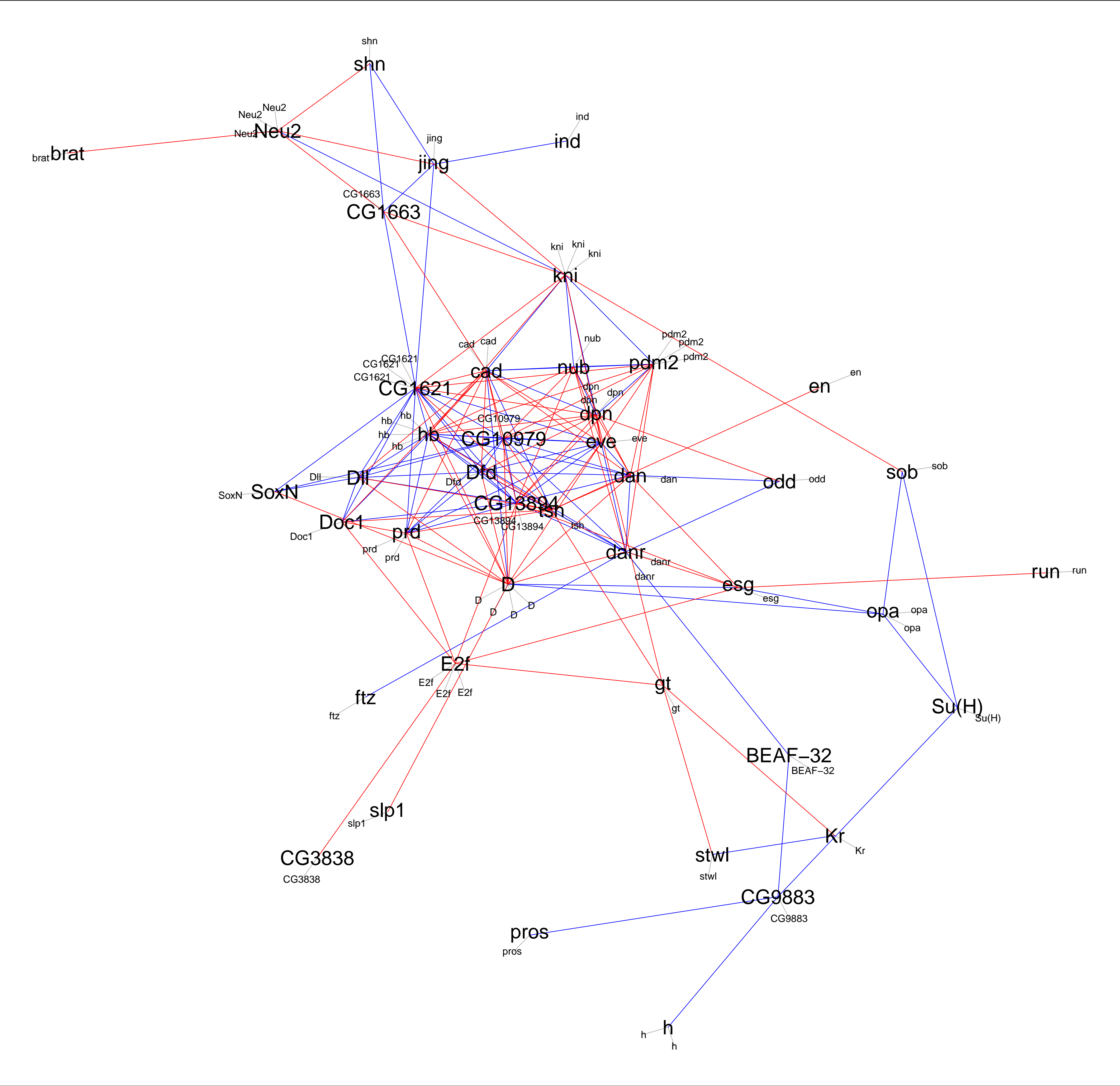
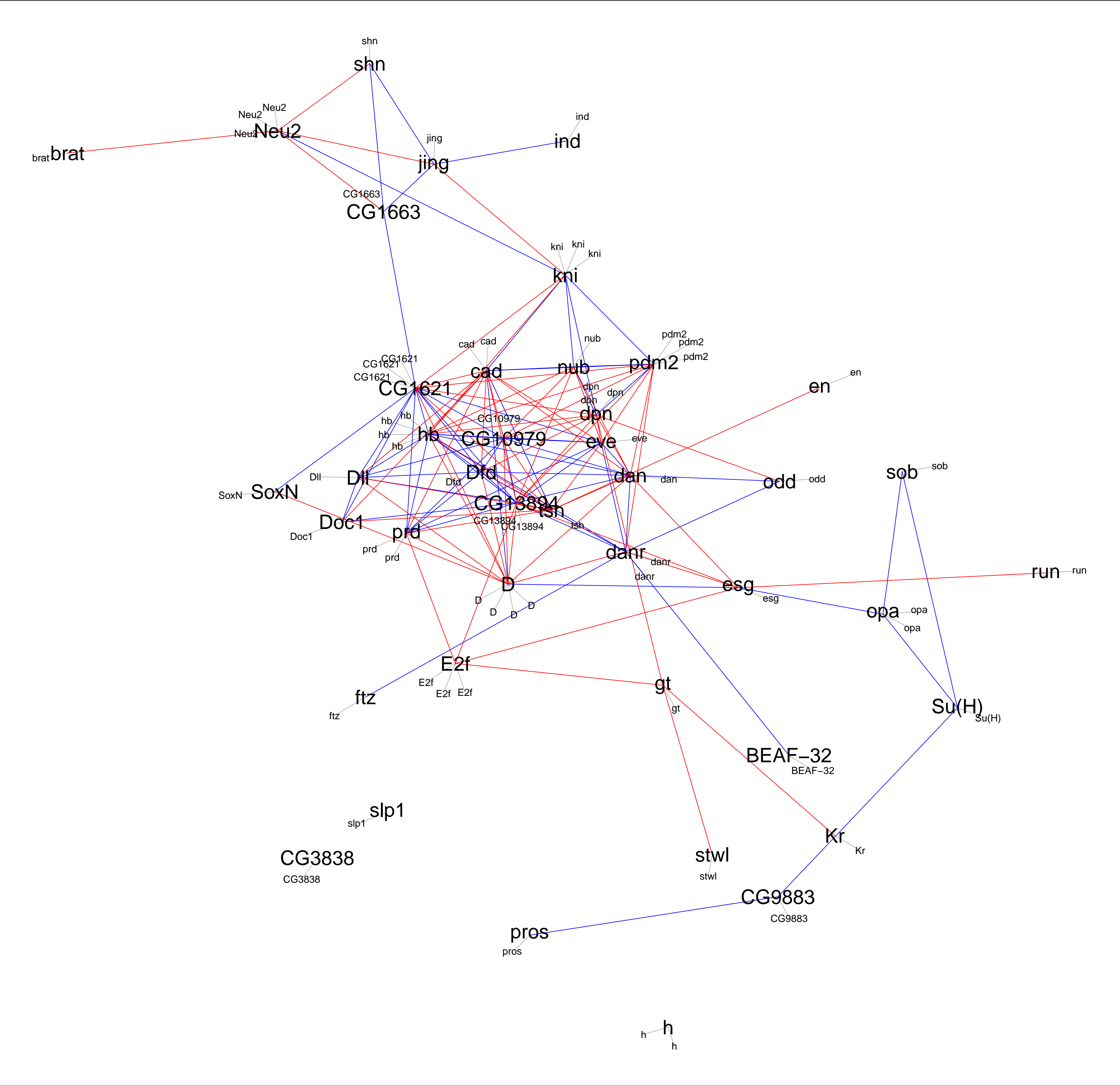


Lower 4.5% correlation = -0.51; upper 4.5% correlation = 0.66



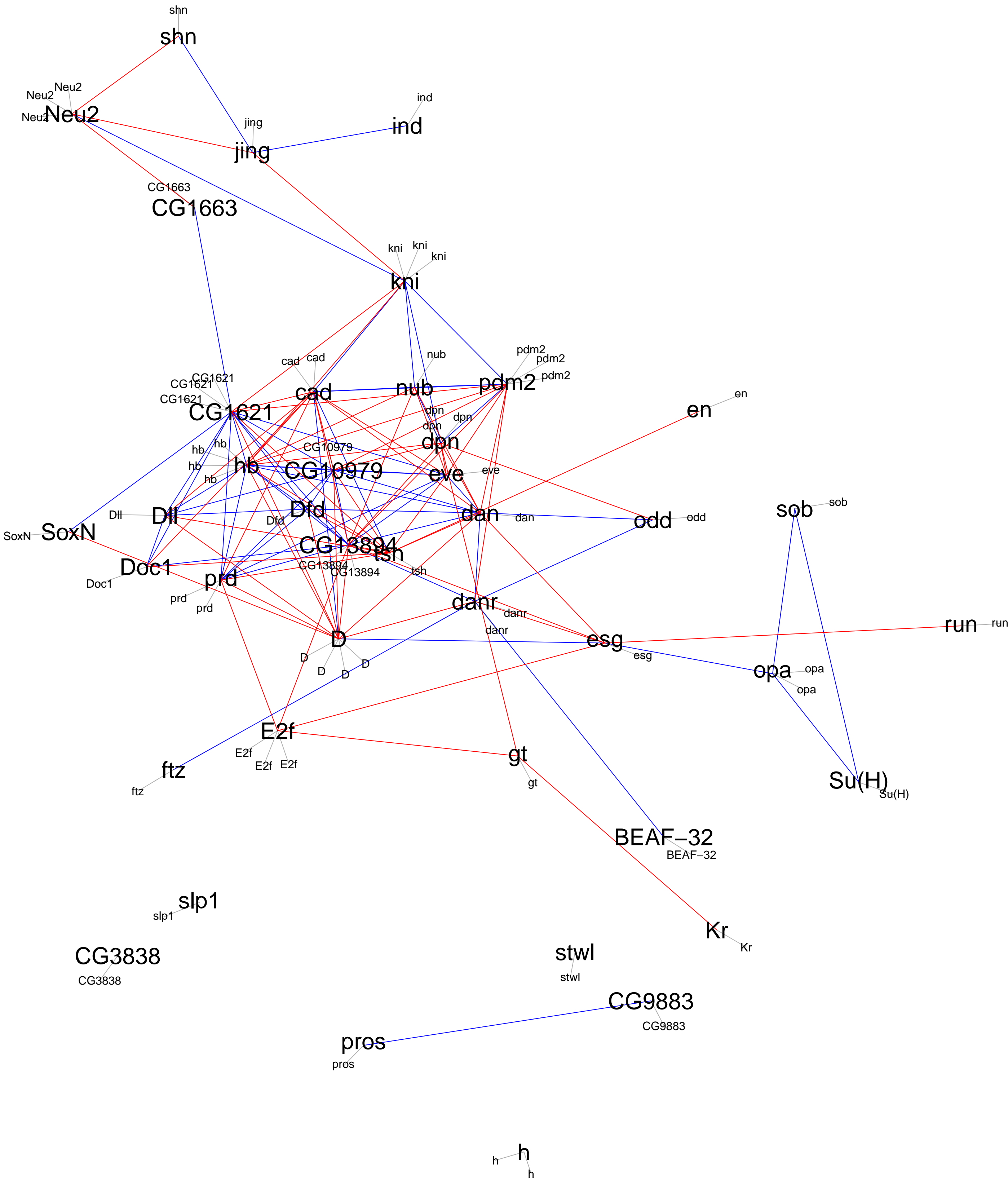
The diagram illustrates a complex gene regulatory network. Nodes represent genes or transcription factors, and the lines represent regulatory interactions. The network is highly interconnected, with many nodes having multiple connections. The nodes are labeled with gene names, and the interactions are color-coded: red lines and blue lines. The network shows a central cluster of genes with many connections, and several peripheral genes with fewer connections. The genes are arranged in a way that suggests functional groups or clusters. The network is a visual representation of the complex regulatory pathways that control gene expression during development.

Lower 3.5% correlation = -0.54; upper 3.5% correlation = 0.69



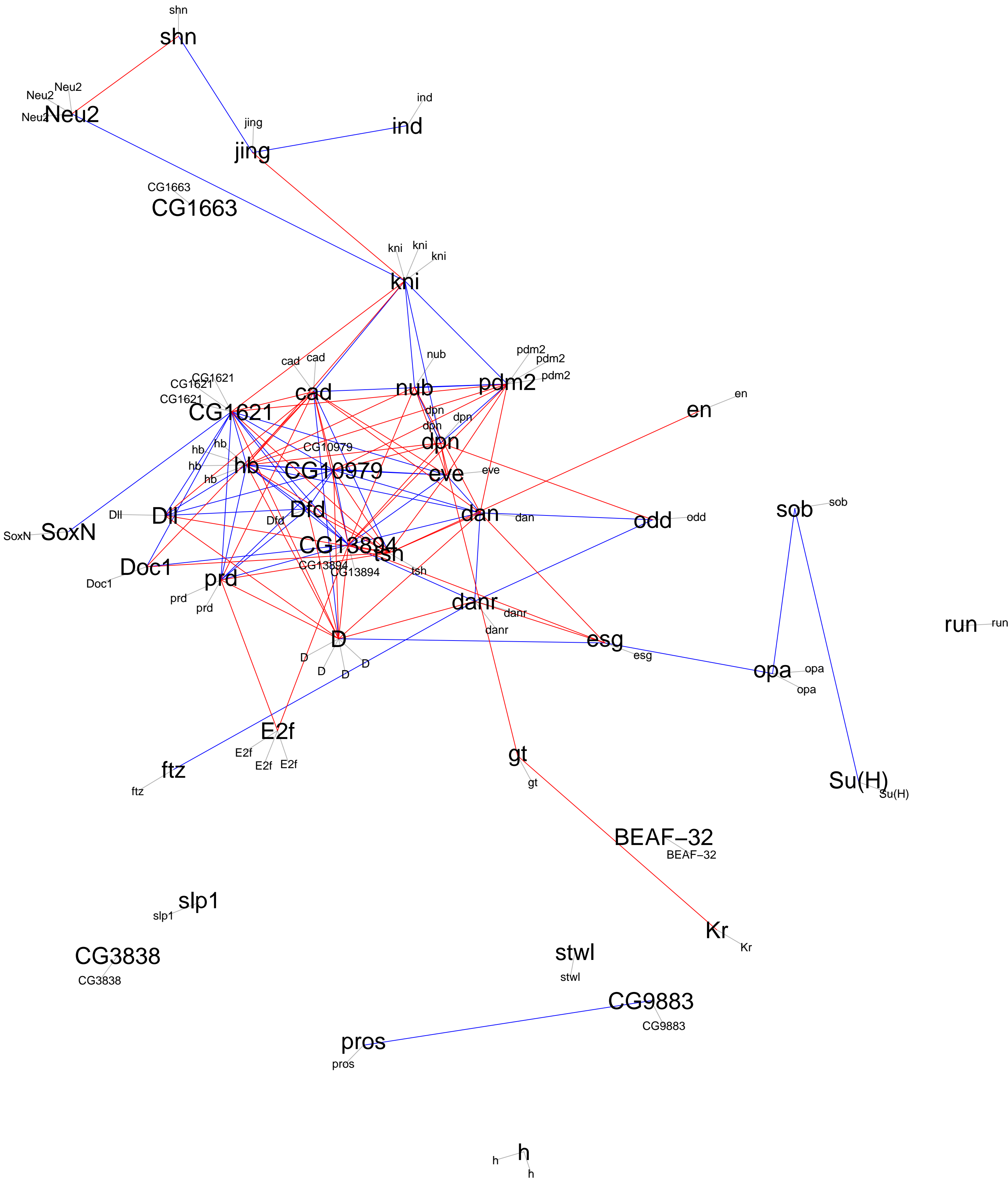
Lower 3% correlation = -0.56; upper 3% correlation = 0.7

brat



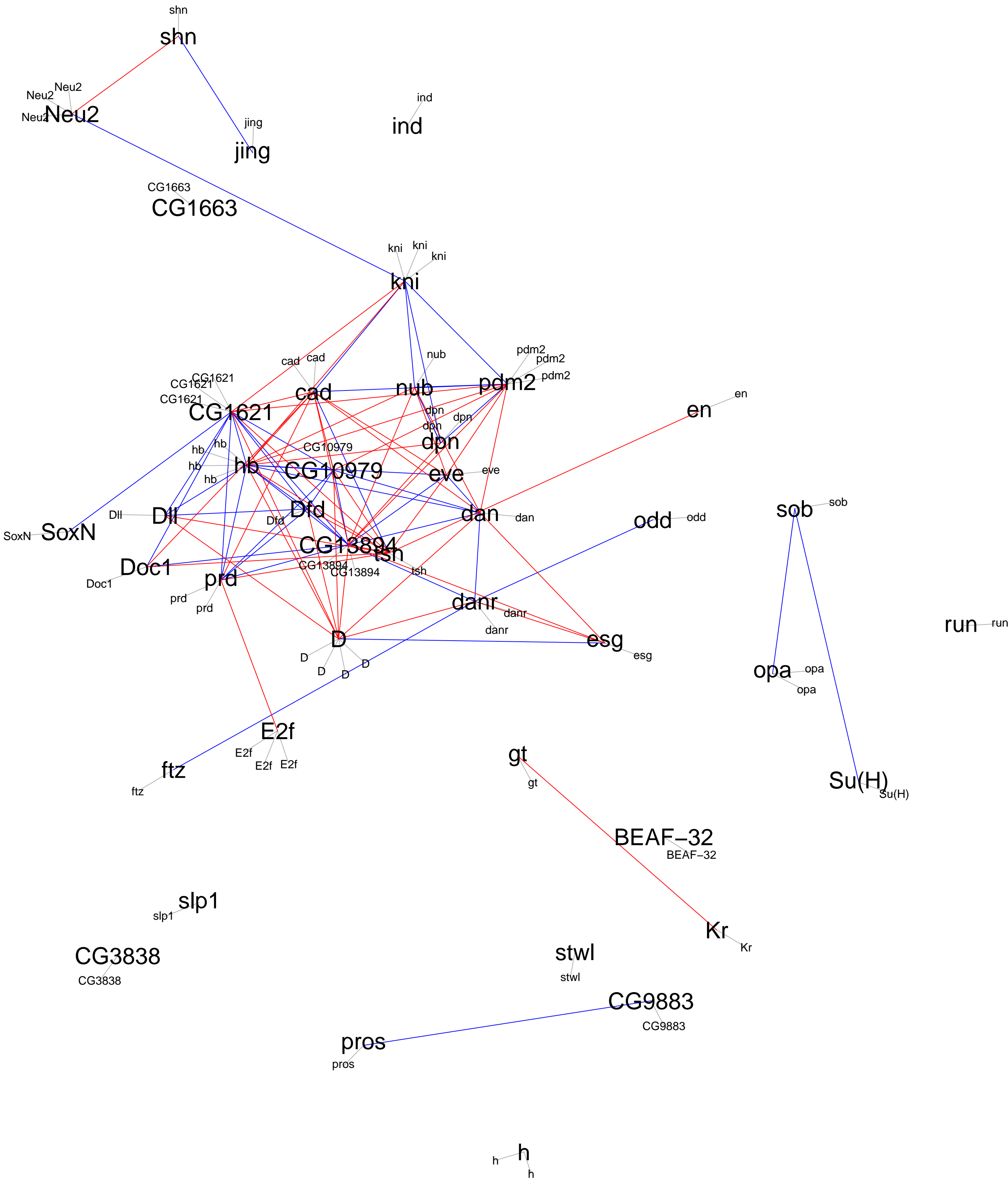
Lower 2.5% correlation = -0.57; upper 2.5% correlation = 0.72

brat

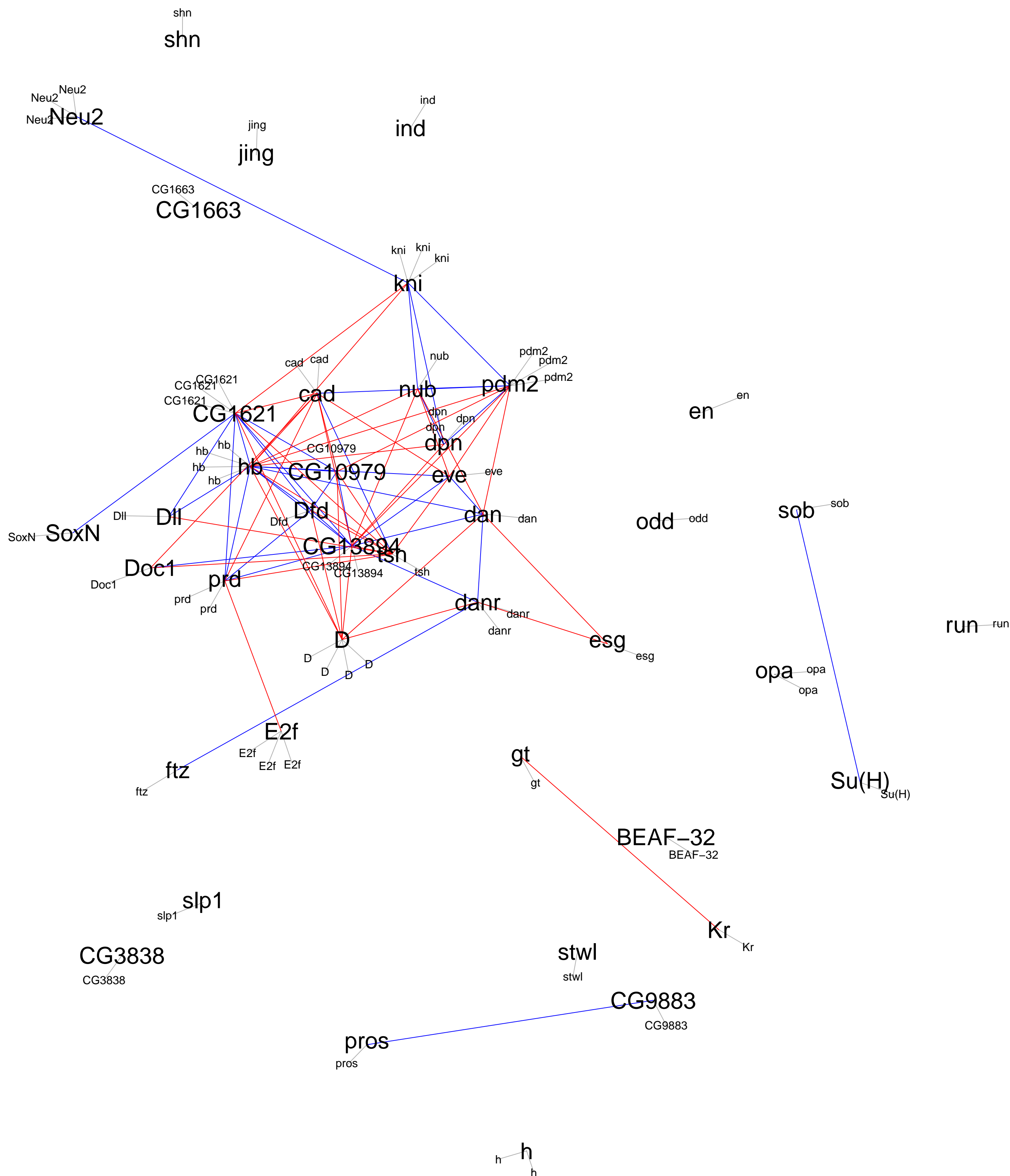


Lower 2% correlation = -0.59; upper 2% correlation = 0.74

brat



bratbrat



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

- Central Cluster (Red Nodes):** A dense network of transcription factors including *cad*, *nub*, *pdm2*, *dpn*, *eve*, *dan*, *danr*, *tsh*, *D*, and *Dfd*, interconnected by numerous red lines.
- Blue Connections:** Nodes like *kni*, *hb*, and *CG10979* are connected to the central cluster via blue lines.
- Peripheral Clusters:**
 - Top:** *shn*, *jing*, *ind*, and *CG1663*.
 - Left:** *SoxN*, *Doc1*, and *DII*.
 - Right:** *en*, *odd*, *sob*, *run*, *opa*, *Su(H)*, and *Kr*.
 - Bottom:** *gt*, *BEAF-32*, *stwl*, *CG9883*, *pros*, *h*, and *ftz*.
- Regulatory Pathways:** A prominent red line connects *gt* to *BEAF-32* and *Kr*. Another red line connects *D* to *Dfd*.