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Plasma proteomics to predict clinical benefit and irAEs In NSCLC treated with anti-PD(L)1 ICI

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Disclosure Information

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Commercial Interest	Relationship(s)
AstraZeneca	Research funding, Consulting/Advisory Board, Data Safety Monitoring Board, Honoraria
Bristol Myers Squibb	Research funding, Consulting/Advisory Board, Data Safety Monitoring Board, Honoraria
Roche/Genentech	Research funding, Consulting/Advisory Board, Honoraria
Amgen	Research funding, Consulting/Advisory Board
Arcus Biosciences	Research funding, Consulting/Advisory Board/Steering committee
NGM Pharmaceuticals	Consulting/Advisory Board
Bayer	Consulting/Advisory Board
Regeneron	Consulting/Advisory Board
Takeda	Consulting/Advisory Board
Pfizer	Consulting/Advisory Board
Elevation Oncology	Consulting/Advisory Board
Abbvie	Consulting/Advisory Board
Kaleido Biosciences	Consulting/Advisory Board
Mirati	Research funding
Daiichi Sankyo	Consulting/Advisory Board Data Safety Monitoring Board, Honoraria

Introduction:

Biomarkers for ICI therapy in NSCLC: Areas of Need

ICI Use for Advanced NSCLC*

PD-L1 $\geq 50\%$

ICI +
chemotherapy

ICI
Monotherapy

PD-L1 1-49%

ICI +
chemotherapy

PD-L1 $< 1\%$

ICI +
chemotherapy

* Preferred treatment (NCCN)

PD-L1 is the only biomarker used to direct ICI therapy in NSCLC

irAEs from ICI Therapy in Advanced NSCLC

Retrospective analysis



36% (114/317) of patients with advanced NSCLC survived > 1 year after initiation of anti-PD-1/PD-L1 therapy.



52% (50/114) of survivors experienced at least one immune-related adverse event (irAE).

20 survivors had multiple irAEs.

27% (31/114) of survivors required ongoing management of irAEs at 1 year



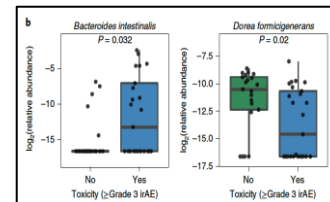
with supportive care, steroids, or additional immunosuppression.

nature medicine

Article

<https://doi.org/10.1038/s41591-022-02094-6>

Germline variants associated with toxicity to immune checkpoint blockade



There are no validated biomarkers for irAEs from ICIs, an area of increasing clinical relevance

Methods:

Study Schema

Prophetic Trial:

Prospective, Observational Trial

Predicting clinical benefit using plasma proteomics profiling (NCT04056247)

- Stage IV NSCLC
- No actionable genomic driver mutations
- 1L systemic therapy

Baseline blood sample
proteomic profiling



PD (L)1 based therapy

PD (L)1 based therapy +
Platinum based chemotherapy

Endpoints (5yr follow-up)

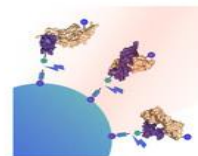
- OS
- PFS
- Clinical Benefit
- Toxicity (AEs; irAEs)

Proteomics profiling

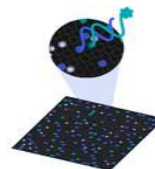
- SomaScan technology (Aptamer-based)
- Examines protein expression levels
- >7000 proteins/sample



Target
binding



UV
cleavage



Array
hybridization



Array
scanning

Study Endpoints:

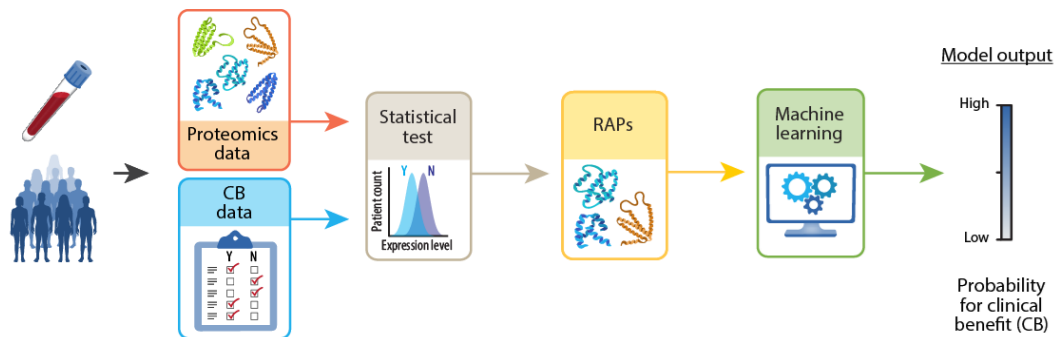
PROphet (Clinical Benefit)

Definition:

- **Clinical benefit** was defined based on PFS at 12 months

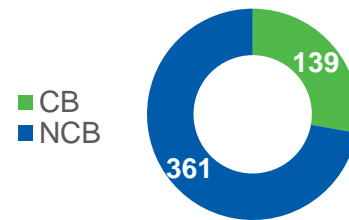
Proteomic Assessment:

- Identify proteomic signature associated with ICI resistance:
- RAP: 'Resistance Associated Proteins'
- Machine learning algorithm associates with clinical benefit



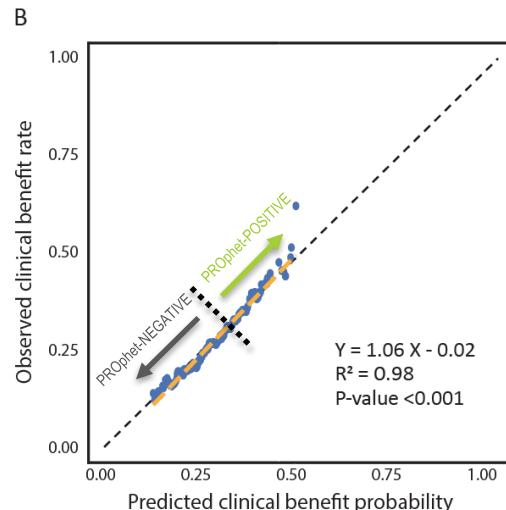
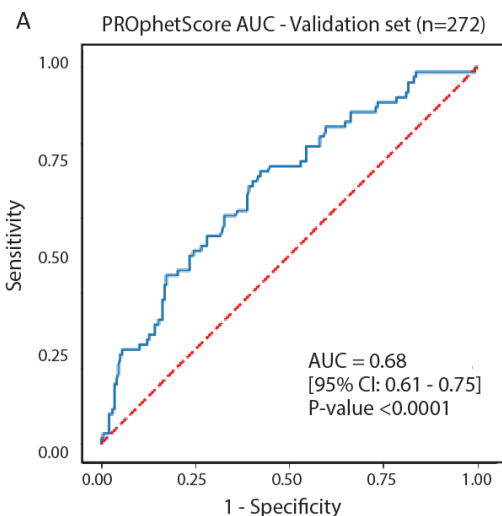
Prophet Trial: Clinical Benefit Cohort (n=500)

Patient Features		Clinical Benefit
Sex	Male	302
	Female	198
ECOG-PS	0	191
	1	270
	2	37
	Unknown	2
PD-L1	High	199
	Low	141
	Negative	131
	Unknown	29
Histology	non-SqCC	370
	SqCC	101
	Unknown	29
Treatment type	ICI+Chemo	290
	ICI	210

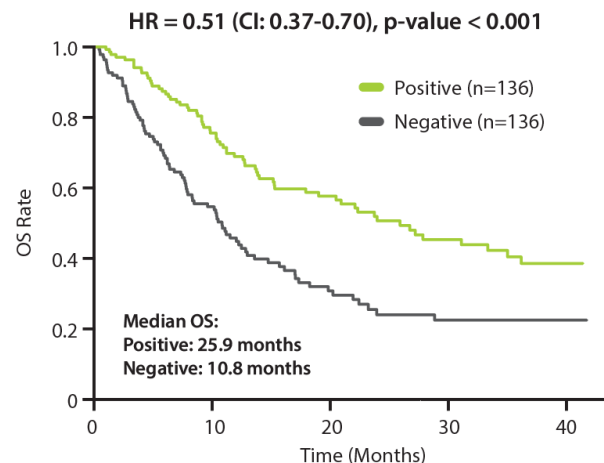


Results:

PROphet (Clinical Benefit)



High correlation between predicted clinical benefit probability and the observed clinical benefit rate ($R^2 = 0.98$)



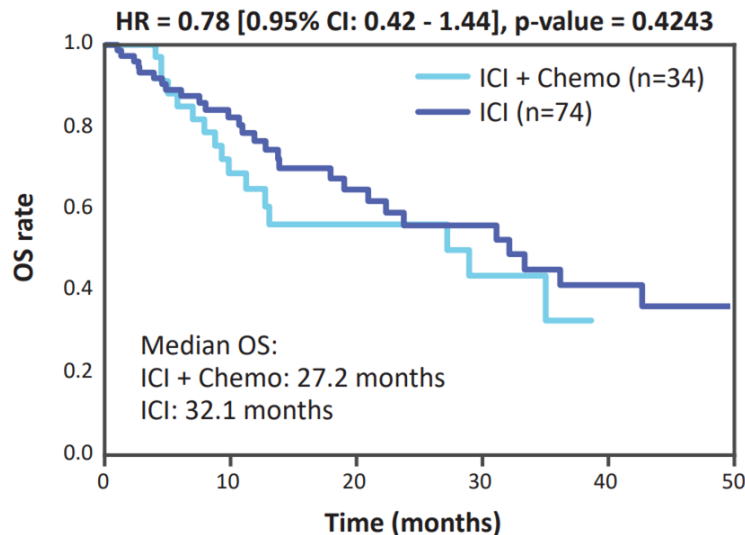
A positive PROphet result is associated with a significant survival benefit

Results:

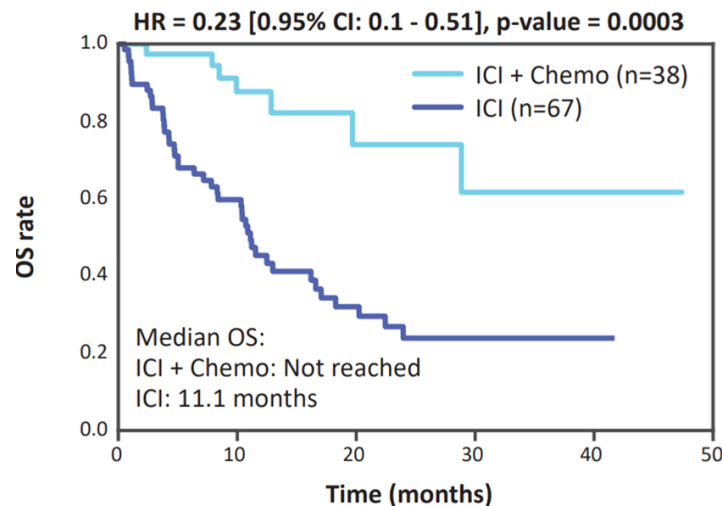
Proteomic Signature + PD-L1: Associates with Clinical Benefit

PD-L1 $\geq 50\%$

'PROphet' POSITIVE + PD-L1 $\geq 50\%$



'PROphet' NEGATIVE + PD-L1 $\geq 50\%$



PROphet result identify NSCLC patients with PD-L1 $>50\%$ who are more likely to benefit from chemo-ICI (compared to ICI)

Study Endpoints:

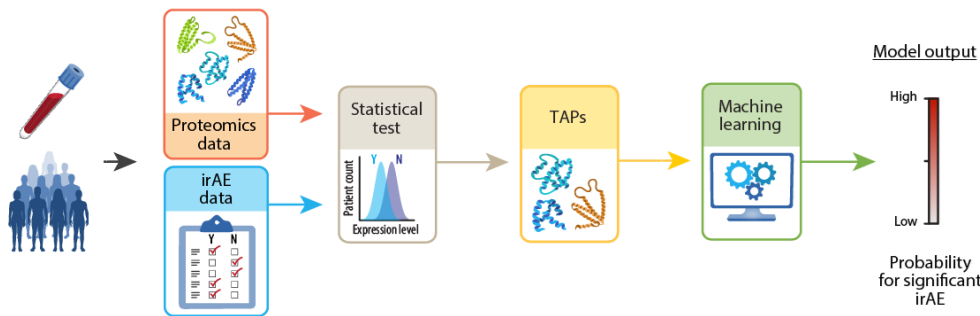
PROphet-irAE Prediction

Definition:

- **Severe irAE:** grade ≥ 3 irAEs within the first 100 days that leading to treatment discontinuation

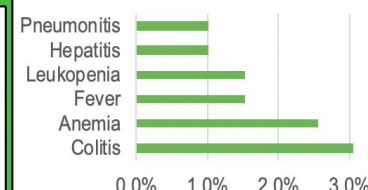
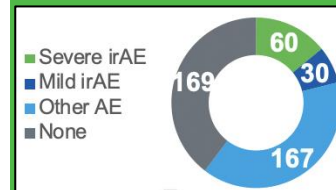
Proteomic Assessment:

- Identify proteomic signature associated with irAEs:
- TAP: 'Toxicity Associated Proteins'
- Machine learning algorithm associates with irAE development
- irAE: AEs that required immunosuppressive therapy, annotated by treating physicians



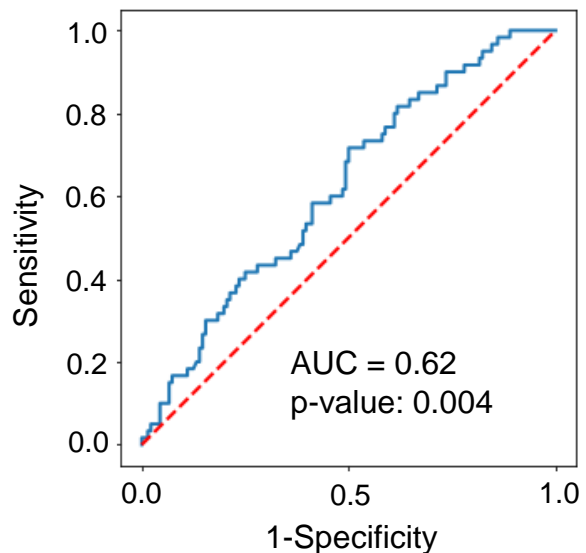
Prophet Trial: irAE Cohort (n= 426)

Category	Parameter	irAE cohort
Sex	Male	249
	Female	177
ECOG	0	136
	1	240
	2	47
	Unknown	3
Histology	non-SqCC	312
	SqCC	97
	Unknown	17
Treatment type	ICI+Chemo	151
	ICI	275

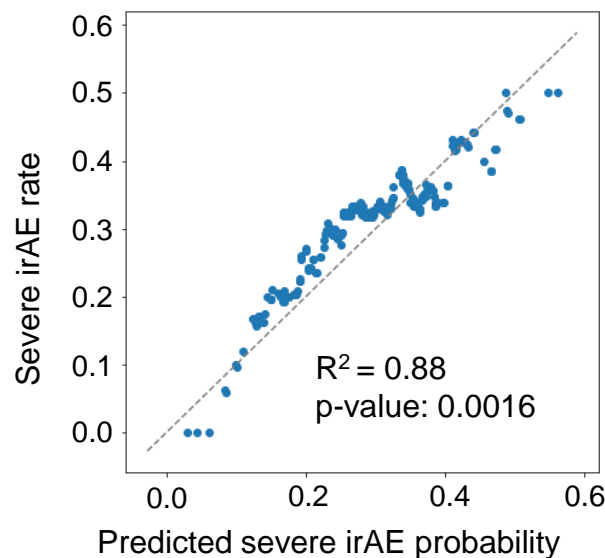


Results:

PROphet-irAE Prediction



irAE model demonstrated statistically significant predictive capabilities

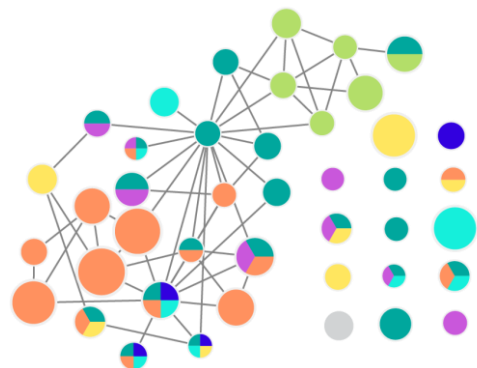


High correlation between predicted severe irAE probability and the observed severe irAE rate

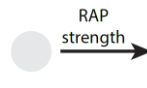
Future Directions:

Mechanistic insights from RAPs and the TAPs

Resistance-Associated Proteins (RAPs)

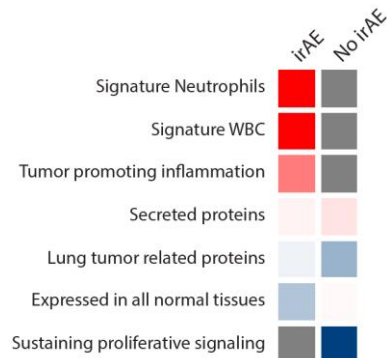


- Cell proliferation
- Chemo-resistance
- Immune modulation
- Angiogenesis
- Invasion and metastasis
- Splicing
- Metabolism



Proteins higher in no clinical benefit are involved in different resistance mechanisms

Toxicity-Associated Proteins (TAPs)



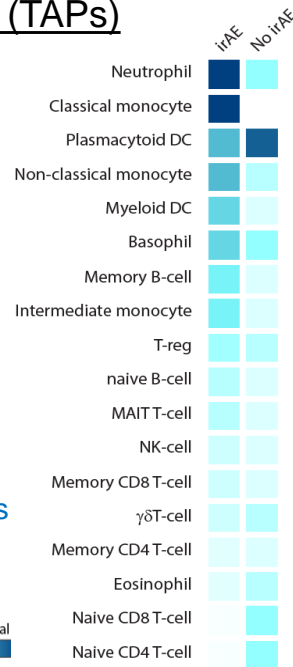
Enrichment factor
De-enriched Enriched

Fisher exact test; $FDR < 0.1$

Mainly
myeloblast-
origin

Mainly
lymphocytes

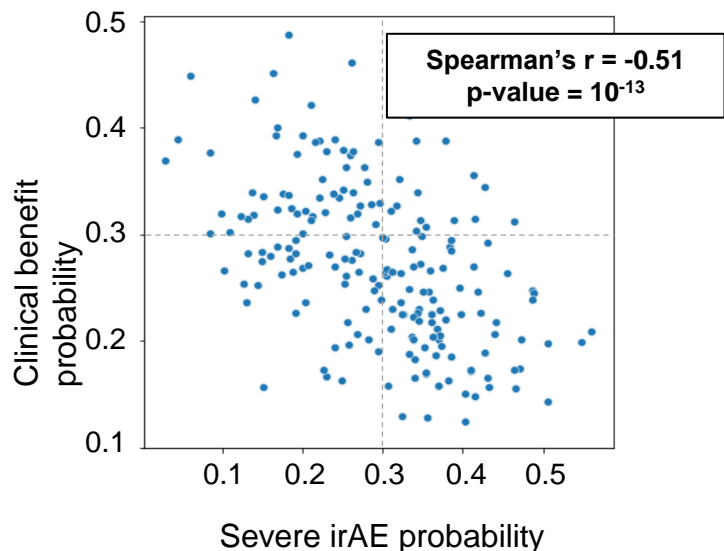
Fraction out of total
Low



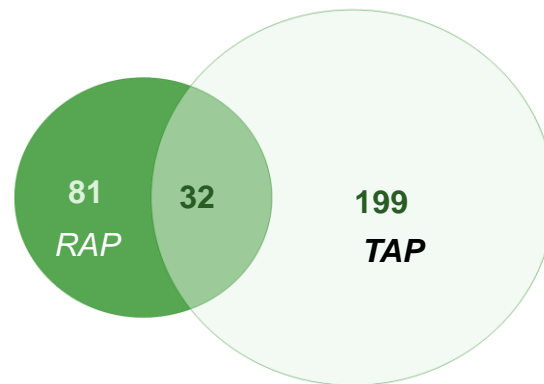
Neutrophil and monocyte related proteins

Future Directions:

Overlap Between PROphet (Clinical Benefit) and PROphet-irAE Predictions



Negative correlation between irAE probability and clinical benefit



RAP = Resistance-Associated Protein
TAP = Toxicity-Associated Protein

Minimal overlap between proteins associated with clinical benefit (RAP) and irAEs (TAP)

Conclusions:

Proteomic signatures and ICI therapy in NSCLC

- A proteomic signature from blood may enrich for prediction of clinical benefit in PD-L1>50% advanced stage NSCLC, based on presence/absence of resistance-associated proteins (RAPs)
- A different proteomic signature from baseline blood, may predict for development of severe irAEs in advanced NSCLC, based on presence of toxicity associated proteins (TAPs)
- There is little overlap between proteomic signatures for response and toxicity
- RAPs are associated with multiple potential resistance mechanisms for treatment
- TAPs are associated with inflammation and neutrophil- and monocyte-related signals, related to irAEs
- Integration of proteomic signatures for clinical benefit and irAEs may be the future of refining ICI-based treatment selection in NSCLC

Colleagues and Collaborators

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All the patients who participated in this study