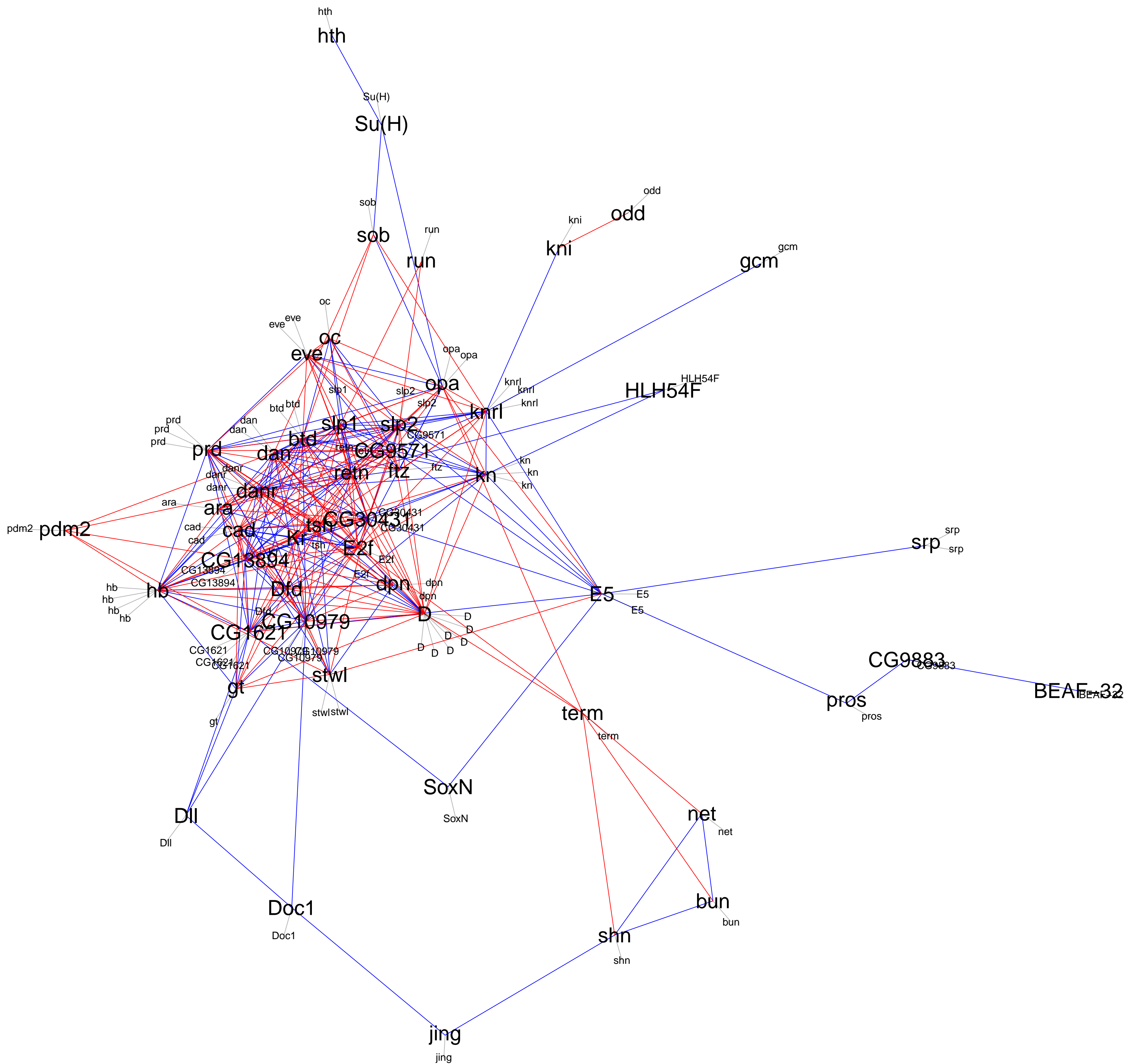


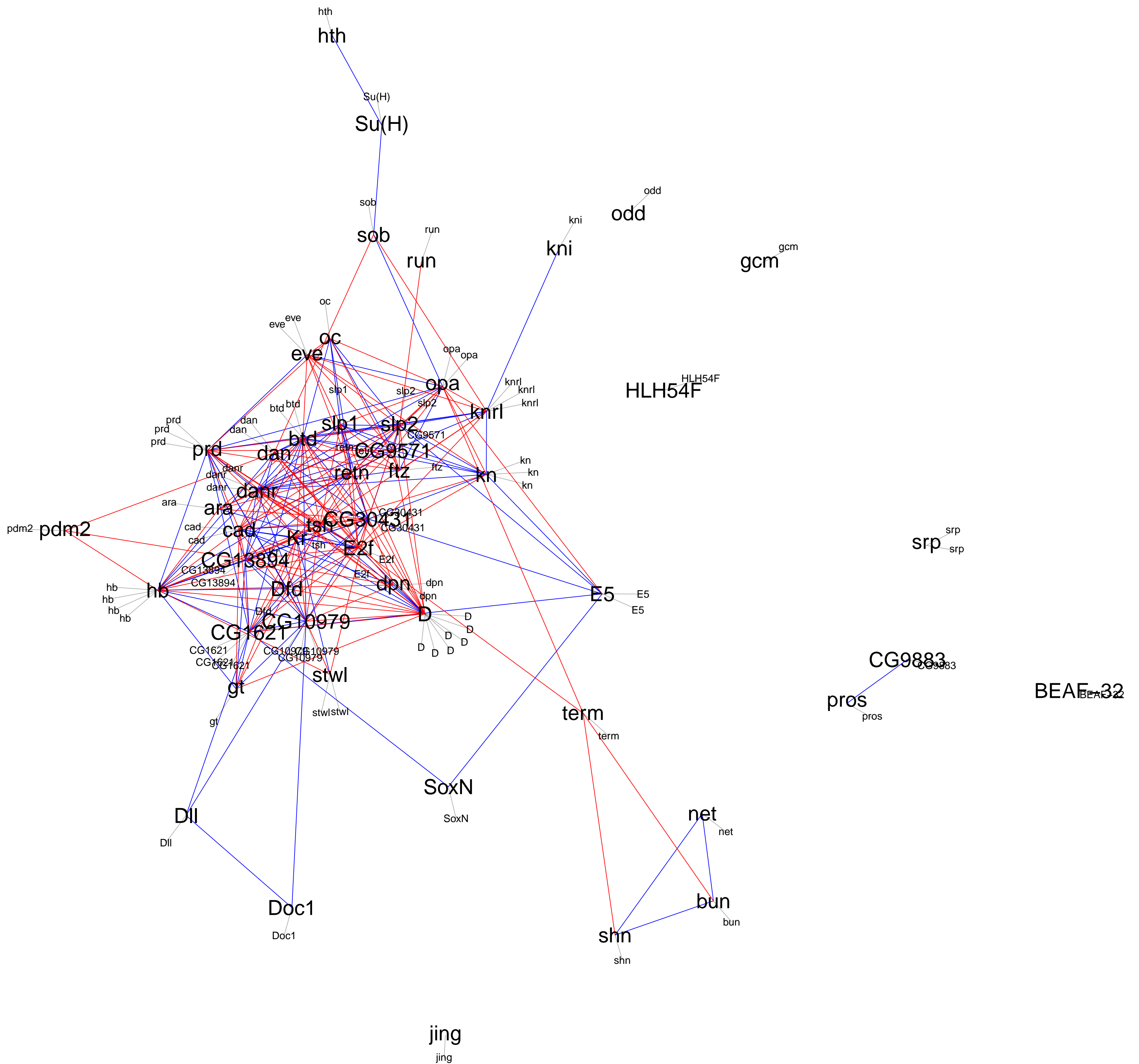
[illegible]

Lower 4.5% correlation = -0.57 ; upper 4.5% correlation = 0.7

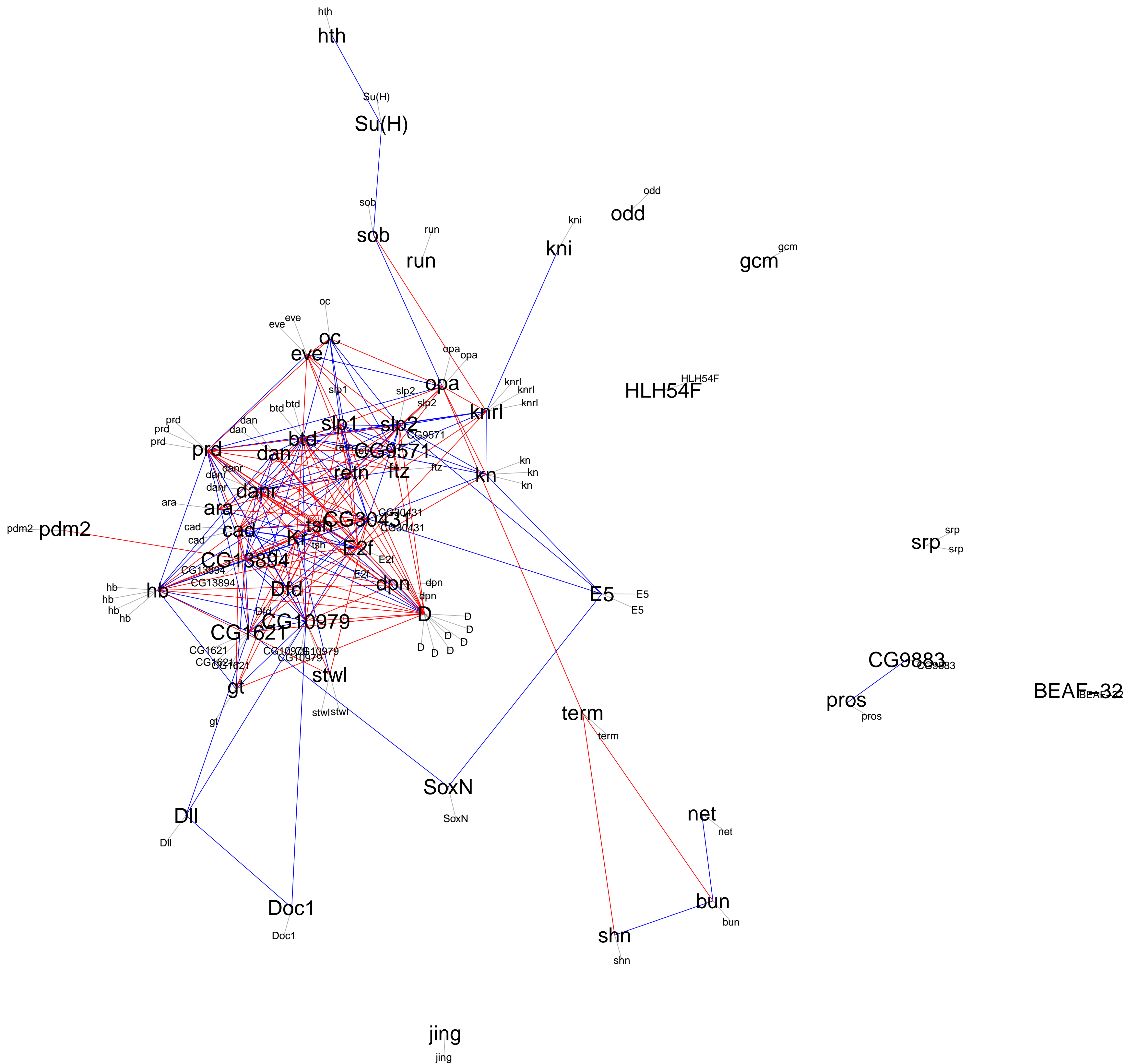


[illegible]

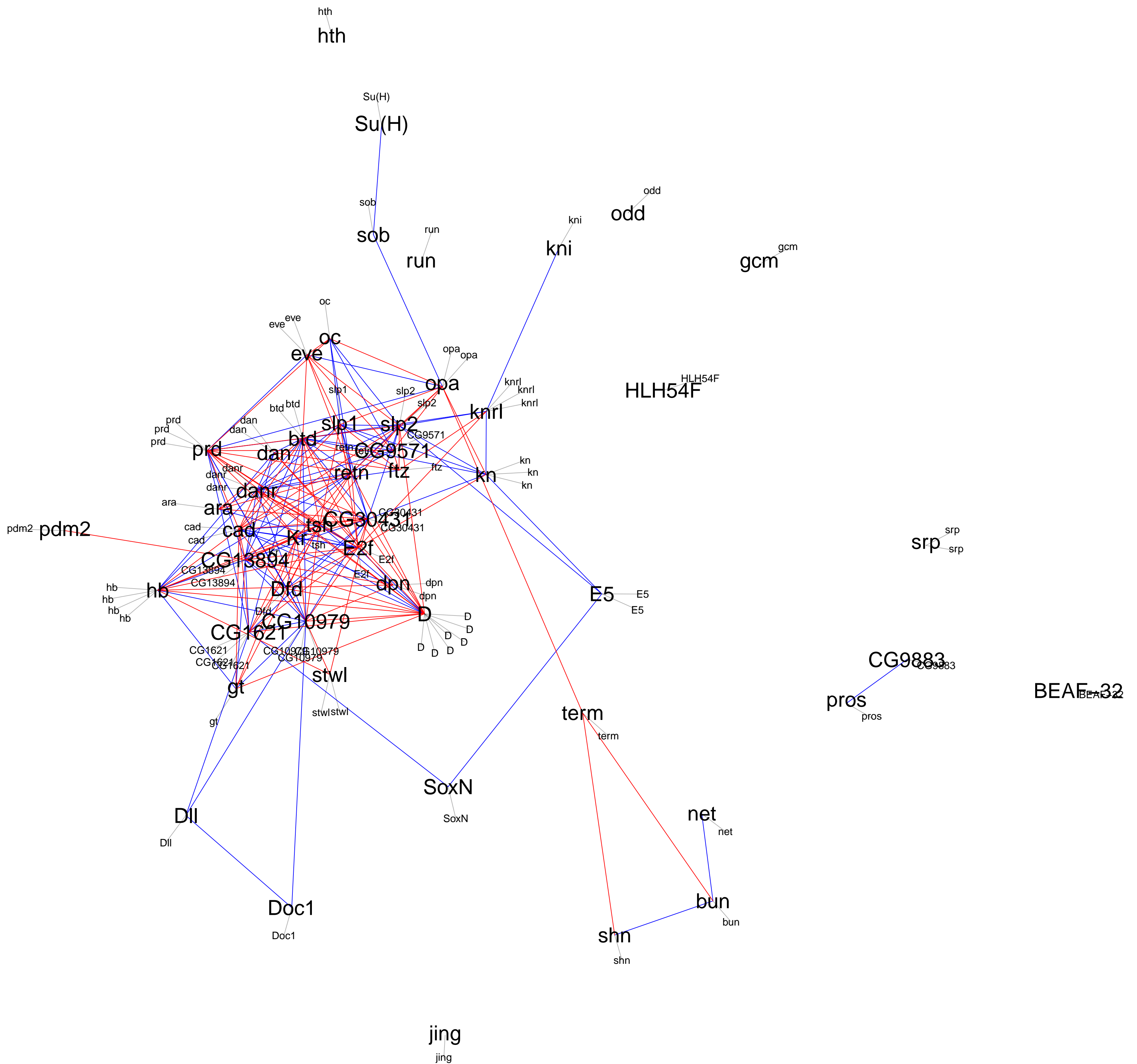
Lower 3.5% correlation = -0.6 ; upper 3.5% correlation = 0.72



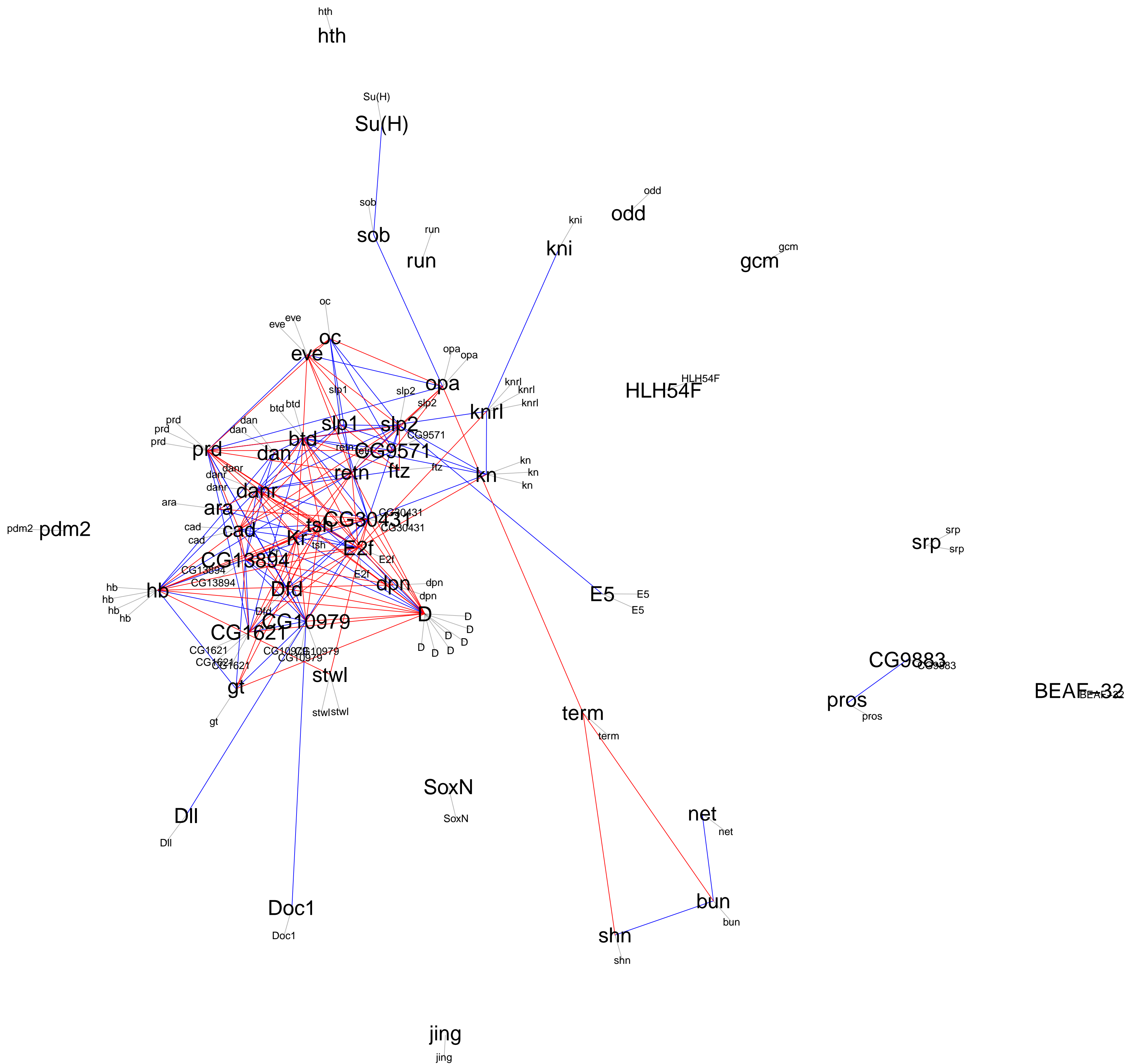
Lower 3% correlation = -0.62; upper 3% correlation = 0.74



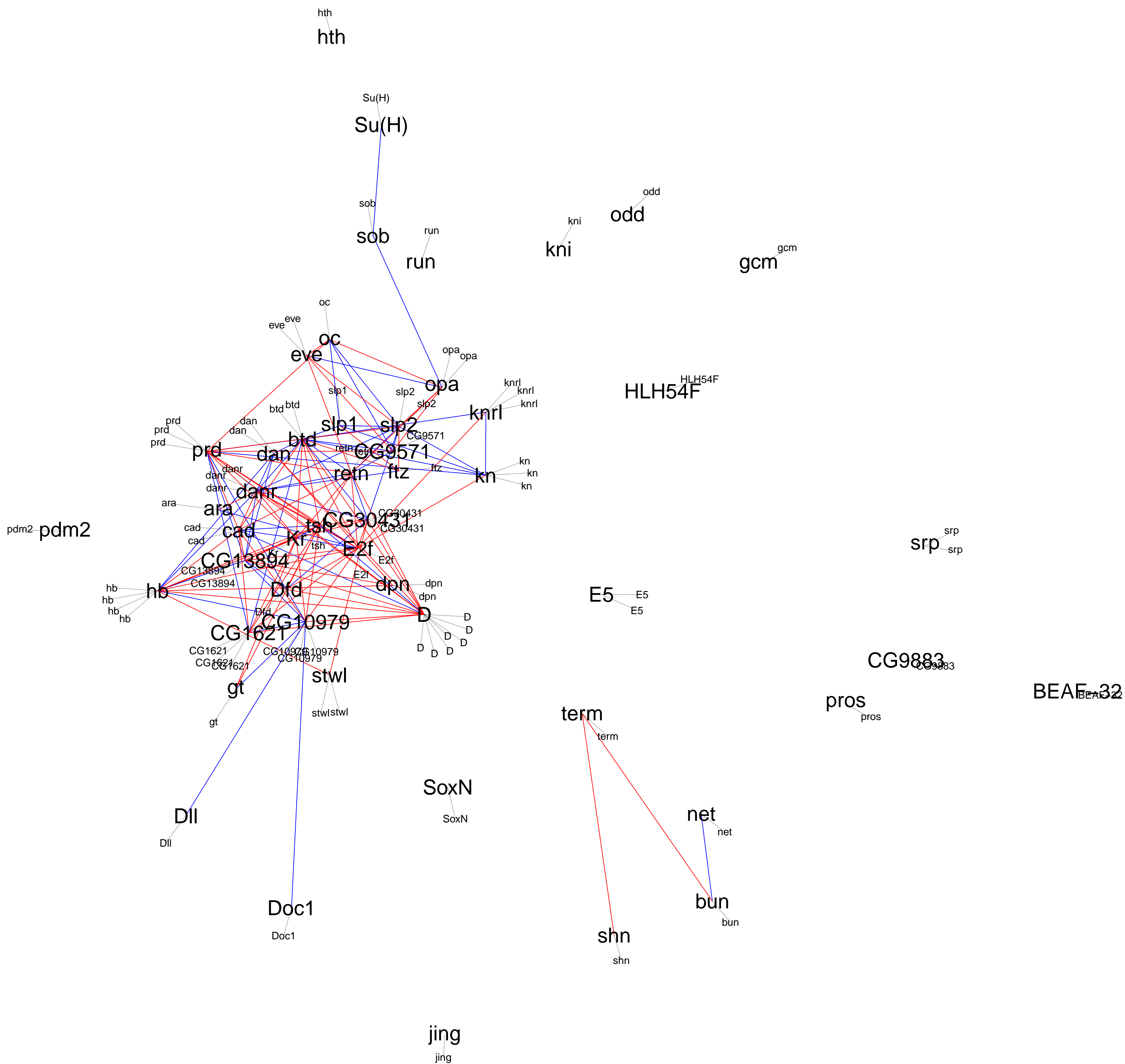
Lower 2.5% correlation = -0.63; upper 2.5% correlation = 0.76



Lower 2% correlation = -0.65; upper 2% correlation = 0.77



Lower 1.5% correlation = -0.68; upper 1.5% correlation = 0.79



The diagram illustrates a complex gene regulatory network. Key components include:

- Transcription Factors (TFs):** hth, Su(H), sob, run, kni, odd, gcm, eve, oc, opa, knrl, kn, retn, ftz, btd, slp1, slp2, dan, danr, ara, cad, hb, Dfd, D, E2f, E5, SoxN, DII, Doc1, jing, term, net, bun, shn, pros, BEAF-32.
- Target Genes:** CG9571, CG30431, CG13894, CG1621, CG10979, CG9883, BEAF-32.
- Regulatory Interactions:** Represented by colored lines (red, blue, green) connecting TFs to their target genes.

