

Historical perspective and future directions: Computational science in immuno-oncology

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April 7, 2022

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Disclosures

- Consulting/Advisory
 - Tango Therapeutics
 - Genome Medical
 - Genomic Life
 - Enara Bio
 - Janssen
 - Manifold Bio
 - Monte Rosa Therapeutics
- Research funding
 - Novartis
 - BMS
- Equity
 - Tango Therapeutics
 - Genome Medical
 - Genomic Life
 - Syapse
 - Enara Bio
 - Manifold Bio
 - Monte Rosa Therapeutics
 - Microsoft

Outline

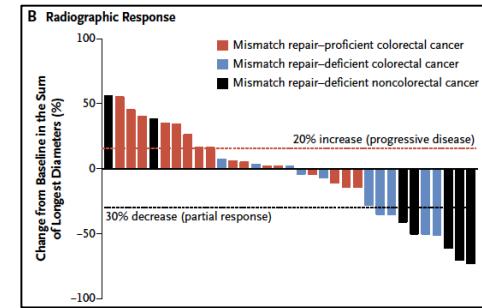
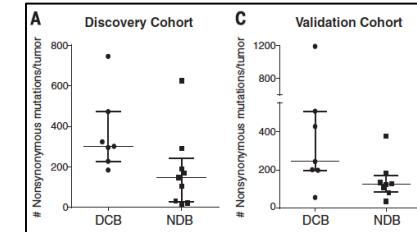
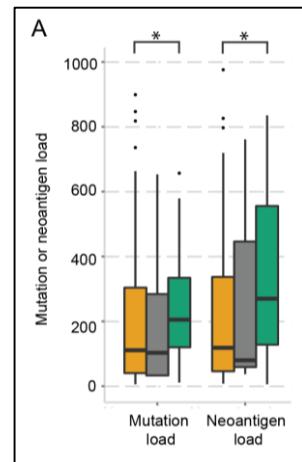
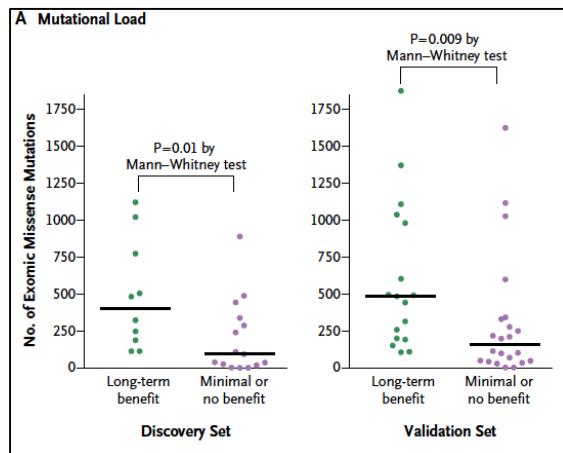
- Genomics and immuno-oncology biomarkers
- Pivoting to reverse translation and genomics
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- Next steps

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Clinical genomics and cancer immunotherapy ca. 2015

Tumor mutational burden



CTLA4 Ab
and melanoma

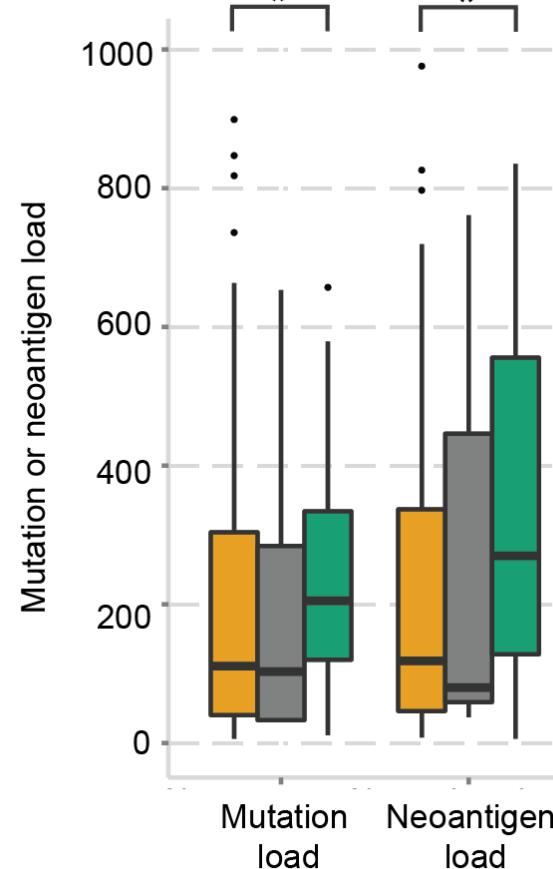
CTLA4 Ab
and melanoma

PD-1 Ab
and NSCLC

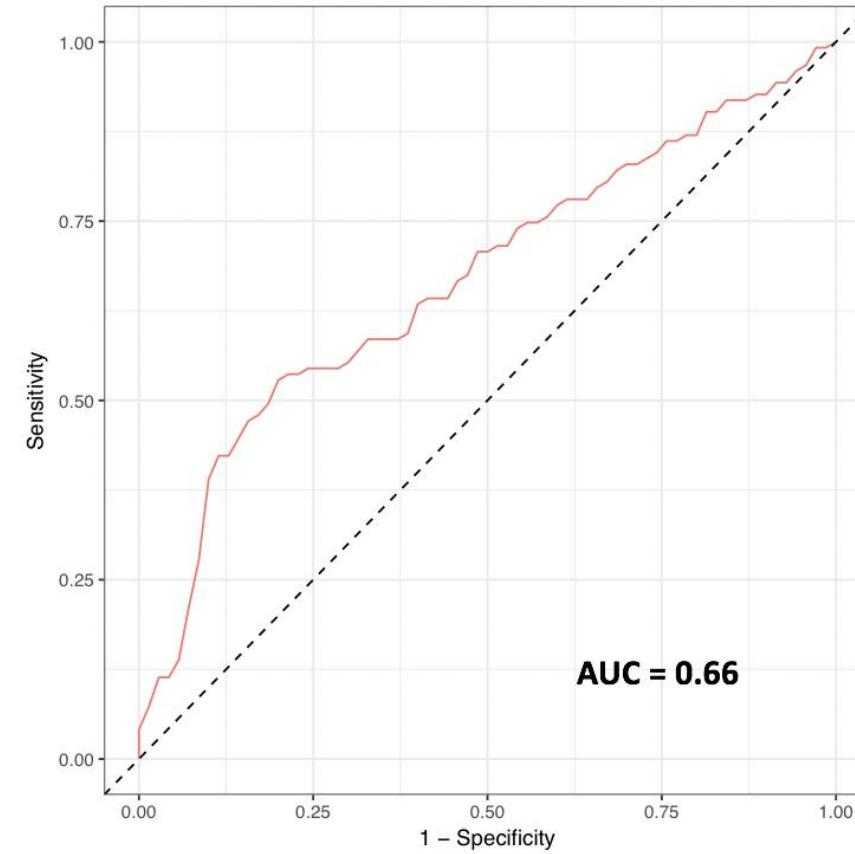
PD-1 Ab and
MSI-high tumors

Is TMB necessary and/or sufficient?

A



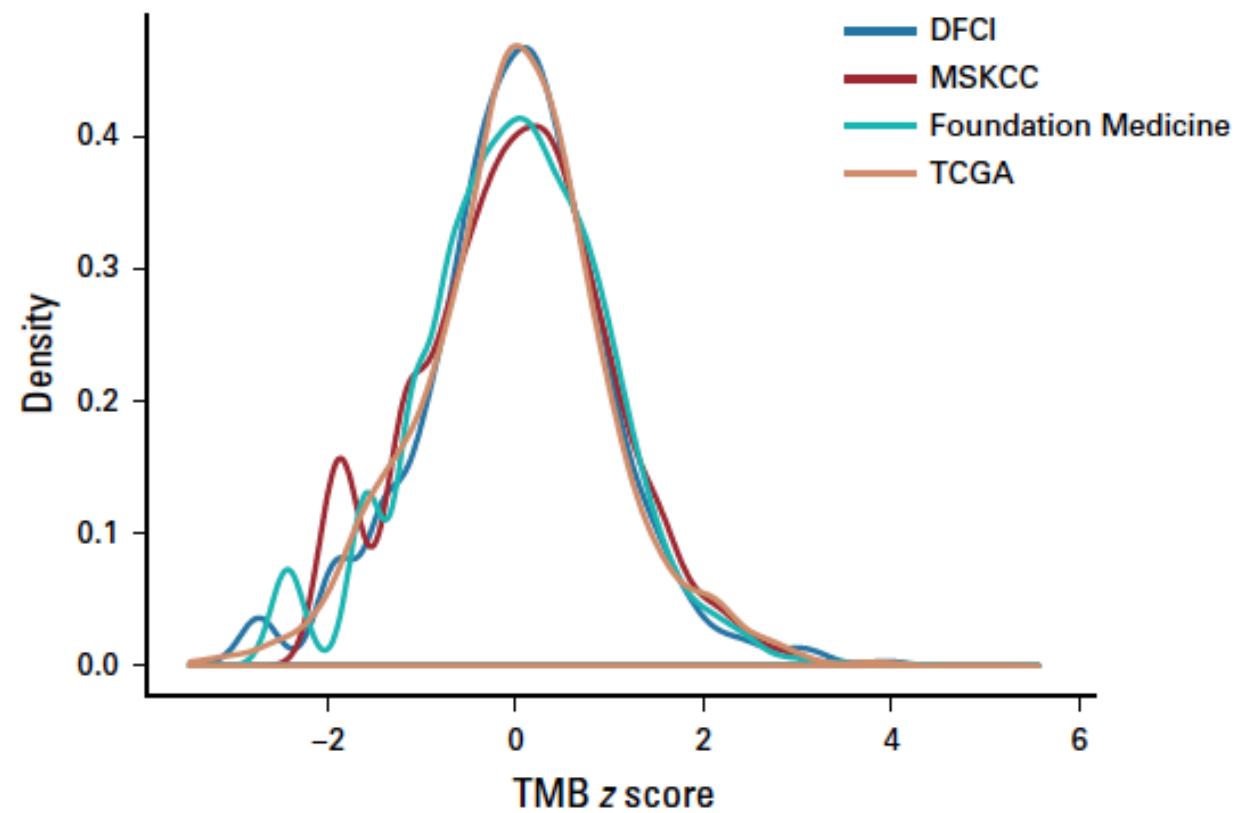
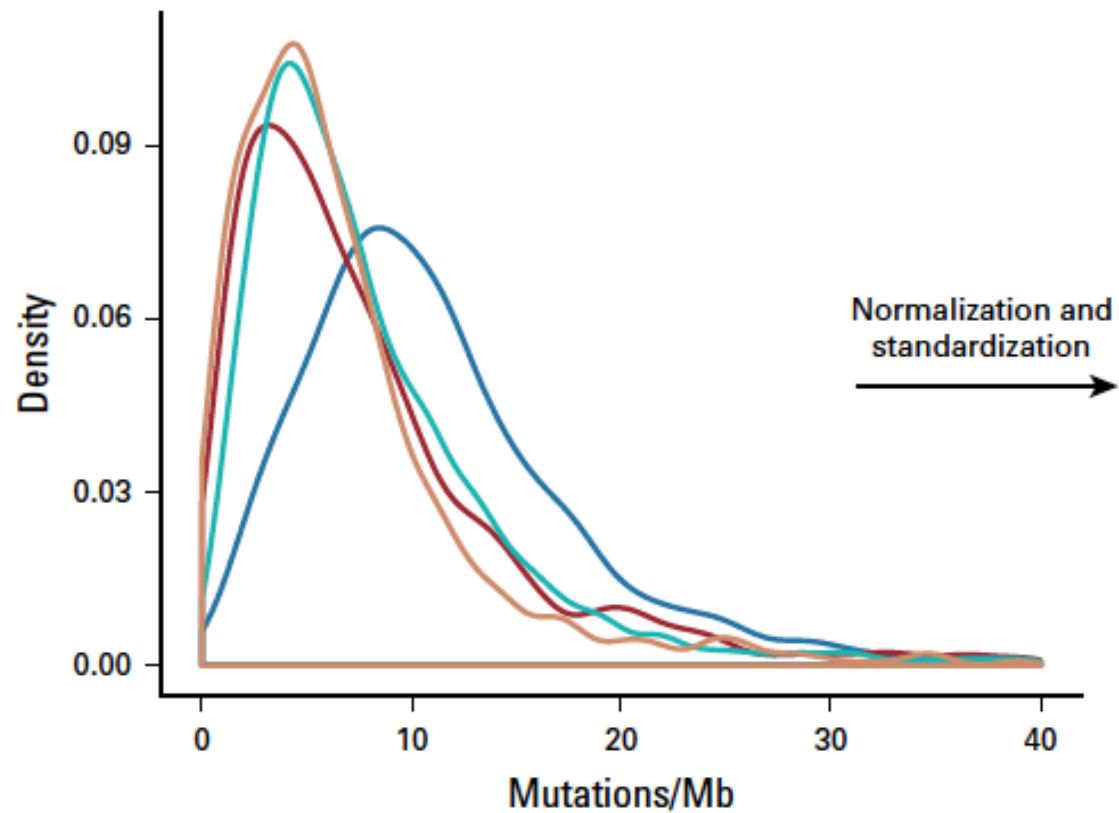
Minimal or no clinical benefit Long-term survival with no clinical benefit Clinical benefit



249 tumors across multiple histologies

Van Allen, Miao, Schilling et al *Science* 2015
Miao, Margolis, Vokes et al *Nature Genetics* 2018

Practical challenges with clinical use of TMB



Practical challenges with clinical use of TMB, cont.

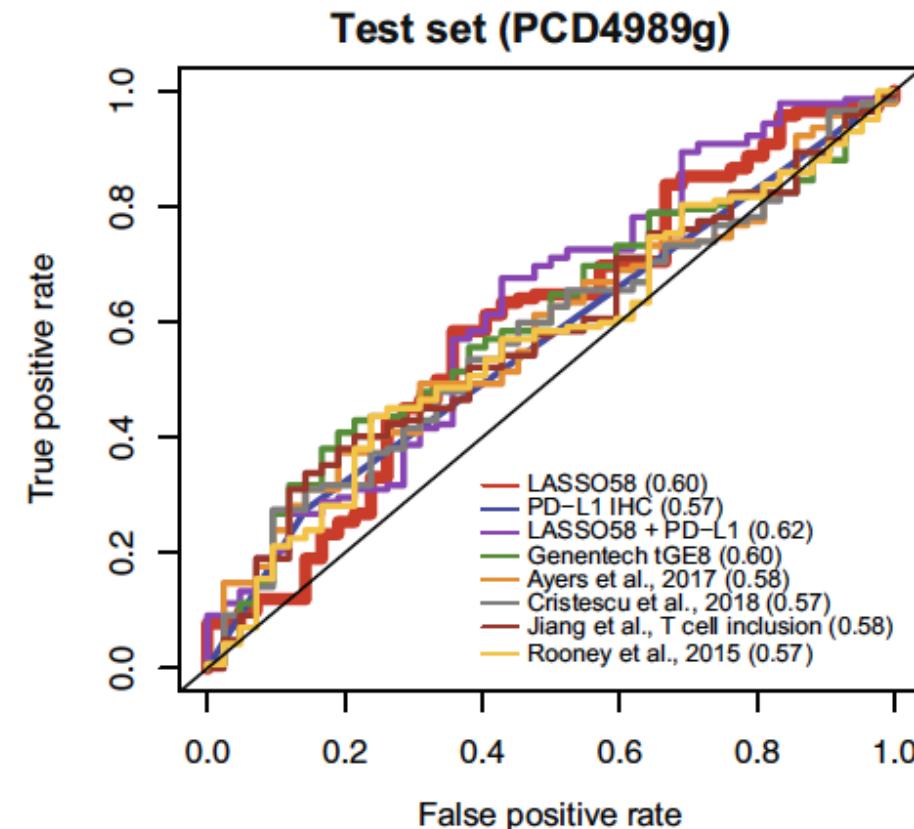
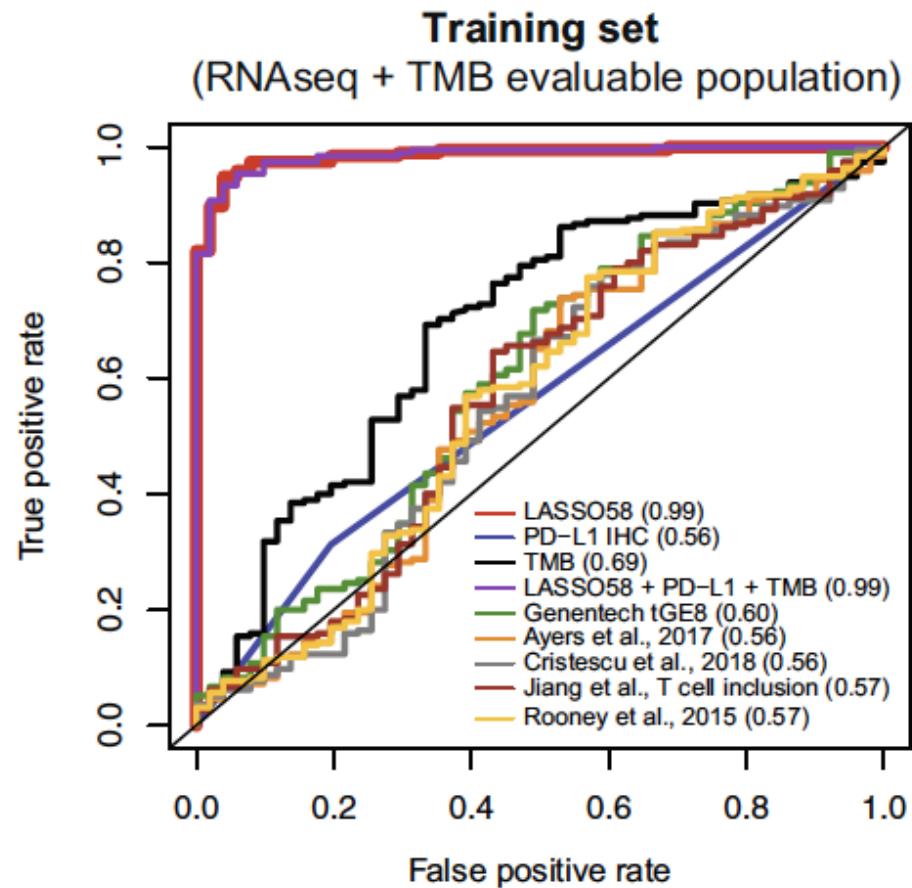
The NEW ENGLAND JOURNAL of MEDICINE

ORIGINAL ARTICLE

Nivolumab plus Ipilimumab in Lung Cancer
with a High Tumor Mutational Burden

Of the 1739 randomly assigned patients, 1649 (94.8%) had tumor samples available to attempt assessment of tumor mutational burden, and 1004 (57.7%) had valid data for tumor mutational burden–based efficacy analyses (Table S2 in the Supplementary Appendix). Baseline char-

Practical challenges with clinical use of more complex signatures



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“First order” genomic events and response to immune checkpoint blockade?

Tumor cell (response mechanisms)

Tumor antigens^{31,32,34–40,54,57,65,67}

Increased tumor mutation burden^{9,37,48}

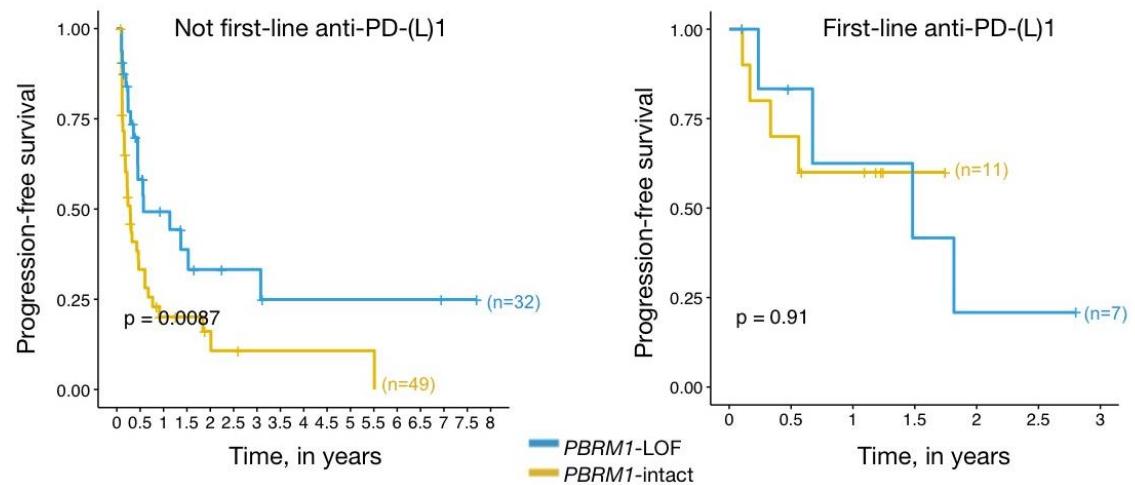
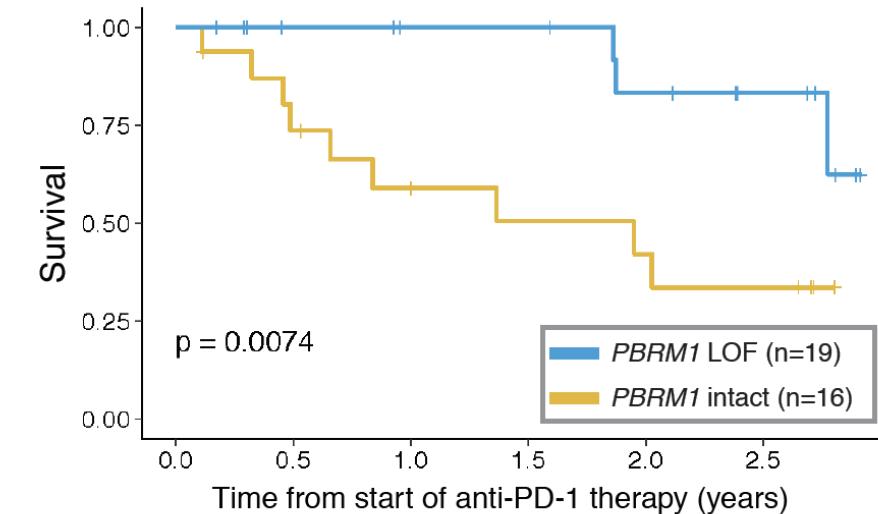
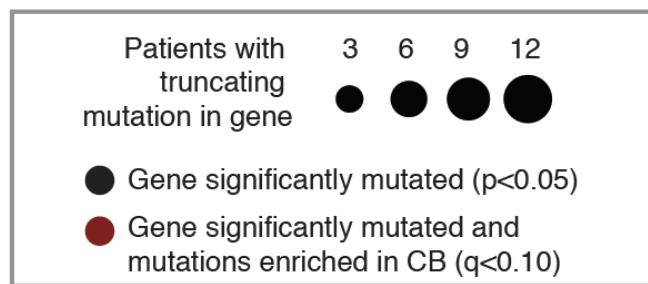
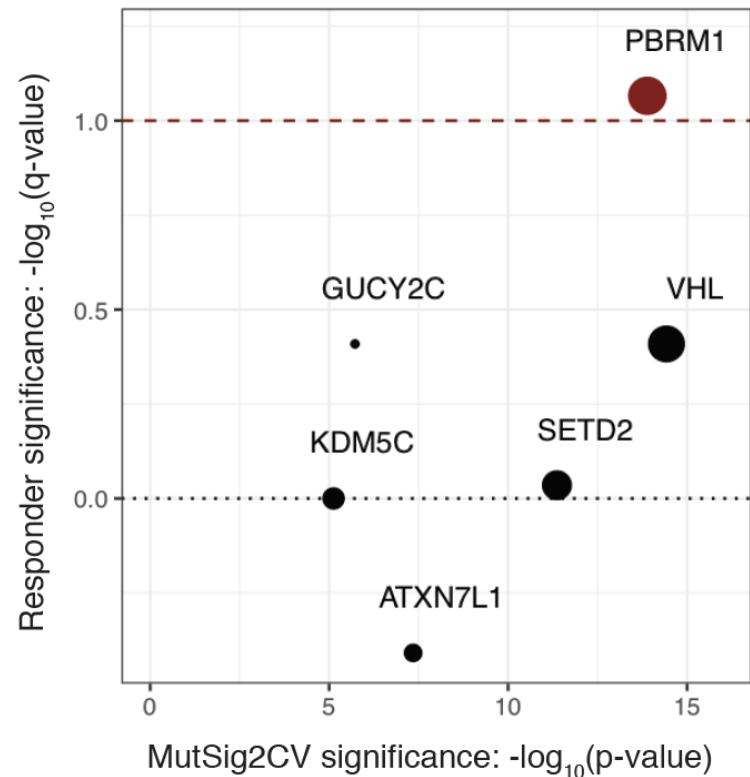
Neoantigens, viral antigens

Mismatch repair deficiency

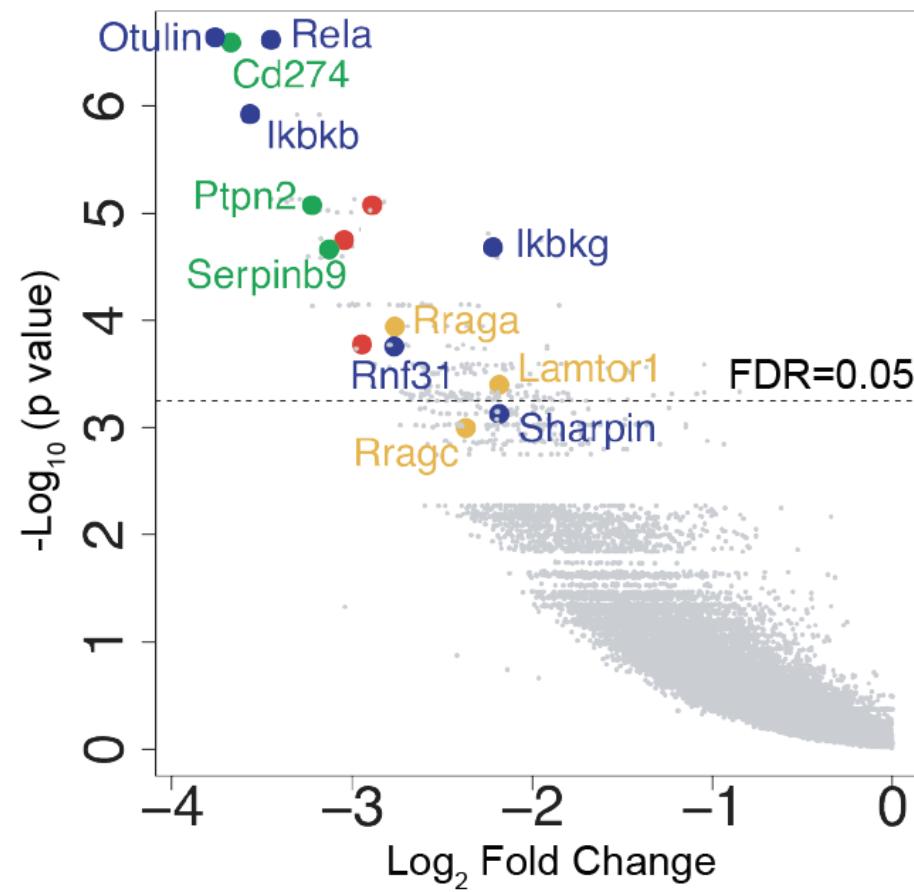
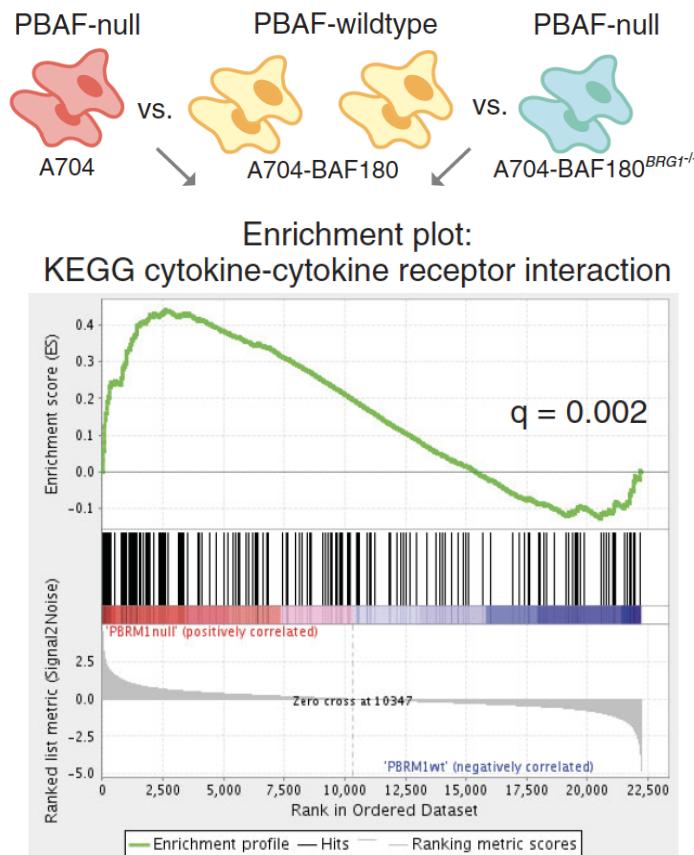


Keenan, Burke & Van Allen,
Nature Medicine 2019

PBRM1 mutations and anti-PD-1 response

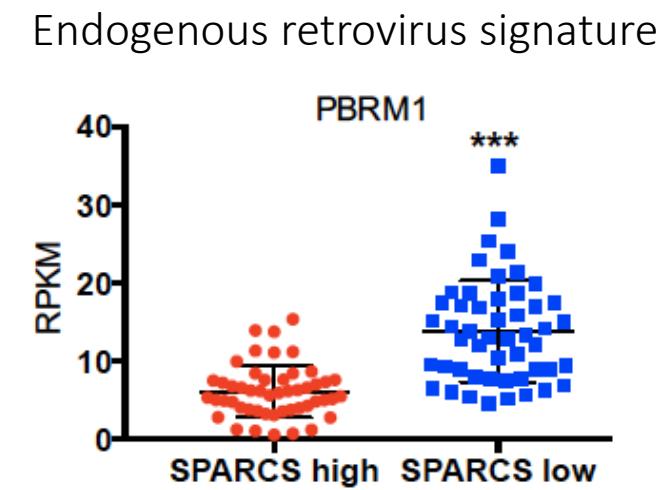


Linking clinical genomics to functional biology



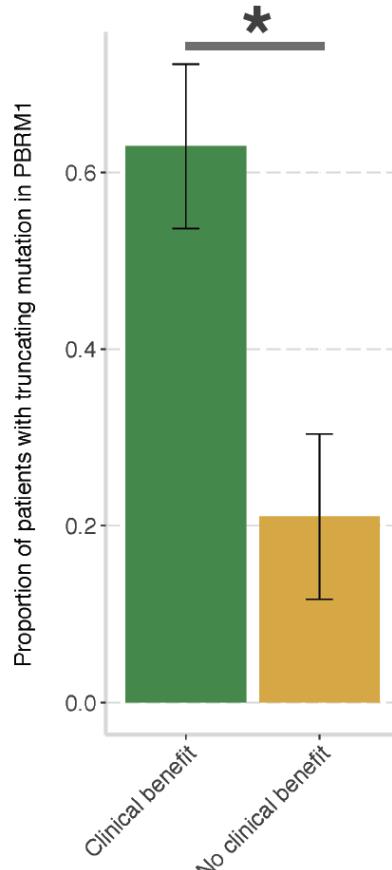
Miao, et al *Science* 2018; Kaelin Lab

Pan, et al *Science* 2018

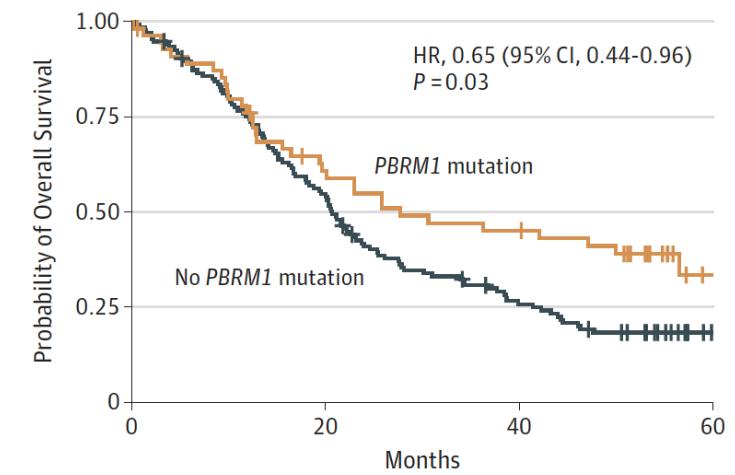
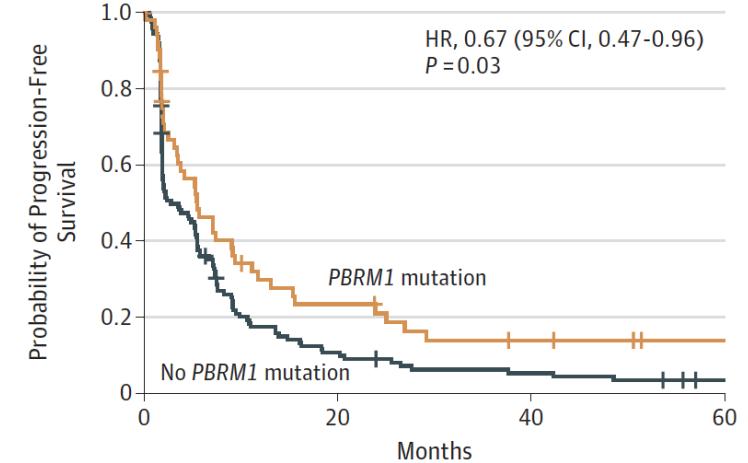
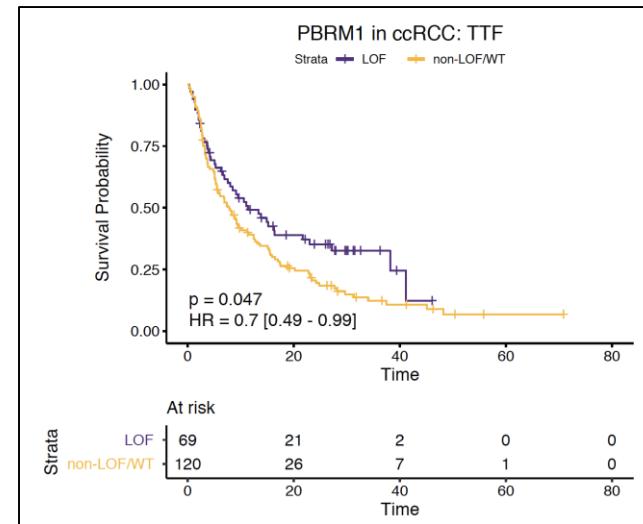
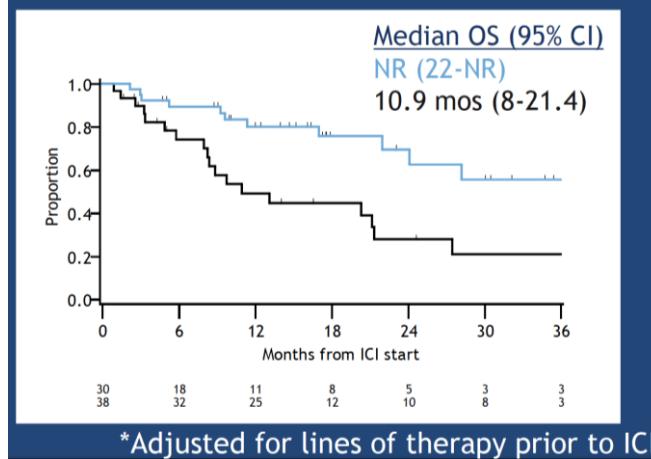


Canadas et al *Nature Med* 2018

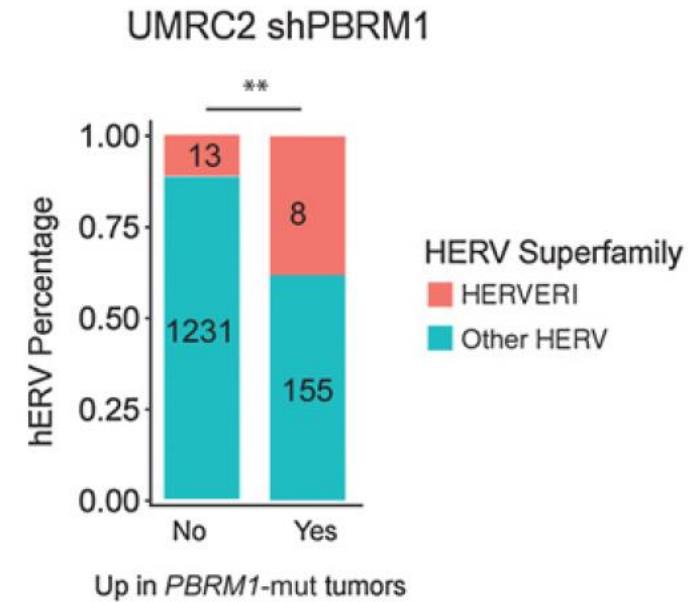
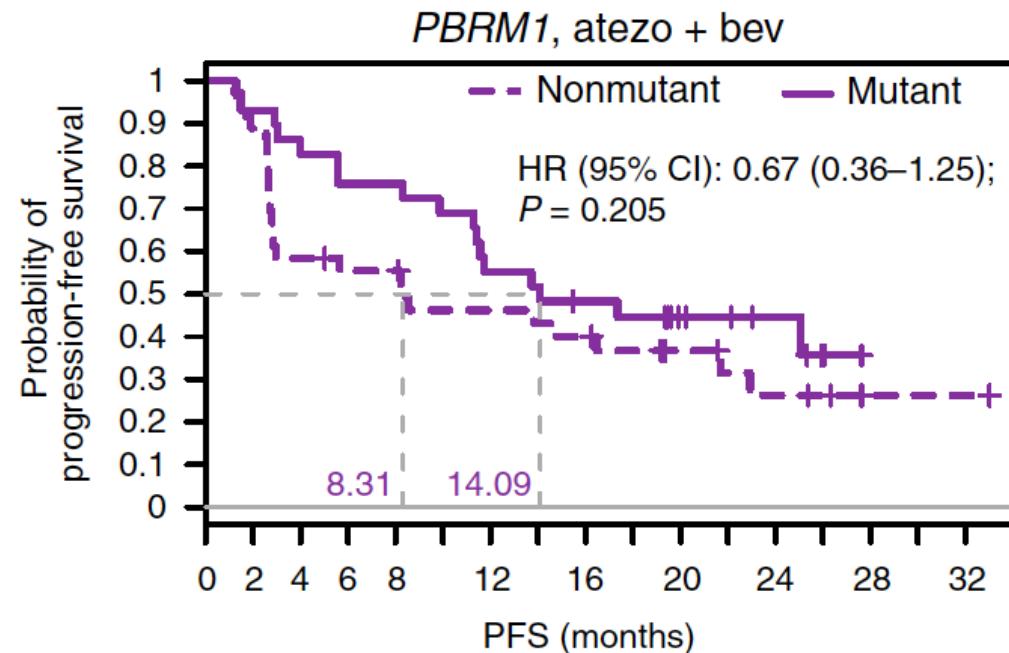
Clinical validation in similar clinical contexts in kidney cancer?



Original Miao et al validation cohort
 $PBRM1 p < 0.01$

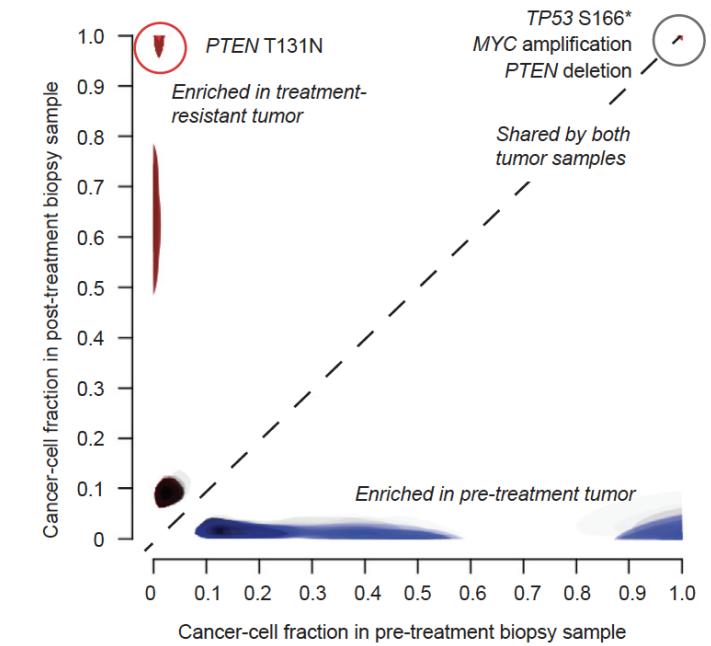
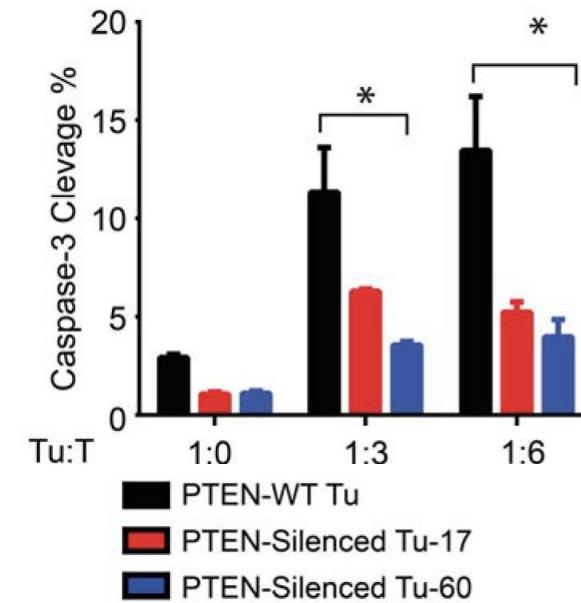
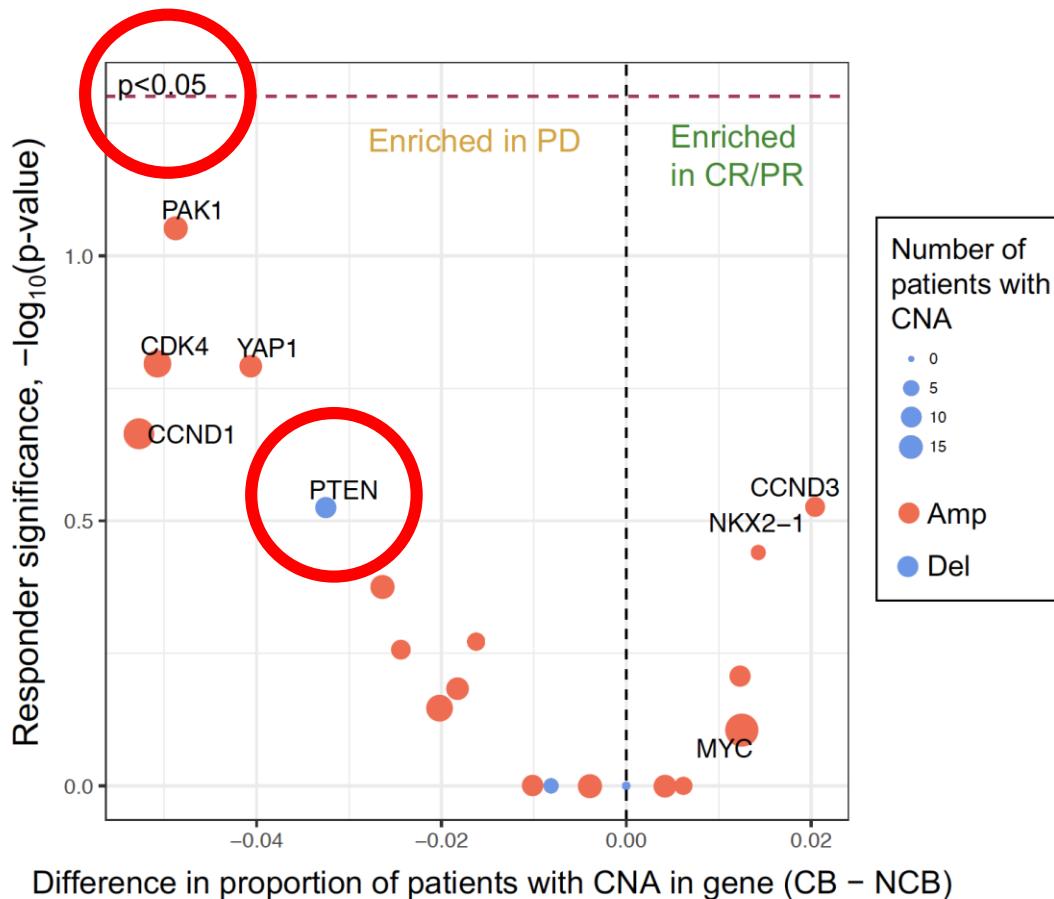


Biology vs. biomarker for immuno-oncology



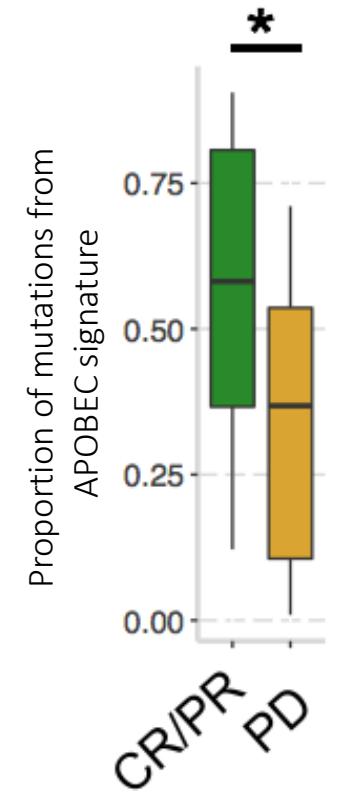
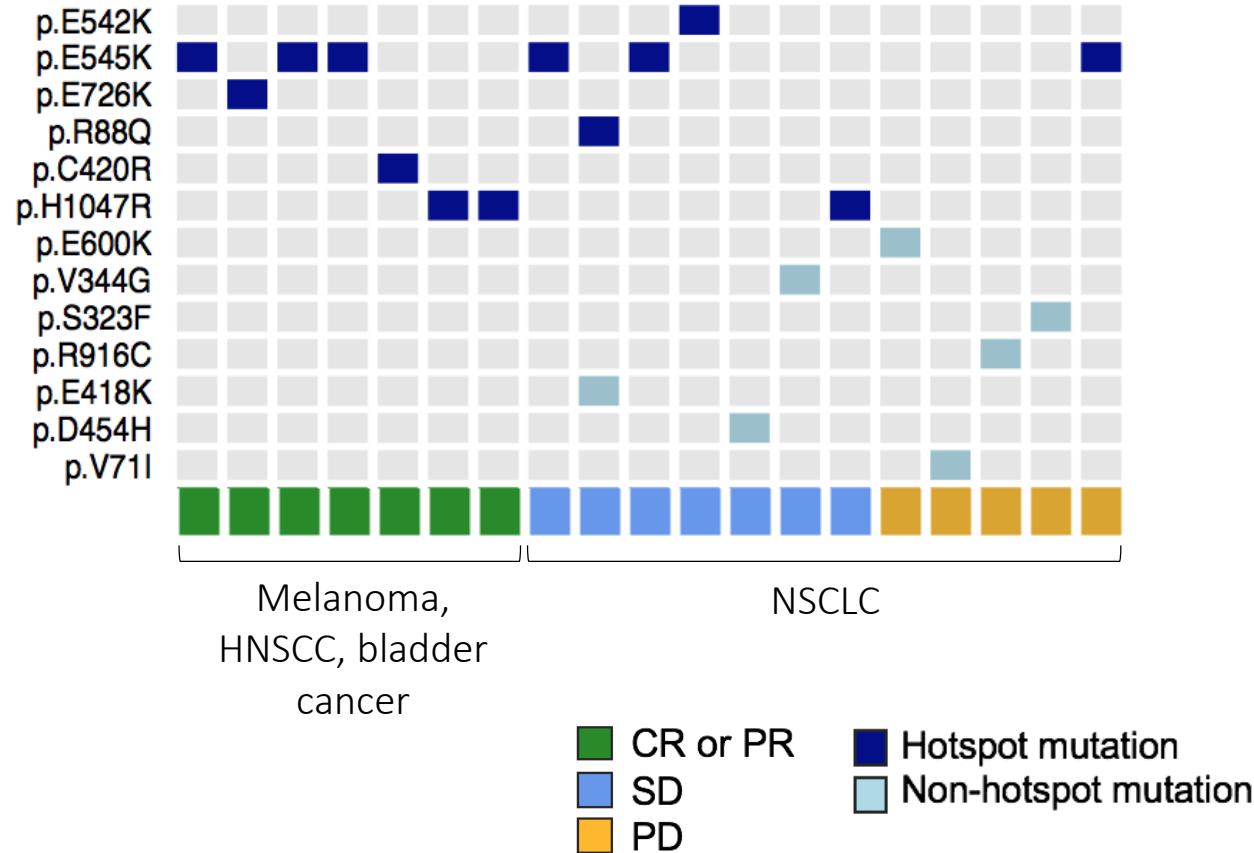
- Numerous interactions suggest complex interplay with other modifiers in distinct clinical contexts
- Additional lineage-specific, tumor heterogeneity, and microenvironmental factors at play
- Functional and larger clinical investigations needed/underway
- **NOT A CLINICAL BIOMARKER!**

PI3K/PTEN and cancer immunotherapy resistance?



Placing single-gene correlates in broader molecular contexts

PIK3CA



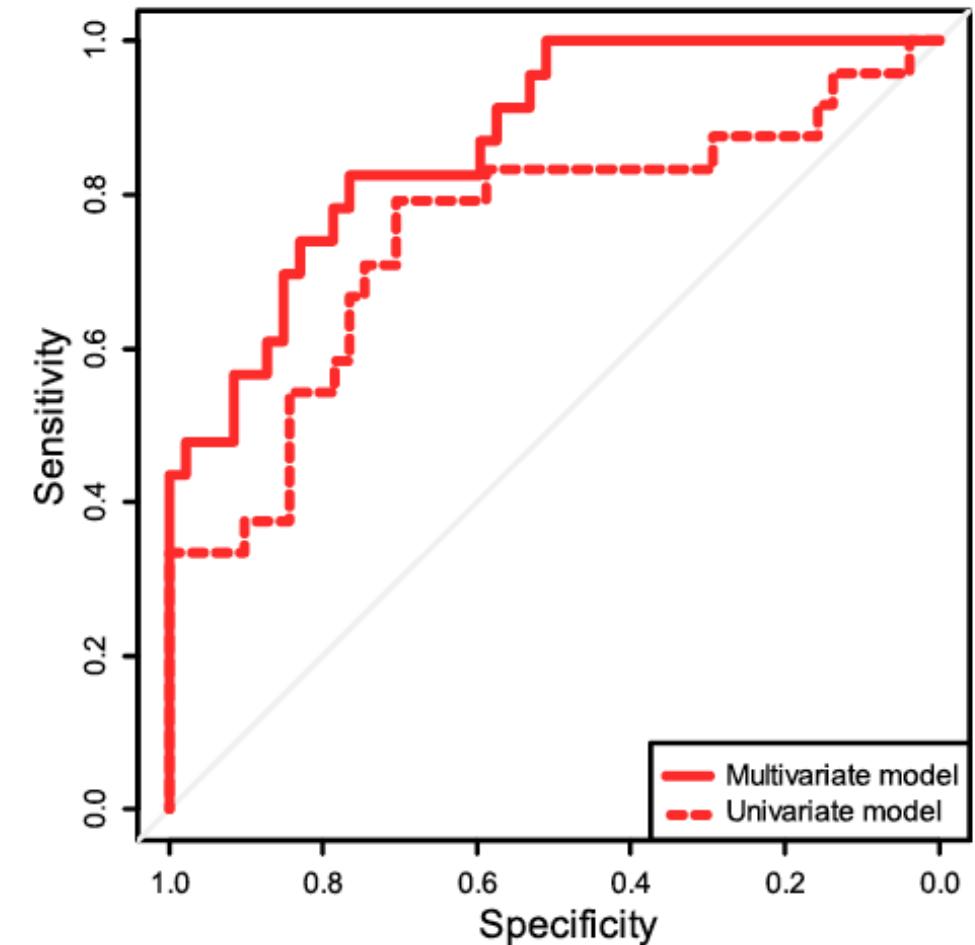
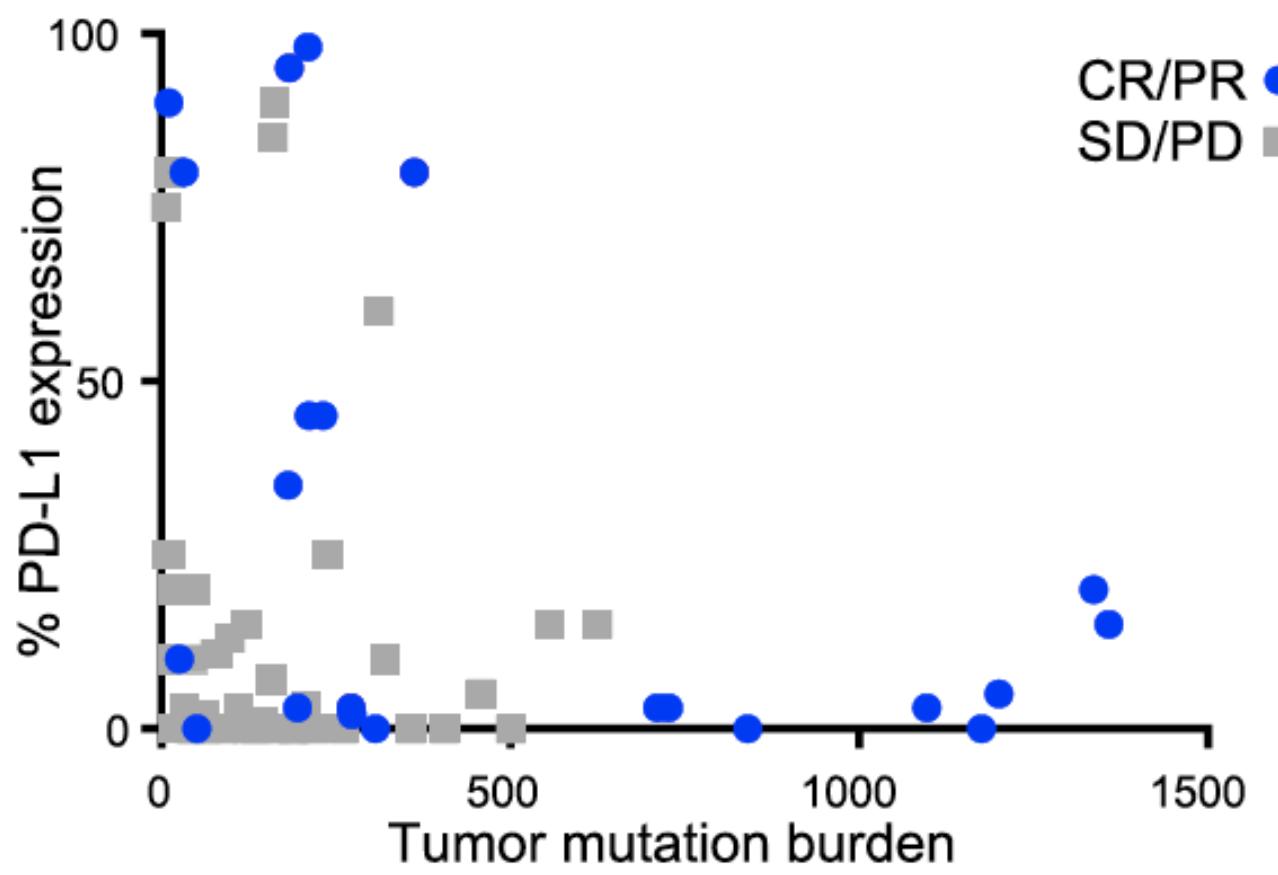
APOBEC

$p=8.1 \times 10^{-3}$

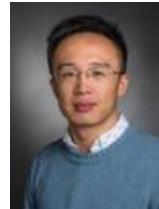
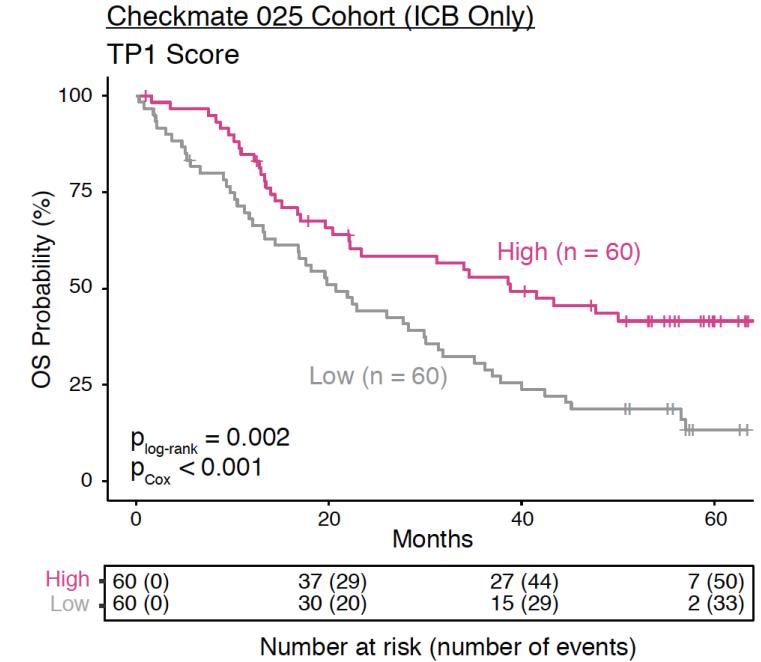
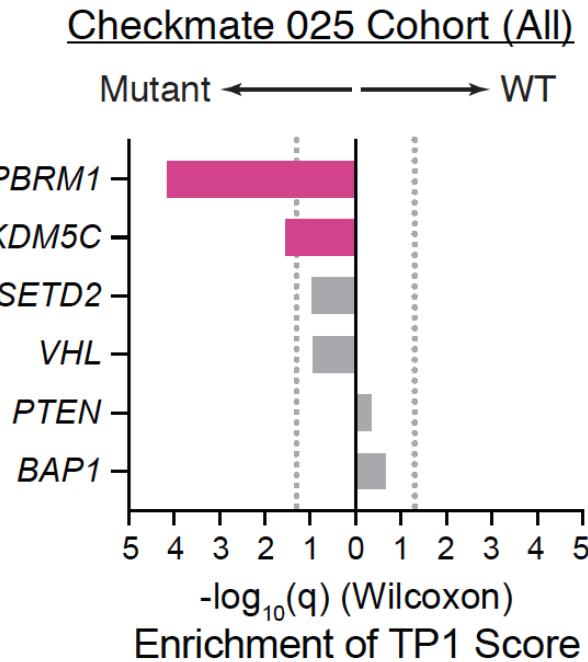
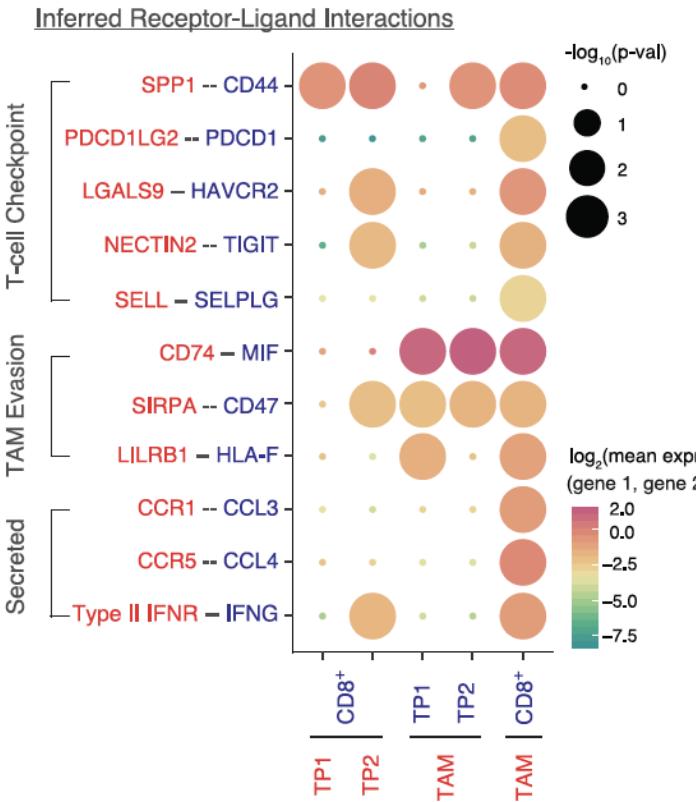
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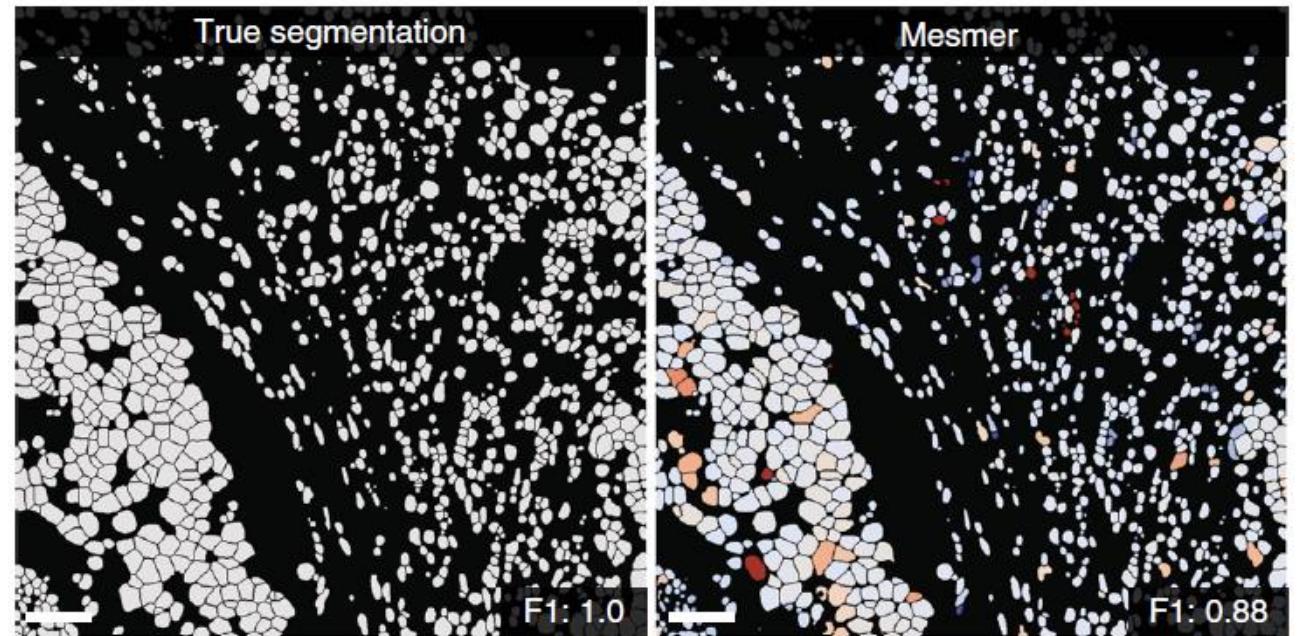
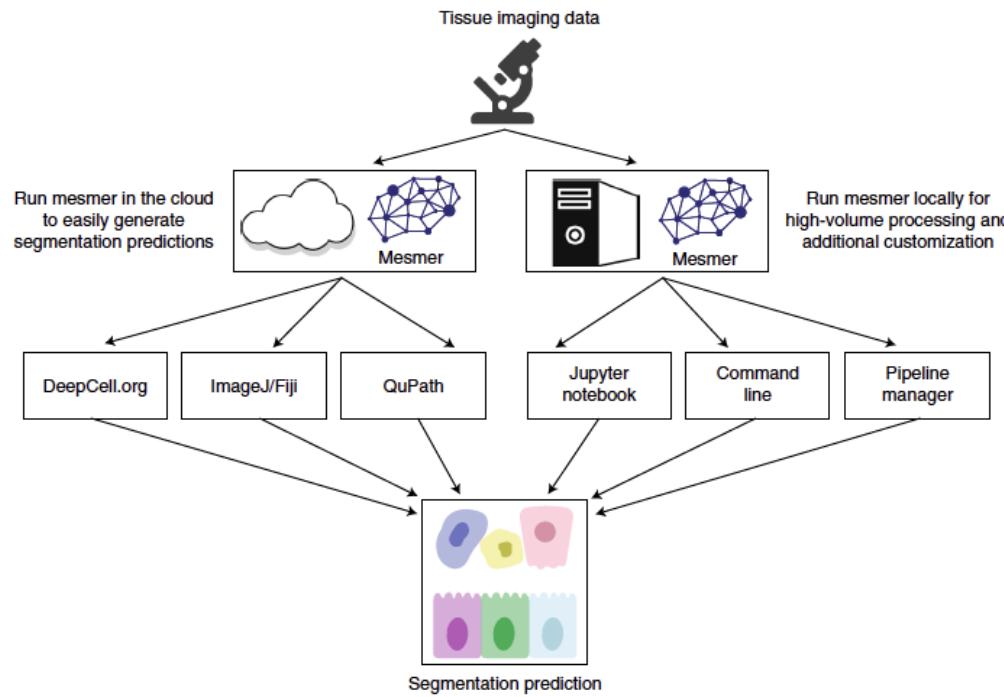
From “first order” genomics to integrated tumor-immune representations



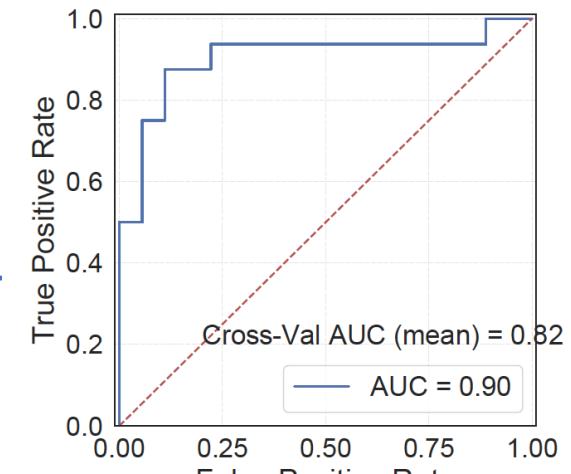
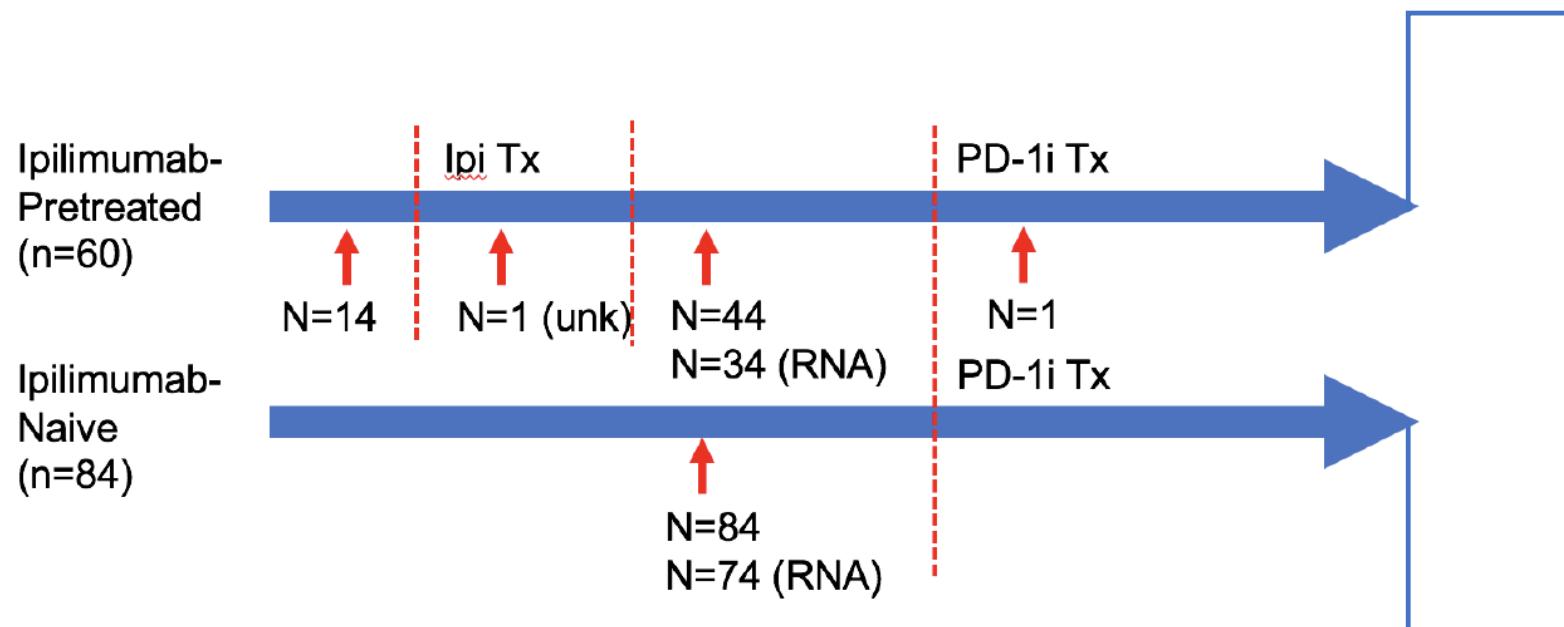
Linking transcriptional programs, mutations, and clinical outcomes



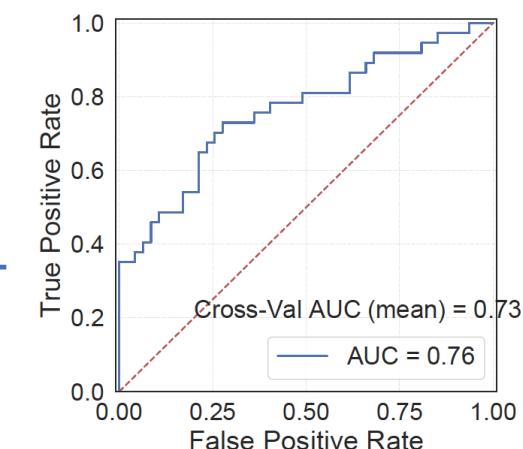
Toward convergent spatial representations of integrated molecular states



Linking integrated molecular representations with complete clinical features



(MHC-II, LN Met, LDH)

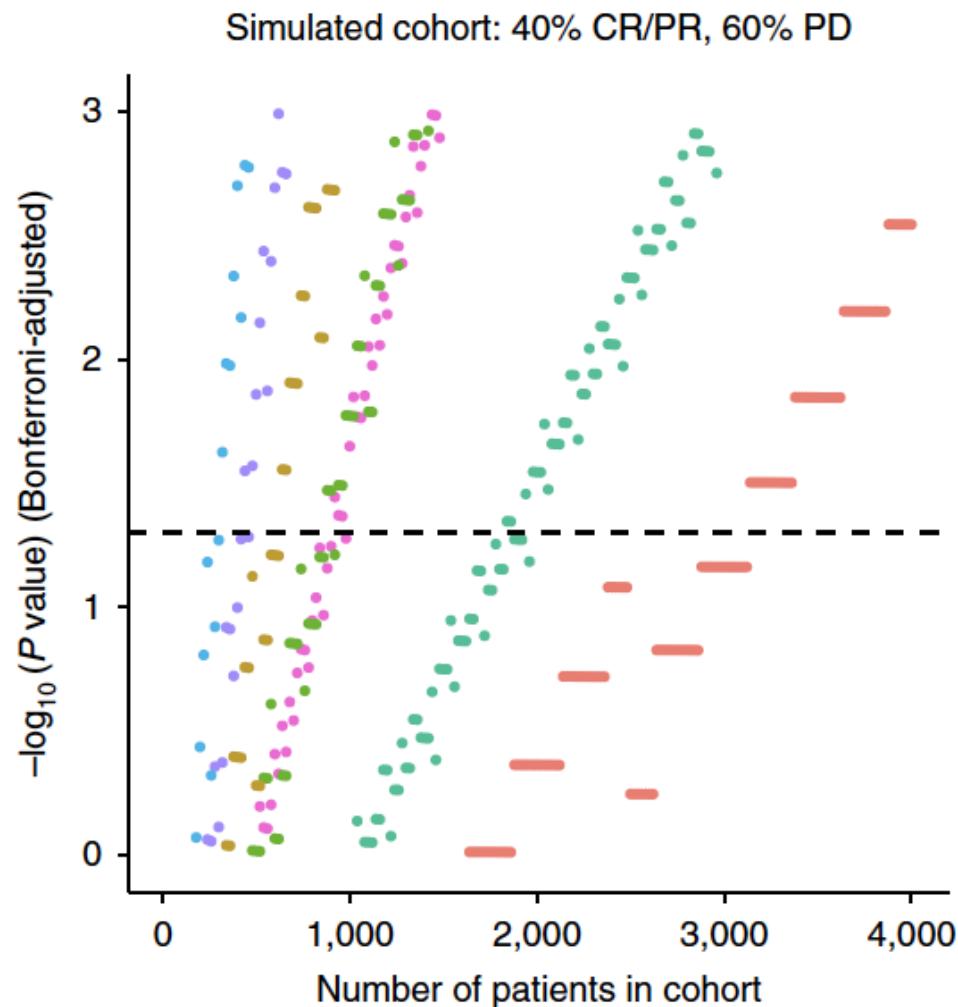


(heterogeneity, ploidy, purity)

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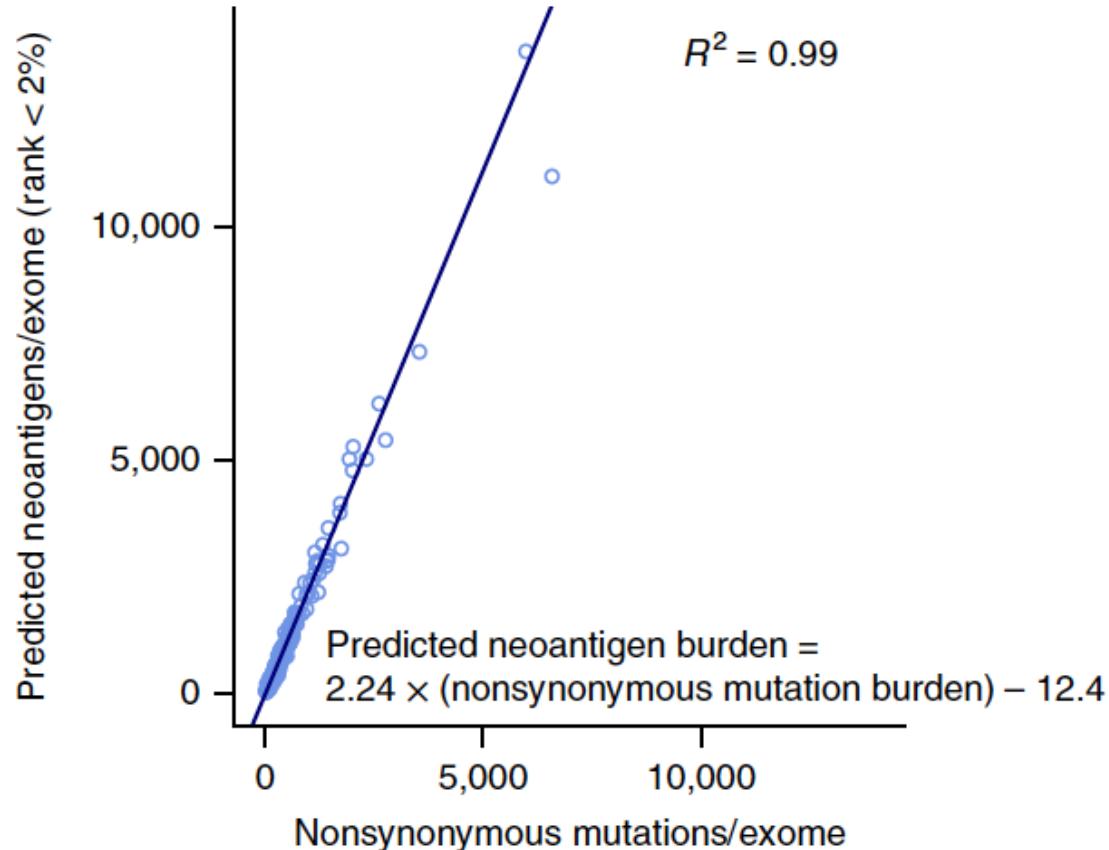
More (and better!) data needed



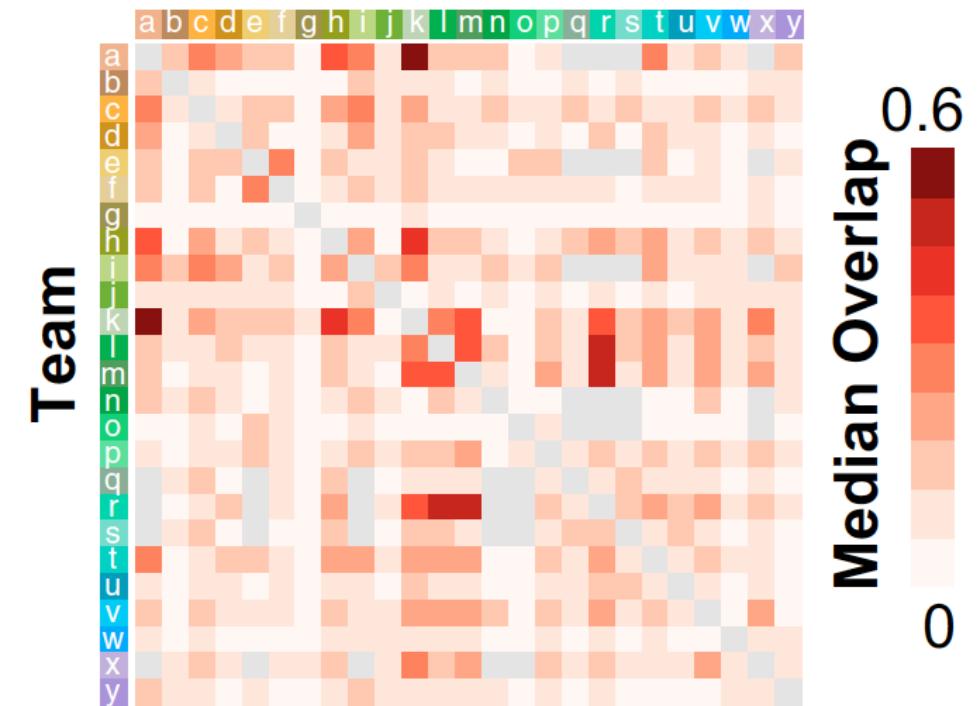
Prevalence of mutation

- 1% CR/PR, 0.01% PD
- 5% CR/PR, 0.5% PD
- 5% CR/PR, 1% PD
- 5% CR/PR, 2% PD
- 10% CR/PR, 1% PD
- 10% CR/PR, 2% PD
- 10% CR/PR, 4% PD

Considering genomics and neoantigen discovery

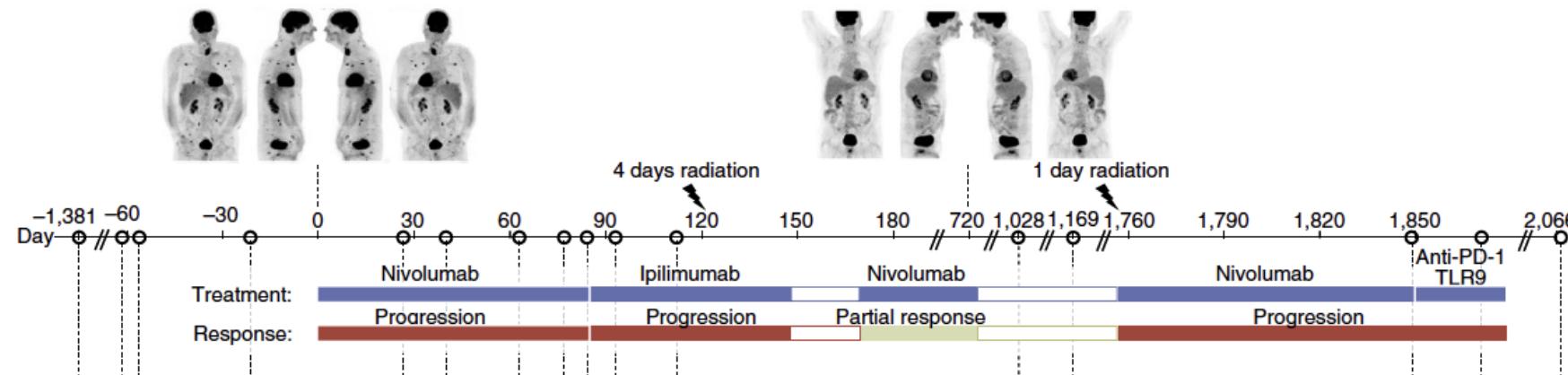


Miao, Margolis, Vokes et al *Nature Genetics* 2018

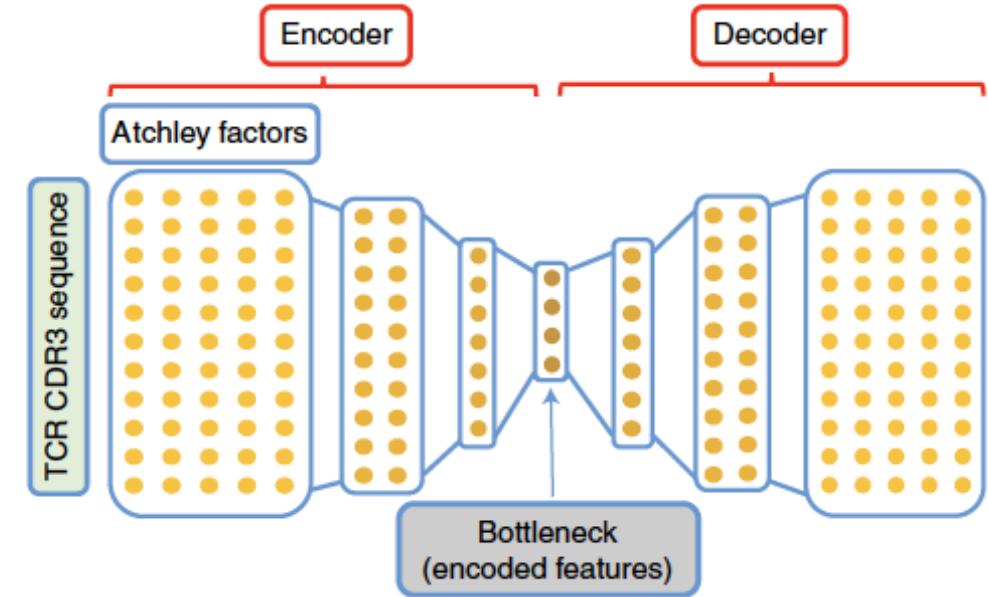
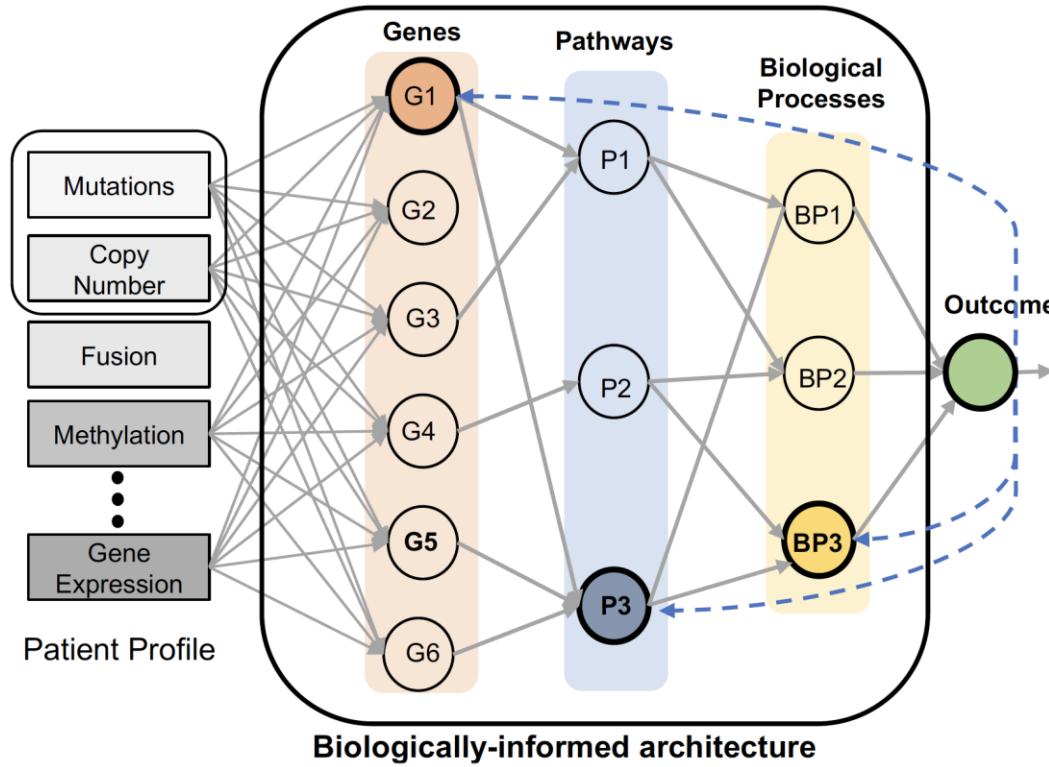


Well et al *Cell* 202

Considering resistance heterogeneity



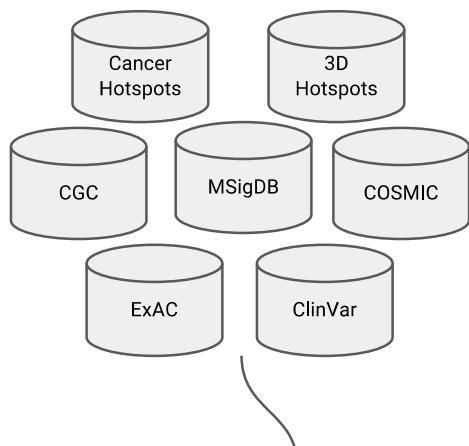
Toward integrating biology and machine learning for immunogenomics discovery



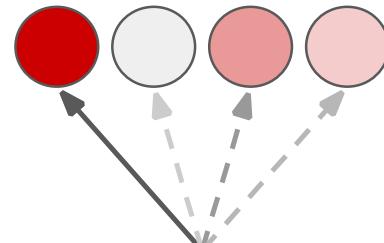
A Molecular Oncology Almanac

www.moalmanac.org

| Patient DNA | |
|-------------------------|--------------------------|
| Mutations | ...ACC... ...TAG... |
| Insertions & Deletions | ...TCG... ...AACCC... |
| Copy number alterations | |

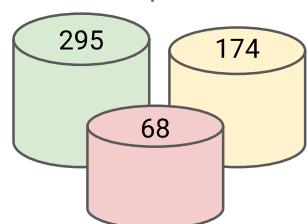


Heuristically evaluate alterations



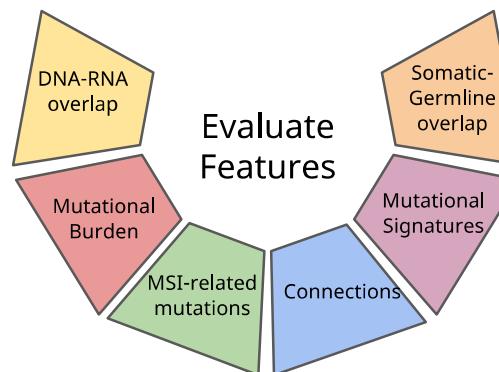
| Patient DNA | |
|--------------------|------------------------|
| Germline Mutations | ...GCT... ...CTA... |
| Patient RNA | |
| Mutations | ...ACC... ...TAG... |
| Fusions | |

Annotate alterations



&

Evaluate Features



Patient - Cell line Similarity
(In Development)

536 action-alteration relationships asserting
sensitivity, **resistance**, and
prognostic claims

Patient Information

| | |
|-------------|---|
| Identifiers | Patient ID: MEL-IPI_Pat02 |
| | Tumor Barcode: MEL-IPI_Pat02-Tumor-SM-4DJZK |
| | Normal Barcode: MEL-IPI_Pat02-Normal-SM-4NFU4 |
| Disease | Code: MEL |
| | Ontology: Melanoma |
| | Stage: Unknown |

Actionability Report

| | | |
|--------|------------------------|------|
| About: | Predictive Implication | Bins |
|--------|------------------------|------|

Variants and Features associated with Therapeutic

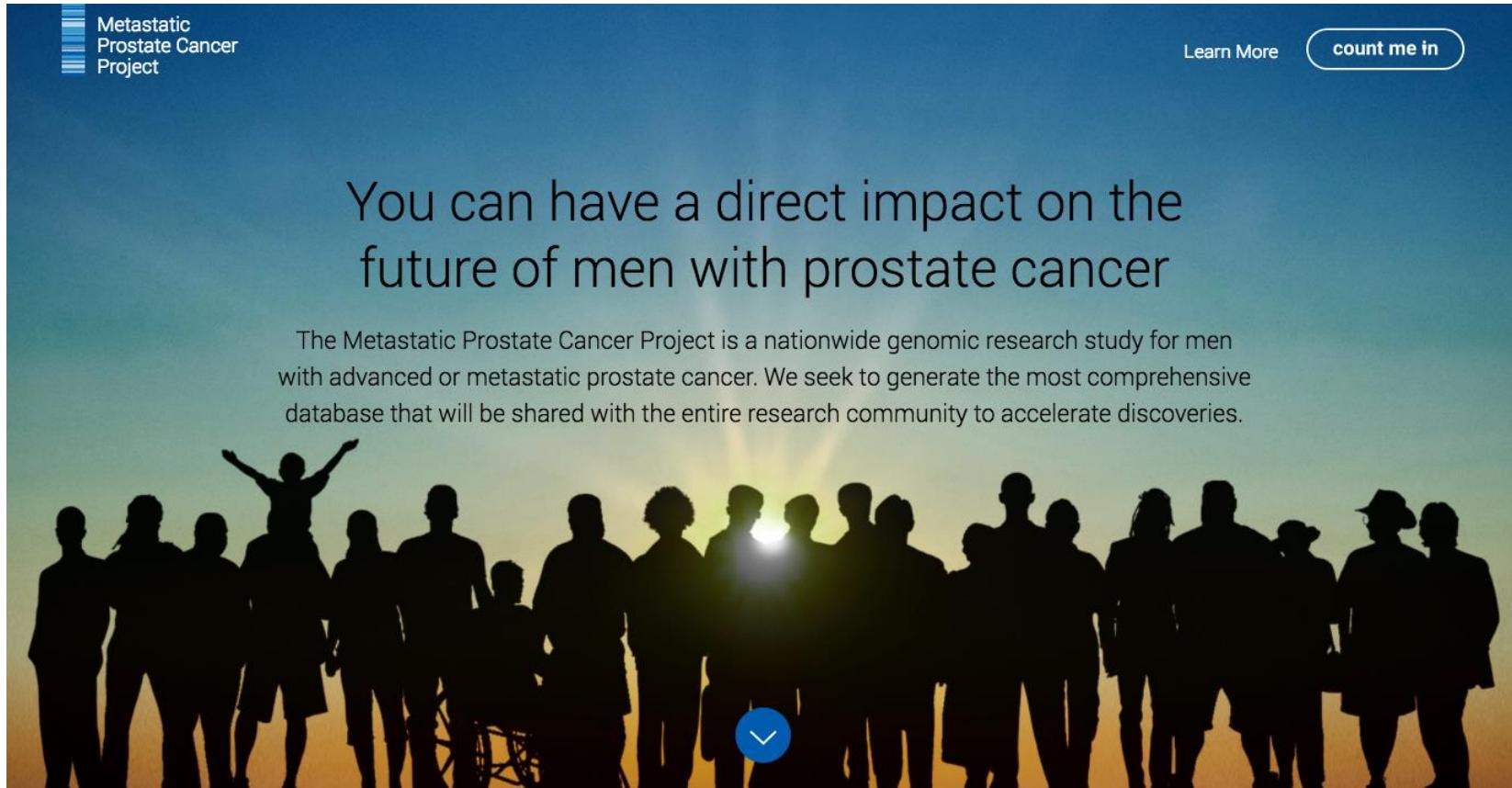
| Predictive Implication | Bin | Feature Type | Feature Alteration |
|------------------------|-----------------------|--------------|--------------------|
| FDA-Approved | Putatively Actionable | Mutation | BRAF Missense |

Generate report

Reardon, et al *Nature Cancer* 2021



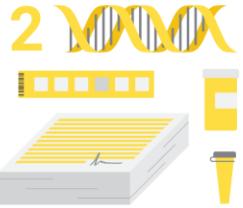
Toward representative clinicogenomic cohorts: The Metastatic Prostate Cancer Project & Count Me In



www.mpcproject.org
joincountmein.org

The Metastatic Prostate Cancer Project

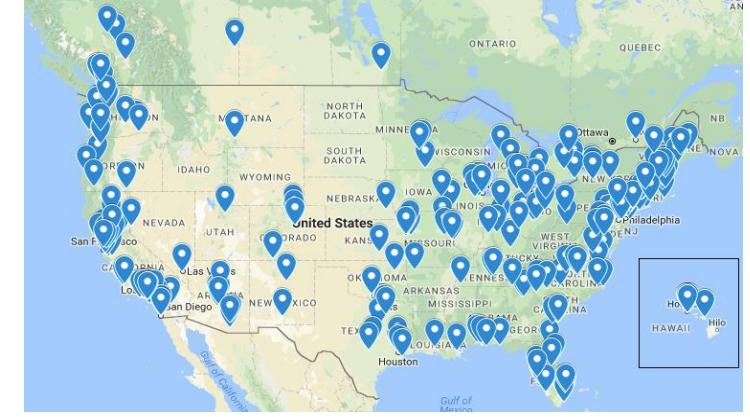
MPCProject.org



Step 1.
Tell us about yourself

Step 2.
Give us permission to collect your samples and data

Step 3.
Learn with us along the way

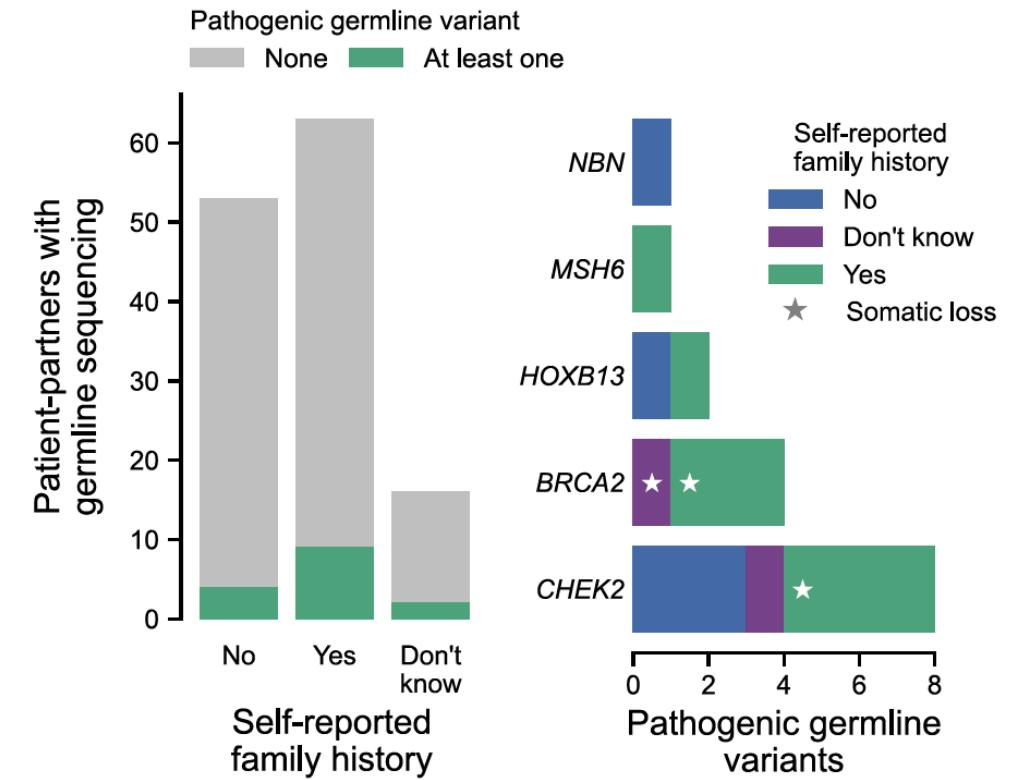
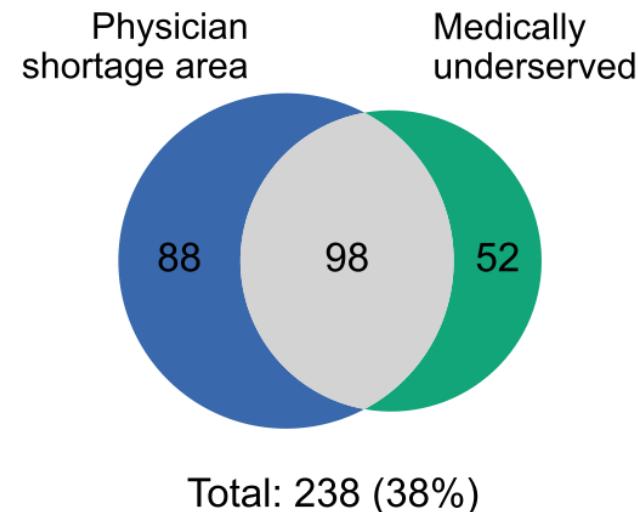
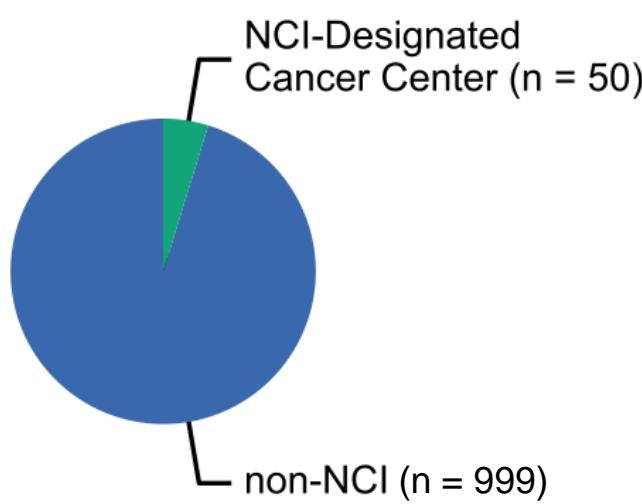


Over 1100 men with
metastatic prostate cancer
have joined the MPCproject
since our launch in January
2018

<http://www.mpcproject.org>
@PrCaProject

The Metastatic Prostate Cancer Project

MPCproject.org



Acknowledgements

The Patients



Let's work together!

vanallenlab.dana-farber.org

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Van Allen Lab

Meng Xiao He
Kevin Bi
Alma Imamovic
Brendan Reardon
Jihye Park
Saud AlDubayan
Jake Conway
Haitham Elmarakaby
Jett Crowdus
Cora Ricker
Jackson Nyman
Seunghun Han
Sabrina Camp
Felix Dietlein
Alok Tewari
Ziad El Bakouny
Riaz Gillani
Shreya Johri
Surya Naranayan

Kathryn Li
Gha Young Lee
Alexis Coolidge
Filipe Carvalho
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Nicita Mehta
Kevin Meli
Camille Mathey-Andrews
Keyan Salari
Theodora Pappa
Lauren Miller-Jones
Aditi Limaye
Bowen Jiang
Jingxin Fu
Erica Pimenta
Julia Schiantarelli
Maha Shady
Natalie Vokes

+ Alumni!

Broad Institute

Klarman Cell Observatory
Mike Cuoco
Count Me In team
Gad Getz
Sachet Shukla
John Doench
Genomics Platform
Picard Team
Firehose Team
Adam Tracy
Kris Cibulskis
Carrie Cibulskis
Will Gibson
Jesse Boehm
Many others...

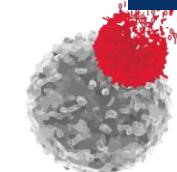
DFCI/BWH + Center for Cancer Genomics

Mary-Ellen Taplin
Bruce Johnson
Entire GU Oncology team
Entire CCPM team
Entire HTAN team
Adam Kibel
Matthew Mossanen
Steve Chang
Mark Preston
Chris Sweeney
Many others...

Friends Near & Far

Dirk Schadendorf
Bastian Schilling
Elizabeth Plimack
Phil Abbosh
Leandro Colli
Many others...

Funding



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- Type your question in the Q&A box, then click “Send”
- Questions will be answered in the Question & Answer session at the end of the webinar (as time permits)

