

Figure 1 displays five network diagrams of protein complexes, where nodes represent proteins and edges represent interactions. Red circles highlight specific proteins of interest in each complex.

- C complex spliceosome:** A large, dense network of proteins. Highlighted proteins (red circles) include HNRNPA1, HNRNPF, and HNRNPA3.
- Large Drosha complex:** A network of proteins. Highlighted proteins (red circles) include SRPK1 and DDX3X.
- IGF2BP1 complex:** A small network of proteins. Highlighted proteins (red circles) include RPS6 and YBX1.
- Cleavage factor IIaM complex:** A small network of proteins. Highlighted proteins (red circles) include U2AF2 and U2AFBP.
- DGCR8 multiprotein complex:** A small network of proteins. Highlighted proteins (red circles) include NCL and DDX5.

Figure 1 displays five network diagrams illustrating protein-protein interactions. The nodes are color-coded: red for proteins with a high degree of connectivity, yellow for proteins with a moderate degree of connectivity, and grey for proteins with a low degree of connectivity. The edges represent interactions between the proteins.

- Toposome:** A central yellow node (DHX9) is connected to four red nodes (TOP2A, HNRNPC, SRPK1, SRPK1) and two grey nodes (DDX21, PRPF8).
- Vigilin-DNA-PK-Ku antigen complex:** A central yellow node (DHX9) is connected to four yellow nodes (XRCC6, HDLBP, PRKDC, XRCC5).
- DHX9-ADAR-vigilin-DNA-PK-Ku antigen complex:** A central yellow node (DHX9) is connected to four yellow nodes (ADAR, HDLBP, XRCC5, XRCC6) and two grey nodes (PRKDC, PRKDC).
- DNA-PK-Ku-eIF2-NF90-NF45 complex:** A central yellow node (DHX9) is connected to six yellow nodes (PRKDC, XRCC5, ILF2, ILF3, EIF2S1, EIF2S3) and two red nodes (EIF2S2, EIF2S3).
- ADAR-DHX9-vigilin-DNA-PK-Ku antigen complex:** A central yellow node (DHX9) is connected to four yellow nodes (ADAR, HDLBP, XRCC5, XRCC6) and two grey nodes (PRKDC, PRKDC).

HDP-RNP complex

SNW1 complex

TLE1 corepressor complex

● Proteins identified in the CIGB-300 pull-down experiment
● Proteins of the CIGB-300 interactome frequently identified in the CRAPome database
 Red border: Well-documented protein kinase CK2 substrates

Figure S2. Protein–protein interaction networks associated with CIGB-300 interacting proteins in NCI-H460 cells. Networks were generated using information gathered from the STRING database and were visualized using Cytoscape. Protein complexes retrieved from the CORUM database are indicated.