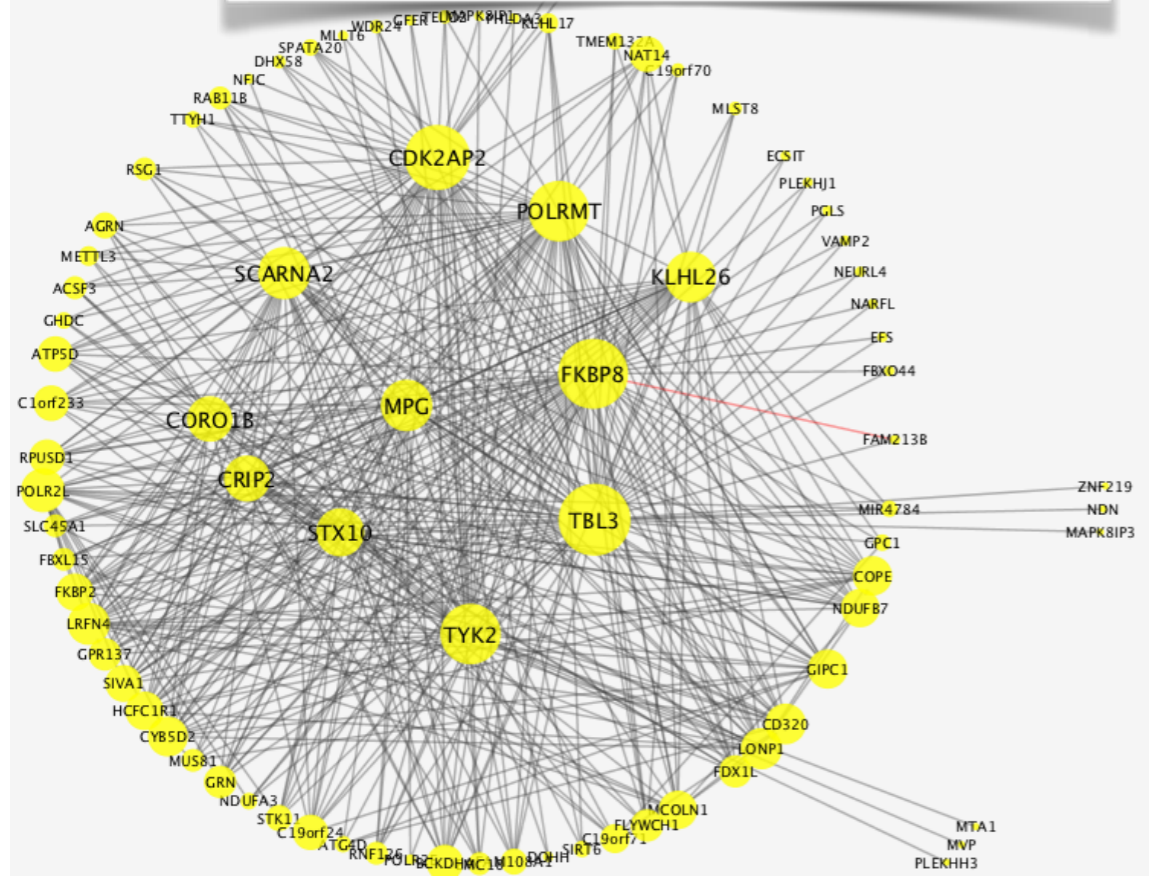
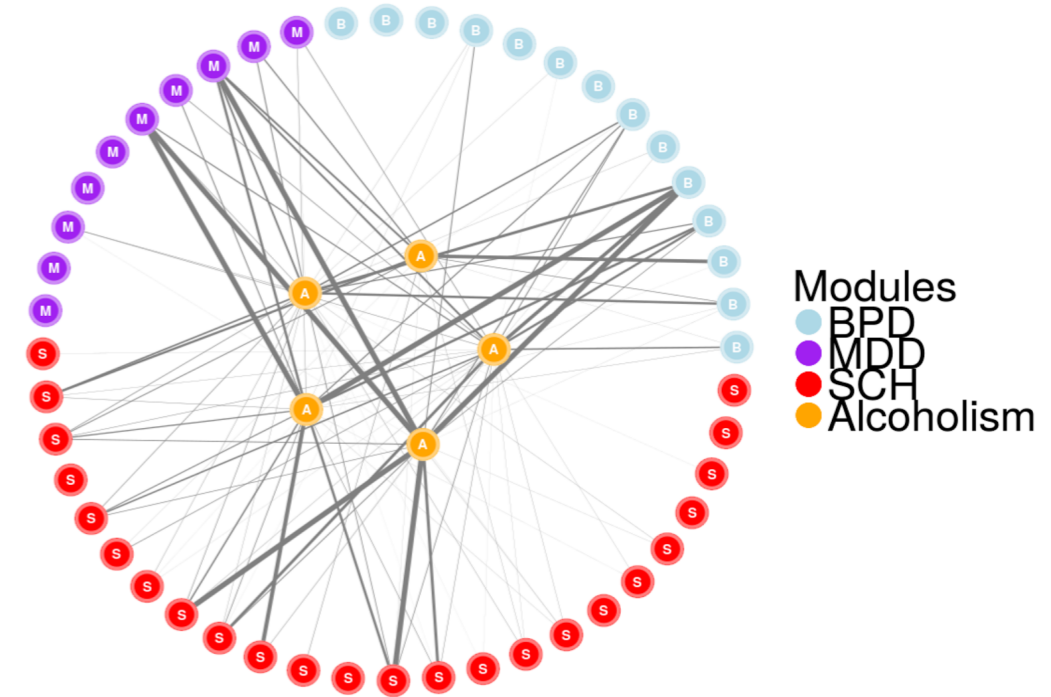
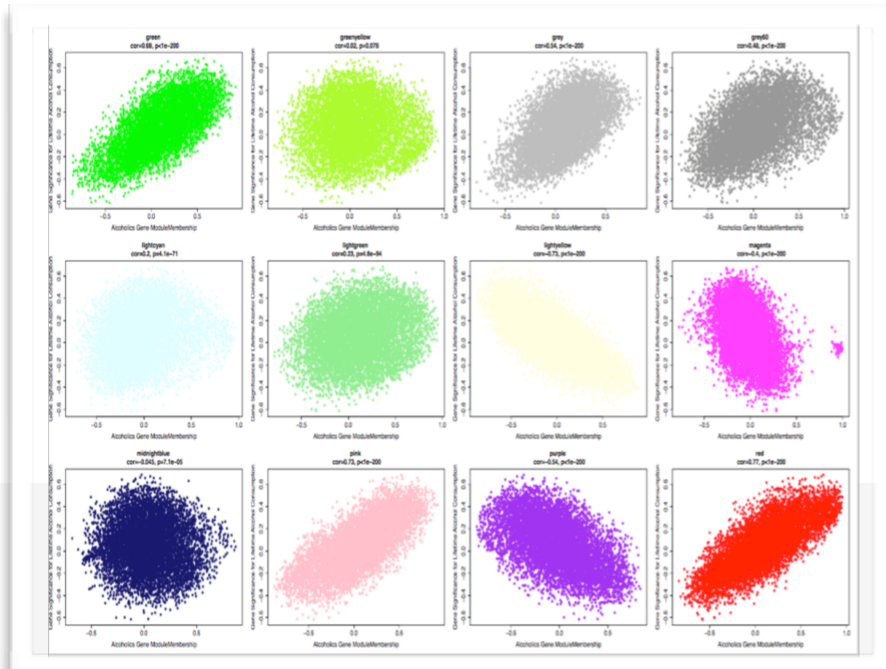


# Transcriptional Profiling of Psychiatric Disorders

In collaboration with Dr. Dayne Mayfield, Waggoner Center for Alcohol & Addiction Research

Identification of transcriptional changes and novel transcripts in the brain related to chronic alcohol abuse (4 brain regions, 30 alc, 30 controls per region)

Comparison of genes co-expressed in alcohol abuse to other psychiatric disorders (Bipolar, depression, schizophrenia) using publicly available data



Identification of FDA approved drugs with an effect on dysregulated gene modules in alcohol abuse (using the Library of Integrative Network-based Cellular Signatures-LINCS)

| Drug Name           | FDA Status                              | Connectivity Score |
|---------------------|---|--------------------|
| formestane          | Approved, Investigational, Withdrawn    | -95.11             |
| metolazone          | Approved                                | -96.17             |
| Erlotinib           | Approved                                | -96.38             |
| timolol             | Approved                                | -95.3              |
| finasteride         | Approved                                | -95.65             |
| flunarizine         | Approved                                | -98.77             |
| alprazolam          | Approved, Illicit, Investigational      | -95.95             |
| ipratropium bromide | Approved                                | -96.71             |
| labetalol           | Approved                                | -95.56             |
| etodolac            | Approved, Investigational, Vet Approved | -95.18             |
| clofibrate          | Approved                                | -95.91             |

# Transcriptional Profiling of Psychiatric Disorders

In collaboration with Dr. Mbemba Jabbi, Dept of Psychiatry, Dell Medical School

RNA-Sequencing of anterior insula samples (100) from individuals with bipolar disorder (37), depression (30) and healthy controls (33).

Identification of differentially enriched transcription factors and pathways

Type II interferon signaling (IFNG)\_Homo sapiens\_WP619

Type II interferon signaling (IFNG)\_Mus musculus\_WP1253

IL-7 Signaling Pathway\_Homo sapiens\_WP205

IL-9 Signaling Pathway\_Mus musculus\_WP10

IL-9 Signaling Pathway\_Homo sapiens\_WP22

IL-2 Signaling Pathway\_Homo sapiens\_WP49

Type III interferon signaling\_Homo sapiens\_WP2113

IL-7 Signaling Pathway\_Mus musculus\_WP297

IL-4 Signaling Pathway\_Homo sapiens\_WP395

Interferon type I signaling pathways\_Homo sapiens\_WP585

Identification of modules of co-expressed genes using WGCNA (Weighted Gene Co-expression Network Analysis)

Module-trait relationships

