

The diagram illustrates a complex gene regulatory network, likely in the context of Drosophila embryonic development. It features numerous genes and transcription factors (TFs) connected by regulatory interactions, color-coded into blue and red lines.

Key Genes and Transcription Factors (TFs) shown:

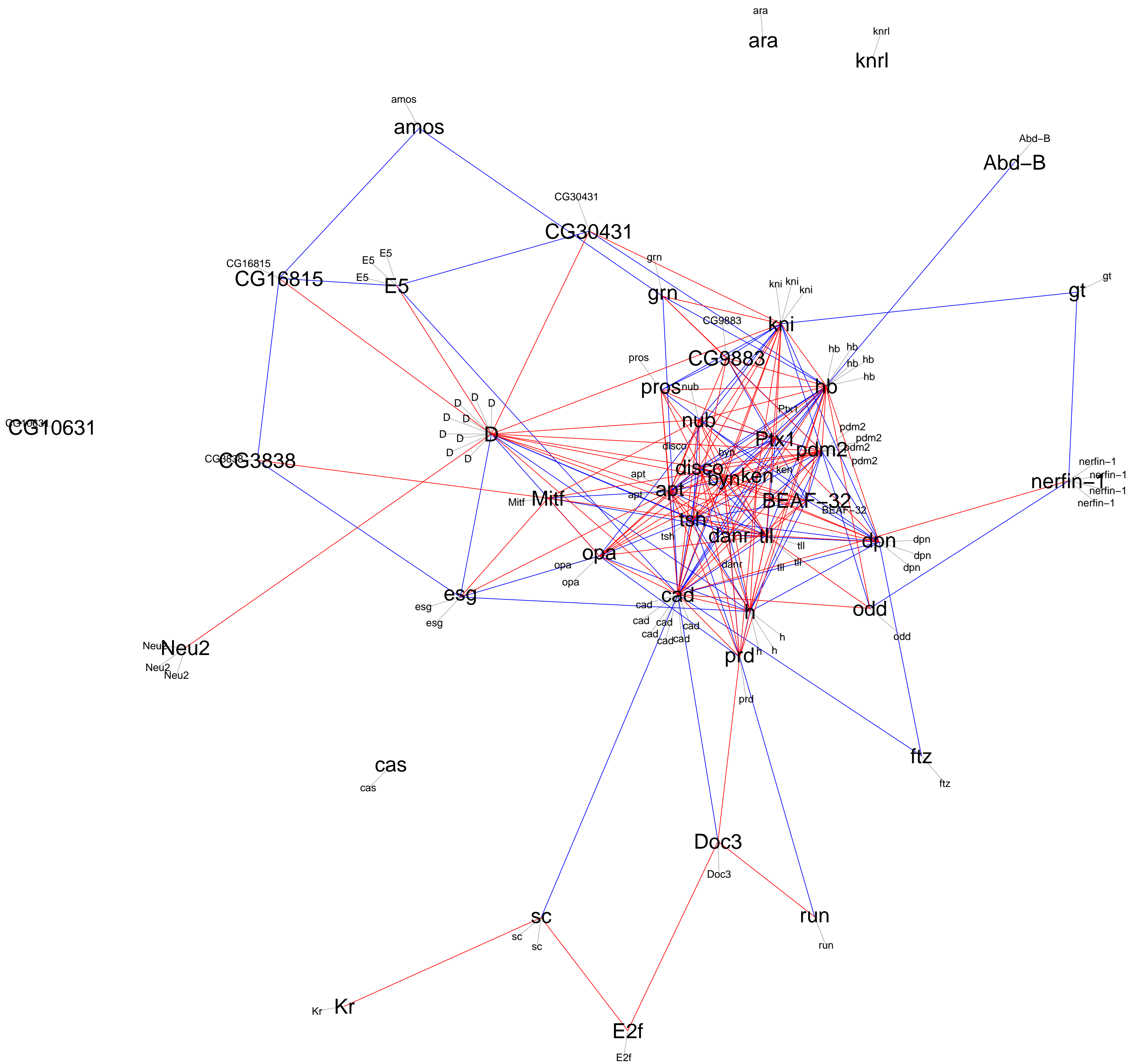
- Top Section (Blue Lines):** amos, E5, CG16815, CG30431, CG9883, kni, hb, Ptx1, pdm2, BEAF-32, danr, tll, odd, ftz, run, Doc3, SC, and Kr.
- Bottom Section (Red Lines):** ara, knrl, Abd-B, gt, nerfin-1, dpn, odd, ftz, run, Doc3, SC, and Kr.

Regulatory Interactions:

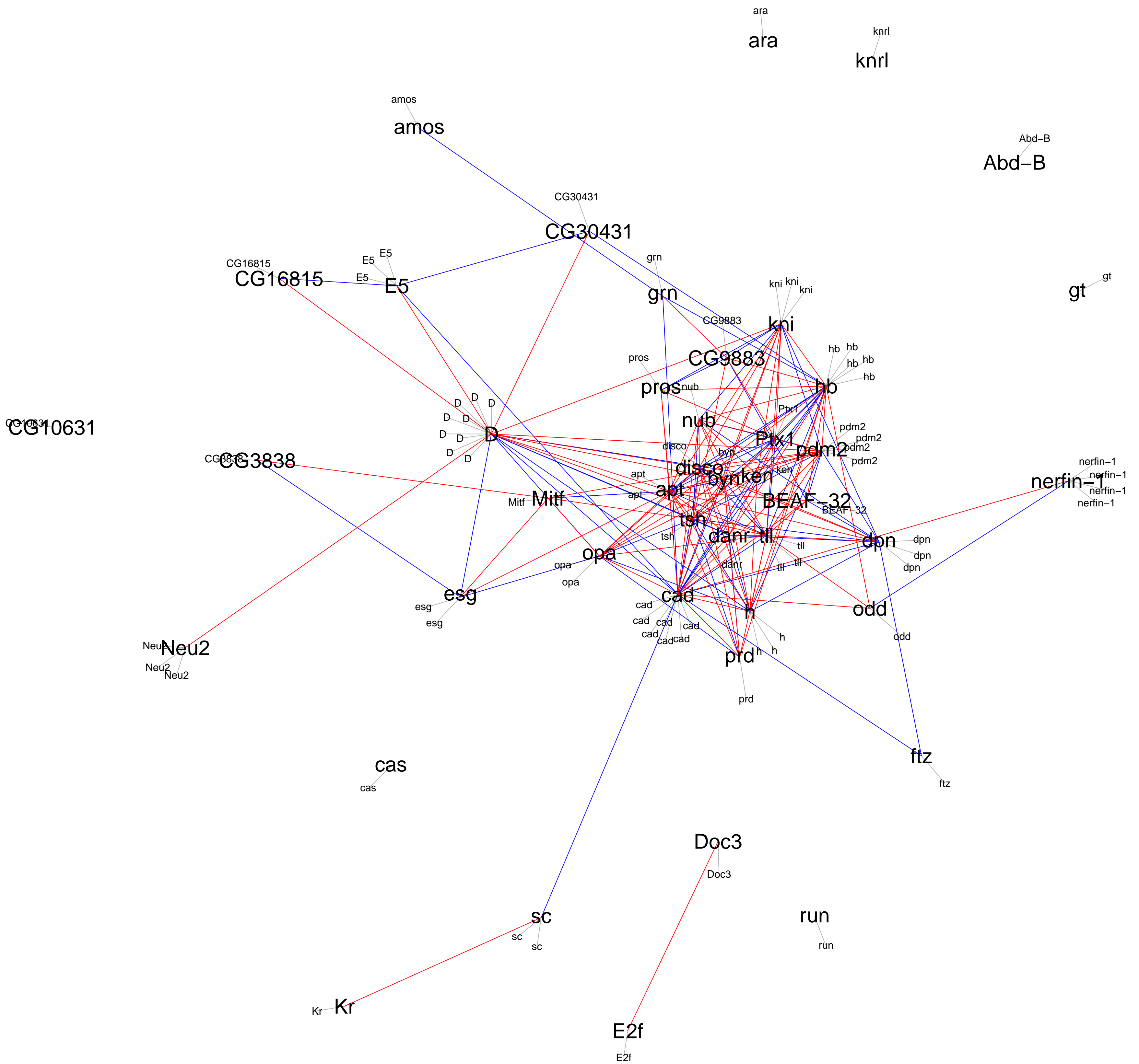
- Blue Lines:** Represent a set of regulatory interactions, often involving TFs like E5, D, Mitf, opa, cad, and Doc3.
- Red Lines:** Represent another set of regulatory interactions, often involving TFs like ara, kni, hb, Ptx1, pdm2, BEAF-32, danr, tll, odd, and run.

The diagram shows a highly interconnected network where many genes are regulated by multiple TFs, and some TFs regulate multiple genes. For example, E5 and D are central nodes in the blue network, while kni and hb are central nodes in the red network. The network structure suggests a hierarchical organization of gene expression during development.

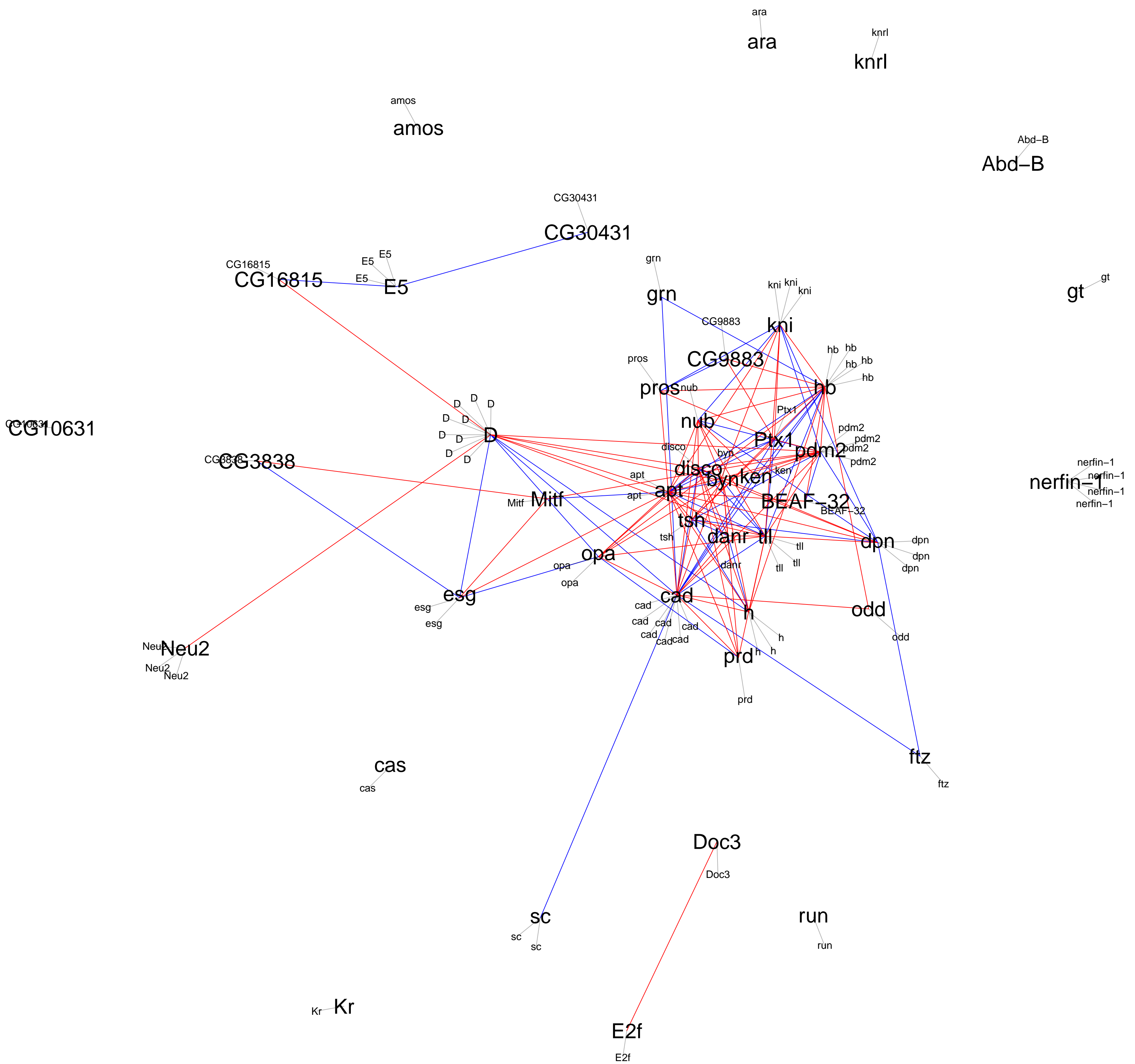
Lower 4.5% correlation = -0.52; upper 4.5% correlation = 0.68



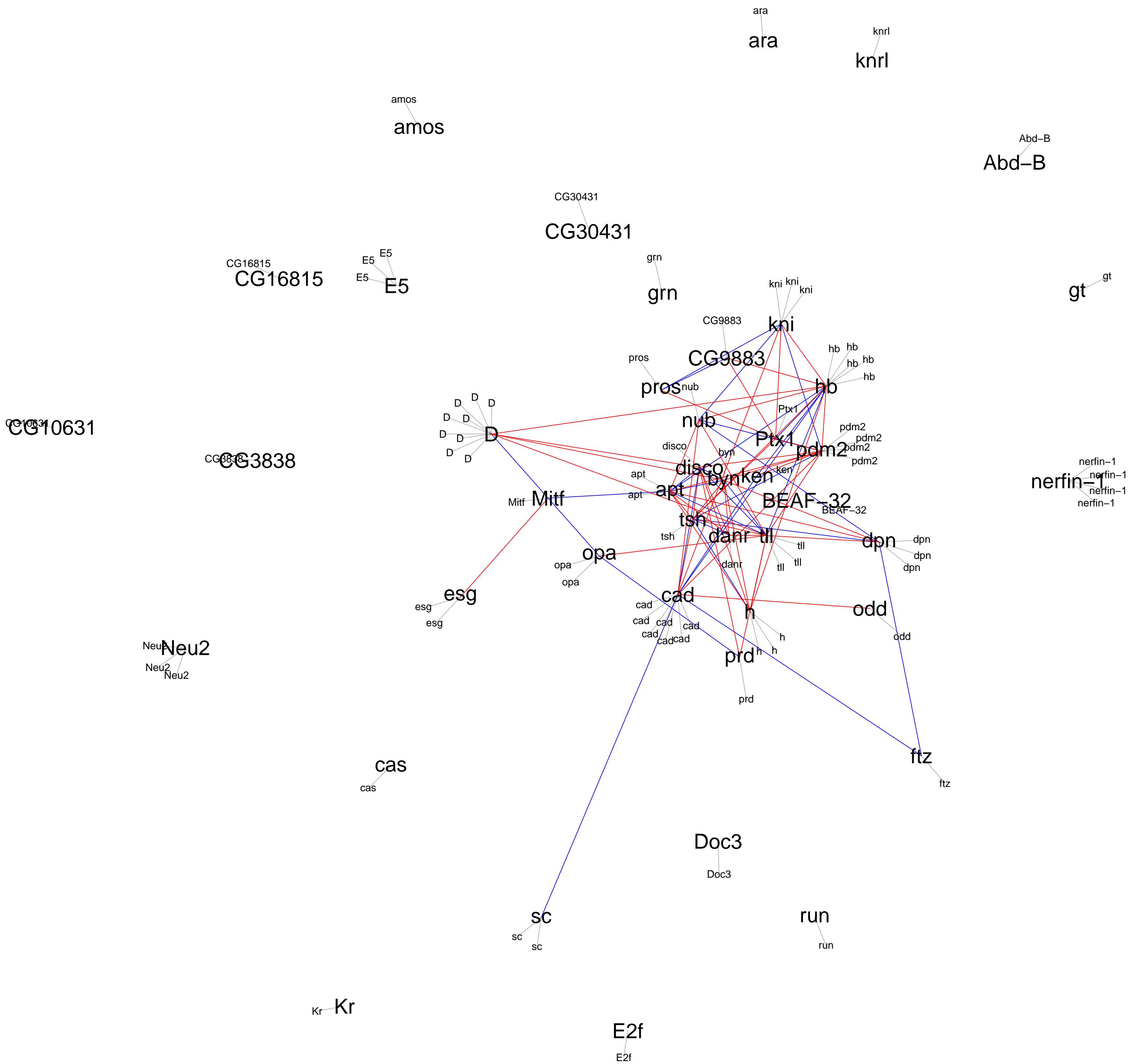
Lower 3.5% correlation = -0.55 ; upper 3.5% correlation = 0.71



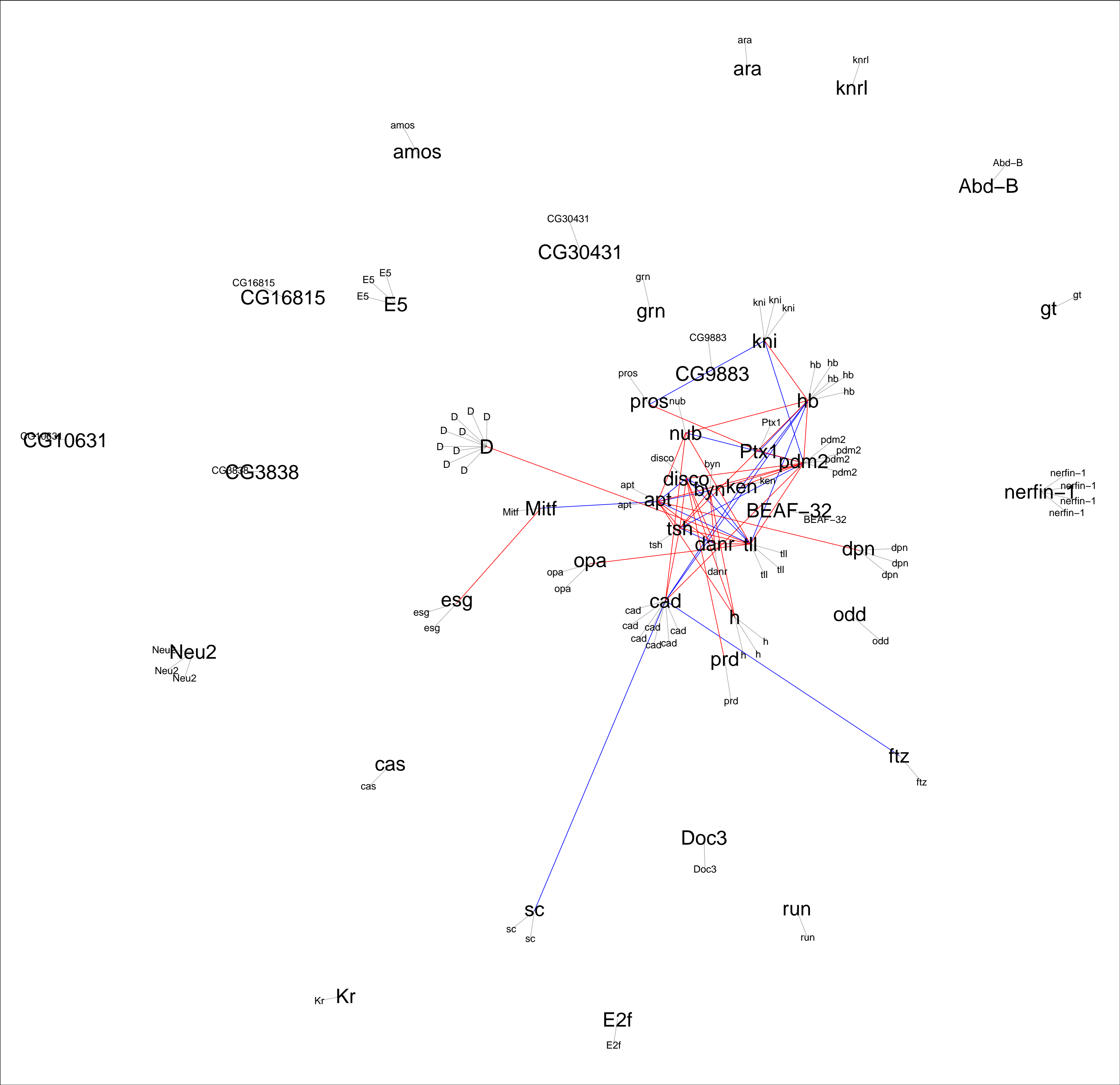
Lower 2.5% correlation = -0.59; upper 2.5% correlation = 0.74



Lower 1.5% correlation = -0.64; upper 1.5% correlation = 0.79



Lower 1% correlation = -0.68; upper 1% correlation = 0.82



Lower 0.5% correlation = -0.73; upper 0.5% correlation = 0.86

