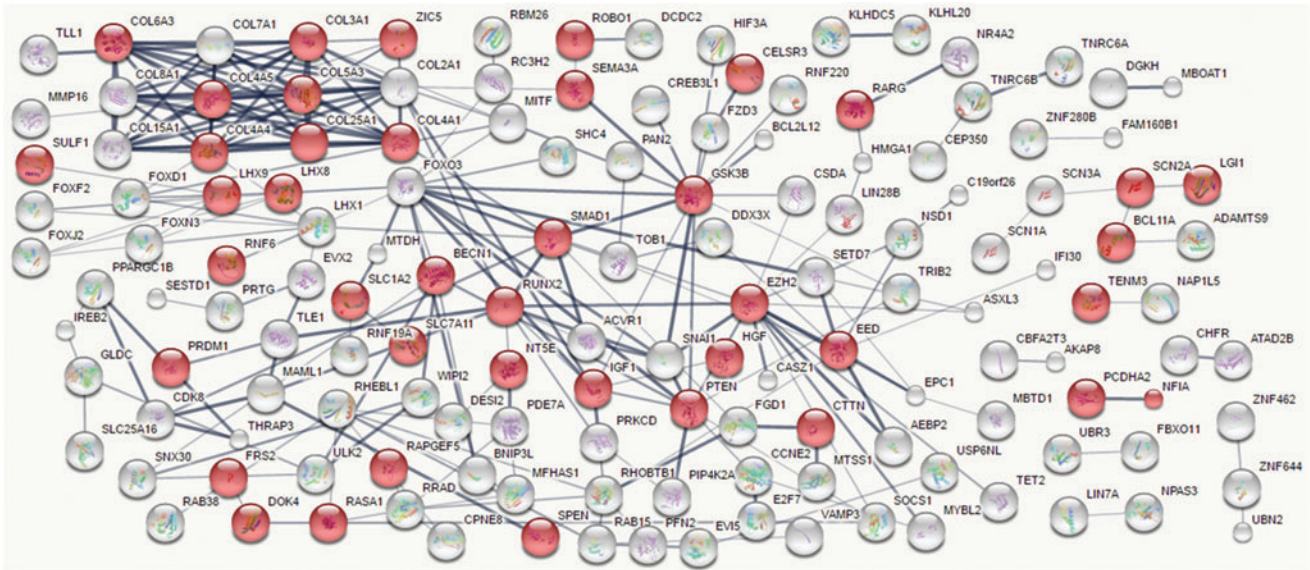# Supplementary Data

SUPPLEMENTARY FIG. S1. Protein interaction network for high-confidence mRNA targets. This network includes 280 mRNAs targeted by the six miRNAs of interest interrogated in String v10 software. Of the 280 mRNAs, 247 have protein products with functional interactions, which represents a clustering coefficient of 0.775 and exceeds the number of interactions expected by chance alone ($p < 0.0001$). The mRNAs in red represent those functionally related to nervous system development (61 genes; $p = 8.56E-09$). Large nodes have known three-dimensional structures, while small node structures are unknown. Edge width defines the meaningfulness of the interaction, with thick edges representing experimentally determined co-expression or homology. miRNA, microribonucleic acid.