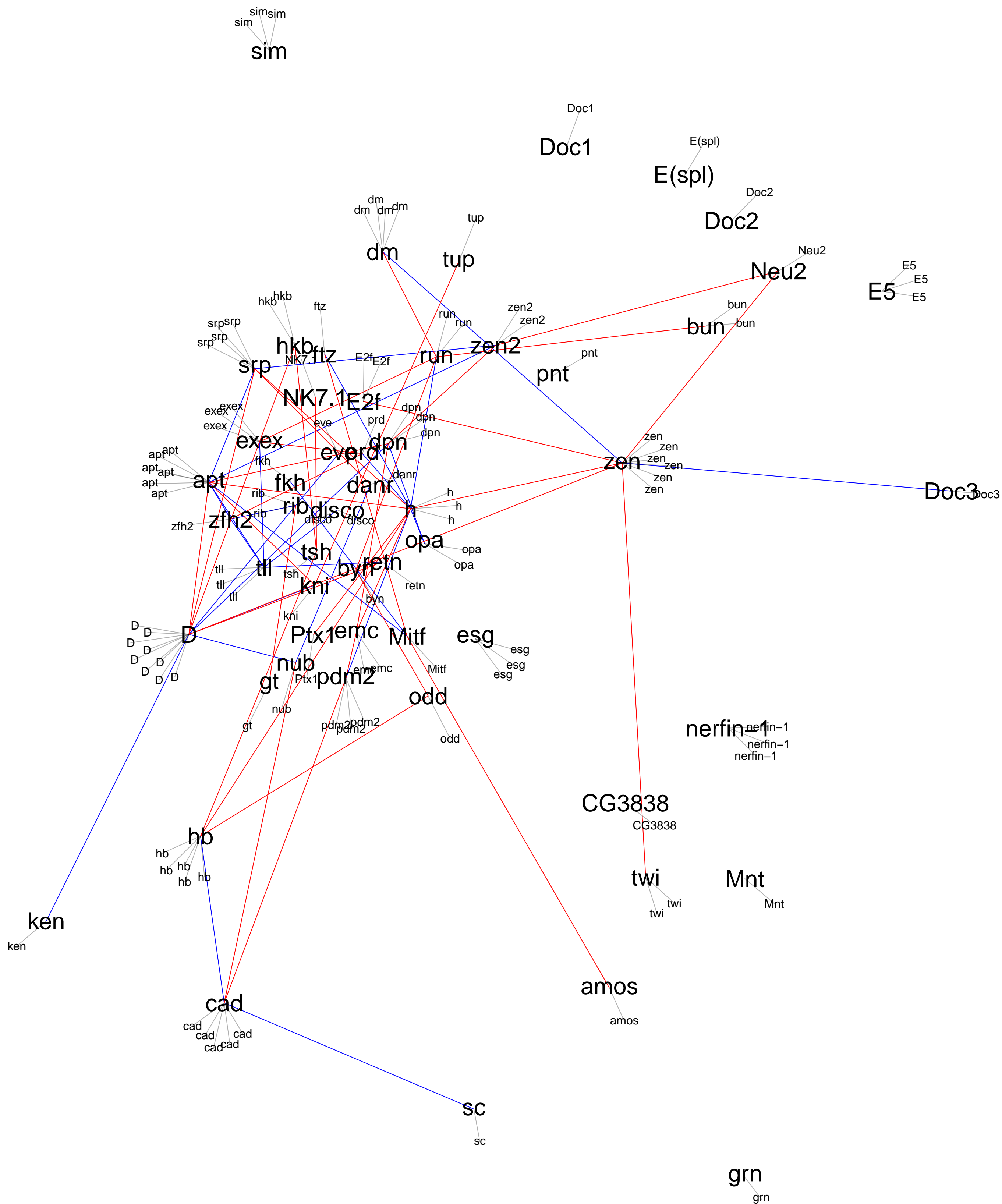


**Lower [4.5%.5%] correlation = [-0.57,-0.56]: Upper [5%.4.5%] correlation = [0.73.0**



The diagram illustrates a complex gene regulatory network. Nodes represent genes, and edges represent regulatory interactions. The network is highly interconnected, with many nodes having multiple incoming and outgoing edges. Key clusters include a large central network of transcription factors and signaling molecules, and several peripheral clusters like 'ken', 'cad', 'hb', 'twi', 'Mnt', 'amos', 'grn', 'SC', 'CG3838', 'CG16815', and 'nerfin-1'.

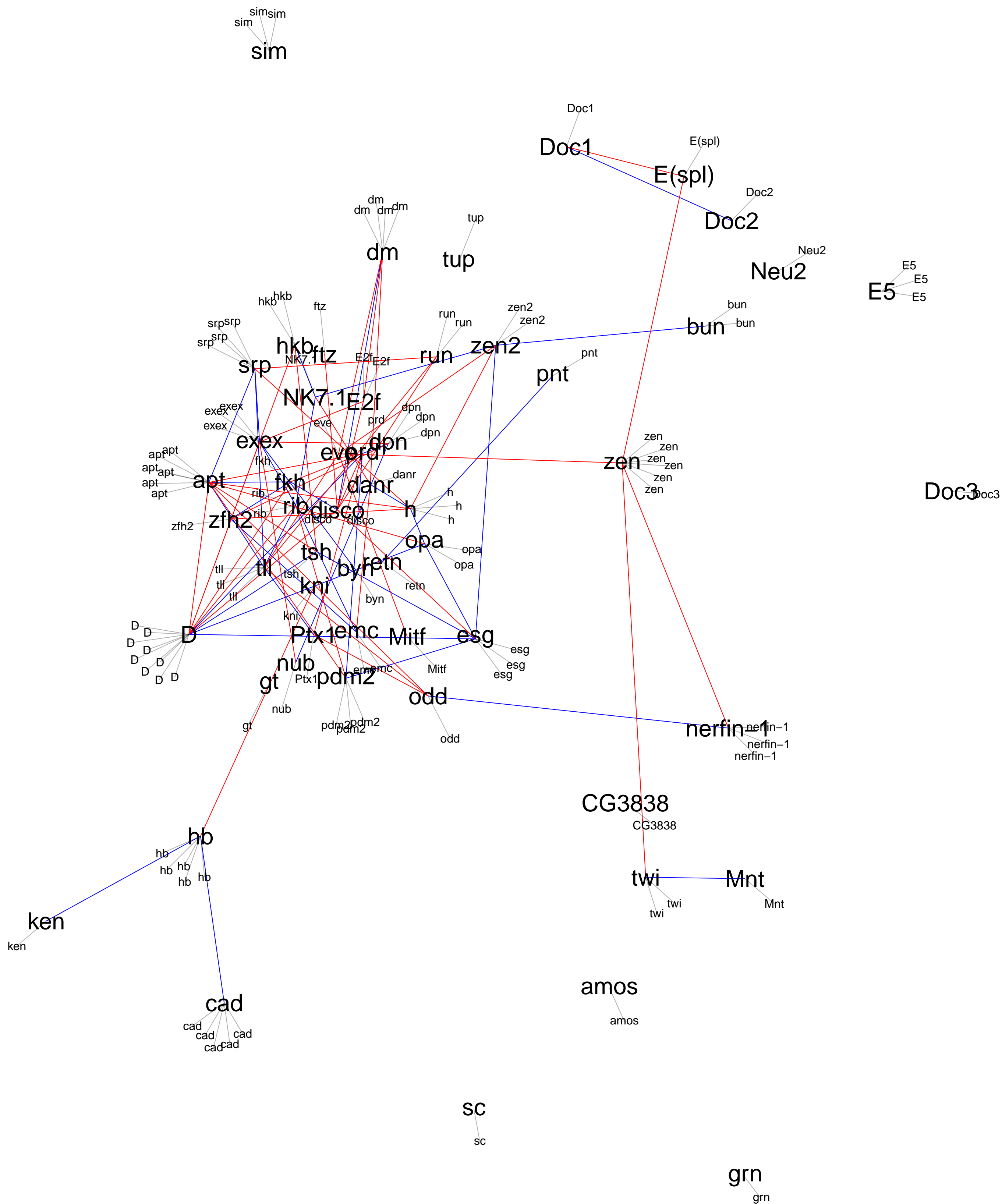
Key nodes and clusters visible in the diagram include:

- Central Network:** A dense cluster of genes including *sim*, *dm*, *tup*, *run*, *zen*, *pnt*, *srp*, *hkb*, *ftz*, *exex*, *apt*, *zfh2*, *rib*, *disco*, *h*, *opa*, *retn*, *byn*, *kni*, *tsh*, *nkx*, *ptx*, *emc*, *mitf*, *esg*, *odd*, *nub*, *gt*, *pdm2*, *nerfin-1*, *Doc1*, *Doc2*, *Doc3*, *E(spl)*, *Neu2*, *E5*, *bun*, *zen2*, *zen*, *hkb*, *ftz*, *srp*, *exex*, *apt*, *zfh2*, *rib*, *disco*, *h*, *opa*, *retn*, *byn*, *kni*, *tsh*, *nkx*, *ptx*, *emc*, *mitf*, *esg*, *odd*, *nub*, *gt*, *pdm2*.
- Peripheral Clusters:**
  - ken*, *cad*, *hb*, *twi*, *Mnt*, *amos*, *grn*, *SC*, *CG3838*, *CG16815*, *nerfin-1*.

The edges are color-coded, likely representing different types of regulatory interactions (e.g., activation, repression, or unknown).

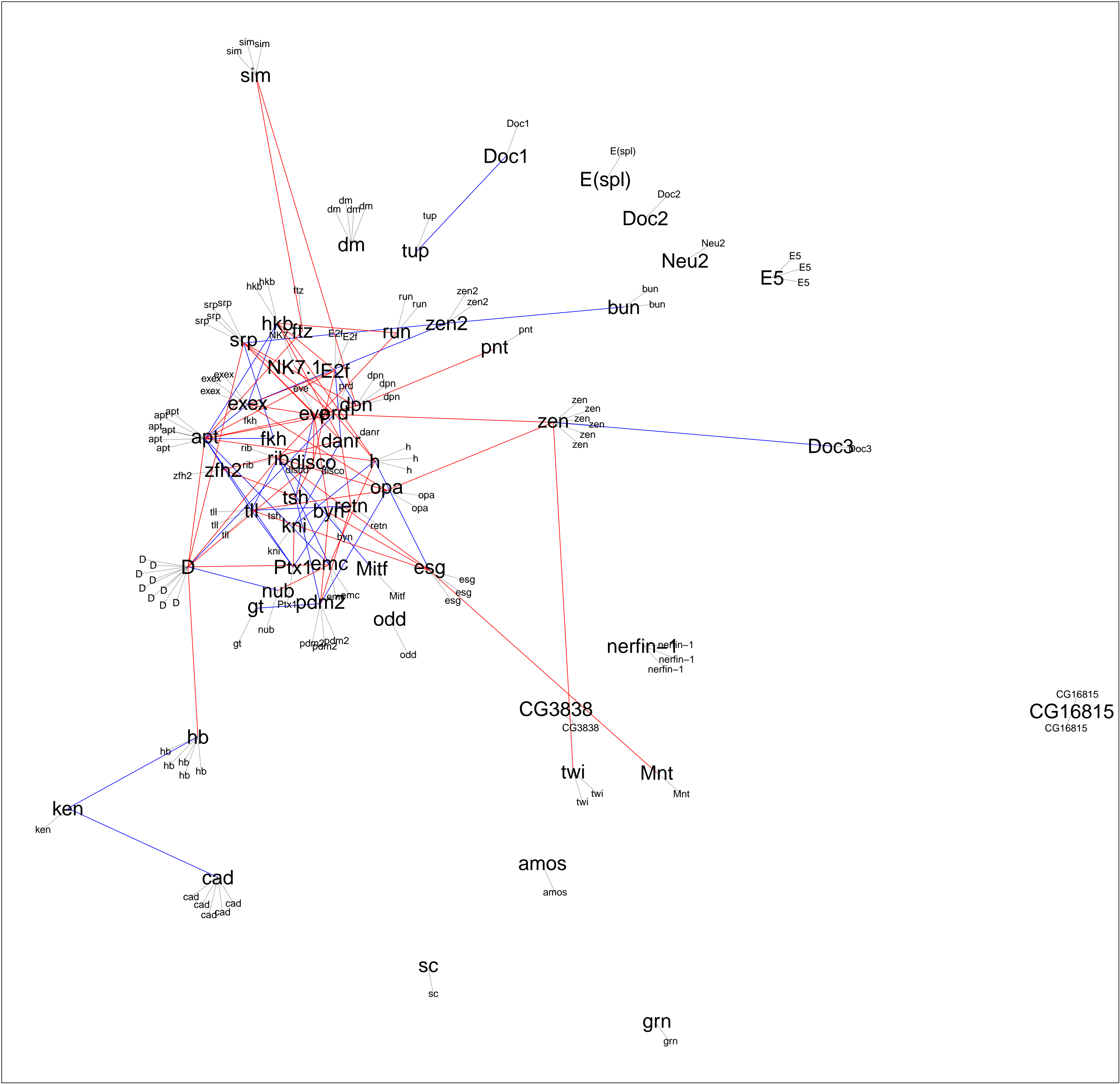
[illegible]

**Lower [3%,3.5%] correlation = [-0.62,-0.6]; Upper [3.5%,3%] correlation = [0.77,0.78]**

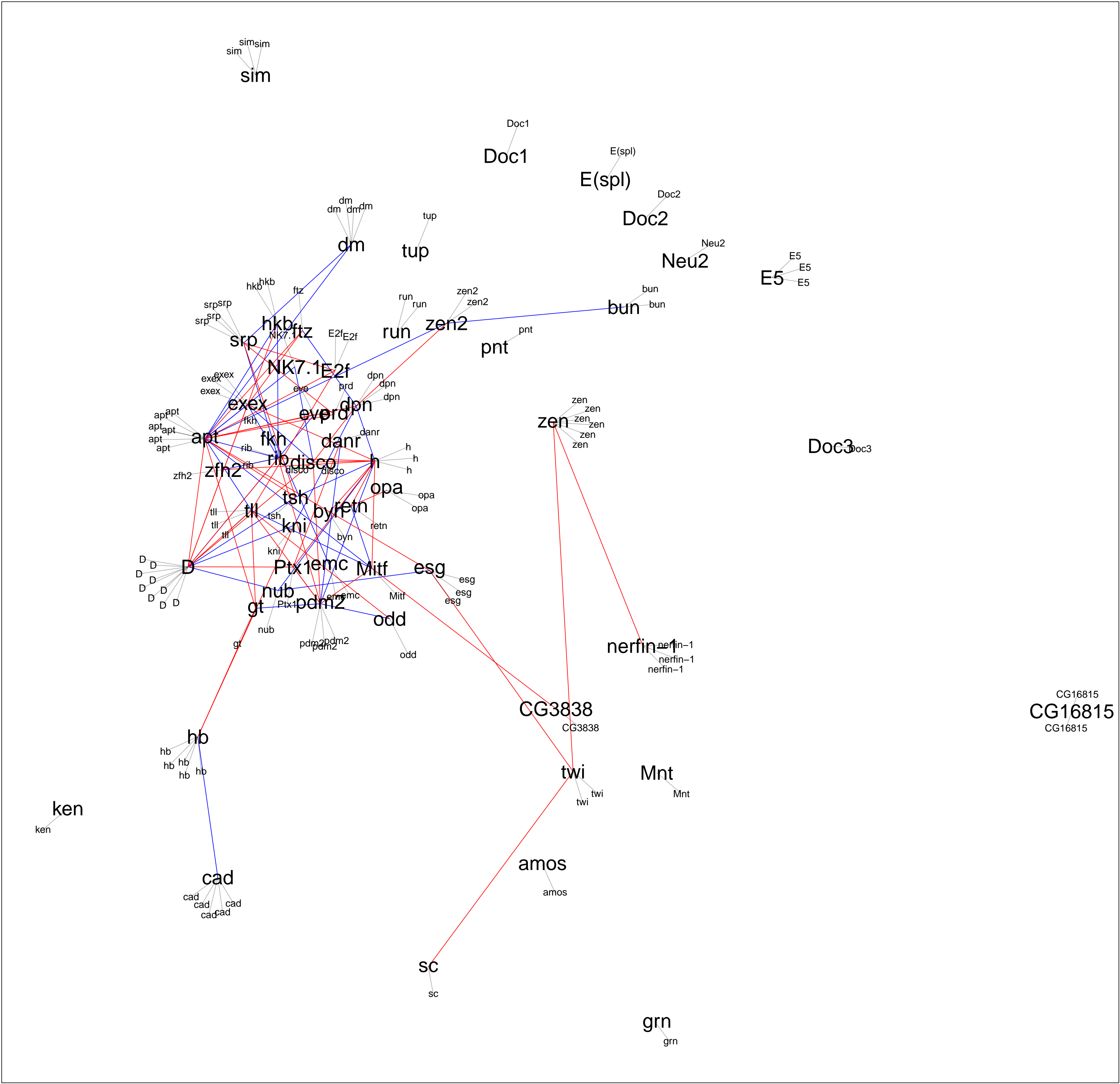




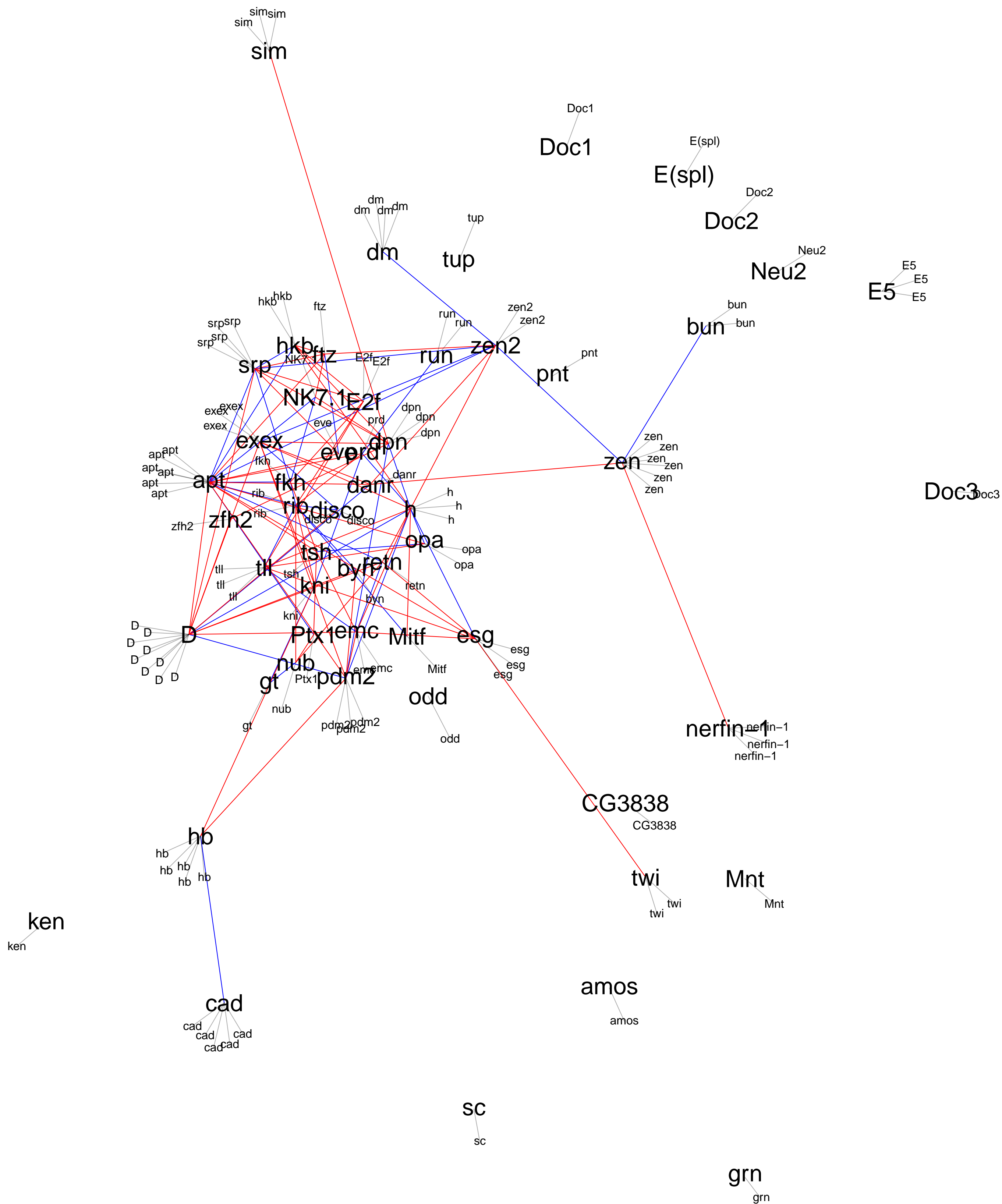
Lower [2.5%,3%] correlation = [-0.65,-0.62]; Upper [3%,2.5%] correlation = [0.78,0.8]



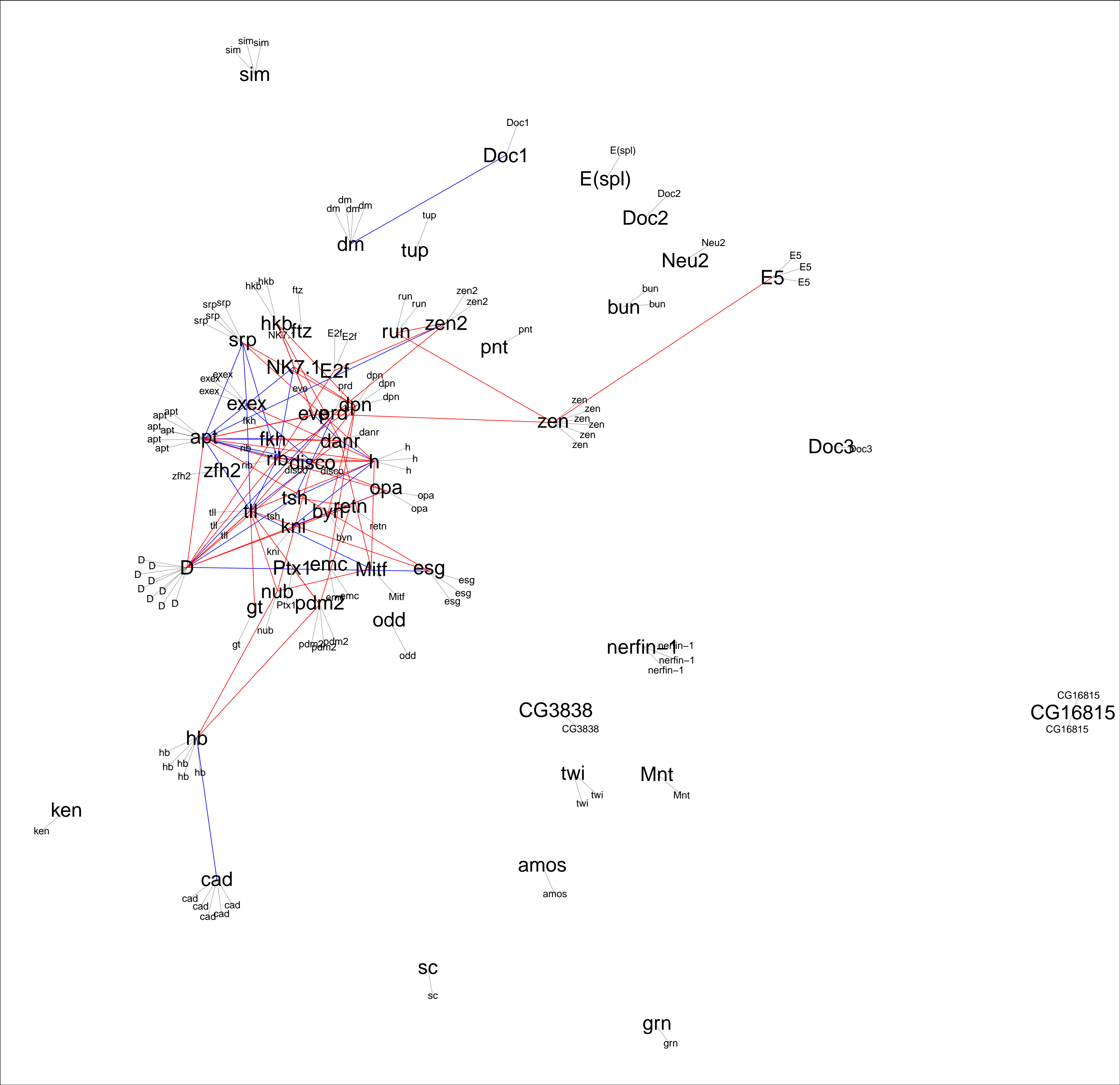
Lower [2%,2.5%] correlation = [-0.67,-0.65]; Upper [2.5%,2%] correlation = [0.8,0.81]



**Lower [1.5%,2%] correlation = [-0.7,-0.67]; Upper [2%,1.5%] correlation = [0.81,0.84]**



Lower [1%,1.5%] correlation = [-0.74,-0.7]; Upper [1.5%,1%] correlation = [0.84,0.86]





[illegible]