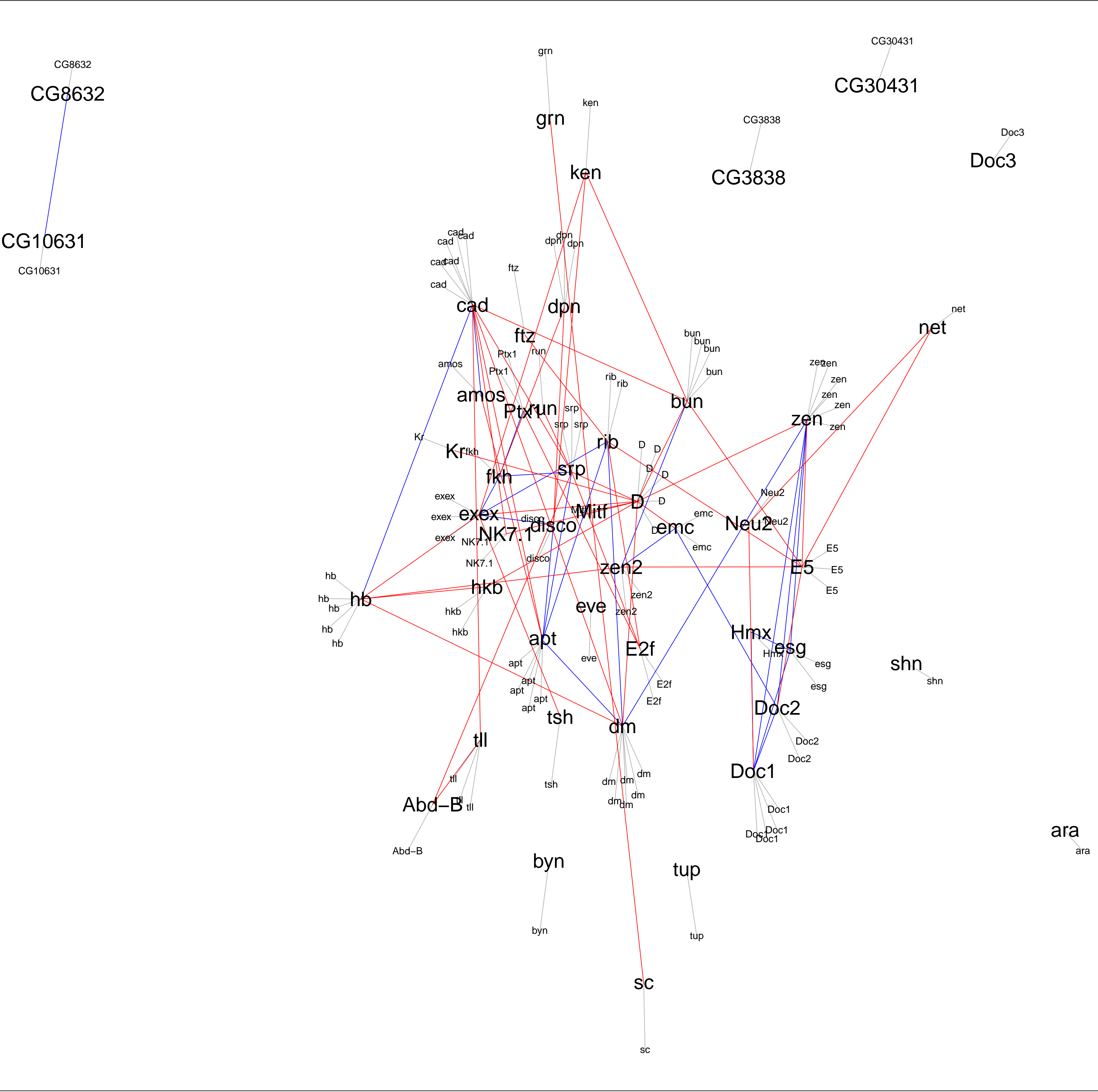
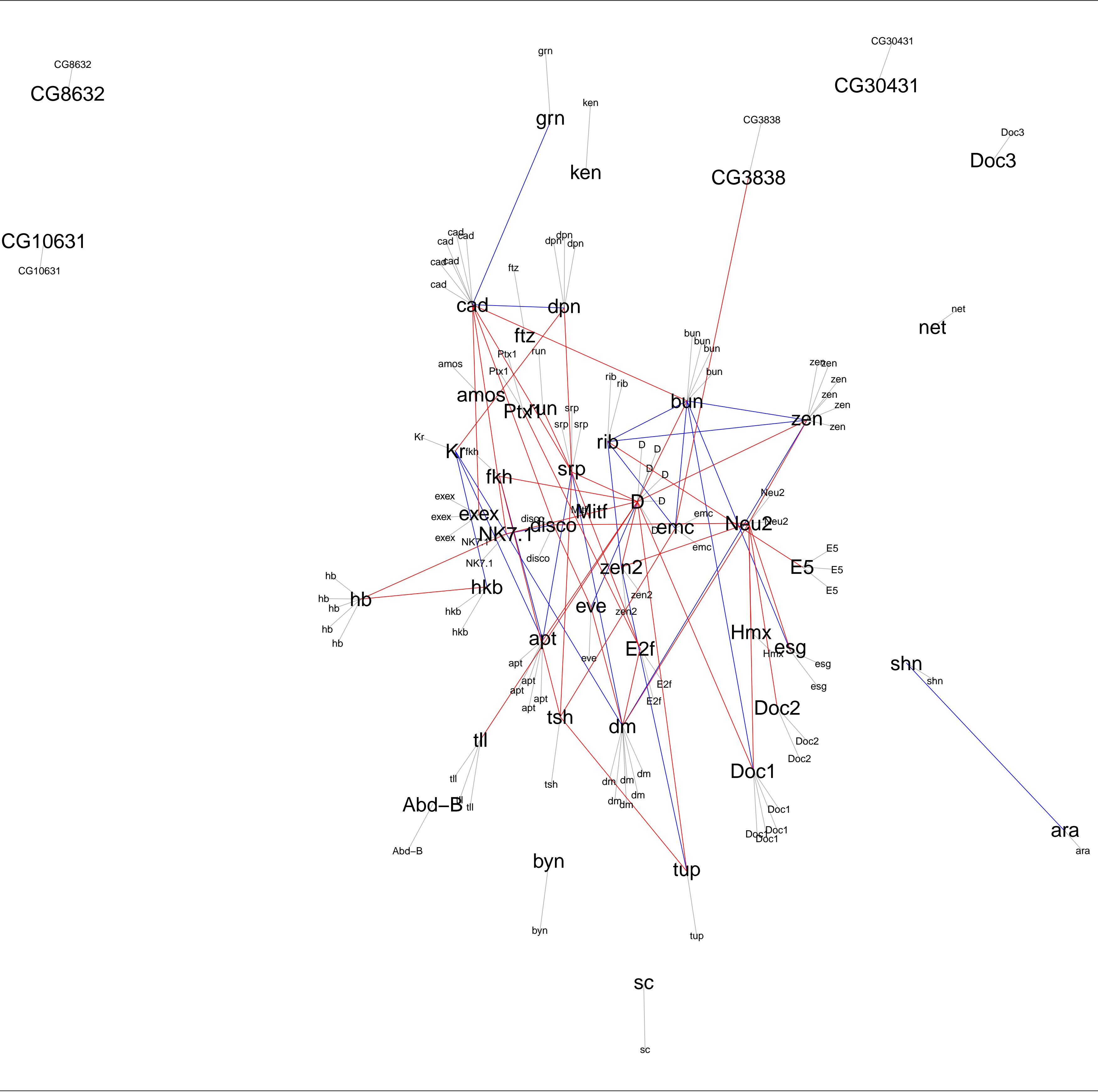


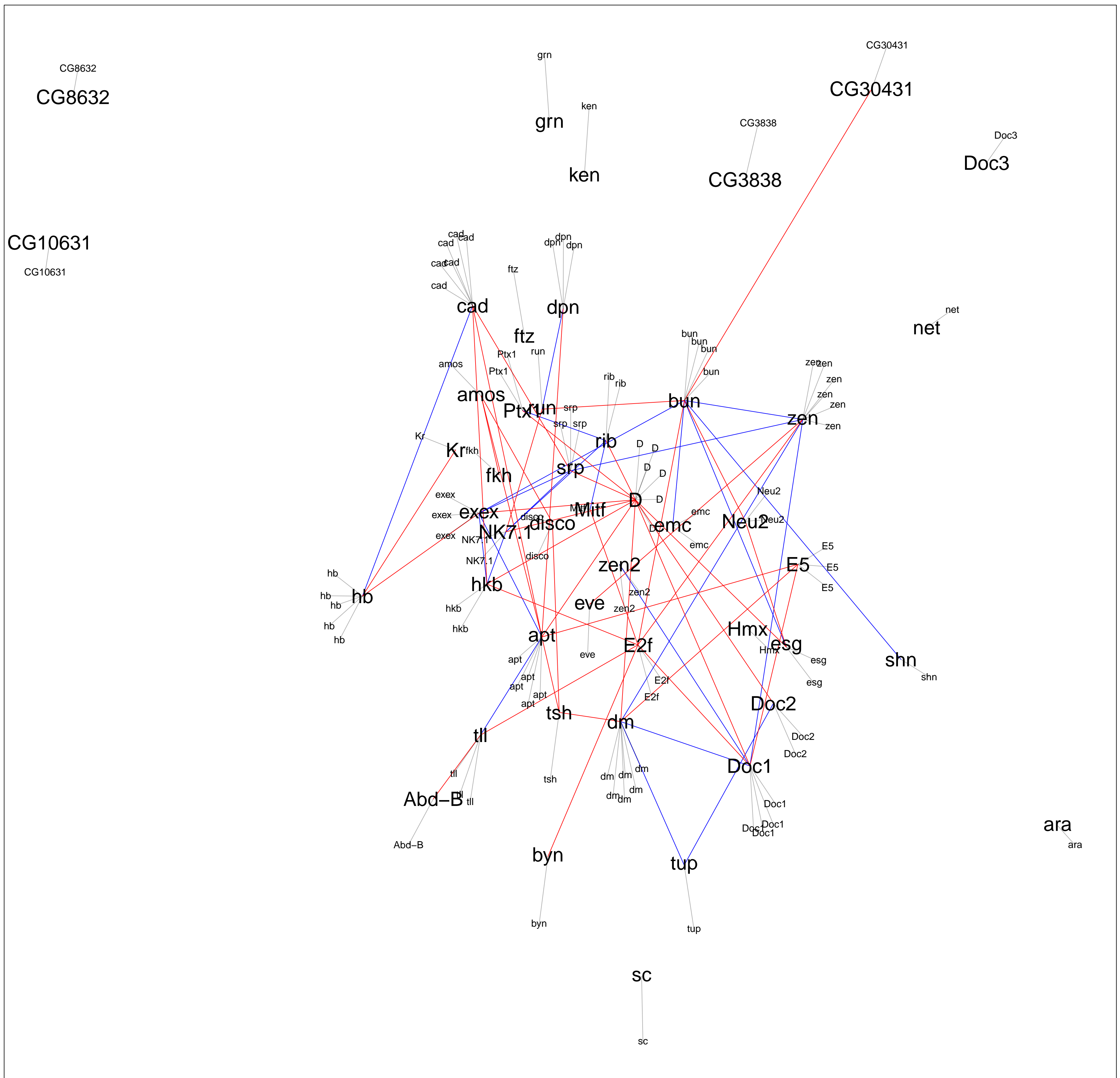
Lower [4.5%,5%] correlation = [-0.53,-0.51]; Upper [5%,4.5%] correlation = [0.77,0.78]



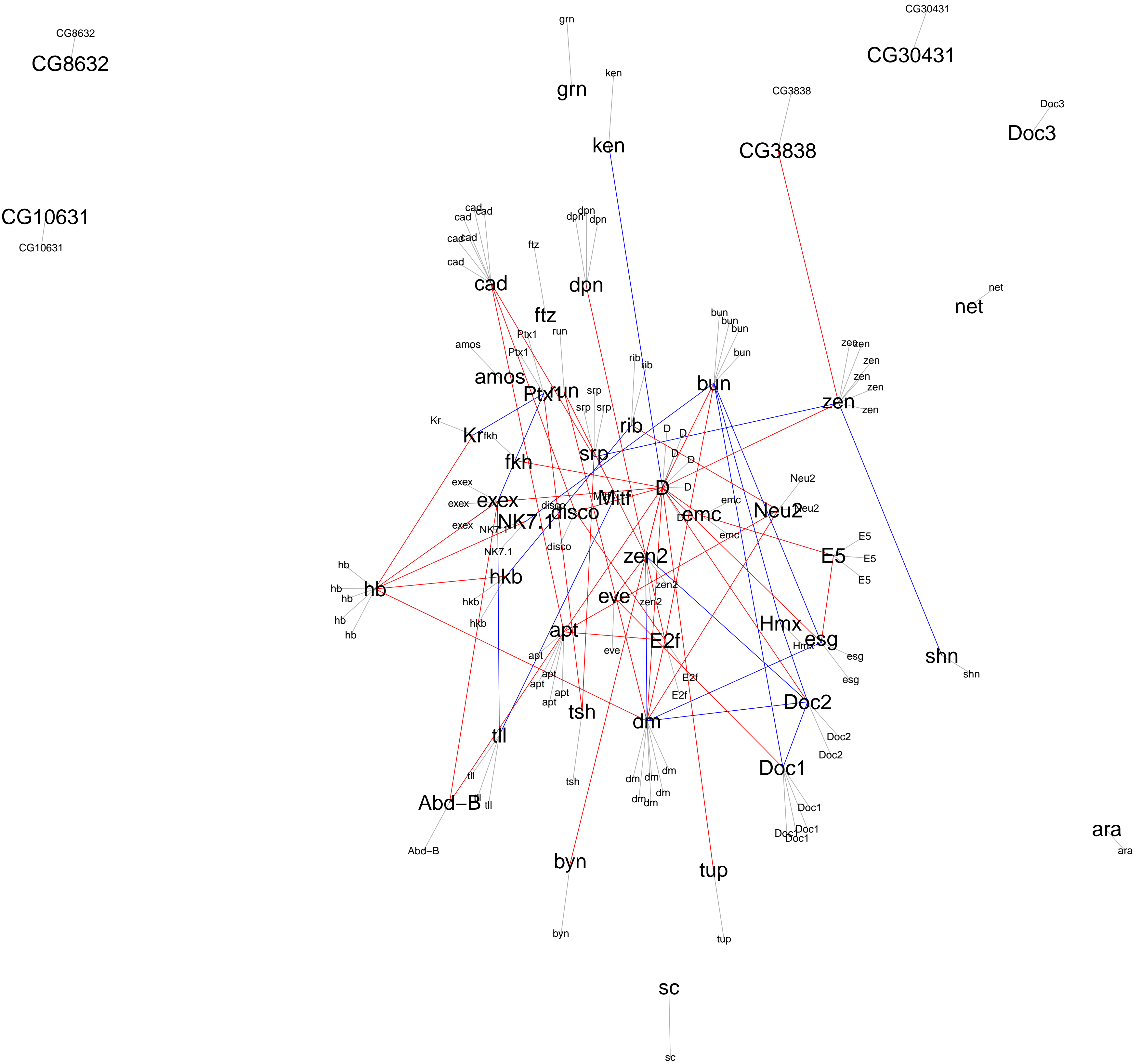
Lower [4%,4.5%] correlation = [-0.54,-0.53]; Upper [4.5%,4%] correlation = [0.78,0.79]



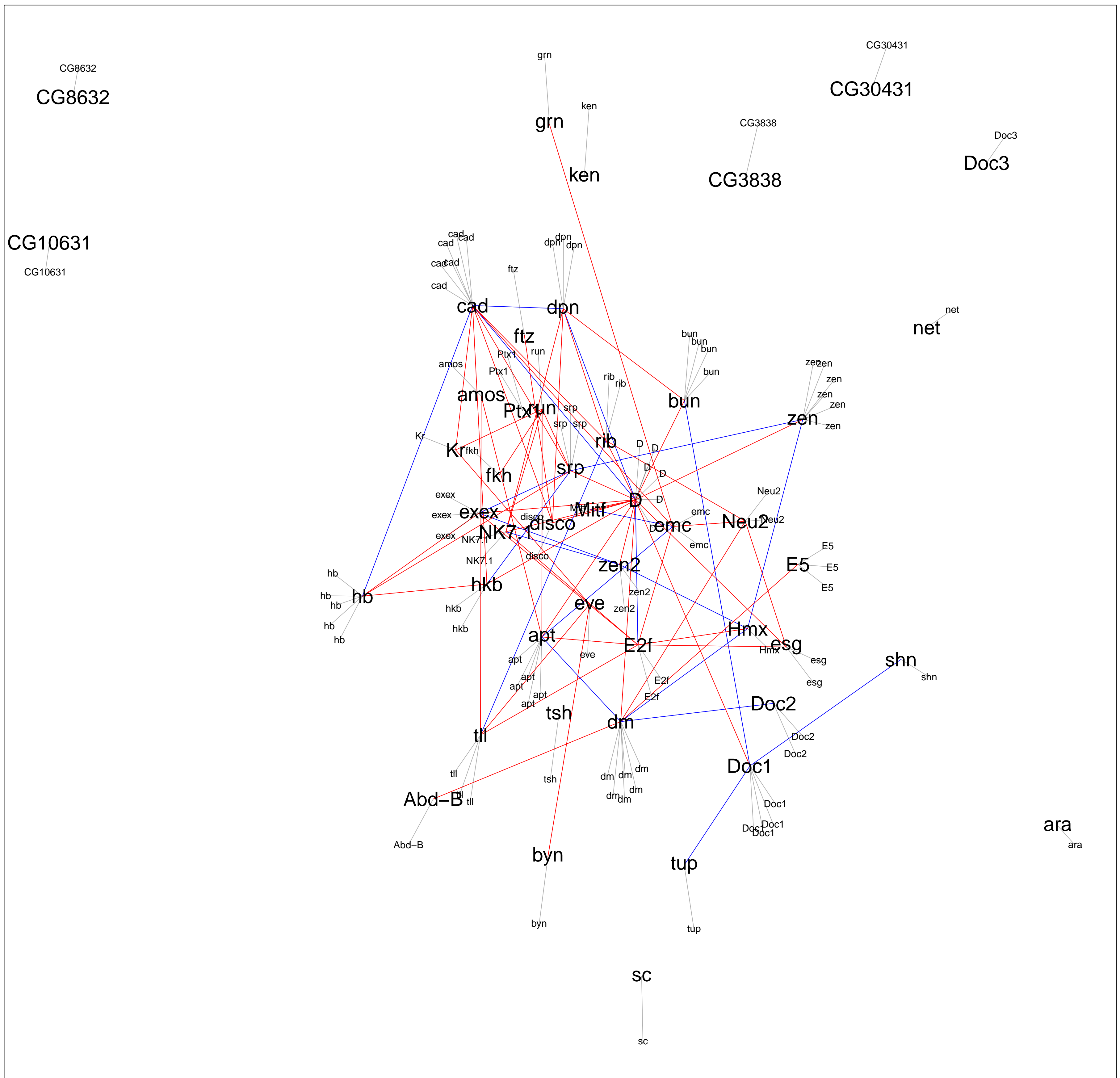
Lower [3.5%,4%] correlation = [-0.56,-0.54]; Upper [4%,3.5%] correlation = [0.79,0.8]



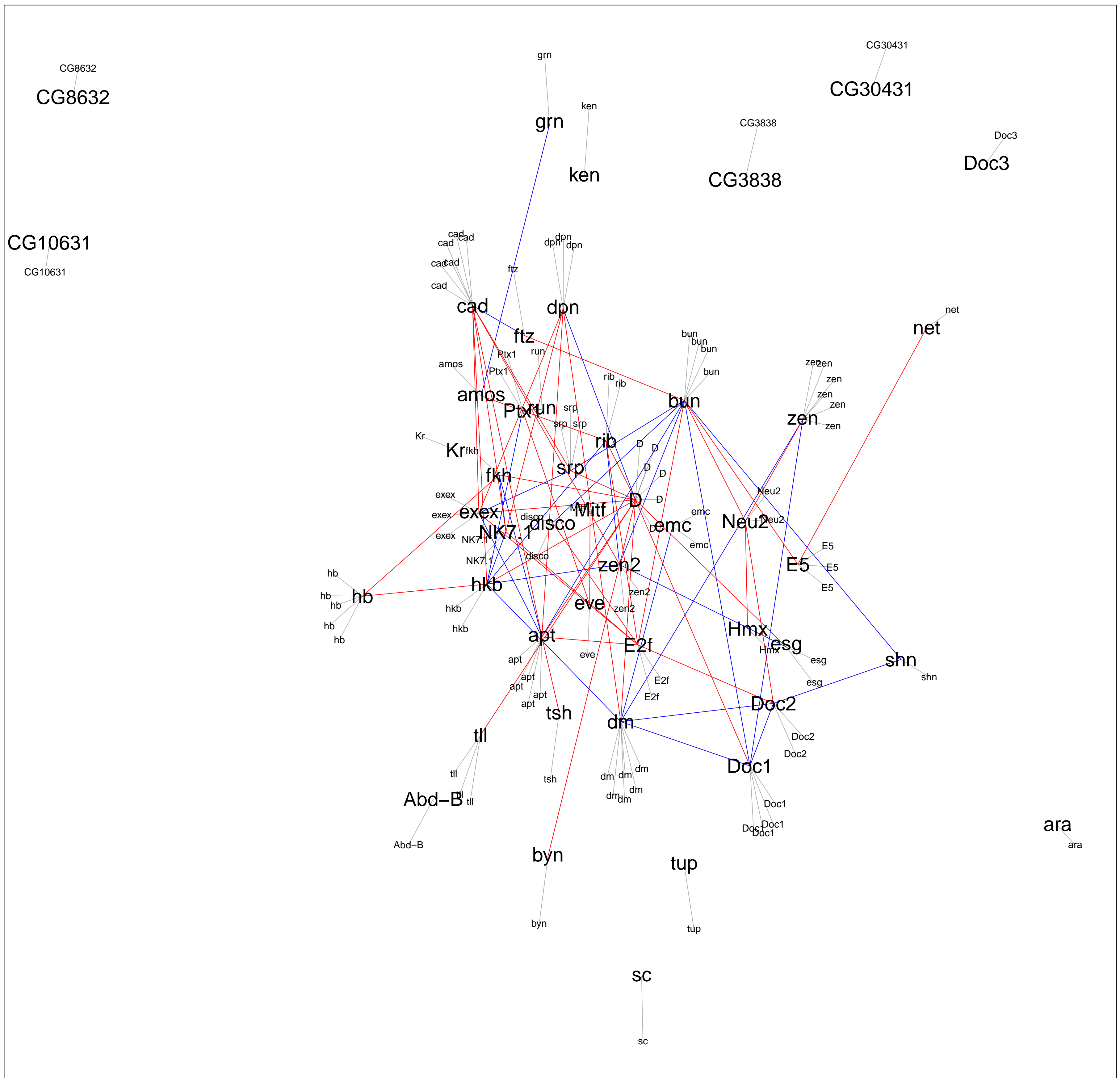
Lower [3%,3.5%] correlation = [-0.58,-0.56]; Upper [3.5%,3%] correlation = [0.8,0.81]



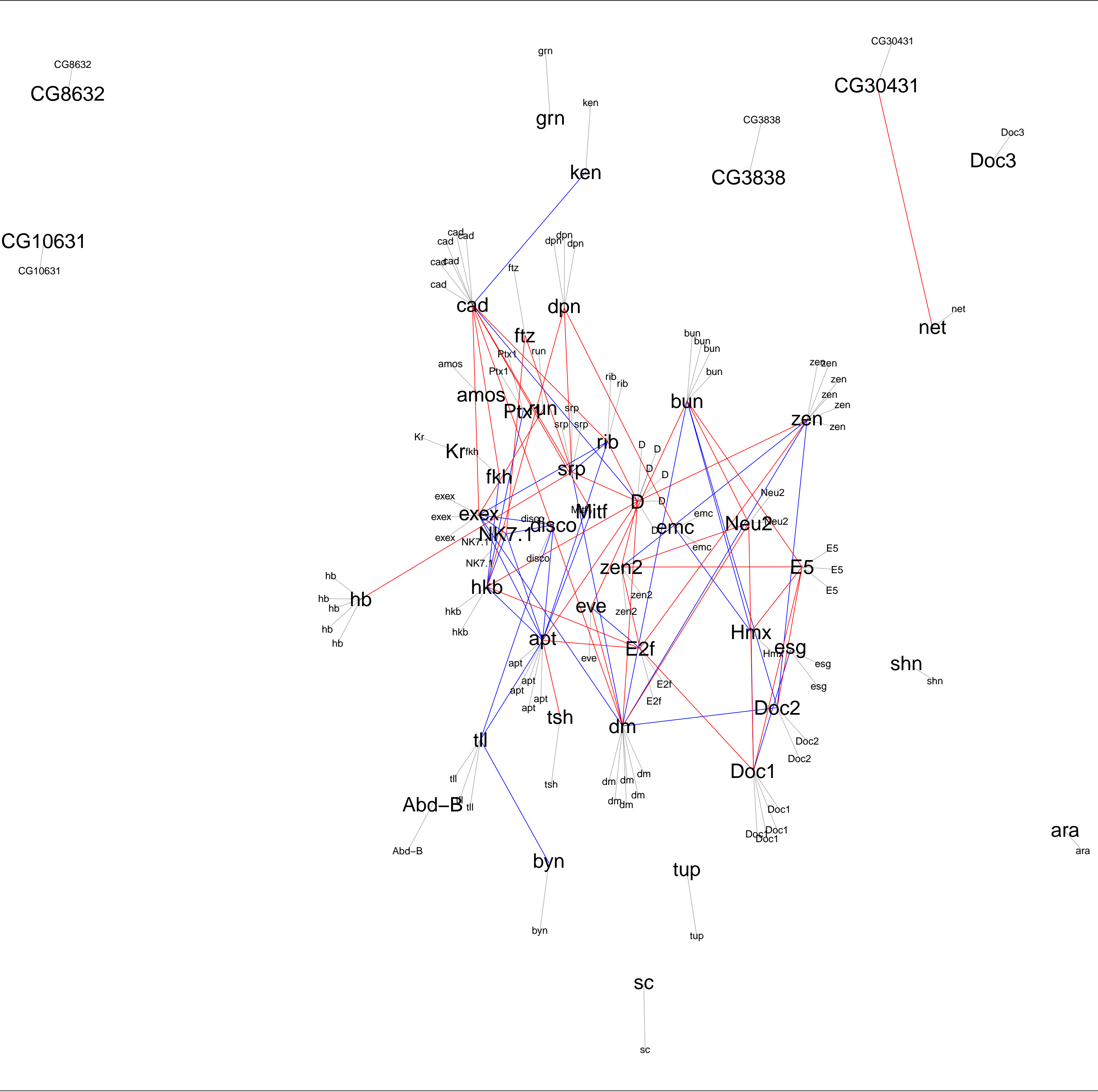
Lower [2.5%,3%] correlation = [-0.6,-0.58]; Upper [3%,2.5%] correlation = [0.81,0.83]



Lower [2%,2.5%] correlation = [-0.62,-0.6]; Upper [2.5%,2%] correlation = [0.83,0.84]



Lower [1.5%,2%] correlation = [-0.65,-0.62]; Upper [2%,1.5%] correlation = [0.84,0.86]



The diagram illustrates a complex gene regulatory network. The network is composed of numerous genes, each represented by a text label. The genes are interconnected by lines of different colors: red, blue, and grey. The network is organized into a hierarchical structure, with genes at the top (e.g., CG8632, CG10631, CG30431, CG3838) and genes at the bottom (e.g., SC, tup, Doc1, Doc2, Doc3). The central part of the network is the most densely connected, with many genes having multiple incoming and outgoing connections. The edges represent regulatory interactions, with the color of the line indicating the type of interaction. The overall layout is a complex web of connections, with some genes acting as hubs and others as peripheral nodes.

Lower [0.5%,1%] correlation = [-0.73,-0.68]; Upper [1%,0.5%] correlation = [0.88,0.9]

