## Study of Gene- microRNA Regulatory Networks across different tissues in a Schizophrenic patients

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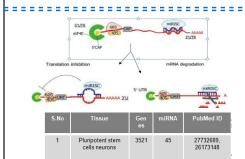
## Abstract

Schizophrenia is one of the most prevalent psychotic disorder that affected an estimated 20 million worldwide, according to WHO estimates in 2019. It is characterized by positive symptoms such as delusions and hallucinations as well as negative symptoms such as reduced speech and apathy. While many factors, including genetic, epigenetic, environmental, and chemical imbalances have been thought to be linked with this disease, the pathogenesis of SCZ still remains elusive without much mechanistic insights. Many functional studies have pointed to a critical role of regulatory elements such as microRNAs and transcription factors. However, a systematic investigation of the gene regulatory networks in SCZ across the various tissues is still missing. In this study, we mapped the several miRNA regulatory networks with biological context in SCZ across 9 different tissue types including various regions of the brain, immune cells, and blood. We identified several SCZ-contextual regulatory hubs that shea liaht on the differential activation of these regulatory elements across the various brain tissues. In particular, miR-34 family is a critical regulatory hub that is activated differentially across the various tissue types.

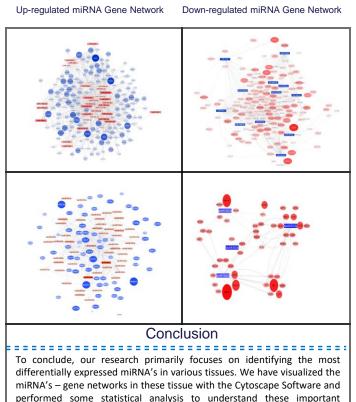
## Introduction

Dorsofrontal Cortex

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orefrontal cortex



miRNA's. Therefore, with this data one can conclude on the important

miRNA targets that can be used for effective drug delivery.

## **Analytics** Up-regulated miRNAs Down-regulated miRNAs