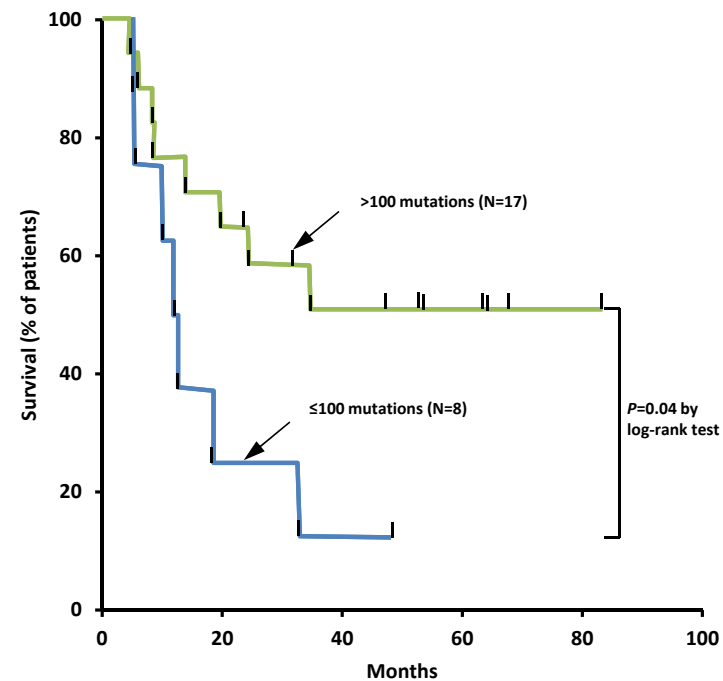
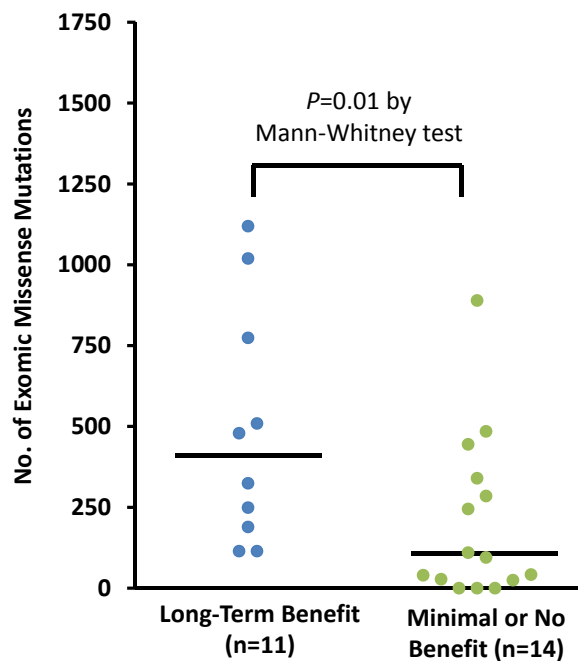


Can genetics be used to select patients for immune checkpoint blockade

Naiyer Rizvi, MD
Director of Thoracic Oncology
Director of Immuno-Oncology
Columbia University Medical Center
New York, New York

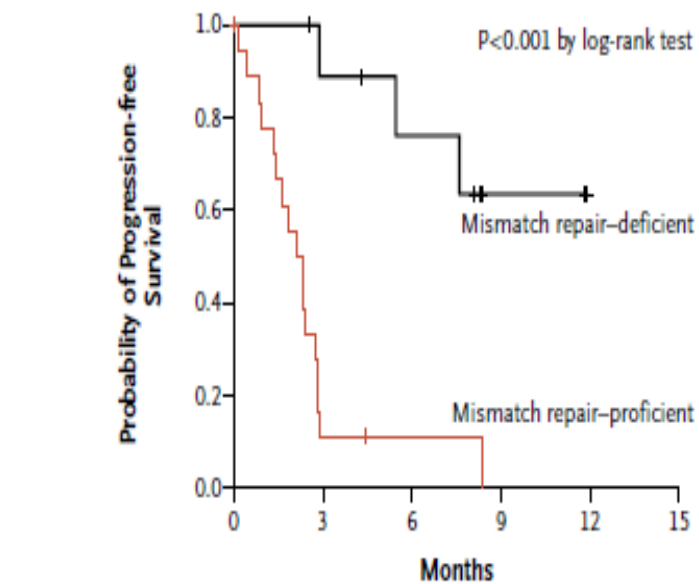
Mutational Load and Clinical Response to CTLA-4 Blockade in Melanoma



Snyder A, et al. *N Engl J Med*. 2014;371(23):2189-2199.

Mutational Burden, MSI, and Response to Anti-PD-1 Therapy

A Progression-free Survival in Cohorts with Colorectal Cancer



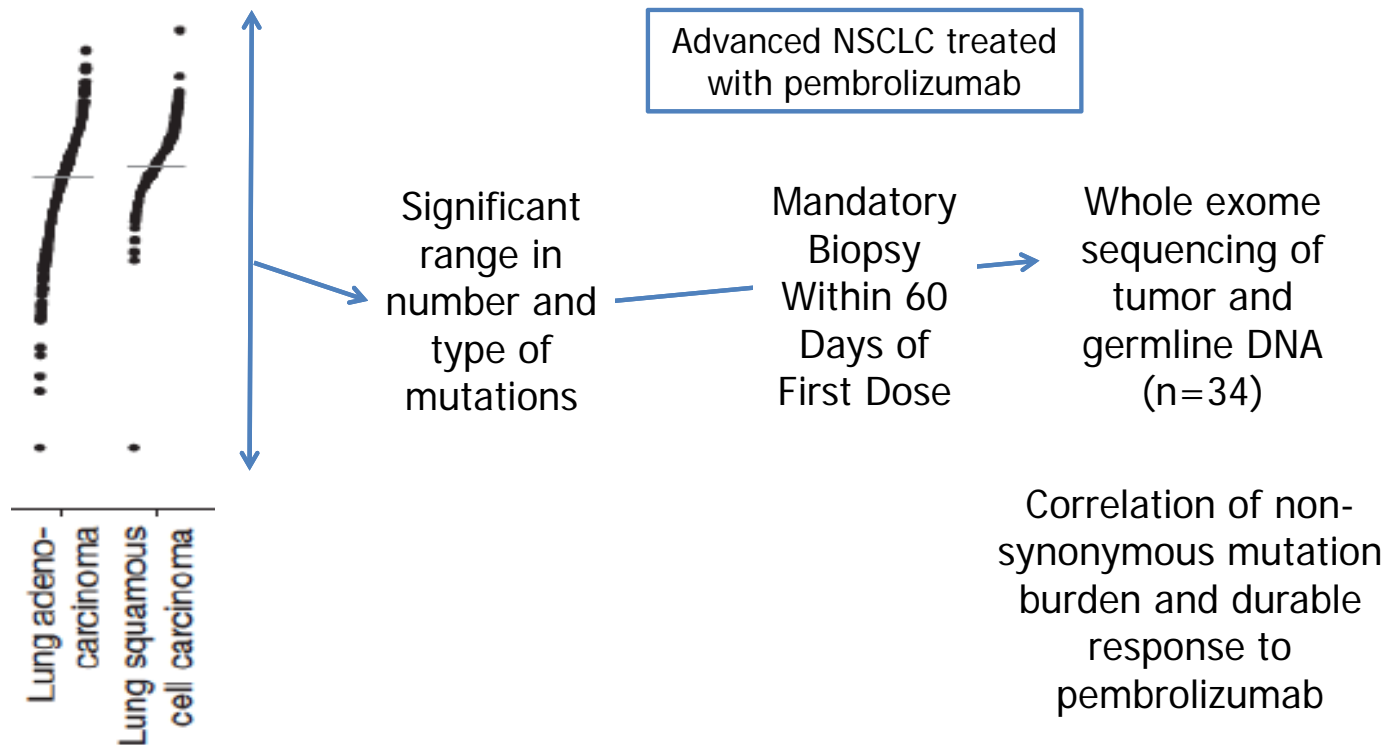
MSI+ 1782 mutations

MSI- 73 mutations

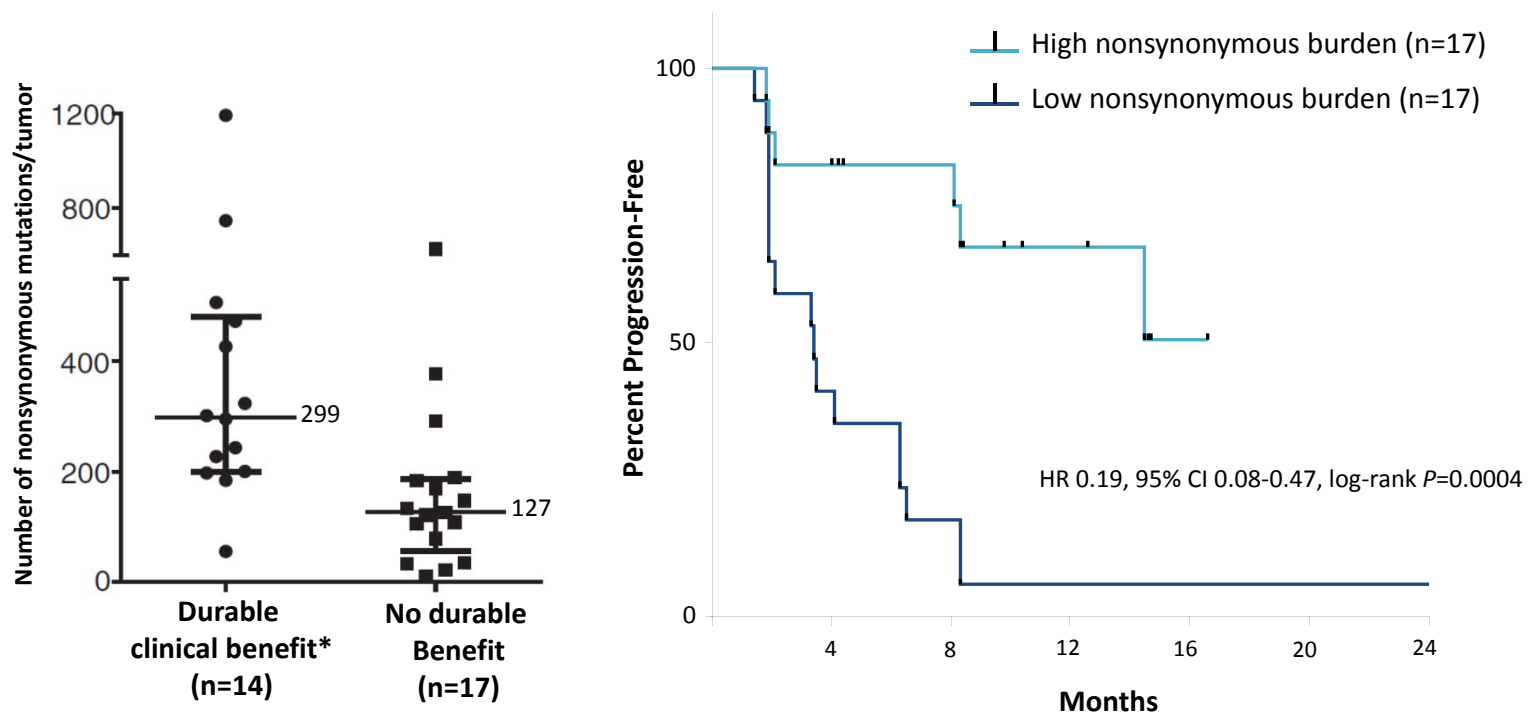
No. at Risk						
Mismatch repair-deficient	11	8	6	2	0	0
Mismatch repair-proficient	21	2	1	0	0	0

Le DT et al, NEJM

Is there a Genetic Basis for Response to PD-1 Blockade ?



Mutation Burden Determines Sensitivity to PD-1 Blockade in NSCLC



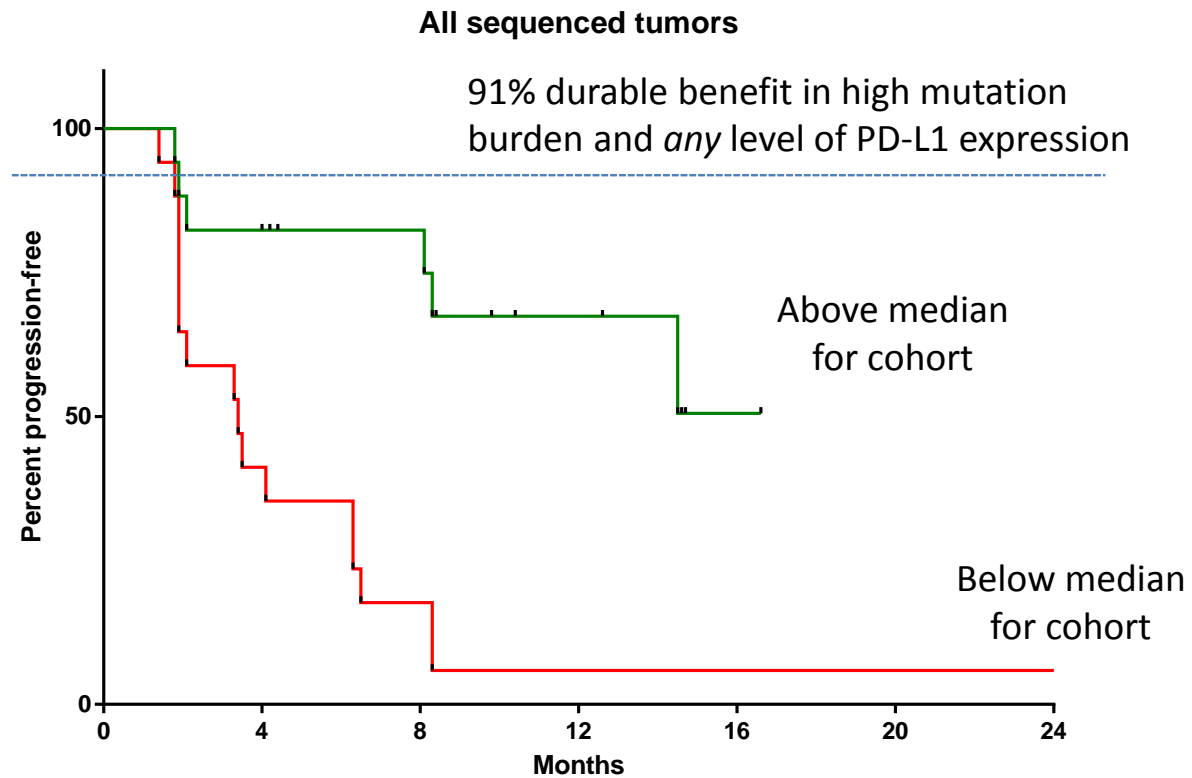
*Partial or stable response lasting >6 months.

Rizvi N, et al. *Science*. 2015;348(6230):124-128.

Mutation burden in PS 1-49%

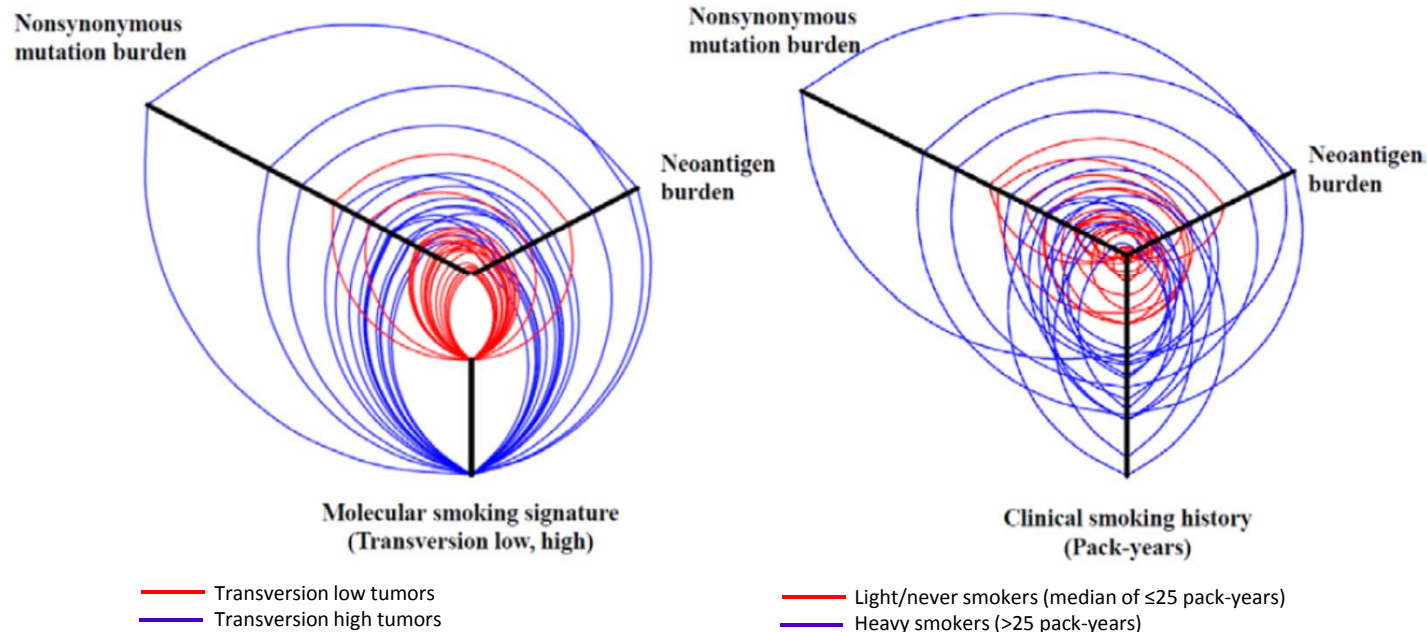
PD-L1	PFS (mos)	Events	RR	DCB	Nonsyn.
1	18.8	0	PR	DCB	1192
40	8.3	1	SD	DCB	507
30	6.2	1	SD	NDB	368
40	14.8	1	PR	DCB	296
40	8.3	1	SD	DCB	185
1	6.5	1	SD	NDB	148
10	1.9	1	POD	NDB	134
33	1.4	1	POD	NDB	122
15	2.1	1	POD	NDB	106
5	3.5	1	SD	NDB	109
2	6.3	1	SD	NDB	79
2	1.9	1	POD	NDB	35
30	1.8	1	POD	NDB	34

Highly significant correlation between non-synonymous mutation burden and durable benefit with pembrolizumab



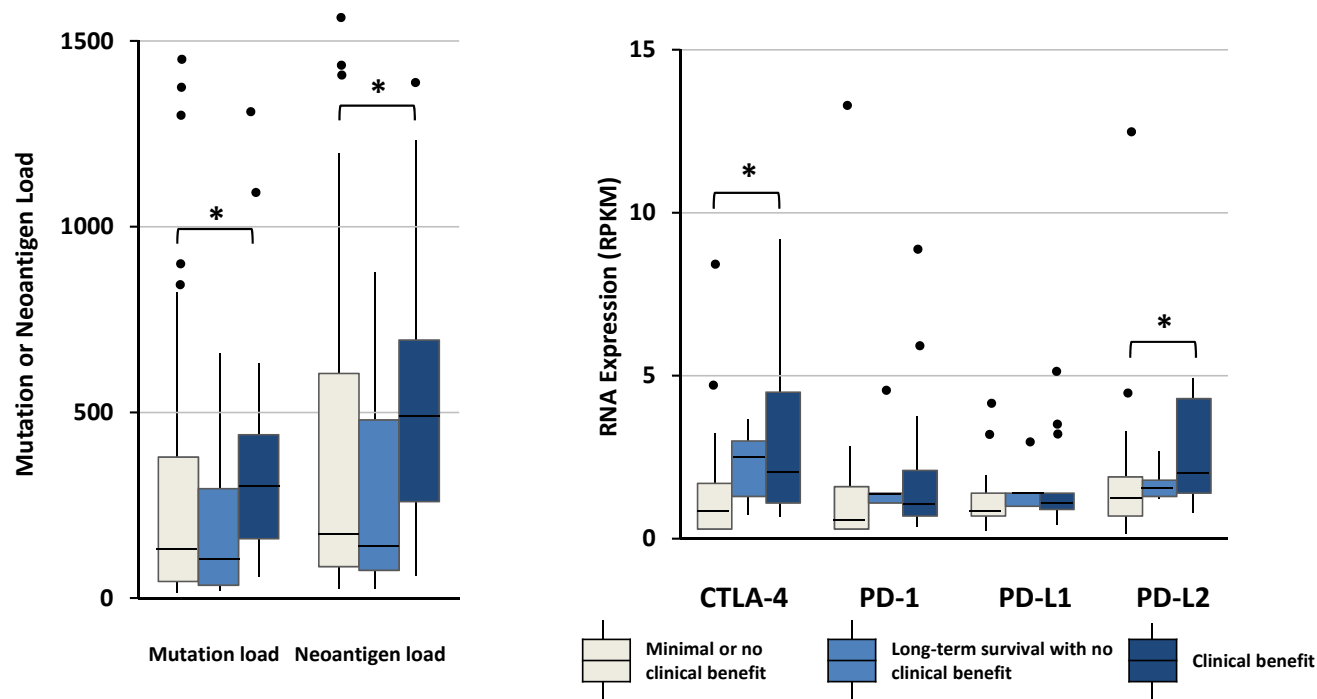
Correlation of Molecular Smoking Signature, Nonsynonymous Mutation Burden, and Neoantigen Burden in NSCLC

- Transversion low tumors have significantly lower mutation and neoantigen burden vs transversion high tumors (Mann Whitney $P < 0.0001$ for both)
- Nonsynonymous mutation burden correlates with neoantigen burden (Spearman ρ 0.91, 95% CI 0.83-0.96, $P < 0.0001$)
- Modest correlation is seen
 - Between pack-years and nonsynonymous mutation burden (Spearman ρ 0.31, 95% CI -0.05-0.59, $P = 0.08$)
 - Between pack-years and neoantigen burden (Spearman ρ 0.35, 95% CI 0-0.62, $P = 0.04$)



Mutational Load and Neoantigen Are Significantly Associated With Clinical Benefit From Ipilimumab

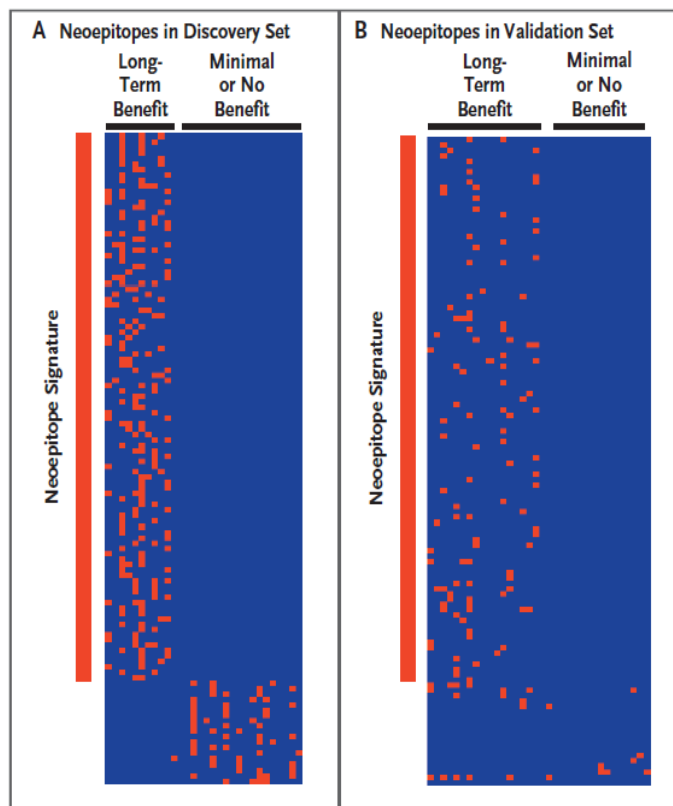
- Whole-exome sequencing performed on pretreatment tumor biopsies and matching germline tissue samples from 110 patients with metastatic melanoma treated with ipilimumab
 - Nonsynonymous mutational load and neoantigen load: significantly associated with clinical benefit ($P=0.0076$ and $P=0.027$)
 - CTLA-4 and PD-L2 expression: significantly elevated in clinical benefit vs no clinical benefit cohort ($P=0.033$ and $P=0.041$)
 - Granzyme A and perforin expression: significantly elevated in clinical benefit vs no clinical benefit cohort ($P=0.042$)



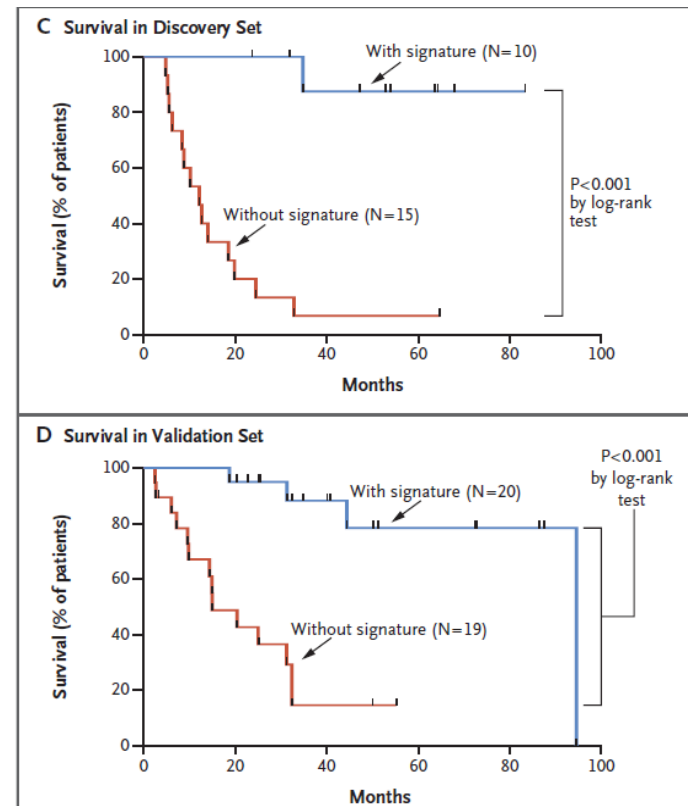
Asterisks indicate $P < 0.05$ (Mann-Whitney). Van Allen EM, et al. *Science*. 2015 Sep 10; Epub ahead of print.

A Robust Neoantigen Signature Identifying Melanoma Patients That Respond to Anti-CTLA4 Therapy

Neoantigen signature

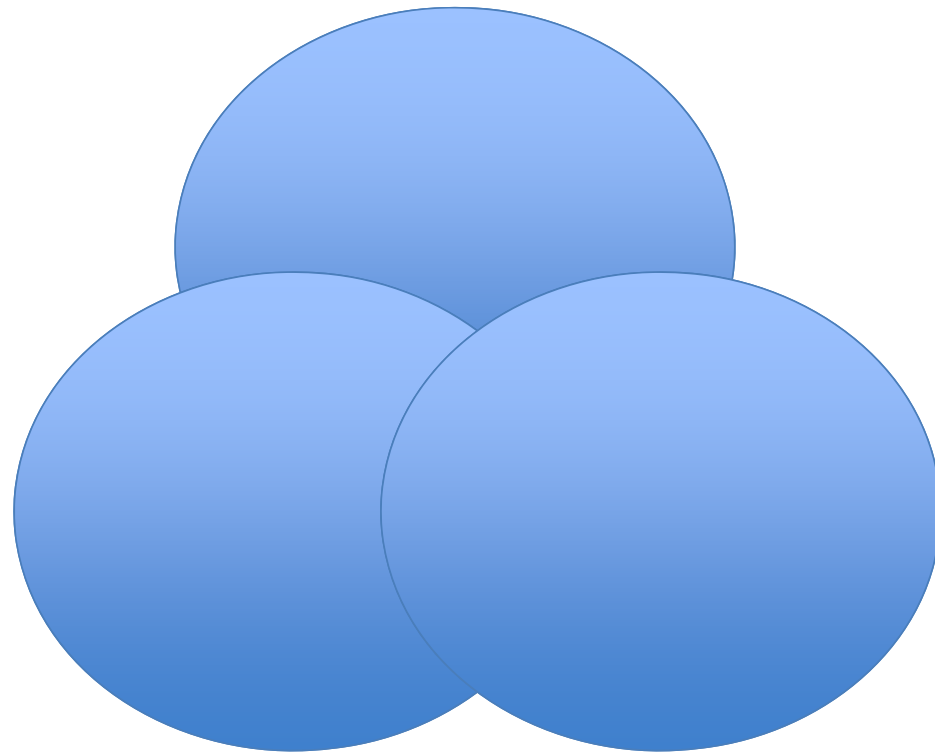


Survival following anti-CTLA4 Rx



Snyder et al. NEJM 2014

Immunotherapy strategy requires multiple lenses



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JHU

*Janis Taube
Drew Pardoll*



Future Biomarkers Panel Discussion

Moderator: Adrian Bot, MD, PhD – Kite Pharma, Inc.

Panelists:

- Lisa H. Butterfield, PhD – University of Pittsburgh
- Suzanne L. Topalian, MD – Johns Hopkins University
- Michael D. Kalos, PhD – Eli Lilly and Company
- Naiyer Rizvi, MD – Columbia University Medical Center