

Multi-Omic Analysis of Glioblastoma Multiforme

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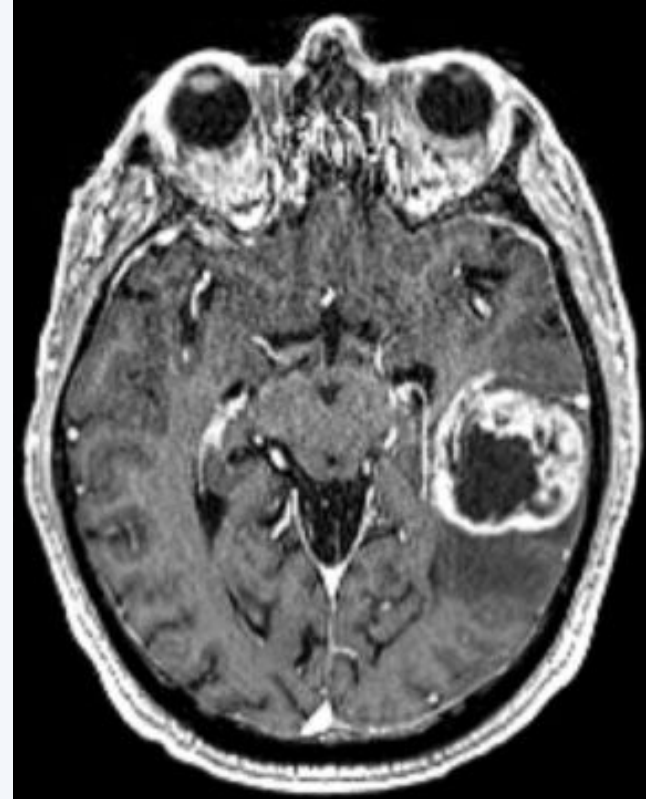
01.



Introduction

Glioblastoma Multiforme

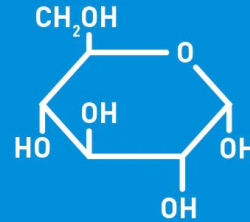
- fast-growing aggressive brain tumor
- invades tissues but doesn't often spread to distant organs
- most common malignant brain tumor
 - 49.1% of cases



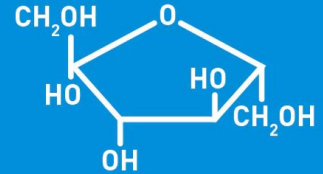
GBM Energy Metabolism

- Primary energy source: glucose
- Low glucose levels → other energy substrates
- Fructose: second most abundant sugar in blood

GLUCOSE

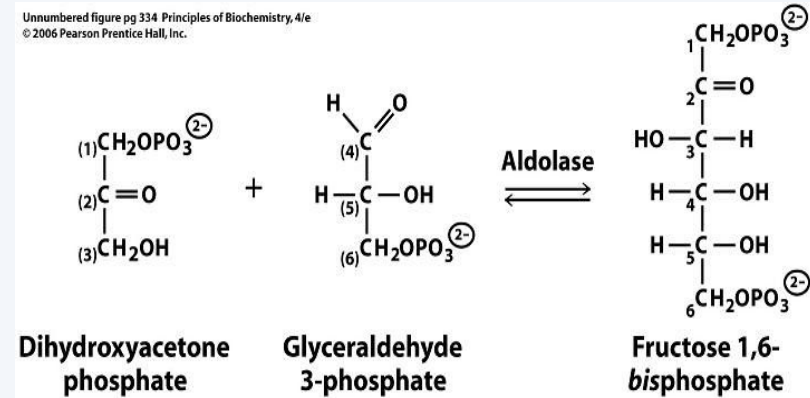


FRUCTOSE



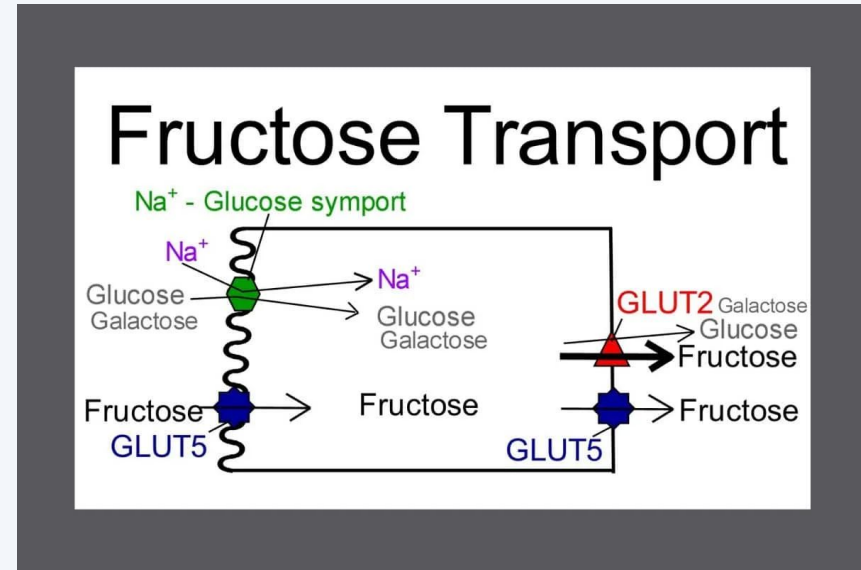
Genes of Interest

- ALDOB: Aldolase for fructose 1,6 biphosphate B
 - Catalyzes fructose 1,6 biphosphate to glyceraldehyde 3 phosphate and dihydroxyacetone phosphate
 - Expressed in low quantities for patients diagnosed with cancer for most malignancies in the human body
 - Low expression typically yields poorer prognosis



Genes of Interest

- SLC2A5: solute carrier family 2 member 5
 - Mediates uptake of of fructose via GLUT5
 - Insulin-independent fructose transporter





Hypothesis

Patients with GBM would have a higher mutation rate in genes ALDOB and SLC2A5, correlating to a lower survivability which could be captured by a machine learning model.

02.



Methods

Methods

Oncoplot

10 frequently mutated genes in GBM

Source: TCGA, n = 305

Kaplan-Meier

ALDOB & SLC2A5 genes

Source: TCGA, n = 338

Scatter Plot

transcription-translation analysis

Source: CPTAC, n = 108

Methods

DGE

differential gene analysis

Source : TCGA, n = 371 | Variables: ~ age + vital status

Machine Learning

classification of patient vital status with RNA/protein expression of ALDOB & SLC2A5

Source: CPTAC, n = 93

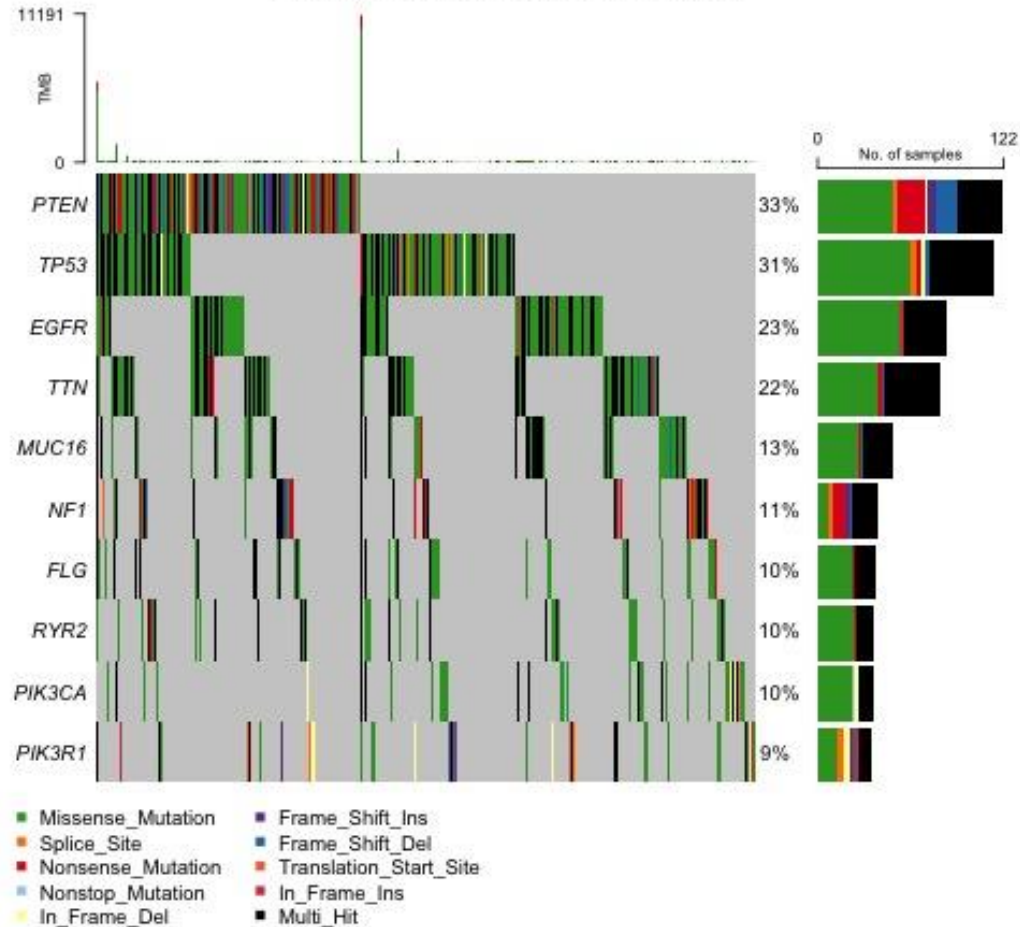
03.



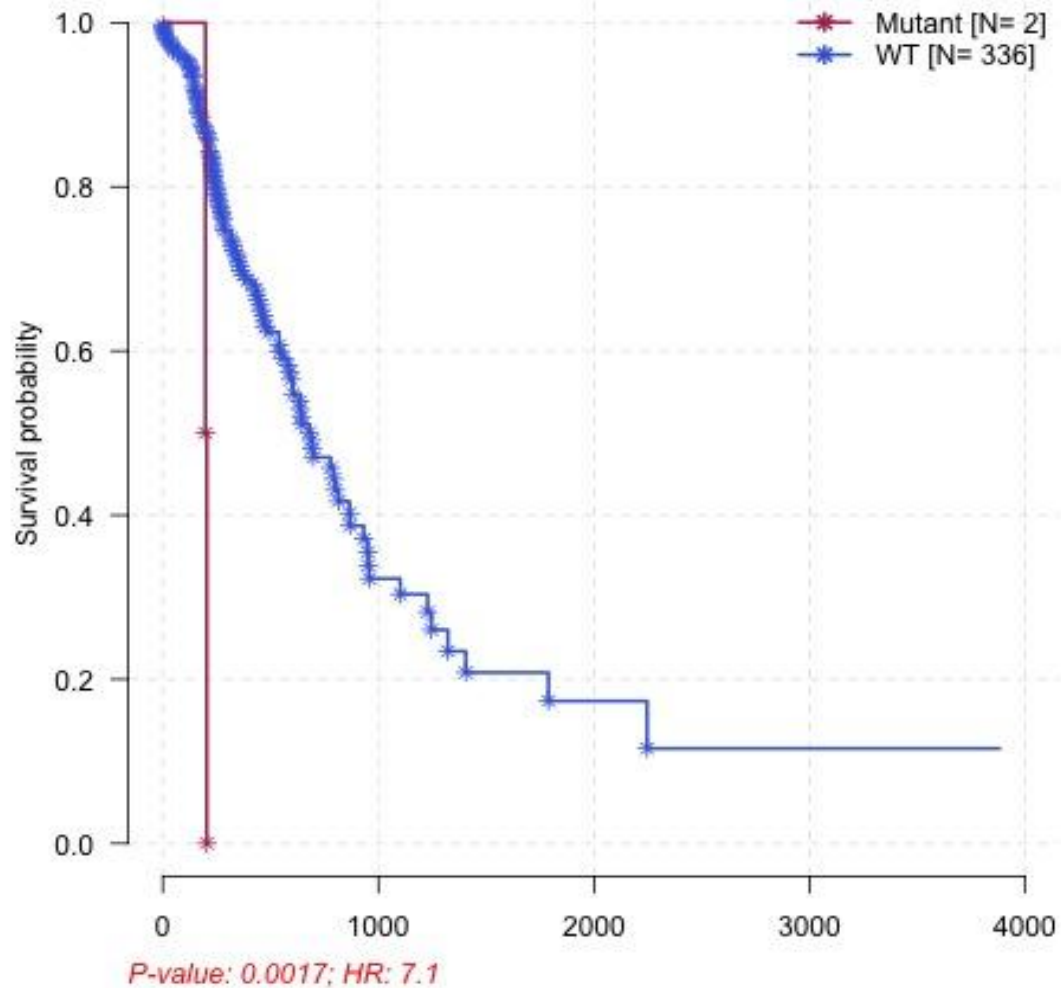
Results

Oncoplot for GBM Patients

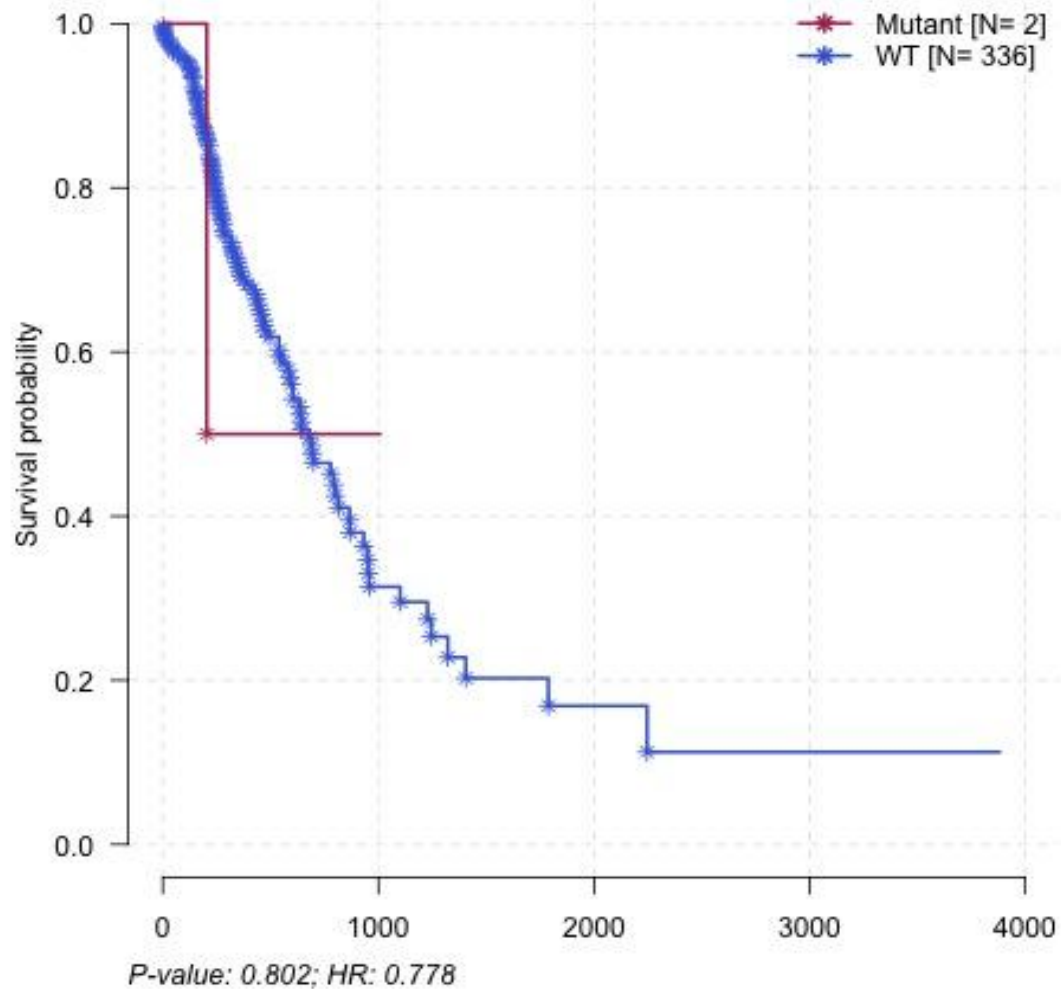
Altered in 305 (82.21%) of 371 samples.



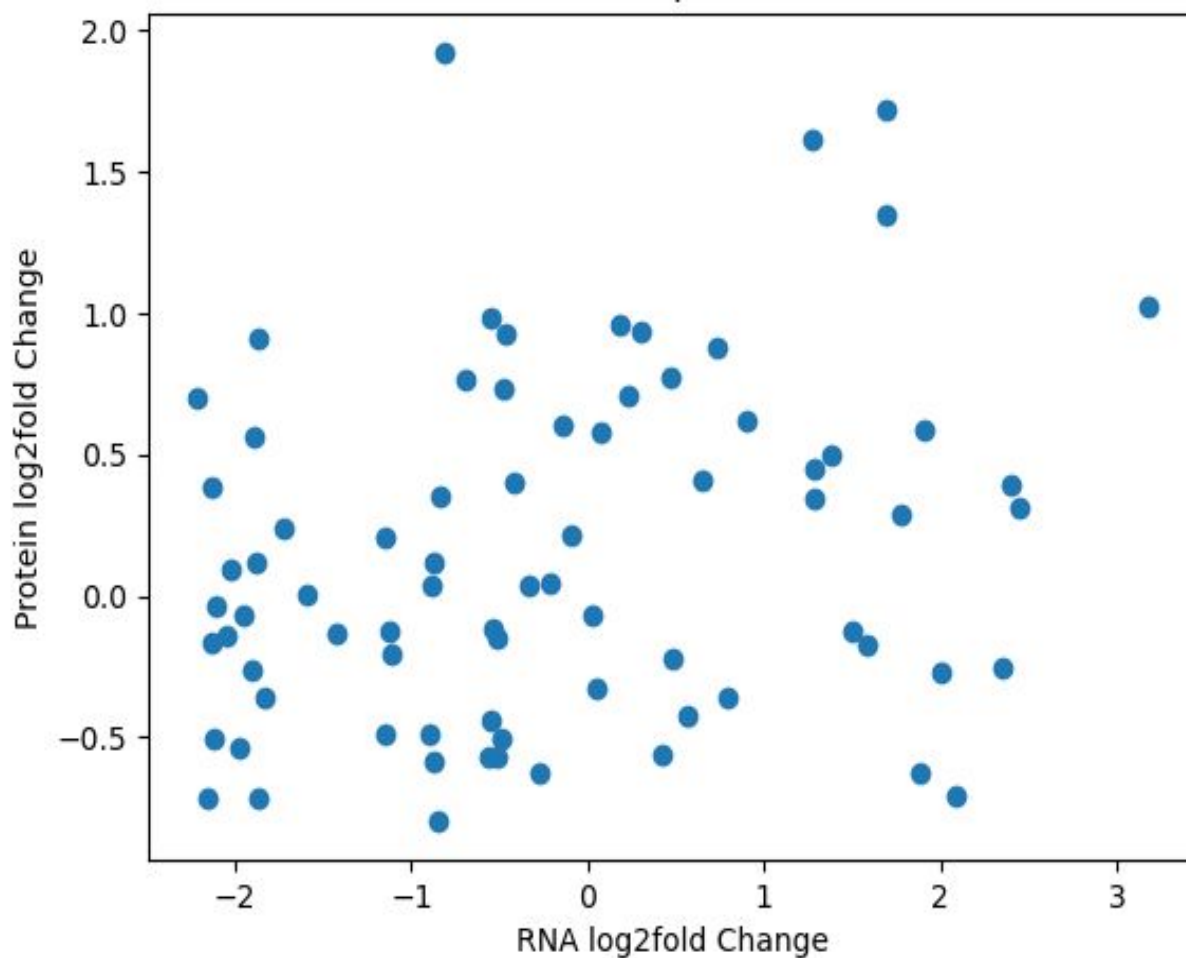
Mutant v/s WT Kaplan-Meier plot for ALDOB



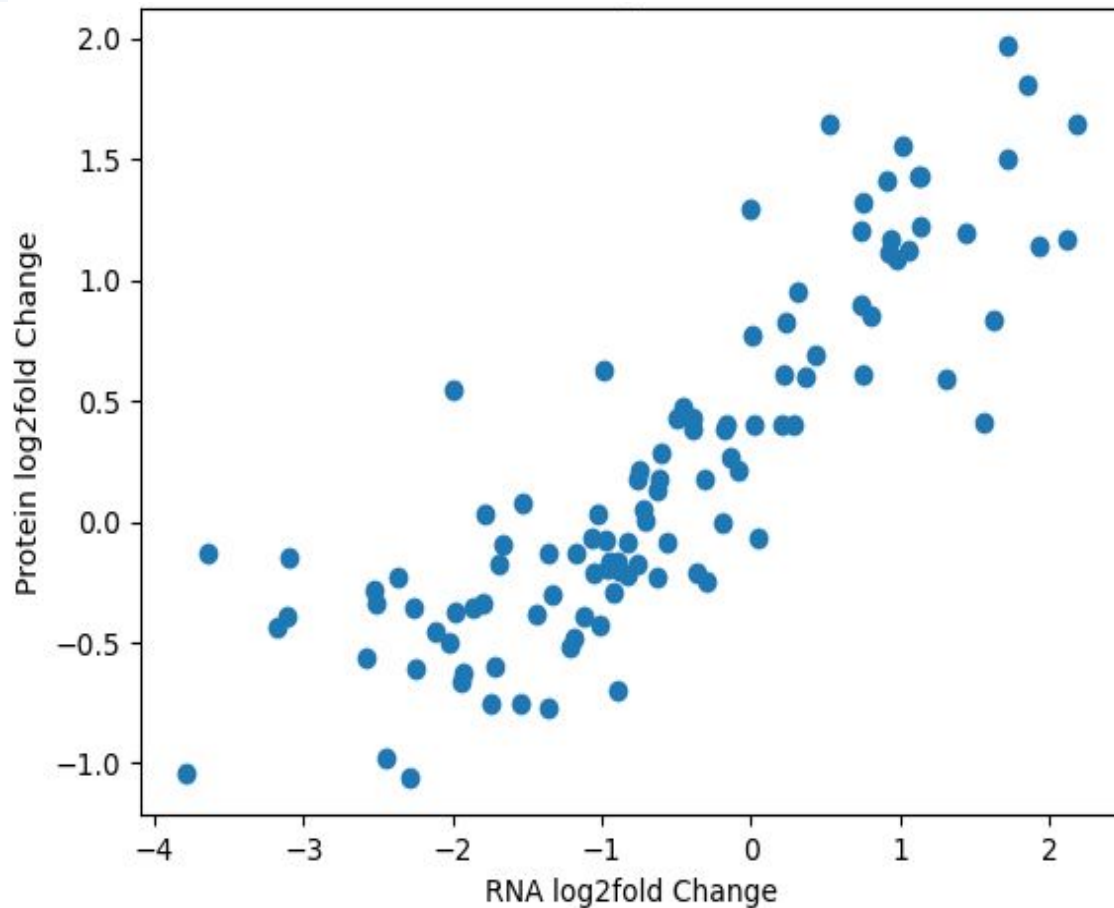
Mutant v/s WT Kaplan-Meier plot for SLC2A5



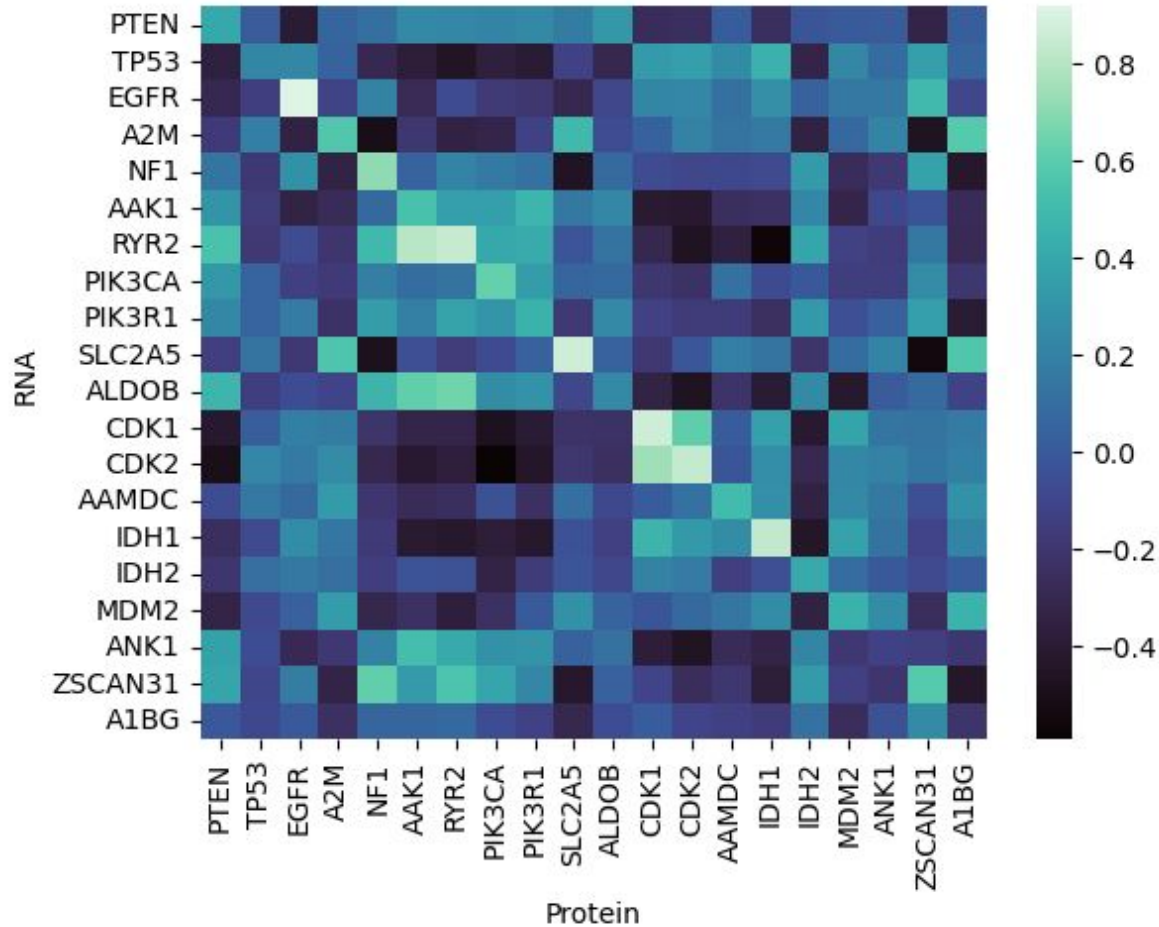
Scatterplot of RNA vs. Protein Expression of ALDOB



Scatterplot of RNA vs. Protein Expression of SLC2A5



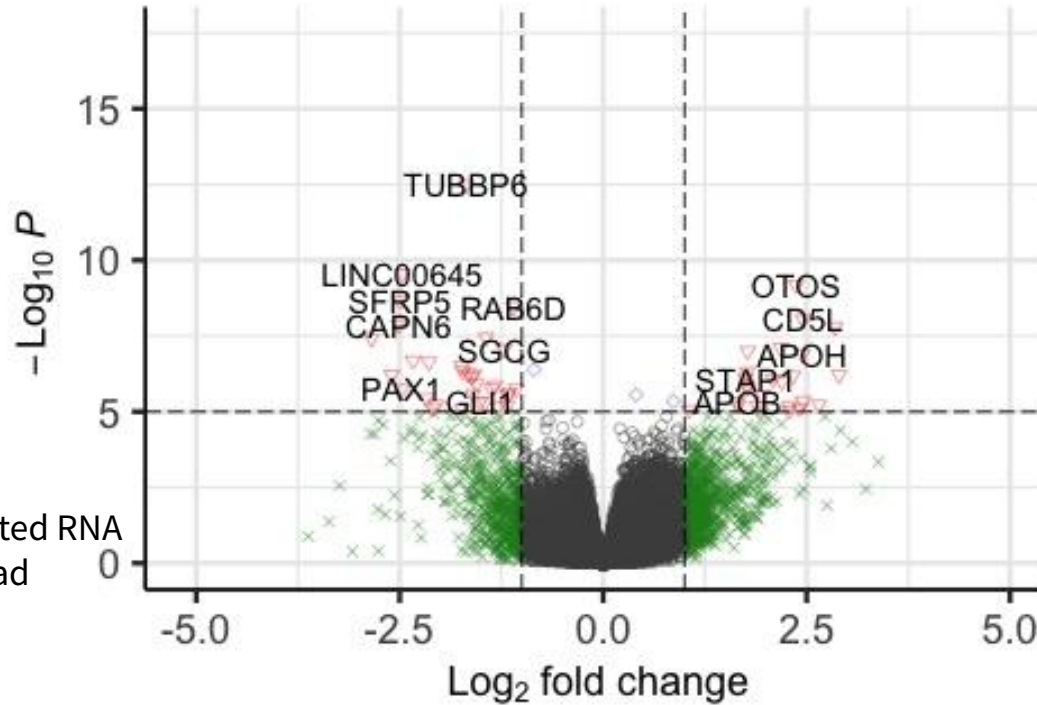
Heatmap for GBM Patients



Volcano Plot

EnhancedVolcano

○ NS × $\text{Log}_2 \text{FC}$ ◇ p-value ▽ p-value and $\text{Log}_2 \text{FC}$

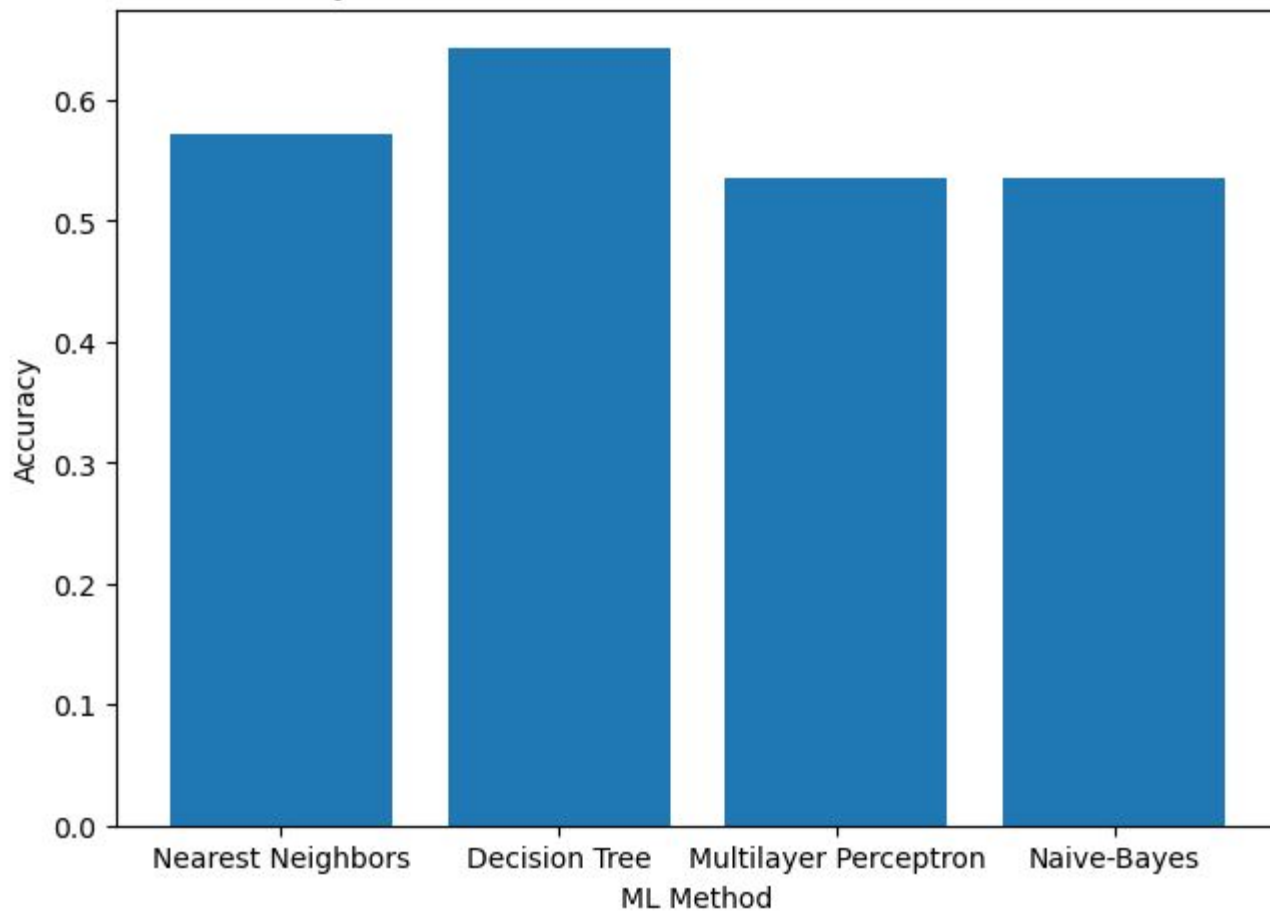


Down-regulated RNA
Count for dead
patients

Up-regulated
RNA Count for
alive patients

total = 48497 variables

Accuracy of ML Methods to Determine Patient's Vital Status





04.



Discussion



General Conclusions

- hypothesis was not supported
 - ALDOB & SLC2A5: not significant indicator of survivability of GBM patients
 - weak mRNA-protein correlation ALDOB gene
 - association between the ALDOB gene and the AAK1, RYR2 and NF1 genes
 - most accurate machine learning method: decision tree
- 
- 

Future Direction



replicate experiments

- increase sample size
- control for more variables
- more significant results

correlation between ALDOB, RYR₂, NF₁

- regulatory mechanisms

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