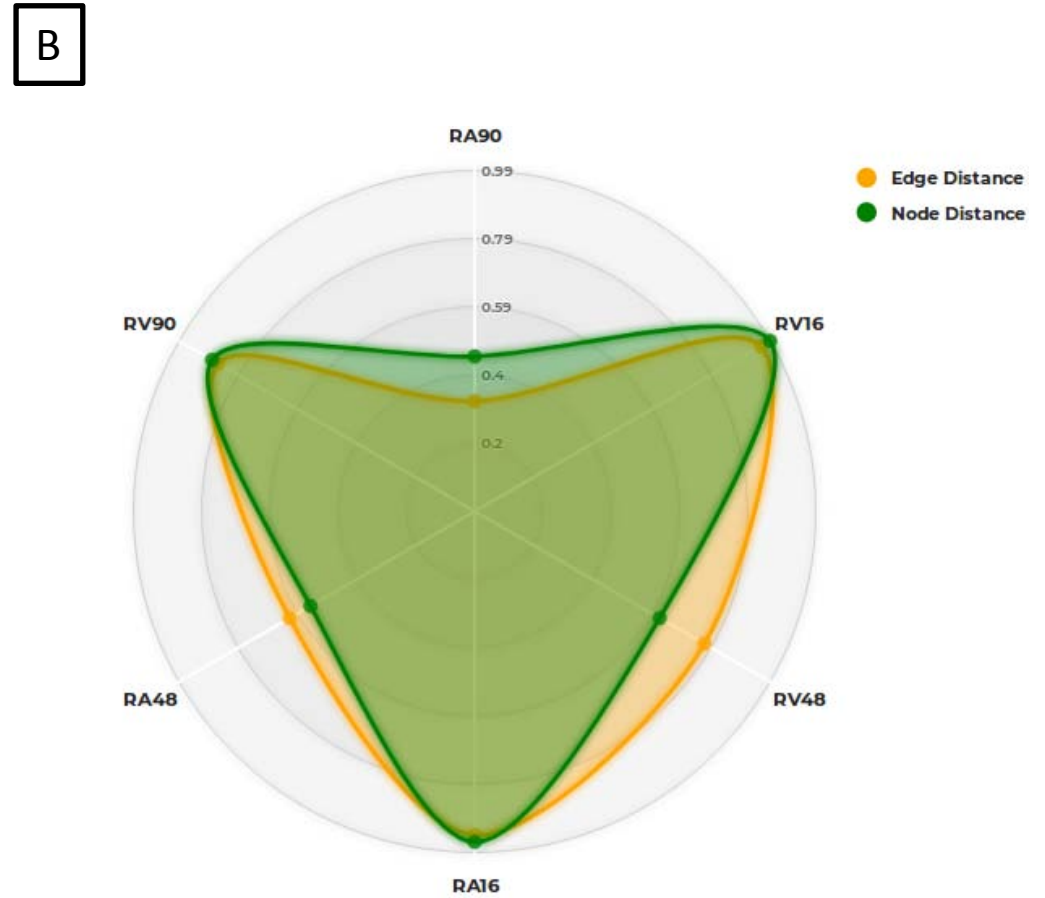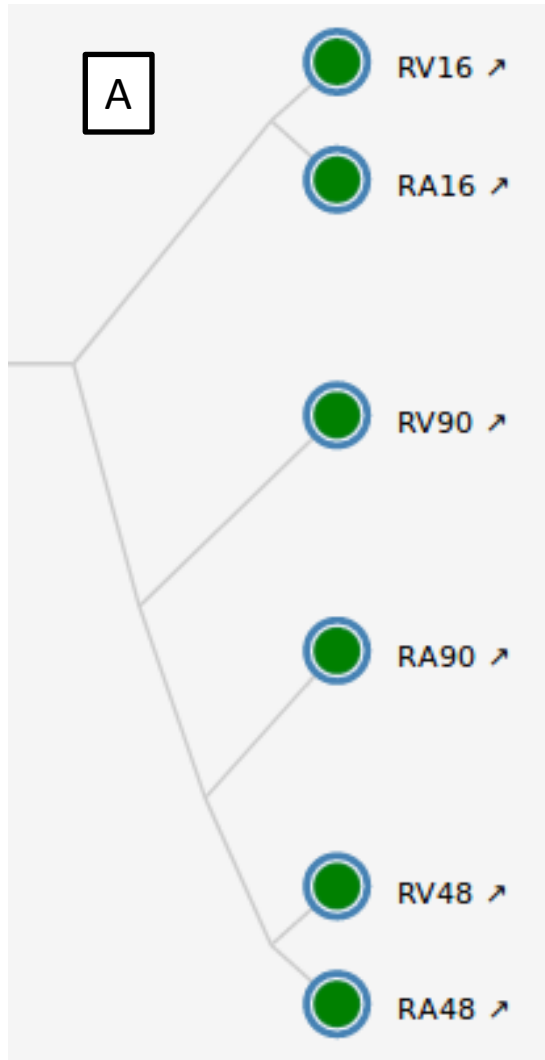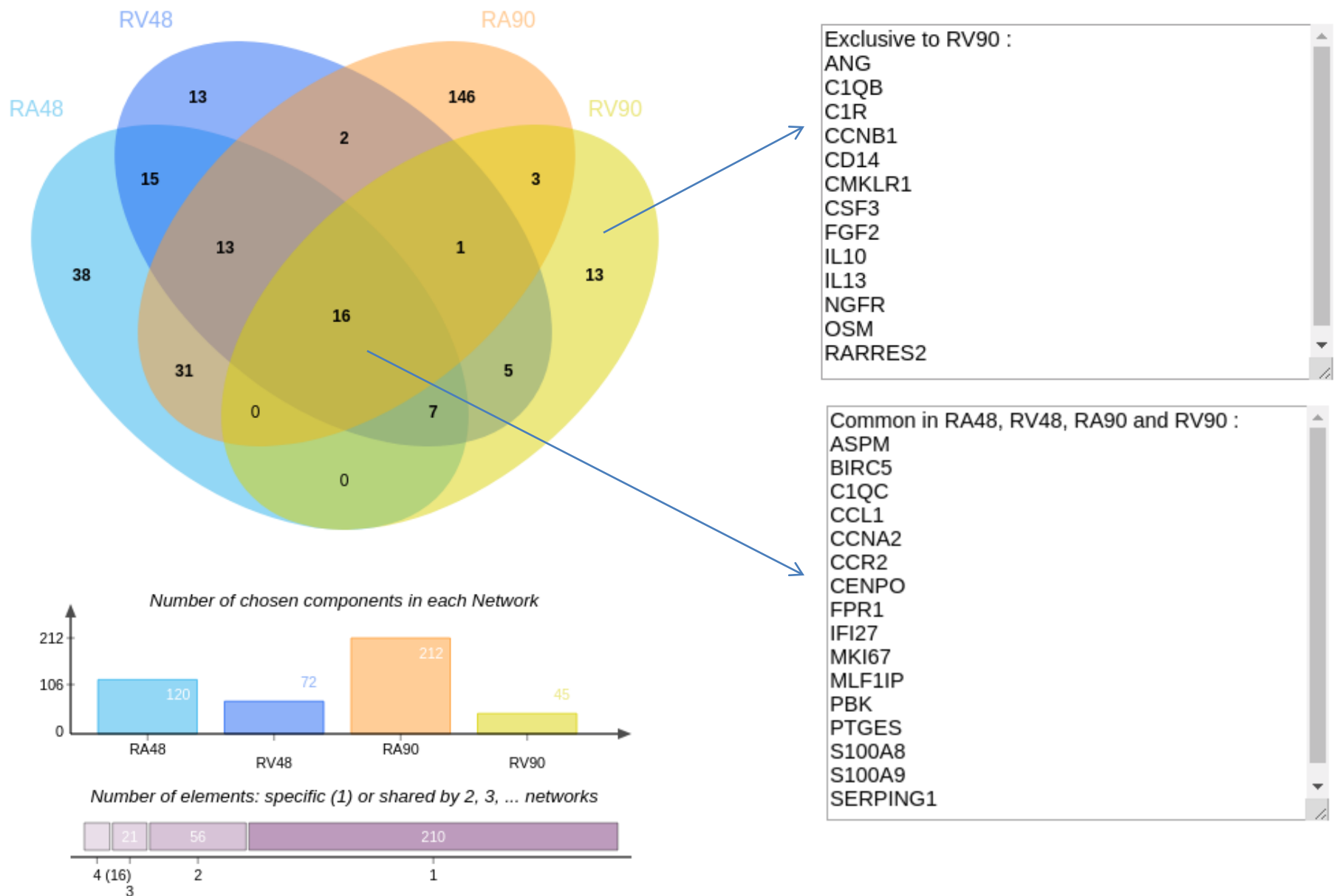**Figure S31**: Global graph properties of four time series human gene perturbation (16hr, 48hr and 90hr) networks corresponding to avirulent (RA) and virulent (RV) strains
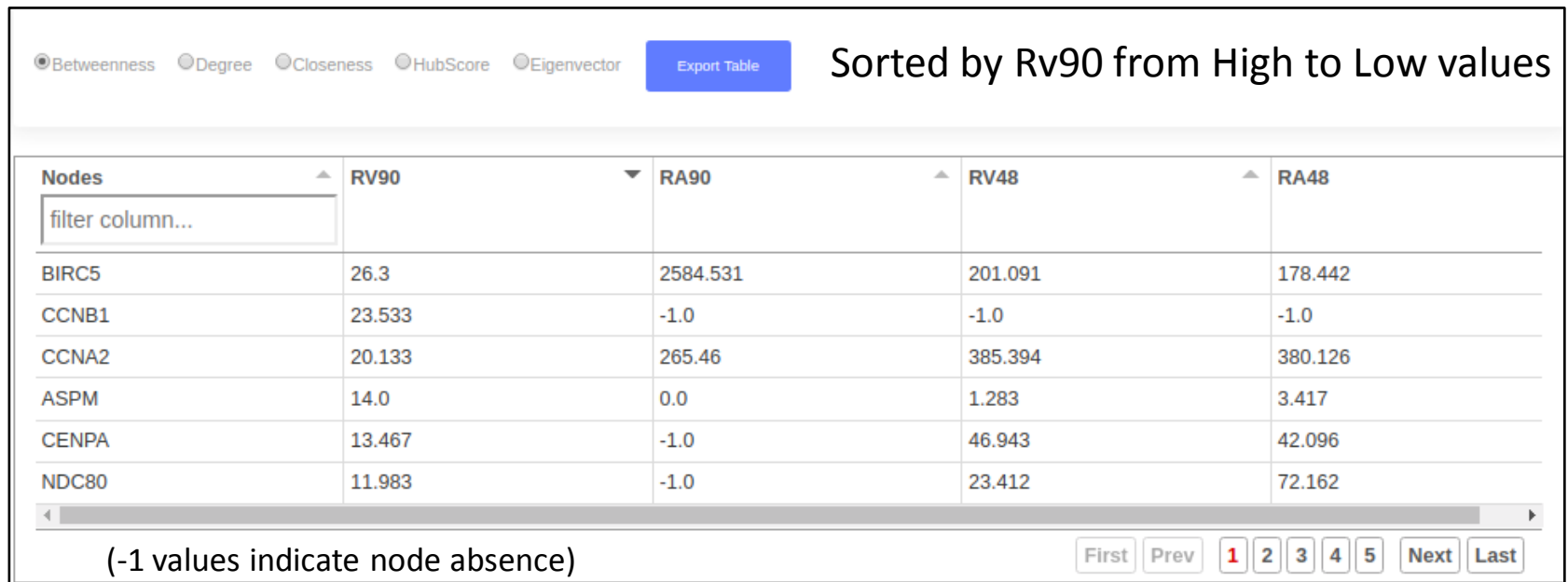
Figure S32: Comparison of the networks using (A) cluster network tree with Jaccard Edge distance and (B) radar plot of node and edge Jaccard distance from the union network
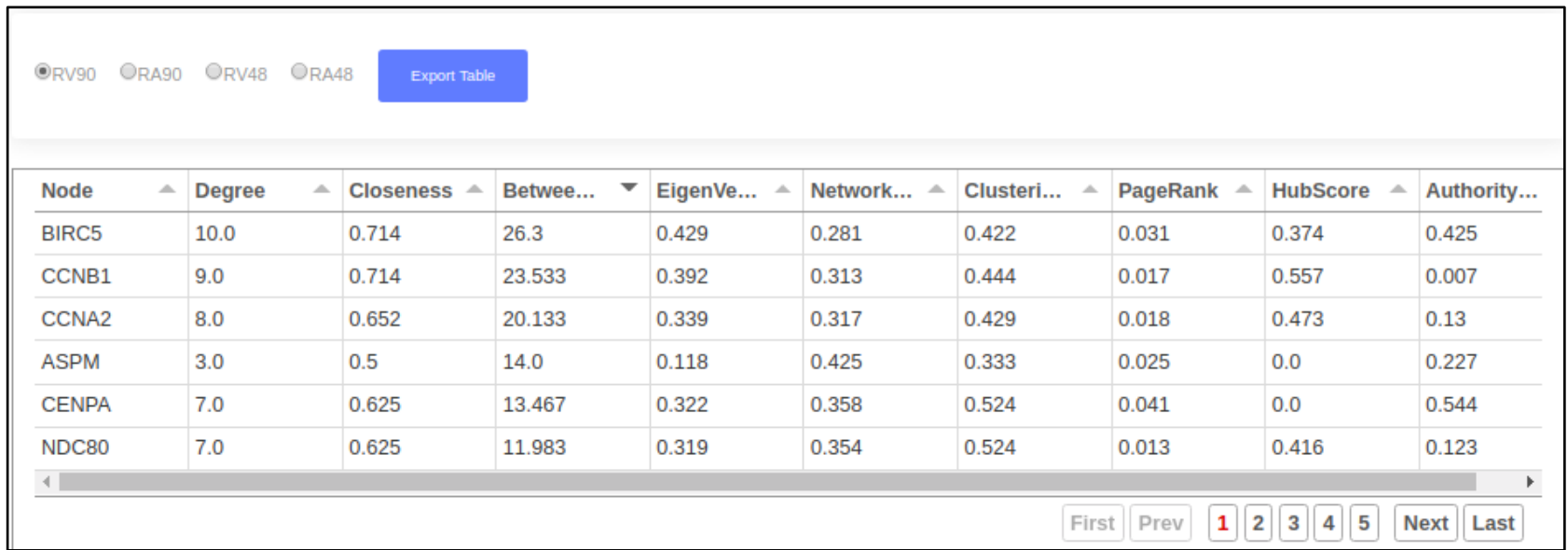
Figure S33: Visualizing similarities and differences between the post infection time point networks in H37Ra and H37Rv

Figure S34: (A) Visualizing nodes sorted with betweenness across various networks (B) visualizing variation of other network properties of the same nodes

| Size	Network	CliqueID	Clique Membership
13	RV 48	Clique-4	BIRC5 BUB1B NDC80 CDCA8 CENPM CENPE SPC25 CENPA CENPF ZWINT CENPN MLF1IP AURKB
13	RV 48	Clique-5	BIRC5 BUB1B NDC80 CDCA8 CENPM CENPE SPC25 CENPA CENPF ZWINT CENPN MLF1IP KIF18A
13	RV 48	Clique-6	BIRC5 BUB1B NDC80 CDCA8 CENPM CENPE SPC25 CENPA CENPF ZWINT CENPN NUF2 AURKB
6	RV 48	Clique-0	BIRC5 BUB1B CCNA2 CENPA CENPE CDCA8
6	RV 48	Clique-2	BIRC5 BUB1B CCNA2 PBK NCAPG RRM2
5	RV 90	Clique-1	BIRC5 CCNB1 CCNA2 MKI67 PBK
5	RV 90	Clique-2	BIRC5 CCNB1 CCNA2 MKI67 CDKN3
5	RV 90	Clique-5	BIRC5 MLF1IP NDC80 KIF18A CENPA
5	RV 48	Clique-1	BIRC5 BUB1B CCNA2 PBK CDCA8
5	RV 48	Clique-7	BIRC5 BUB1B NDC80 CDCA8 PBK

Figure S35: Clique containing BIRC5 in the virulent strain infection networks
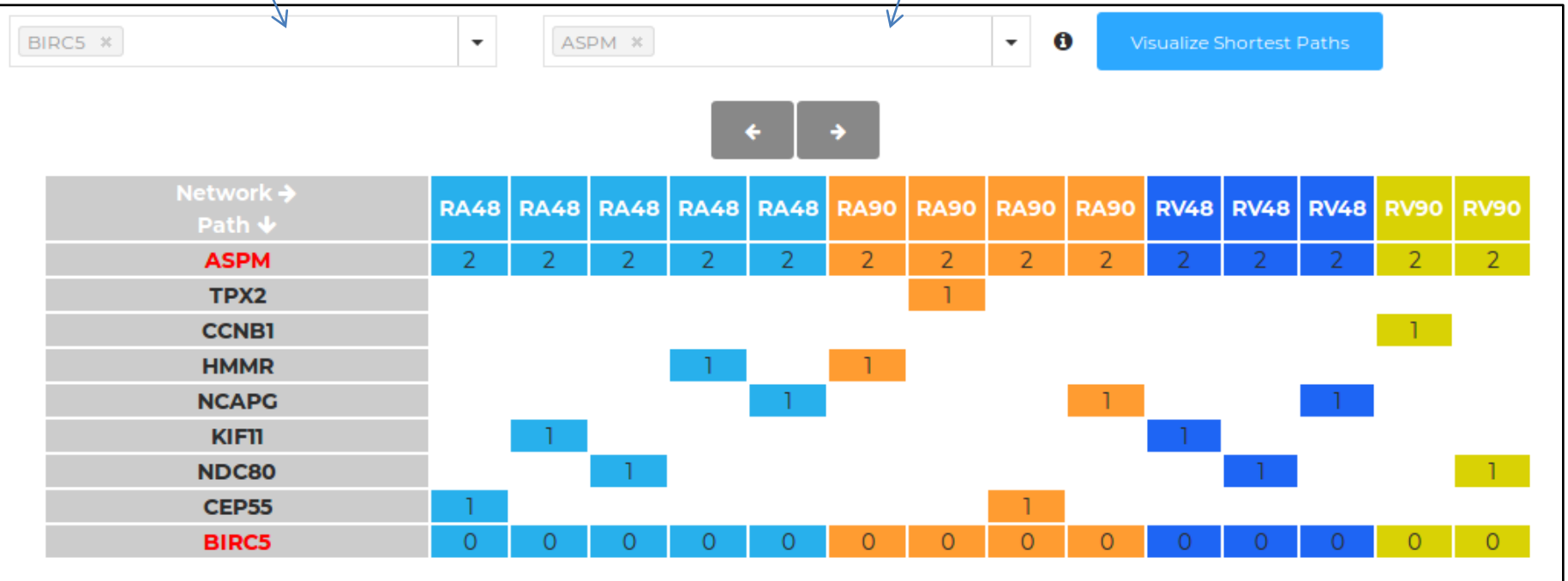
Figure S36: Visualizing differential shortest paths for connected perturbation
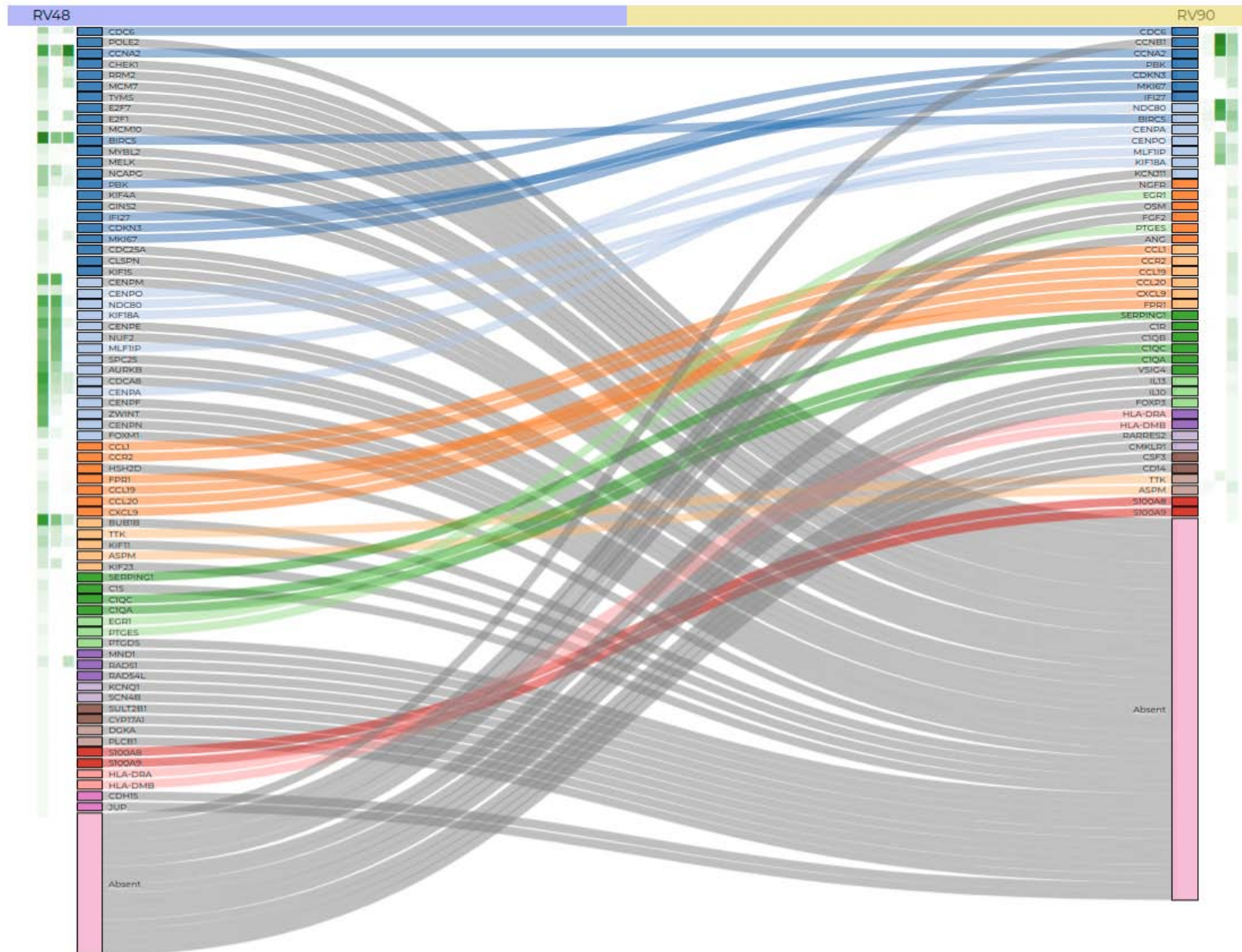
Figure S37: Visualizing changes in community structure between the 48ᵗʰ and 90ᵗʰ hour network of H37Rv infected human cells