

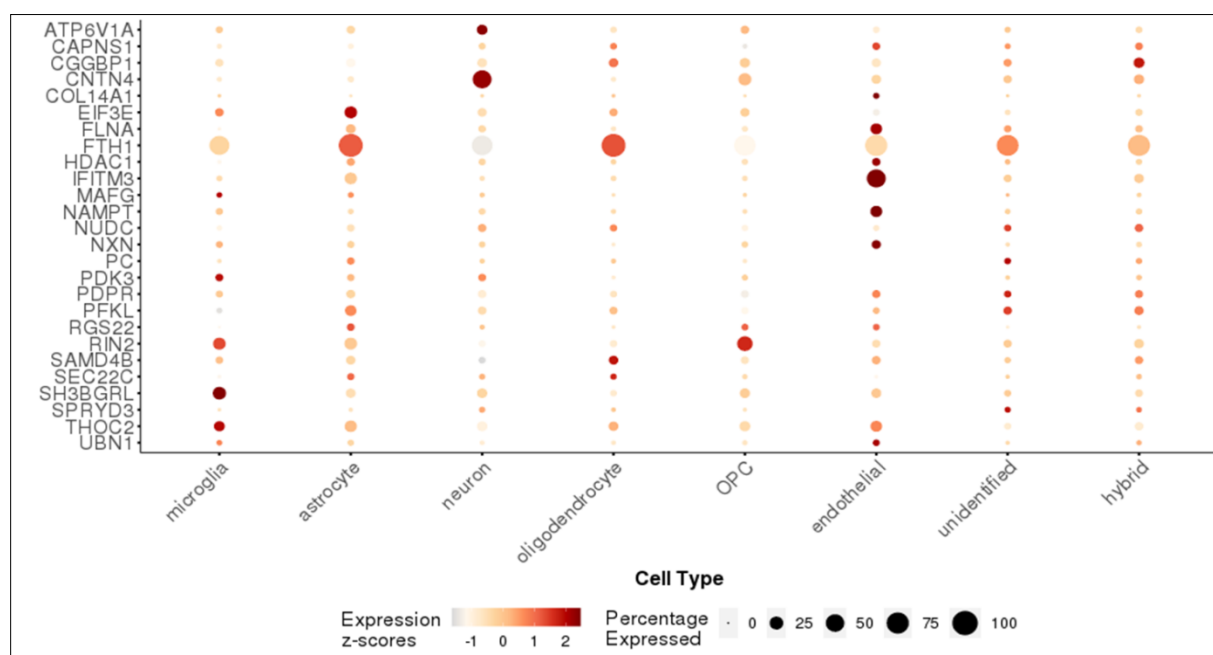


Fig. 1 Transcriptomic specificity of the circRNA genes. Cell types with the largest magnitude Z-score found in the entorhinal cortex. The size and color grades of each point indicate the abundance of the gene. 26 out of 34 input genes are found in the dataset. The following genes are not found: ADAMTS13, EXPH5, FOXO3B, ITPRIPL2, MYO1G, PCDH1, PPP1R14B, USP51.

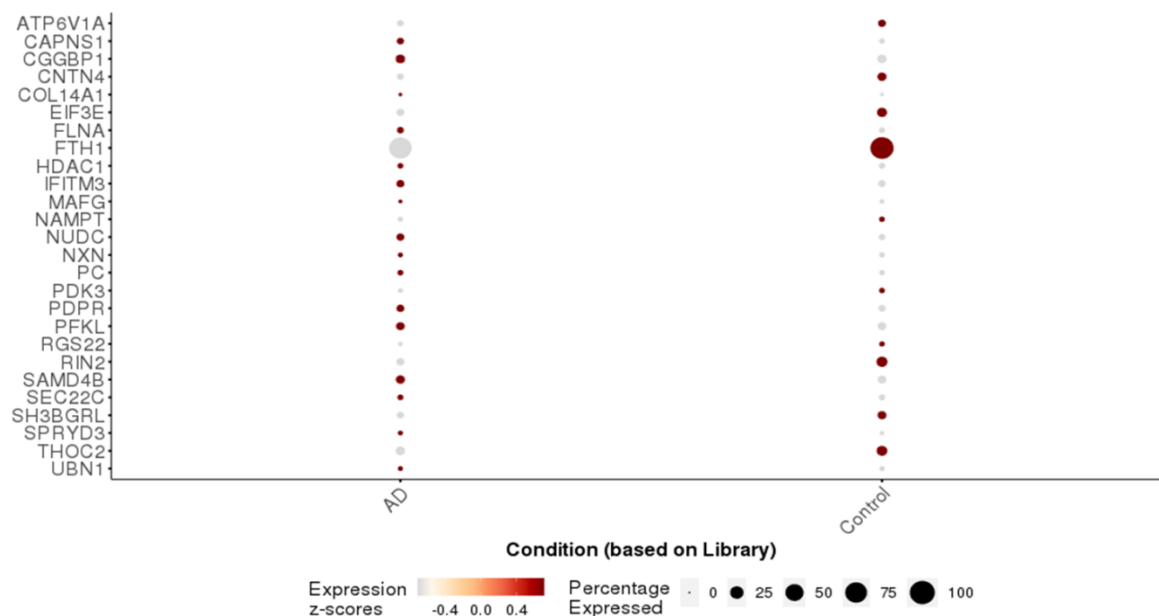


Fig. 2 Transcriptomic specificity of the circRNA genes in AD compared to control group.

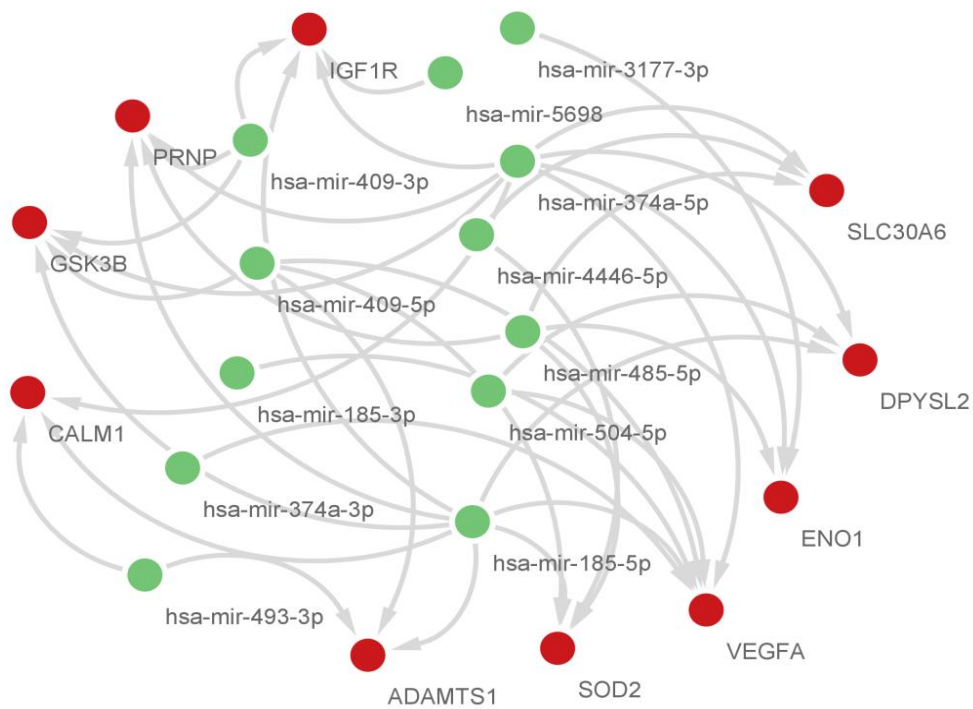


Fig 3 A sub-network constructed from the intersection of possible target genes of up/down regulated miRNAs and includes genes related to AD disease. Red nodes represents downregulated miRNAs

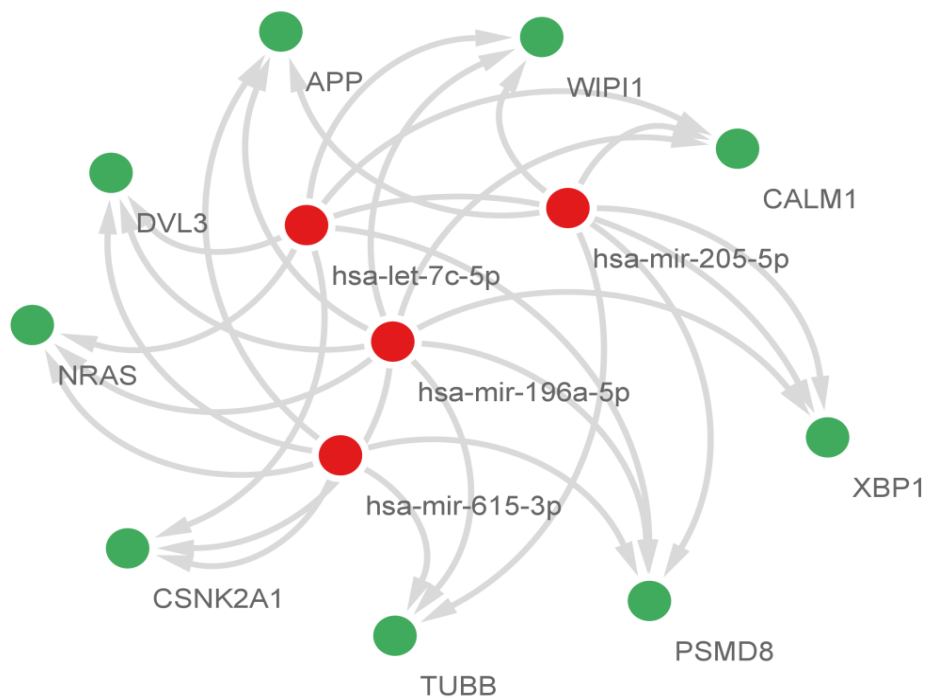


Fig. 4 A sub-network constructed from the intersection of possible target genes of upregulated miRNAs and includes genes related to AD disease. Red nodes represents upregulated miRNAs.

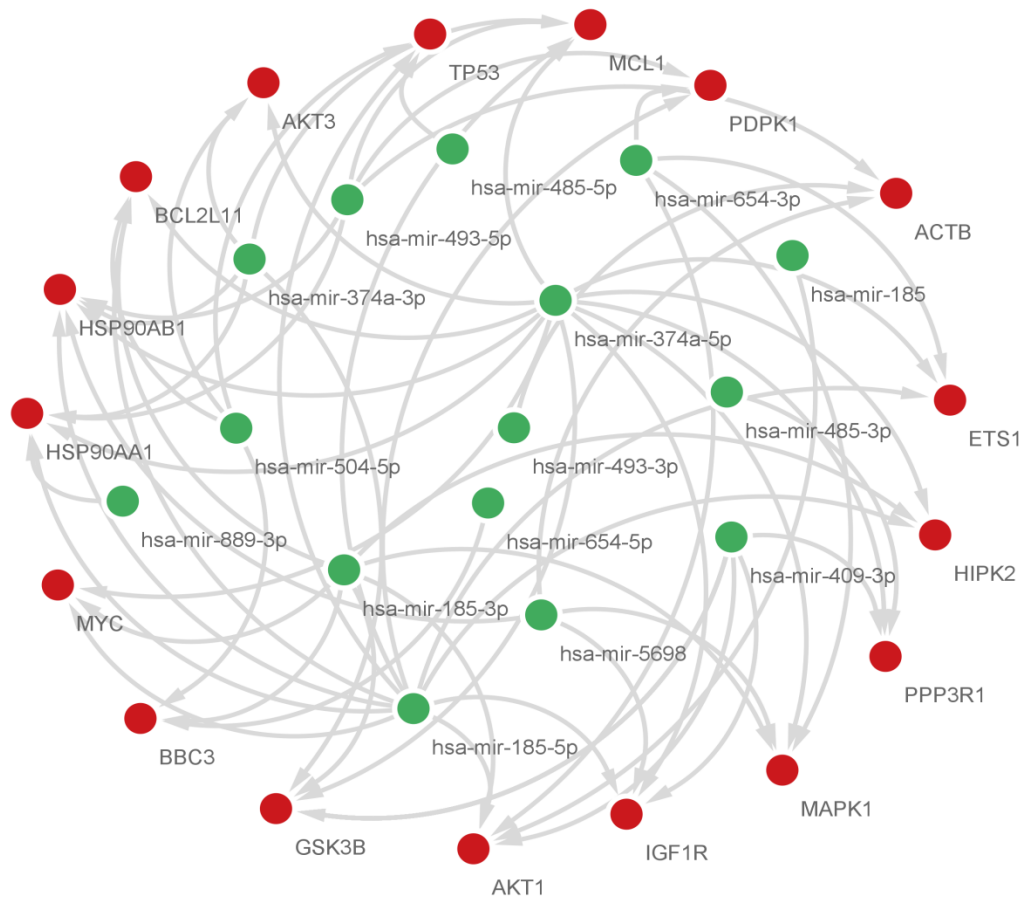


Fig. 5 A network is constructed from the target genes of downregulated miRNAs involved in the PI3K-Akt signaling, p53 signaling, cellular senescence, insulin signaling, mTOR and Apoptosis pathway and GO categories related to AD. Green nodes represents downregulated miRNas.