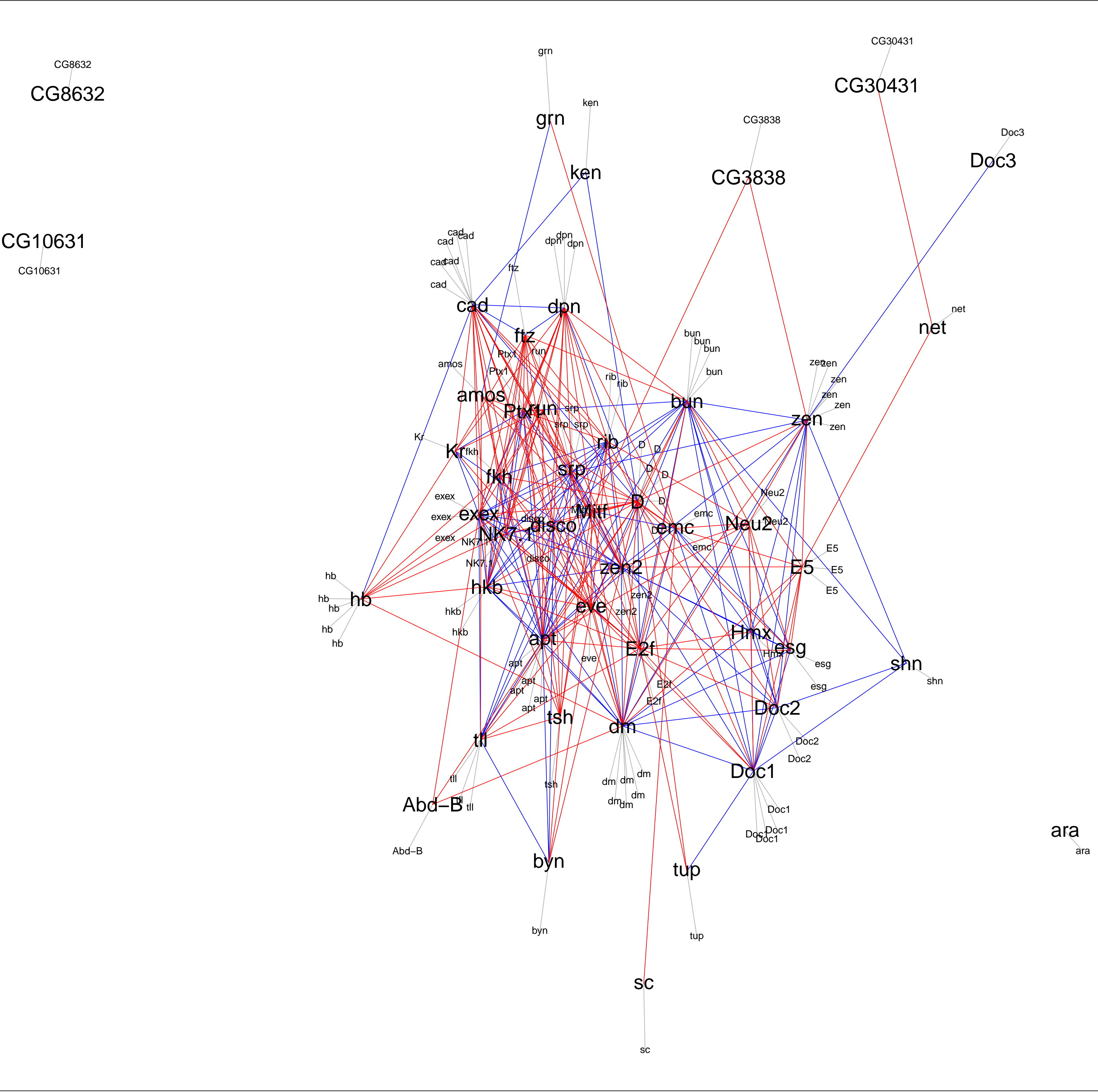


[illegible]

[illegible]

[illegible]

Lower 3.5% correlation = -0.56; upper 3.5% correlation = 0.8

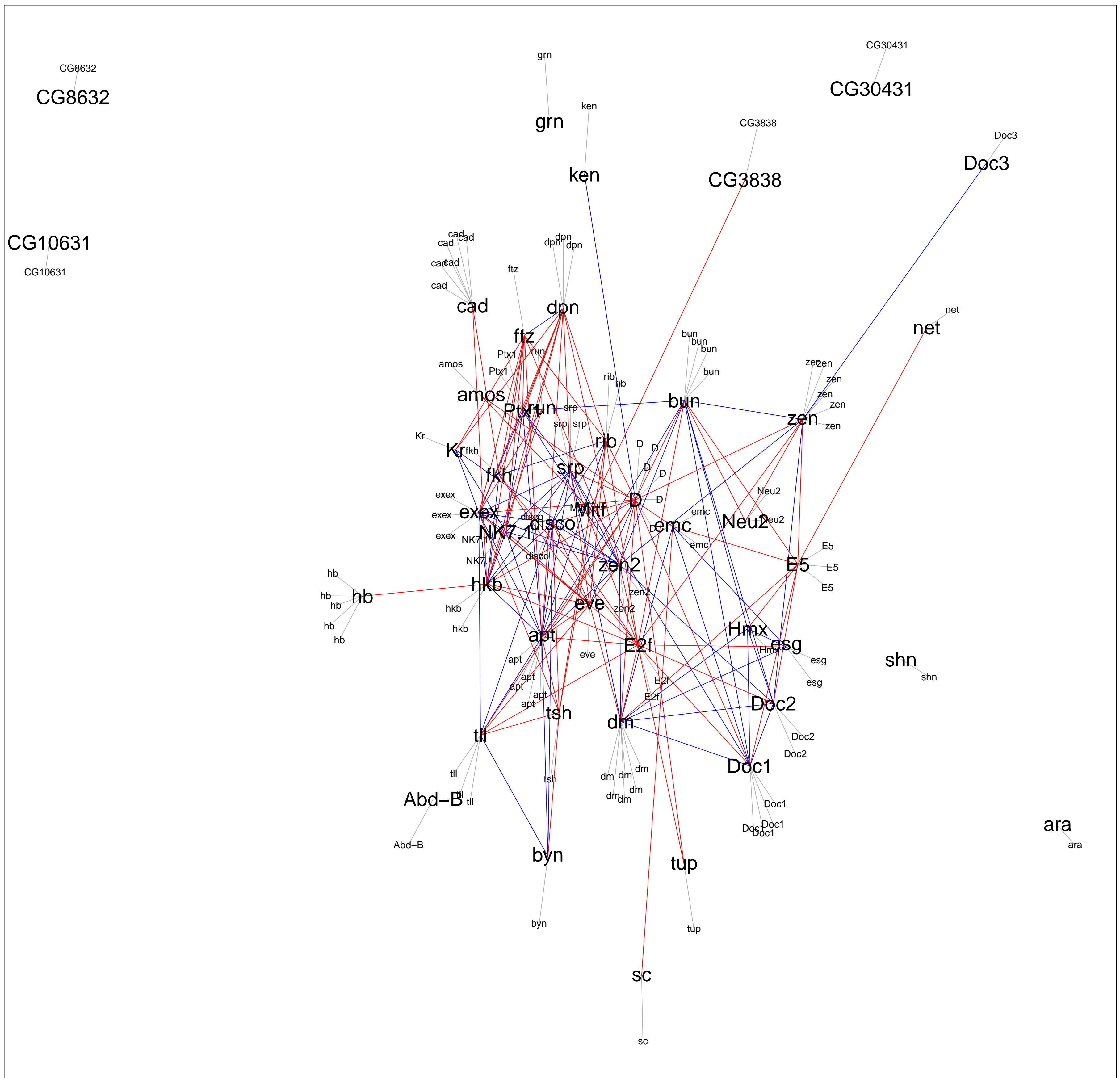


The diagram illustrates a complex gene regulatory network. The central part of the network is a dense cluster of genes, including **cad**, **fkh**, **exex**, **hkb**, **tll**, **dm**, **zen2**, **ap1**, **ap2**, **ap3**, **ap4**, **ap5**, **ap6**, **ap7**, **ap8**, **ap9**, **ap10**, **ap11**, **ap12**, **ap13**, **ap14**, **ap15**, **ap16**, **ap17**, **ap18**, **ap19**, **ap20**, **ap21**, **ap22**, **ap23**, **ap24**, **ap25**, **ap26**, **ap27**, **ap28**, **ap29**, **ap30**, **ap31**, **ap32**, **ap33**, **ap34**, **ap35**, **ap36**, **ap37**, **ap38**, **ap39**, **ap40**, **ap41**, **ap42**, **ap43**, **ap44**, **ap45**, **ap46**, **ap47**, **ap48**, **ap49**, **ap50**, **ap51**, **ap52**, **ap53**, **ap54**, **ap55**, **ap56**, **ap57**, **ap58**, **ap59**, **ap60**, **ap61**, **ap62**, **ap63**, **ap64**, **ap65**, **ap66**, **ap67**, **ap68**, **ap69**, **ap70**, **ap71**, **ap72**, **ap73**, **ap74**, **ap75**, **ap76**, **ap77**, **ap78**, **ap79**, **ap80**, **ap81**, **ap82**, **ap83**, **ap84**, **ap85**, **ap86**, **ap87**, **ap88**, **ap89**, **ap90**, **ap91**, **ap92**, **ap93**, **ap94**, **ap95**, **ap96**, **ap97**, **ap98**, **ap99**, **ap100**. The network is highly interconnected, with many genes having multiple connections. The diagram uses blue and red lines to represent different types of interactions. The central cluster is surrounded by several other genes, including **hb**, **Abd-B**, **byn**, **tup**, **SC**, **ara**, **shn**, **Doc2**, **Doc1**, **esg**, **Hmx**, **E5**, **Neu2**, **emc**, **zen**, **bun**, **rib**, **srp**, **disco**, **exex**, **hkb**, **tll**, **dm**, **zen2**, **ap1**, **ap2**, **ap3**, **ap4**, **ap5**, **ap6**, **ap7**, **ap8**, **ap9**, **ap10**, **ap11**, **ap12**, **ap13**, **ap14**, **ap15**, **ap16**, **ap17**, **ap18**, **ap19**, **ap20**, **ap21**, **ap22**, **ap23**, **ap24**, **ap25**, **ap26**, **ap27**, **ap28**, **ap29**, **ap30**, **ap31**, **ap32**, **ap33**, **ap34**, **ap35**, **ap36**, **ap37**, **ap38**, **ap39**, **ap40**, **ap41**, **ap42**, **ap43**, **ap44**, **ap45**, **ap46**, **ap47**, **ap48**, **ap49**, **ap50**, **ap51**, **ap52**, **ap53**, **ap54**, **ap55**, **ap56**, **ap57**, **ap58**, **ap59**, **ap60**, **ap61**, **ap62**, **ap63**, **ap64**, **ap65**, **ap66**, **ap67**, **ap68**, **ap69**, **ap70**, **ap71**, **ap72**, **ap73**, **ap74**, **ap75**, **ap76**, **ap77**, **ap78**, **ap79**, **ap80**, **ap81**, **ap82**, **ap83**, **ap84**, **ap85**, **ap86**, **ap87**, **ap88**, **ap89**, **ap90**, **ap91**, **ap92**, **ap93**, **ap94**, **ap95**, **ap96**, **ap97**, **ap98**, **ap99**, **ap100**. 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[illegible]

Lower 1.5% correlation = -0.65 ; upper 1.5% correlation = 0.86



The diagram illustrates a complex gene regulatory network. The central part of the image is dominated by a dense web of interconnected gene nodes. These nodes are represented by text labels, and their interactions are shown by colored lines: red, blue, and grey. The network is highly interconnected, with many nodes having multiple connections. The layout is organized such that genes at the periphery are connected to a central hub. Labels like CG8632, CG10631, CG3838, CG30431, Doc3, net, shn, ara, and SC are placed around the network, often with lines pointing to specific nodes or clusters. The network is color-coded: red lines represent one type of interaction, blue lines represent another, and grey lines represent a third. The layout is organized with genes at the periphery connected to a central hub.

The diagram illustrates a complex gene regulatory network. The central cluster contains a dense web of interactions between genes such as *grn*, *ken*, *cad*, *dpn*, *ftz*, *amos*, *Ptx1*, *run*, *srp*, *rib*, *bun*, *zen*, *net*, *exex*, *fkh*, *disco*, *eve*, *apt*, *tsh*, *tll*, *Abd-B*, *byn*, *dm*, *tup*, *SC*, *Hmx*, *Doc1*, *Doc2*, *Doc3*, *E5*, *Neu2*, *emc*, *D*, and *shn*. The network is characterized by a high degree of connectivity, with many genes having multiple incoming and outgoing edges. The edges are color-coded: blue for activation, red for repression, and grey for unknown interactions. The diagram is organized into a hierarchical structure, with a central core of highly interactive genes and several peripheral clusters of genes that are less interconnected. The overall layout is a complex, interconnected web of nodes and edges, representing the intricate regulatory pathways in the system.