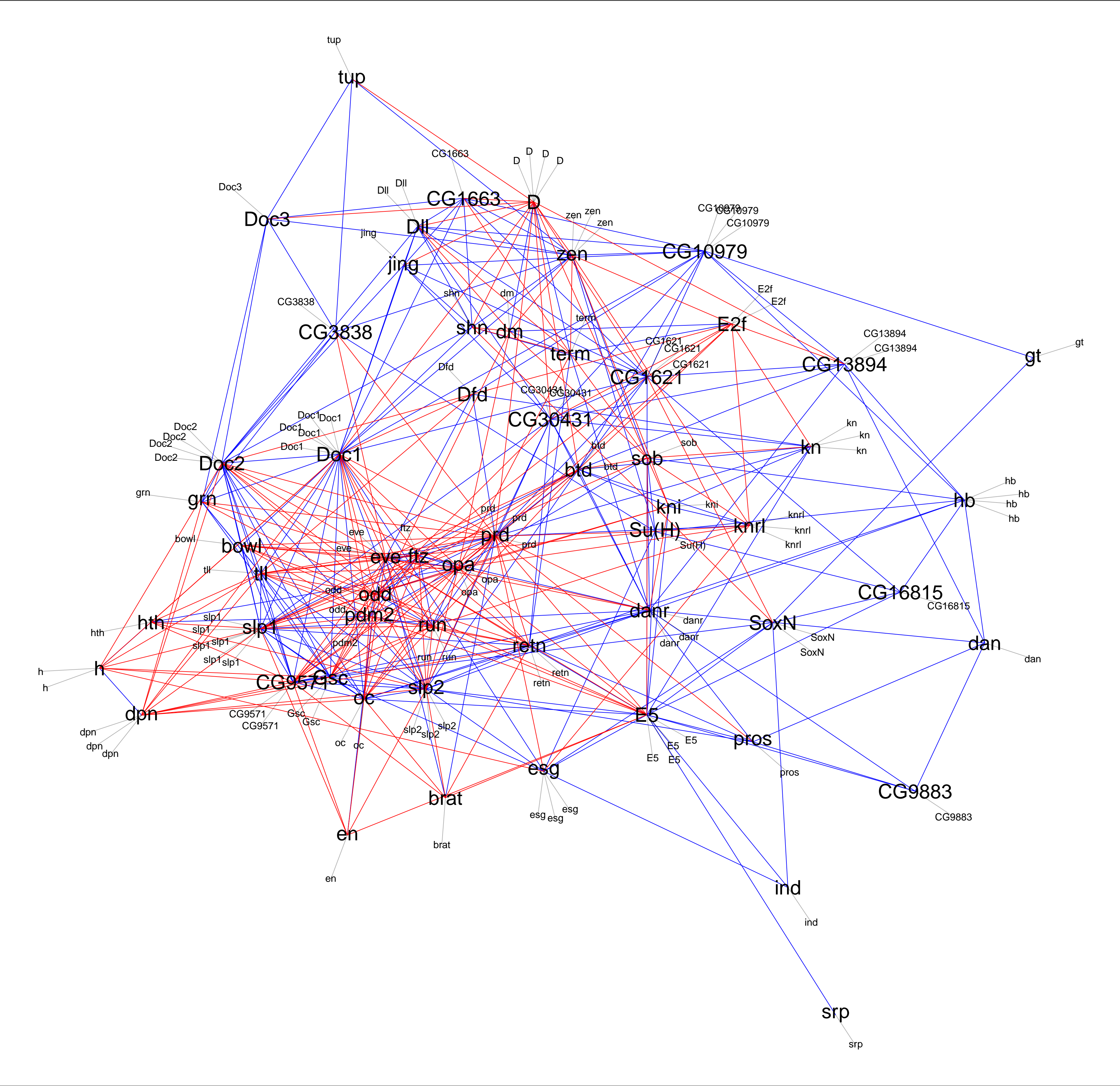


Lower 5% correlation = -0.47; upper 5% correlation = 0.65

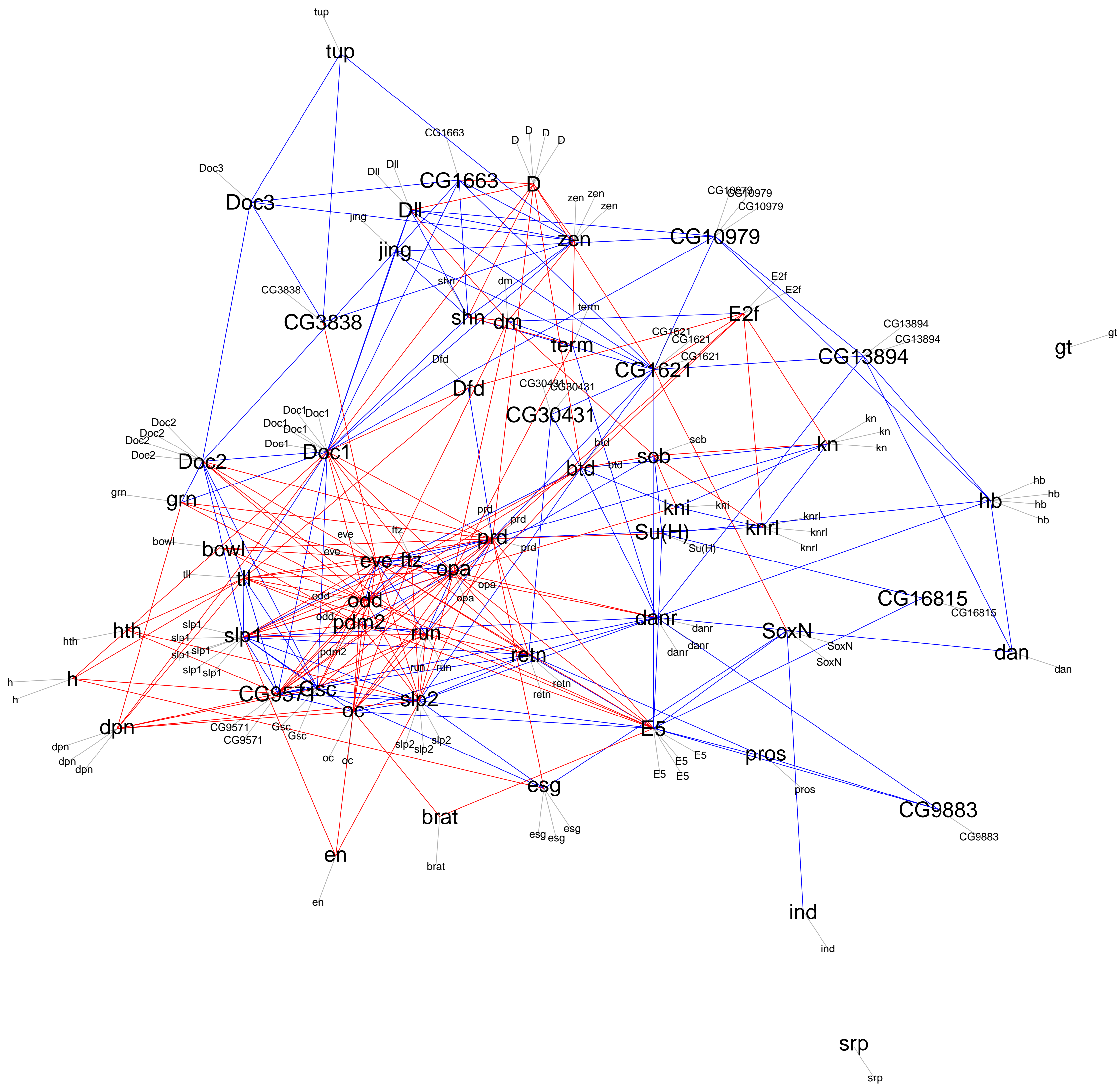


The diagram illustrates a complex network of interactions between various genes and proteins. The nodes are labeled with names such as Doc1, Doc2, Doc3, D, Dfd, E2f, E5, SoxN, and many others. The edges are colored red and blue, representing different types of interactions. The network is highly interconnected, with many nodes having multiple connections. Some nodes are highlighted in red, including D, Dfd, and E5. The layout is dense, with nodes clustered together and many overlapping edges.

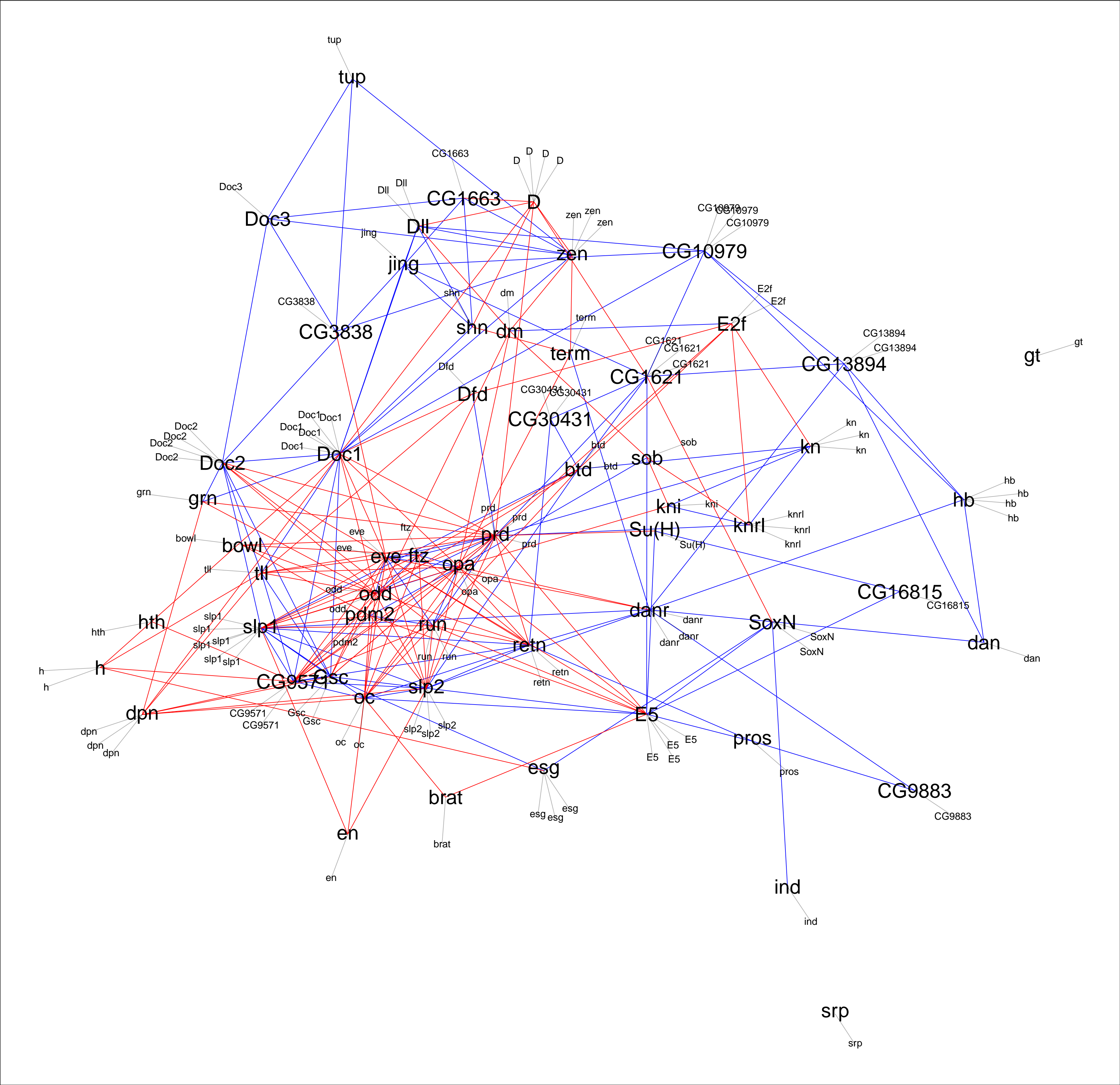
[illegible]

[illegible]

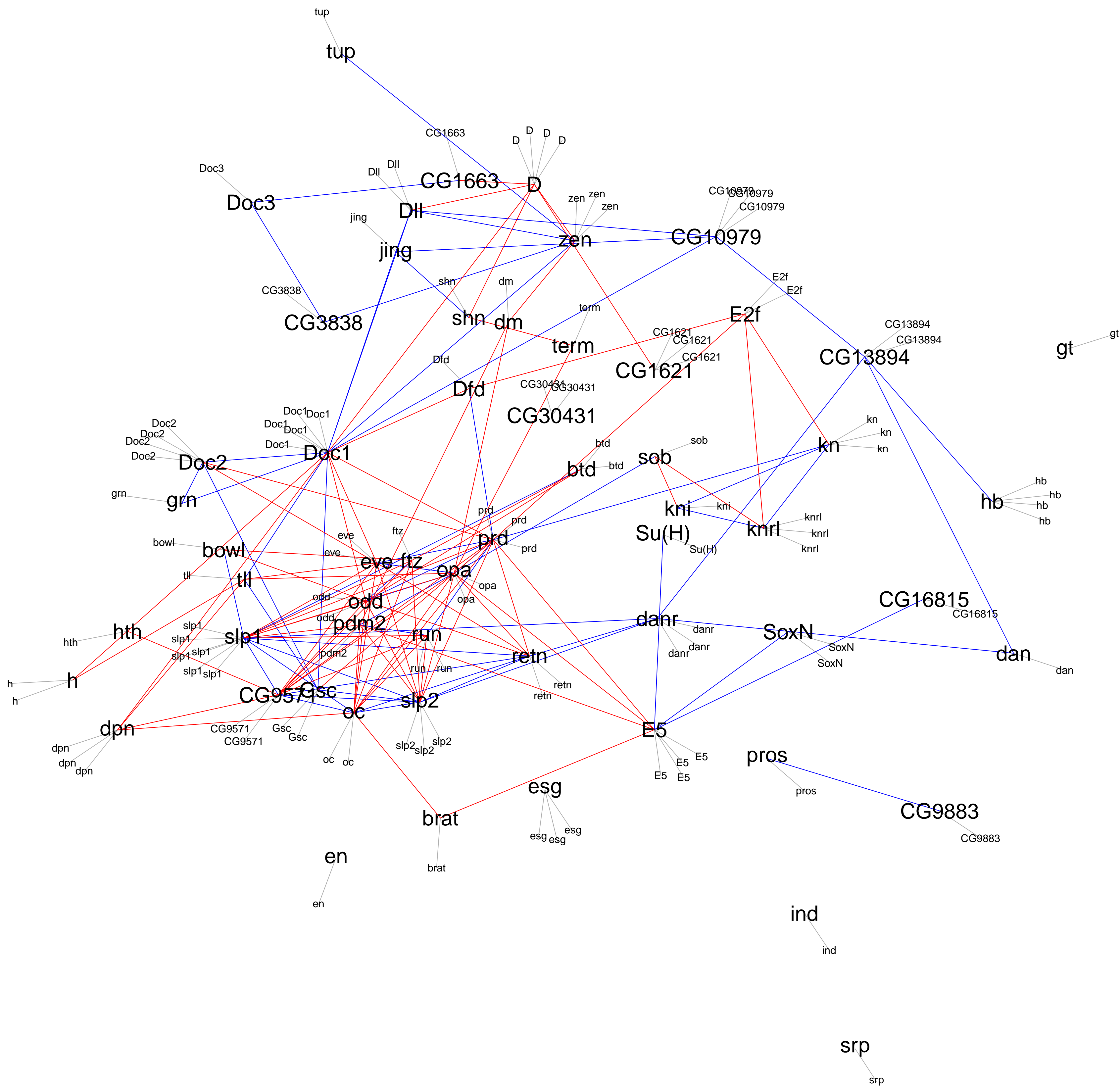
Lower 3% correlation = -0.53; upper 3% correlation = 0.7



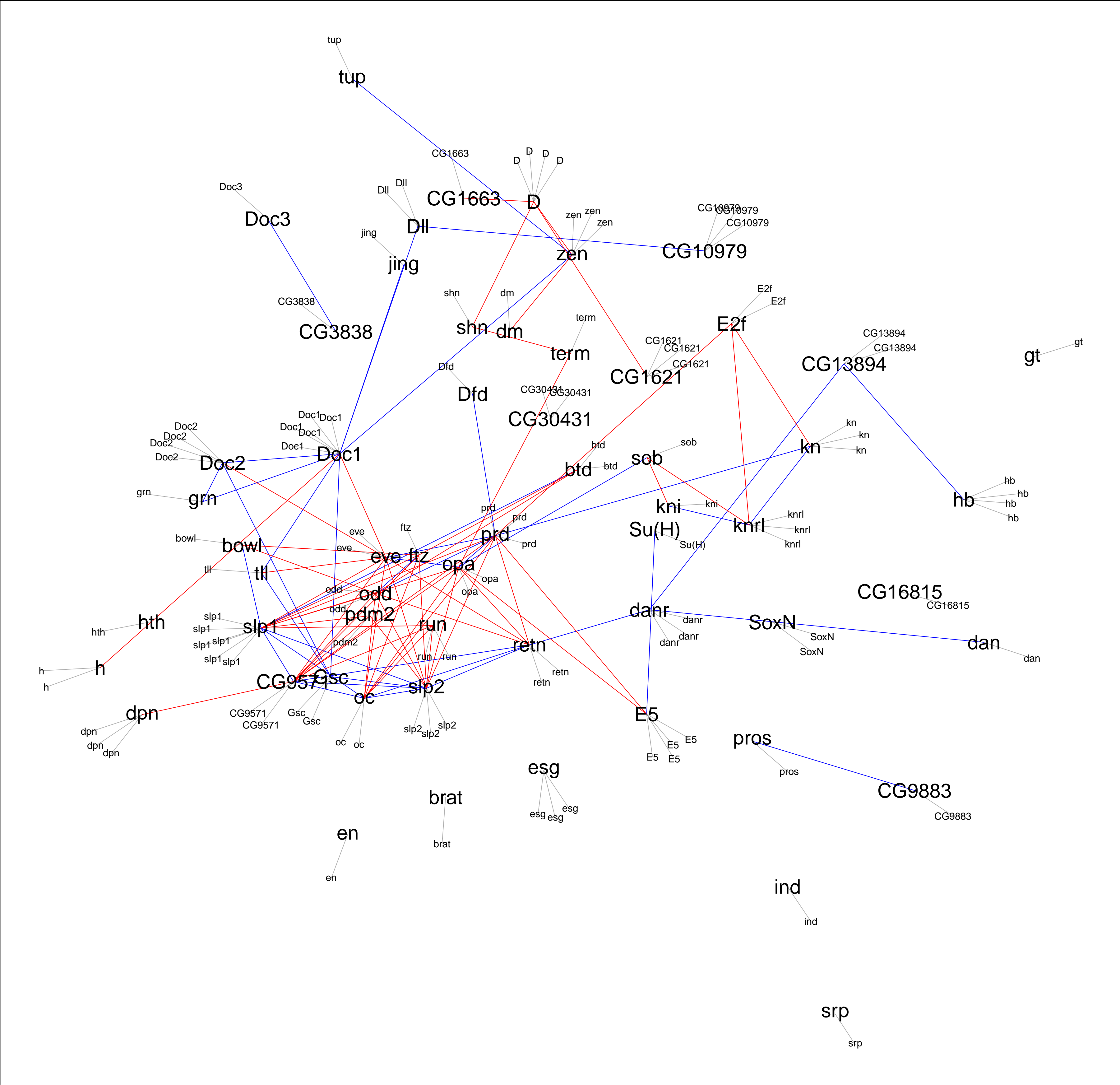
Lower 2.5% correlation = -0.55; upper 2.5% correlation = 0.72



Lower 1.5% correlation = -0.6; upper 1.5% correlation = 0.76



Lower 1% correlation = -0.64; upper 1% correlation = 0.79



The diagram illustrates a complex gene regulatory network. It features a central cluster of red nodes, including **D**, **zen**, **shn**, **dm**, **term**, **btd**, **opa**, **prd**, **run**, **retn**, and **odd**, which are interconnected by red lines. Surrounding this central hub are several clusters of blue nodes, such as **Doc1**, **Doc2**, **grn**, **bowl**, **tll**, **hth**, **h**, **dpn**, **slp1**, **slp2**, **Gsc**, **oc**, **brat**, **en**, **danr**, **SoxN**, **dan**, **pros**, and **srp**, connected by blue lines. Other nodes, including **tup**, **Doc3**, **CG1663**, **DII**, **jing**, **CG3838**, **CG10979**, **E2f**, **CG13894**, **gt**, **kn**, **hb**, **Su(H)**, **knrl**, **CG16815**, **CG9883**, **ind**, and **esg**, are also present, some with multiple instances or associated with specific genomic coordinates (e.g., CG1663, CG10979, CG3838, CG1621, CG30431, CG9571, CG16815, CG9883). The network is highly interconnected, with many nodes having multiple incoming and outgoing regulatory links.