

[illegible]

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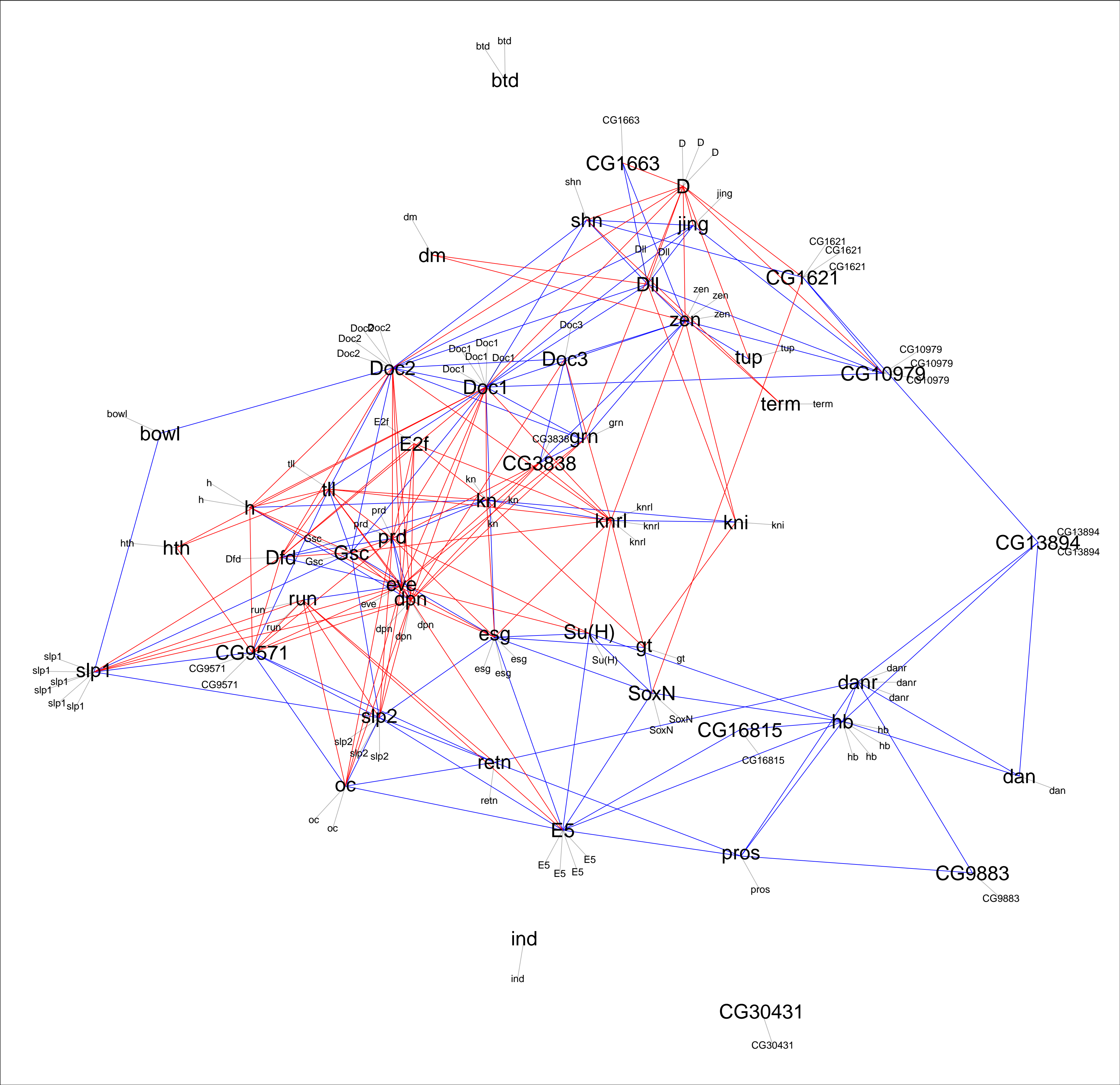




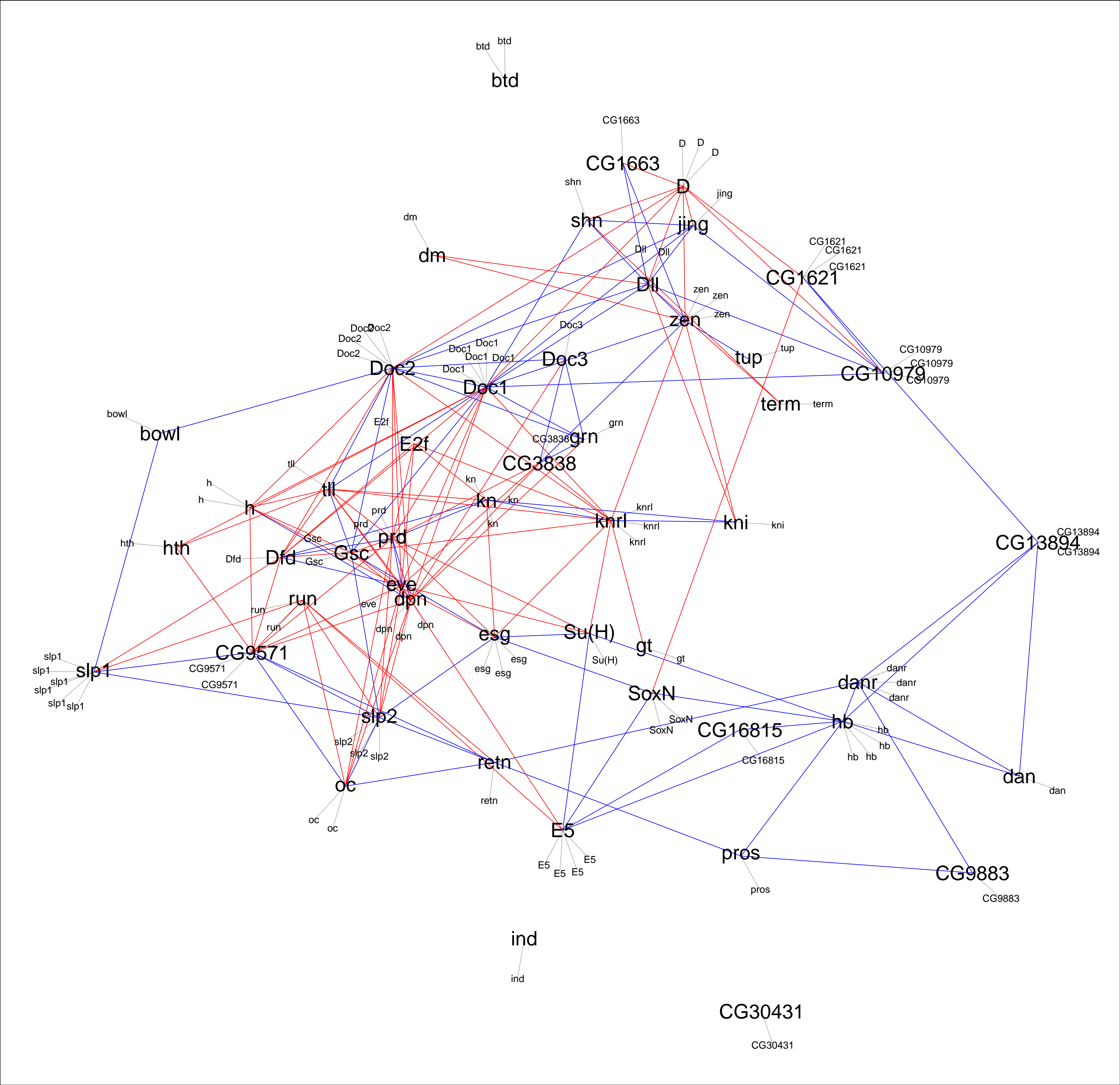




Lower 3% correlation = -0.54; upper 3% correlation = 0.74



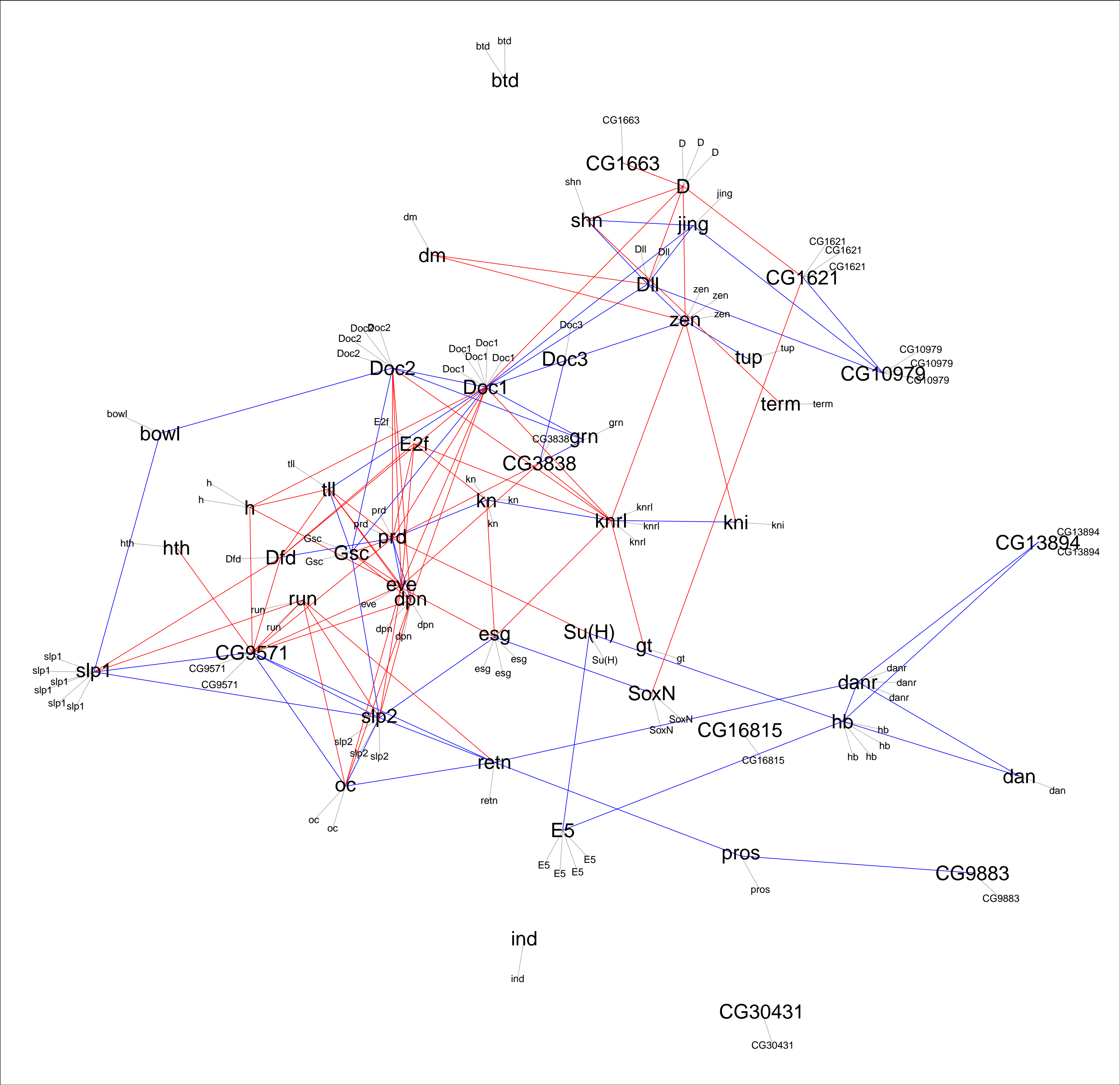
Lower 2.5% correlation = -0.56; upper 2.5% correlation = 0.75



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Lower 1.5% correlation = -0.61; upper 1.5% correlation = 0.79





The diagram illustrates a complex gene regulatory network. Nodes represent genes or transcription factors, and edges represent regulatory interactions. The network is highly interconnected, with many nodes having multiple incoming and outgoing edges. The nodes are labeled with gene names, often followed by a cluster ID (e.g., CG1663, CG1621, CG10979, CG3838, CG9571, CG16815, CG9883, CG30431, CG13894). The edges are colored, with red lines indicating one type of interaction and blue lines indicating another. The network is organized into several clusters, with some nodes acting as hubs. The overall structure suggests a complex regulatory hierarchy and feedback loops.

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