



FIG. 8. STRING output for the first bicluster ($\alpha = 0.5$, $\beta = 0.6$). Transcription factors are represented by nodes, and a variety of associations between the nodes are represented by the colored edges. The following associations between nodes are shown in the graph: (1) “neighborhood” indicating frequent occurrence of genes in the same genomic neighborhood (dark green); (2) “co-occurrence” of linked orthologous groups across species (dark blue); (3) “gene fusion” indicating whether fusion occurred (red); (4) “co-expression” representing evidence of mRNA co-expression of the associated genes (black); (5) “experiments” representing experimental evidence for an interaction (purple); (6) “databases” representing evidence from pathway databases for association (turquoise); and (7) “text mining” representing co-publication information (light green).