

Applying Germ-line MicroRNA Mutations to Predict Response and Toxicity to Immune Therapy

Cancer Immune Responsiveness Workshop, May 2018
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Disclosure Information

Joanne B. Weidhaas

I have the following financial relationships to disclose:

Consultant for: MiraDx

Stockholder in: MiraDx

I will not discuss off label use and/or investigational use in my presentation.

Hypothesis: Germ-line biomarkers will help



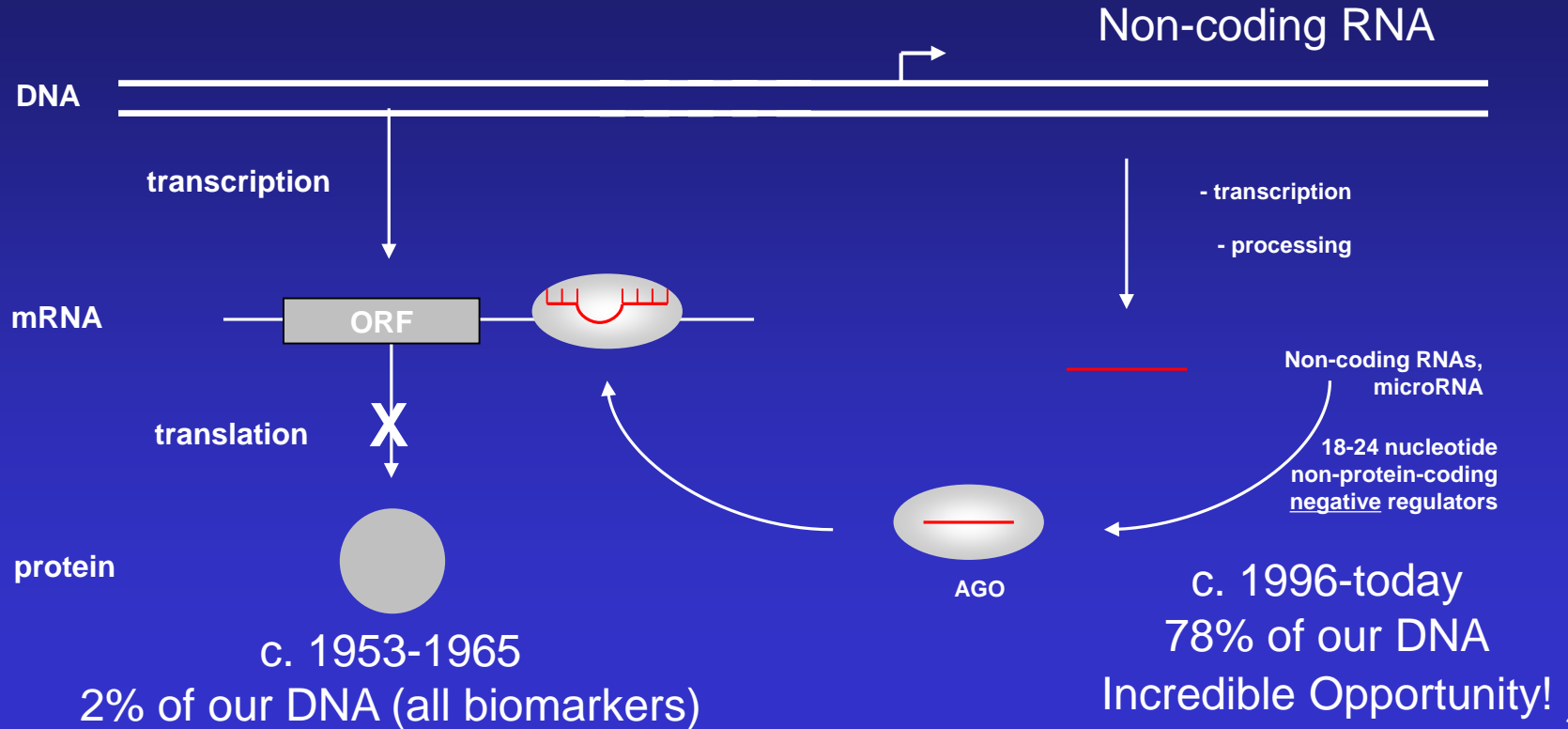
1. What You're
Born With
(Germ-line Genetics)



2. Same biomarkers
predict systemic treatment
response and toxicity

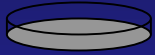
While accepted in most diseased states, not so in cancer

Also apply new insights into DNA



Why? MiRNAs lead the systemic stress response

A549/CRL2741



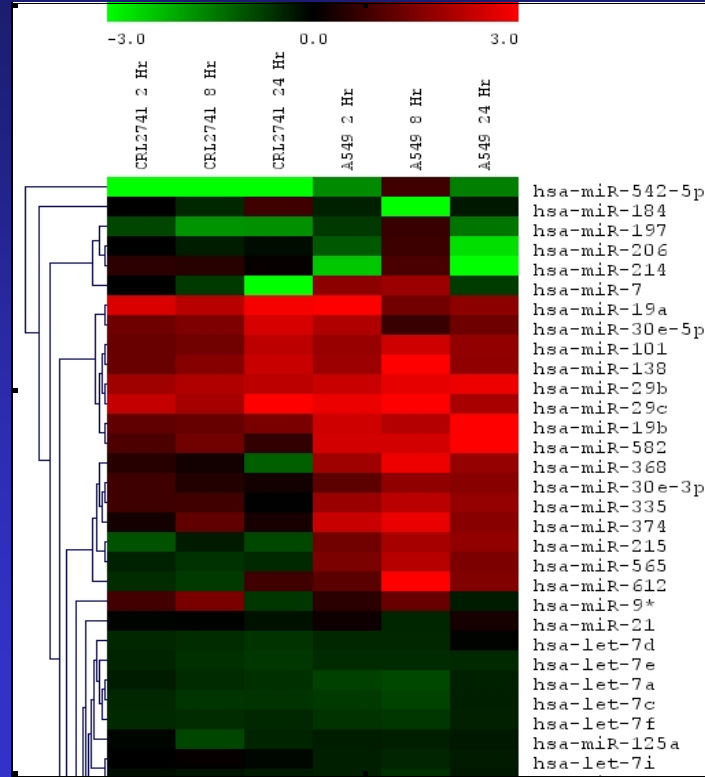
+/- IR



total

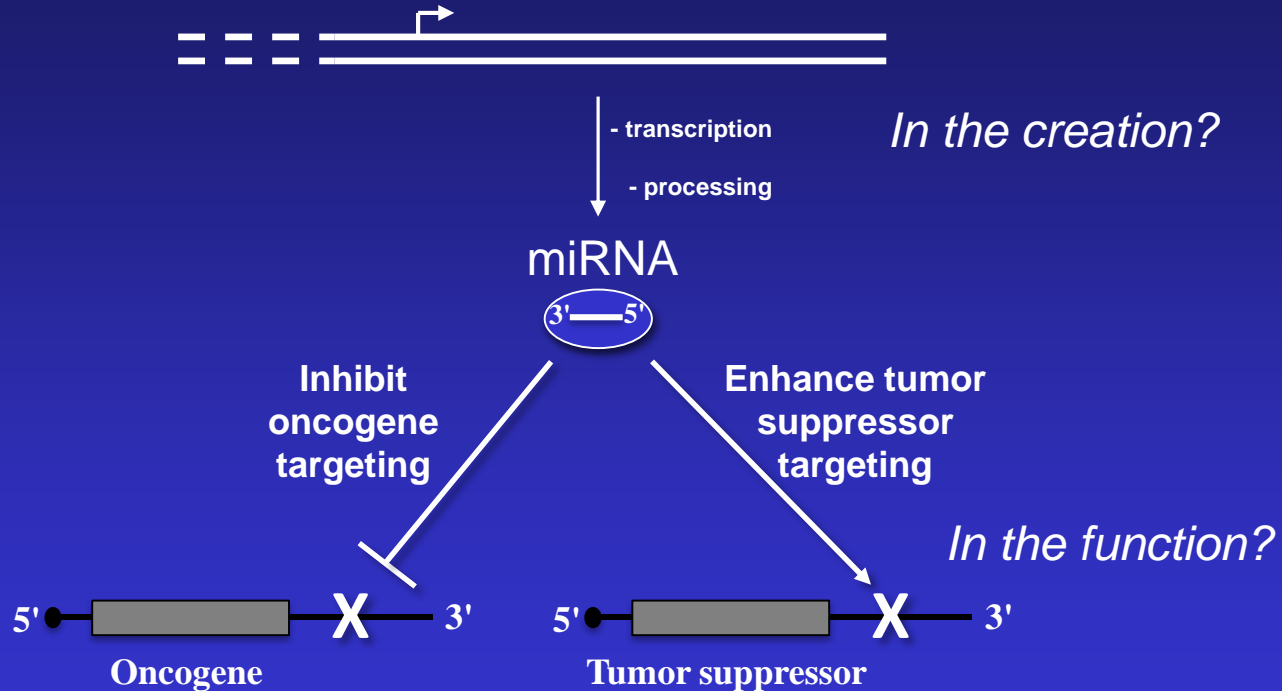
lyse

miRNA



- Immediate
- Conserved
- Systemic

Are there germ-line differences in microRNAs?



Are missed on RNA seq, exon sequencing, and SNP platforms

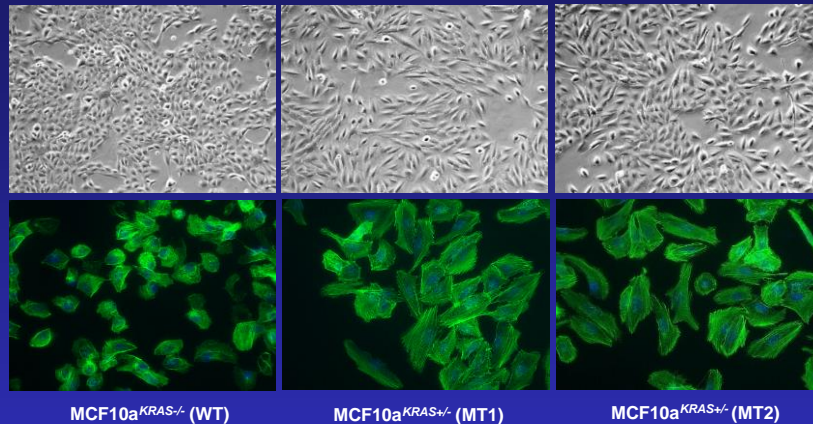
First example: *KRAS*-variant impacts normal biology

Non-variant (-/-)
Epithelial morphology
(rounded/cuboidal)

KRAS-variant (+/-)
Mesenchymal morphology
(long/spindle-like)

Phase contrast

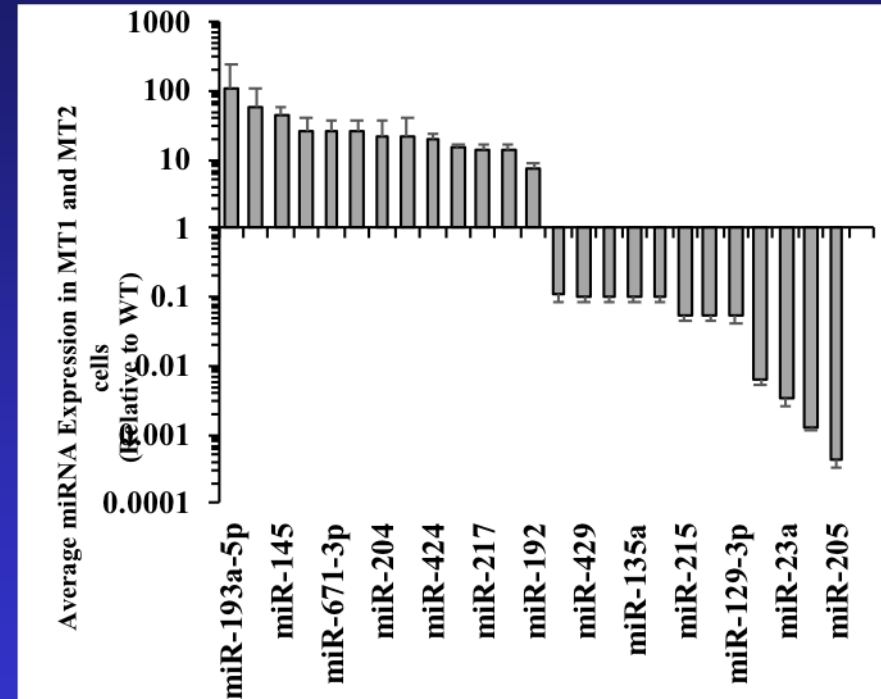
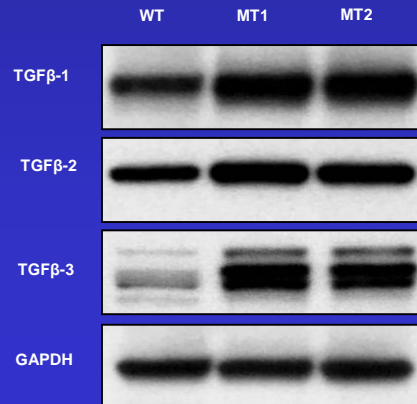
F-actin



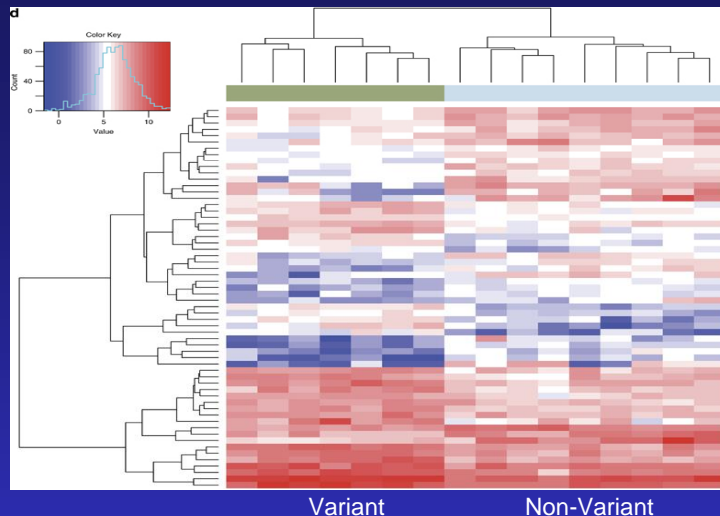
MCF10a^{KRAS}-/- (WT)

MCF10a^{KRAS}+/- (MT1)

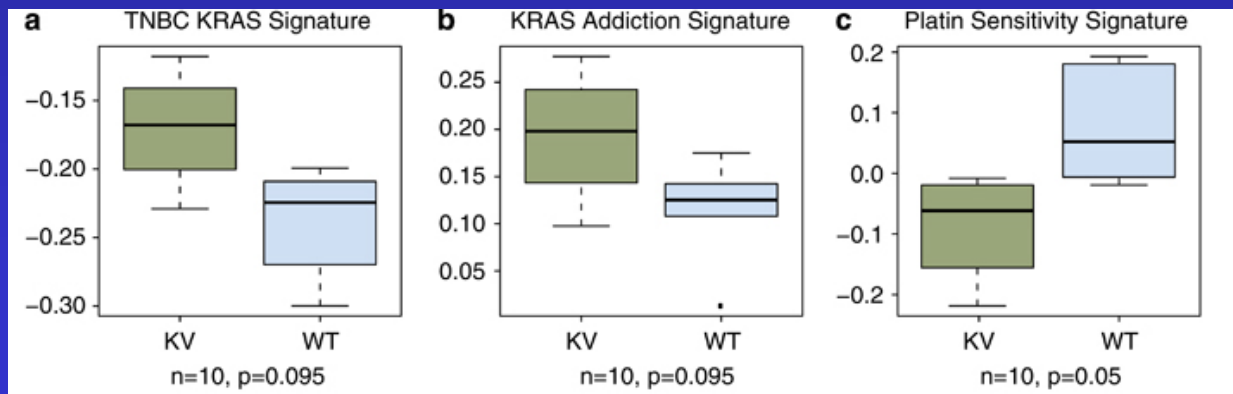
MCF10a^{KRAS}+/- (MT2)



KRAS-variant impacts tumor biology

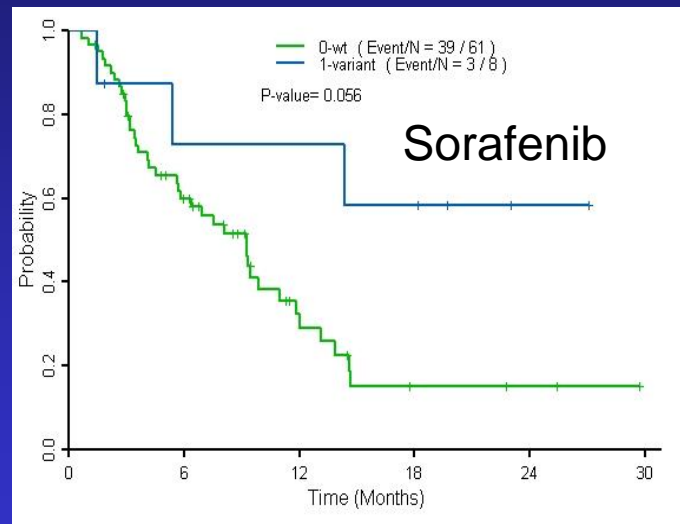
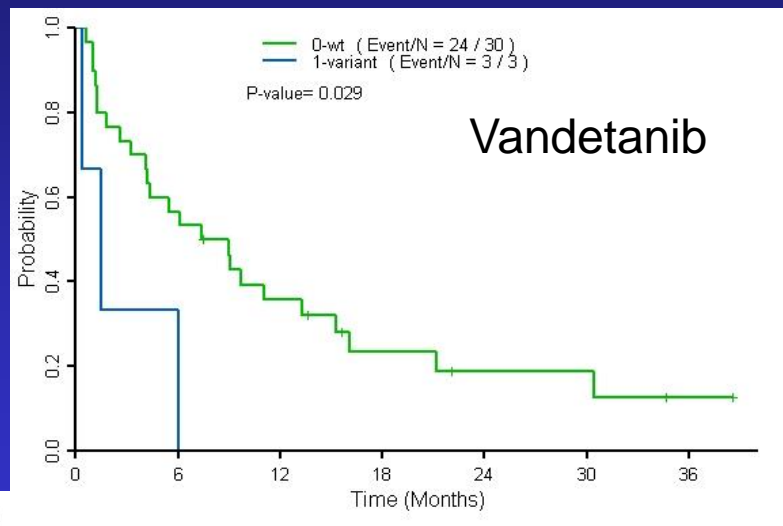


Expression Signature	TT vs TG/GG TNBC Tumor	<i>p</i> K-S Test
NRAS	up	0.02
BRCA mutant-like	up	0.04
Luminal Progenitor	up	0.04
MAPK Creighton	up	0.06
PCA Estrogen	down	0.04



KRAS-variant predictive biomarker of response

- Metastatic NSCLC patients
- Two phase II trials



KRAS-variant

Pan-Cancer, Drug Specific

- Over 11,000 patients, including 3 phase III trials

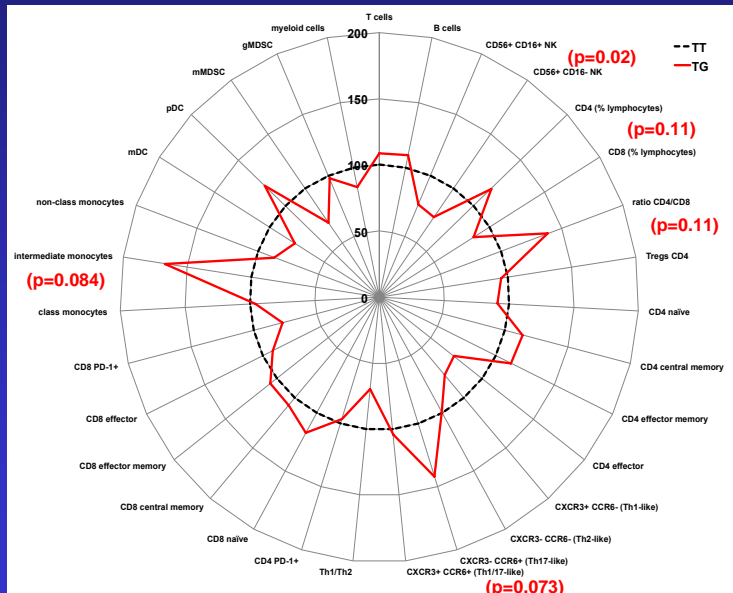
Agents	Cancer types	Phase Trial	Improvement in Progression Free Survival (PFS)	Improvement in Overall Survival (OS)
Sorafenib	NSCLC trials	Two Phase II	2x increase in PFS	>3x increase in OS
MK2206	NSCLC trail	One Phase II	1.3x increase in PFS	6x increase in OS when combined with Erlotinib
Cetuximab	Colon, Head & Neck, Lung	Phase II and III	2x increase in PFS	2x increase in OS
Cisplatin	Ovarian, Head & Neck, Lung	Phase II and III	3x decrease in PFS	2x decrease in OS
Erlotinib	NSCLC trials	Two Phase II	2x decrease in PFS	3x decrease in OS
Vandetanib	NSCLC trial	One Phase II	1.2x decrease in PFS	8x decrease in OS

THERAPY specific not TUMOR type specific



KRAS-variant patients are immunologically altered

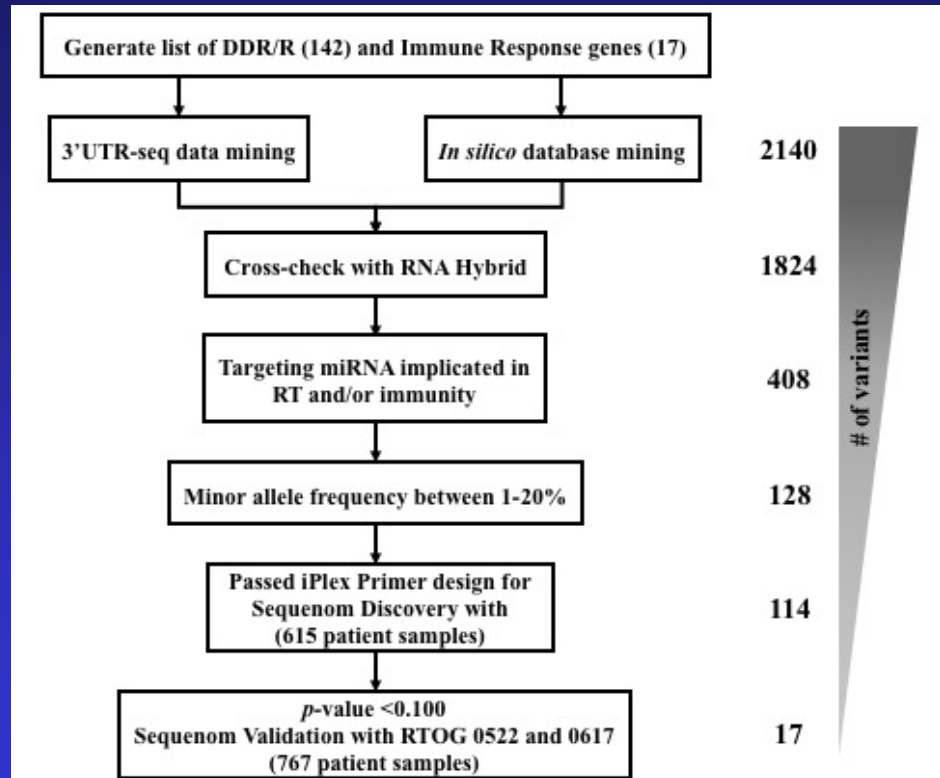
- Depressed NK cells and altered monocytes
- Immunologically suppressed (*high TGFB*), DNA repair deficient



	n	Min	Q1	Median	Q3	Max
KRAS-non-variant	311	2261.42	8837.00	18476.52	32379.43	123264.70
KRAS-variant	65	5034.35	12574.03	23376.49	44809.10	109759.72

Identification of Additional Mutations

- Sequencing all 3'UTRs, promoter regions and miRNAs
- Identified novel and known variants
- Validated for function in silico
- ~2100 for additional study
- Confirm disrupt miRNAs relevant in response
- Common enough to be clinically relevant
- Apply to relevant well vetted clinical data sets

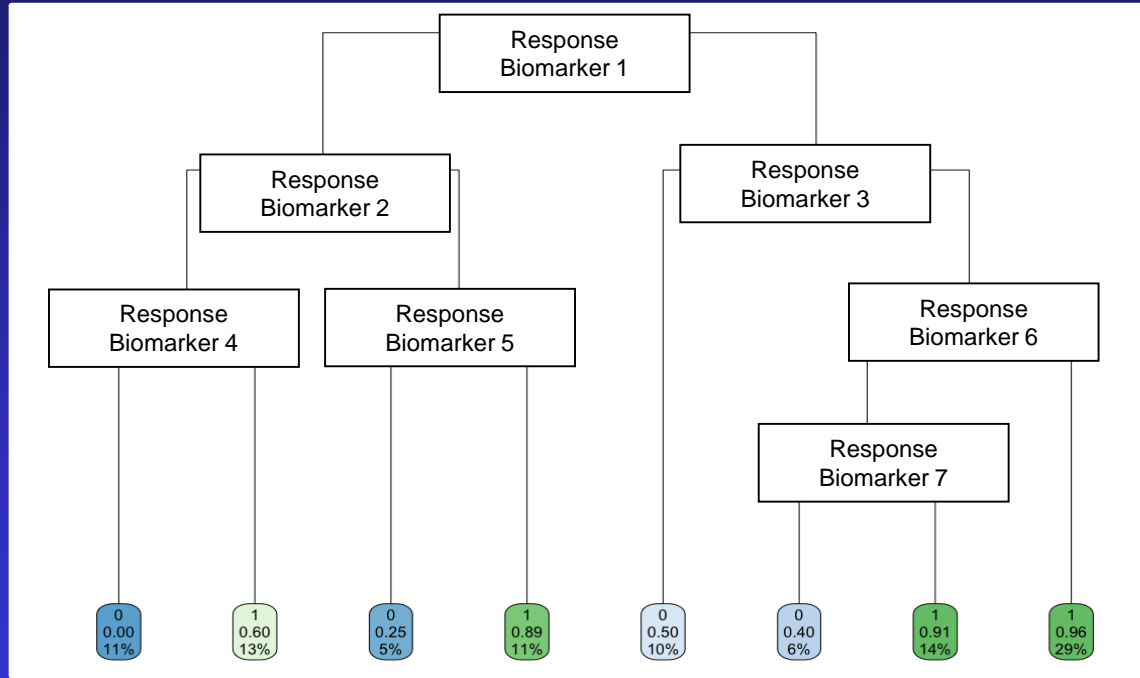


Applying these biomarkers to systemic response

- Cohorts:
 - anti-PD1/PDL1 treated melanoma patients with known response and toxicity (n=55)
 - anti-PD1/PDL1 NSCLC, GU, prostate, GYN, sarcoma (n~100)
- Screened a panel of ~325 vetted biomarkers
- Model response
- Model toxicity

Anti-PD1/PDL1 biomarkers of response

- Melanoma only training set, 55 patients
- Progressive and relapsed versus sustained responders



71% accuracy, 80% sensitivity and 65% specificity

How does this compare to PDL1 and TMB?

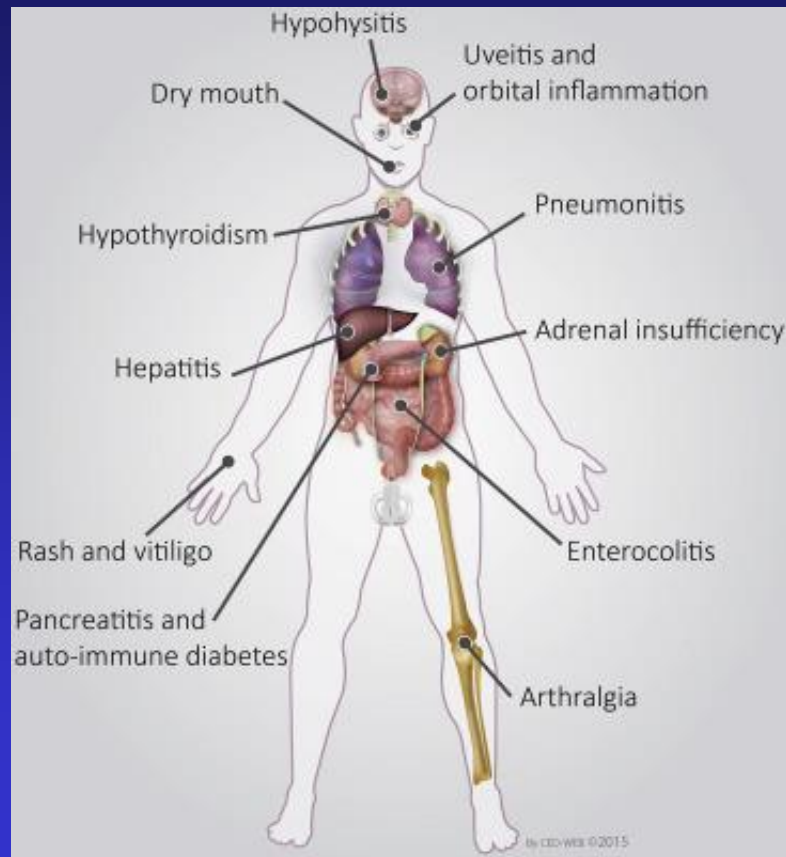
- In this cohort, PDL1 staining performed in ~50%
- TMB on ~90% of patients
- Compared head to head

	Accuracy	Sensitivity	Specificity
PDL1 \geq 50	33%	0%	67%
TMB>10	60%	69%	50%
TMB>20	52%	31%	75%
Mir-variants	68%	77%	58%

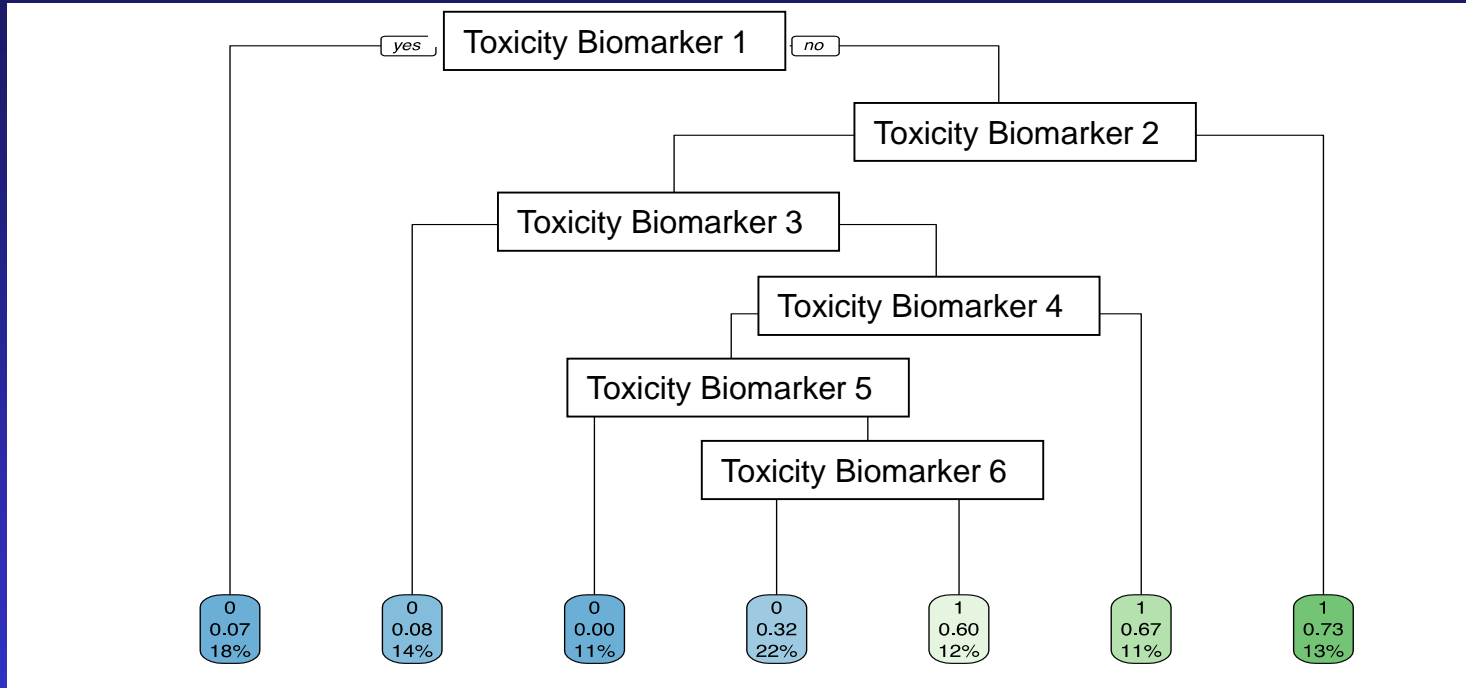
- Found independent from each other

iRAEs – immune related adverse events

- What is this?
 - Reflect “over-zealous” immune system
 - Grade 2 or > irAEs develop on 24-30% of patients treated with single agents
 - Can lead to significant morbidity
- Analysis
 - Training set 54 melanoma patients
 - Validation cohort 100 patients other cancer types (NSCLC, prostate, GU)
 - Pan-cancer signature



Anti-PD1/PDL1 biomarkers of toxicity



Accuracy of 75%, Sensitivity of 70%, Specificity of 86%

Independent validation: 80% accuracy (82% sensitivity and 87% specificity)

Pan cancer signature: 81% accuracy, 84% sensitivity and 75% specificity

Future Directions

- Validate response in the extended cohort
- For toxicity consider
 - Exposure
 - Toxicity type
 - Higher grades
 - Combinations

Conclusions

- Germ-line microRNA-based genetic variants can predict:
 - Different cellular biology
 - Tumor biology
 - Unique systemic reactions to cancer therapy (good or bad)
- Promising will predict response to immune therapy
- Strong evidence do predict toxicity to IOs
- Pan-cancer biomarkers of toxicity

Acknowledgements

The (Old) Weidhaas Yale Lab



Funding

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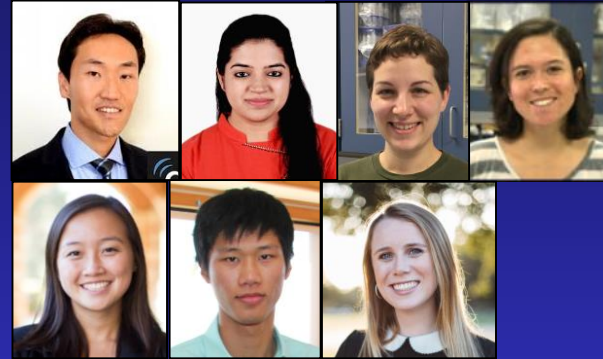
CMCR

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Great Collaborations

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