

Sparkathon Project TimIOs: A Pooled Analysis of Durable vs. Transient Responders on Immunotherapy Trials

- **Yana G. Najjar, MD**
 - *Assistant Professor of Medicine, University of Pittsburgh*
- **Randy Sweis, MD**
 - *Instructor of Medicine, University of Chicago*
- **On behalf of Team TimIOs**



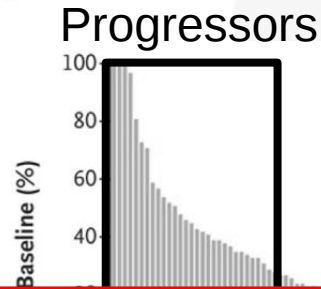
Disclosures

- Research funding: Merck (YGN), Bayer (RFS), BMS (RFS)
- Consulting: Array BioPharma (YGN), Puma (RFS), BMS (RFS), Eisai (RFS), Exelixis (RFS)
- Honoraria: BMS (RFS), Exelixis (RFS), Medscape (RFS)

Background

- Immunotherapy is standard of care for many solid tumor types
- 20-40% of patients respond to anti-PD-1
- The majority of patients do not respond
- Little is understood about distinct differences between responders and non-responders
- Compartmentalization of clinical and tissue-derived data
- Need for a unified platform to pool and analyze existing data

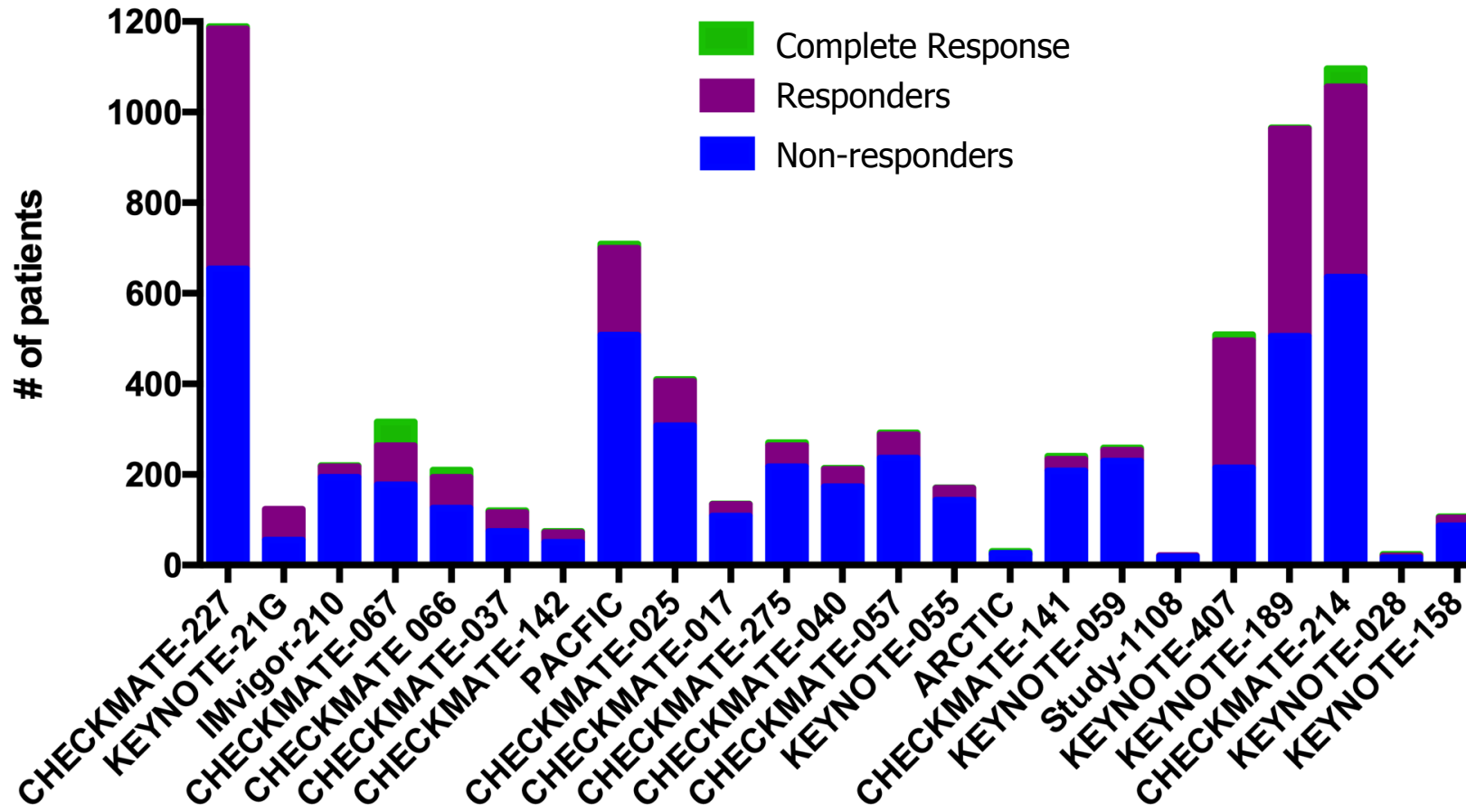
Responses to anti-PD-1 are heterogeneous



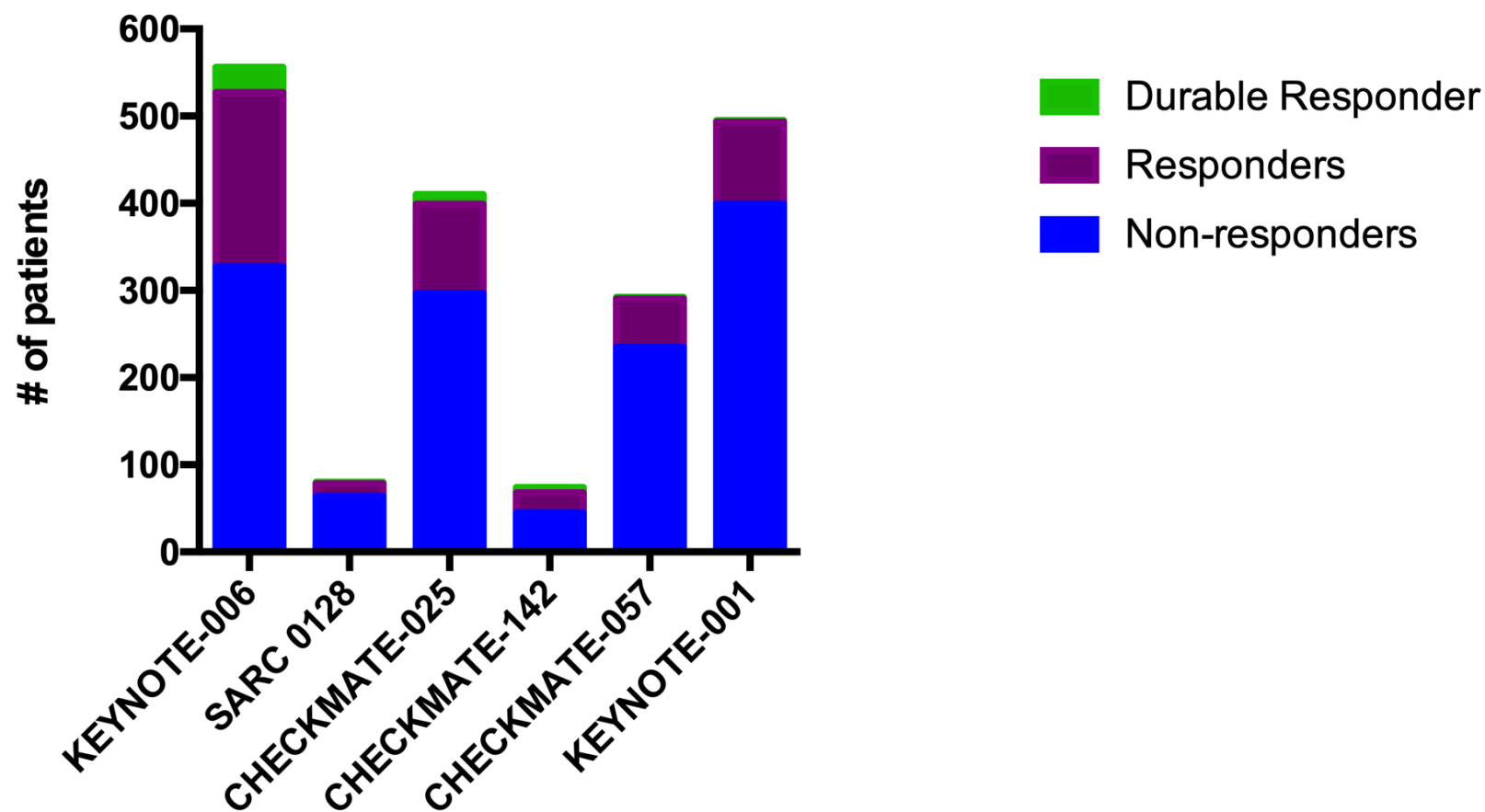
Understanding tumor heterogeneity is critical for developing the tools to predict clinical response to immunotherapy



Responses to anti-PD-1 across studies



Responses to anti-PD-1 across studies



Innovative Solution

- A unified public/private consortium
- An honest broker to facilitate cross-institutional collaboration
- To develop a platform identifying fundamental differences between:

Durable responders vs. Transient responders

Elite responders vs. Rapid progressors

Definitions

Standard (RECIST 1.1):

- Complete Response CR (100%↓)
- Partial response PR ($\geq 30\%$ ↓)
- Stable disease SD (29%↑ - 19%↓)
- PD ($\geq 20\%$ ↑)

Non-Standard:

- Rapid PD ($\geq 50\%$ ↑) by 12 weeks
- Transient response (PR/CR < 6 months)
- Durable response (PR/CR > 2 years)

Comparative populations to analyze:

- 1- Transient vs. durable response
- 2- CR ('elite' responders) vs. rapid PD

Core Teams

Project Lead: Yana Najjar/Project Co-Lead: Randy Sweis

Assay Optimization

Houssein Sater
Cara Haymaker
Maria Ascierto
Praveen Bommarreddy
Roberta Zappasodi
Vali Barsan
Sara Valpione

Clinical design

Heather McGee
Houssein Sater
Cara Haymaker
Wungki Park
Nicholas Tschernia
Uqba Khan
Erik Wennerberg
Vali Barsan

Bioinformatics

Nils Rudqvist
Randy Sweis
Vali Barsan
Anne Monette
Maria Ascierto

External Affairs

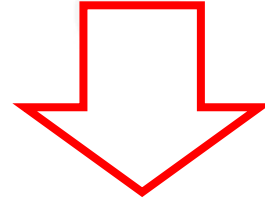
Erik Wennerberg
Heather McGee
Nicholas Tschernia
Vinita Popat
Wungki Park
Anne Monette
Alexandria Cogdill

Legal/Administrative

Erik Wennerberg
Alexandria Cogdill
Anne Monette
Vinita Popat

Project Goal

Define gene expression signatures associated with resistance to PD-1 blockade



- Inform on potential mechanisms of resistance
- Develop novel rational combination strategies
- Spare toxicity in patients less likely to benefit

Study Design

1A) Unsupervised approach using existing RNA-seq datasets from pretreatment biopsies to identify immune gene expression signatures distinguishing:

- Transient responders vs. durable responders (primary analysis)
- Elite responders vs. rapid progression of disease (secondary analysis)

Hypothesis: Tumors from durable vs. transient responders have different immune gene expression profiles, which can be used as biomarker of response, patient selection, and novel therapeutic targets.

Study Design

1B) Supervised approach using existing RNA-seq datasets from pretreatment biopsies to determine the impact of known immunosuppressive molecules on the outcome of PD-1 blockade:

- Focus on: PD-1, LAG3, TIM3, IDO1, PD-L1, PD-L2, TIGIT, ITGAM, ARG1, ADORA2A, CD39, CD73 and TGFB1, Foxp3

Hypothesis: Negative immune regulators are overexpressed by tumor and immune cells in the TME of transient vs. durable responders, and in patients with CR vs. rapid PD.

Data Elements

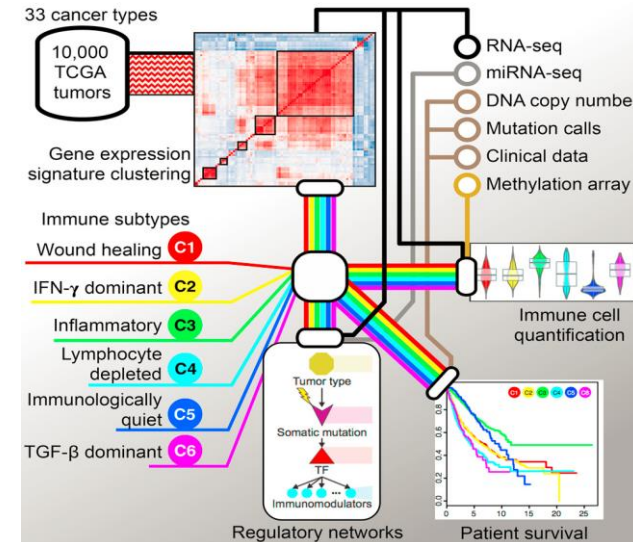
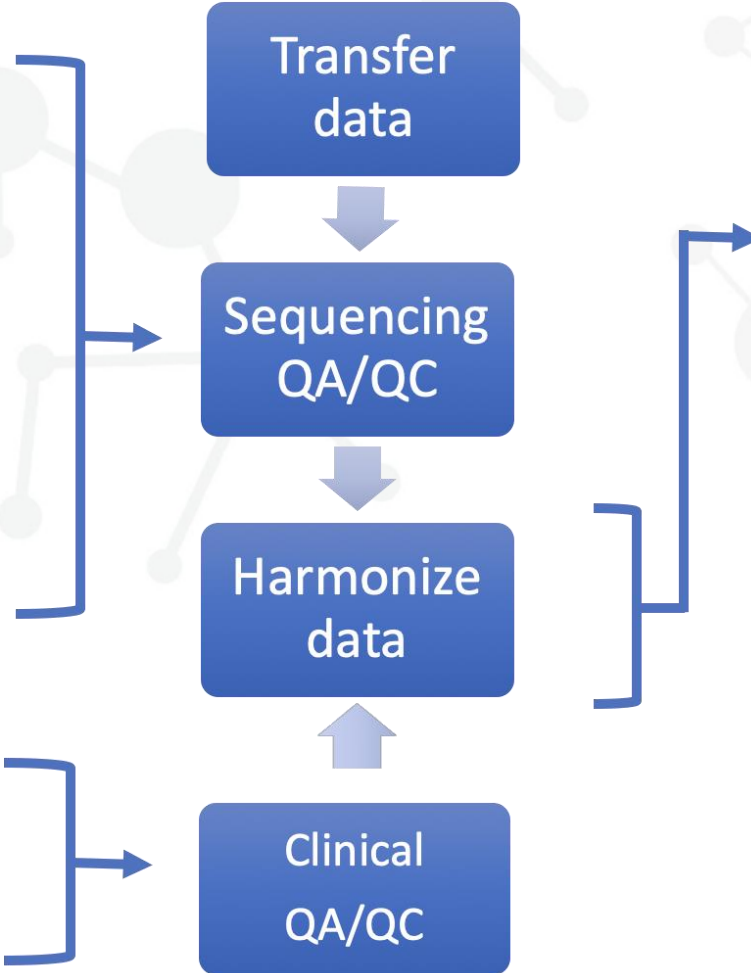
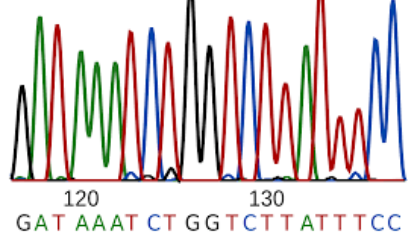
Clinical:

- Primary diagnosis
- Age, sex, race
- Date of metastatic diagnosis
- DFS, PFS, OS on trial
- date of biopsy, biopsy site
- Treatment on trial
- Number of cycles
- Prior therapies

Bioinformatic:

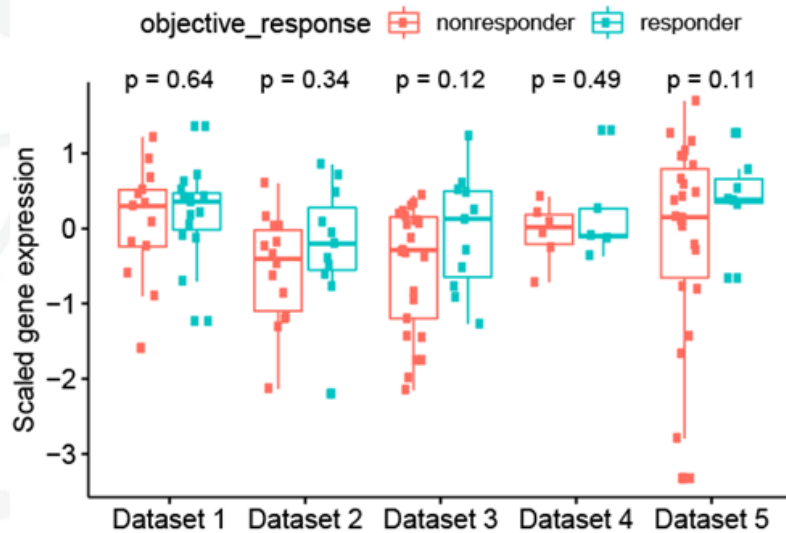
- Summarized gene level expression data
- Raw gene expression data
- Date of sequencing

Proposed Analysis Workflow



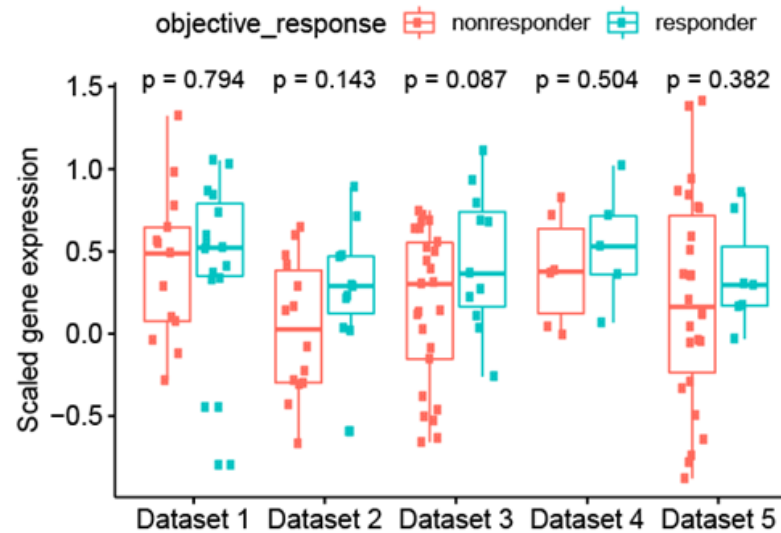
Selected Pilot Data (N = 170)

CD3



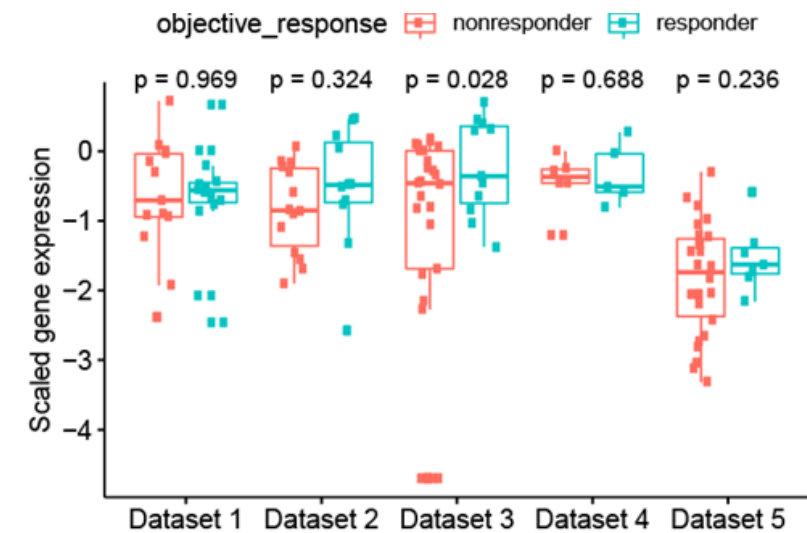
ANOVA, $p=0.036$

IRF1



ANOVA, $p=0.042$

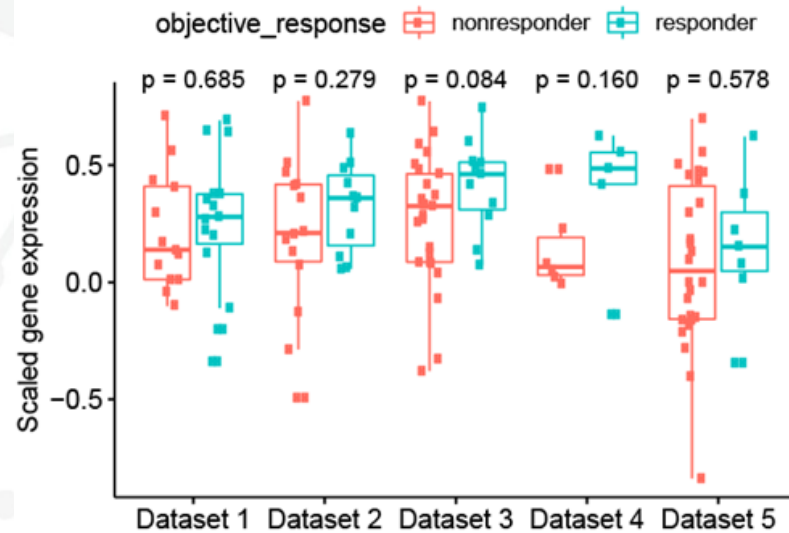
TIGIT



ANOVA, $p=0.044$

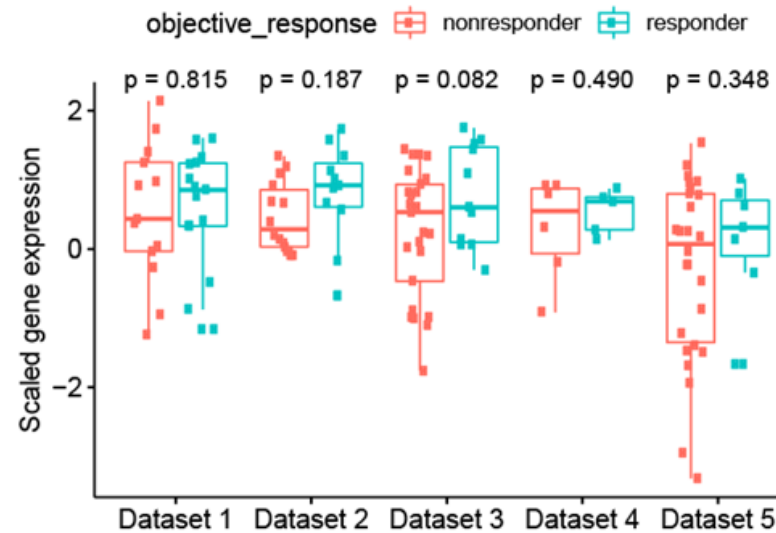
Selected Pilot Data N=170

BCL6



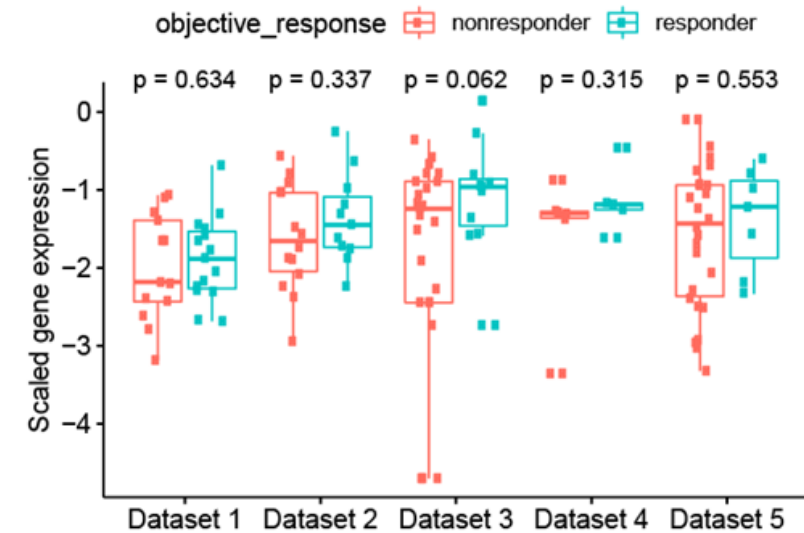
ANOVA, $p=0.038$

CXCL9



ANOVA, $p=0.053$

FLT3



ANOVA, $p=0.041$

Summary

- Pilot study demonstrates ability to integrate data across datasets in terms of clinical response
- Increasing the pool of harmonized datasets from individual onco-immunology trials is expected to increase power of analyses
- We continue to expand our collaborations with several partners
- Additional partners and datasets are needed and welcome

Acknowledgements - Thank you!



Advisory Committee

Lisa H. Butterfield, PhD
Mario Sznol, MD
Howard L. Kaufman, MD, FACS
Sandra Demaria, MD
Leisha A. Emens, MD, PhD
Kristen Hege, MD
Samir N. Khleif, MD
Willem W. Overwijk, PhD
Pedro J. Romero, MD
Francesco Marincola, MD

Institute for Systems

Biology

Vésteinn Þórsson, PhD
Ilya Shmulevich, PhD

Financial Support

AstraZeneca
Incyte
Amgen
Genentech
Anonymous Donor

SITC Staff

Rebecca Borzon
Mary Dean, JD, CAE
Anne Hahn, MPH
Alicia Schuessler, CAE
Donnette Tinsley, MSED
Tara Withington, CAE



Ken Carter, PhD

