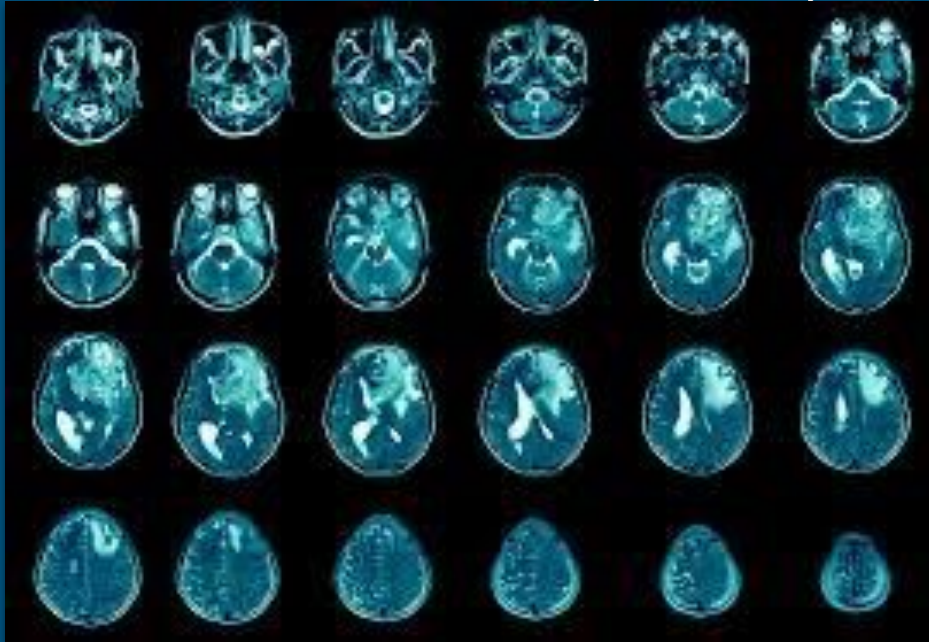


An Investigation into Glioblastoma Multiforme Survival

Kayla Xu, Joshua Gabbay, Jenna
Jacobs

Glioblastoma Multiforme (GBM)



The uncontrolled division of cells in the central nervous system

Kills 13,000 Americans annually

Risk factors:

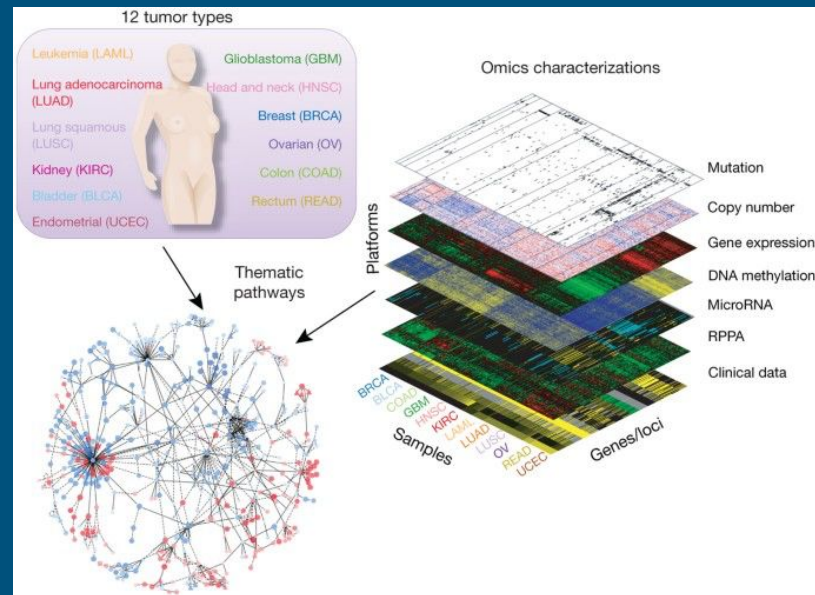
- Genetic
 - PTEN, EGFR, CDKN2A, CDH1
- Environmental
 - Radiation exposure

The Data

What is TCGA and how will we be using it?

What is CPTAC?

Analysing problems from a multi-omic perspective.

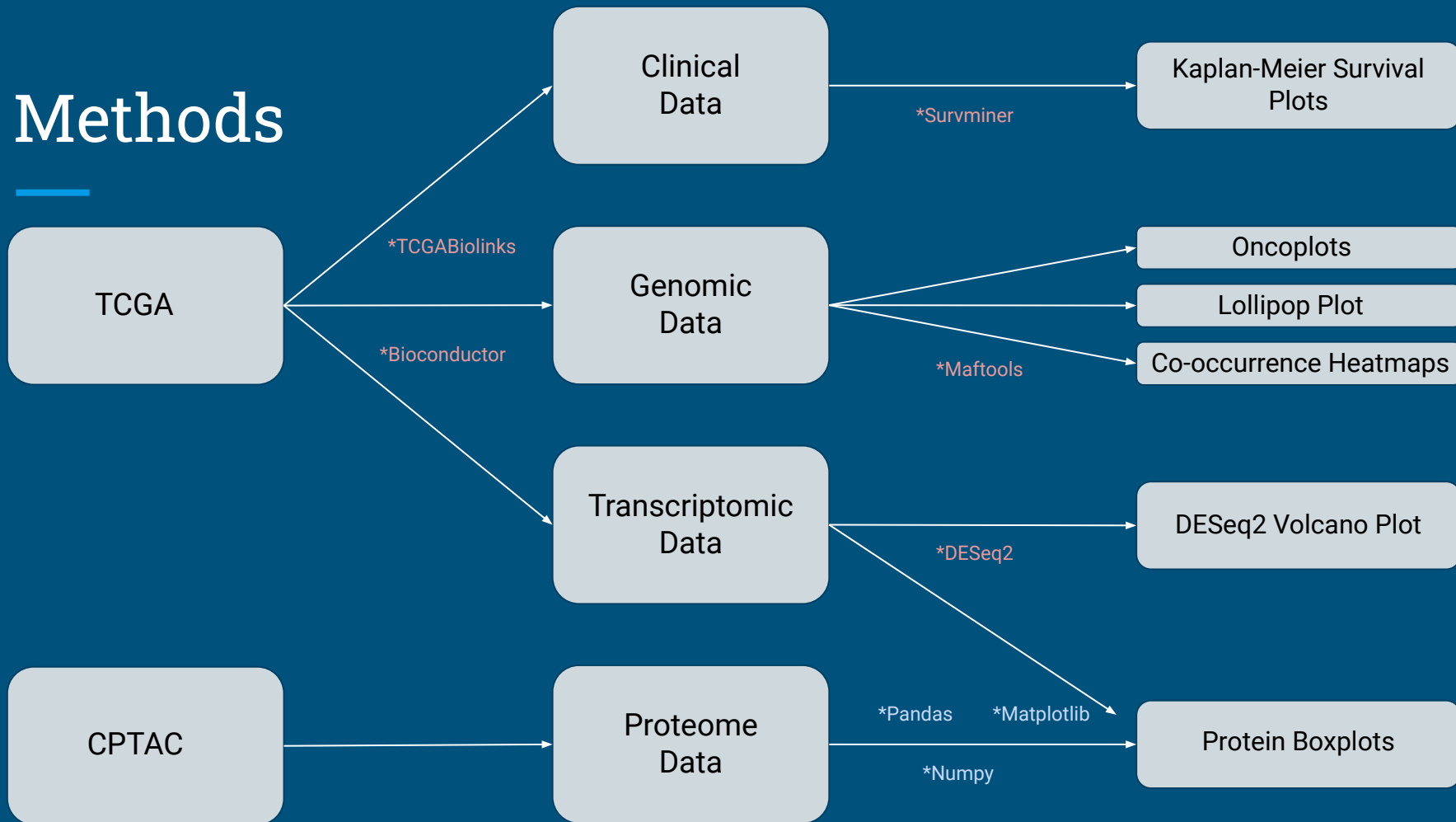


<https://www.nature.com/articles/ng.2764>

The Investigation

Hypothesis: There will be significant differences in genomic, transcriptomic, proteomic, and clinical profiles between surviving patients and non-surviving patients.

Methods



Dataset Breakdown

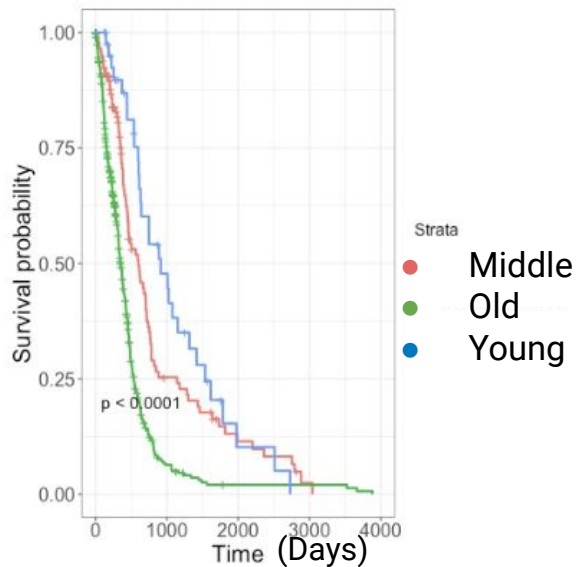
Survivors = 101

Non-Survivors = 492

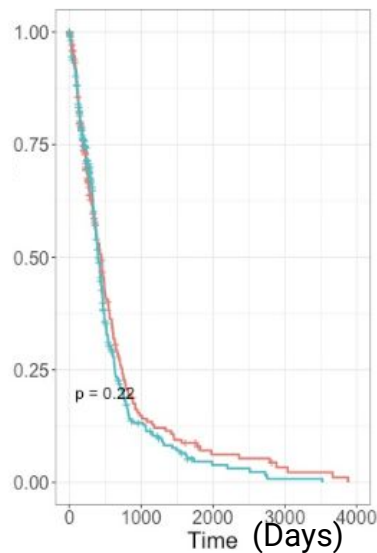
Age	Sex	Race
Old patients = 556	Male patients = 368	White patients = 509
Middle-aged patients = 119	Female patients = 231	Black patients = 52
Young patients = 44		Asian patients = 13

Kaplan-Meier plots show age and, possibly, race impact a patient's survival rate

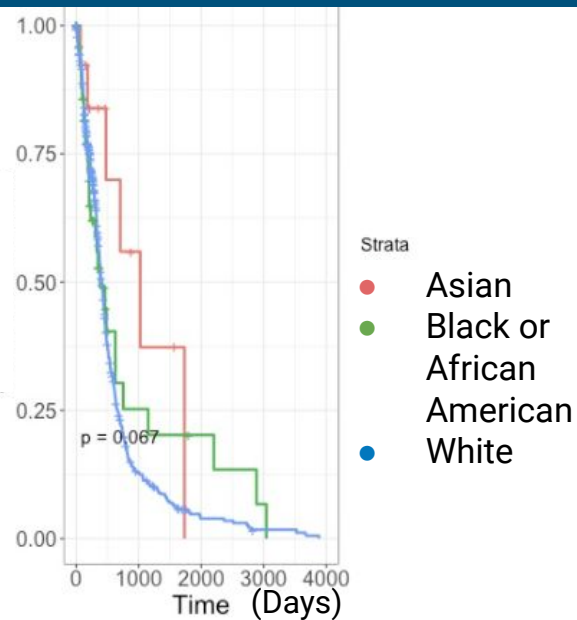
Figure 1. 1a: Age



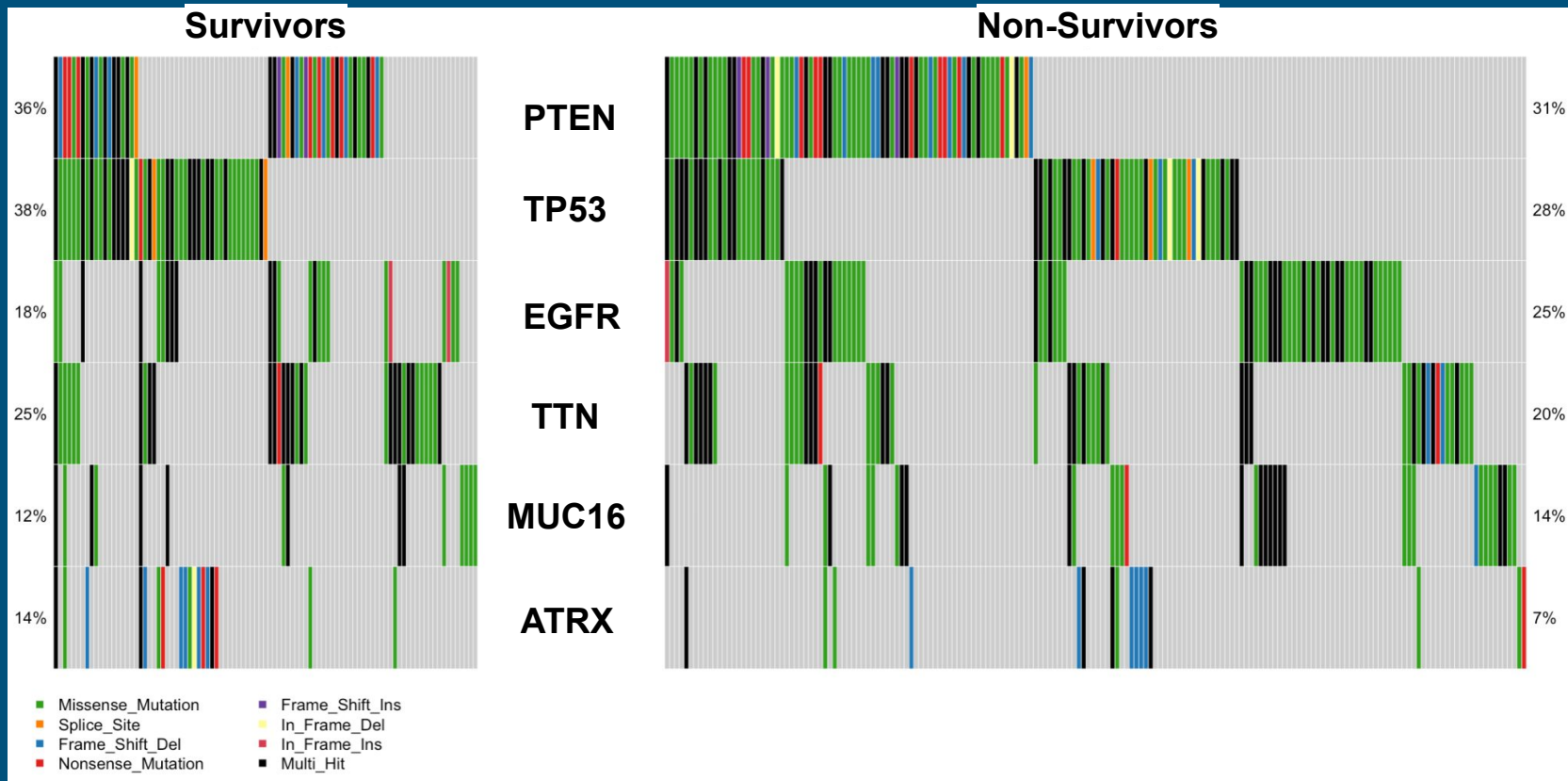
1b: Sex



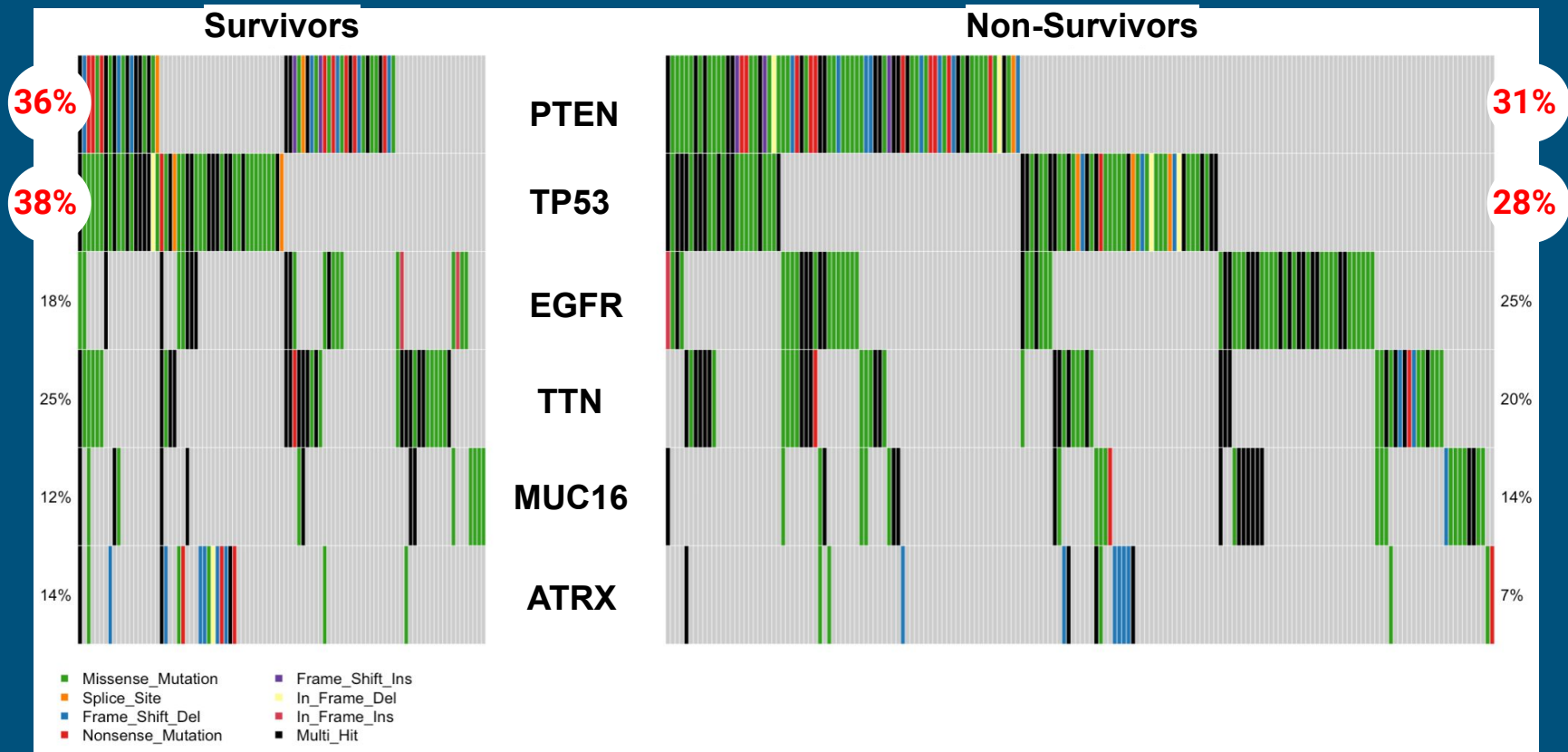
1c: Race



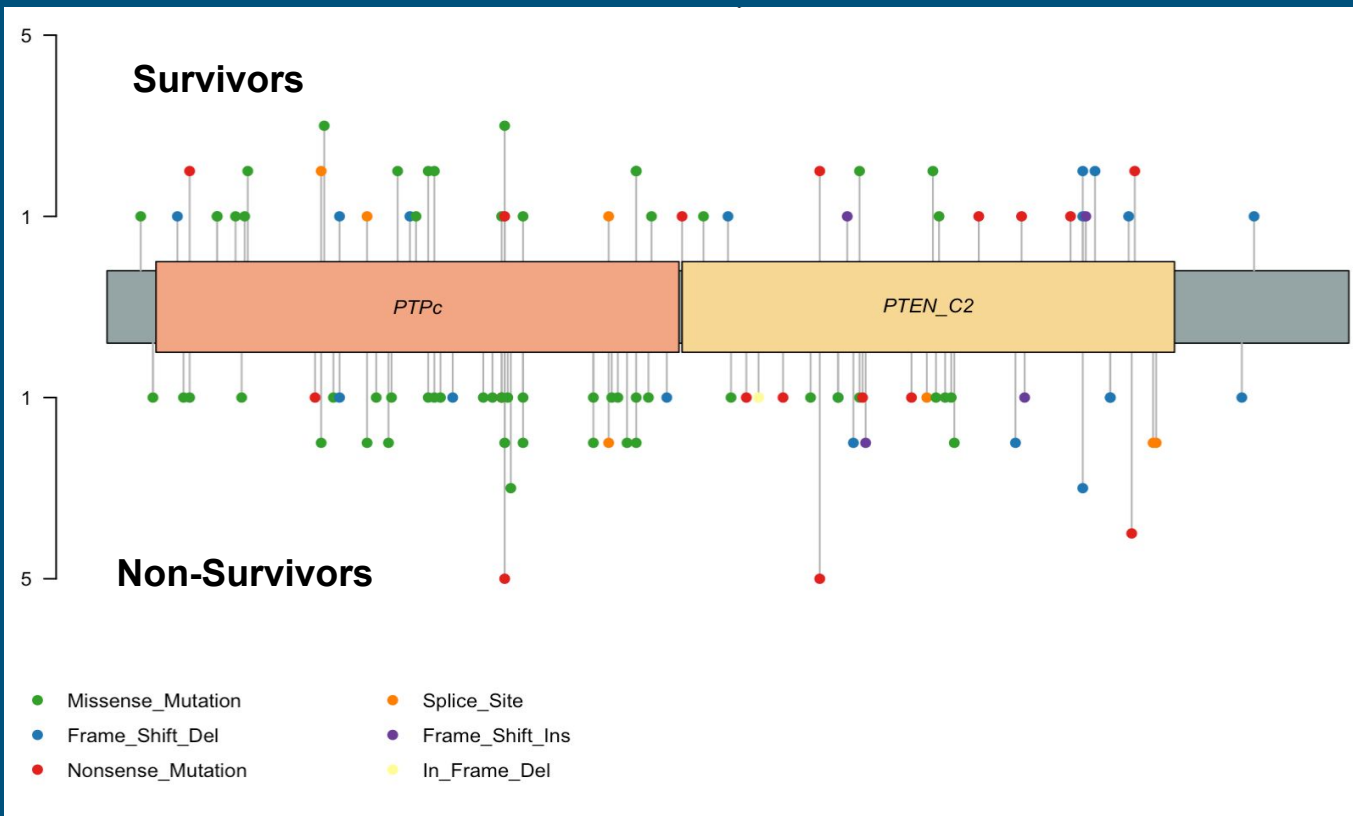
Oncoplot Between Survivors and Non-survivors



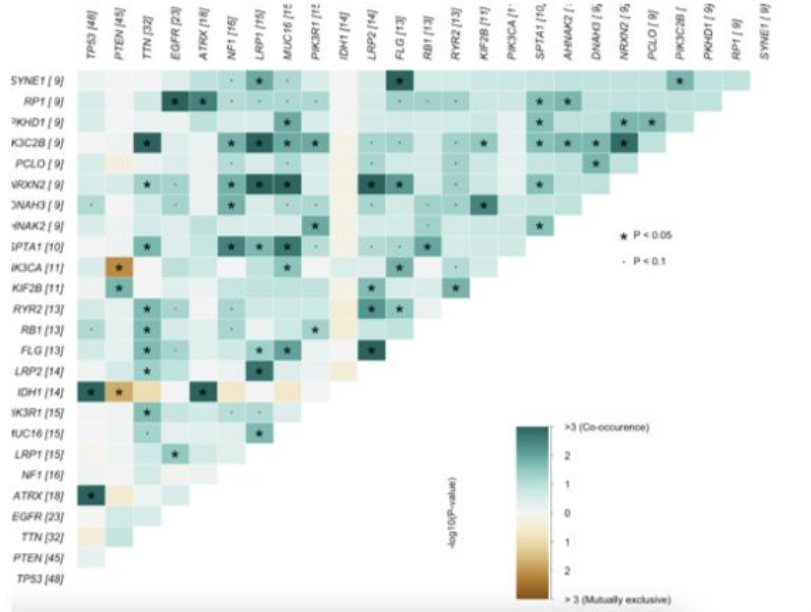
Oncoplots Between Survivors and Non-survivors



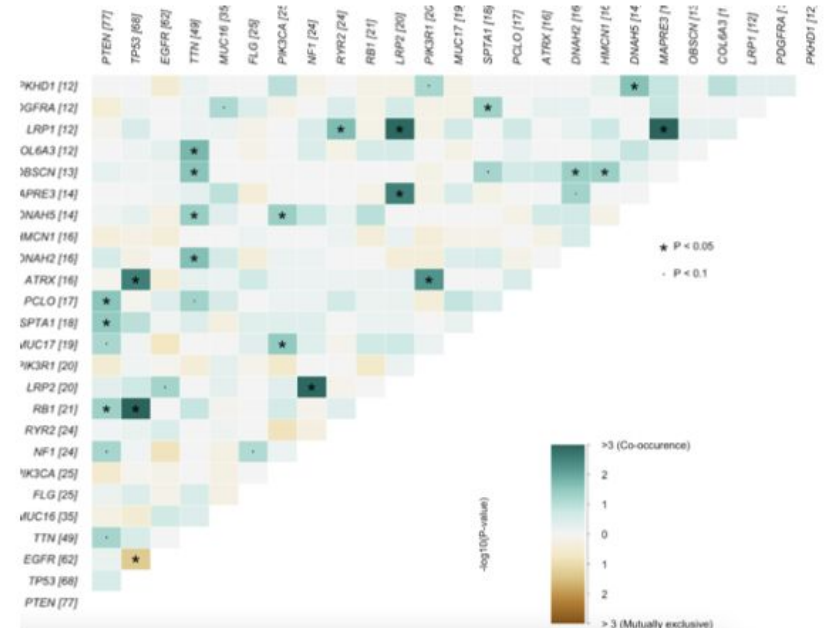
Gene Mutations: PTEN



Mutation Co-occurrence



Survivors

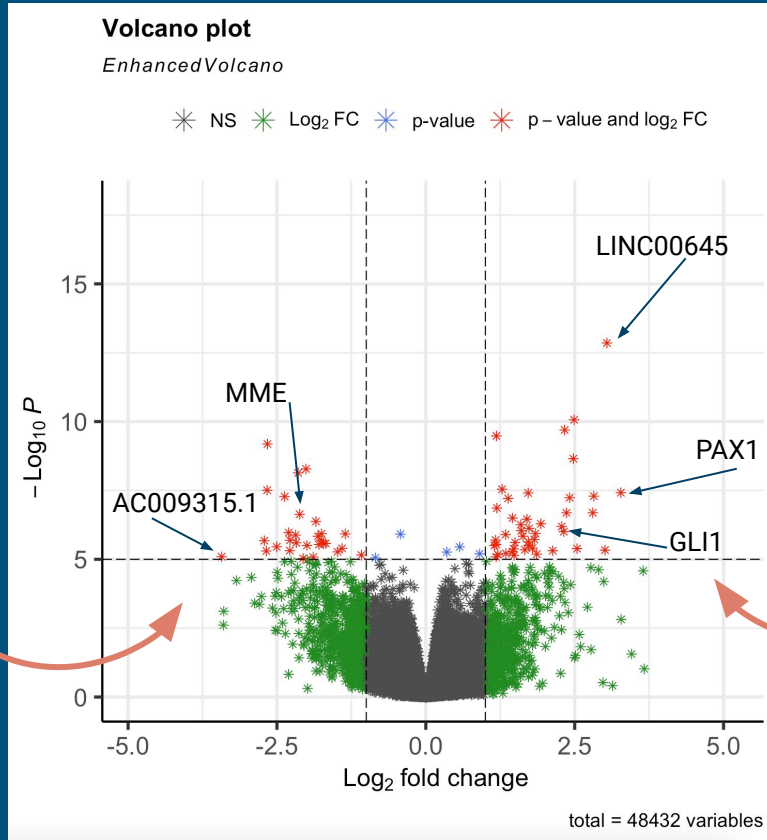


Non-Survivors

Volcano plot between survivors and non-survivors shows several upregulated genes in each group

- upregulation in non-survivors

- upregulation in survivors

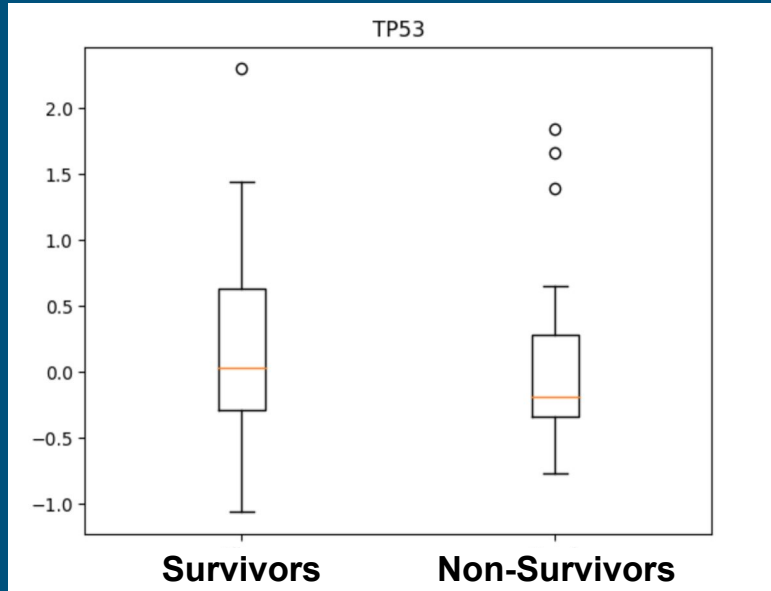


- Mostly non-coding RNAs
- Differences from oncoplots

Figure 5.

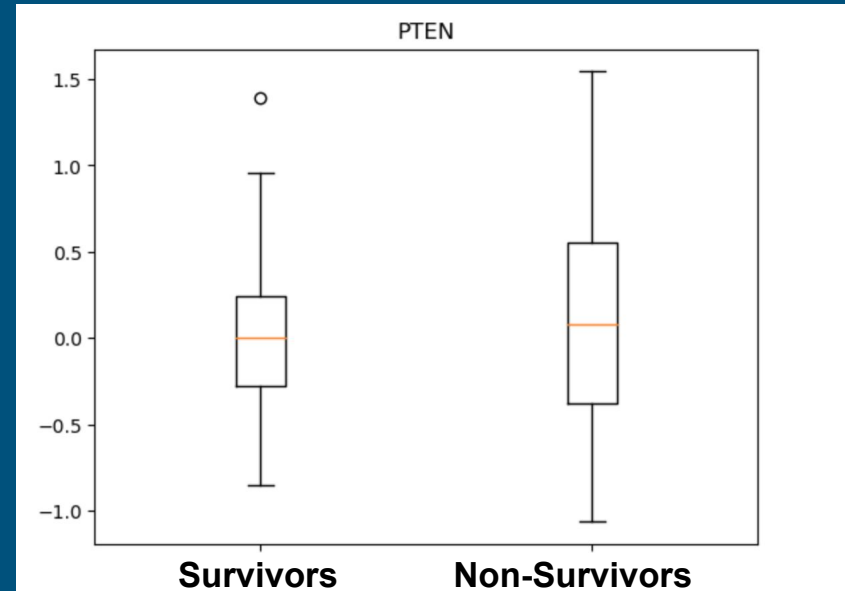
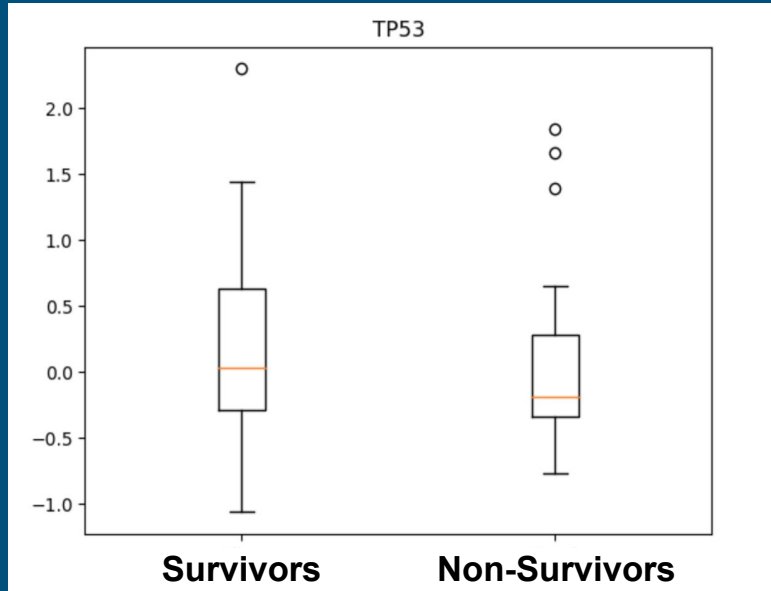
Protein Expression

For commonly mutated genes



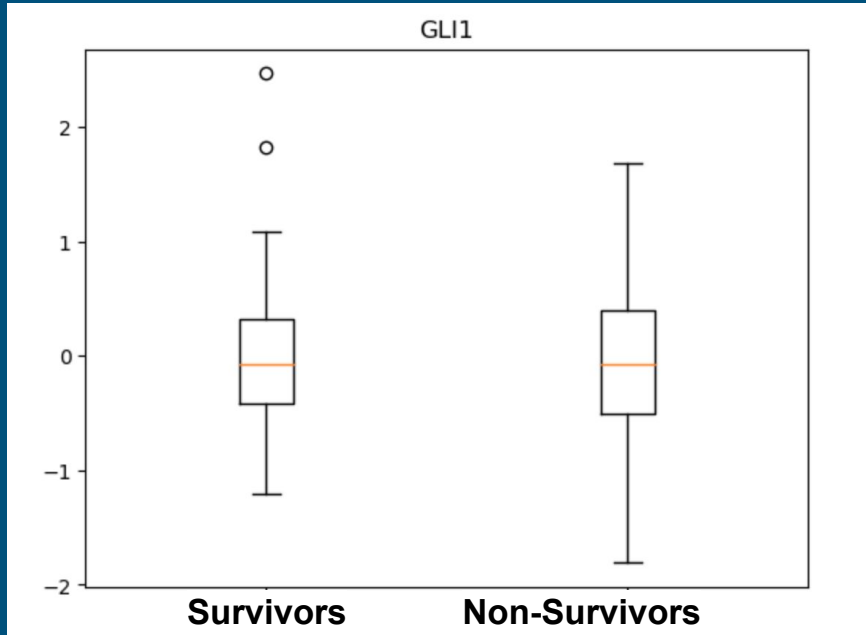
Protein Expression

For commonly mutated genes



Protein Expression

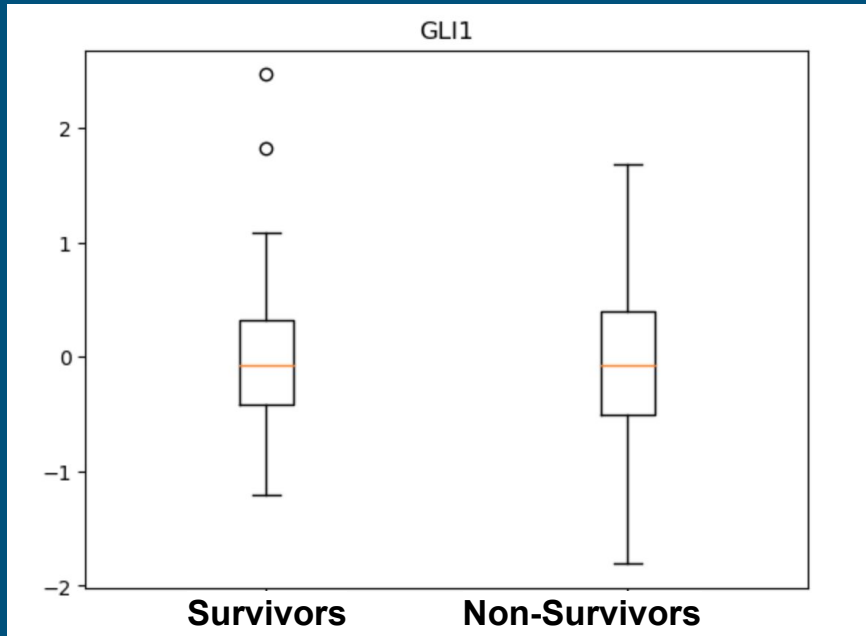
For differentially expressed RNA



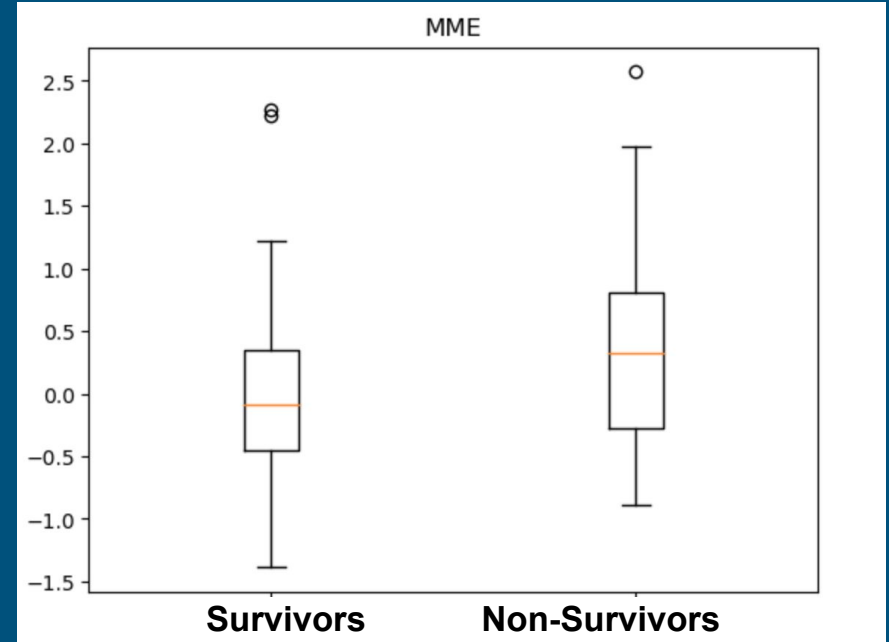
Survivor - upregulated

Protein Expression

For differentially expressed RNA



Survivor - upregulated



Non-Survivor - upregulated

Key Takeaways

- Differences between age and race
- Transcriptomic Differences -> non-coding RNAs
 - PAX1 and AC009315.1 importance
- Differences in mutations
 - PTEN PTPc domain
- Limited continuity between mutations, RNA, protein
 - Exception: MME

Moving Forwards

Non-coding upregulated gene

-(LINC00645)

Demographics and survivals

-African-American/Black and Asian patients

Larger sample size

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Thank You For Listening



Questions?

