



Figure S17: Detailed protocol followed in co-expression network analysis. To perform co-expression analysis, initially a correlation matrix was constructed based on expression data of RBP and its PPI partners. Adjacency matrix of co-expression network was created based on the correlation matrix of RBP and its PPI partners. In the next step those edges having correlation coefficient $< |0.8|$ were removed. From the remaining edges of adjacency matrix, network was constructed based on MST algorithm. The co-expressed modules were identified based on the edge betweenness property. For visualization of networks in positive association between nodes green colored edge and for negative association red colored edges are used. To differentiate the nodes, RBPs are given in spherical and proteins in circular shape. Expression levels of nodes were scaled. Those nodes highly expressed are larger in size compared to the low expressed nodes. Also those proteins belonging to same module are visualized with same color.