

Network Modeling

Bioinformatics Modeling for the Regulatory Network of circRNA hsa-circ-0000064

Regulatory interactions between circRNA-miRNA and miRNA-mRNA, were predicted computationally by Targetscan^[1] and miRanda algorithm ^[2], then integrated to represent the regulatory network of ceRNA network of circRNA hsa-circ-0000064 which is HCC related. Both species have been subjected to adjacency matrix set up based on the weight of interaction between predicted targets, circRNA hsa-circ-0000064 and its' target miRNAs as well as miRNA mir-1825 and its target mRNAs were represented by weight matrix describing relation strength from selected databases. Finally, the final proposed ceRNA network was constructed using Cytoscape 3.5.1 ^[3]. Network analysis suggested the TRIM2 tumor suppressor which we used to experimentally assess the regulatory function of ceRNA network. The ceRNA network and it's graphical representation helped us to interpret the interaction mechanisms and signalling of circRNAs, miRNAs, and regulated mRNAs that have significant association to circRNAs regulatory role in HCC.

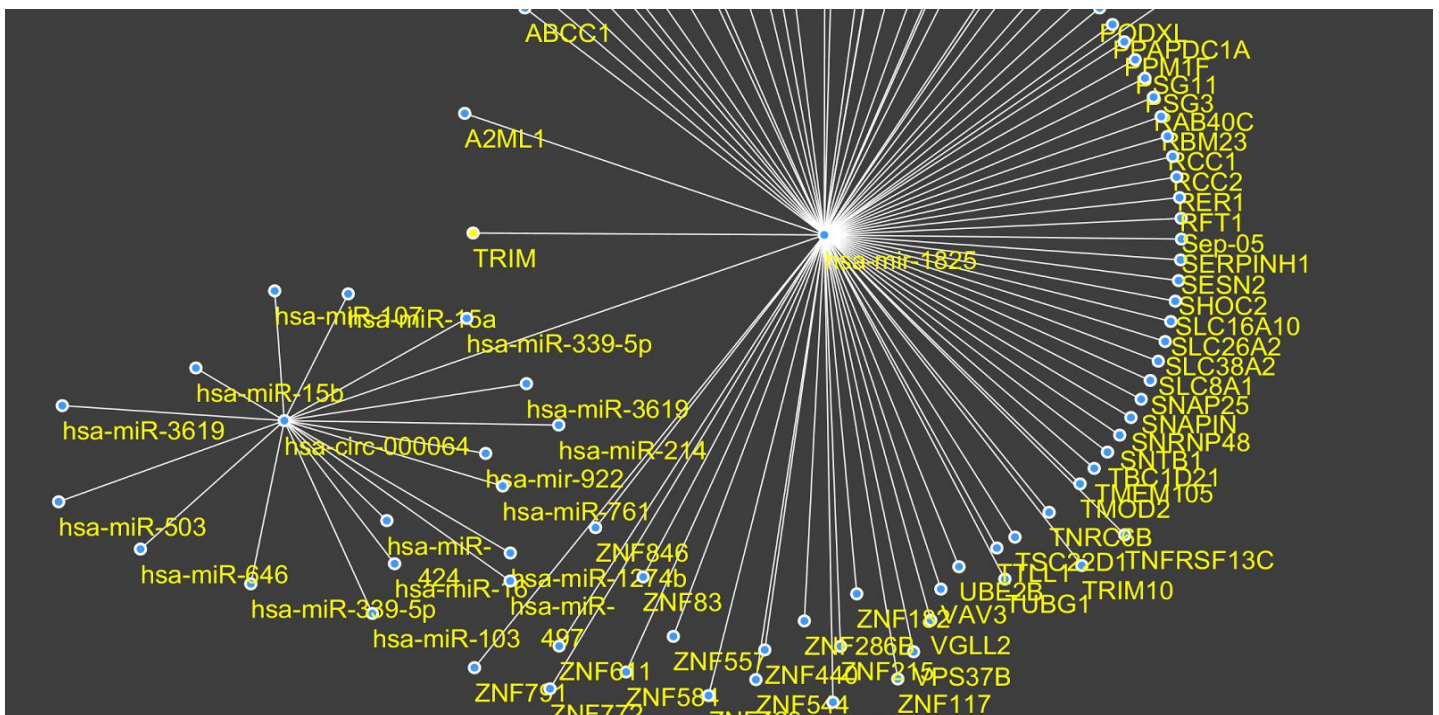


Figure-1 Regulatory network of circular RNA

References

- 1- Miranda KC, Huynh T, Tay Y, et al. A pattern-based method for the identification of MicroRNA binding sites and their corresponding heteroduplexes. *Cell*. 2006;126(6):1203-17
- 2- Lewis BP, Burge CB, Bartel DP. Conserved seed pairing, often flanked by adenosines, indicates that thousands of human genes are microRNA targets. *Cell*. 2005;120(1):15-20.
- 3- Shannon P, Markiel A, Ozier O, et al. Cytoscape: A Software Environment for Integrated Models of Biomolecular Interaction Networks. *Genome Research*. 2003;13(11):2498-2504. doi:10.1101/gr.1239303.