

The diagram illustrates a complex network of protein-protein interactions. The nodes are categorized by color and shape: red squares and circles (left cluster), blue squares and diamonds (right cluster), and black squares (other nodes). The interactions are represented by lines of varying thickness, suggesting different levels of interaction strength or type. The left cluster is highly interconnected, while the right cluster shows a more sparse network of interactions.

The diagram illustrates a complex gene-gene interaction network. Central nodes, such as *FGFR1*, *FGF2*, *FGF10*, *FGFR2*, and *FGFR3*, are highly connected hubs. Other prominent nodes include *ANOS1*, *GPC4*, *HSPG2*, *FGF1*, *FGF7*, *TNFAIP6*, *SDC2*, *DGN*, *FGF18*, *TGFBR3*, *KL*, *FGF9*, *FGF13*, *GPC3*, *FGF12*, *FGF17*, and *KL*. These central nodes are interconnected with peripheral nodes like *FGFBP1*, *CD44*, *PTX3*, *FGFBP3*, *KLB*, *FGF22*, *FIBP*, *GPC1*, *SDC1*, and *SDC4*. The color coding highlights functional groups: red for core FGF pathway components, black for related signaling molecules, blue for extracellular matrix and growth factors, and grey for highly connected hub genes.

