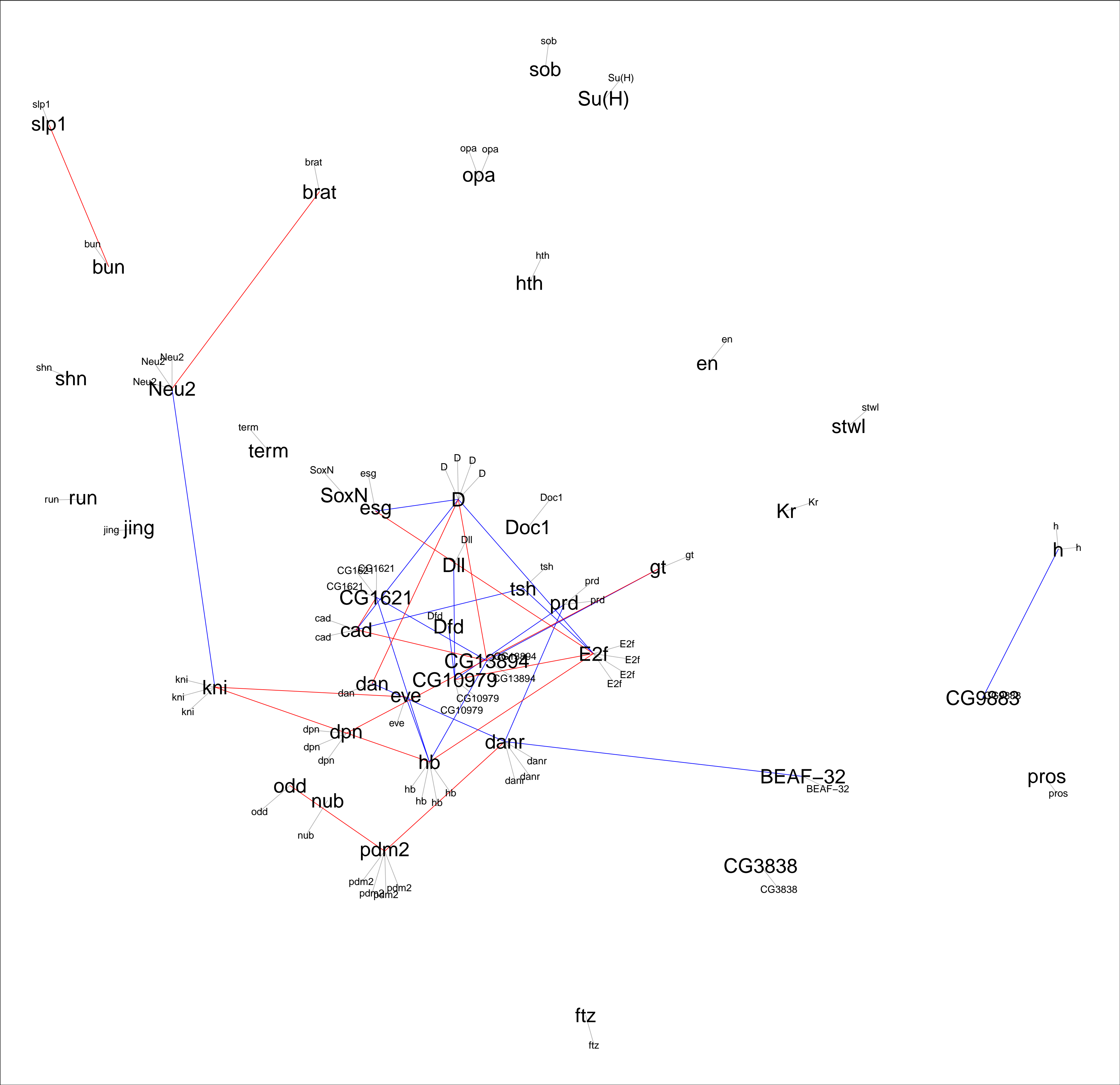


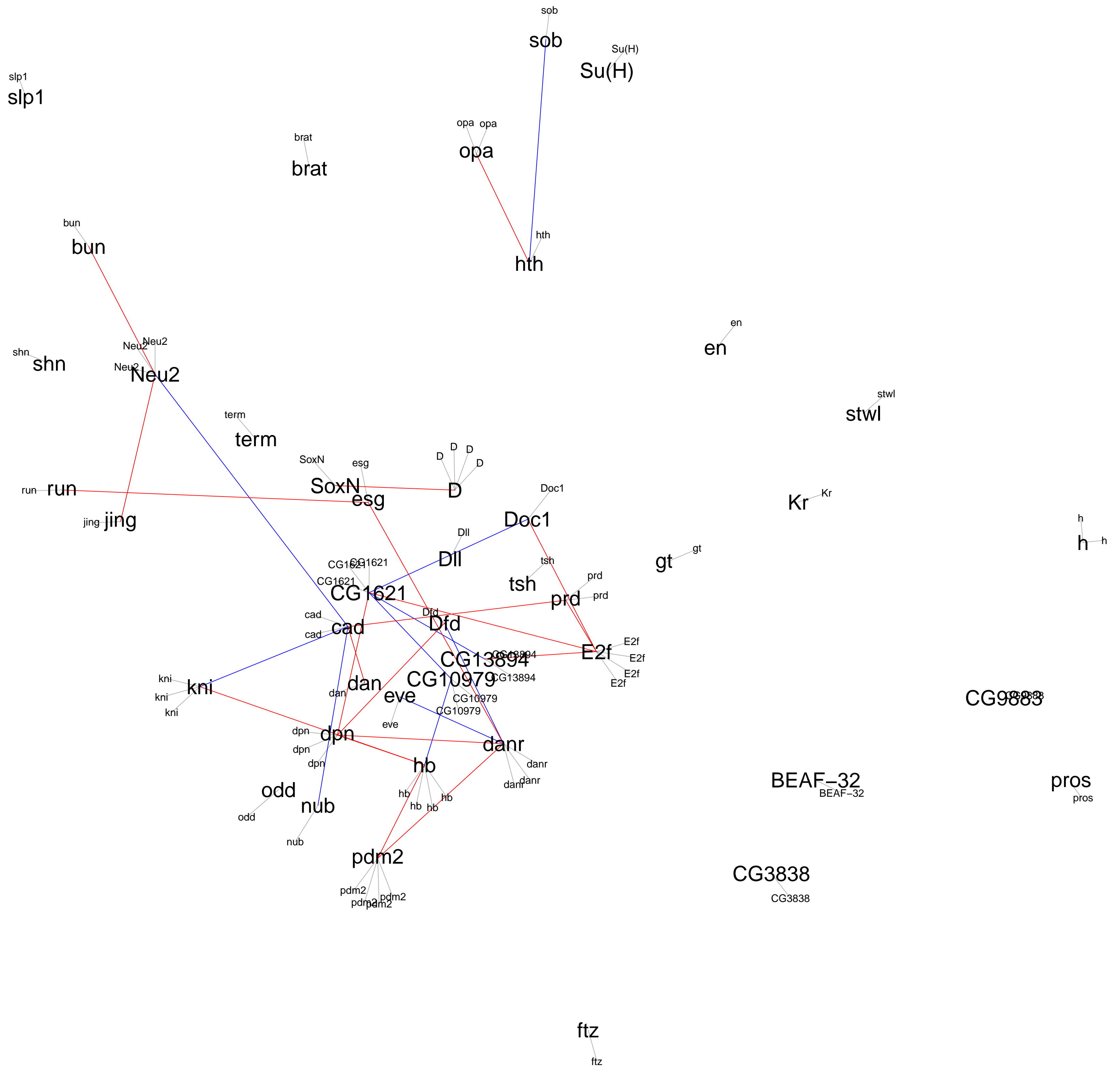
[illegible]

The diagram illustrates a complex network of gene and protein interactions. The nodes are labeled with gene names or protein identifiers, and the edges represent interactions between them. The network is organized into several clusters, with a central hub of genes like SoxN, Dll, Dfd, D, Doc1, tsh, prd, E2f, CG13894, CG10979, dan, eve, hb, danr, odd, nub, pdm2, and kni. Other clusters include shn, Neu2, term, run, jing, bun, slp1, brat, opa, hth, en, stwl, Kr, gt, h, pros, ftz, BEAF-32, CG3838, CG9883, and CG9882. Red lines indicate strong or specific interactions, while blue lines indicate other types of interactions. Grey lines represent weaker or less specific interactions. The diagram is set against a white background with a black border.

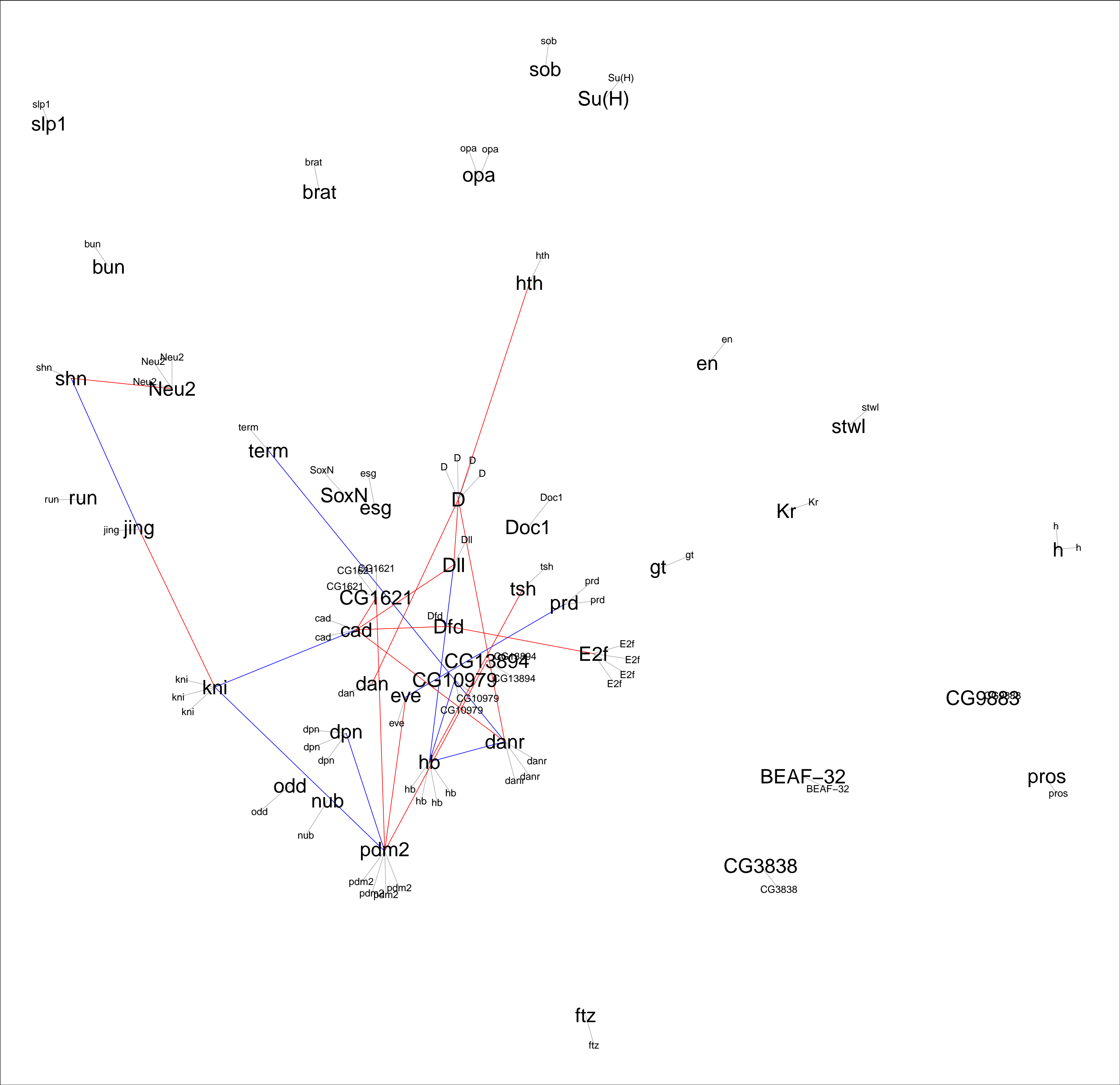
Lower [3.5%,4%] correlation = [-0.58,-0.56]; Upper [4%,3.5%] correlation = [0.7,0.71]



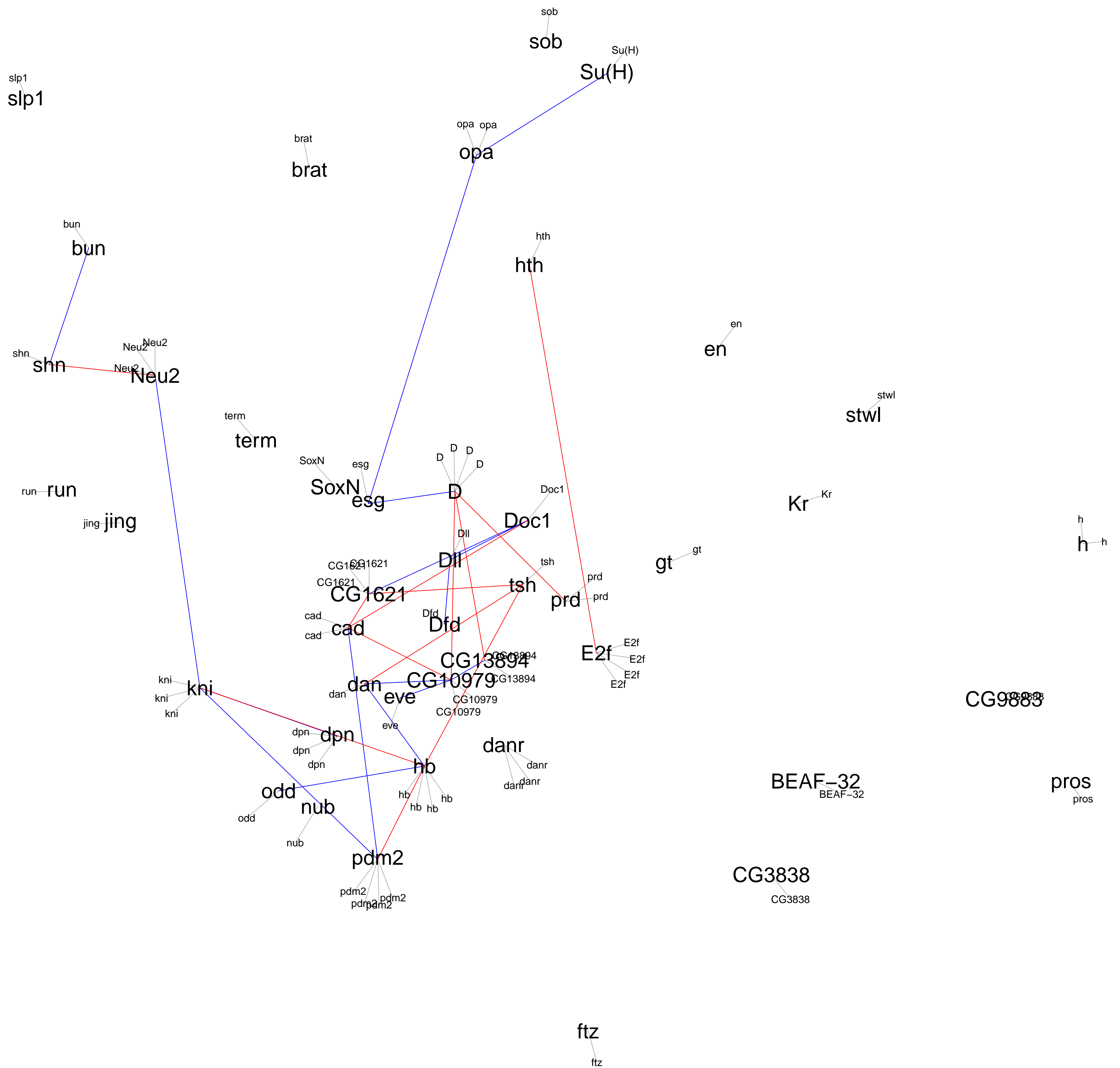
**Lower [3%,3.5%] correlation = [-0.59,-0.58]; Upper [3.5%,3%] correlation = [0.71,0.73]**



Lower [2.5%,3%] correlation = [-0.61,-0.59]; Upper [3%,2.5%] correlation = [0.73,0.74]



**Lower [2%,2.5%] correlation = [-0.63,-0.61]; Upper [2.5%,2%] correlation = [0.74,0.76]**



The diagram illustrates a complex gene regulatory network. Key features include:

- Central Cluster:** A dense network of genes including *SoxN*, *D*, *Dll*, *Dfd*, *Doc1*, *tsh*, *prd*, *E2f*, *dan*, *eve*, *hb*, *danr*, *odd*, *nub*, *pdm2*, and *kni*. These are interconnected by numerous red and blue lines.
- Peripheral Clusters:**
  - slp1*, *bun*, *shn*, *Neu2*, *brat*, *opa*, *hth*, *en*, *stwl*, *Kr*, *h*, *gt*, *BEAF-32*, *CG3838*, *CG9883*, *pros*, *ftz*, and *CG1621* are located around the periphery, often with fewer connections.
- Interaction Types:** Red lines represent strong or direct regulatory interactions, while blue lines represent weaker or indirect interactions.
- Layout:** The network is organized in a way that groups related genes together, with a central hub-and-spoke structure and several peripheral nodes.



The diagram illustrates a complex gene regulatory network. The top section shows a series of genes and transcription factors, including *slp1*, *bun*, *shn*, *Neu2*, *brat*, *opa*, *hth*, *sob*, *Su(H)*, *en*, *stwl*, and *Kr*. The bottom section features a dense cluster of genes and transcription factors, including *SoxN*, *esg*, *D*, *Dll*, *Doc1*, *tsh*, *prd*, *gt*, *E2f*, *dan*, *eye*, *hb*, *danr*, *odd*, *nub*, *pdm2*, *kni*, *dpn*, *cad*, *CG1621*, *CG13894*, *CG10979*, *CG9883*, *BEAF-32*, *CG3838*, *ftz*, and *pros*. Red lines indicate activation, and blue lines indicate repression. The bottom section is highly interconnected, with many genes having multiple connections.



The diagram illustrates a complex gene regulatory network. Nodes represent genes or transcription factors, and edges represent regulatory interactions. The network is highly interconnected, with many nodes having multiple incoming and outgoing edges. The nodes are arranged in a way that suggests functional clusters or pathways. Key clusters include a central group of genes like SoxN, D, Dfd, tsh, prd, E2f, and a group of genes like kni, dpn, odd, nub, pdm2. Other genes are more isolated, such as slp1, bun, shn, Neu2, brat, opa, hth, sob, Su(H), en, stwl, Kr, gt, h, CG9883, BEAF-32, CG3838, and pros. The edges are colored (red, blue, black) to indicate different types of regulatory relationships.