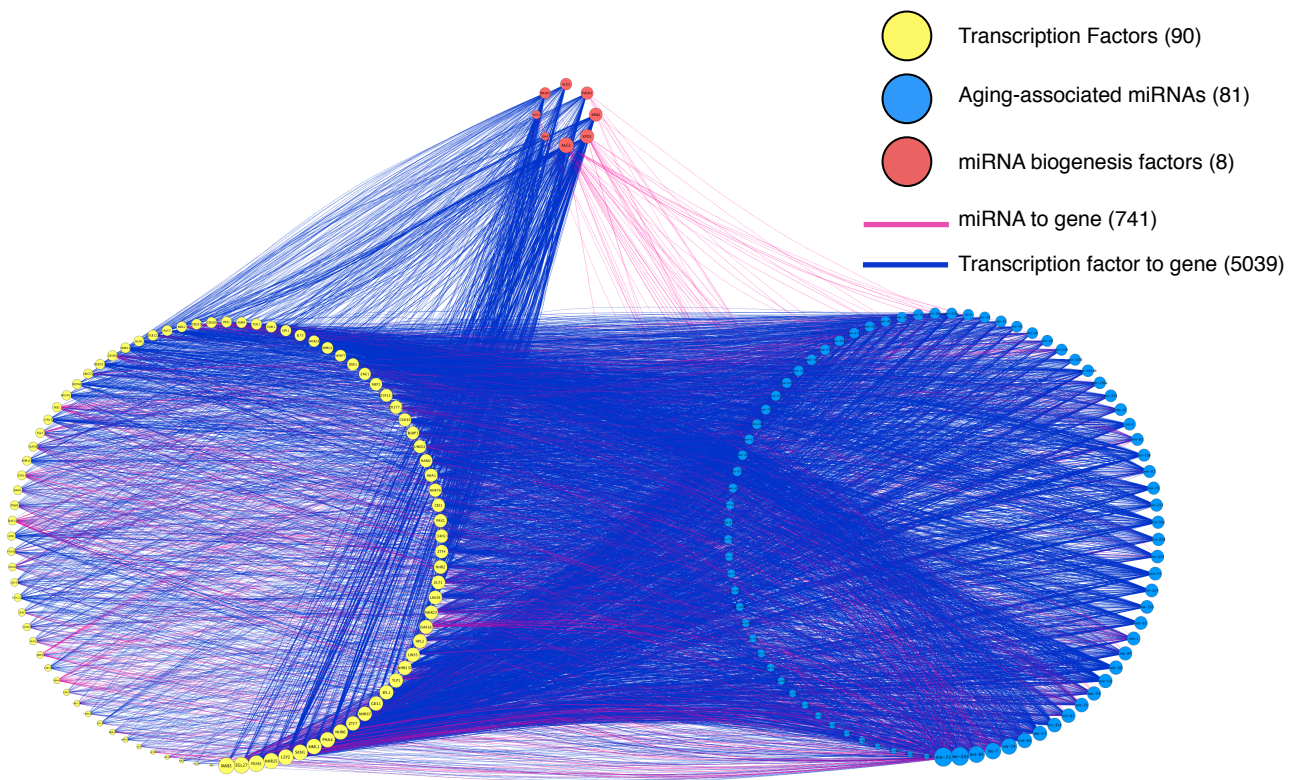
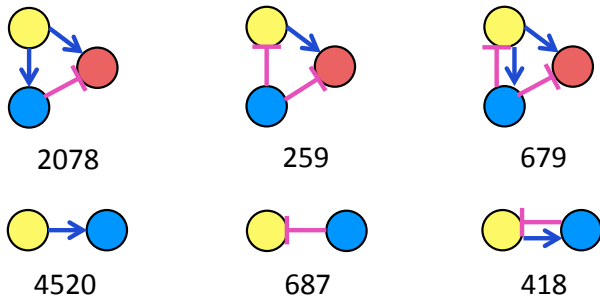


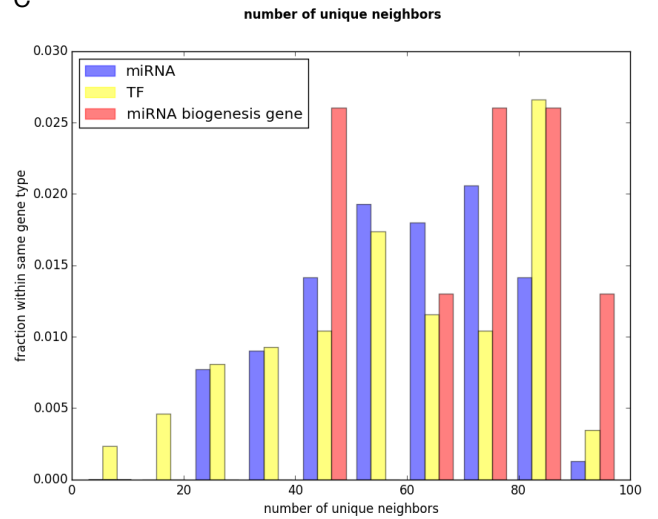
A



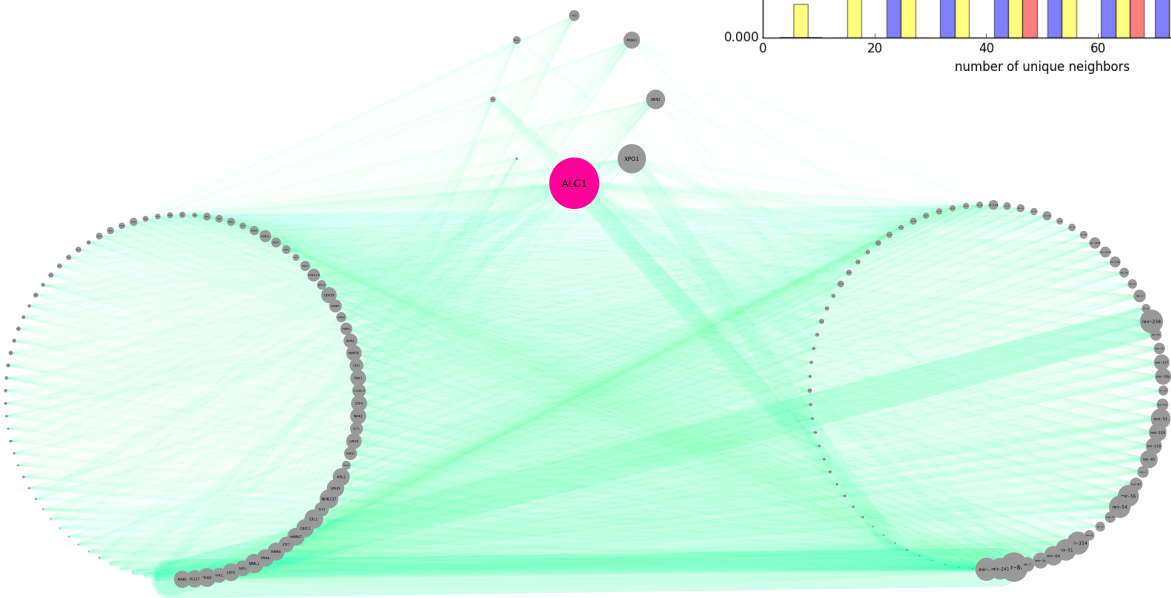
B



C



D



**Figure S1: Regulatory Gene Network of Aging. Related to Figure 1.**

(A) Network consists of 90 transcription factors, 81 aging-associated miRNAs and 8 miRNA biogenesis factors. Network shown in degree sorted layout by gene type using Cytoscape (Cline et al., 2007). Node sizes reflect node degrees. Yellow: TFs, blue: aging-associated miRNAs; red: miRNA biogenesis factors. Pink edges: miRNA-to-gene regulation; blue edges: TF-to-gene regulation. (B) Summary of interactions in the network. Interaction types are shown as diagrams and the numbers of those interactions represented in the network are indicated below. Color scheme same as in (A). (C) Histogram of number of unique first neighbors, scaled by frequency for each gene type. (D) The regulatory gene network in degree sorted layout by gene type, as in (A). Node and node label sizes reflect the betweenness centrality index of the node. Edge width and stroke transparency reflect edge betweenness. *alg-1* is shown in pink.