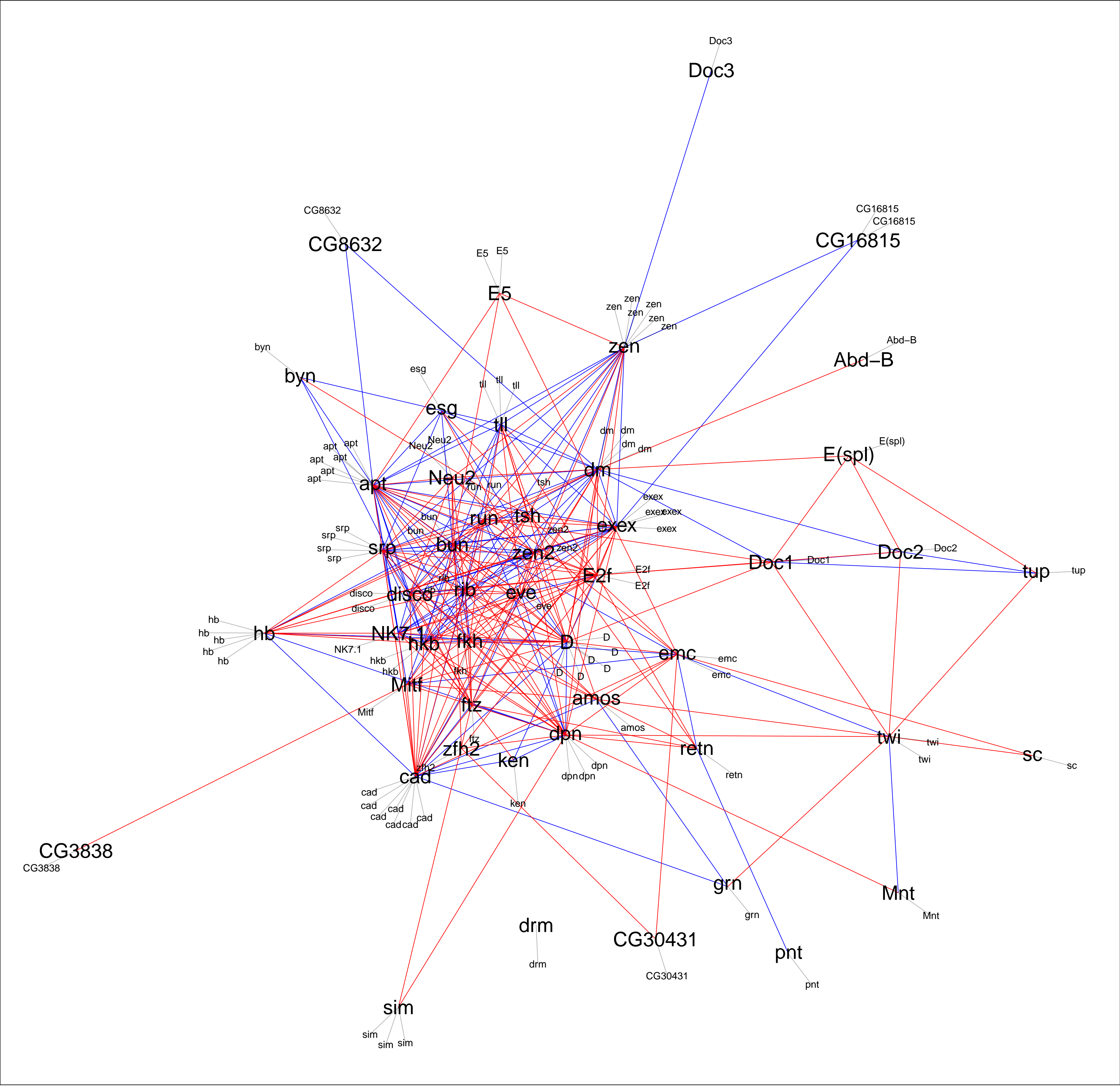
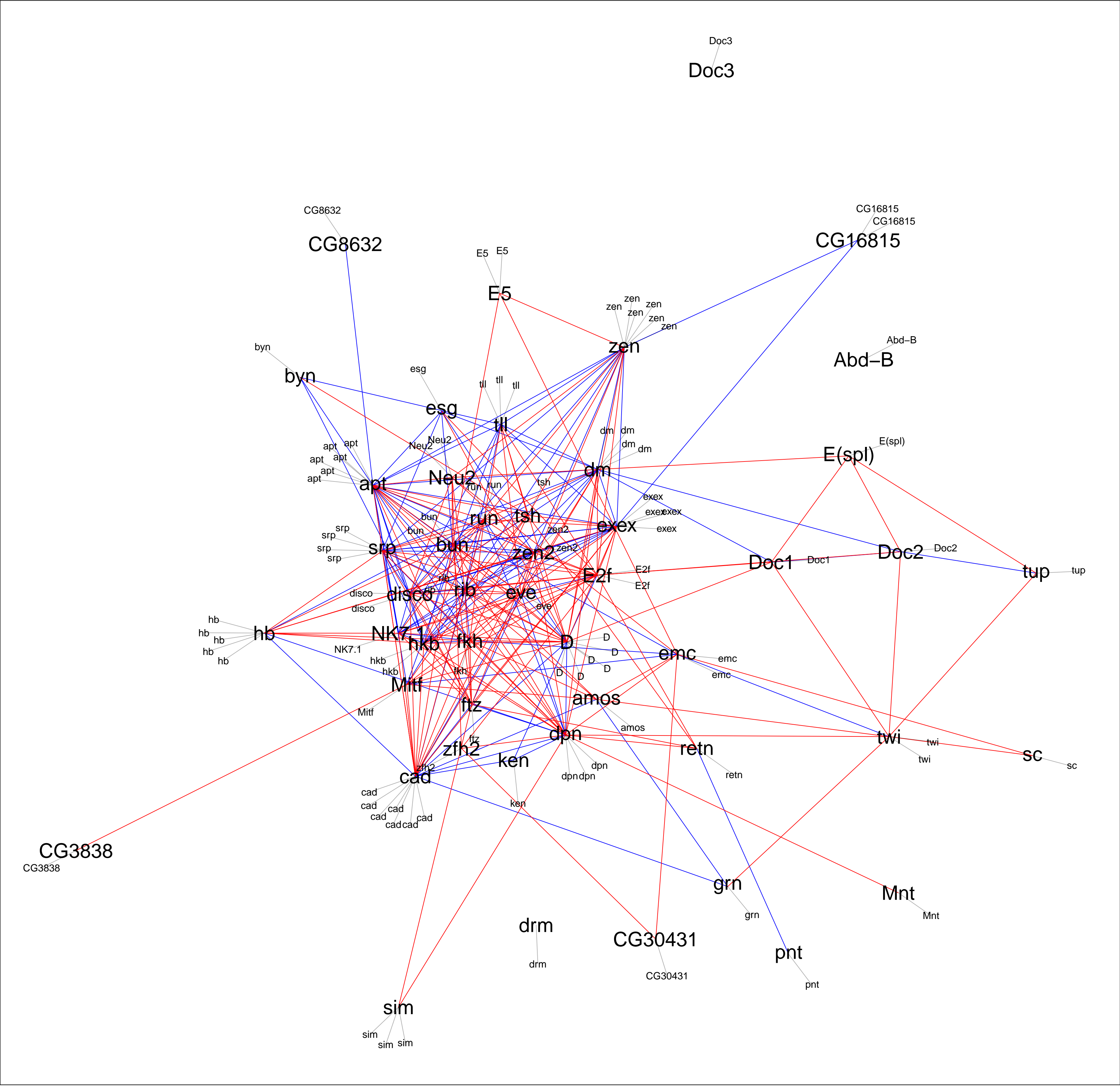


The diagram illustrates a complex gene regulatory network. The central part of the network is a dense cluster of genes, including *zen*, *dm*, *exex*, *E2f*, *D*, *amos*, *dpm*, *ken*, *cad*, *zfh2*, *fitz*, *hkb*, *hkh*, *disco*, *NK7.1*, *hb*, *srp*, *apt*, *esg*, *Neu2*, *run*, *tsh*, *zen2*, *eve*, *emc*, *retn*, *twi*, *sc*, *Mnt*, *pnt*, *grn*, *drn*, *sim*, *CG30431*, *CG3838*, *CG8632*, *CG16815*, *Doc3*, *Doc1*, *Doc2*, *Abd-B*, *E(spl)*, *tup*, *byn*, *esg*, *Neu2*, *run*, *tsh*, *zen2*, *eve*, *emc*, *retn*, *twi*, *sc*, *Mnt*, *pnt*, *grn*, *drn*, *sim*, *CG30431*, *CG3838*, *CG8632*, *CG16815*, *Doc3*, *Doc1*, *Doc2*, *Abd-B*, *E(spl)*, *tup*, *byn*, *esg*, *Neu2*, *run*, *tsh*, *zen2*, *eve*, *emc*, *retn*, *twi*, *sc*, *Mnt*, *pnt*, *grn*, *drn*, *sim*, *CG30431*, *CG3838*, *CG8632*, *CG16815*, *Doc3*, *Doc1*, *Doc2*, *Abd-B*, *E(spl)*, *tup*, *byn*, *esg*, *Neu2*, *run*, *tsh*, *zen2*, *eve*, *emc*, *retn*, *twi*, *sc*, *Mnt*, *pnt*, *grn*, *drn*, *sim*, *CG30431*, *CG3838*, *CG8632*, *CG16815*, *Doc3*, *Doc1*, *Doc2*, *Abd-B*, *E(spl)*, *tup*, *byn*, *esg*, *Neu2*, *run*, *tsh*, *zen2*, *eve*, *emc*, *retn*, *twi*, *sc*, *Mnt*, *pnt*, *grn*, *drn*, *sim*, *CG30431*, *CG3838*, *CG8632*, *CG16815*, *Doc3*, *Doc1*, *Doc2*, *Abd-B*, *E(spl)*, *tup*, *byn*, *esg*, *Neu2*, *run*, *tsh*, *zen2*, *eve*, *emc*, *retn*, *twi*, *sc*, *Mnt*, *pnt*, *grn*, *drn*, *sim*, *CG30431*, *CG3838*, *CG8632*, *CG16815*, *Doc3*, *Doc1*, *Doc2*, *Abd-B*, *E(spl)*, *tup*, *byn*, *esg*, *Neu2*, *run*, *tsh*, *zen2*, *eve*, *emc*, *retn*, *twi*, *sc*, *Mnt*, *pnt*, *grn*, *drn*, *sim*, *CG30431*, *CG3838*, *CG8632*, *CG16815*, *Doc3*, *Doc1*, *Doc2*, *Abd-B*, *E(spl)*, *tup*, *byn*, *esg*, *Neu2*, *run*, *tsh*, *zen2*, *eve*, *emc*, *retn*, *twi*, *sc*, *Mnt*, *pnt*, *grn*, *drn*, *sim*, *CG30431*, *CG3838*, *CG8632*, *CG16815*, *Doc3*, *Doc1*, *Doc2*, *Abd-B*, *E(spl)*, *tup*, *byn*, *esg*, *Neu2*, *run*, *tsh*, *zen2*, *eve*, *emc*, *retn*, *twi*, *sc*, *Mnt*, *pnt*, *grn*, *drn*, *sim*, *CG30431*, *CG3838*, *CG8632*, *CG16815*, *Doc3*, *Doc1*, *Doc2*, *Abd-B*, *E(spl)*, *tup*, *byn*, *esg*, *Neu2*, *run*, *tsh*, *zen2*, *eve*, *emc*, *retn*, *twi*, *sc*, *Mnt*, *pnt*, *grn*, *drn*, *sim*, *CG30431*, *CG3838*, *CG8632*, *CG16815*, *Doc3*, *Doc1*, *Doc2*, *Abd-B*, *E(spl)*, *tup*, *byn*, *esg*, *Neu2*, *run*, *tsh*, *zen2*, *eve*, *emc*, *retn*, *twi*, *sc*, *Mnt*, *pnt*, *grn*, *drn*, *sim*, *CG30431*, *CG3838*, *CG8632*, *CG16815*, *Doc3*, *Doc1*, *Doc2*, *Abd-B*, *E(spl)*, *tup*, *byn*, *esg*, *Neu2*, *run*, *tsh*, *zen2*, *eve*, *emc*, *retn*, *twi*, *sc*, *Mnt*, *pnt*, *grn*, *drn*, *sim*, *CG30431*, *CG3838*, *CG8632*, *CG16815*, *Doc3*, *Doc1*, *Doc2*, *Abd-B*, *E(spl)*, *tup*, *byn*, *esg*, *Neu2*, *run*, *tsh*, *zen2*, *eve*, *emc*, *retn*, *twi*, *sc*, *Mnt*, *pnt*, *grn*, *drn*, *sim*, *CG30431*, *CG3838*, *CG8632*, *CG16815*, *Doc3*, *Doc1*, *Doc2*, *Abd-B*, *E(spl)*, *tup*, *byn*, *esg*, *Neu2*, *run*, *tsh*, *zen2*, *eve*, *emc*, *retn*, *twi*, *sc*, *Mnt*, *pnt*, *grn*, *drn*, *sim*, *CG30431*, *CG3838*, *CG8632*, *CG16815*, *Doc3*, *Doc1*, *Doc2*, *Abd-B*, *E(spl)*, *tup*, *byn*, *esg*, *Neu2*, *run*, *tsh*, *zen2*, *eve*, *emc*, *retn*, *twi*, *sc*, *Mnt*, *pnt*, *grn*, *drn*, *sim*, *CG30431*, *CG3838*, *CG8632*, *CG16815*, *Doc3*, *Doc1*, *Doc2*, *Abd-B*, *E(spl)*, *tup*, *byn*, *esg*, *Neu2*, *run*, *tsh*, *zen2*, *eve*, *emc*, *retn*, *twi*, *sc*, *Mnt*, *pnt*, *grn*, *drn*, *sim*, *CG30431*, *CG3838*, *CG8632*, *CG16815*, *Doc3*, *Doc1*, *Doc2*, *Abd-B*, *E(spl)*, *tup*, *byn*, *esg*, *Neu2*, *run*, *tsh*, *zen2*, *eve*, *emc*, *retn*, *twi*, *sc*, *Mnt*, *pnt*, *grn*, *drn*, *sim*, *CG30431*, *CG3838*, *CG8632*, *CG16815*, *Doc3*, *Doc1*, *Doc2*, *Abd-B*, *E(spl)*, *tup*, *byn*, *esg*, *Neu2*, *run*, *tsh*, *zen2*, *eve*, *emc*, *retn*, *twi*, *sc*, *Mnt*, *pnt*, *grn*, *drn*, *sim*, *CG30431*, *CG3838*, *CG8632*, *CG1*

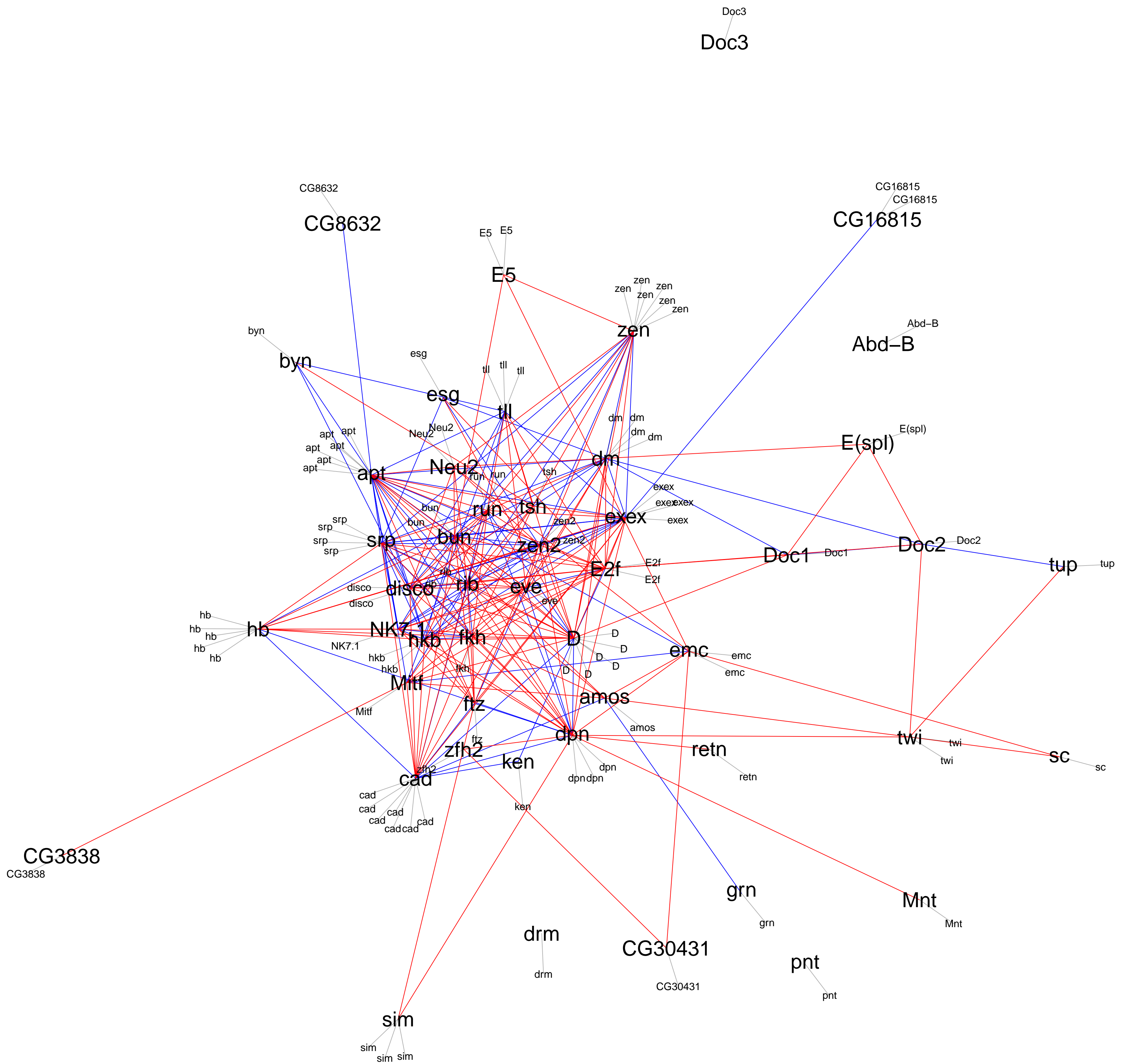
Lower 4.5% correlation = -0.54; upper 4.5% correlation = 0.76



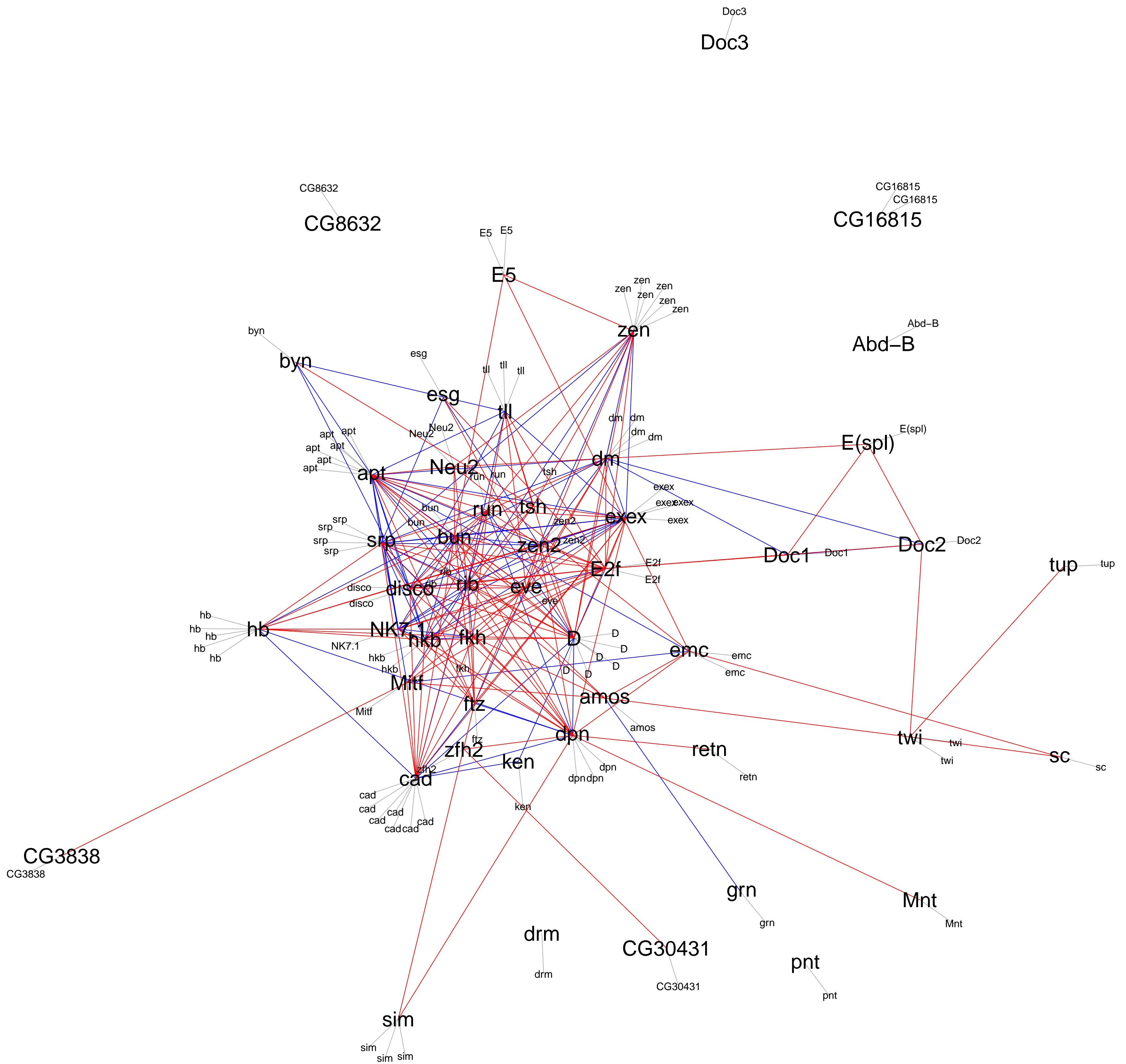
Lower 4% correlation = -0.55; upper 4% correlation = 0.78



Lower 3.5% correlation = -0.57 ; upper 3.5% correlation = 0.79



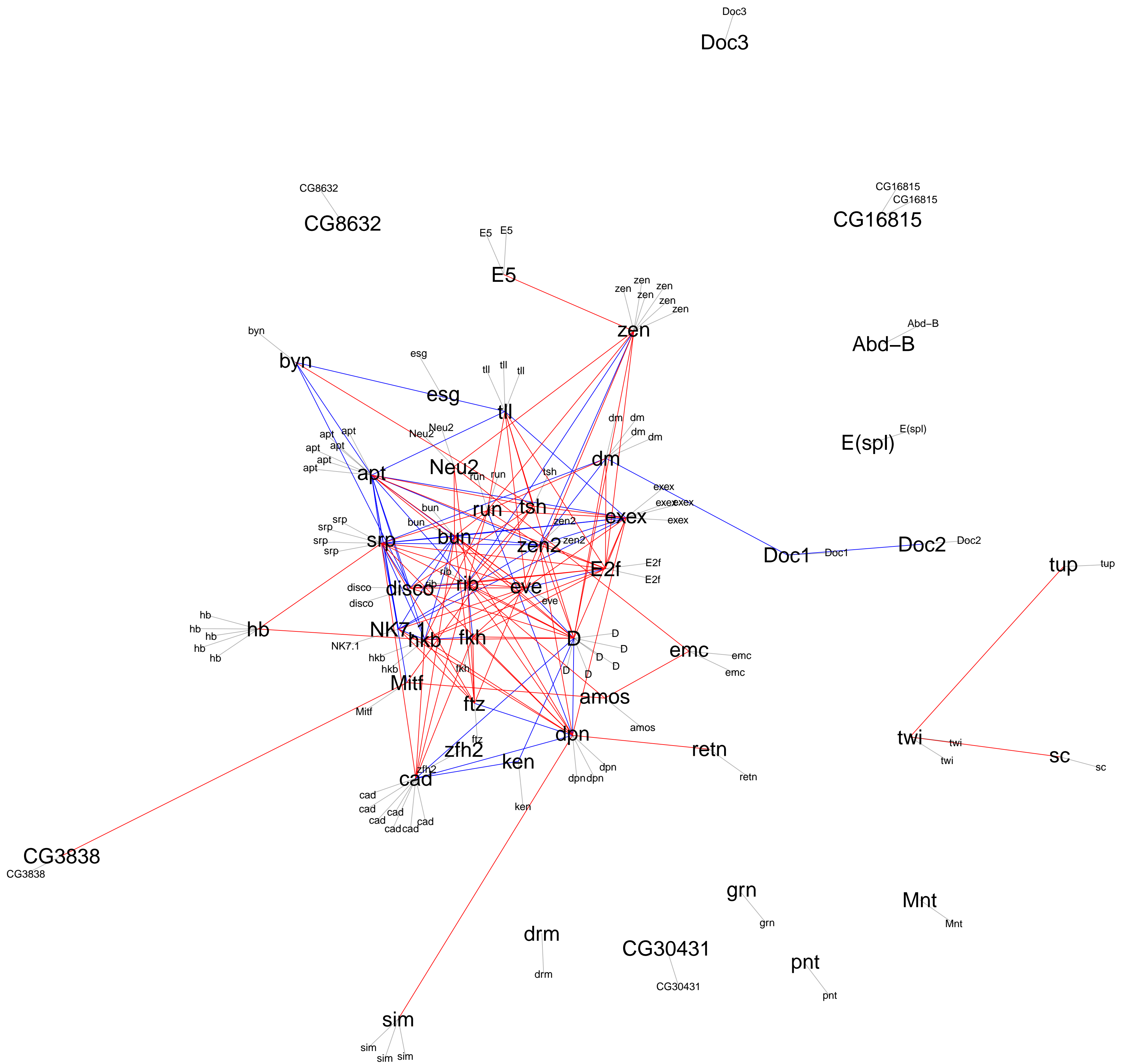
Lower 3% correlation = -0.58; upper 3% correlation = 0.8



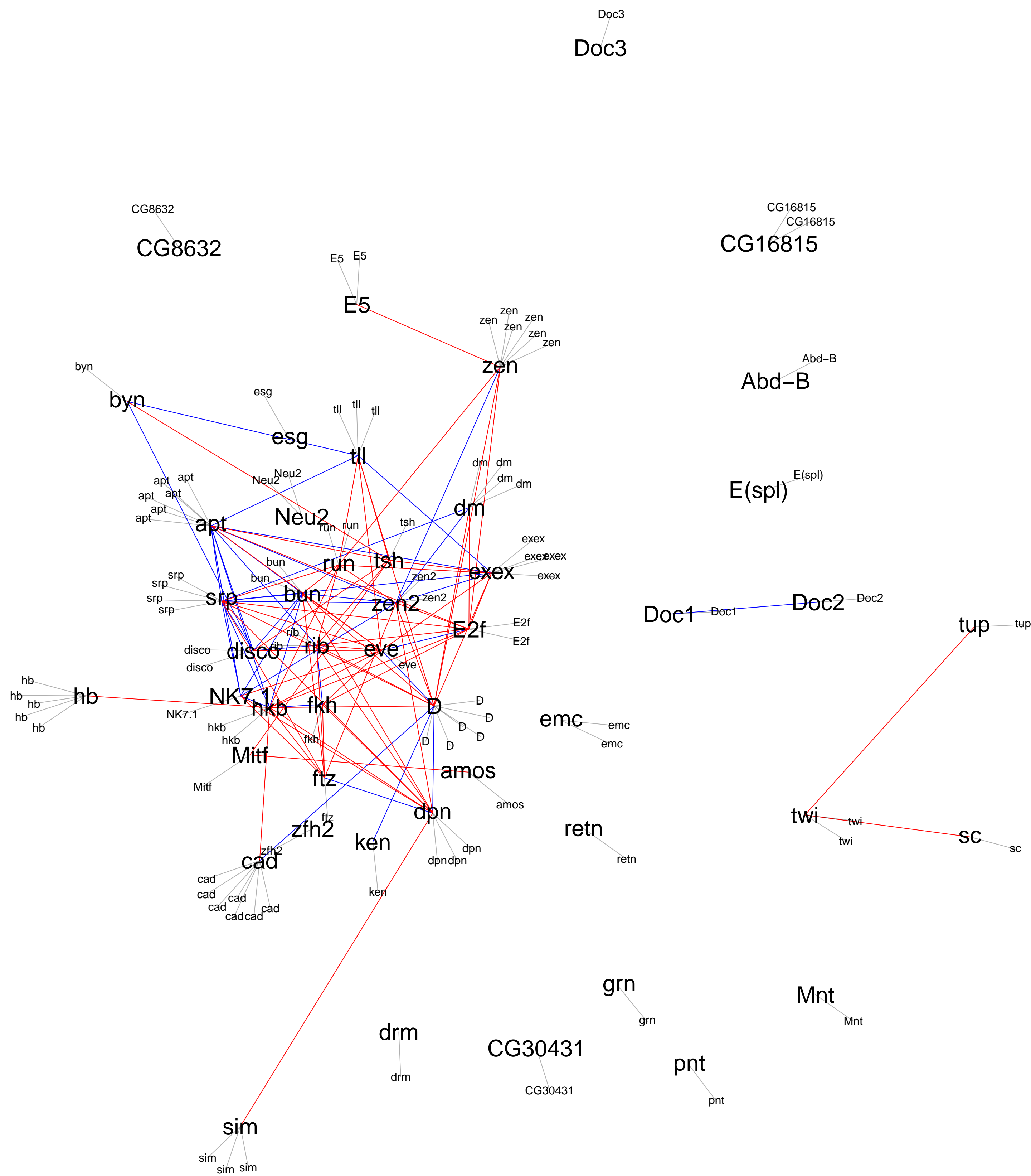
[illegible]

The diagram illustrates a complex gene regulatory network. At the top, several peripheral nodes are connected to the main network: Doc3, CG8632, CG16815, and Doc3. The central part of the diagram is a dense cluster of genes and transcription factors, including apt, srp, bun, run, tsh, zen, exex, E2f, D, amos, dpn, ken, zfh2, cad, Mitf, hkb, fkh, ftz, and others. These central nodes are interconnected by a complex web of red and blue lines, representing different types of regulatory interactions. The bottom part of the diagram shows more peripheral nodes and clusters, including CG3838, CG30431, Doc3, Doc1, Doc2, E(spl), Abd-B, tup, twi, sc, Mnt, pnt, grn, drm, and sim. The overall structure suggests a hierarchical organization of gene expression, with peripheral genes and clusters regulating the central core.

Lower 1.5% correlation = -0.65; upper 1.5% correlation = 0.85



Lower 1% correlation = -0.68; upper 1% correlation = 0.87



Lower 0.5% correlation = -0.73; upper 0.5% correlation = 0.89

