**Aggressive cancer** is not caused by **one change alone** . This dashboard brings together **many cancer signals,** including **DNA changes** , **mutation levels** , **cancer subtypes,** and **pathways** to show each **patient's risk** more clearly.

# Patient-Level Molecular Driver Visualization and Aggressiveness Profiling Using SAPCS Data

## INTRO

- Prostate cancer is the most prevalent cancer among men of African ancestry, yet the molecular landscape of the disease in this population remains poorly characterized and clinically underrepresented in global genomic studies

### Problem

- There is a critical gap in tools that integrate and visualize the molecular complexity of African prostate cancer, specifically how driver mutations, oncogenic subtypes, mutational signatures, and pathway alterations collectively associate with clinical disease aggressiveness in the SAPCS cohort

### Objectives

- Visualize Driver Mutations
- Characterize Oncogenic Subtypes
- Summarize Mutation Counts
- Profile Mutational Signatures
- Summarize Enriched Pathways
- Explore Association with Disease Aggressiveness

## METHODS

### Project Scoping & Exploratory Data Analysis

| | | |
|---|---|---|
| Project scope, objectives & constraints definition | Cleaning and integration of data using analytics tools | Identifying trends and co-occurrence in the data |

African → Data Source → Non African

1. Clinical
2. Somatic Driver Genes
3. Global Mutational Subtypes
4. Mutational Signatures
5. Oncogenic Pathways

### Model Development and Selection

| | | |
|---|---|---|
| Machine learning model development | Model accuracy and stability evaluation | Model selection and validation |

Best model:
**LASSO Logistics regression**

### Final Dashboard & Patient Scoring

| | | |
|---|---|---|
| Development of final dashboard: Streamlit | Dashboard Model Integration | Patient-level Scoring |

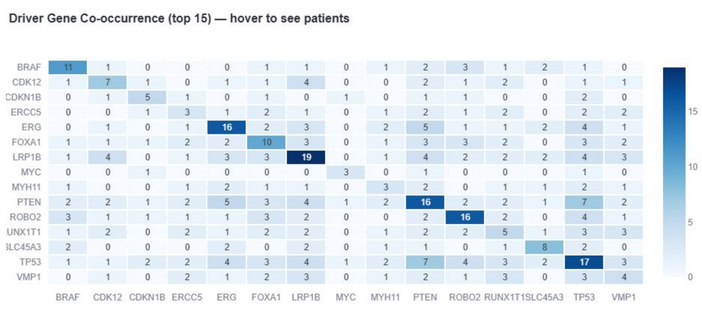


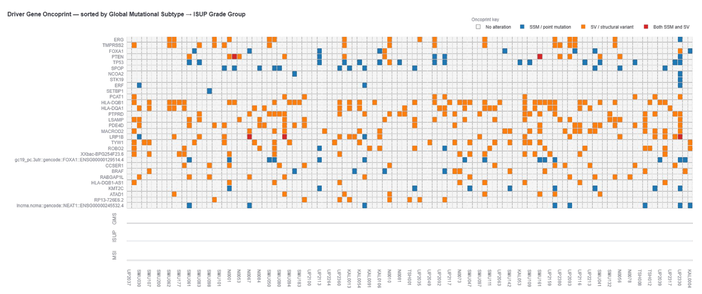

## RESULTS

## DISCUSSION

- No single driver alteration independently explained disease aggressiveness. The signal was distributed across multiple molecular layers.
- Due to the small sample size (n=100) and a low-risk minority class (n=24), the model is strictly for research/investigative use and must not be used to direct clinical patient care.

## Visualizations





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