





### Advances in Cancer Immunotherapy™

### **Emerging Immune Biomarkers**

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# Types of Immune Related Cancer Biomarkers

- Prognostic Biomarkers may identify the likelihood of a clinical event, such as disease progression, disease recurrence, or death, independent of the therapy received
- Predictive Biomarkers are present at diagnosis and may identify whether individuals are more likely to experience a favorable or unfavorable response to treatment
- Pharmacodynamic Biomarkers may show that a biologic response has occurred in an individual who has received treatment

- Immune score in colorectal cancer (good prognosis)
- T-regulatory cells in ovarian cancer (poor prognosis)

- MSI<sup>high</sup> in CRC (response to ICI)
- PD-L1 expression in NSCLC (response to ICI)

- Level of antigen specific immunity after vaccination
- Immune related adverse event after ICI

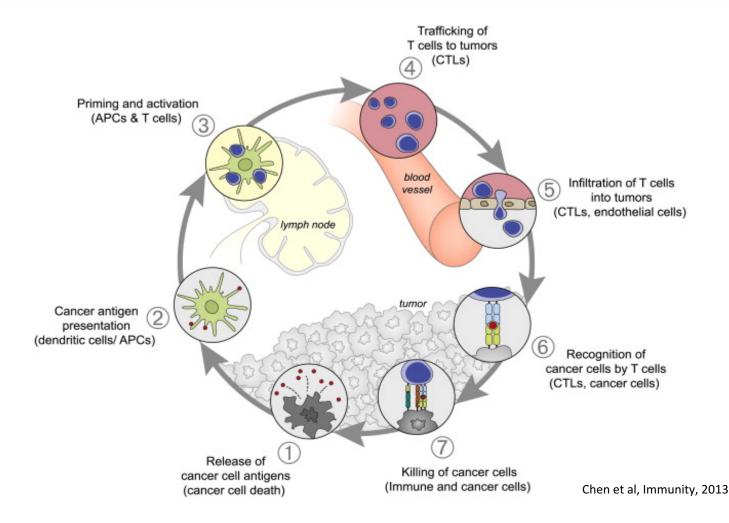


Many prognostic biomarkers are also predictive

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## **Effective Anti-Cancer Immunity**

Biomarker locations
Blood
Lymph node
Tumor





### **Current Predictive Immune Biomarkers**

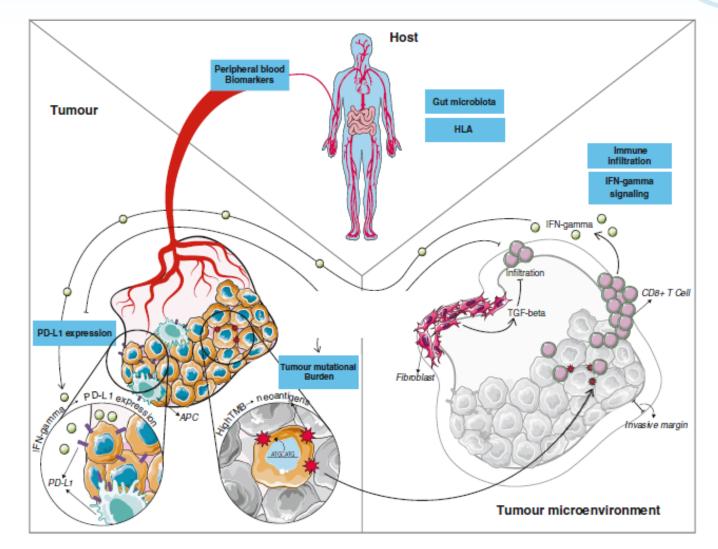
FDA approved for selection

PD-L1

**TMB** 

**dMMR** 

**MSI**high





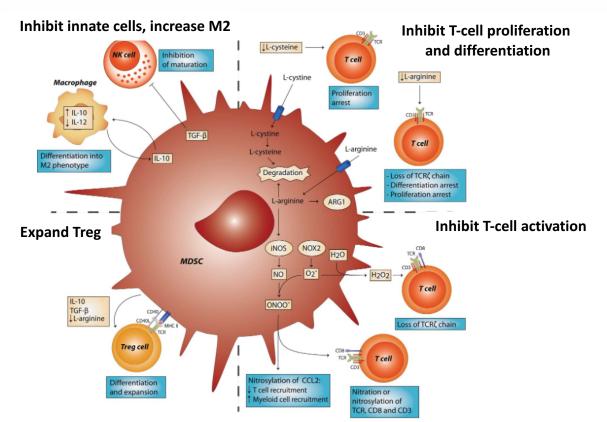
## **Emerging Immune Biomarkers**

- Systemic review of predictive biomarkers for outcomes of ICI in melanoma
- Melanoma trials of ICI, Phase II/III, biomarkers associated with clinical outcomes: screened 2536 trials, analyzed 177 studies inclusive of 128 biomarkers
- QUIPS risk of bias six domains: study participation, study attrition, prognostic factor measurement, outcome measurement, adjustment for other prognostic factors, and statistical analysis. Most with high or moderate risk of bias.
- Peripheral blood markers: Myeloid derived suppressor cells, CD8<sup>+</sup> memory T-cells, T-cell receptor diversity, circulating tumor cells or DNA
- Tumor associated markers: TIL, gene expression profiles
- Specific species in the gut microbiome
- Clinical biomarkers\*



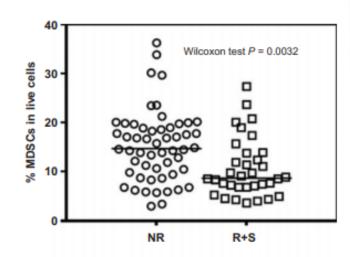


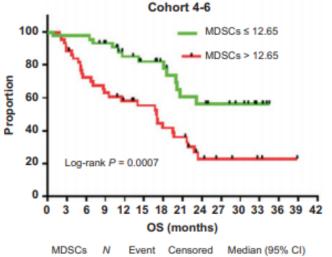
### **MDSC**



de Koning et al, Oncoimmunology, 2016

- >90 patients
- Phase I/II trial
- Advanced melanoma
- Ipilimumab refractory
- Treated with nivolumab
- +/- vaccine
- Low baseline MDSC correlated with outcome
- MoMDC stronger inverse predictor of outcome



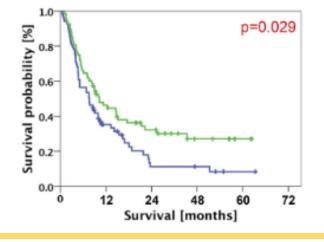


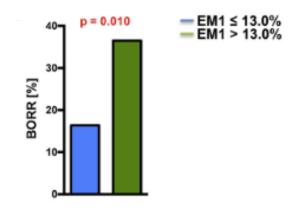
MDSCs N Event Censored Median (95% CI)
≤12.65 44 13 (30%) 31(70%) NA (19.9–NA)
>12.65 44 30 (68%) 14 (32%) 16.9 (8.7–21.7)



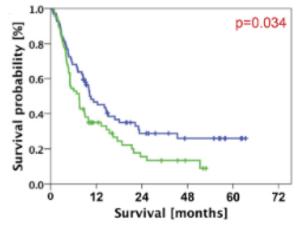
# CD8+ Memory T-cells

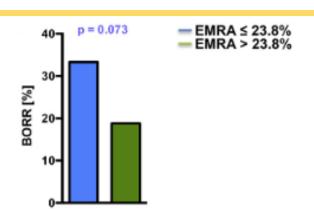
Effector memory





Terminally differentiated effector memory





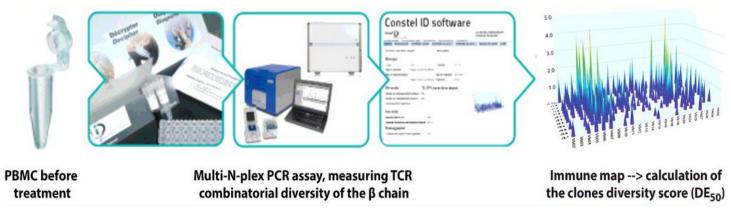
- 137 patients
- Advanced melanoma
- Treated ipilimumab
- Baseline blood
- High effector memory, positive correlation
- High terminally differentiated EM, negative correlation





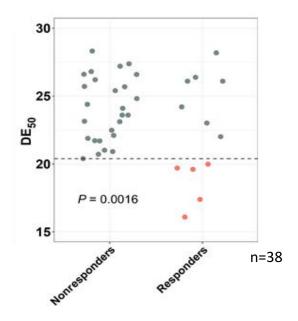
### TCR Diversity

T-cell repertoire diversity evenness (DE<sub>50</sub>)



- Advanced melanoma treated with ICI
- Even frequency distribution=low clonality=high DE<sub>50</sub> score
- Specific frequencies abundant=high clonality=low DE<sub>50</sub> score
- Low DE<sub>50</sub> (<20.4) is an independent predictor of increased OS (p=0.034)</li>

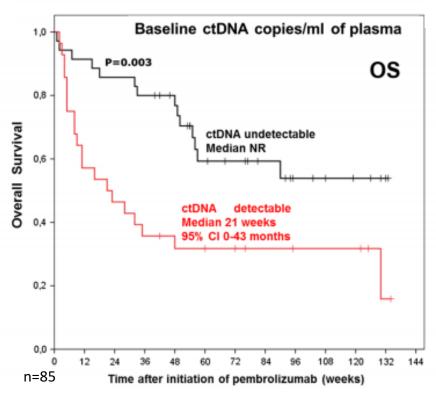
### Predictive of response to anti-PD-1

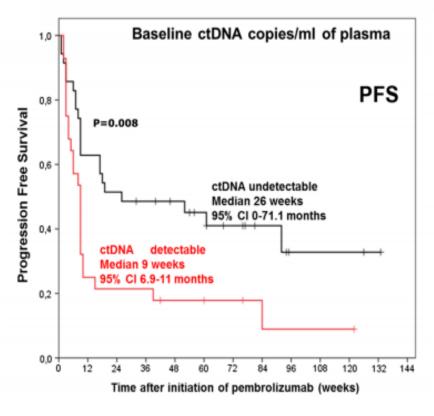


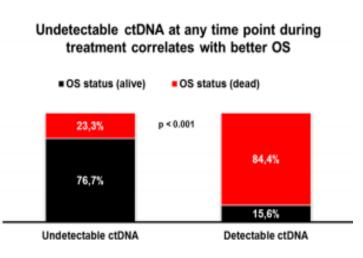


Hogan et al, Ca Immunol Res, 2019

# Circulating Tumor Cells or DNA







Seremet et al, J Trans Med, 2019

Society for Immunotherapy of Cancer

- Advanced melanoma
- Treated with anti-PD-1
- Baselines ctDNA an independent predictor of PFS and OS
- Potential as a pharmacodynamic biomarker



## Tumor Infiltrating Lymphocytes

- 300 studies
- 70,000 patients

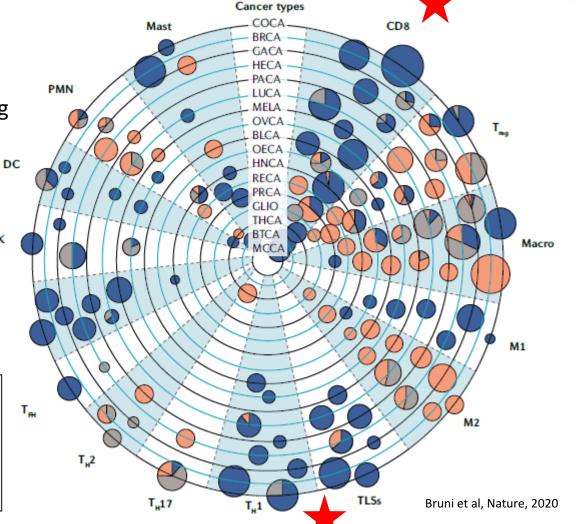
Prognostic association

Number of patients

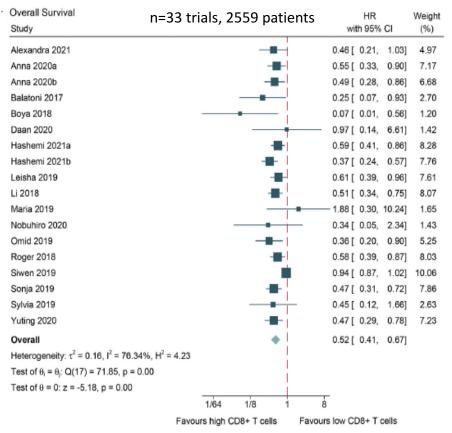
1,001-

5,000

- 17 cancers
- 15 tumor infiltrating immune cell types



#### Baseline CD8 TIL and OS after ICI

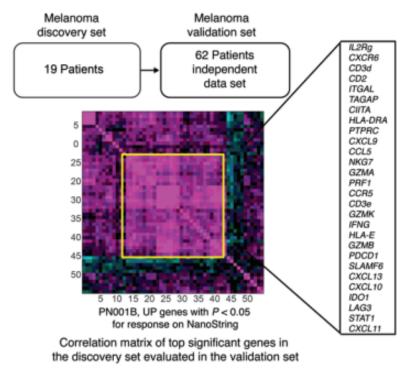


Li et al, eClinical Medicine, 2021

501- 101-

1,000 500

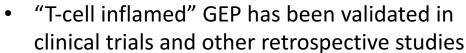
# Gene Expression Profiles: T-cell Inflammation



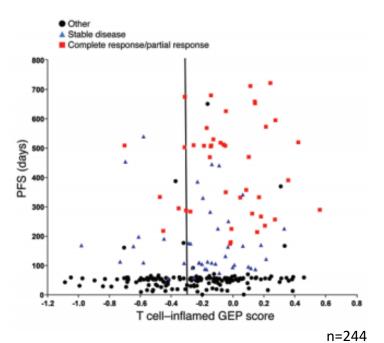
Ayers et al, JCI, 2017



IFN-γ	Expanded immune gene signature	
IDO1	CD3D	IL2RG
CXCL10	IDO1	NKG7
CXCL9	CIITA	HLA-E
HLA-DRA	CD3E	CXCR6
STAT1	CCL5	LAG3
IFNG	GZMK	TAGAP
	CD2	CXCL10
	HLA-DRA	STAT1
	CXCL13	GZMB



 Most advanced candidate for a predictive biomarker

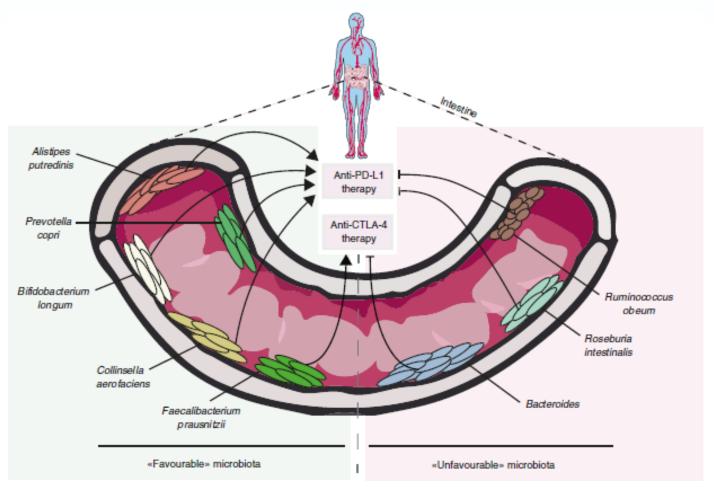


KEYNOTE 012, 028 9 cancer cohorts

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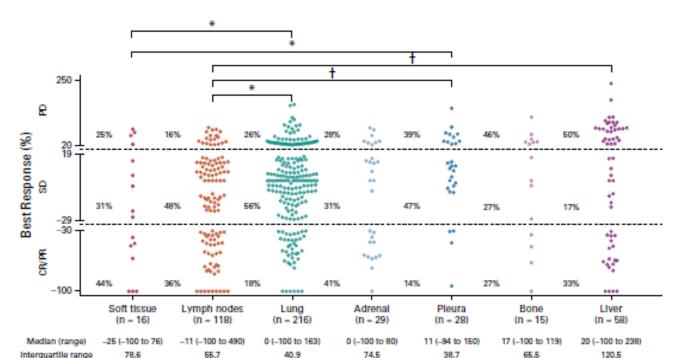
## Changes in the Gut Microbiome





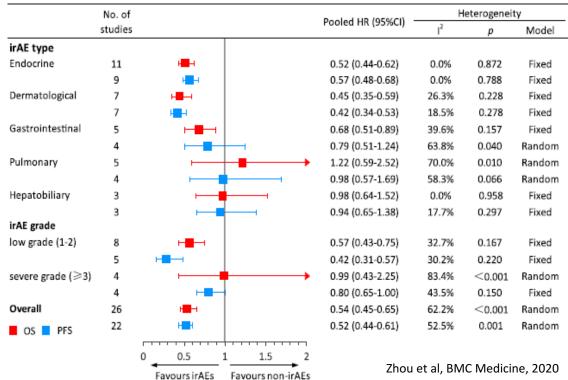
## Clinical Biomarkers: Disease Sites/irAE

761 lesions from 214 NSCLC, 290 lesions from 78 MMRD Best Overall Response



Osorio et al, JCO, 2019

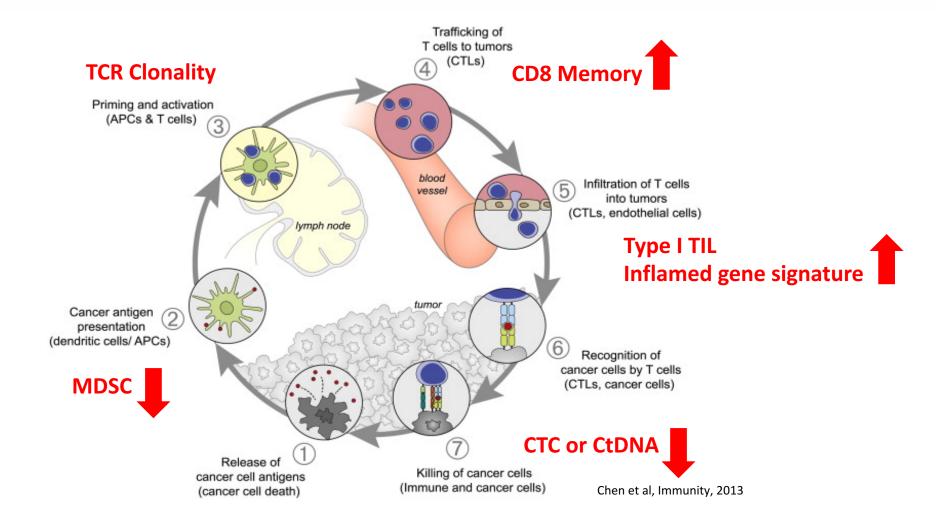
### 22 studies, multiple tumor types, 3297 patients Progression Free Survival





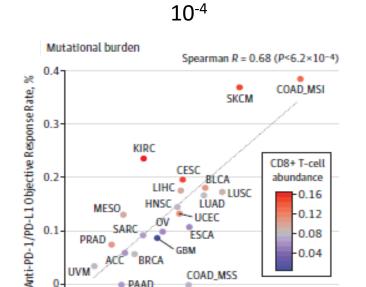
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## Multiple Markers Needed



2.0

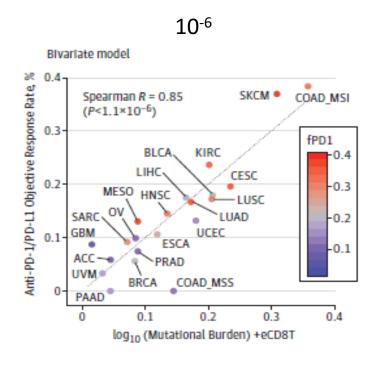
COAD MSS

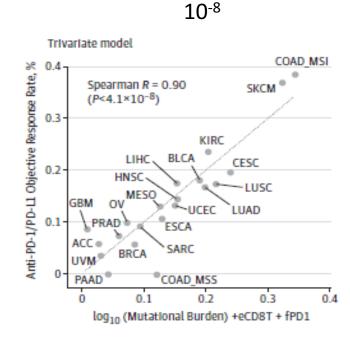
log<sub>10</sub> (Mutational Burden)

2.5

3.0

3.5





Lee et al, JAMA Oncology, 2019

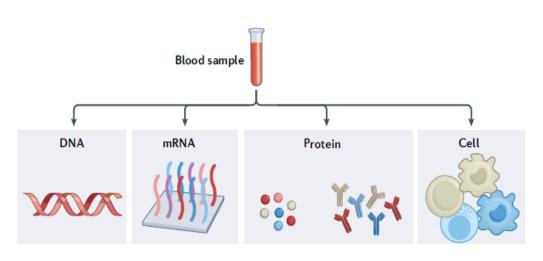
- TCGA, 7187 patients, 21 cancer types, 36 variables
- Whole exome and RNA sequencing
- Predict objective response to ICI



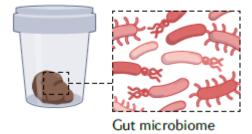
1.0

1.5

## Systems Approach to Predictive Biomarkers



#### Stool sample



Tumour sample

Jing et al, Nat Rev Clin Oncol, 2022

#### Tumor foreignness Mutational load Tumor sensitivity to Infiltrating immune cells Intratumoral T cells, immune effectors myeloid cells IFNg expression profile Absence of inhibitory Absence of inhibitory tumor metabolism checkpoints LDH, IDO PD-1, CTLA-4 Absence of soluble Desirable general performance inhibitors and immune status TGF-B, IL-10, VEGF NLR. WHO score Van Dijk et al, Eur Urol, 2019 Tumor foreignness Tumor sensitivity to Infiltrating immune cells immune effectors myeloid cells IFNg expression Absence of inhibitory Absence of inhibitory tumor metabolism checkpoints LDH, /DO PD-L CTLA-4 Absence of soluble Desirable general performance inhibitors and immune status

NLR, WHO store

TOY-A, A-10, VEGF