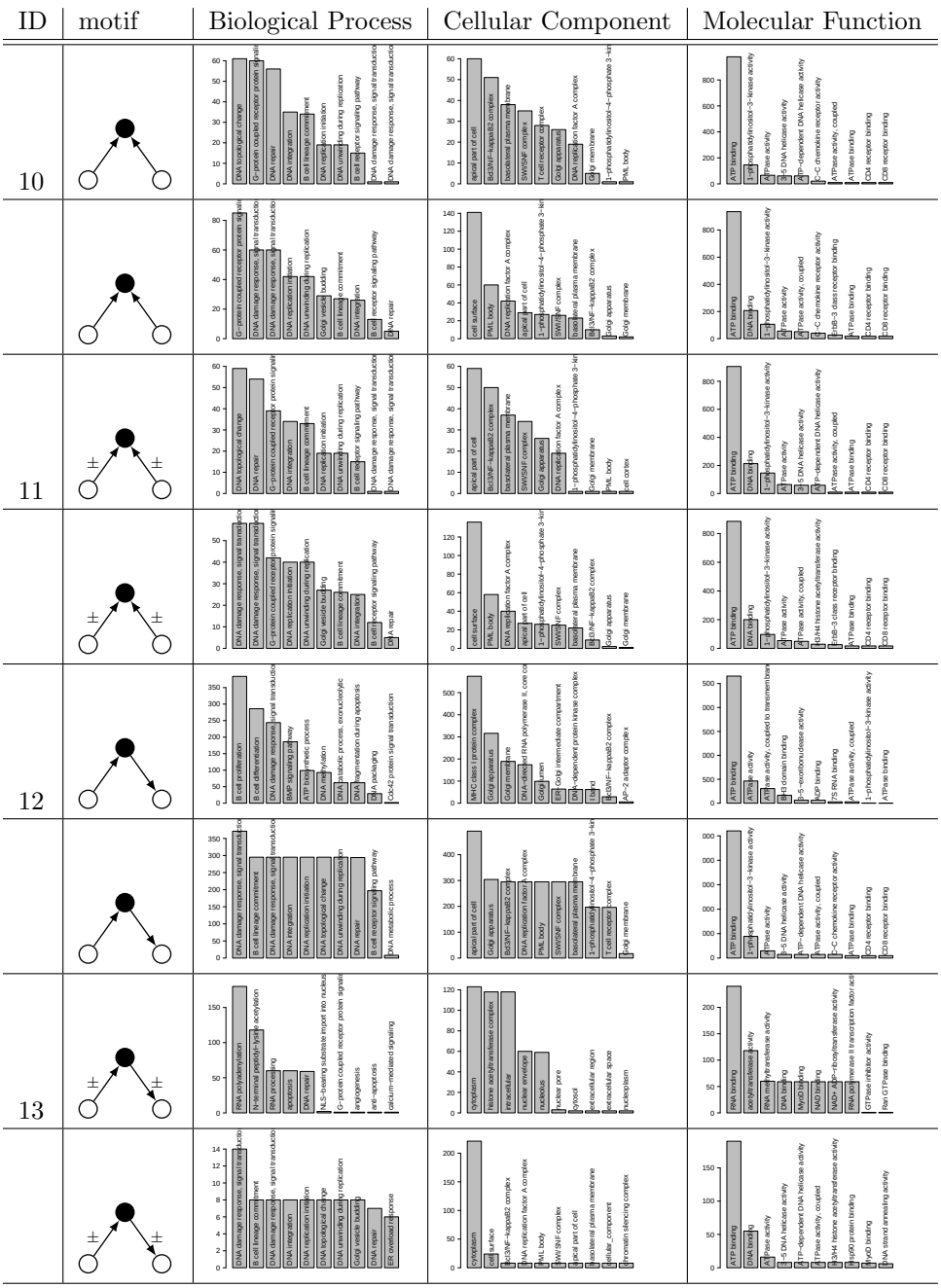


Table 10: Gene Ontology annotation of human proteins involved in network motifs of HIV-human regulatory network.

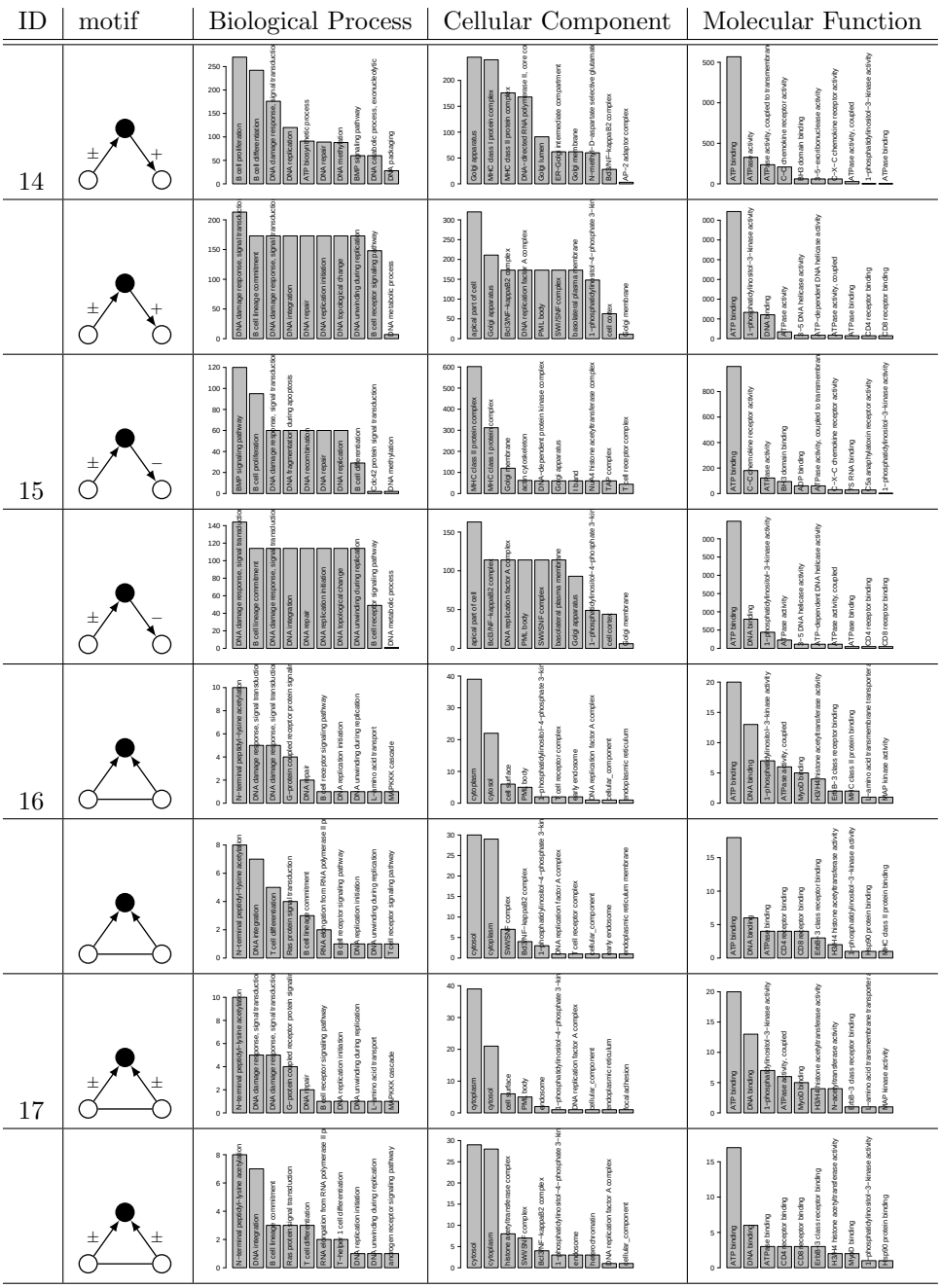


Table 11: Gene Ontology annotation of human proteins involved in network motifs of HIV-human regulatory network.

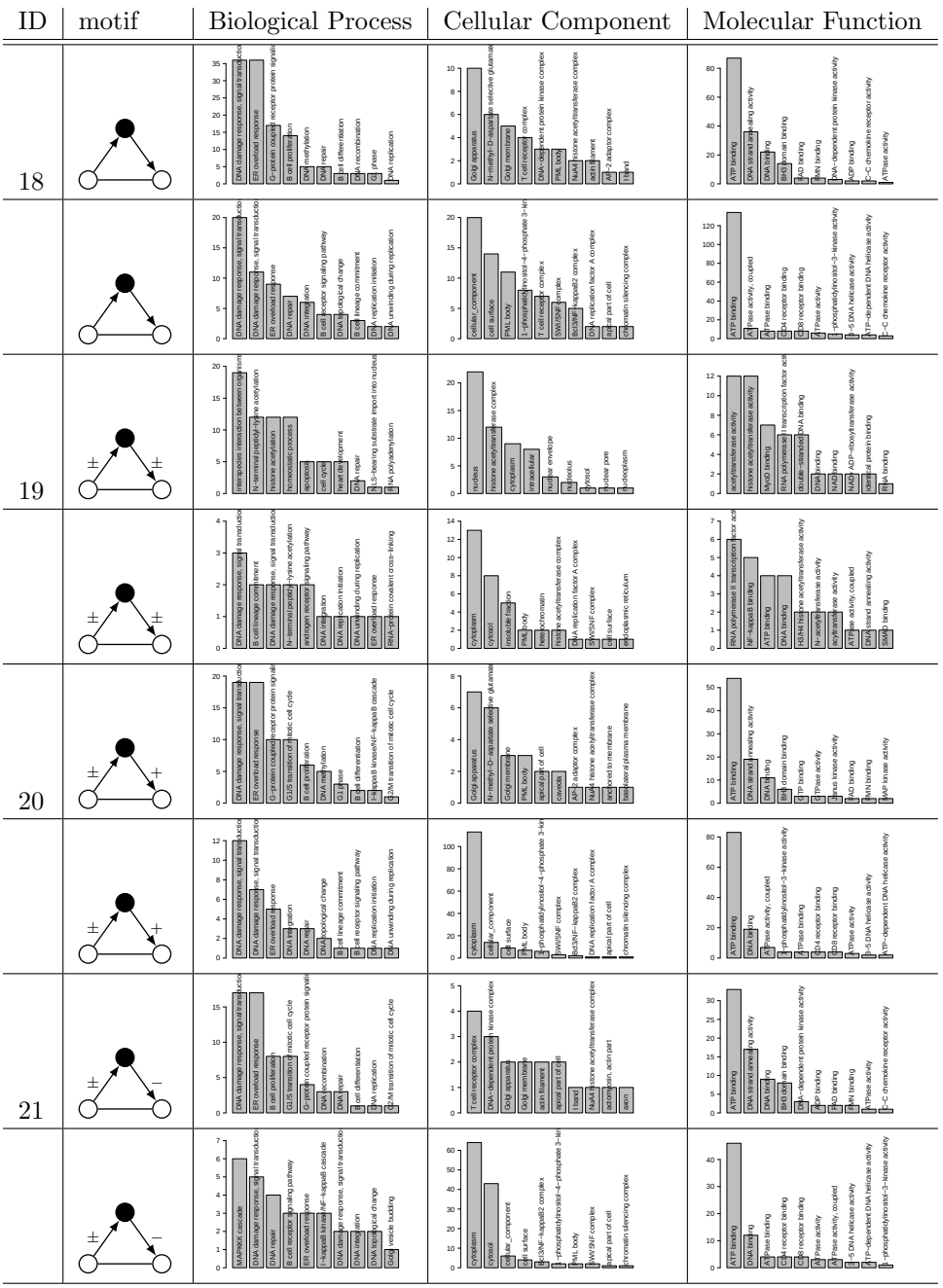


Table 12: Gene Ontology annotation of human proteins involved in network motifs of HIV-human regulatory network.

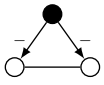
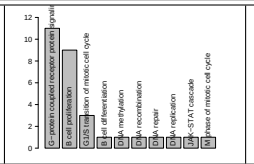
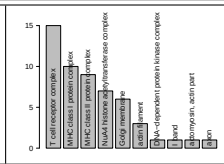
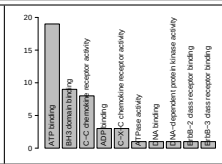
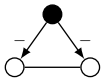
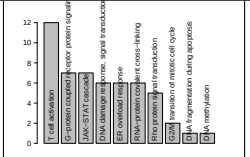
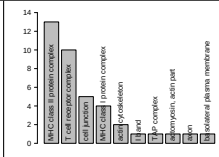
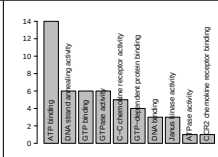
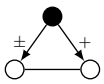
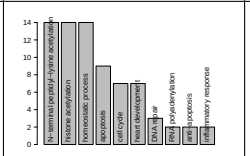
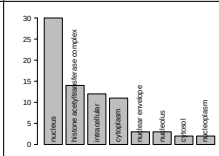
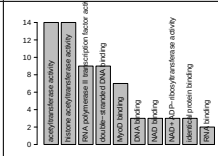
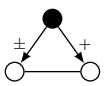
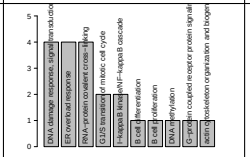
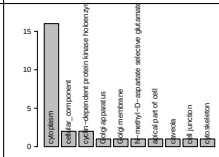
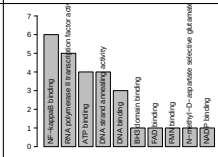
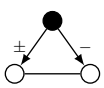
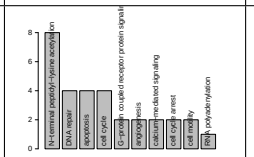
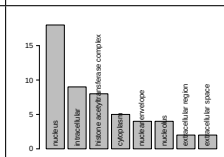
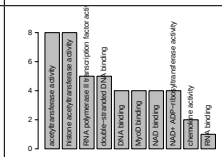
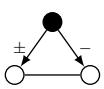
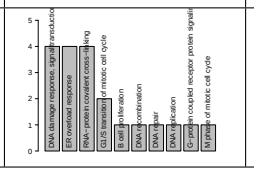
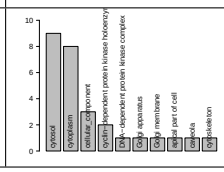
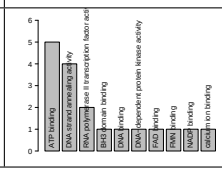
ID	motif	Biological Process	Cellular Component	Molecular Function
22				
				
23				
				
24				
				

Table 13: Gene Ontology annotation of human proteins involved in network motifs of HIV-human regulatory network.

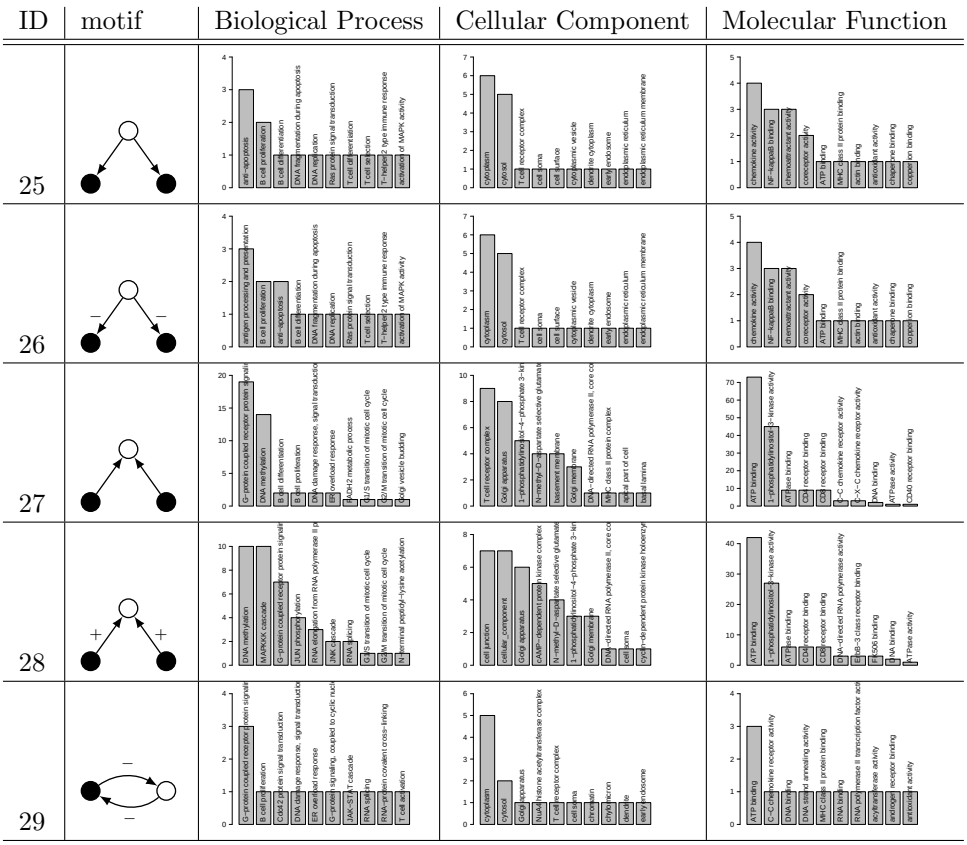


Table 14: Gene Ontology annotation of human proteins involved in network motifs of HIV-human signaling network.

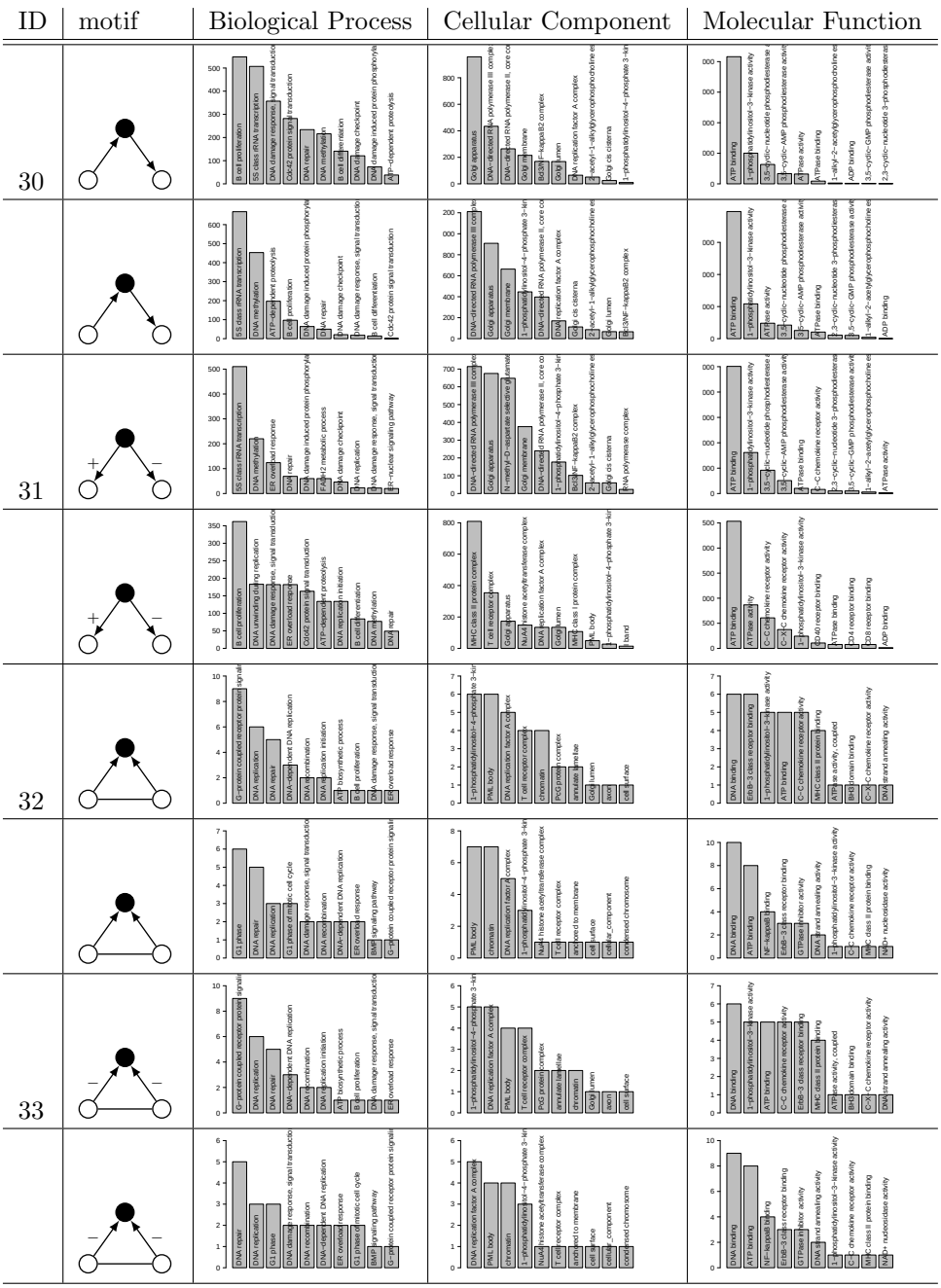


Table 15: Gene Ontology annotation of human proteins involved in network motifs of HIV-human signaling network.

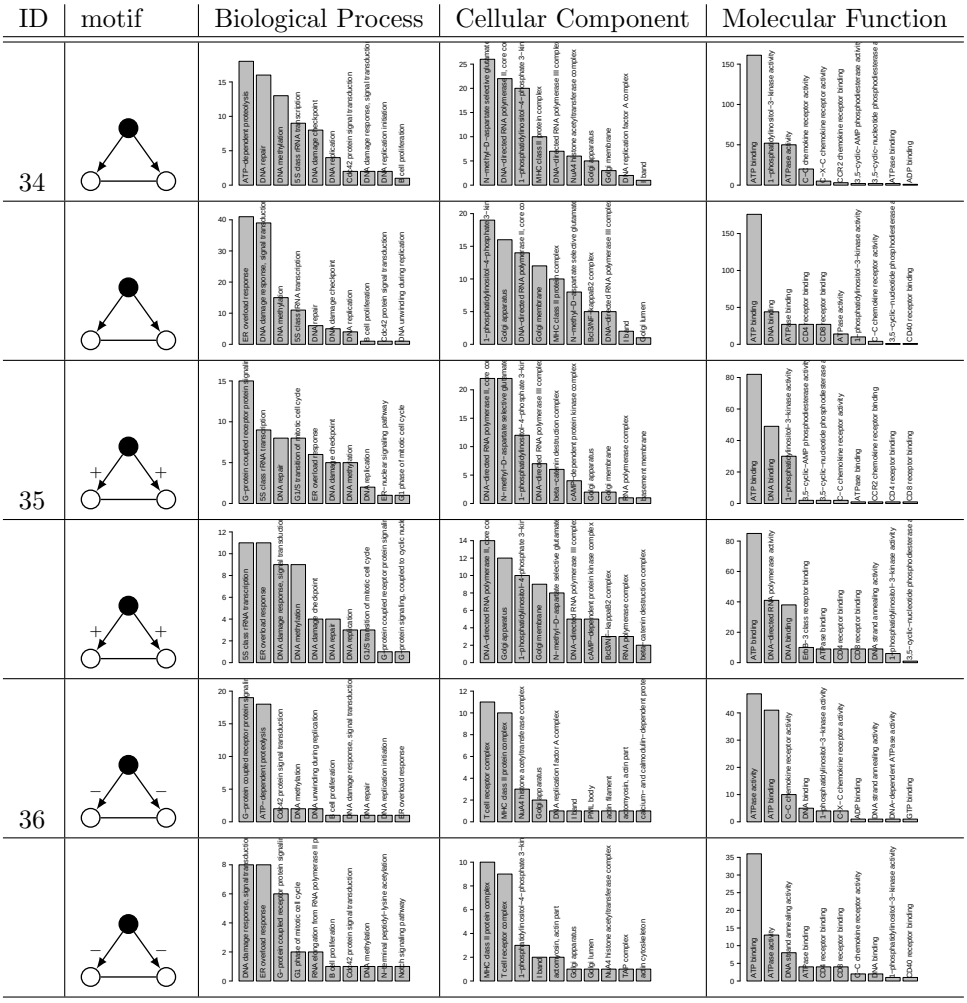


Table 16: Gene Ontology annotation of human proteins involved in network motifs of HIV-human signaling network.