

Genomics of Prostate Cancer Disparities

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Disclosures

- Funding sources: National Cancer Institute grants (R-01, U01, P20 PACHE, P20 SPORE), Department of Defense, Prostate Cancer Foundation, V-Foundation, Movember Foundation, Susan G. Komen Foundation
- U.S. patents issued and pending, licensing in progress. TheraSplice Inc recently founded, not funded yet.
- Consulting and stock relationship with several companies, unrelated to any aspect of this research



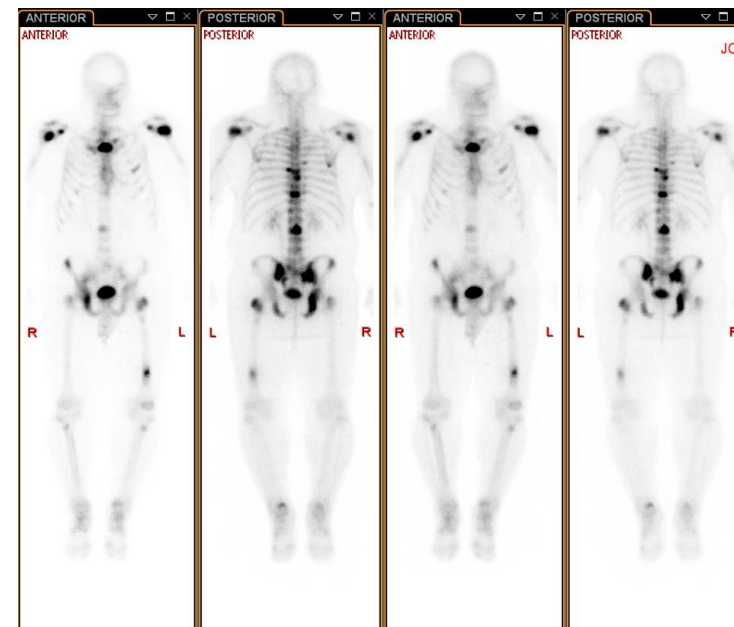
Learning objectives

- Understand the multi-level contributors to cancer disparities.
- Explain how SEOH-related and/or ancestry-related biology may contribute to cancer disparities.
- Recognize the importance of precision oncology approaches to achieving cancer health equity.

Case Presentation



- MB is a 55 yo AAM with tobacco-related COPD
- Has no health insurance - Does not own a car – takes public transportation
- Seen in a clinic for the underserved with inconsistent healthcare
- Had not been seen in clinic for 16 months
- After addressing the dyspnea, provider noticed he had lost 25 lbs since last visit 1.5 years prior
- Asked if he had ever discussed cancer screening at previous visits including colonoscopy and PSA testing
- Patient noted “nobody in my family has cancer so I don’t need that”
- Also stated “I don’t want to be experimented on”
- Declined lab work and colonoscopy
- 3 months later – presents to the ED with back pain and leg weakness, found to have spinal cord compression and PSA 1300



Specimen: A. LEFT ILIUM BIOPSY

DIAGNOSIS AND INTERPRETATION:

"LEFT ILIUM BIOPSY":

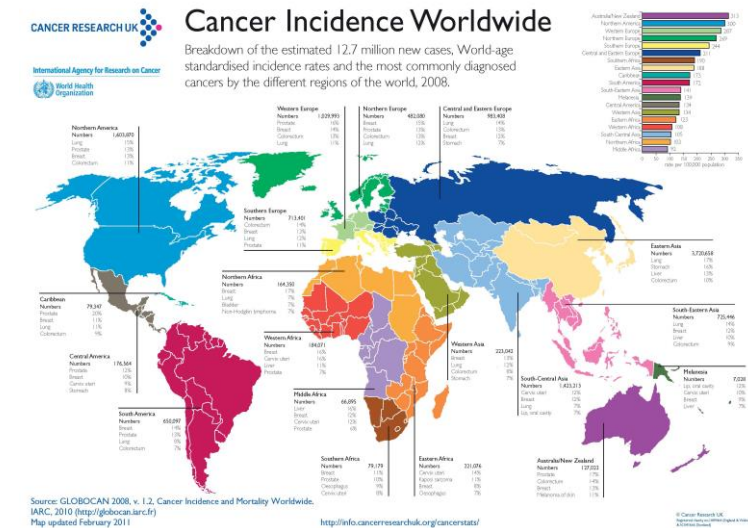
- METASTATIC POORLY-DIFFERENTIATED CARCINOMA; CONSISTENT WITH PROSTATIC PRIMARY.
88307, 88342, 88341X7, 88311

COMMENT: The carcinoma involving the bone is very poorly differentiated, so a panel of immunostains is performed to identify a possible primary site. The tumor cells are positive for pancytokeratin and PSA and are negative CK7, CK20, Gata3, S100, CD45, and synaptophysin. This pattern is consistent with a prostatic primary. An intradepartmental review is performed on this case prior to sign out.

What Are Cancer Health Disparities?



- **The unequal burden of cancer among minoritized and marginalized persons/populations and the medically vulnerable and underserved**
- **This problem is local, regional, national, global, urban and rural**

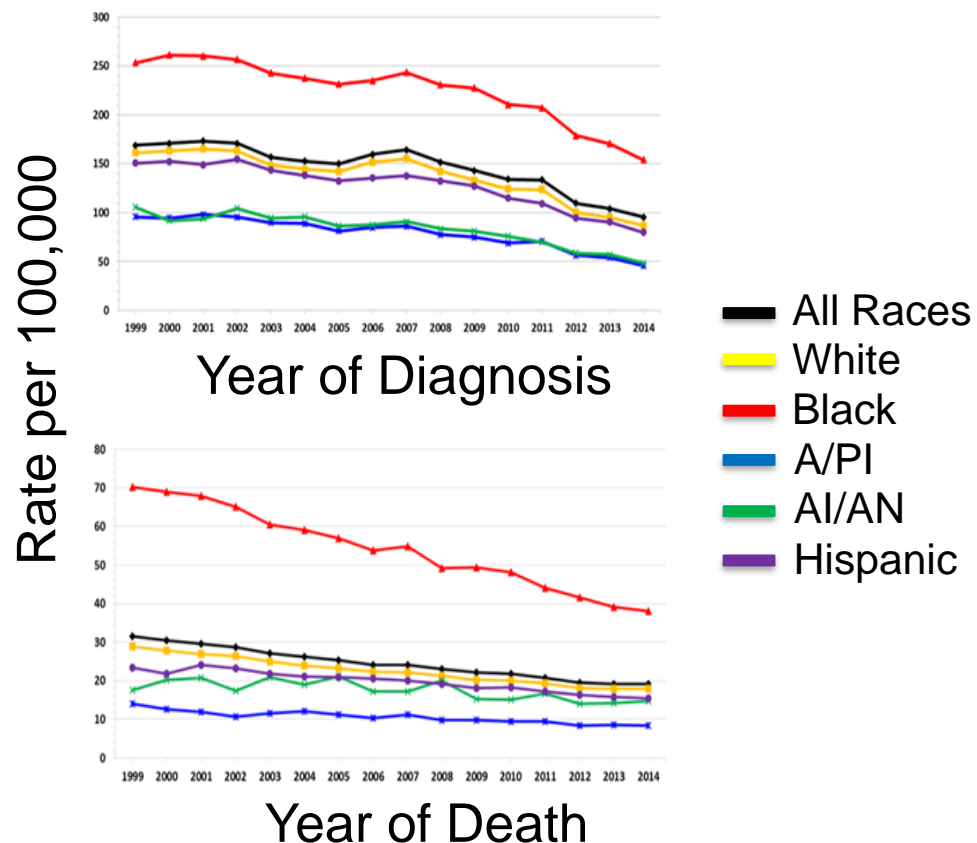


Prostate Cancer Disparities Among Racial Groups



Incidence Rates by Race and Ethnicity US, 1999-2014

Death Rates by Race and Ethnicity US, 1999-2014



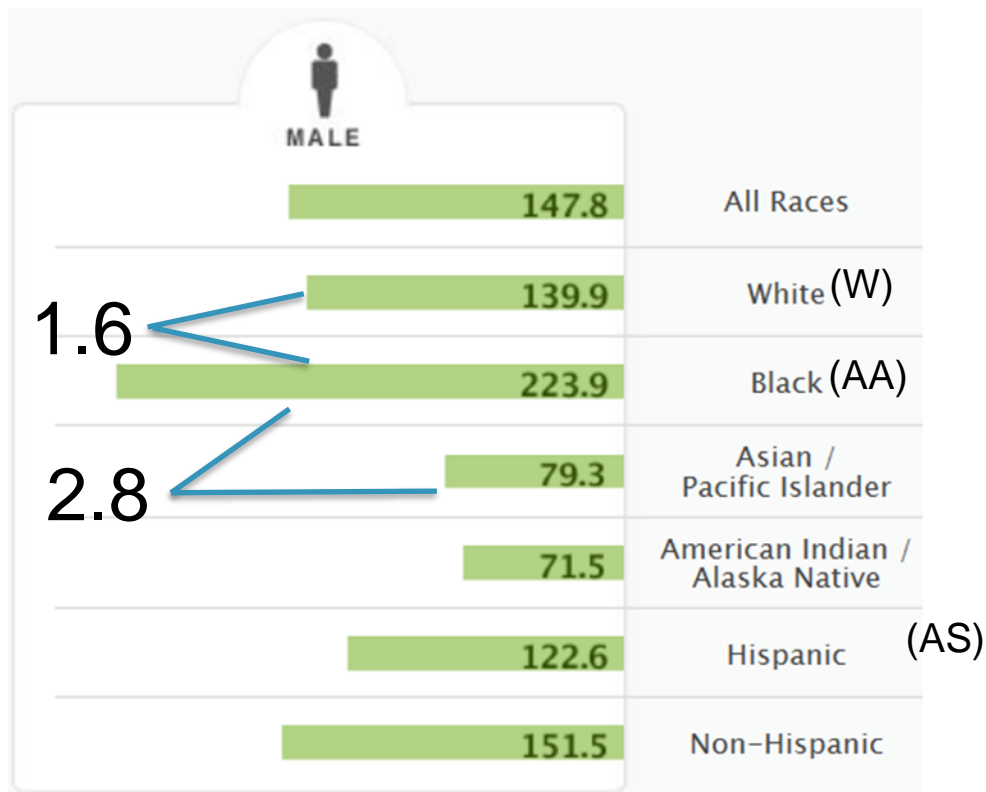
Disparities in Prostate Cancer Aggressiveness

- Earlier mean age at diagnosis
- Shorter mean survival
- More common advanced stage diagnosis
- Greater risk of early recurrence
- More common metastasis
- **Much the same in equal access health systems**
- **Exacerbated by the dramatic drop in screening after 2012 – increased # and % of men being diagnosed with late stage disease**

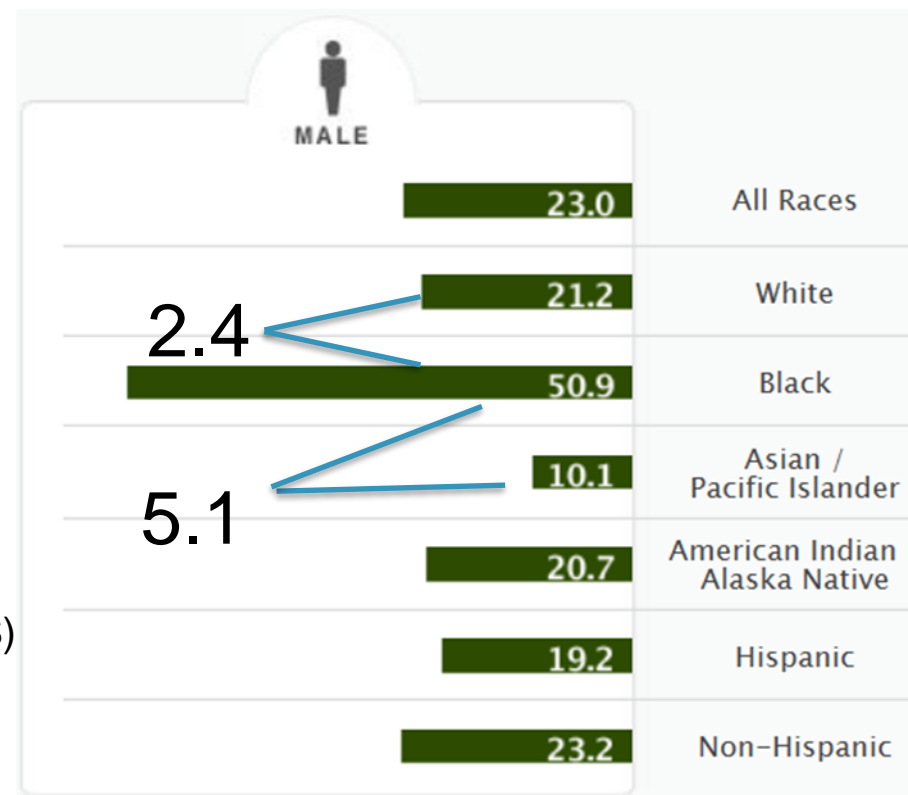
Prostate Cancer Disparities Among Racial Groups



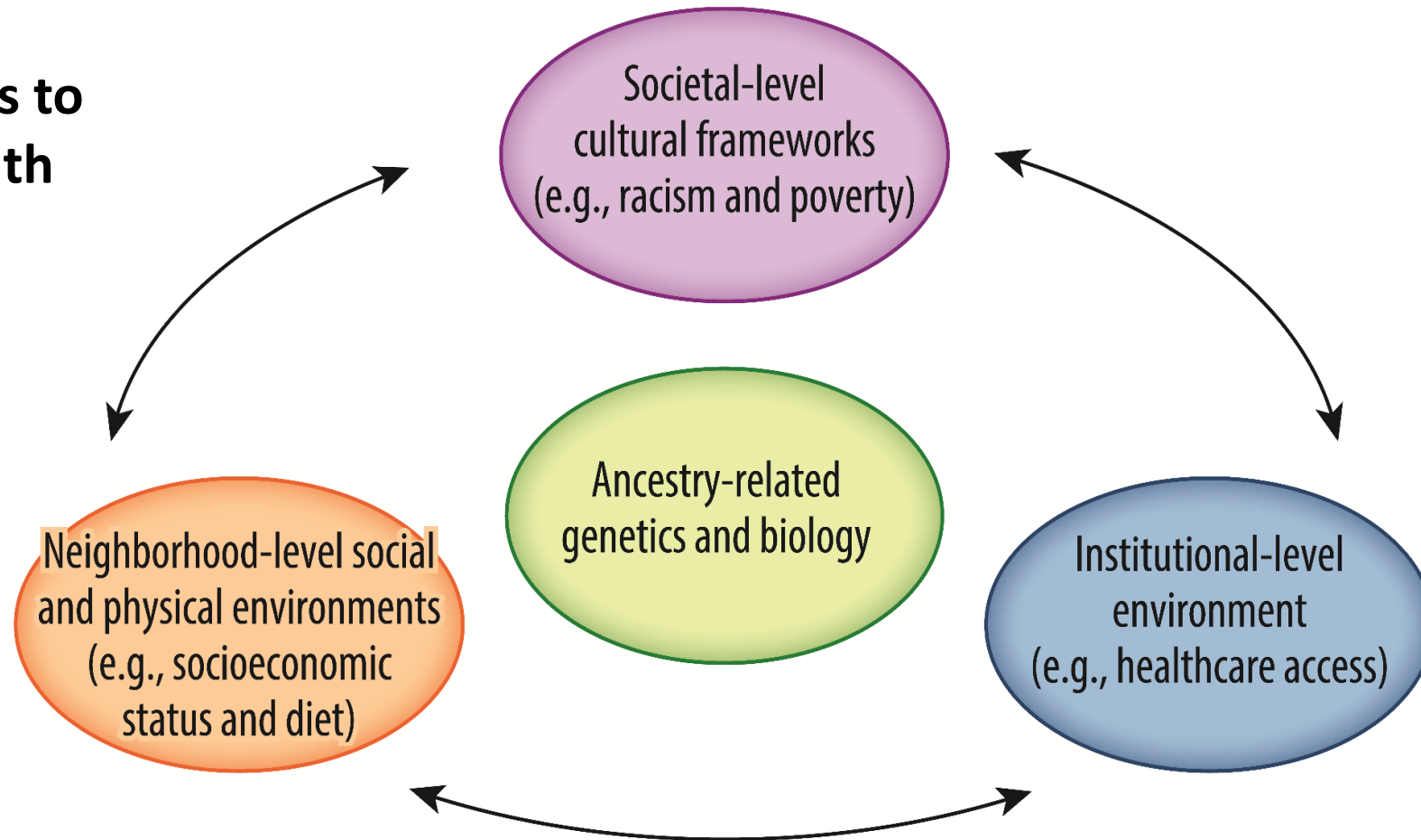
Number of New Cases per 100,000 Persons



Number of Deaths per 100,000 Persons



Multi-level Contributors to Cancer Health Disparities



Cancer health disparities

Annual Review of Medicine
Biological Aspects of Cancer Health Disparities
Jennifer A. Freedman, Muthana Al Abo, Tyler A. Allen, Sean A. Piwarski, Kara Wegermann, Steven R. Patierno

Intersecting Contributors to Cancer Disparities



Social & Environmental

Personal Health Beliefs
Individual Responsibility
Socioeconomic Status
Environmental Exposures

Biological

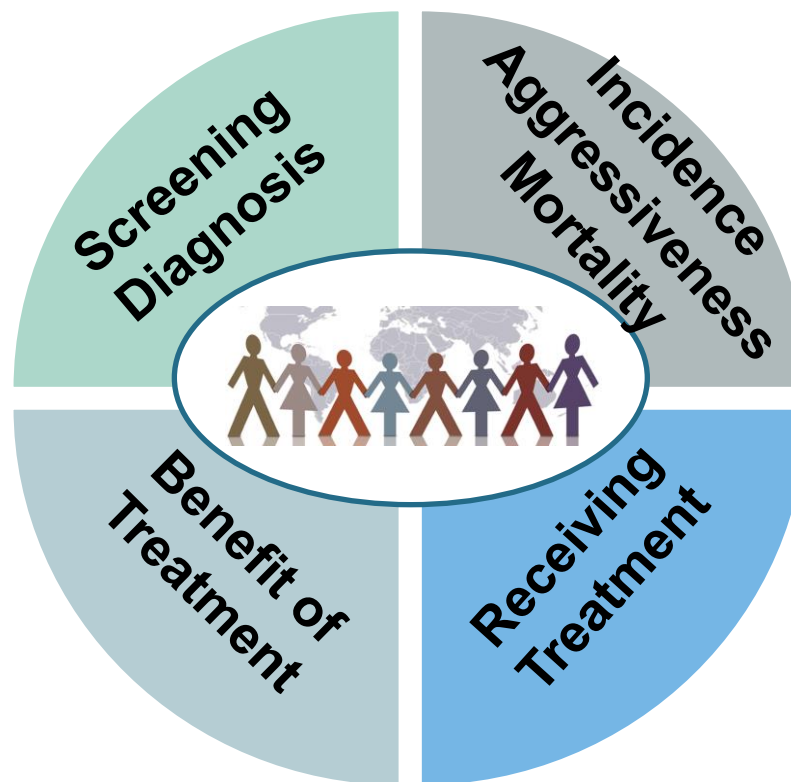
Germline/Somatic
Genome
Epigenome
Transcriptome
Proteome
Metabolome

Lifestyle

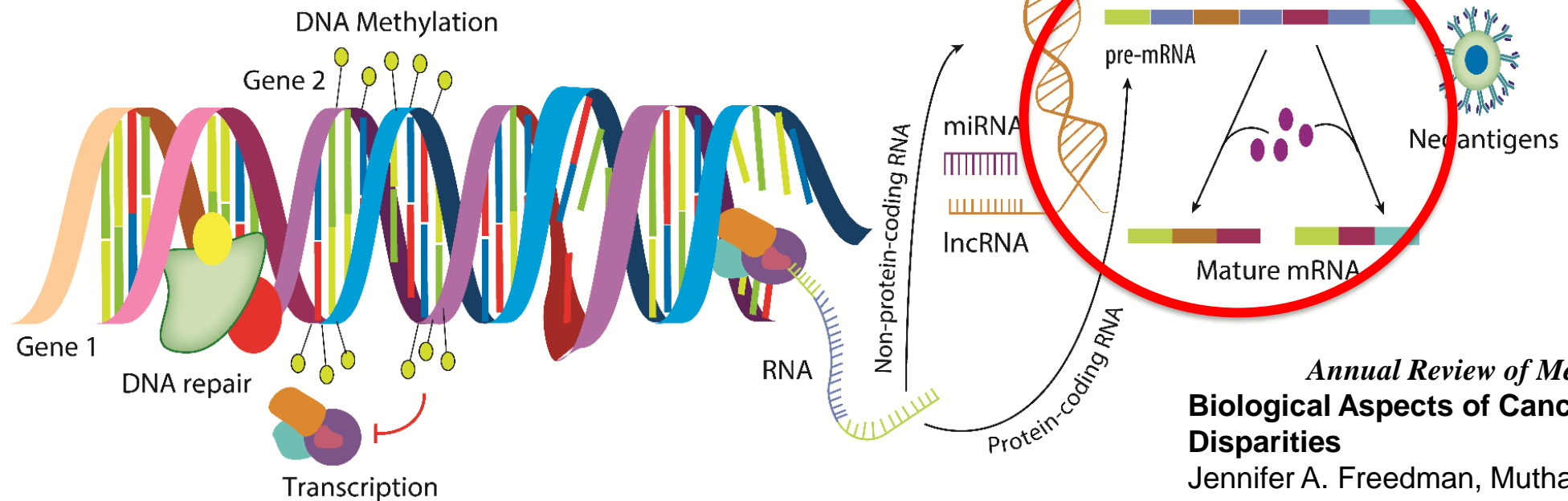
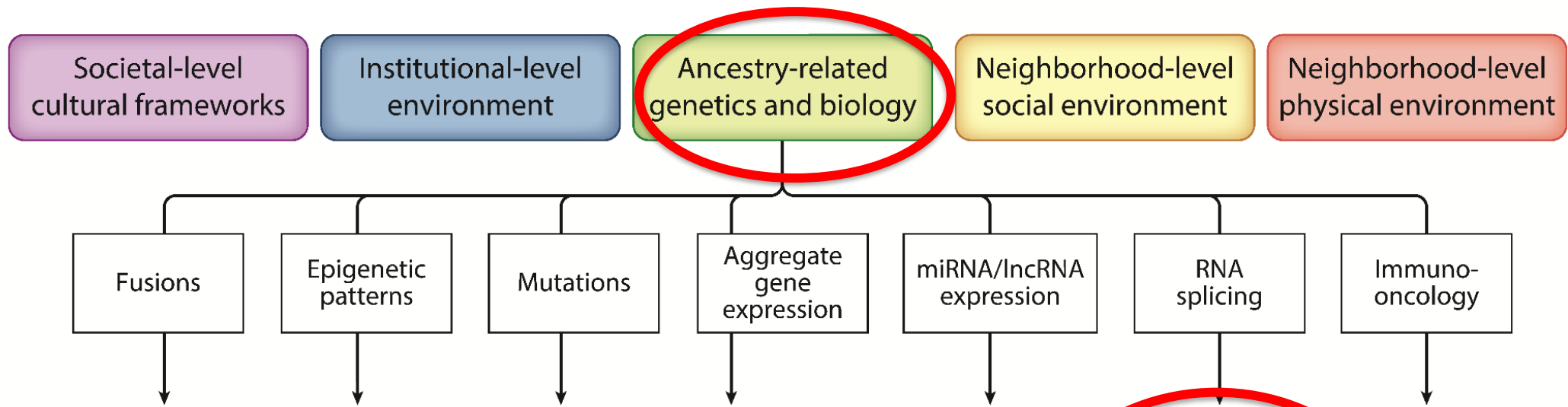
Smoking Status
Diet
Exercise
Obesity
Comorbidities
Physical Environment

Structural

Health System
Access To Care
Policy
Physical Environment



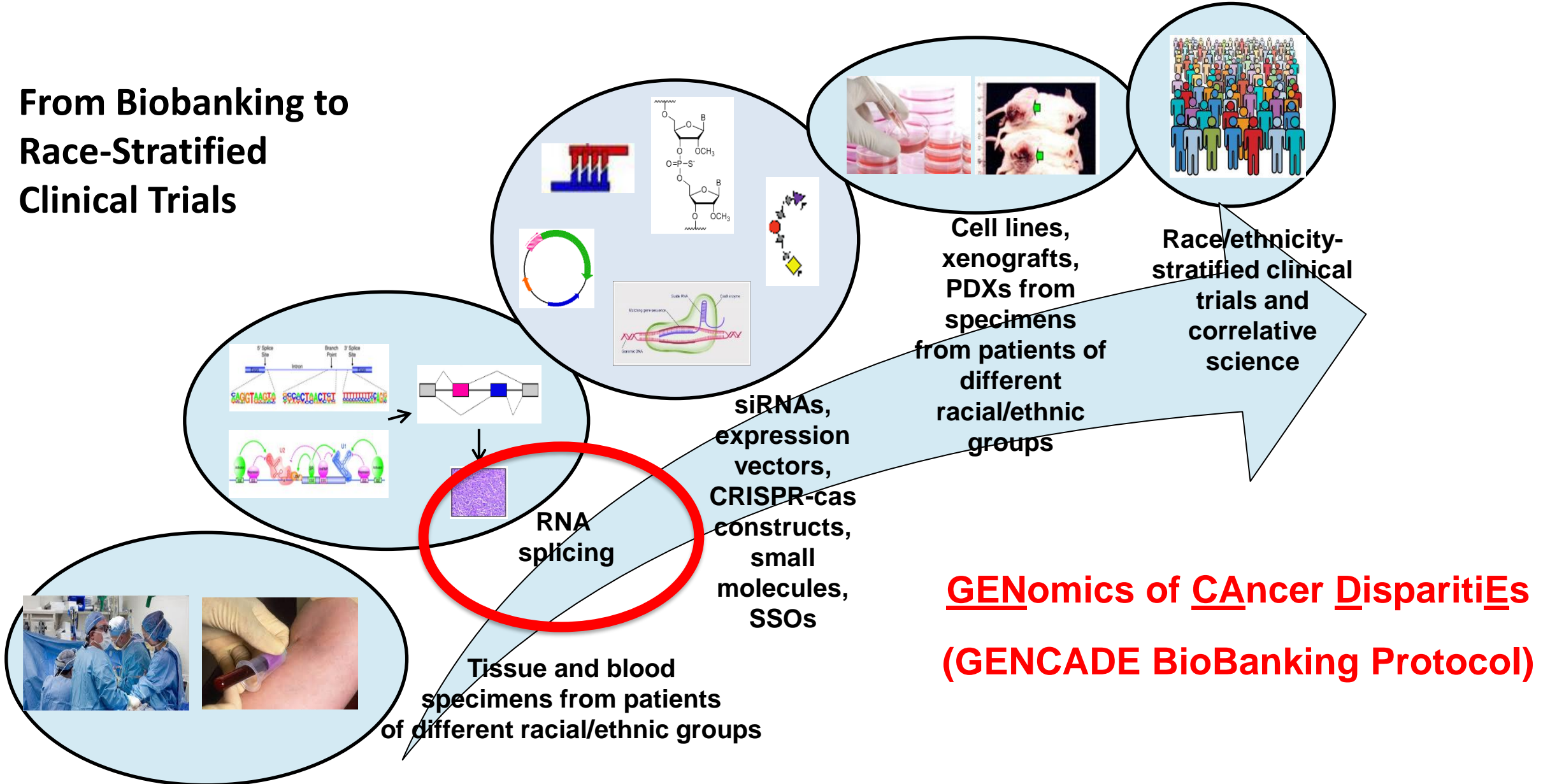
Illustrates the need for new
methodologies in “convergence
science”



Annual Review of Medicine
Biological Aspects of Cancer Health Disparities
Jennifer A. Freedman, Muthana Al Abo,
Tyler A. Allen, Sean A. Piwarski, Kara
Wegermann, Steven R. Patierno

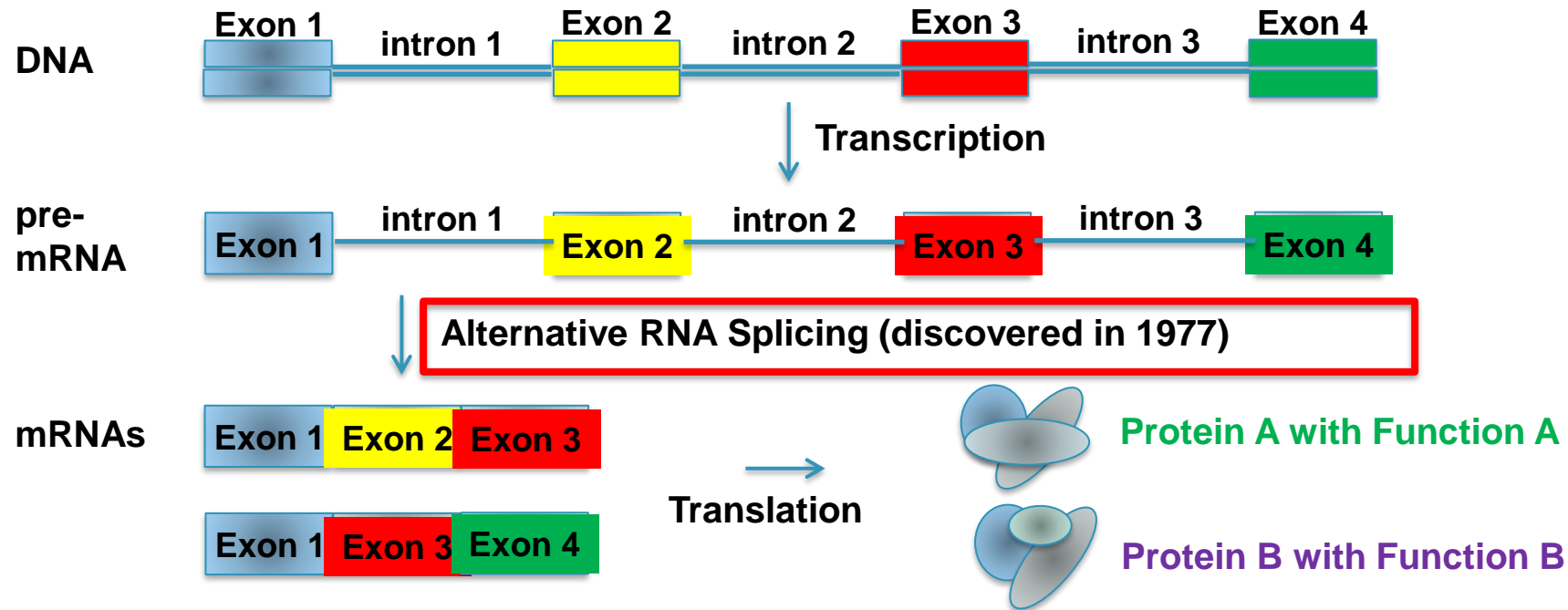
Translational Cancer Disparities Laboratory Research

From Biobanking to Race-Stratified Clinical Trials



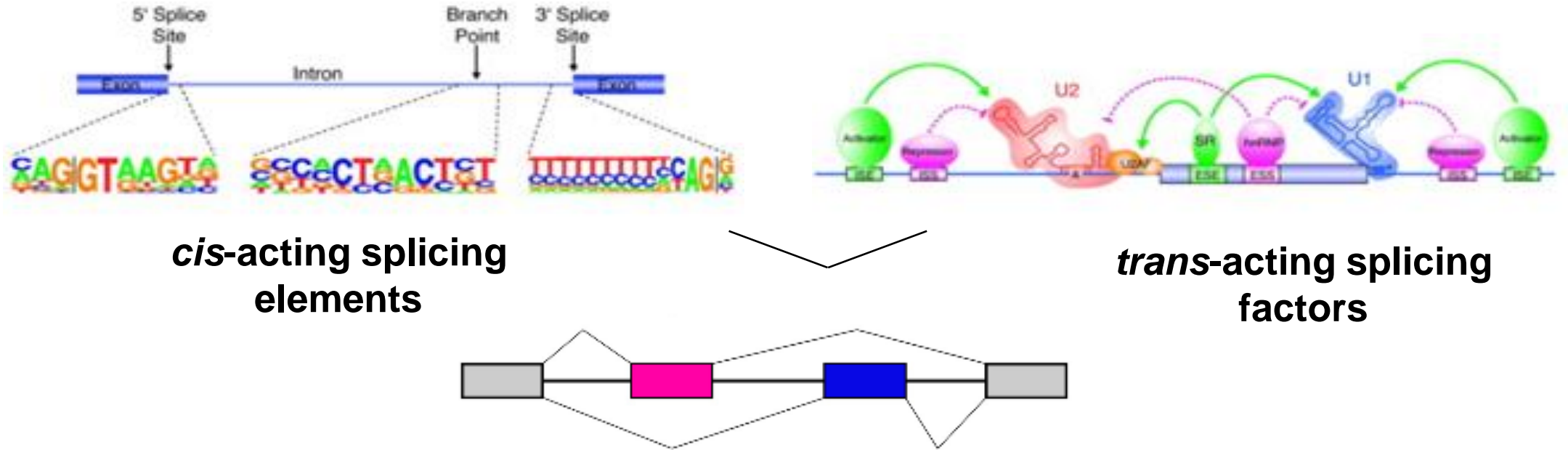


Central Dogma of Biology: Splicing 101



- Drives evolutionary biological diversity, increasingly recognized as a principle driver of tumor biology
- “Functions of proteins produced from RNA splice variants from a given gene (proteoforms) can be as different as proteins encoded by entirely different genes” Yang et al., Cell, 2016
- **Alternative RNA Splicing Impacts Every Hallmark of Cancer**

What regulates Alternative RNA Splicing?



Does Alternative RNA Splicing differ by race, ethnicity or ancestry?

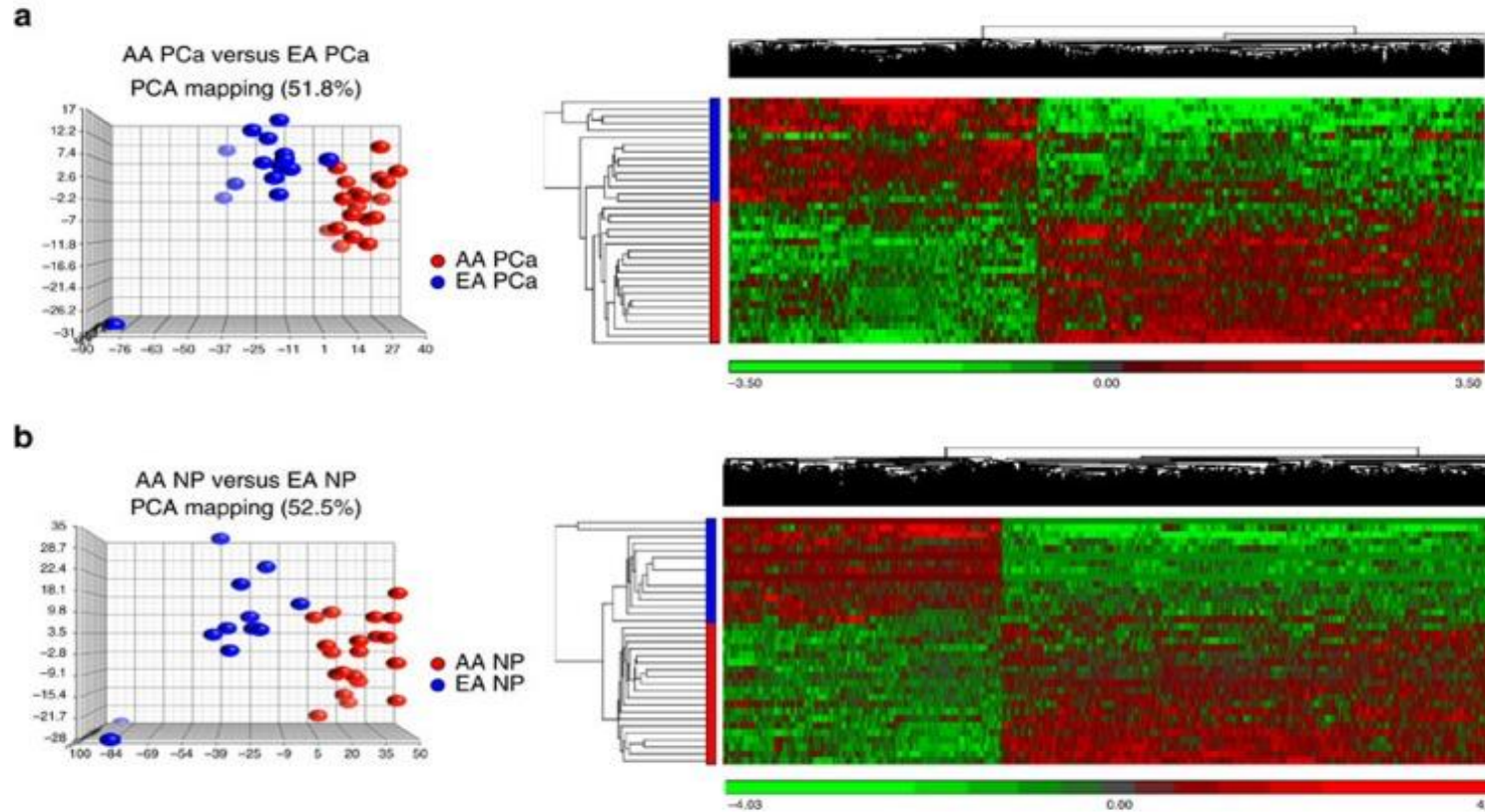
How does it affect tumor biology?

Can ARS help predict risk or survival?

Is it clinically meaningful and targetable?



Bi-dar Wang, PhD GWU,
now at
U. MD Eastern Shore



Norman Lee, PhD GW
Cancer Center

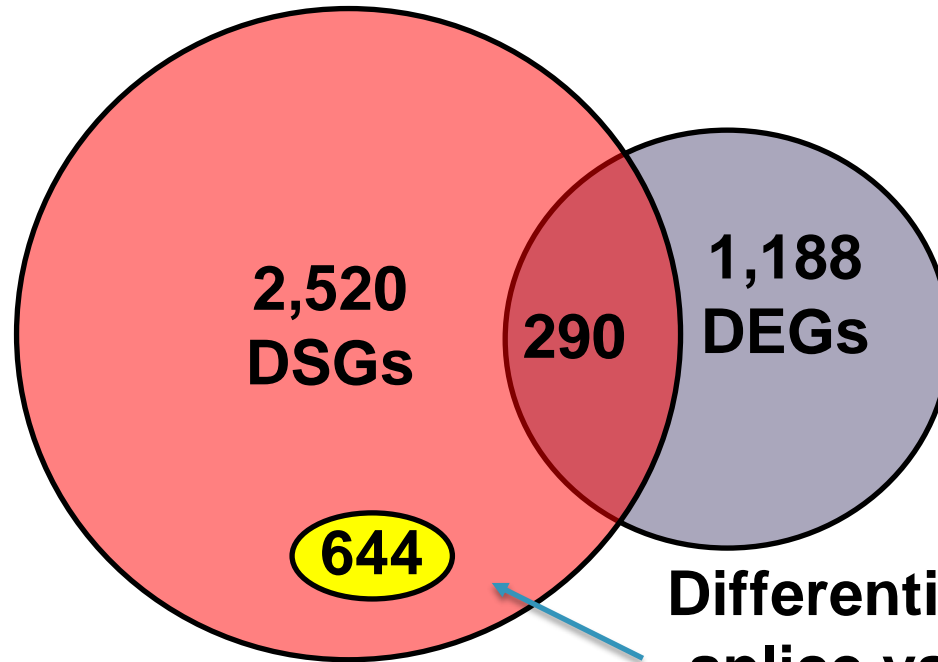
Alternative splicing promotes tumour aggressiveness and drug resistance in African American prostate cancer

Bi-Dar Wang, Kristin Ceniccola, SuJin Hwang, Ramez Andrawis, Anelia Horvath, Jennifer A. Freedman, Jacqueline Olender, Stefan Knapp, Travers Ching, Lana Garmire, Vyomesh Patel, Mariano A. Garcia-Blanco, Steven R. Patierno, Norman H. Lee. Nat Comm 2017



Race-related ARS in Prostate Cancer by Exon Arrays

**Prostate Cancer Biopsy Samples
Self-identified AA vs W Patients
Analyzed by exon array**

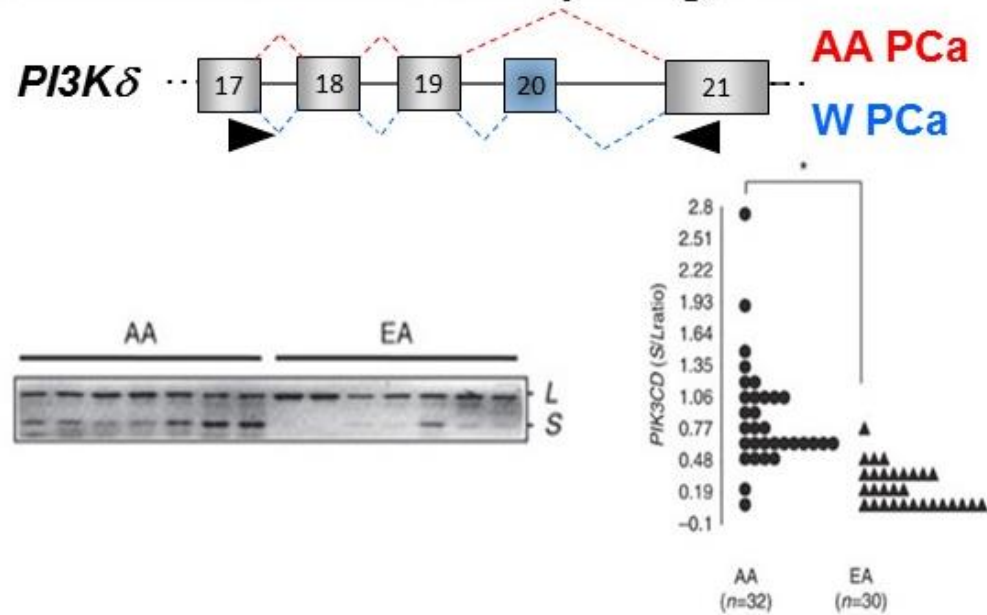


**72% of these DSG were
previously implicated in
cancer**

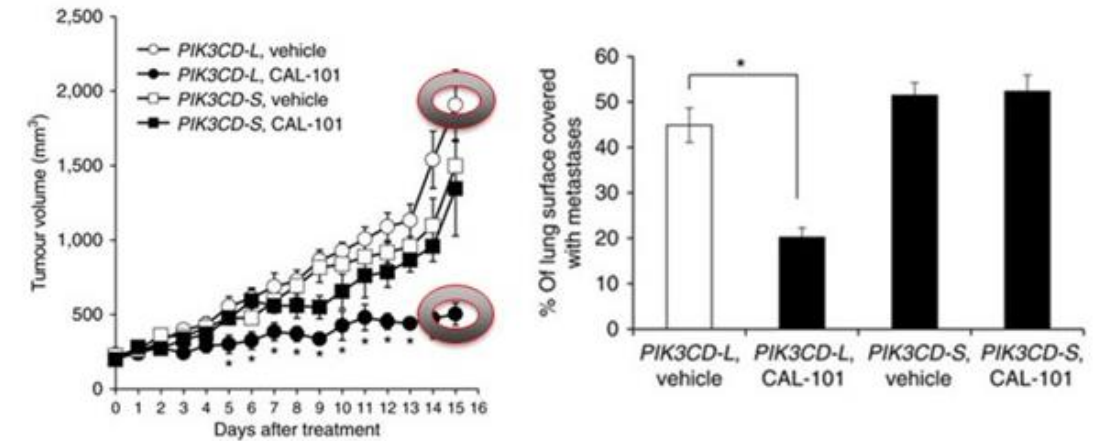
**Differential RNA
splice variants
also present in the
patient's adjacent
normal prostate
tissue**

Functional Impact of Race-related $PI3K\delta$ ARS

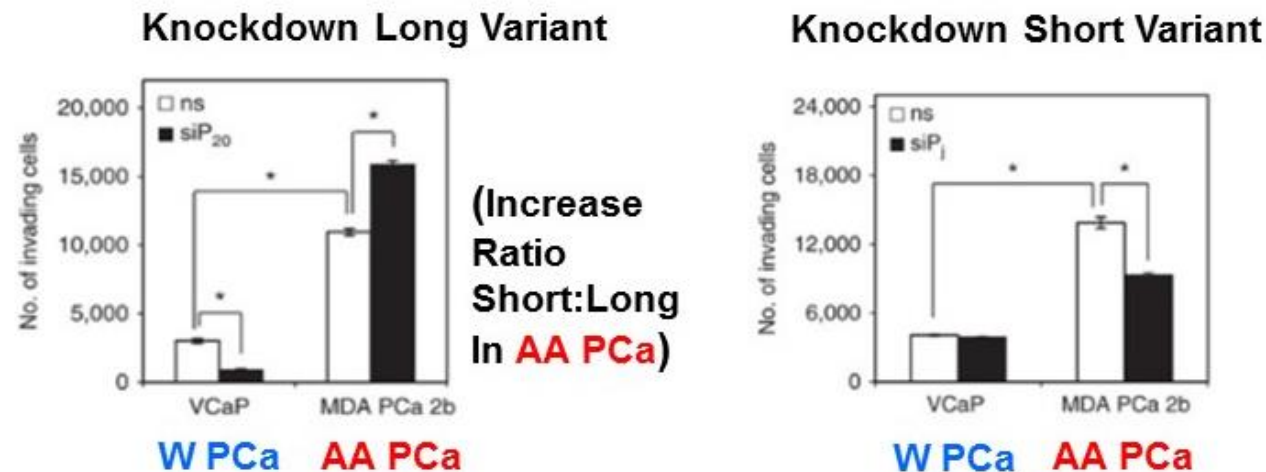
A. $PI3K\delta$ differential RNA splicing, PCa



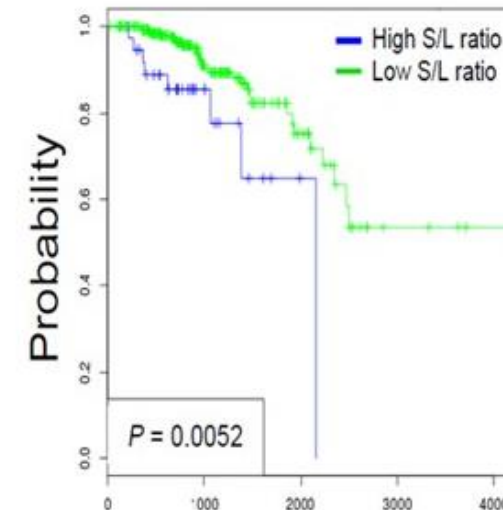
C. $PI3K\delta$ -S is resistant to $PI3K\delta$ inhibition



B. $PI3K\delta$ -S drives race-related PCa aggressiveness



D. Lower DFS, PRAD patients high $PI3K\delta$ -S/ $PI3K\delta$ -L ratio



CanSplice®

visualizes TCGA data and compares ARS, aggregate gene expression, and survival in cancers of patients of different races

Select tumor type

Select tumor type

TCGA-BRCA

Select analysis

Splice

Aggregate

Correlation

Survival

White

African American

Asian

Not reported

Tumor

751

182

61

94

Normal

105

6

1

1

Number of samples

Input gene name

Input Gene Name

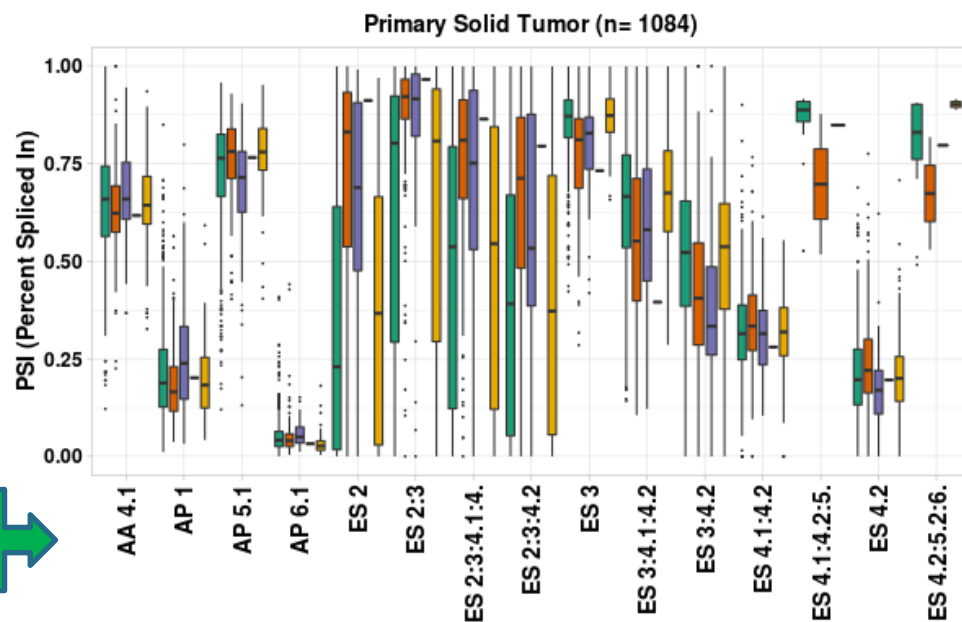
SLC3A2

Select ARS/T type

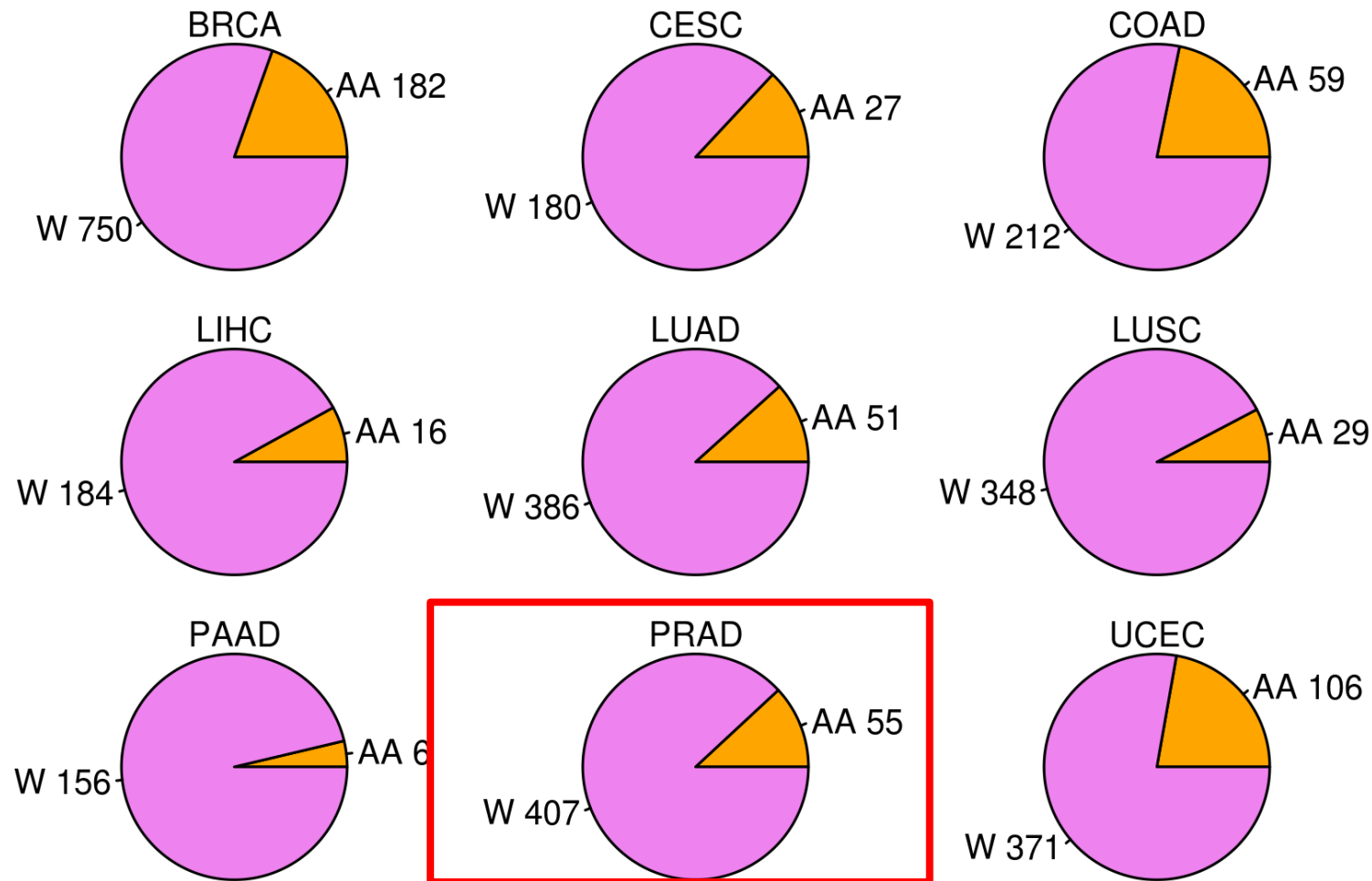
All

Interactive output of all ARS/T in the selected gene

ARS/T



TCGA samples included in our analysis



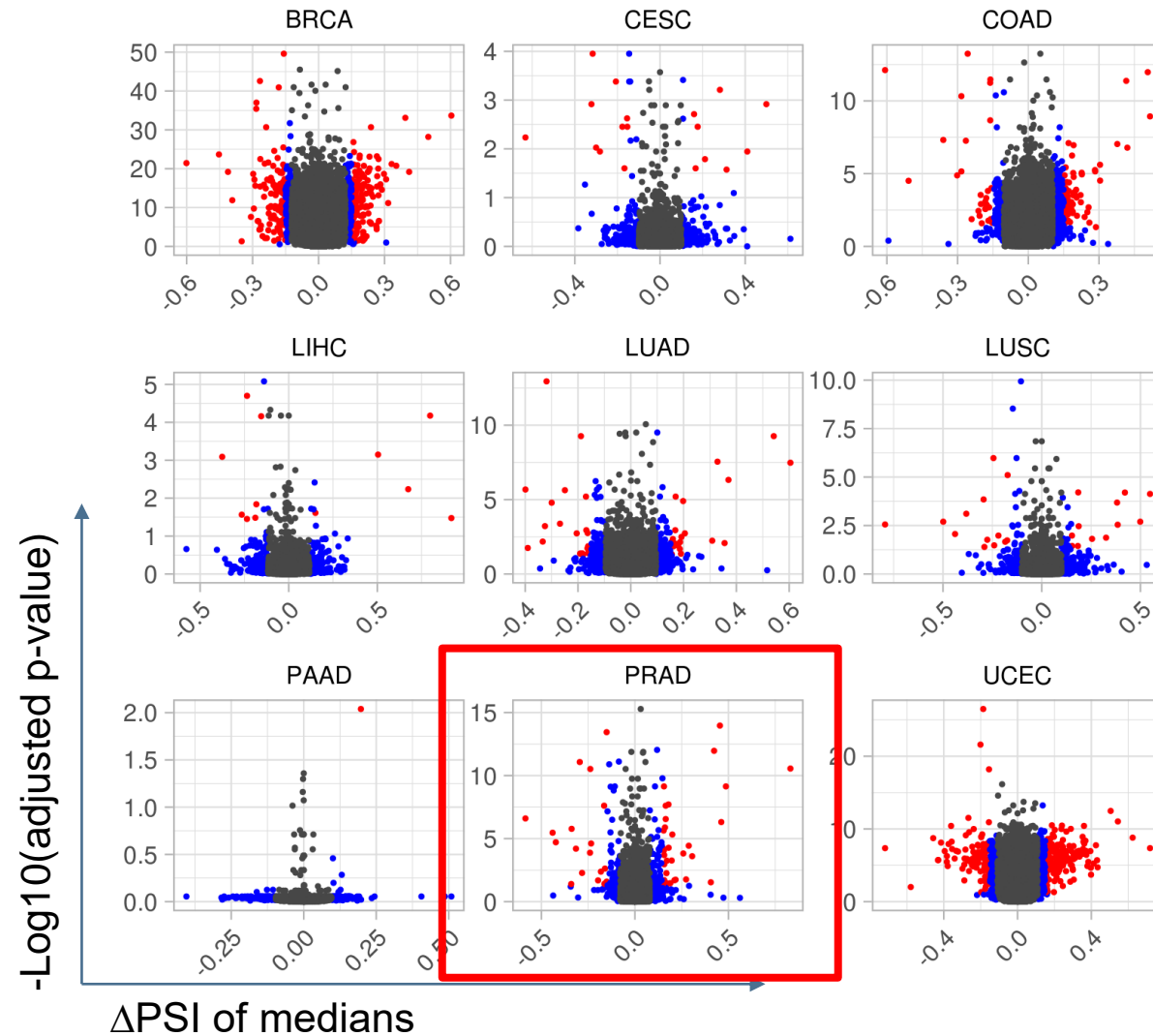
AA: African American
W: White

Cancer	TCGA Study Abbreviation
Breast	BRCA
Cervical Cancer	CESC
Colon	COAD
Liver	LIHC
Lung adeno	LUAD
Lung squamous	LUSC
Pancreatic	PAAD
Prostate	PRAD
Uterine	UCEC

Al Abo et al., 2021



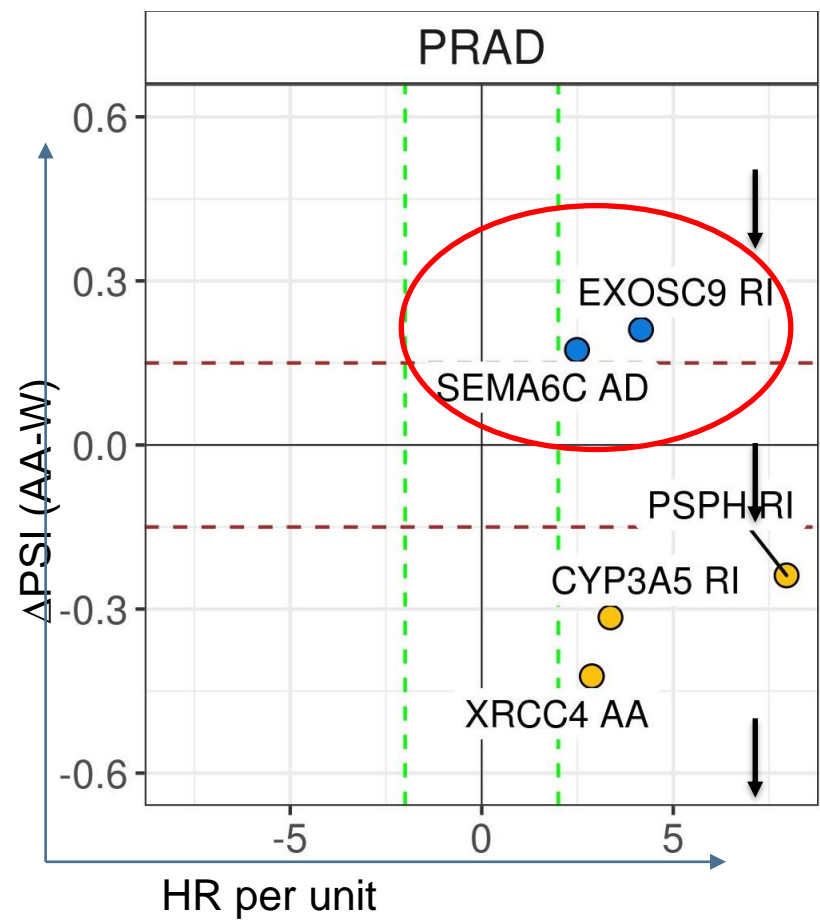
Identification of race-related ARS in TCGA



● **Top-ARS:** top 500 D-ARS ranked by absolute ΔPSI between AA and W

● **D-ARS:** top D-ARS exhibiting absolute $\Delta\text{PSI} > 15\%$ between AA and W and adjusted p-value < 0.05





PSI: Percent Spliced In
 Δ PSI: difference in splicing level



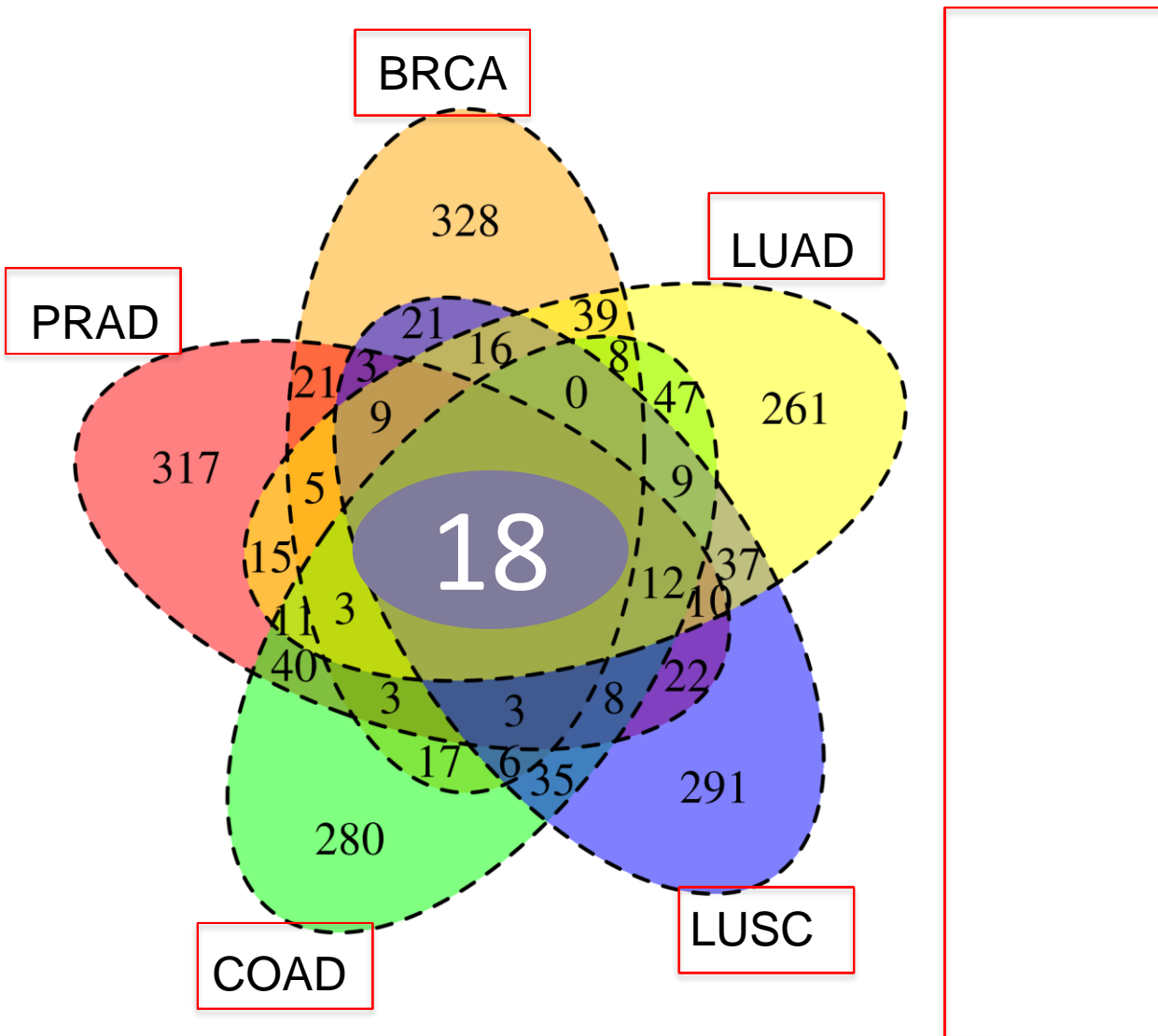
D-ARS associated with poor survival probability in AA (better in W)



D-ARS associated with poor survival probability in W (better in AA)

Al Abo et al., 2021





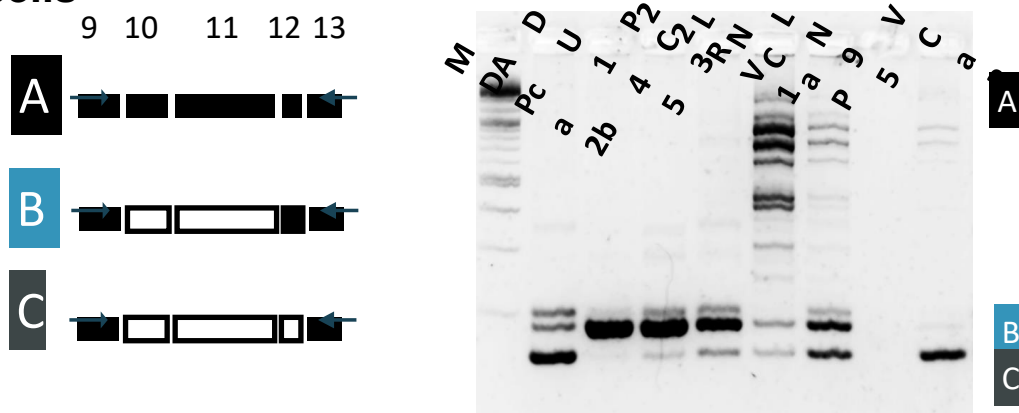
Al Abo et al., Genomics 2021

Targets in Common to PRAD, BRCA, LUAD, LIHC	Gene Description	Alternative Splicing Event
INSR	Insulin receptor	Skip of exon 11
CD44	Receptor for hyaluronic acid	Skip of exon v1-v10
ITGA6	Integrin, alpha 6	Skip of exon 5
RELN	Extracellular matrix serine protease	Skip of last exon
ABLIM3	Actin binding LIM protein family, 3	Skip of exon 14
BPTF	Bromodomain PHD finger transcription factor	Skip of exon 5
COL6A3	Collagen, type VI, alpha 3	Skip of exon 4
EHBP1	EH domain binding protein 1	Skip of exon 15
FN1	Fibronectin 1	Skip of exon 40
LMO7	LIM domain 7 – modulates actin signaling	Skip of exon 12

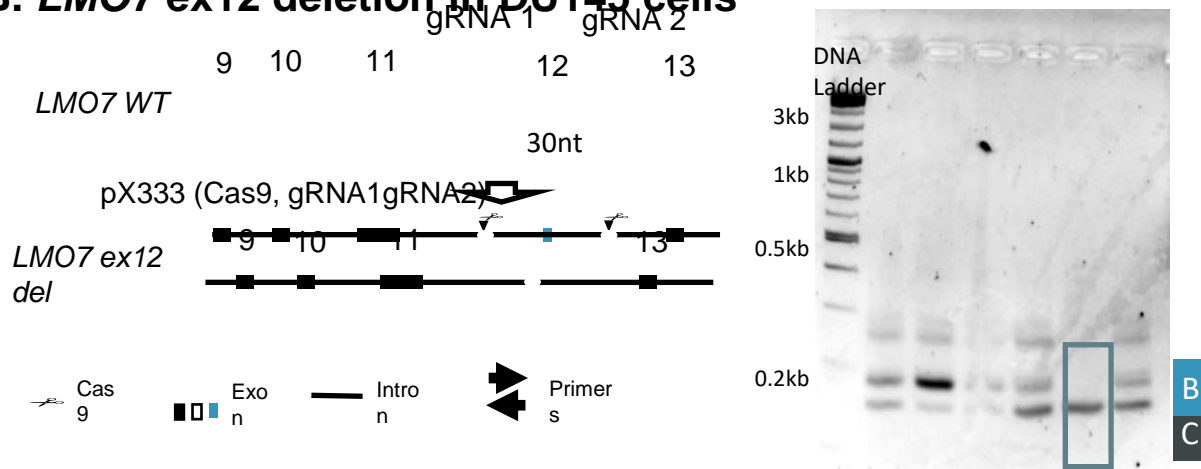
Functional Impact of Race-related *LMO7* ARS – exon 12



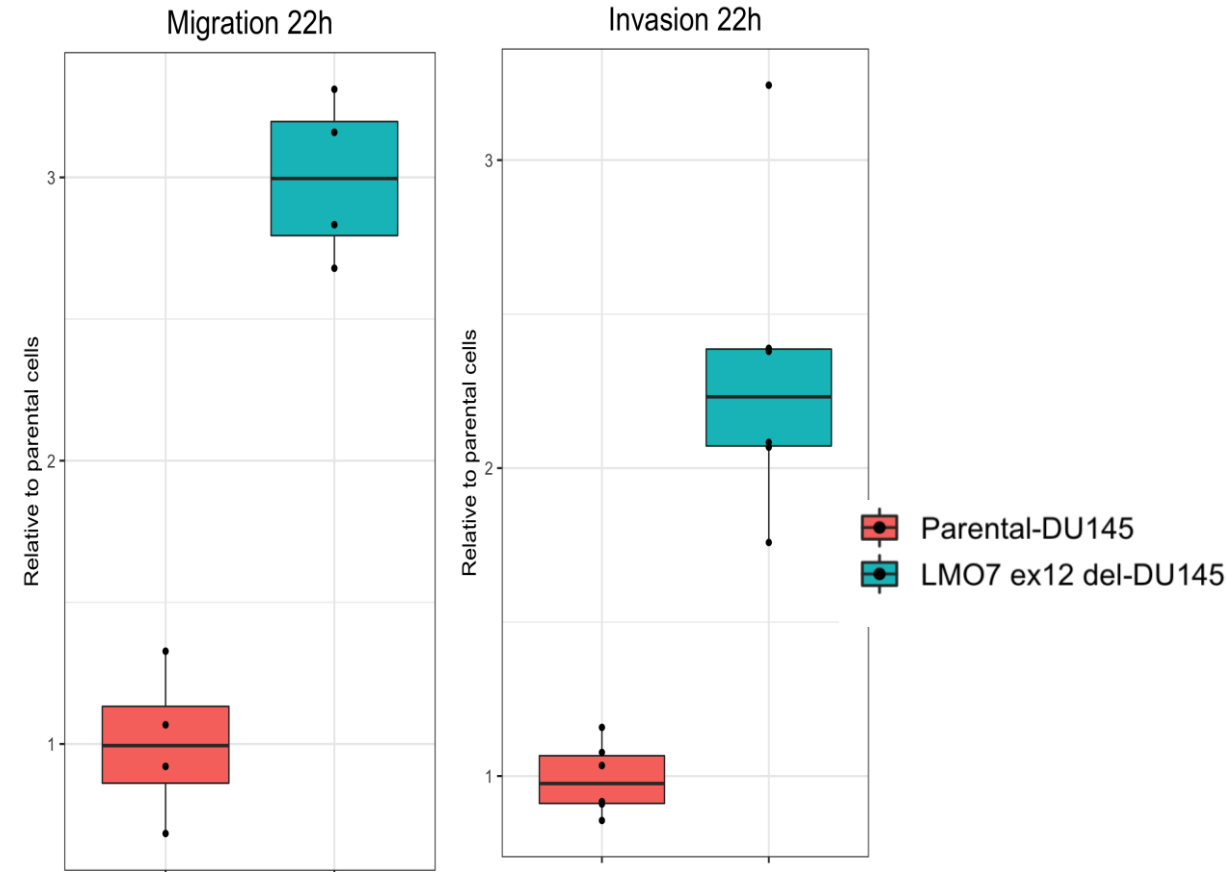
A. *LMO7* differential RNA splicing, prostate cancer cells



B. *LMO7* ex12 deletion in DU145 cells



C. Increased migration and invasion in *LMO7* ex12 del cells

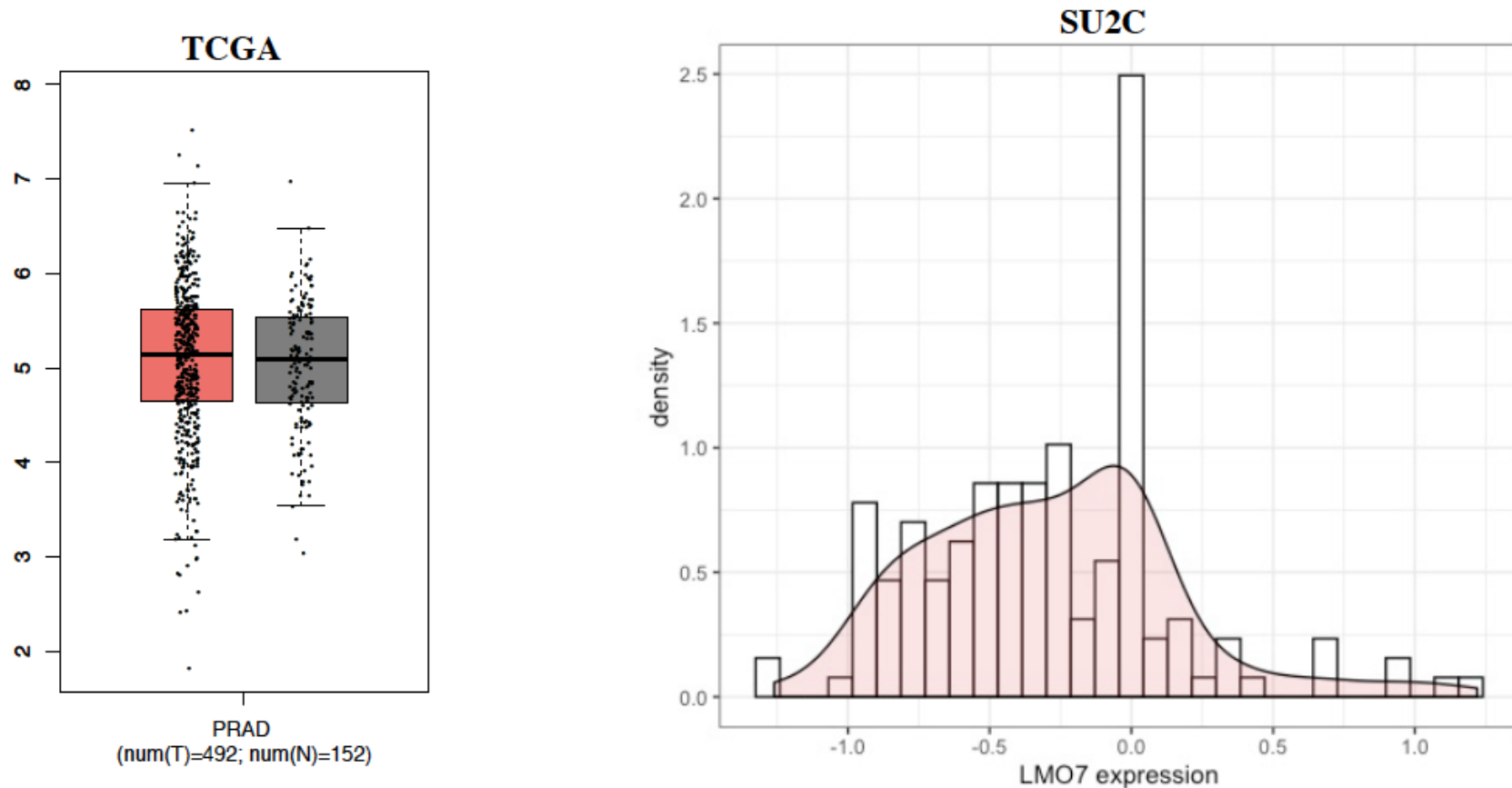


LMO7 in primary vs metastatic PC



TCGA (primary cancer): No difference in aggregate expression of LMO7 in Normal vs Tumor in PC

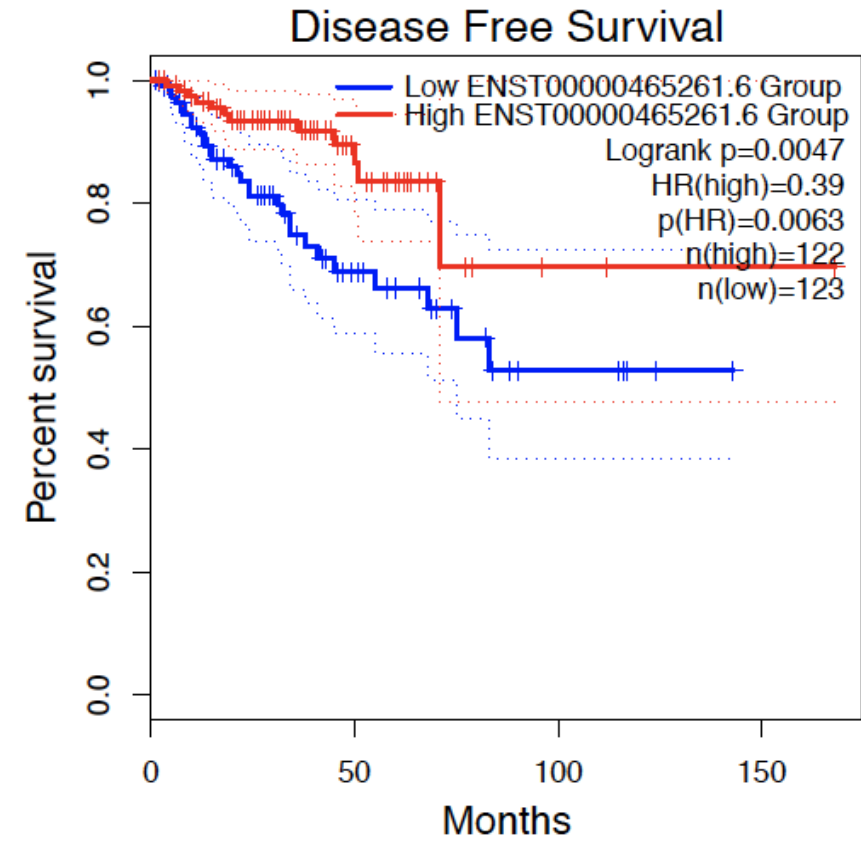
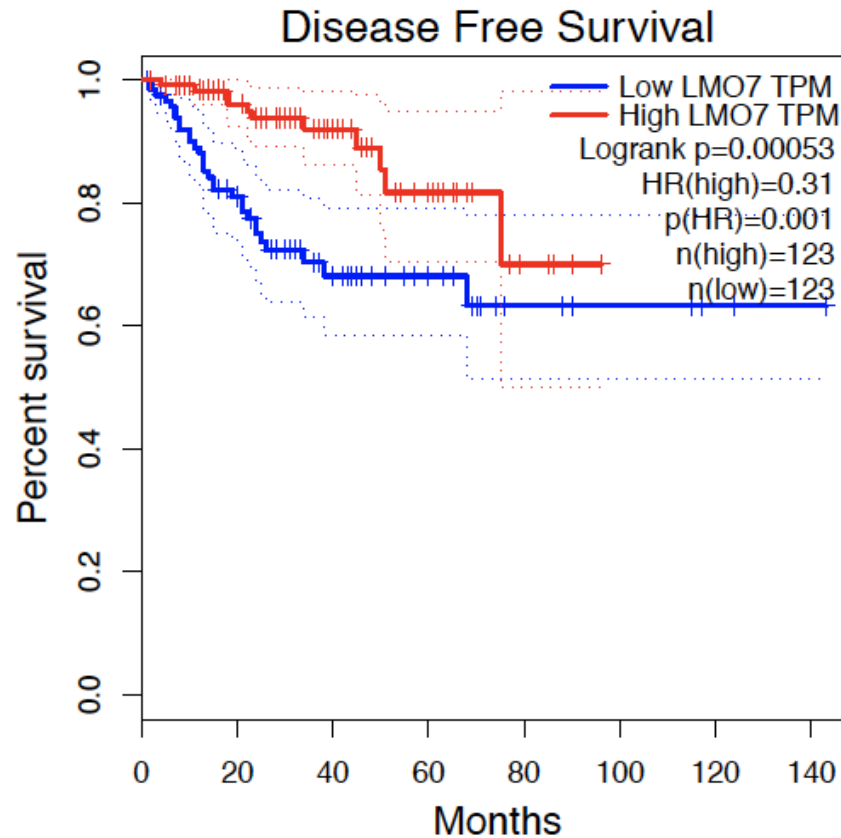
SU2C (metastatic): Big difference in frequency of loss of expression of LMO7



Clinical Impact of Race-related *LMO7* ARS in PC



Association between *LMO7* low expression or ex12 skipping and disease free survival in PCa

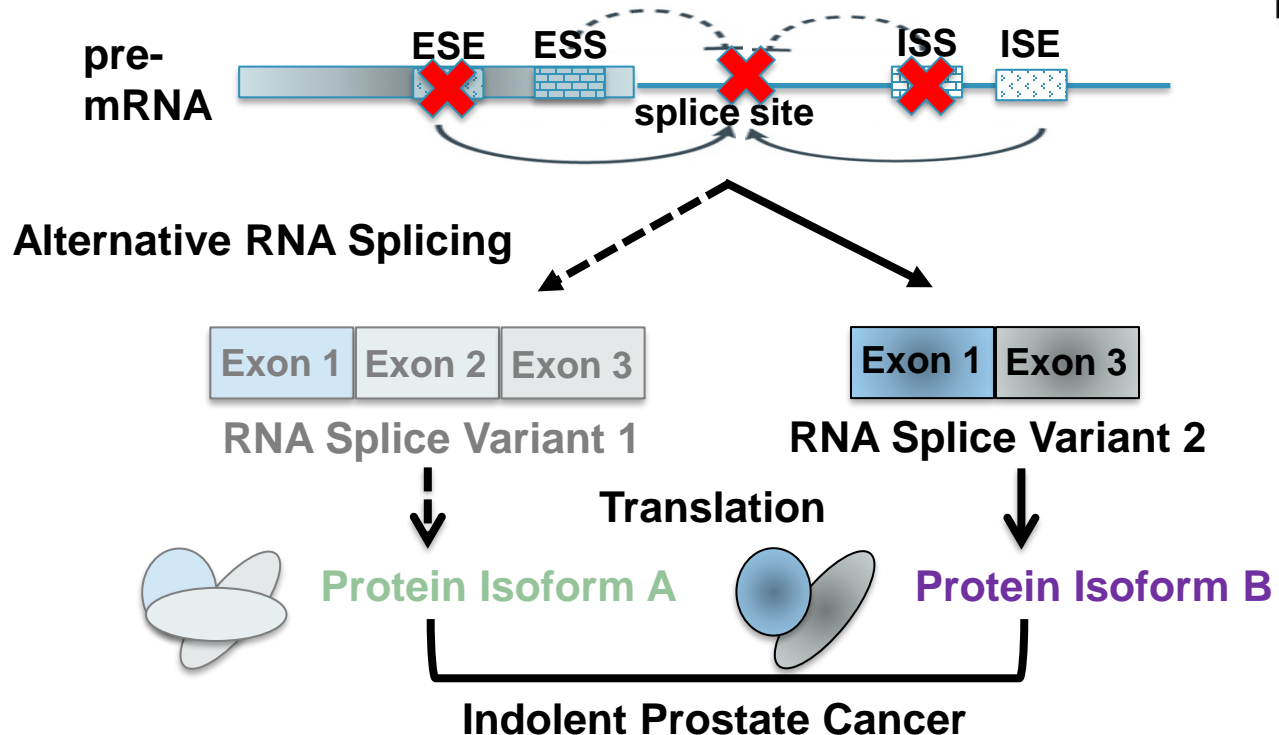




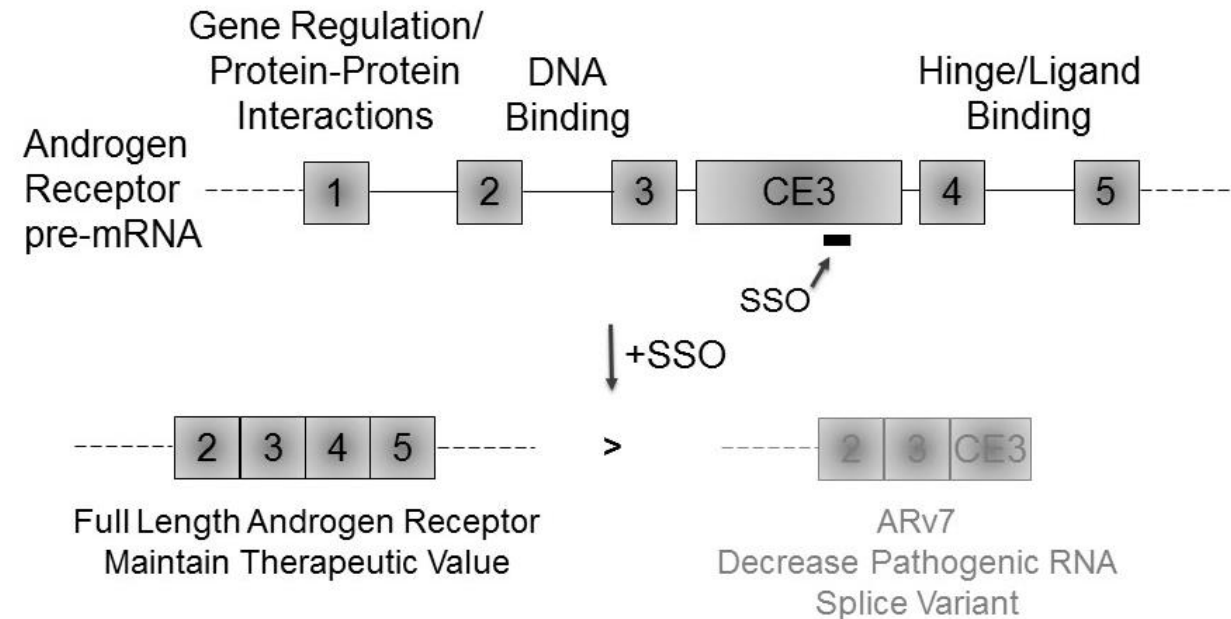
Therapeutic Targeting of Alternative RNA Splicing

Splicing regulatory regions can be targeted with
Splice-Switching Oligonucleotides
SSOs

Simultaneously limit pathogenic RNA
splice variants and maintain/induce RNA
splice variants with therapeutic value

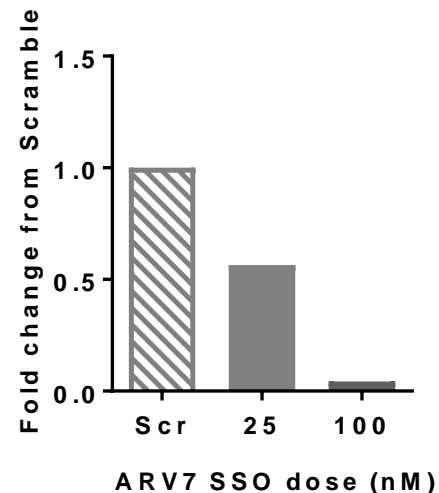
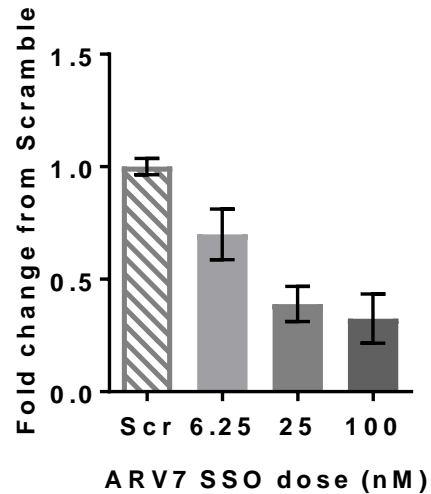


SSOs against the AR-V7 variant of the Androgen Receptor

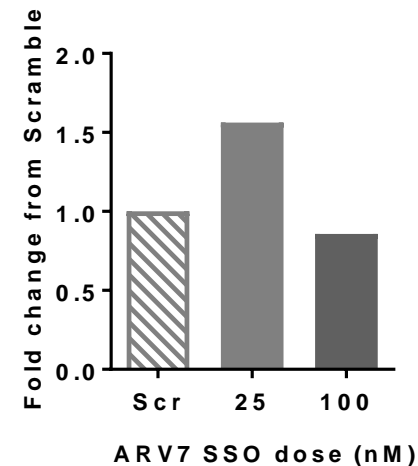
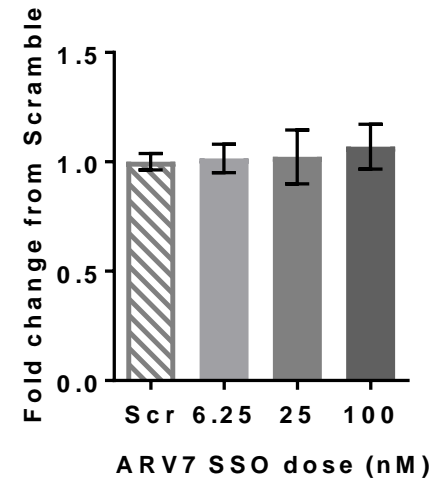


Targeting ARS: Splice-Switching Oligonucleotides (SSO)

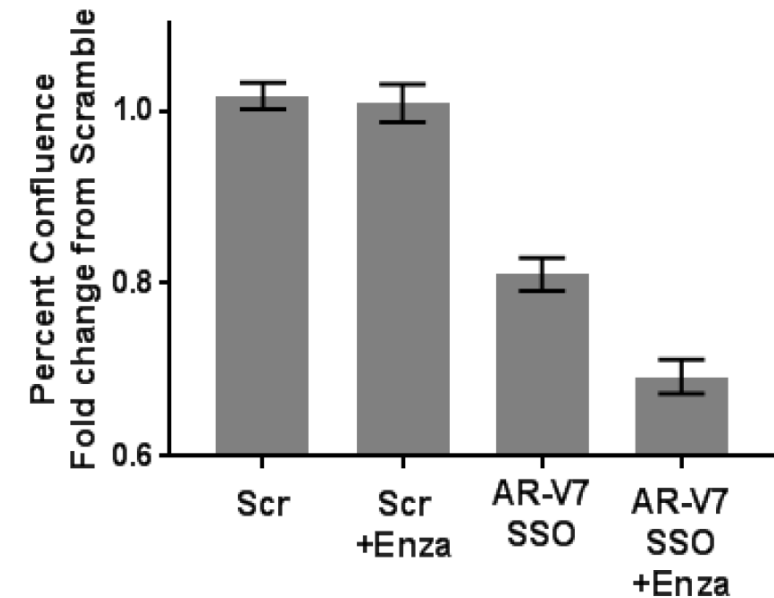
ARv7 SSO decreases ARv7 RNA and protein



ARv7 SSO maintains full length AR RNA and protein



ARv7 SSO decreases proliferation, restores sensitivity to enzalutamide



LaCroix *et al.*,

Deep RNAseq of GENCADE



72 patients (Blacks and Whites)

Fresh frozen – tumor and adjacent

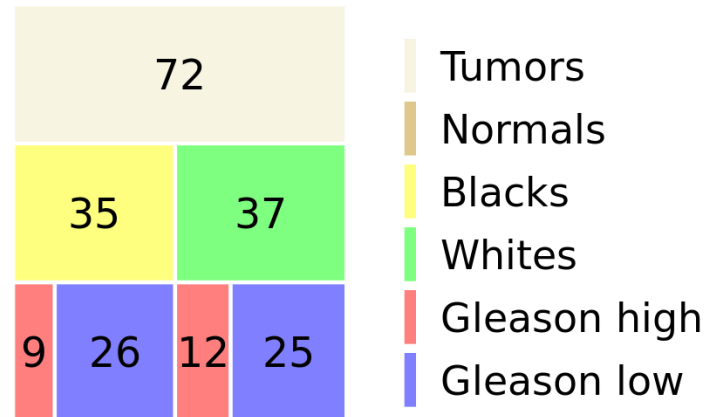
Extensive MR data available

DNA for ancestry

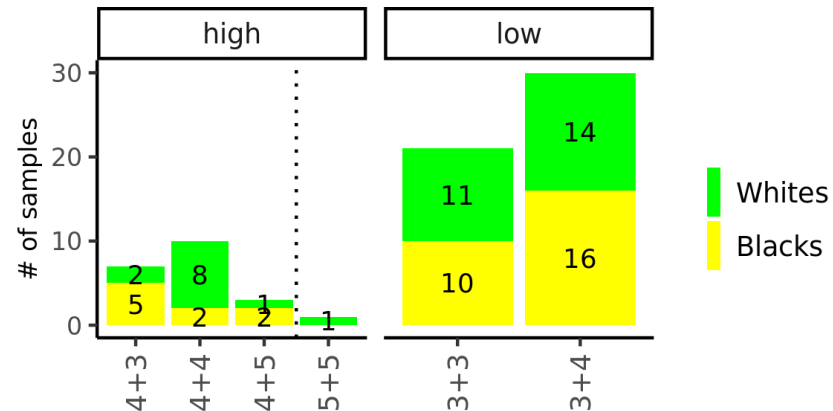
**RNA for deep RNAseq – 150 length reads
And >100 million read per samples**

Aggregate gene expression by STAR2 pass and htseq

Splicing by SpliceSeq

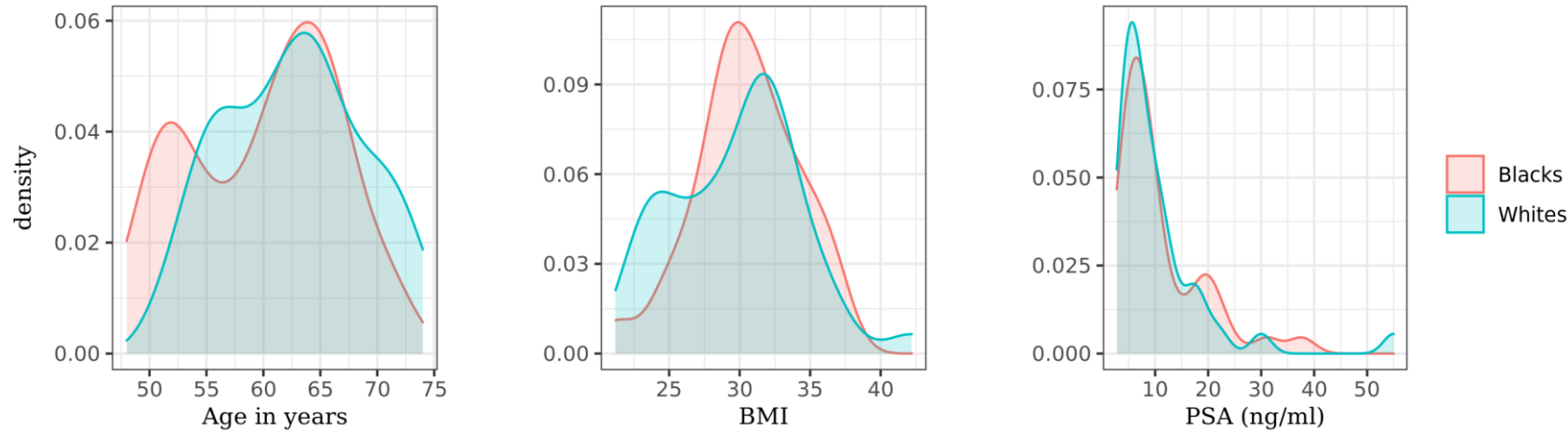


← Tumor samples have matching adjacent normal samples

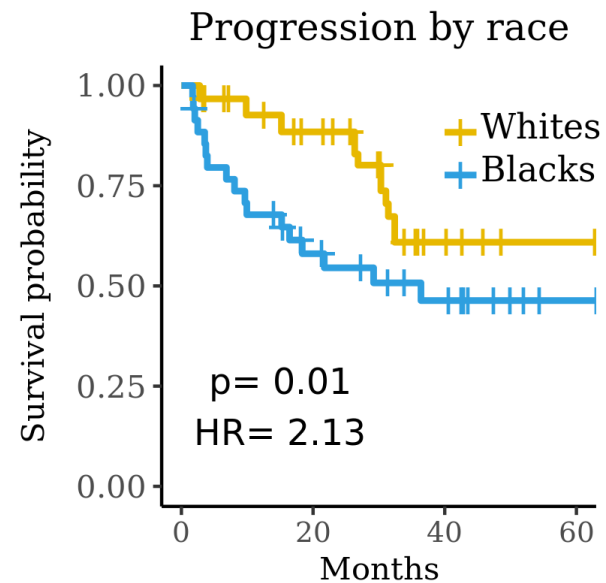


← Breakdown of the samples by Gleason scores and race.

Deep RNAseq of GENCADE



Density plots showing age, BMI and PSA levels in Black and White GENCADE prostate cancer patients



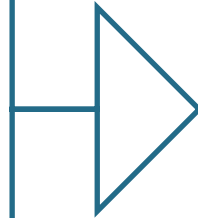
Survival analysis of GENCADE prostate cancer patients shows significant increase in progression in Black patients compared to White patients

DO NOT POST

Gene Set Enrichment Analysis (Hallmark 50 pathways)

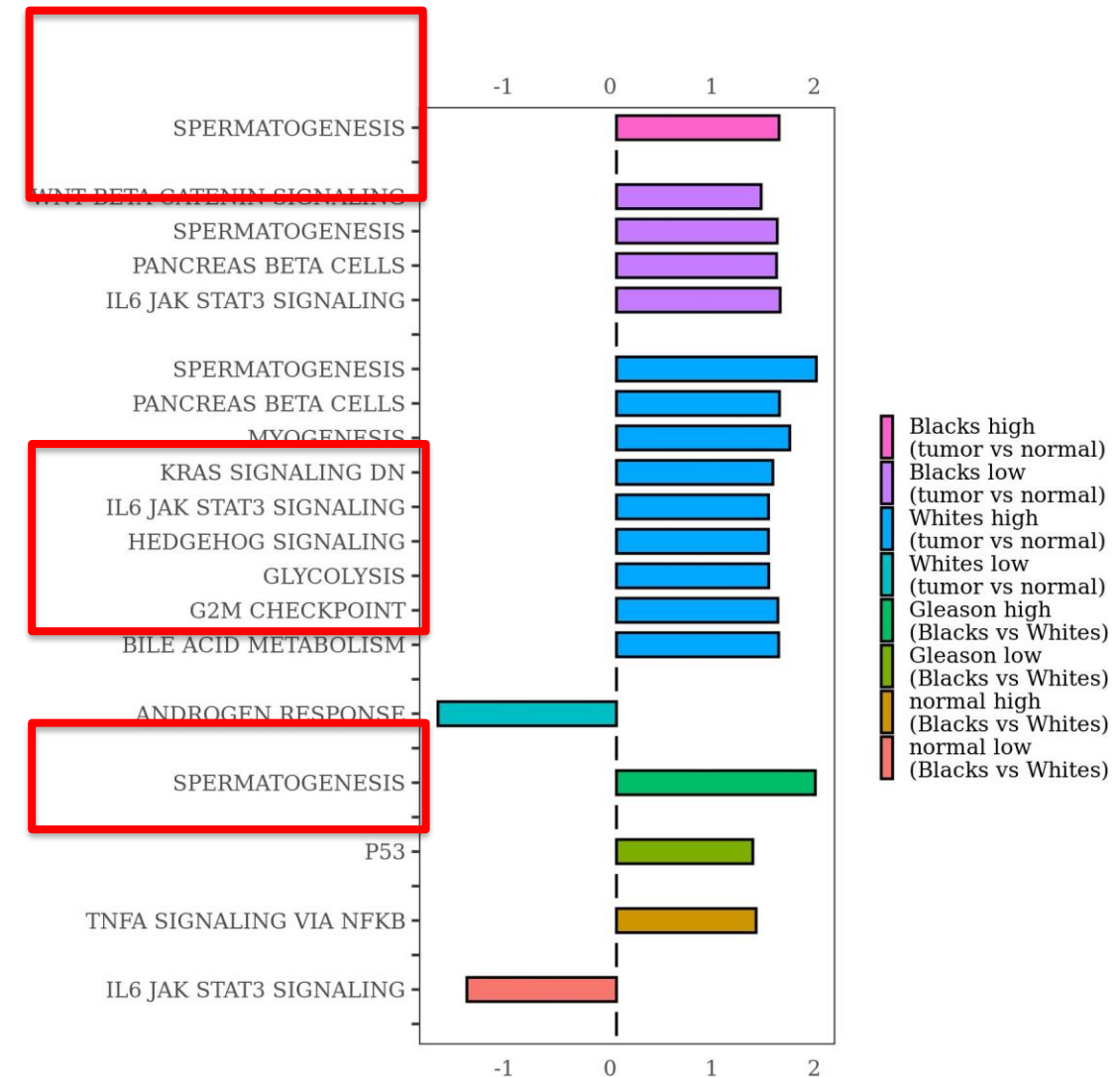


The gene set enrichment analysis for the identified race-related ARSTs in tumors or adjacent normal tissue and between tumors and adjacent normal tissue within Blacks and Whites exhibit enrichment in cancer-related pathways.



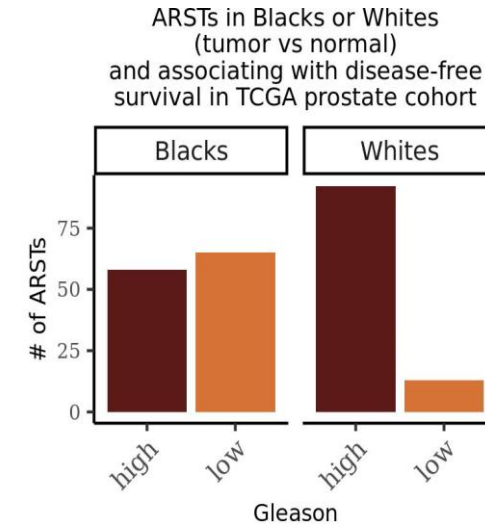
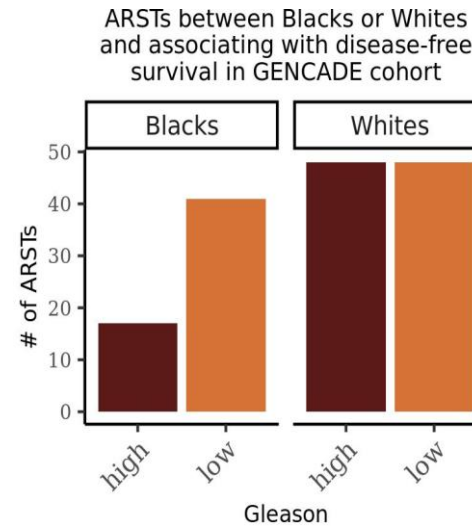
Cancer-related “spermatogenesis” genes showing race-related differential RNA splicing:

NF2, MTOR, AURKA, RADS17, BRCA, CDK1, PARP2, HOXB1

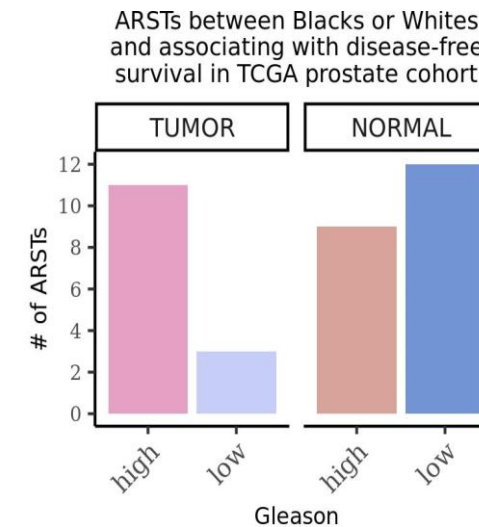
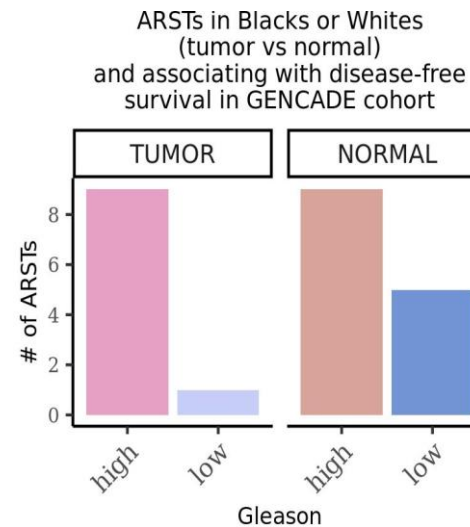


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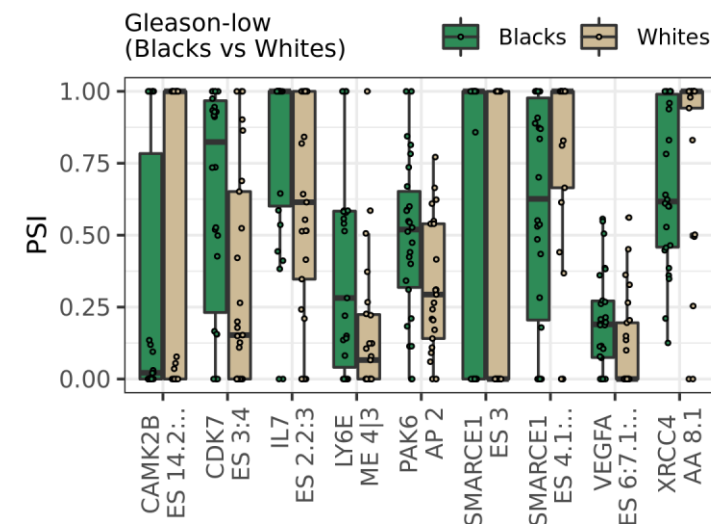
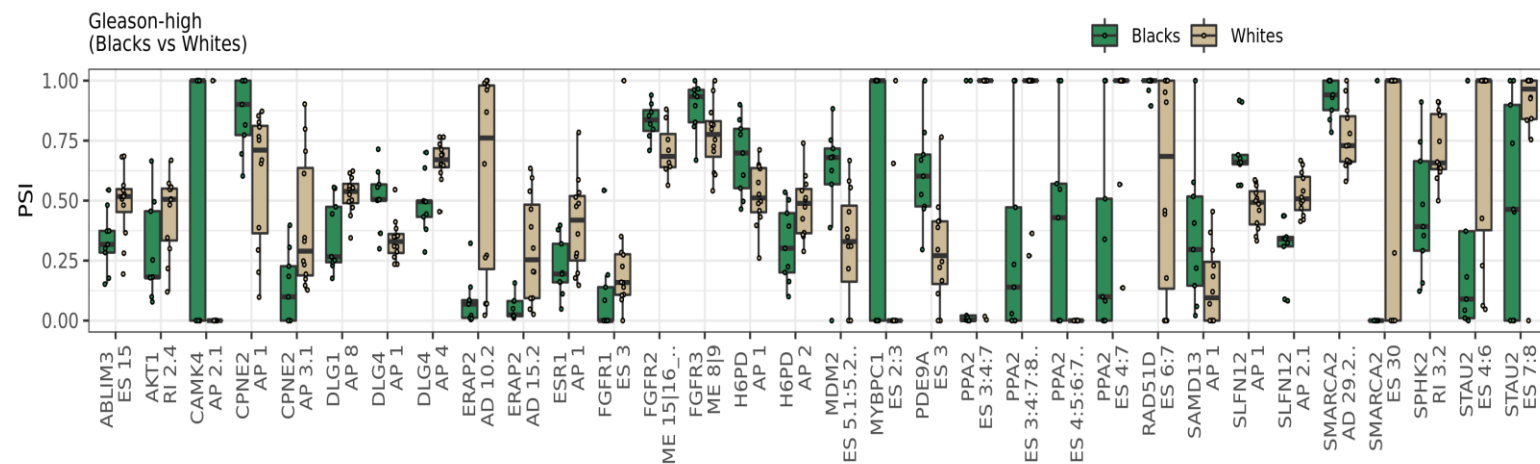
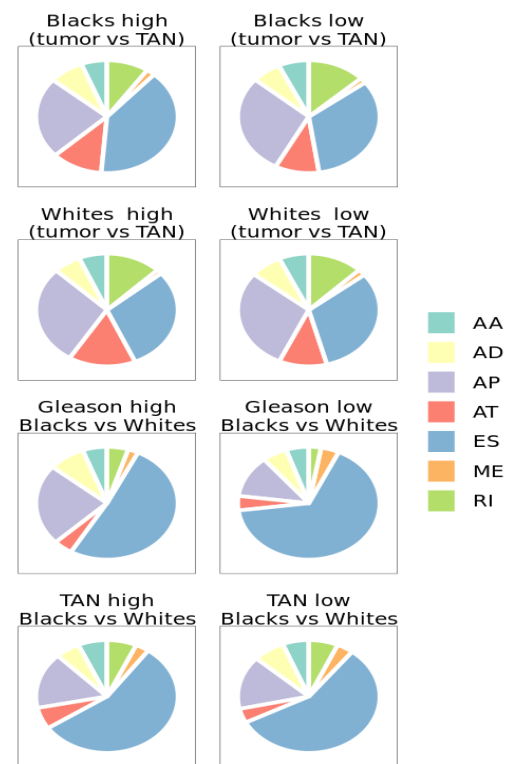
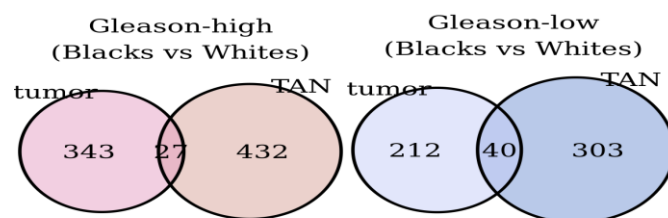
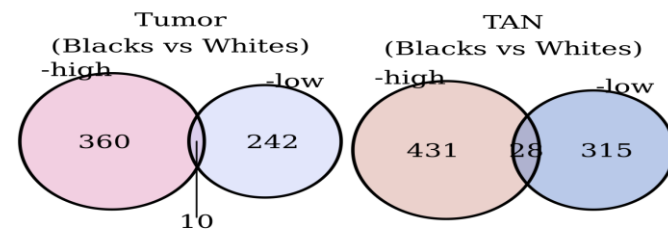
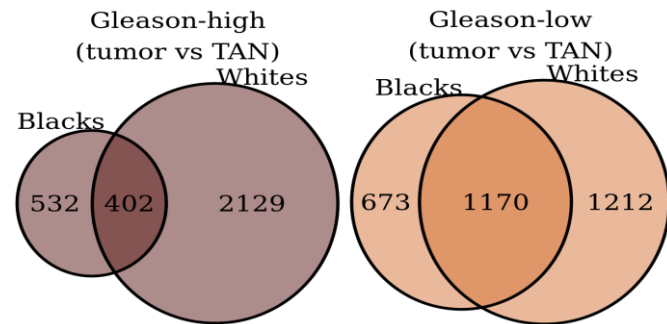
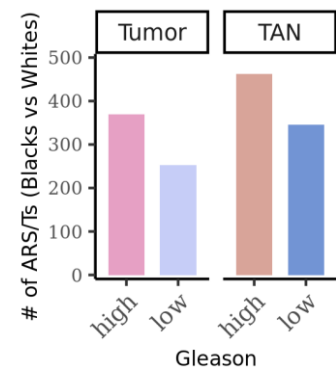
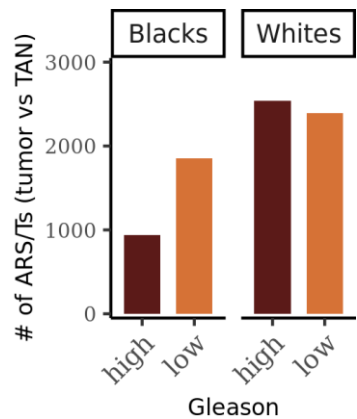
Number of race-related differentially spliced genes associated with disease-free survival - Hazard ratio > 2 and p-value < 0.05



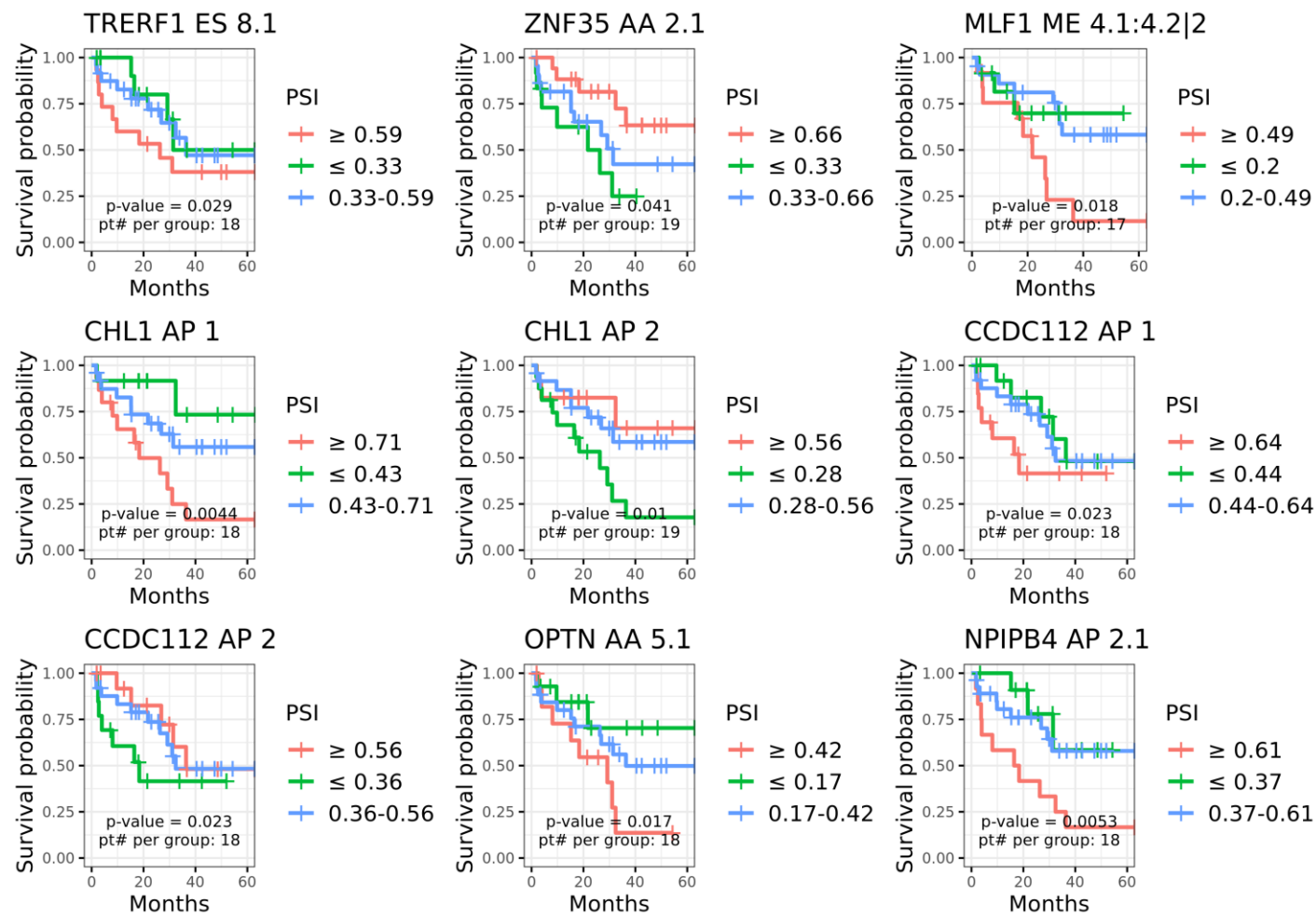
Race-related ARSTs identified in adjacent normal tissue are also associated with survival. This implicates differences in the tumor microenvironment that may play a critical role in differential cancer progression.



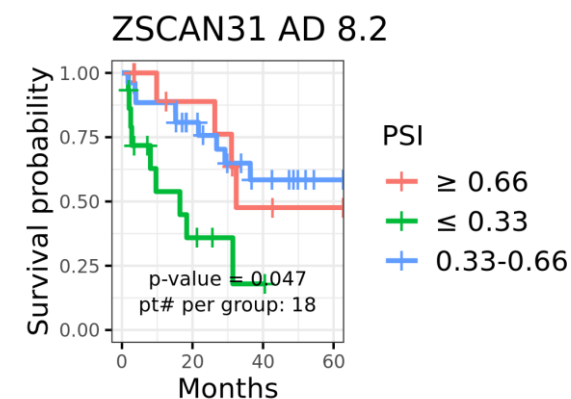
DO NOT POST



Disease-free survival Analysis: association between race-related differentially spliced genes in High or Low Gleason tumors (GENCADE)



PSI = Percent Spliced In:
An arbitrary measure of
frequency of exon skipping
in a particular gene



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Rationale for Comparative Ancestral Transcriptomics (CAT) Approach

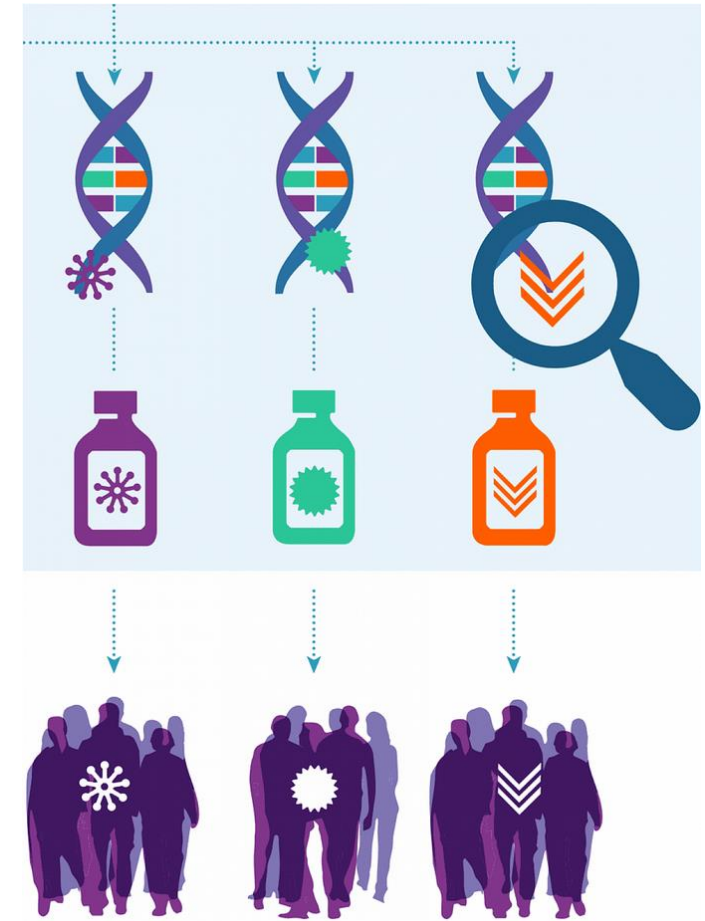


This approach is focused on patient-centered precision oncology, NOT race-based medicine

Population-level differences in RNA splicing allow us to hone in on targets driving tumor aggressiveness



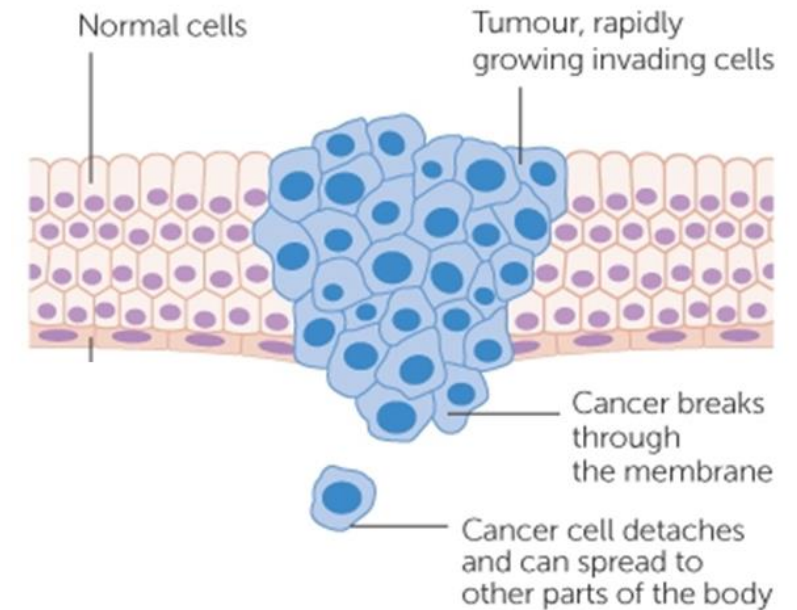
Once identified, these targets can become the basis for biomarker stratified precision clinical trials for ALL patients whose cancer expresses the pathological splice variant



<https://www.nih.gov/news-events/news-releases/nci-match-precision-medicine-clinical-trial-releases-new-findings-strengthens-path-forward-targeted-cancer-therapies>

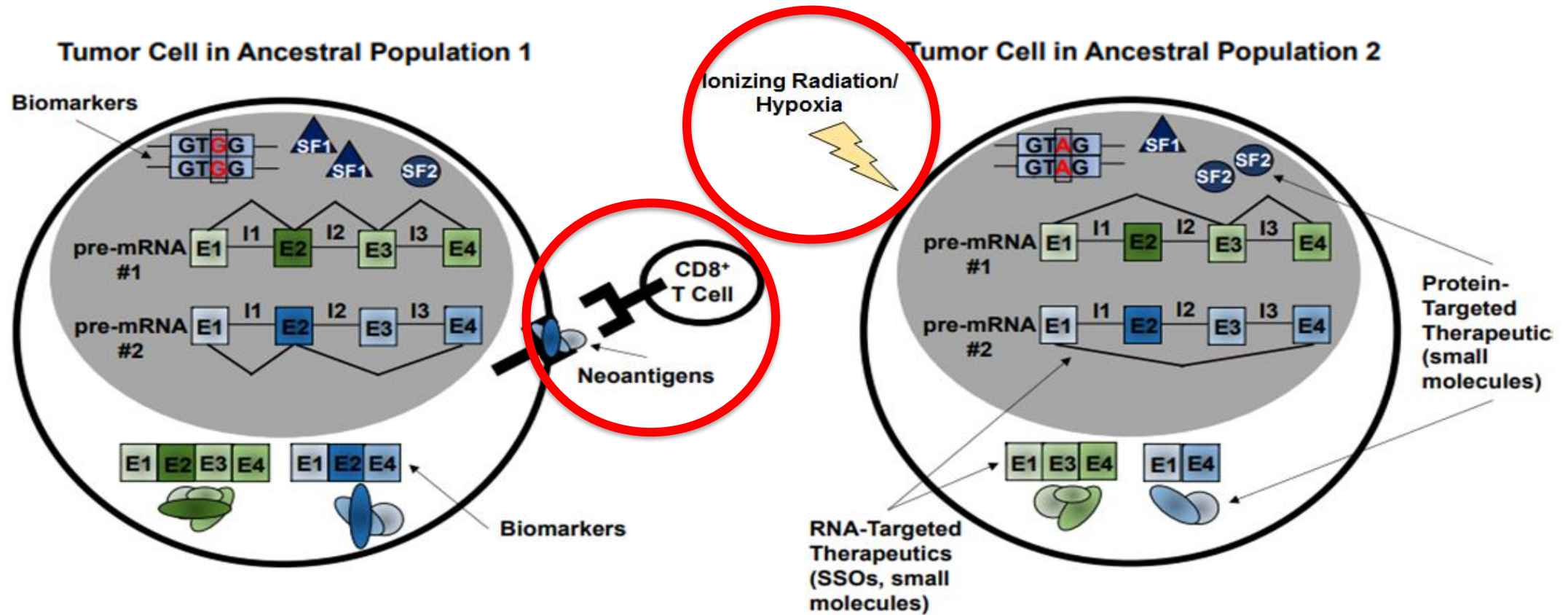
Thousands of novel pathological splice variants across 9 tumors that:

- Increase cancer cell growth
- Decrease cancer cell death
- Increase cancer spread
- Drive resistance to therapy
- Correlate with worse survival



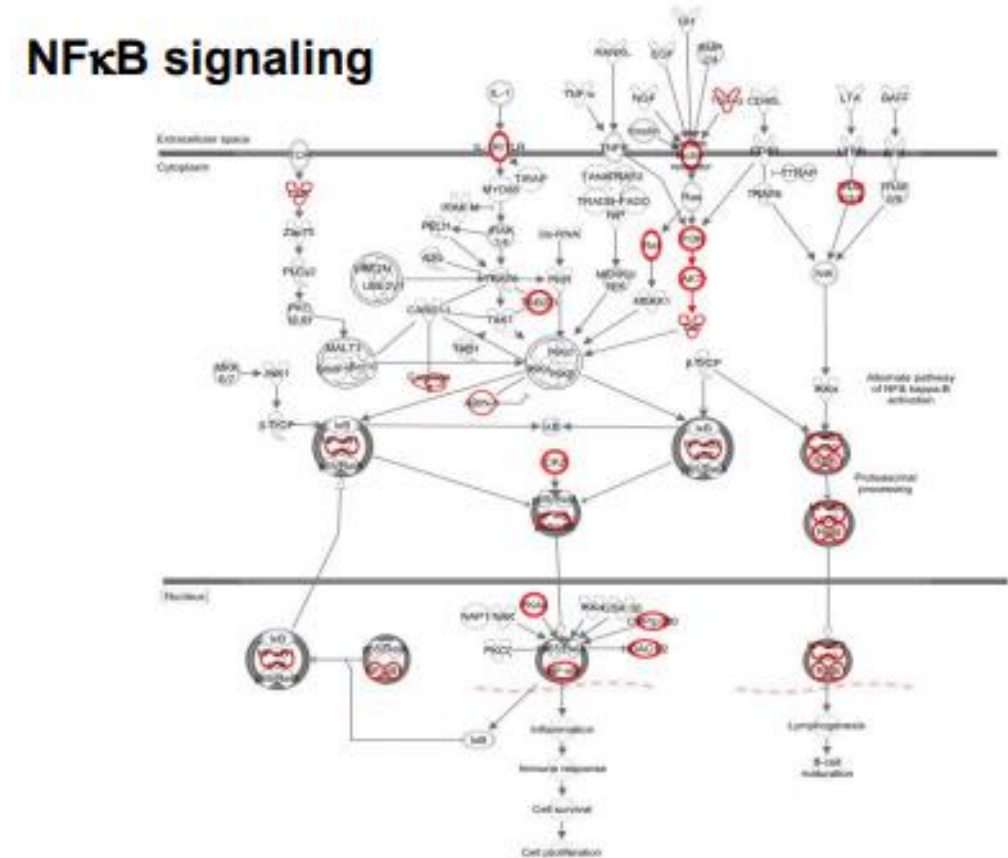
Can target the pathological RNA splicing event with Splice Switching Oligonucleotides (SSOs)

Can target the pathological splice variant proteoforms (small molecules)

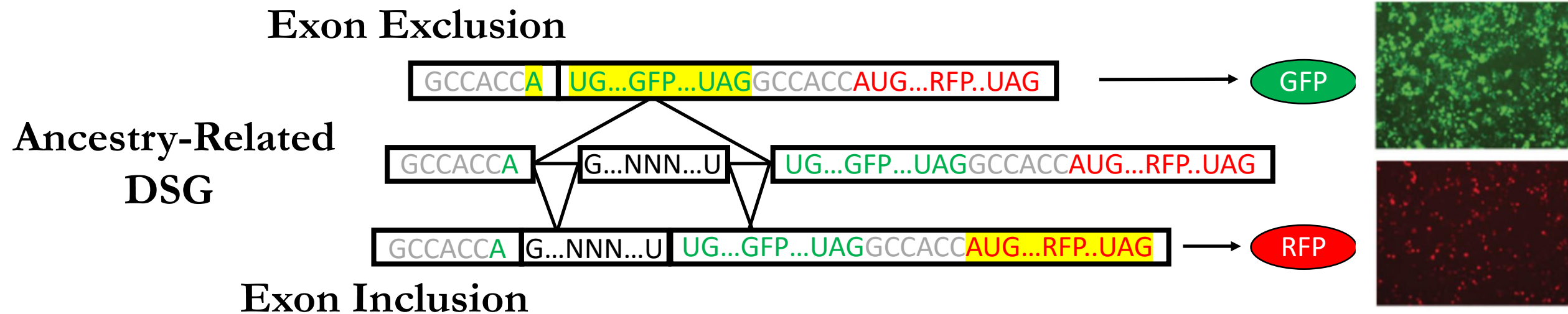


Alternative RNA Splicing as a Potential Major Source of Untapped Molecular Targets in Precision Oncology and Cancer Disparities: Timothy Robinson, Jennifer Freedman, Muthana Al Abo, April Deveau, Bonnie LaCroix, Brendon Patierno, Daniel George, Steven Patierno, 2019

- Adaptive immunity
- Defense response to bacteria
- Defense response to viruses
- NF κ B signaling
- Innate immunity
- Inflammasome signaling



Oncogenic signaling pathway of D-ARS over-represented in AA PC vs EA PC

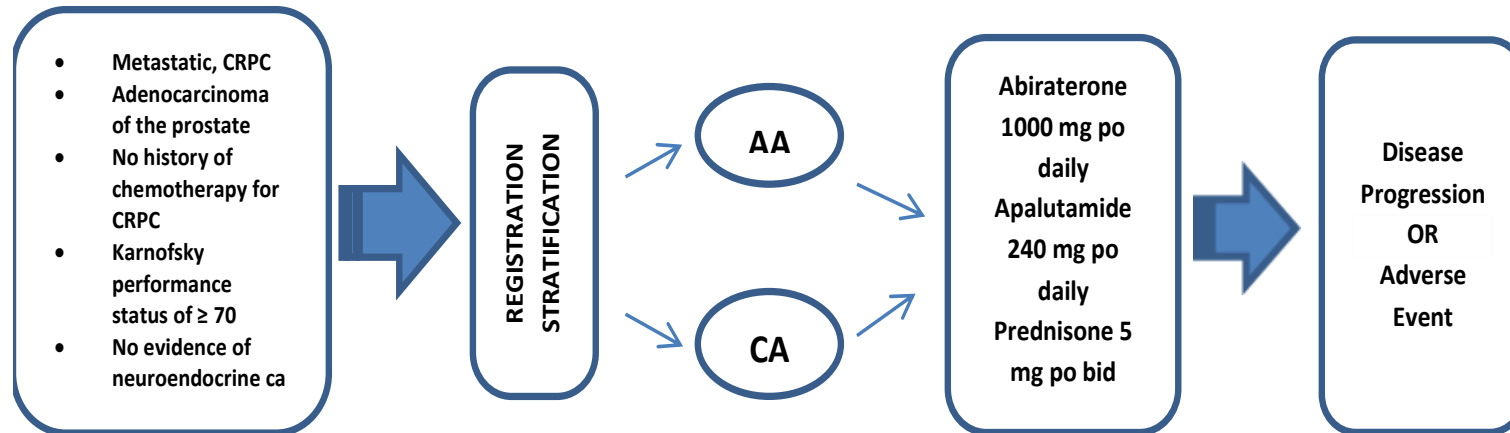


- High-throughput, screening, development and optimization of drugs targeting RNA splicing with real-time analysis and accurate quantitation
- **RNA splicing plasticity:** readout in response to drug treatment, environmental agents
- Identification of factors driving ancestry-related RNA splicing

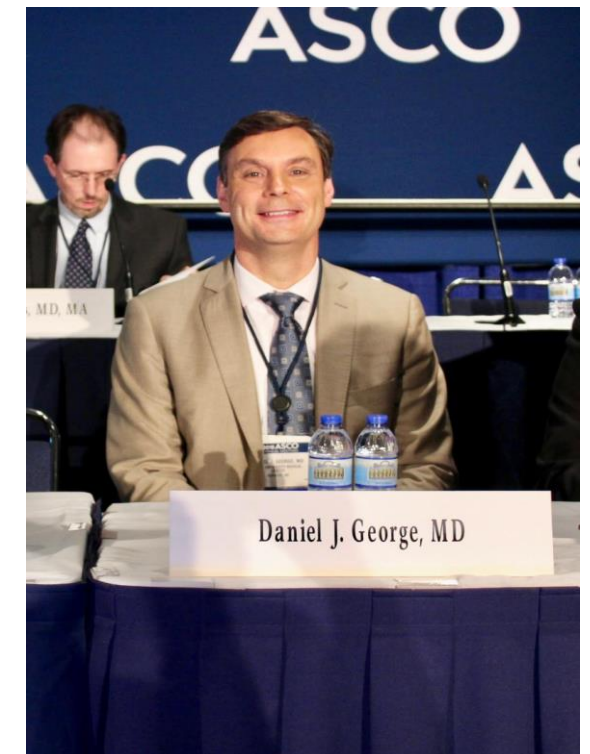
Extraordinary Results from Race-Stratified or Equal Representation by Race Clinical Trials

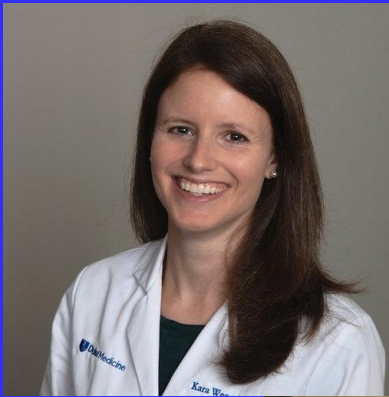


- *ABI-RACE:** Abiraterone + Prednisone (EQR)
- PROCEED:** Sipuleucil-T stratified by race
- DOCETAXEL:** Docetaxel retrospective meta-analysis by race
- *PANTHER:** Apalutamide, Abiraterone, Pred (EQR) (in progress)
- *ASPIRE:** ADT, PARP Inhibitor in localized disease (EQR)



Improved biochemical response for African-American men with advanced prostate cancer and a stronger response to both hormone and chemotherapy therapy: Duke's Prostate & Urologic Cancer Center





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DCI Shared Resources

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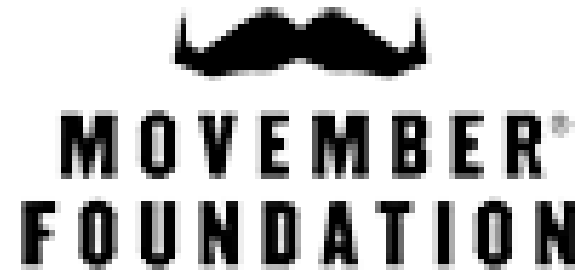


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Disparities

P20 PACHE: Duke-NCCU
Translational Cancer
Disparities Research
Partnership

Duke Cancer Disparities
SPORE

RO1's



Prostate and Lung

