Transcriptomic Analysis of Hyperglycemic and Hypoglycemic Effects on Ocular Tissues: Unraveling the Molecular Landscape in Ophthalmology

Introduction

Transcriptomic analyses are essential in deciphering the complex world of gene expression, providing valuable insights into the molecular underpinnings of biological processes. By studying the complete set of RNA transcripts, transcriptomics helps uncover how genes are regulated and how they respond to various conditions and treatments. This knowledge is critical for advancing our understanding of disease mechanisms, identifying potential biomarkers, and developing targeted therapies. As an experienced bioinformatician, I recognize the significance of transcriptomic analyses in driving groundbreaking discoveries and advancing our understanding of intricate cellular processes. It serves as a powerful tool to explore the genetic basis of health and disease, propelling advancements in diverse areas of biological research.

Problem

The aim of this study was to comprehensively investigate and understand the effects of glucose treatment on eye tissue. Glucose, as a fundamental energy source for cells, plays a crucial role in various physiological processes. However, elevated glucose levels have been associated with several ocular disorders, including diabetic retinopathy and cataracts, highlighting the need for a thorough examination of its impact on the eye tissue transcriptome. By conducting a transcriptomic analysis, we seek to unravel the molecular alterations induced by glucose treatment in the ocular environment. This research is crucial in elucidating the underlying mechanisms and pathways affected by glucose, providing valuable insights into the potential role of glucose metabolism in ocular health and disease. The findings from this investigation hold the promise of advancing our understanding of ocular physiology and may have implications for the development of targeted interventions and therapeutic strategies to mitigate glucose-related ocular pathologies.

Approach

In this transcriptomic analysis aimed at understanding the effect of glucose treatment on eye tissue, a rigorous suite of bioinformatics approaches was systematically employed to gain comprehensive insights into the molecular mechanisms at play. Initially, raw RNA-Seq data underwent thorough preprocessing, including quality filtering and alignment to a suitable reference genome. Quantification of gene expression levels was achieved using robust tools such as featureCounts with meticulous parameter optimization to suit the experimental design. Careful normalization procedures were implemented to account for confounding factors, ensuring accurate and reliable comparisons between samples.

To investigate the gene of interest, EGR1, in greater detail, a network analysis was conducted using the STRING database and Cytoscape. This analysis unveiled intricate protein-protein interactions and regulatory networks involving EGR1, shedding light on its potential role as a central regulatory element in the context of glucose treatment effects in eye tissue.

In addition to examining individual gene expression, miRNA-mRNA interactions were mapped to explore potential post-transcriptional regulatory mechanisms. This step provided insights into the impact of glucose treatment on miRNA-mediated gene regulation, revealing several miRNA-mRNA pairs and their relative pathways implicated in the response to glucose treatment.

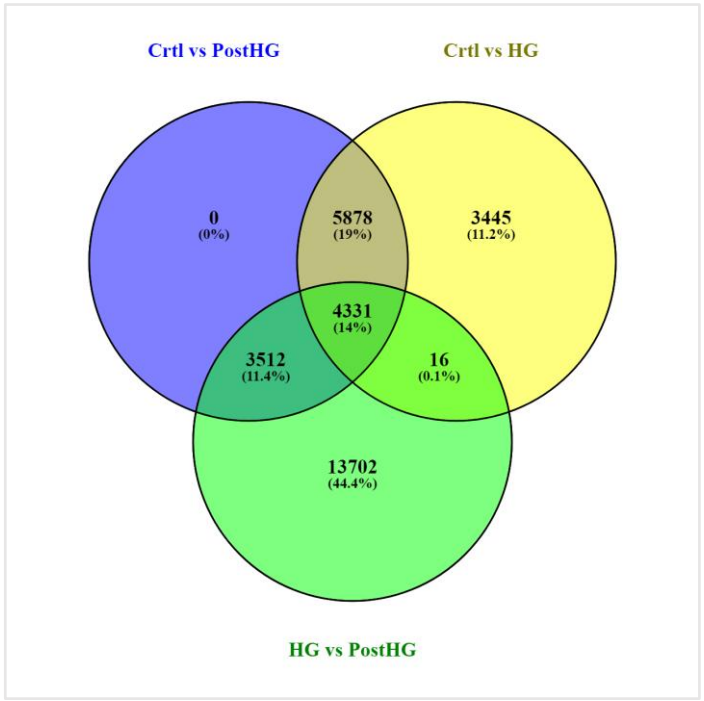
Furthermore, the involvement of long non-coding RNAs (lncRNAs) in the regulatory landscape was explored. By mapping lncRNAs to their respective miRNA-mRNA targets and pathways, we gained a deeper understanding of their potential role in modulating gene expression in response to glucose treatment.

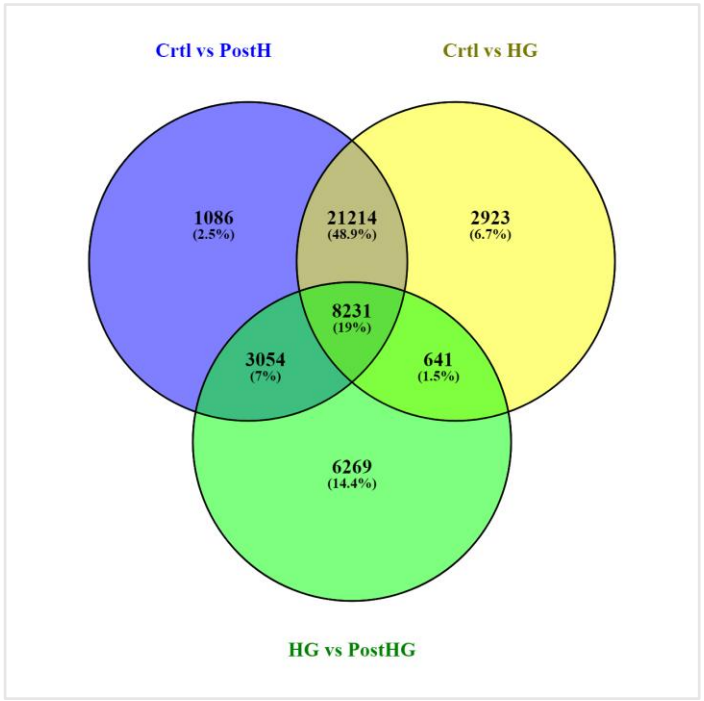
Given EGR1's role as a transcription factor, we sought to elucidate potential binding motifs in the identified differentially expressed genes (DEGs) for EGR1. This analysis was performed prior to annotation and pathway enrichment to discern EGR1's potential direct transcriptional targets and further contribute to understanding its regulatory impact in the context of glucose treatment.

In conclusion, the comprehensive bioinformatics approaches undertaken in this study facilitated a comprehensive characterization of the transcriptomic changes induced by glucose treatment in eye tissue. The integration of network analysis, miRNA-mRNA interactions, and lncRNA regulatory networks, alongside the investigation of EGR1's binding motifs, provided valuable insights into the molecular mechanisms underlying the observed effects. These findings contribute to a deeper comprehension of the interplay between glucose metabolism and ocular health, paving the way for potential therapeutic strategies targeting glucose-related ocular conditions.

Results

In our transcriptomic analysis investigating the effect of glucose treatment on eye tissue, we observed significant changes in gene expression profiles. Functional enrichment analysis revealed that several biological pathways were significantly affected, including glucose metabolism, oxidative stress response, and inflammation regulation. Additionally, the network analysis focusing on the gene of interest, EGR1, unveiled its central role in a protein-protein interaction network associated with glucose treatment. These results collectively provide critical insights into the molecular alterations induced by glucose treatment in eye tissue, highlighting potential mechanisms underlying glucose's impact on ocular physiology and warranting further investigations for targeted therapeutic interventions in glucose-related ocular conditions.

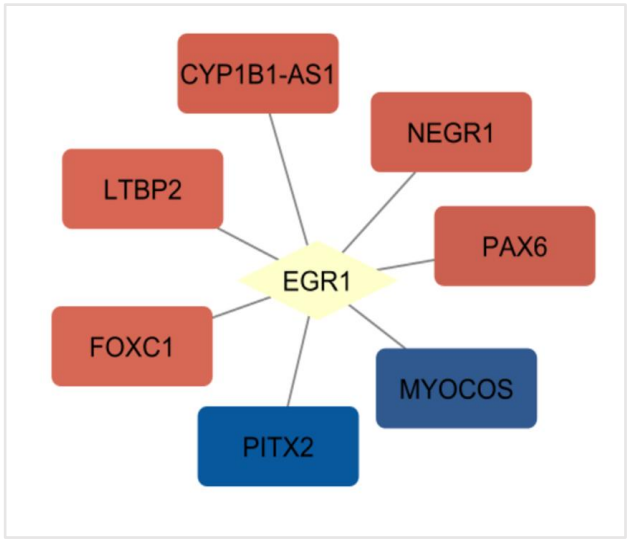




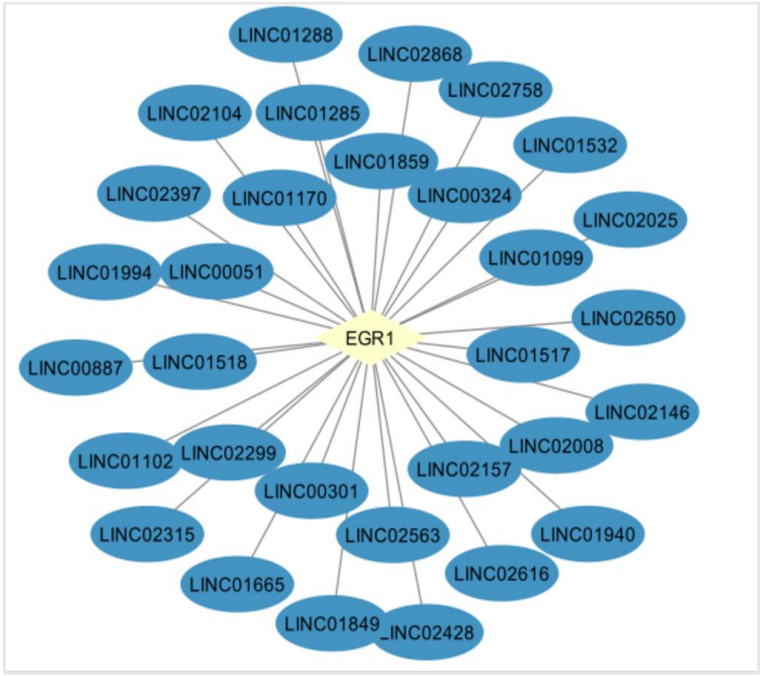
Upregulated and downregulated genes across all treatment groups were estimated

Results

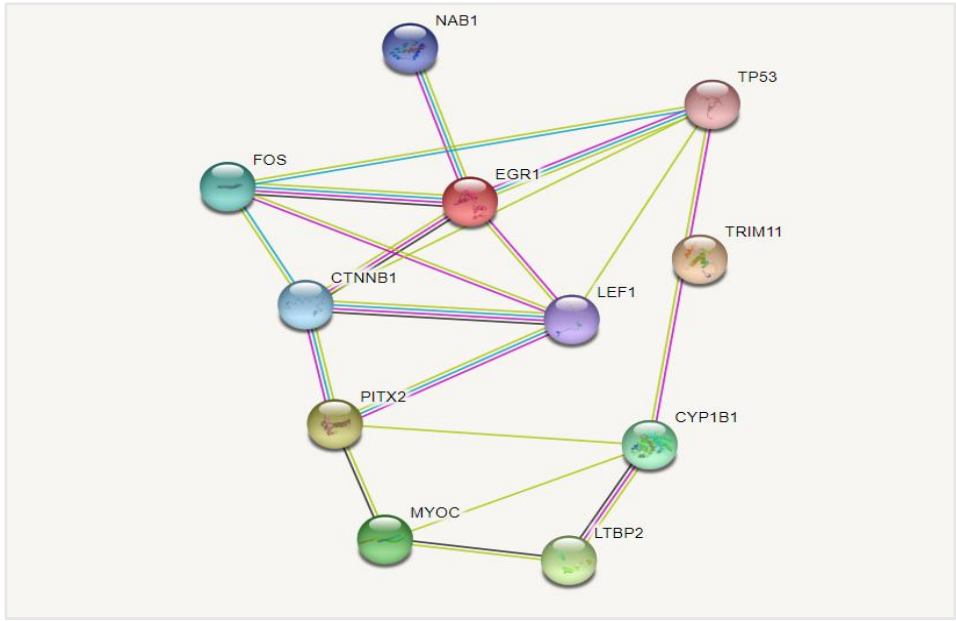
Cytoscape and STRING database - performed to identify genes interacting with EGR1



Eye associated genes are interacting with EGR1



Non-coding RNAs are interacting with EGR1

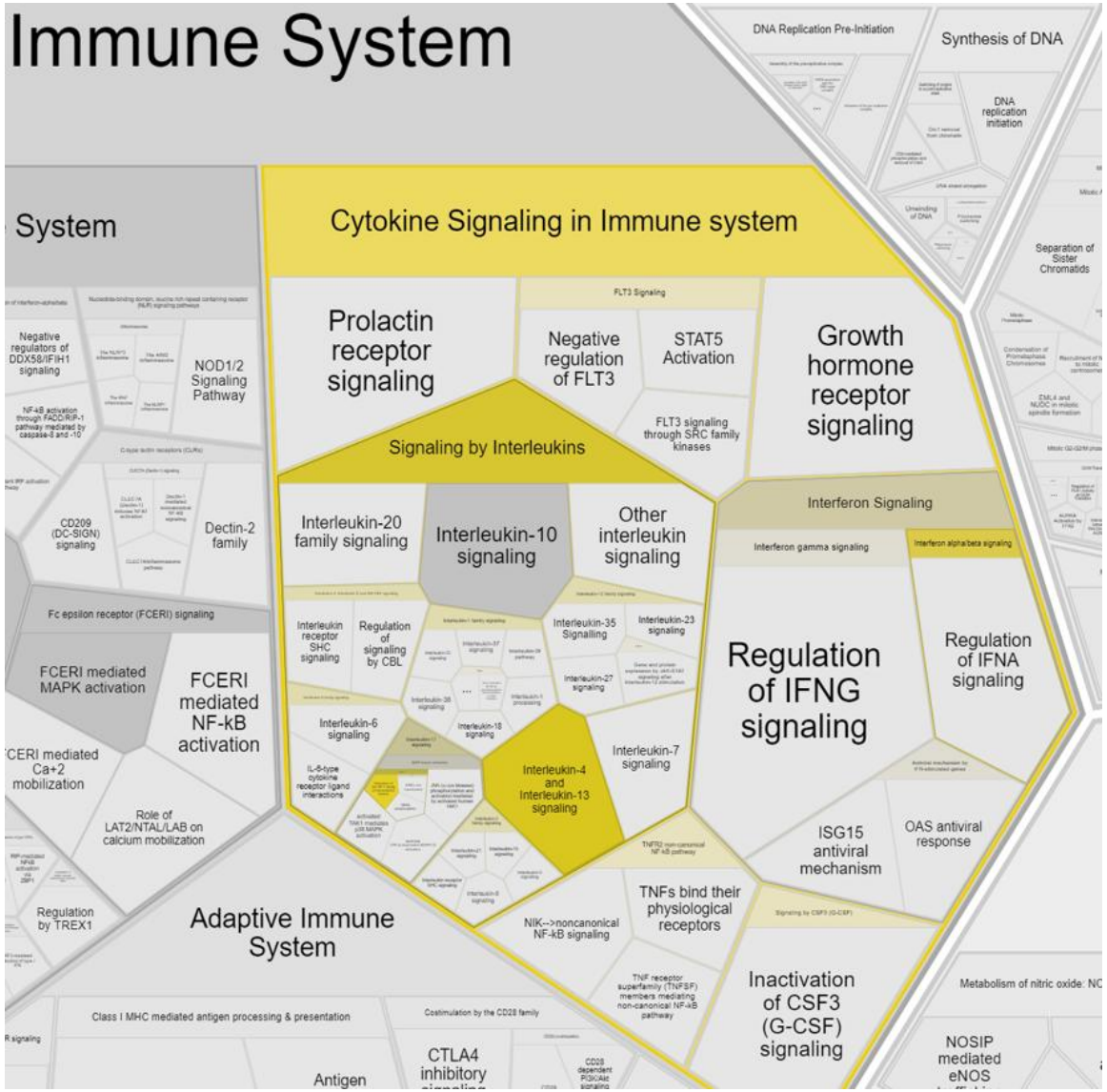


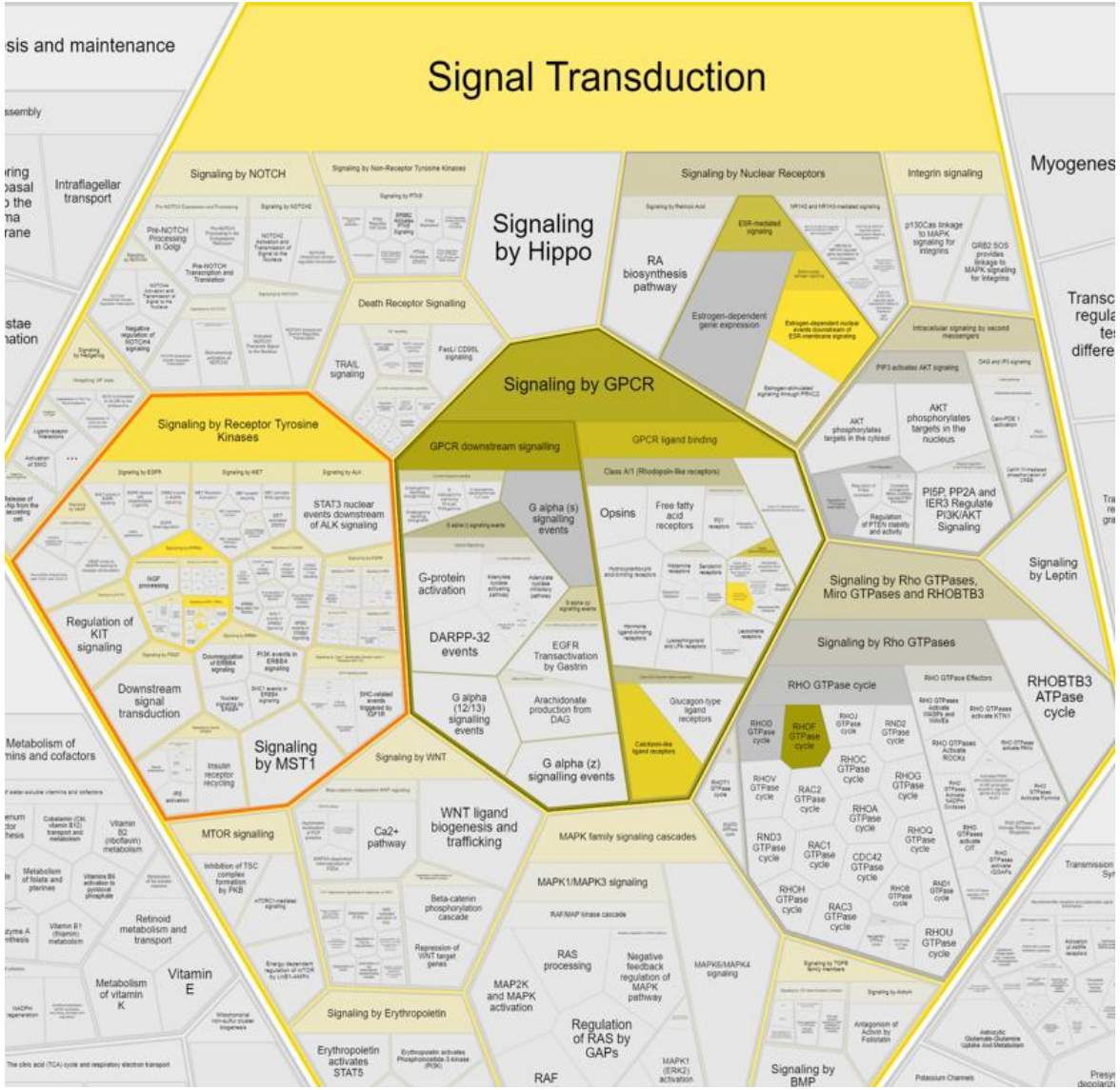
NETWORK FROM STRING DATABASE- at **protein-protein level**

These are eye associated genes interacting with EGR1

The STRING database contains information from numerous sources, including experimental data, computational prediction methods and public text collections.

TP53 looks like the connecting protein for all the eye-associated genes





Reactome pathways for upregulated genes identified