

# Precision medicine in the era of comprehensive genomic profiling

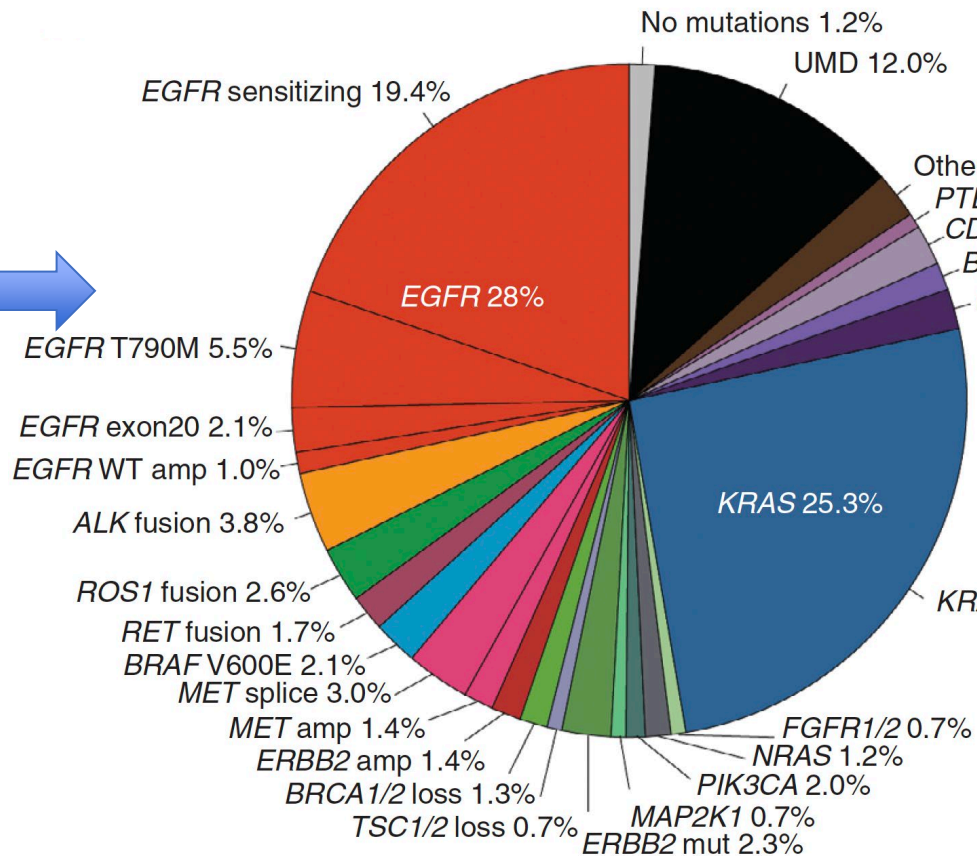
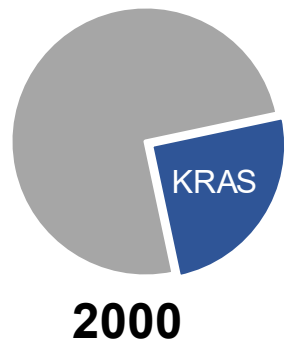
Charles M. Rudin MD PhD  
Deputy Director, MSKCC



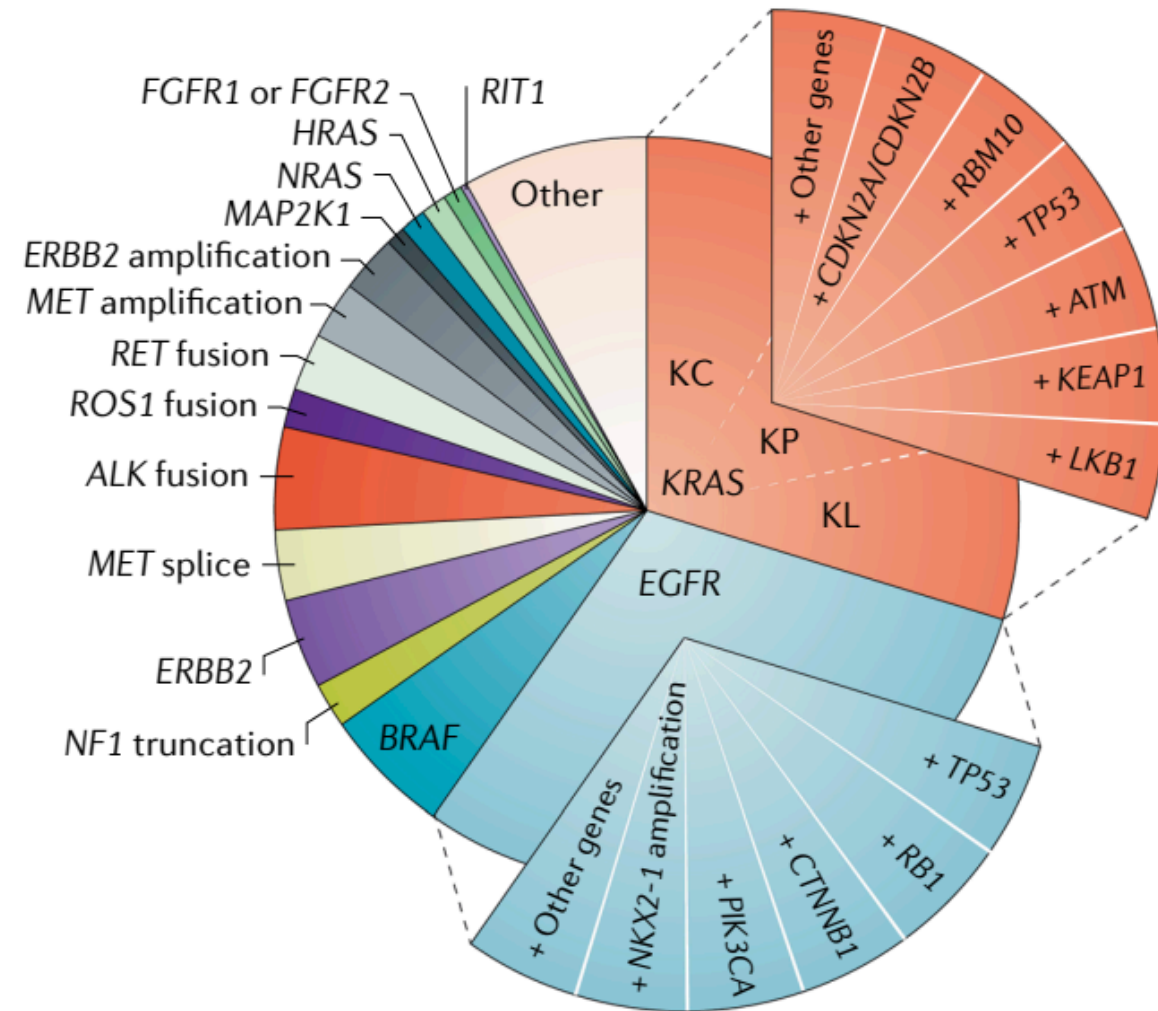
Memorial Sloan Kettering  
Cancer Center

**Clinically actionable drivers are on the rise**

# The number of drivers has risen in lung adenocarcinomas



Jordan et al, *Cancer Discov* 2017

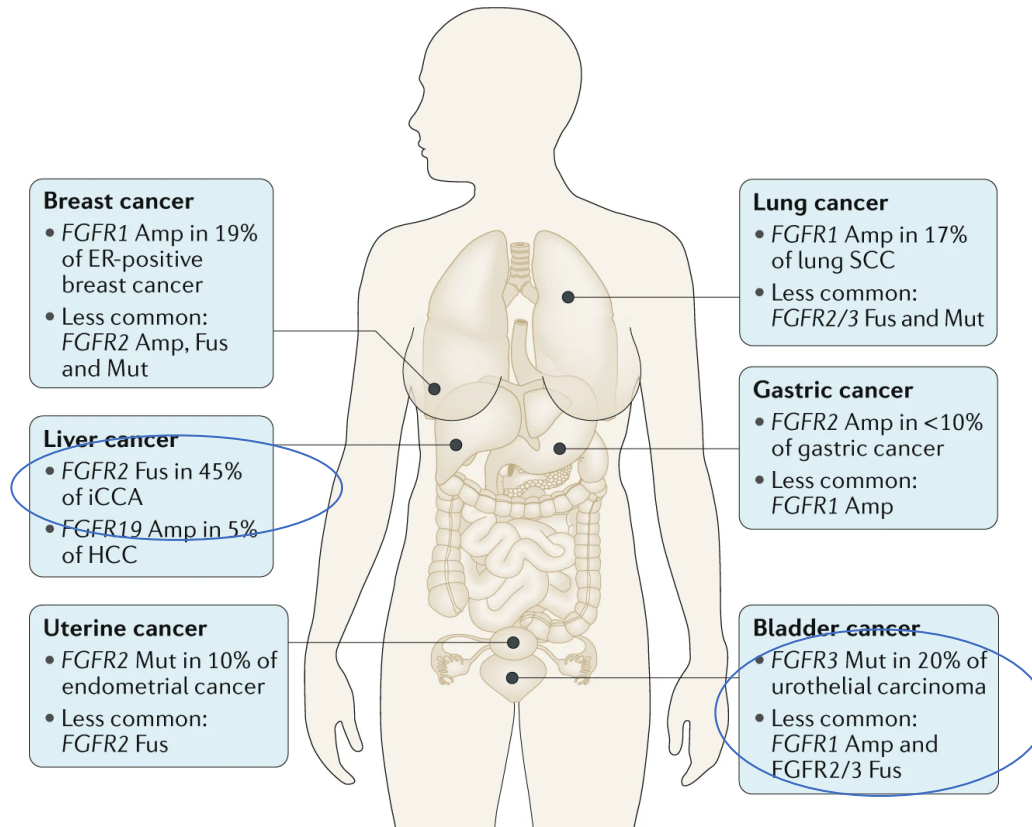


Skoulisdis et al, *Nat Rev Cancer* 2019

# A rise in targetable drivers in other cancer types

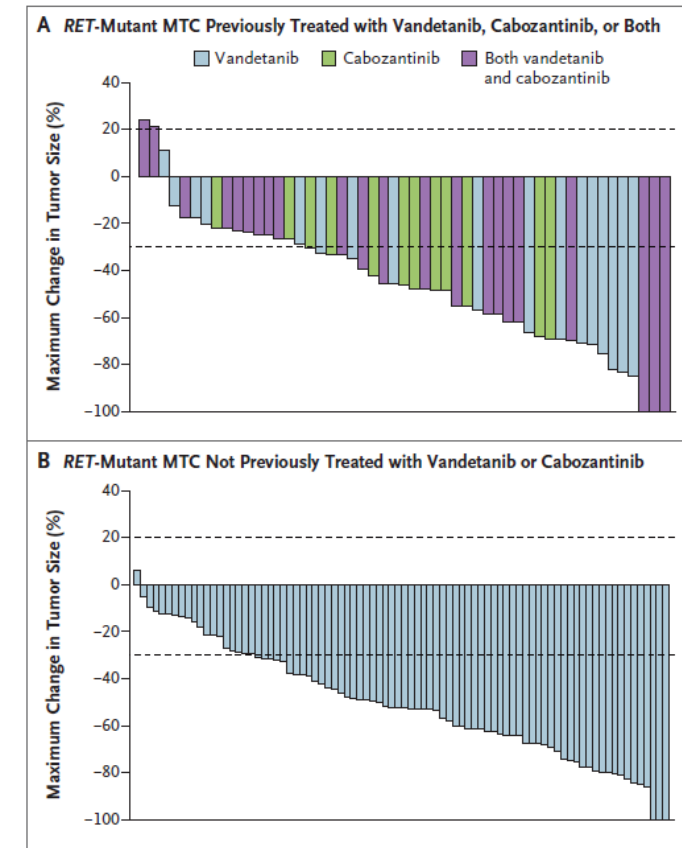
## FGFR-dependent cancers

- Erdafitinib (pan-FGFR): urothelial cancers
- Pemigatinib (FGFR1-3): cholangiocarcinoma



## RET-dependent cancers

- Selitrectinib: *RET*-mutant medullary thyroid cancers
- Pralsetinib: *RET* fusion-positive lung cancers





# TRK inhibitors approved in a tumor-agnostic fashion for adult and pediatric cancers with *NTRK* fusions

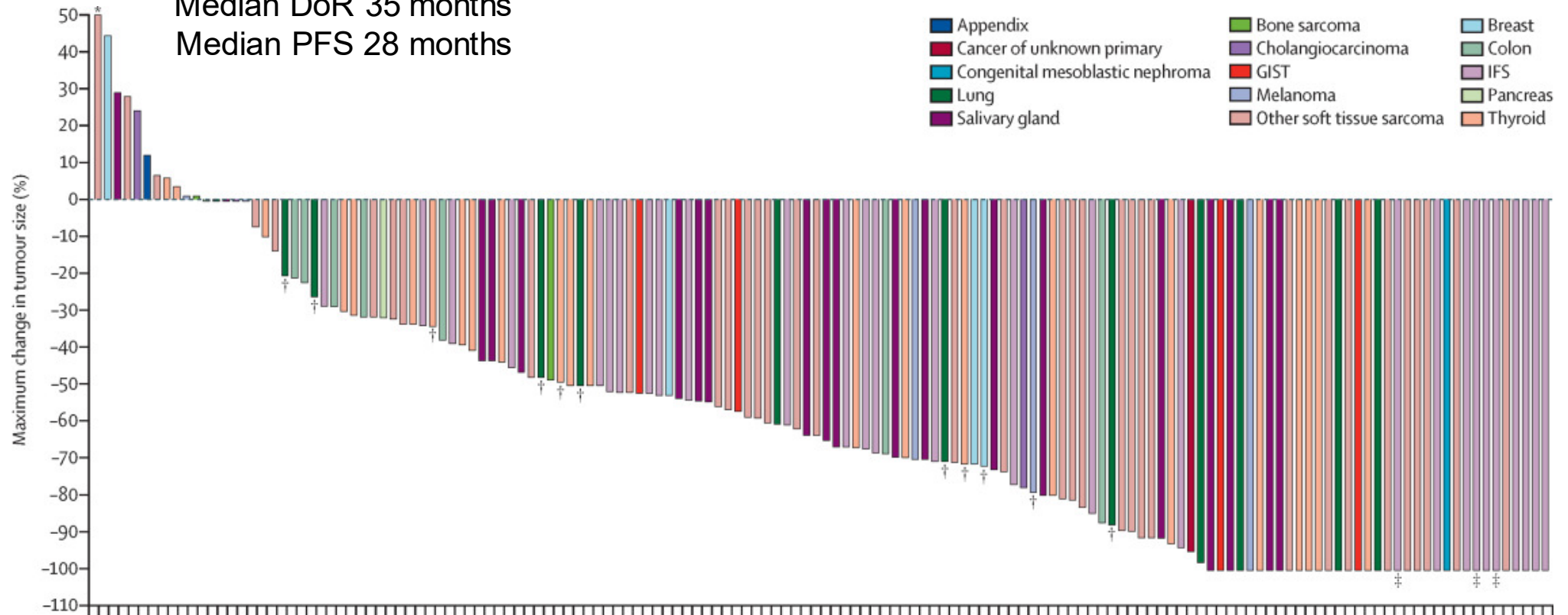
## Larotrectinib

ORR 79%

(95% CI 72-85%, n=159)

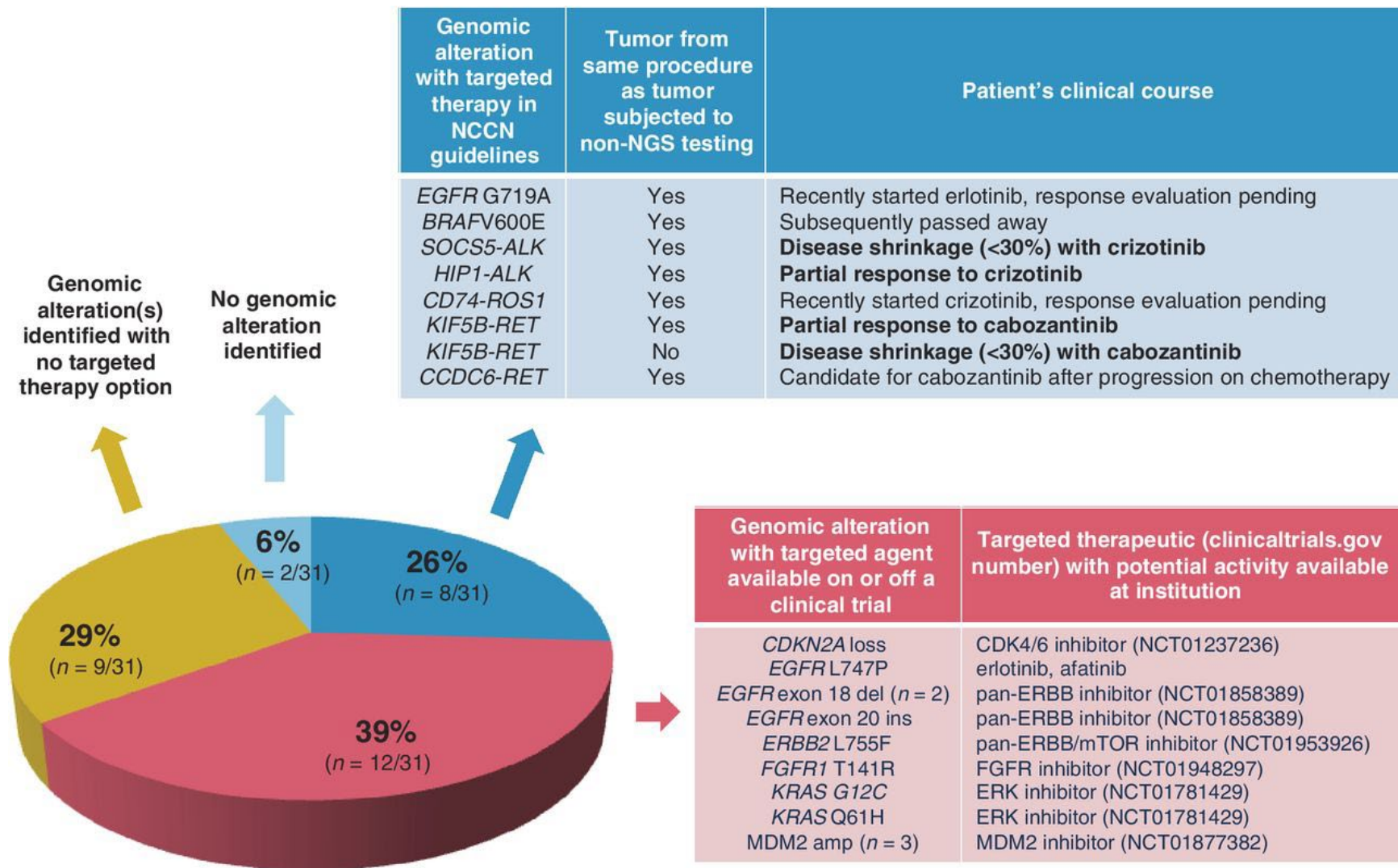
Median DoR 35 months

Median PFS 28 months



**Diagnostic migration toward increasingly  
comprehensive sequencing approaches**

# Next-gen sequencing identifies clinically relevant alterations missed by “piecemeal” sequencing



# NGS *decreases* care costs compared to smaller panels

- newly diagnosed with mNSCLC → genomic alteration tests compared (*EGFR/ALK/ROS1/BRAF/MET/HER2/RET/NTRK1*)
  - upfront NGS (all alterations tested simultaneously plus *KRAS*)
  - sequential testing (sequence of single-gene tests)
  - exclusionary testing (*KRAS* + sequential testing)
  - hotspot panels (*EGFR/ALK/ROS1/BRAF* tested simultaneously + single-gene tests or NGS for *MET/HER2/RET/NTRK1*)

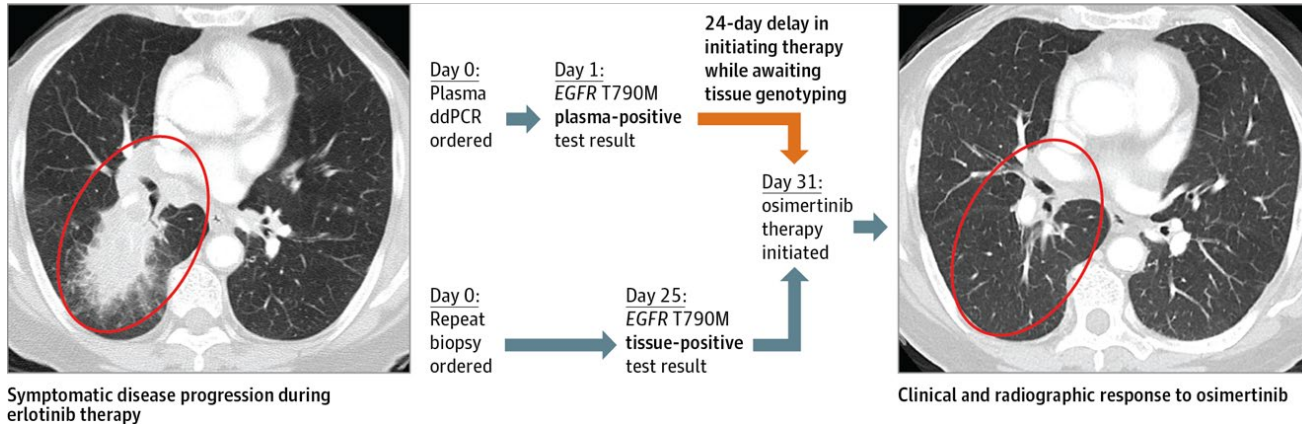
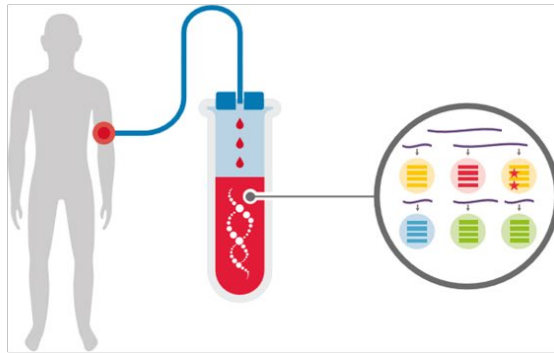
**TABLE 3.** Total Cost and Cost Difference Versus NGS

Testing Strategy	Medicare-Insured Patients (n = 2,066)		Commercially Insured Patients (n = 156)	
	Total Cost	Cost Difference v NGS	Total Cost	Cost Difference v NGS
NGS	2,190,499	—	620,369	—
Sequential	3,721,368	1,530,869	747,771	127,402
Exclusionary	3,584,177	1,393,678	624,178	3,809
Hotspot panel	4,331,295	2,140,795	871,211	250,842

NOTE. Costs are given in 2017 US dollars.

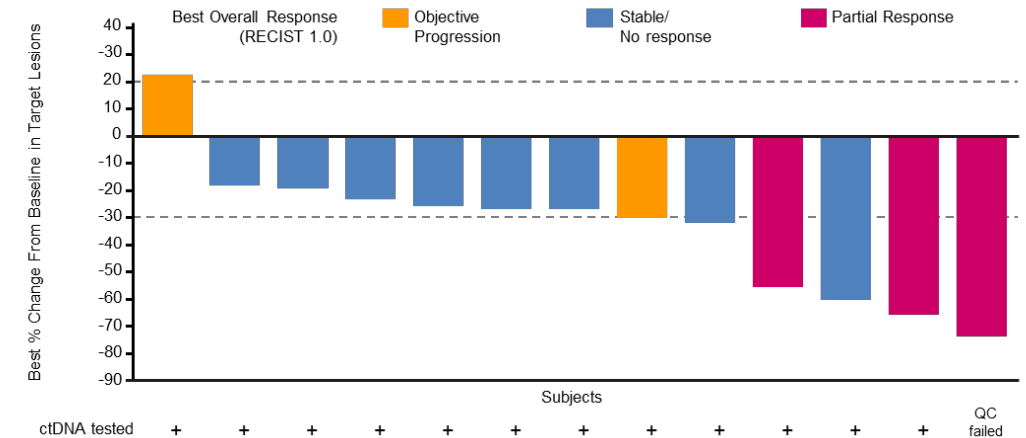
\*although **unit cost** of NGS was higher than individual single-gene tests, **overall cost** (included testing and rebiopsy cost) was the lowest for NGS

# Liquid biopsies complement tumor tissue sequencing and can effectively match patients to therapies

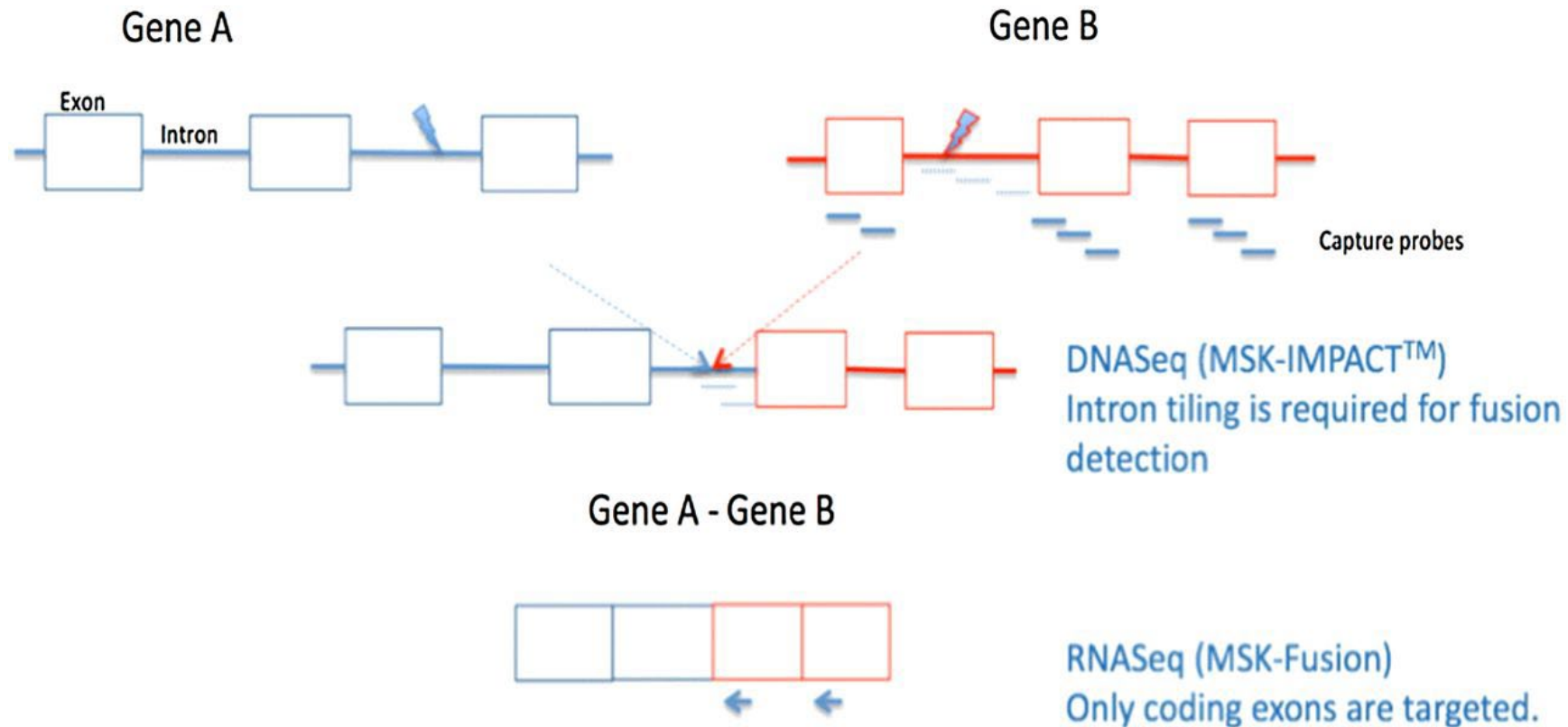


## Crizotinib in *MET* exon 14-altered NSCLCs (ctDNA cohort)

Best Percent Change from Baseline in Size of Target Lesions in ctDNA Cohort in Patients with Measurable Disease (n=13)\*



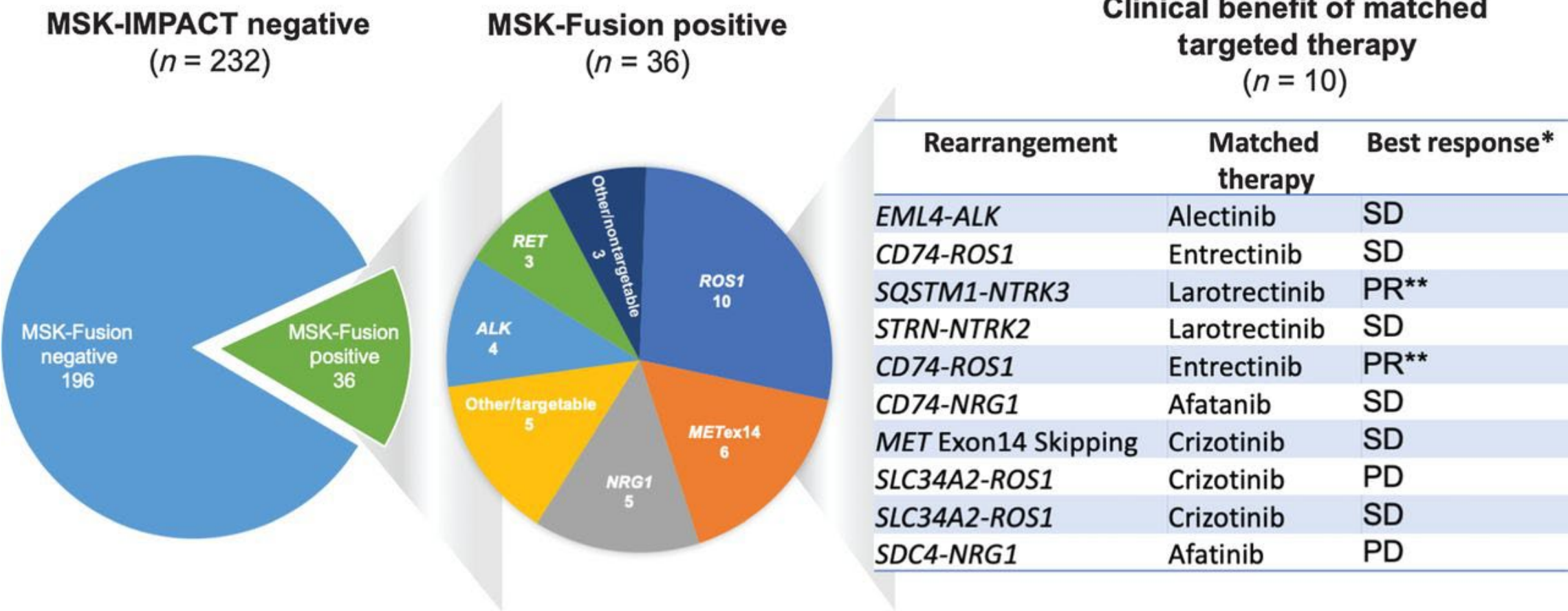
# Fusion detection by DNA vs. RNA-based NGS



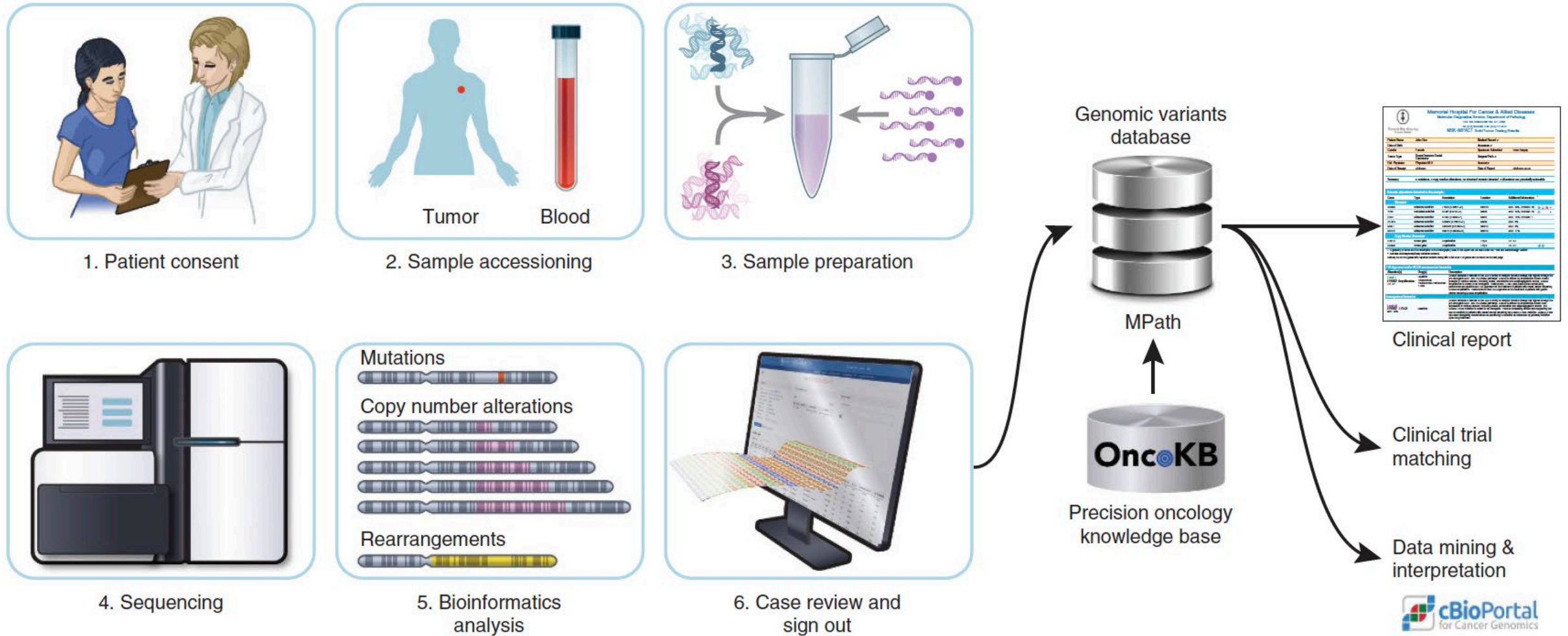
**Large intronic regions** (e.g. *NTRK2* and *NTRK3*) and **repetitive elements at fusion breakpoints** (e.g. *ROS1*) make even the best DNA-based hybrid capture assays suboptimal at capturing all actionable genomic events.



# Patients with drivers identified by RNA matched to therapy



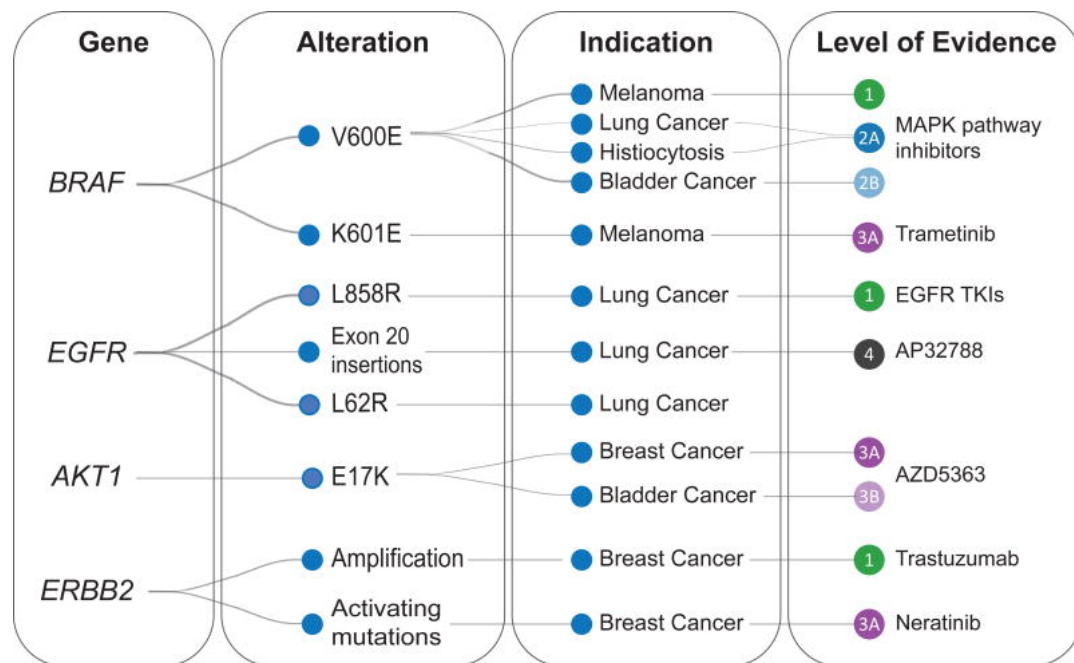
# Clinical workflow at MSKCC



Over 125,000 served!!!

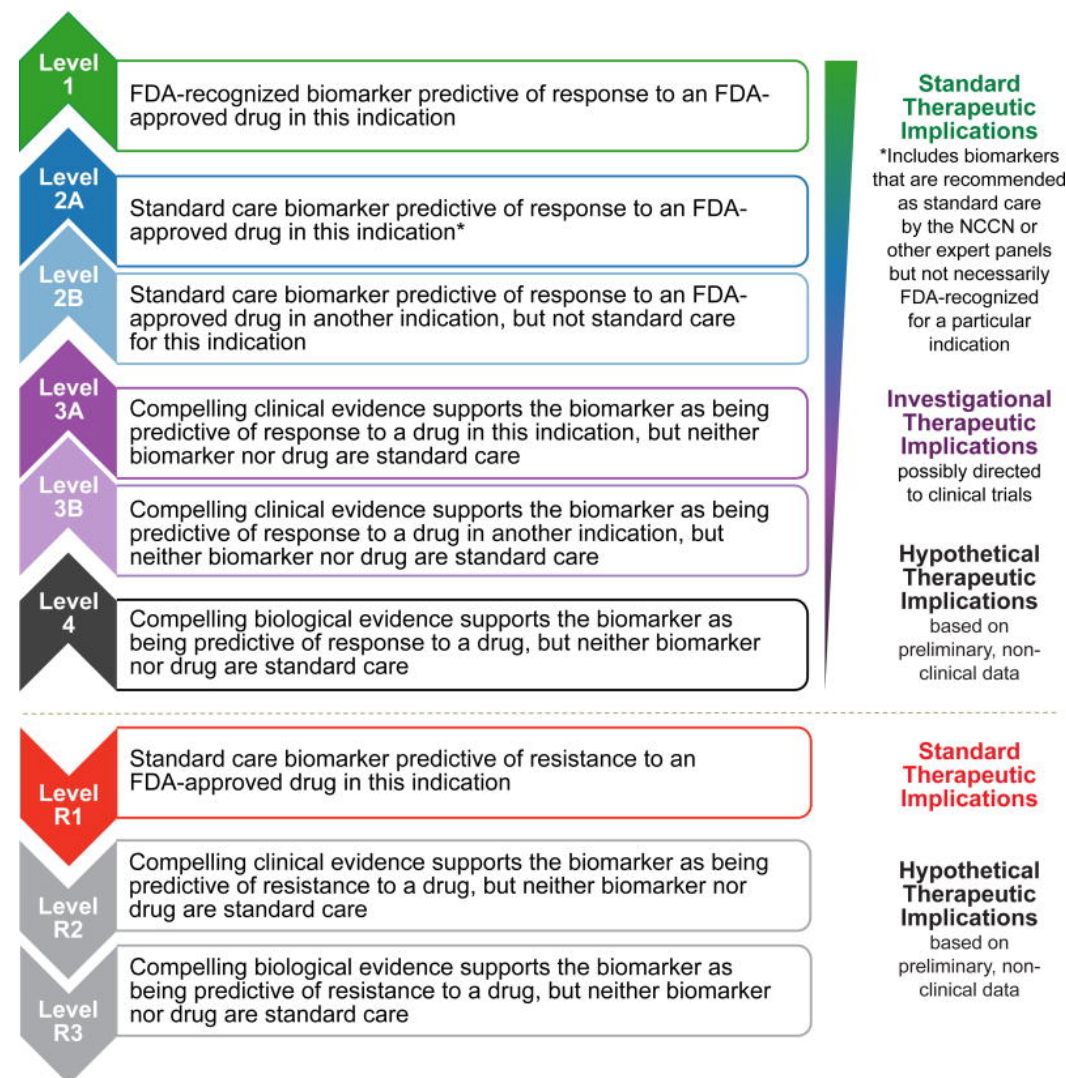


# Alterations filtered through curated database of actionability



**Data sources for clinical genomics annotation committee:**  
variant databases, treatment guidelines, scientific literature, recurrence

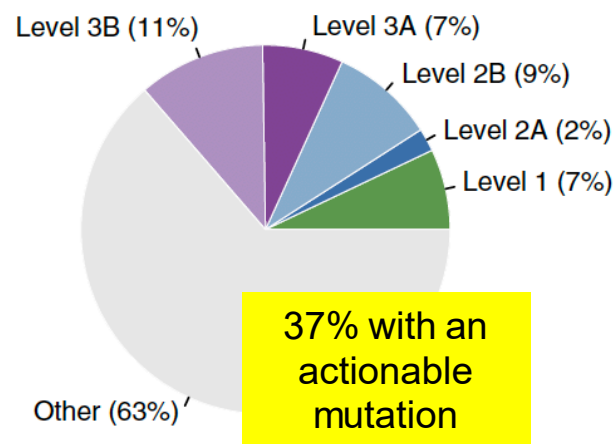
**Posts to:** oncokb.org website, cBioPortal, clinical reports



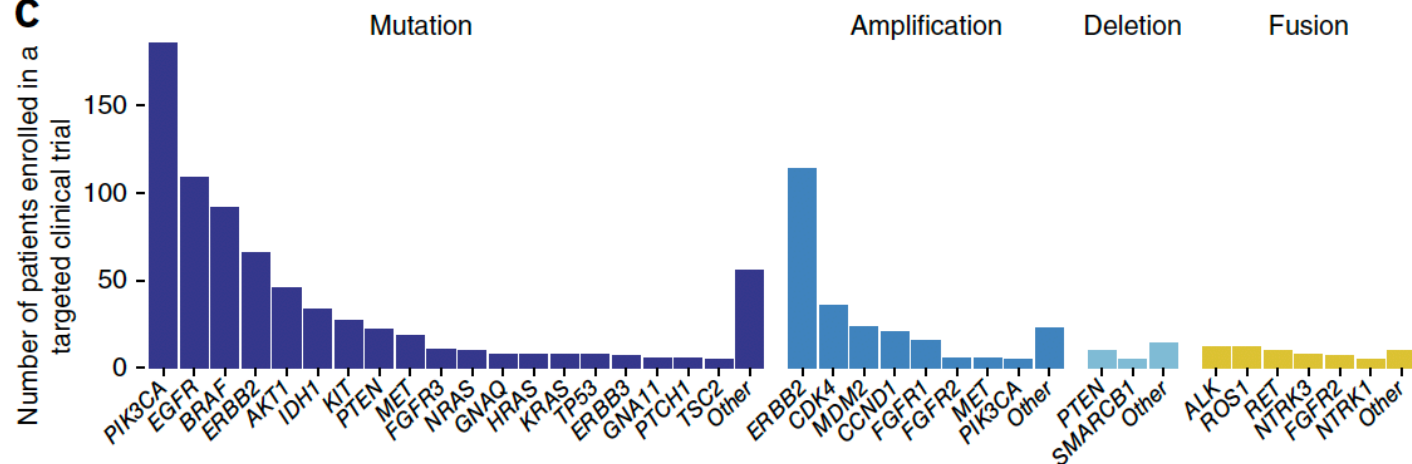
# How has this impacted clinical research and clinical practice?

**a**

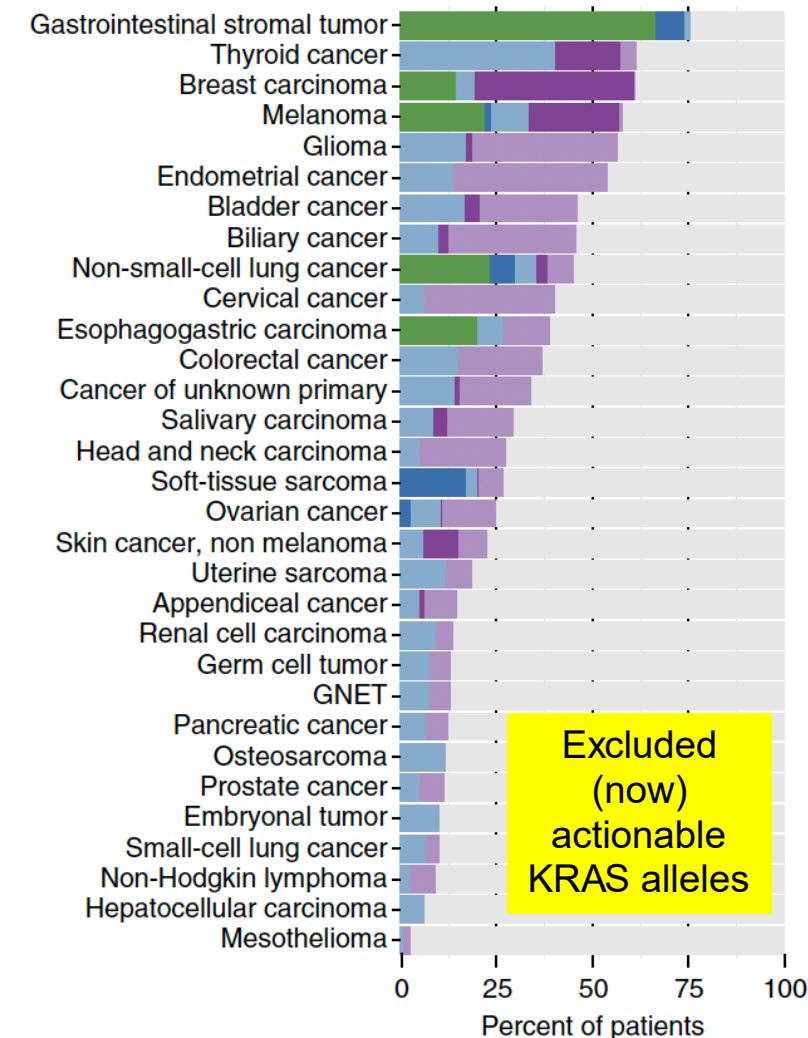
Level 1	FDA-recognized biomarker for an FDA-approved drug in the same indication
Level 2A	Standard of care biomarker for an FDA-approved drug in the same indication
Level 2B	Standard of care biomarker for an FDA-approved drug in another indication
Level 3A	Compelling clinical evidence supporting the biomarker as being predictive of drug response in the same indication
Level 3B	Compelling clinical evidence supporting the biomarker as being predictive of drug response in another indication



**c**

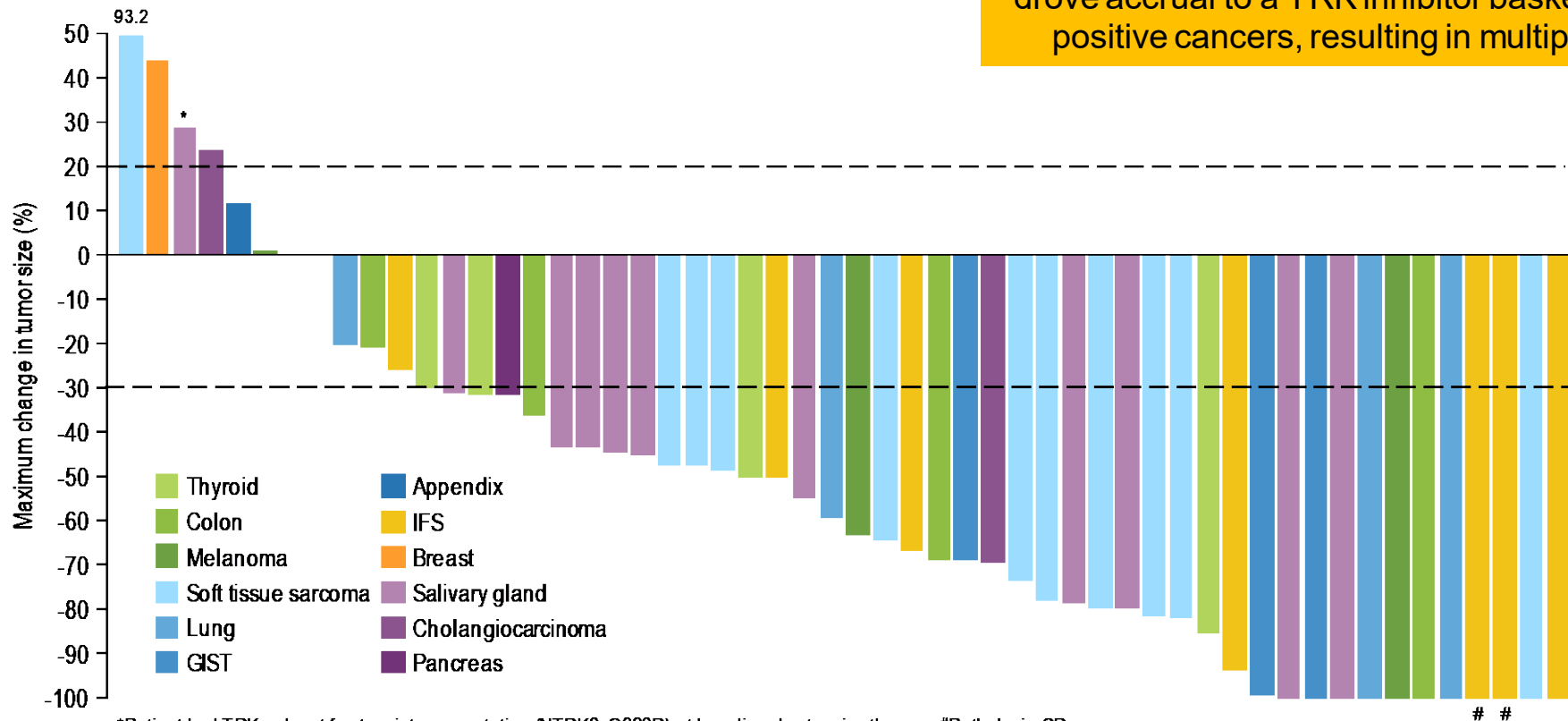


**b**



# Enterprise-scale NGS drives basket trial accrual

**MSK-IMPACT and Darwin Cohort Management System** drove accrual to a TRK inhibitor basket trial for TRK fusion-positive cancers, resulting in multiple global approvals



\*Patient had TRK solvent front resistance mutation (NTRK3 G623R) at baseline due to prior therapy; #Pathologic CR  
Note: One patient not shown here. Patient experienced clinical progression and no post-baseline tumor measurements were recorded.

**Contemporary comprehensive sequencing platforms offer advantages over limited panels**

# NGS detects germline alterations across multiple cancer types

1566 patients with MSK-IMPACT germline sequencing

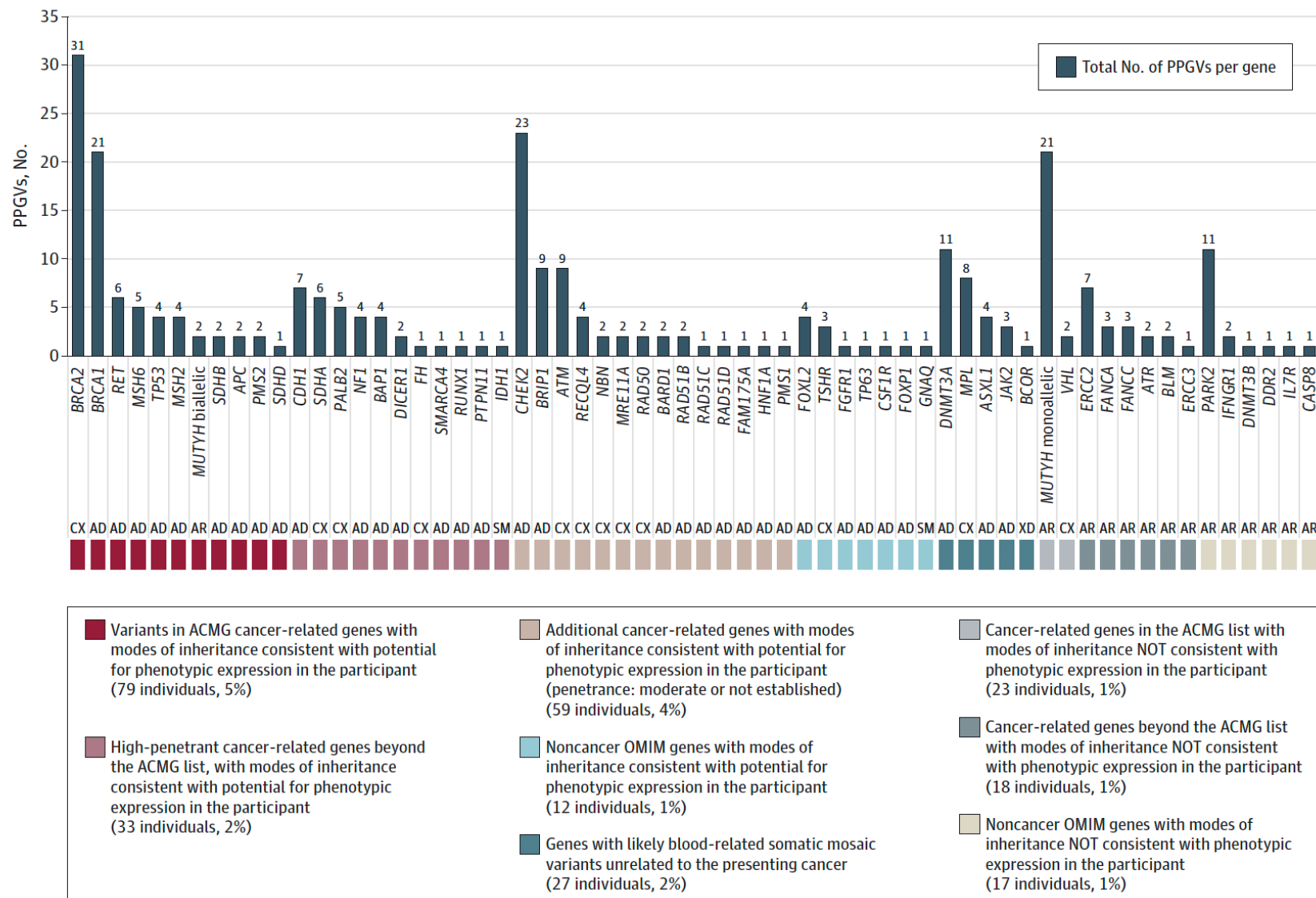
16% with potentially pathogenic germline variant

92% retained in tumor

80% in cancer

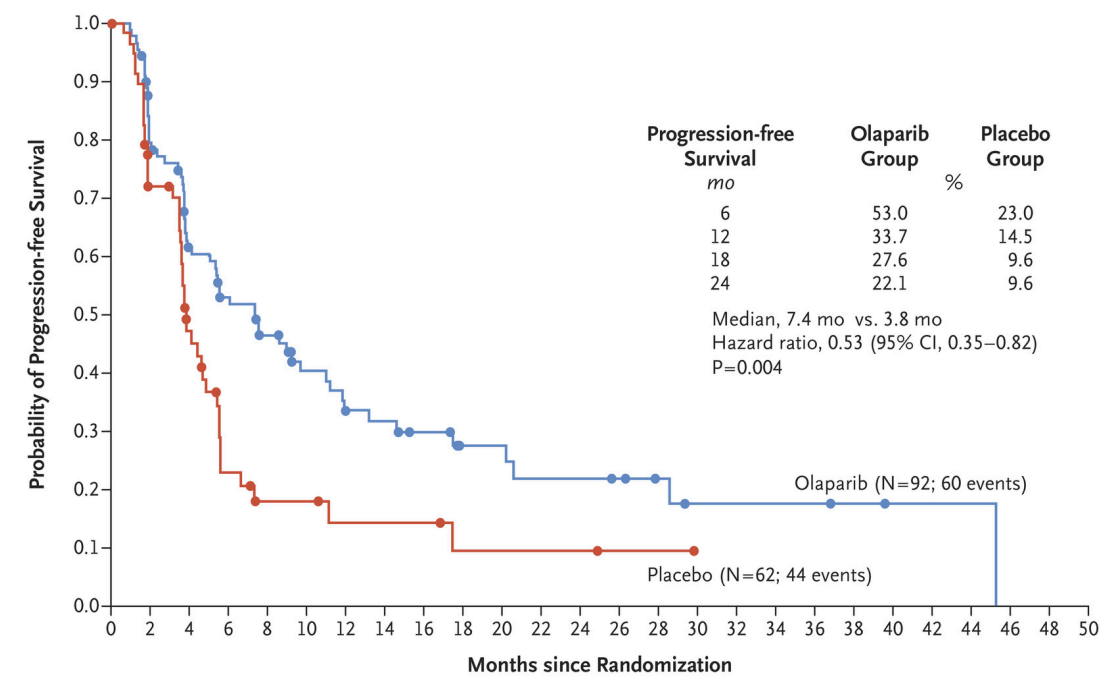
susceptibility genes

5% actionable (e.g. BRCA)

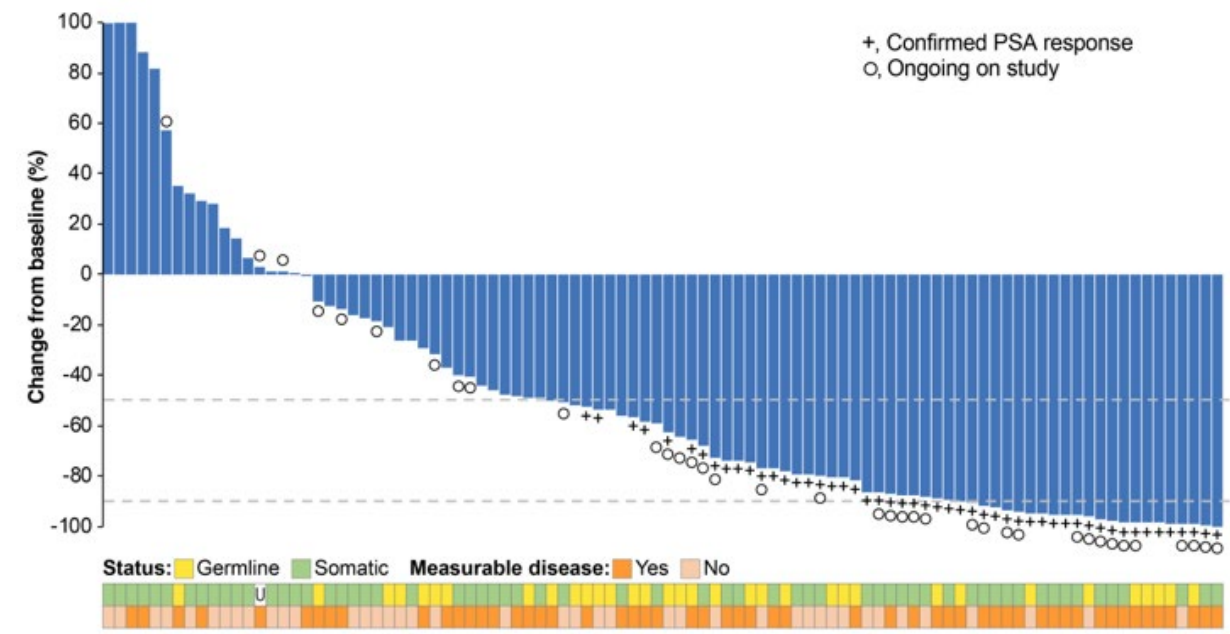


# PARP inhibition in cancers with *BRCA1/2* mutations including germline alterations

**POLO trial**  
olaparib in pancreatic CA



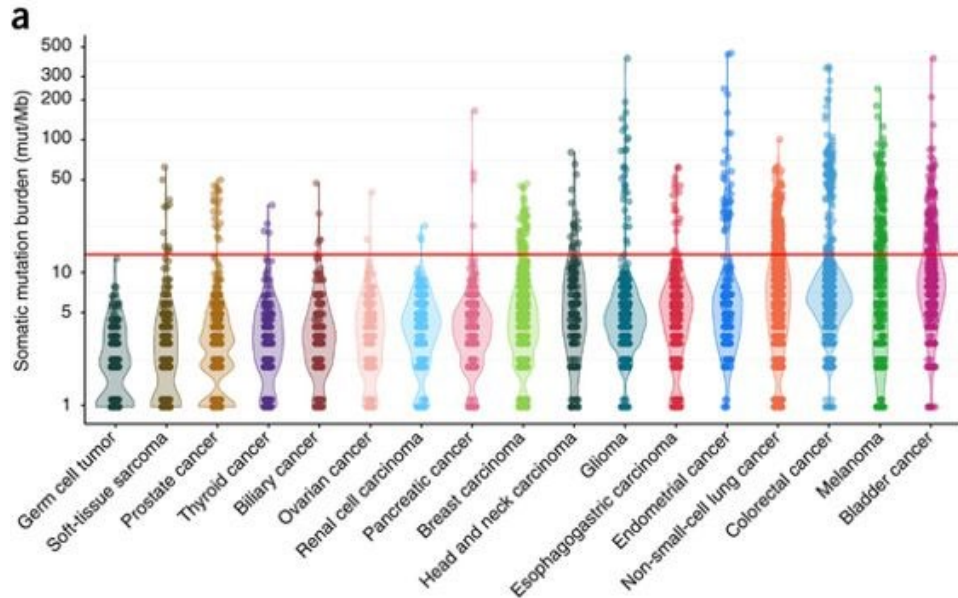
**TRITON2 trial**  
rucaparib in prostate cancer



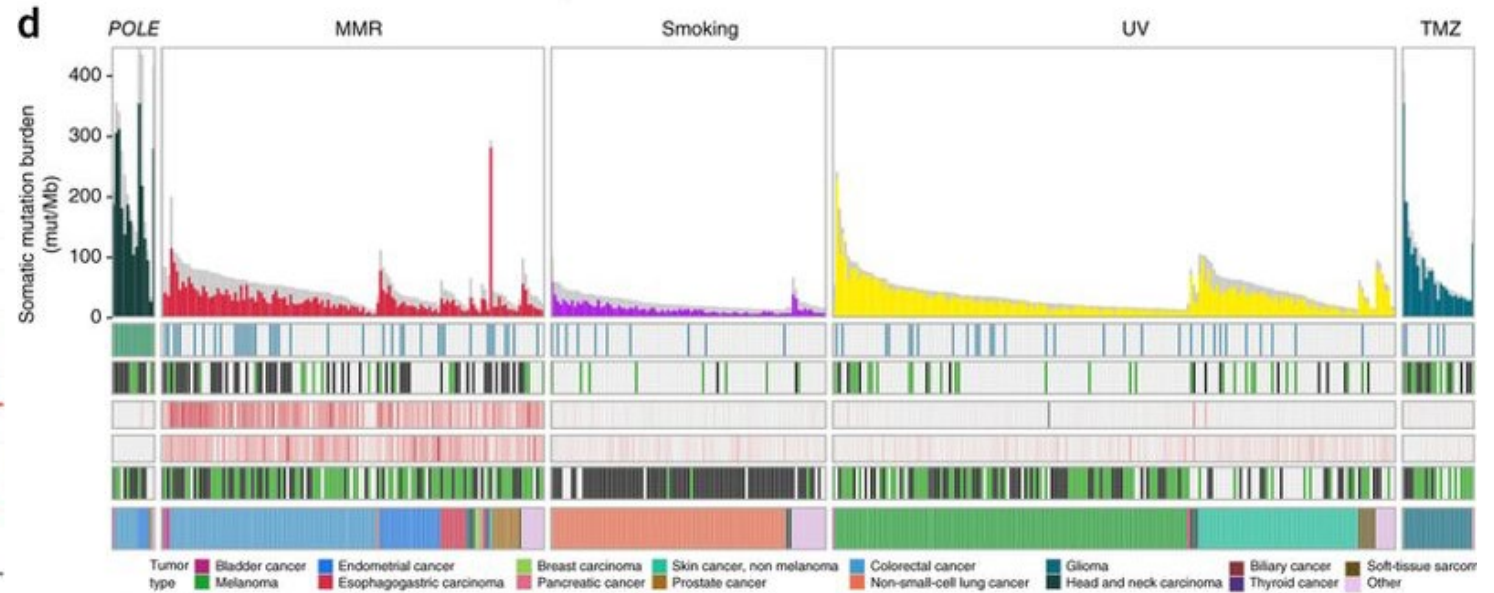


# Genomic signatures of response to immunotherapy can be identified by NGS

Tumor mutational burden calculated across cancer types.



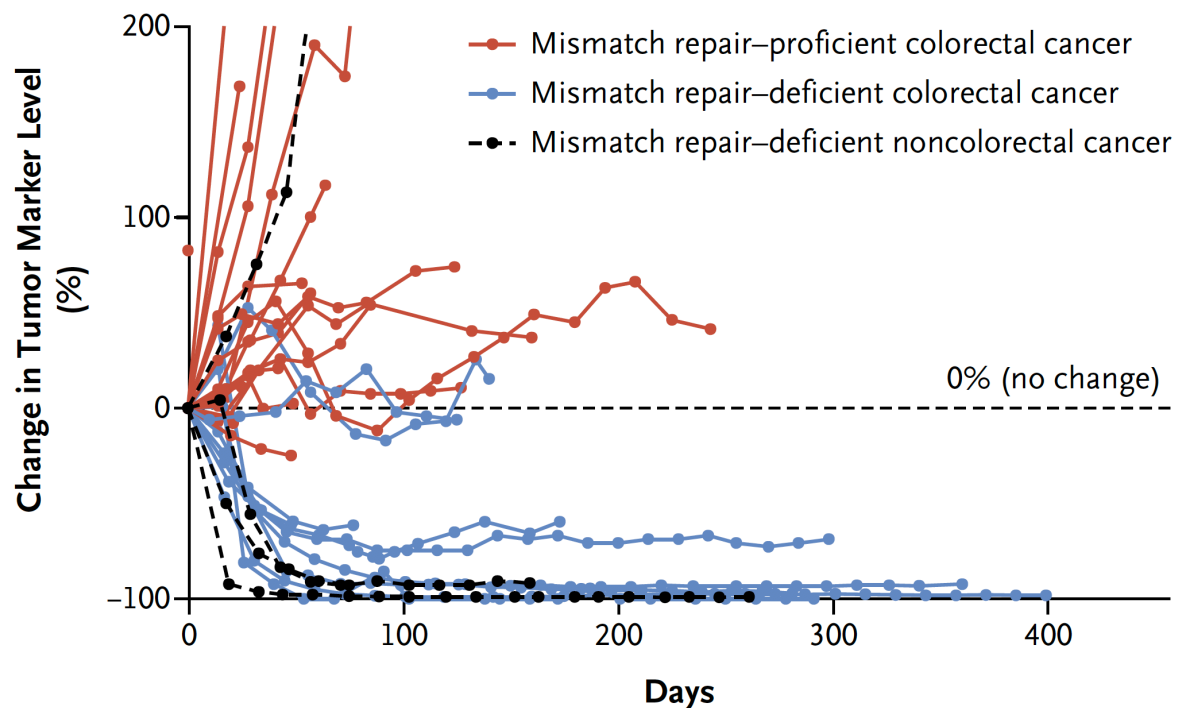
Exogenous mutagen signatures may inform disease etiology



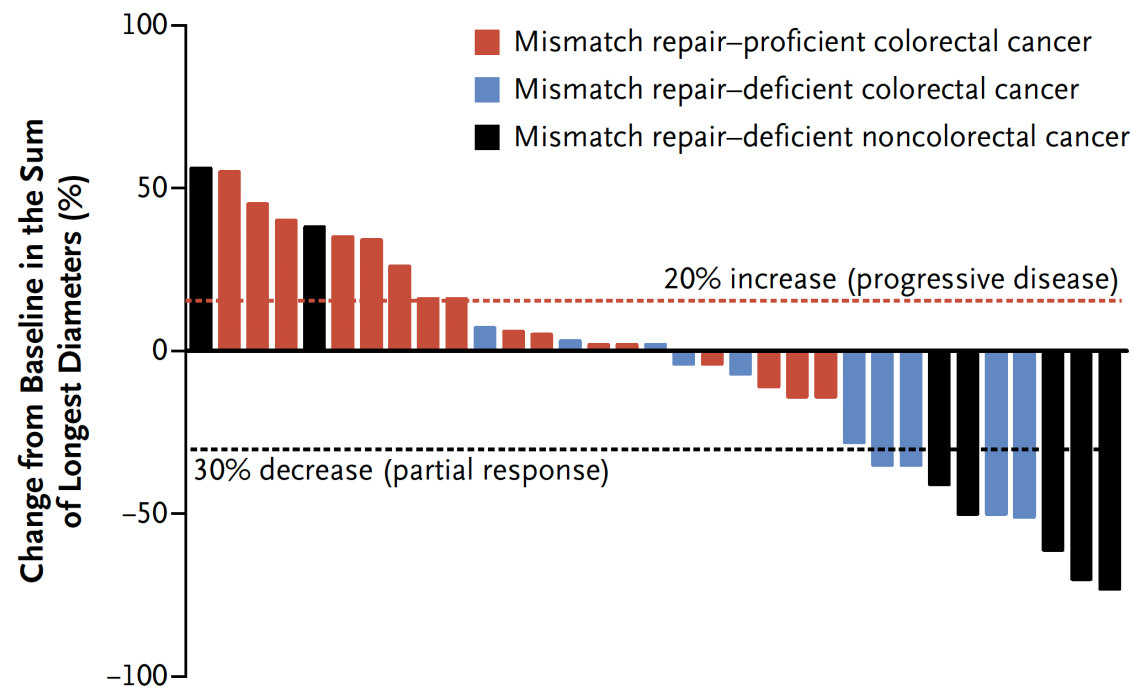
Can detect MSI status, matching MSI-high patients of any cancer type to immunotherapy

# MSI as a predictor of response to immunotherapy

**A Biochemical Response**



**B Radiographic Response**



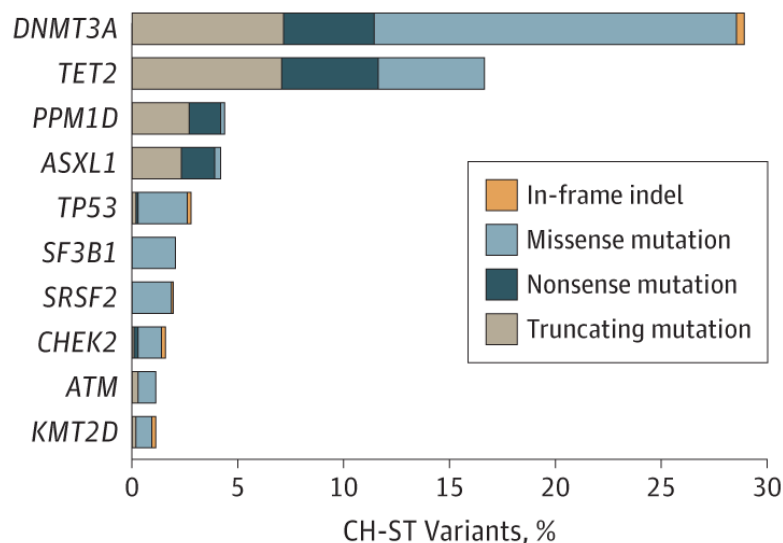


# Clonal hematopoiesis identified in MSK-IMPACT sequencing

17,469 patients: clonal hematopoiesis (CH) interrogated in peripheral blood leukocytes by MSK-IMPACT

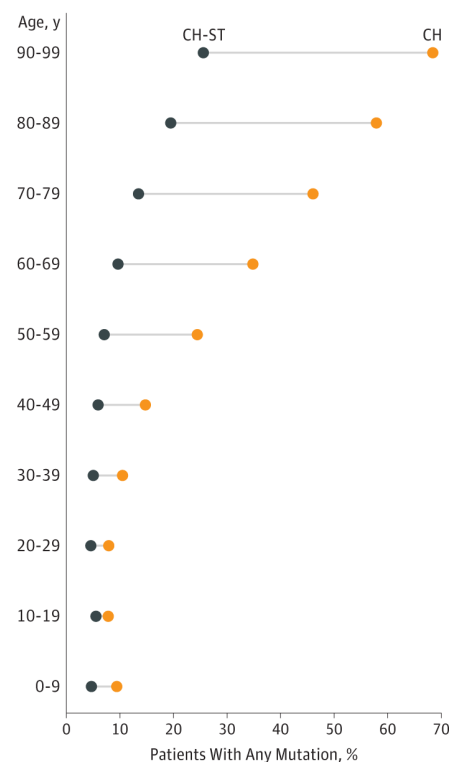
- **26% had CH mutations in blood**

**A** 10 Most frequently altered genes

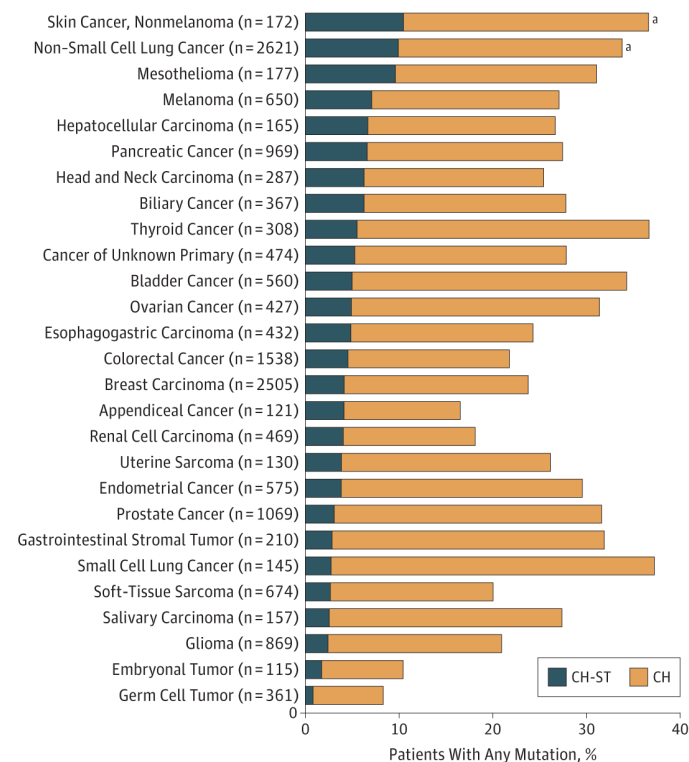


CH mutations increased with age  
Most commonly found in skin cancer and NSCLC.

**A** Frequency by age



**B** Frequency by cancer type



# Clonal hematopoiesis mutations can be categorized as “actionable” and lead to erroneous treatment recommendations

Table. Clonal Hematopoiesis in Solid Tumor Mutations With Treatment Implications Based on OncoKB Database

Sex/Age at Blood Sampling, y	Gene	Amino Acid Change	VAF		Cancer Type	Highest OncoKB Level <sup>a</sup>
			Blood	Tumor		
M/84	<i>BRCA2</i>	Q3156*	0.344	0.118	Melanoma	2B
M/74	<i>IDH2</i>	R140Q	0.405	0.082	Pancreatic	2B
F/72	<i>IDH2</i>	R140Q	0.298	0.063	NSCLC	2B
M/68	<i>IDH2</i>	R140Q	0.162	0.048	NSCLC	2B
M/76	<i>IDH2</i>	R140Q	0.270	0.039	NSCLC	2B
F/59	<i>BRCA1</i>	E1836Q	0.332	0.036	Endometrial	2B
F/74	<i>NRAS</i>	G12R	0.442	0.119	NSCLC	3B
F/80	<i>NRAS</i>	G12V	0.081	0.037	Uterine sarcoma	3B
F/83	<i>IDH1</i>	R132H	0.077	0.033	Melanoma	3B
F/70	<i>IDH1</i>	R132C	0.048	0.022	Melanoma	3B
M/43	<i>PTEN</i>	D24G	0.348	0.174	Colorectal	4
F/50	<i>NF1</i>	R2616*	0.237	0.095	Breast carcinoma	4
M/68	<i>KRAS</i>	G60D	0.297	0.094	Prostate	4
M/55	<i>NF1</i>	X1554_splice	0.105	0.049	Melanoma	4
M/79	<i>NF1</i>	F256Lfs*	0.141	0.043	Prostate	4
M/78	<i>KRAS</i>	A146P	0.132	0.035	Skin cancer, nonmelanoma	4
F/77	<i>KRAS</i>	G12R	0.087	0.041	Colorectal	R1

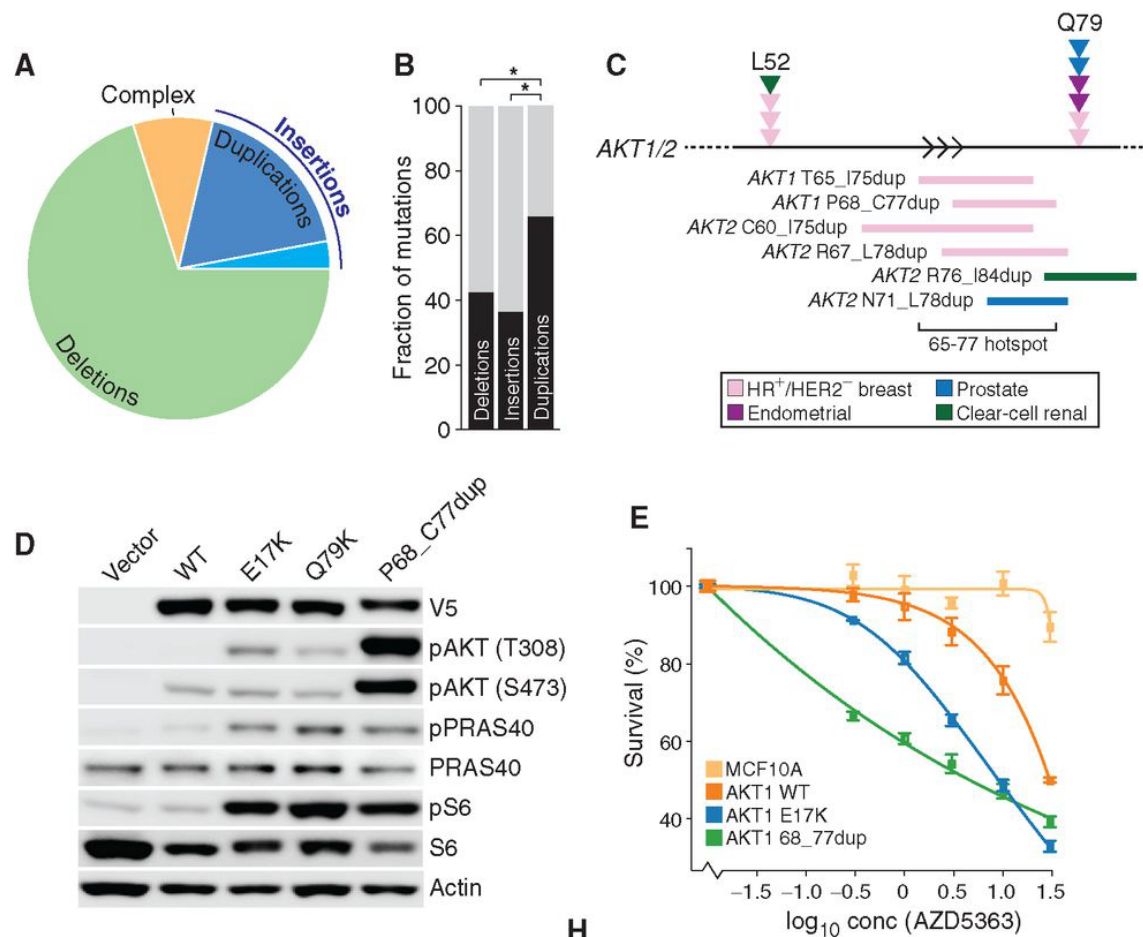
**Next gen sequencing drives discovery science**

# Comprehensive NGS assays drive discovery

Unbiased discovery of recurrent oncogenic indels from population-scale data

## Variants of unknown significance (VUS)

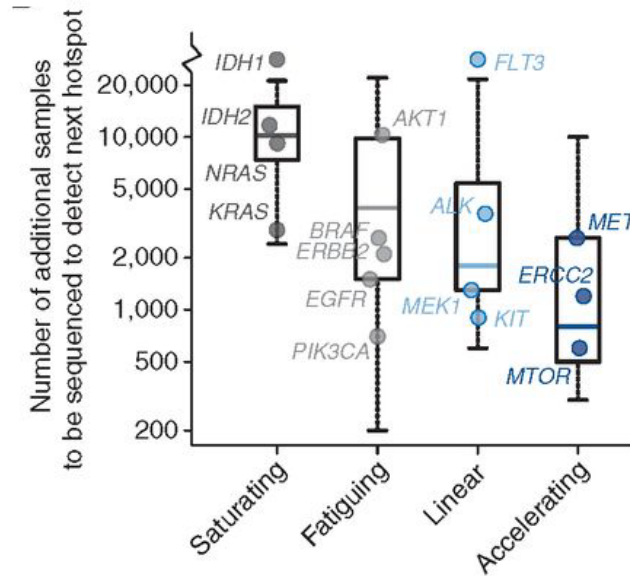
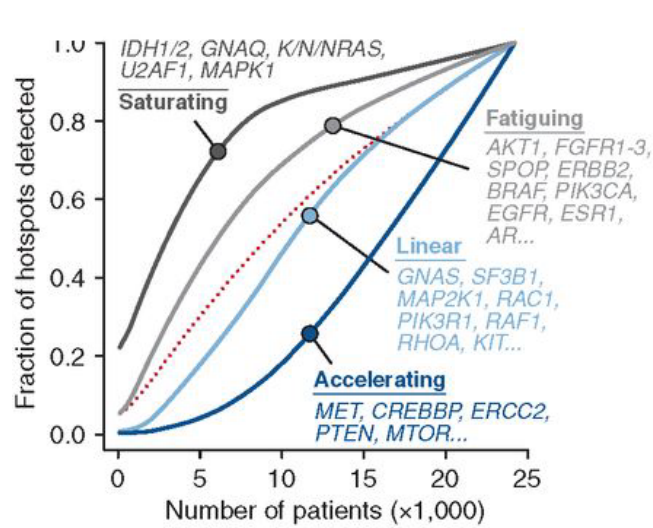
- Some may be clinically actionable.
- Laboratory validation can take years.
- Computational weight of evidence can be used to identify potentially oncogenic variants.



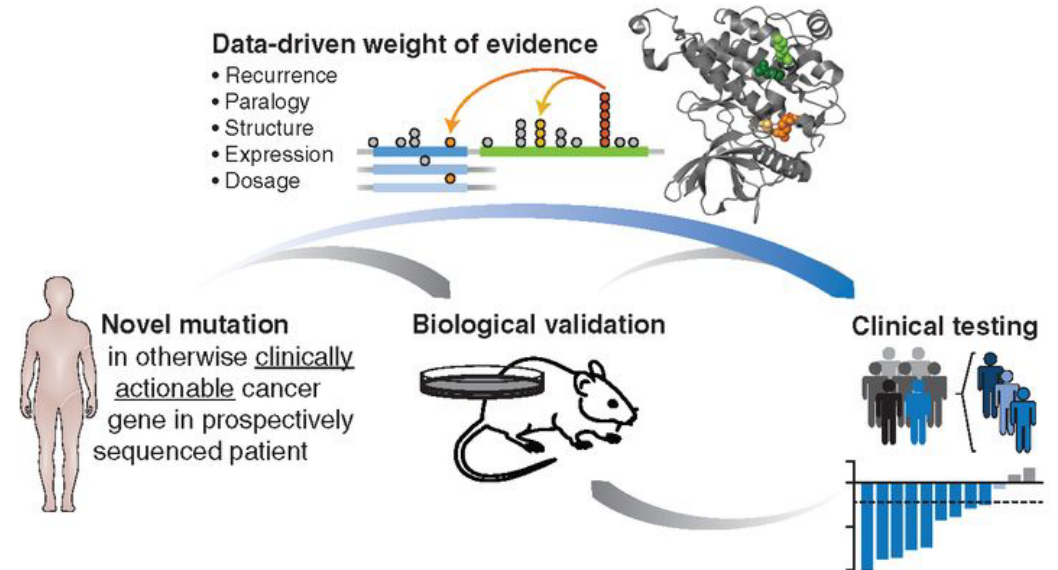
- Duplications more commonly occurred in oncogenes
- Paralogous AKT 1/2 hotspot duplications identified.
- **AKT1/2 duplications found to be oncogenic**
  - downstream signaling more active
  - increased sensitivity to AKT inhibitor
  - used to select patients for AKT inhibitor basket trial

# Computational vetting can identify potentially actionable variants

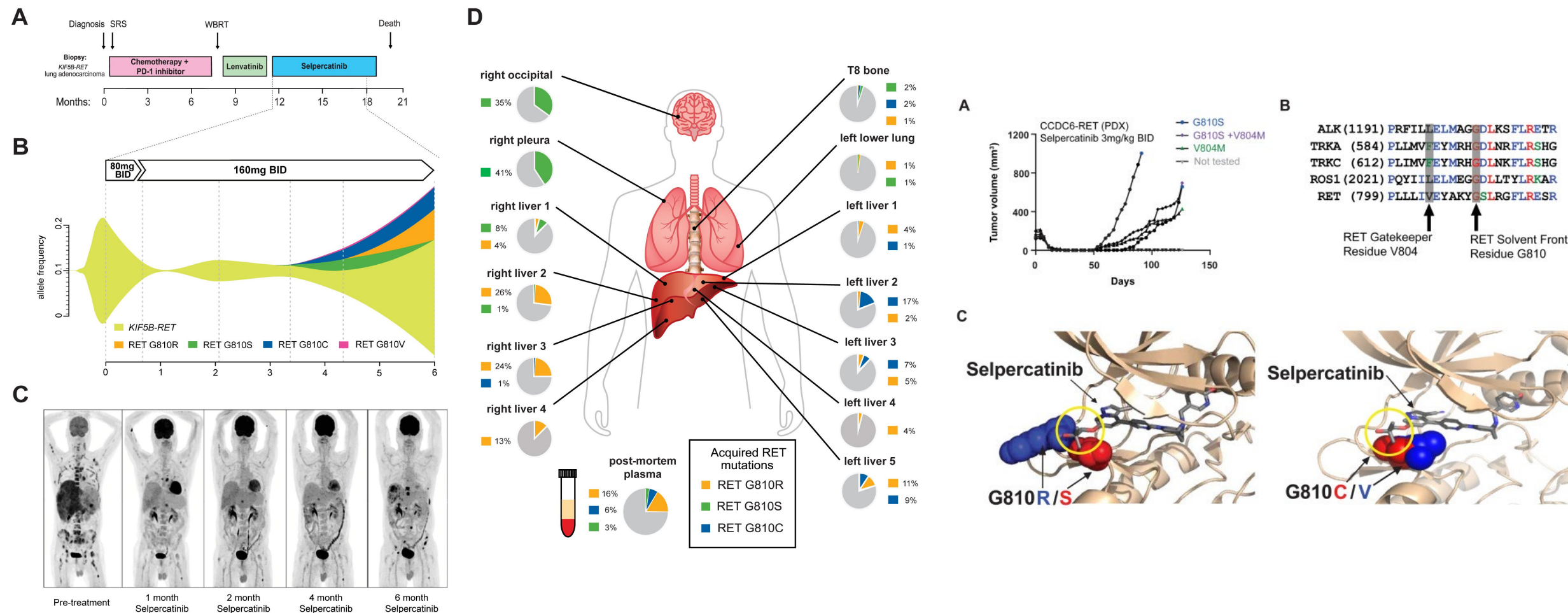
Increased likelihood of hotspot identification the more patient samples are sequenced and analyzed



Using prospective sequencing, computational analyses can nominate select variants for exploration both in the clinic and in the laboratory.

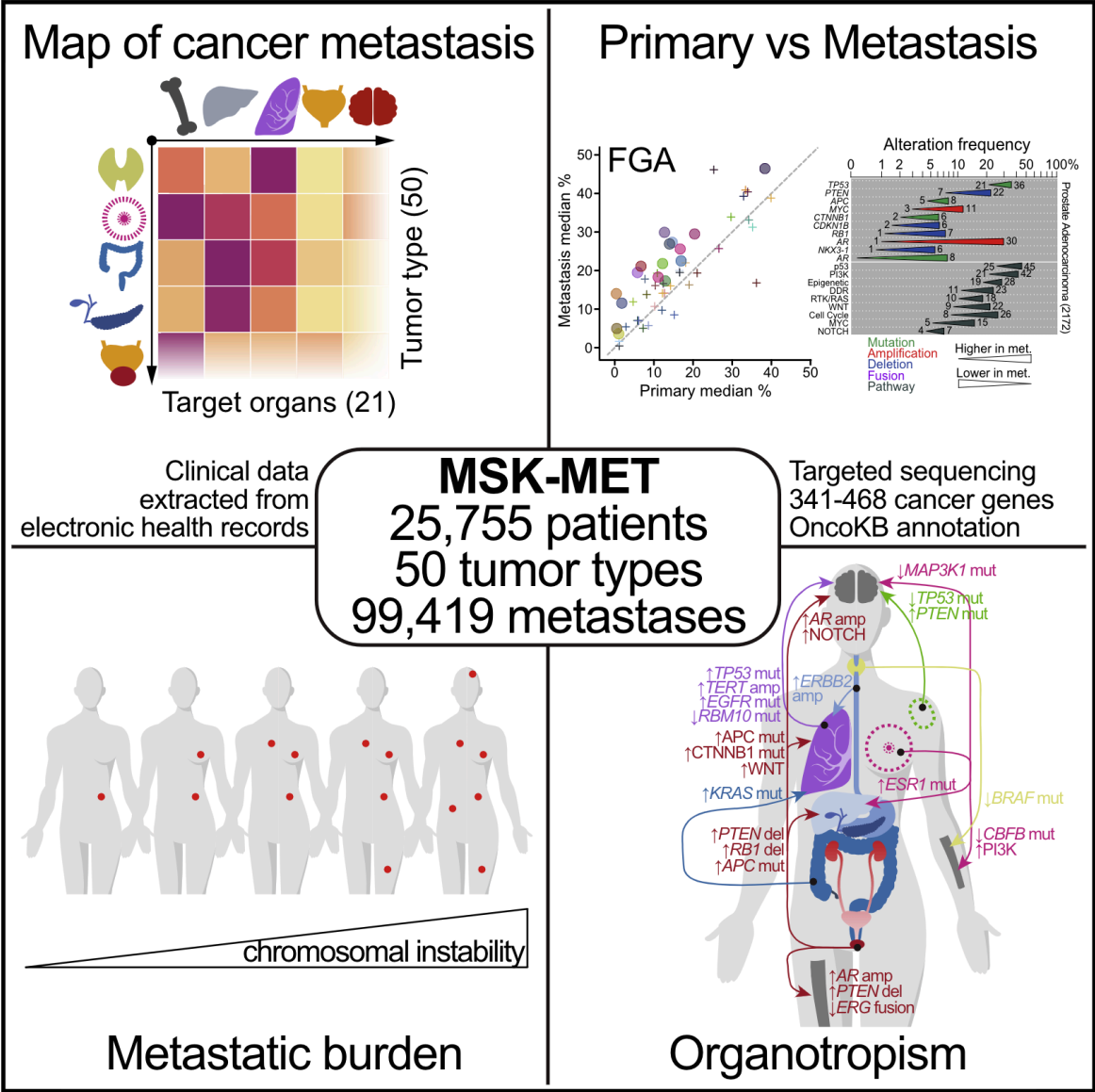


# Sequencing identifies mechanisms of therapeutic resistance





# Genomic profiles of metastatic tropisms



# Summary

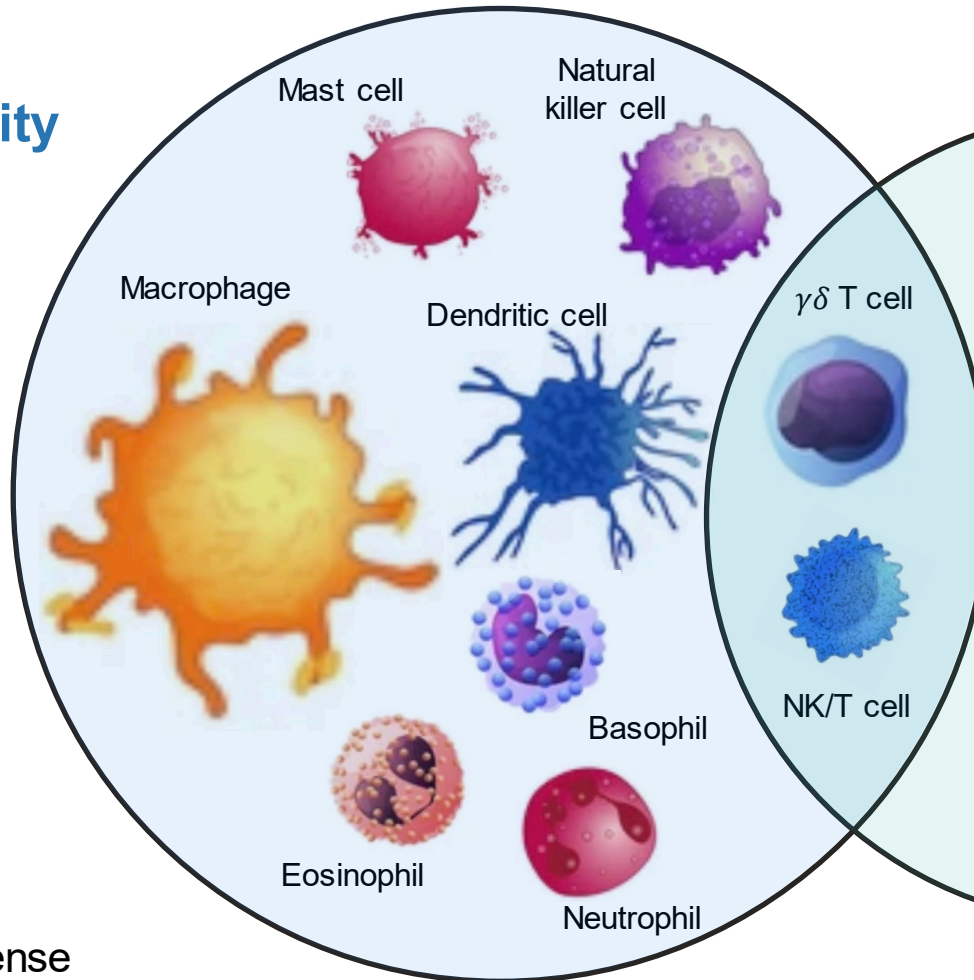
- The list of actionable molecular drivers with approved targeted therapies continues to grow
- Comprehensive DNA/RNA-based cancer sequencing
  - improves the detection of clinically actionable drivers vs older strategies
  - is potentially cost-saving
- NGS assays can also detect
  - potentially pathogenic germline variants
  - clonal hematopoiesis mutations in solid tumors
  - potential immunotherapy biomarkers and other mutational signatures
- NGS assay data can be leveraged to
  - aid driver discovery, capitalizing on computational analyses
  - develop prospectively monitored cohorts that aid therapy matching



**Next gen sequencing and applications to improving immunotherapy**

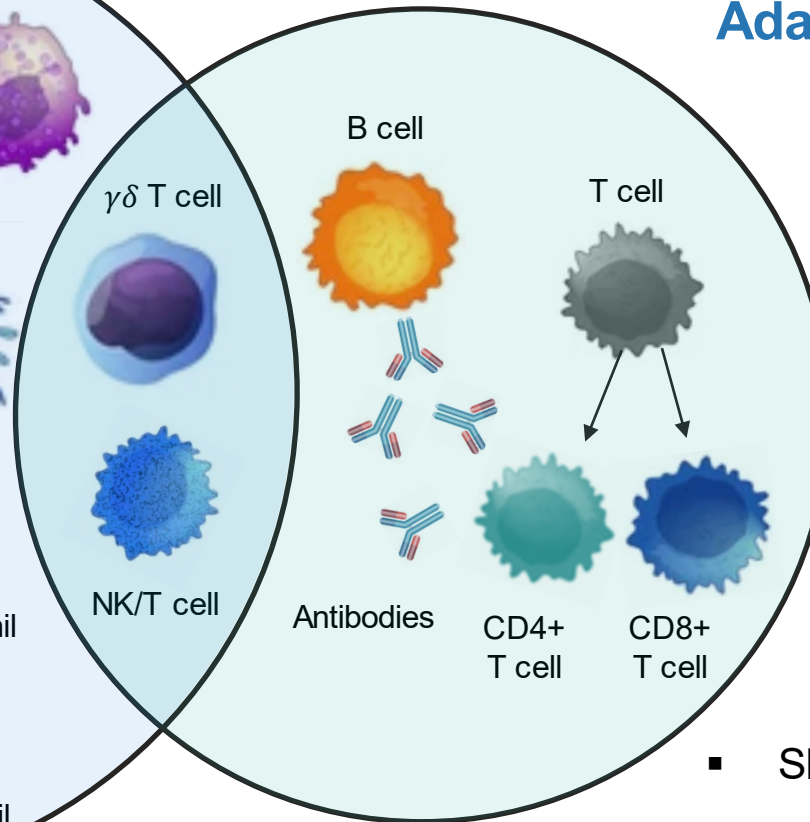
# A broad look at anti-cancer immune effectors

## Innate Immunity



- Nonspecific
- First line of defense
- Can prime activation of adaptive immunity

## Adaptive Immunity

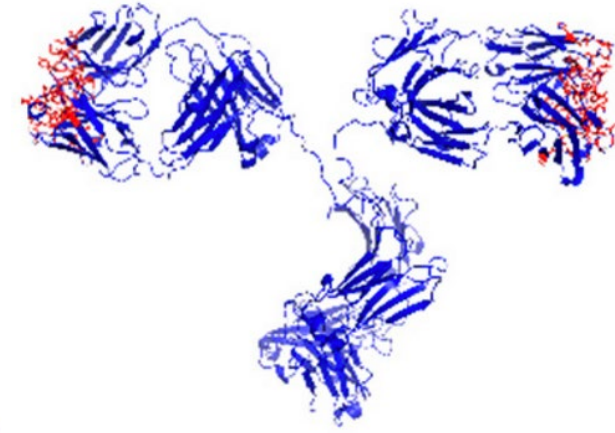


- Slower to develop
- Specific target recognition
- Memory functions
  - Faster, stronger subsequent responses

# Anti-cancer applications of adaptive immunity

## Naked antibodies (or antibody fragments)

- Blocking
- Activating



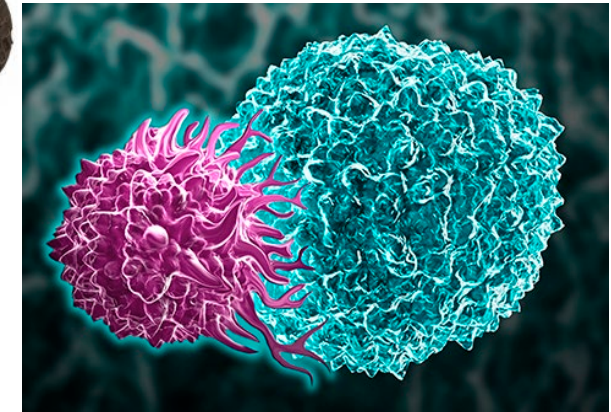
## Trojan horse strategies

- Antibody-drug conjugates
- Radioimmunoconjugates

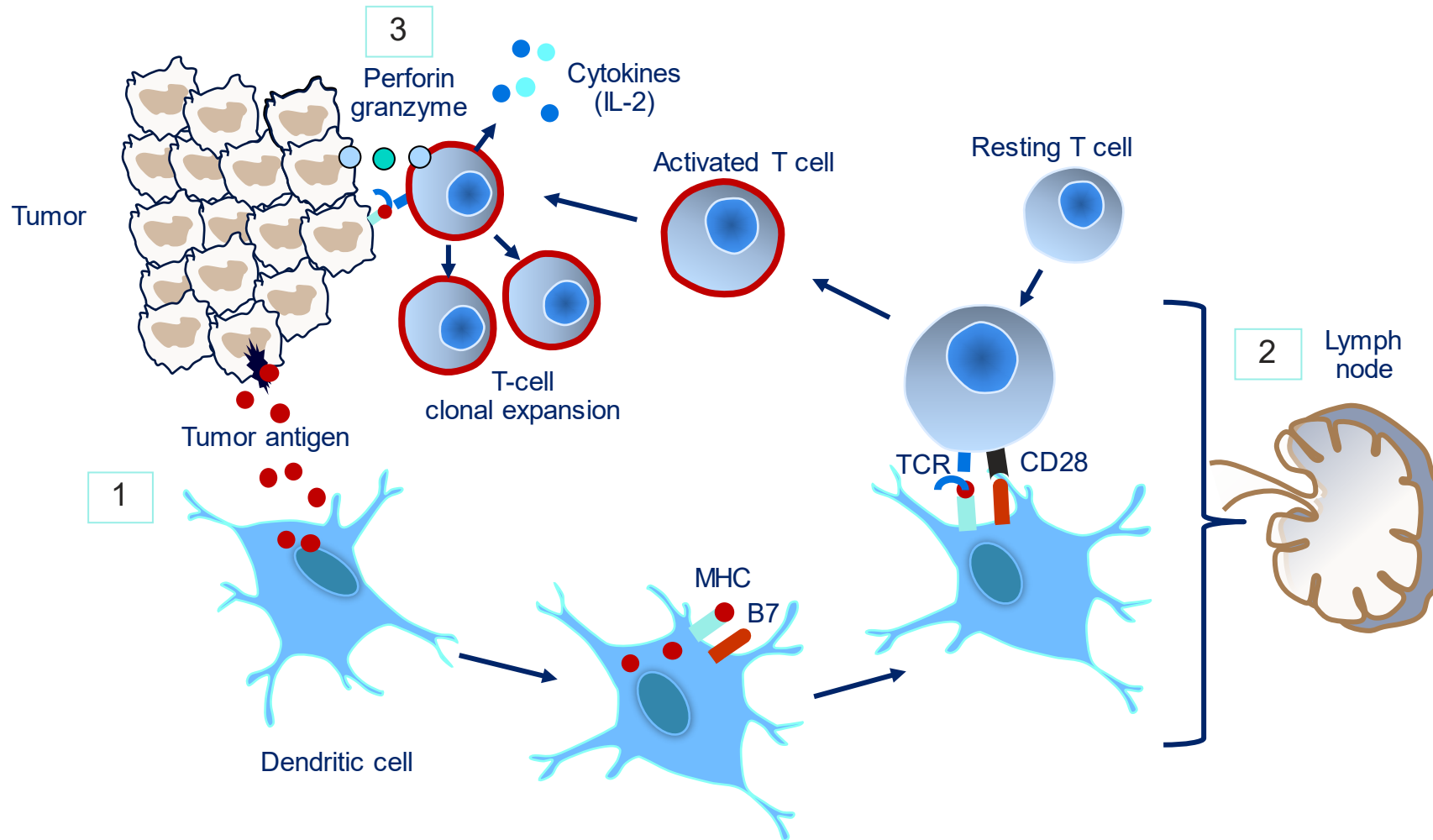


## Cell therapies

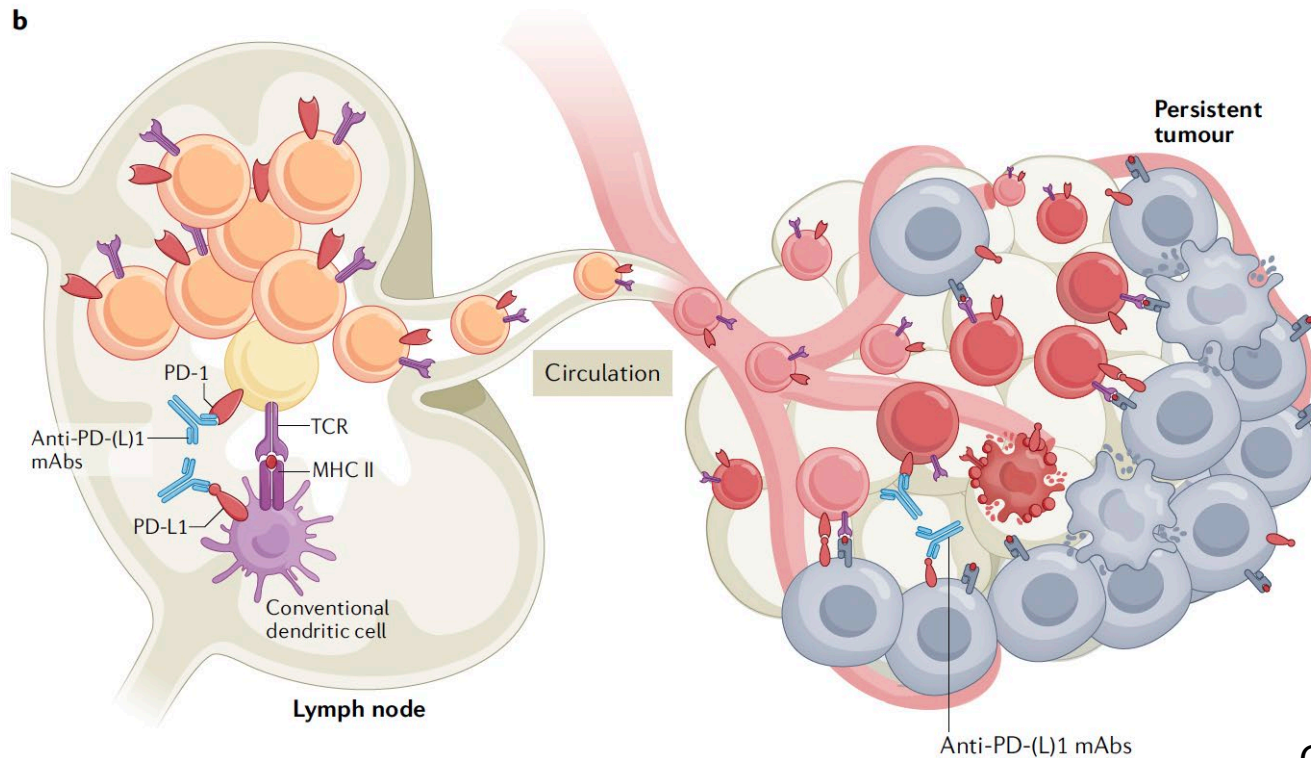
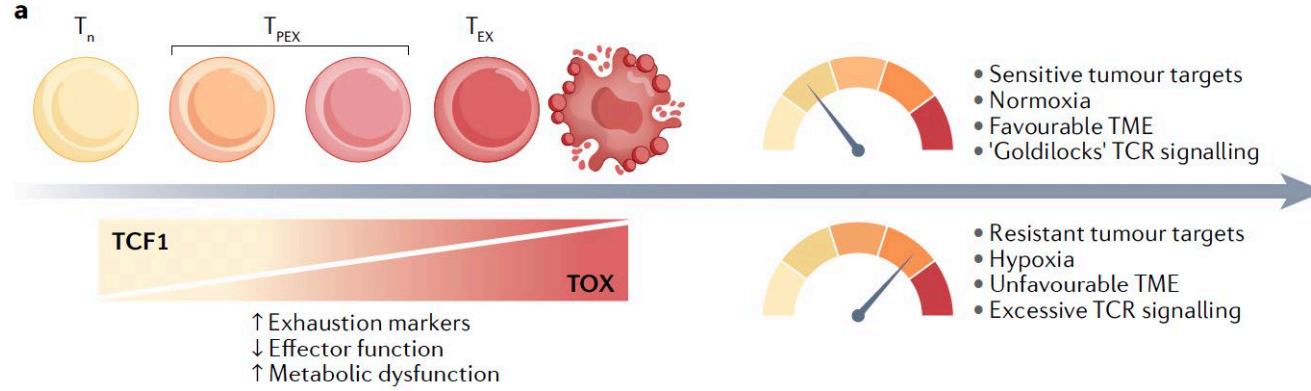
- TIL
- TCR and TCR-like structures
- CAR-Ts



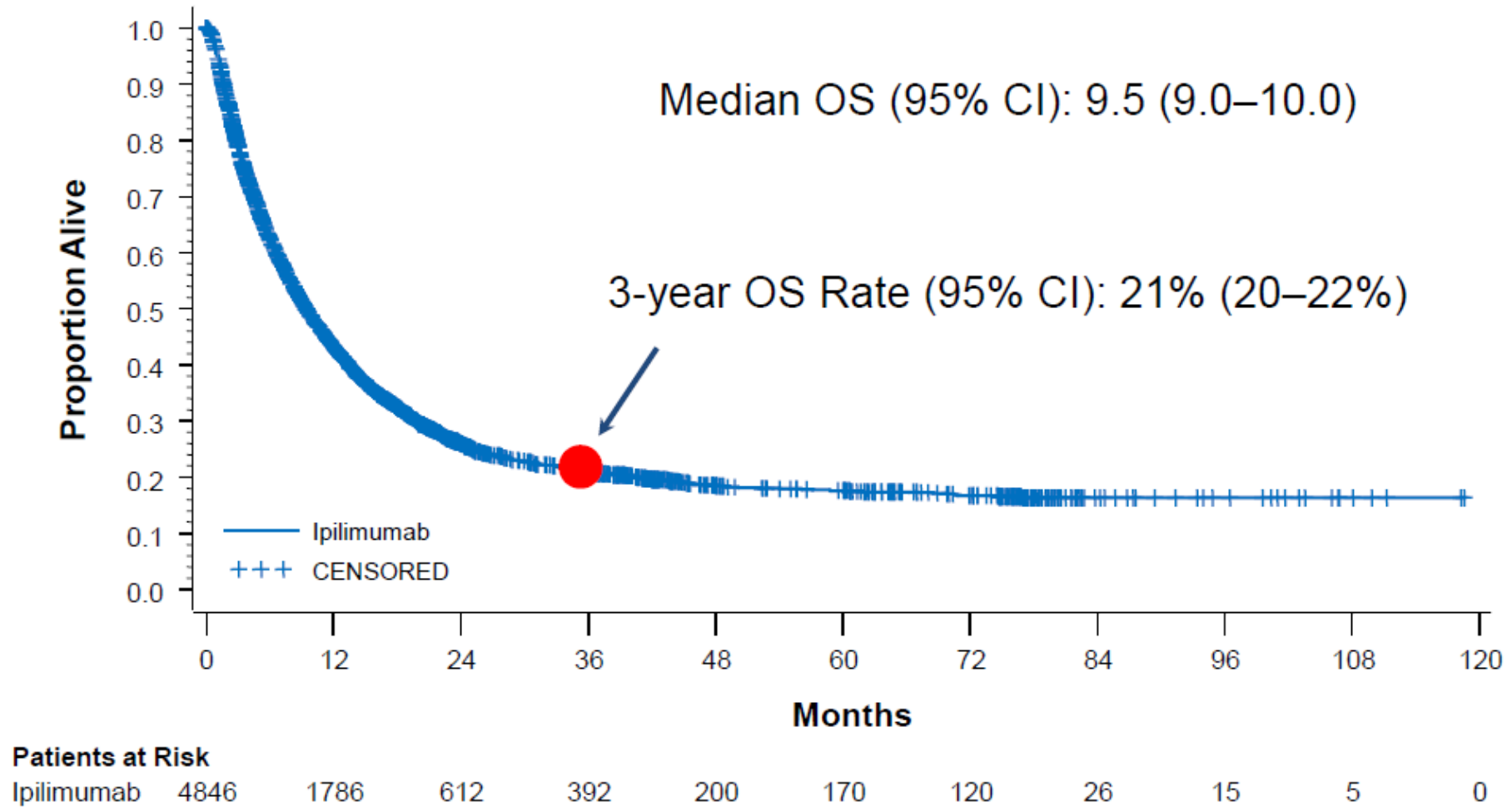
# T cell activation in anti-tumor immunity: an overview



# But is that right? A more nuanced, view

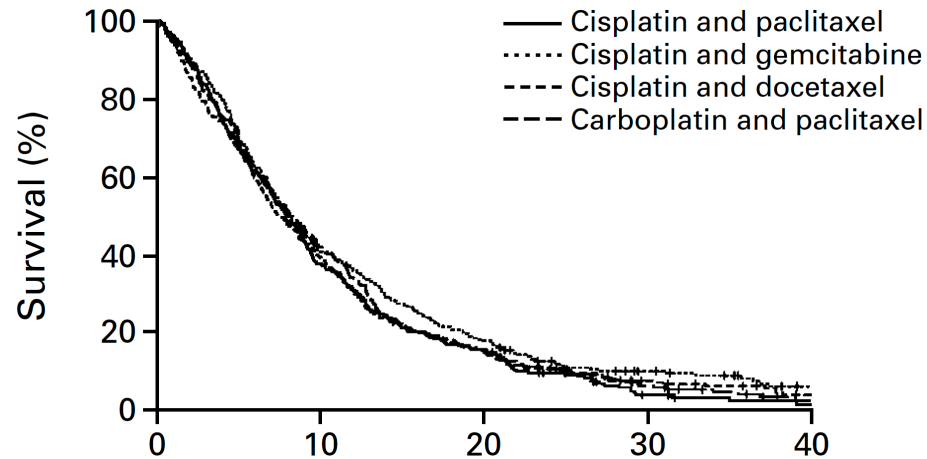


# Metastatic melanoma – ipilimumab





# Non-small cell lung cancer: where we were, where we are

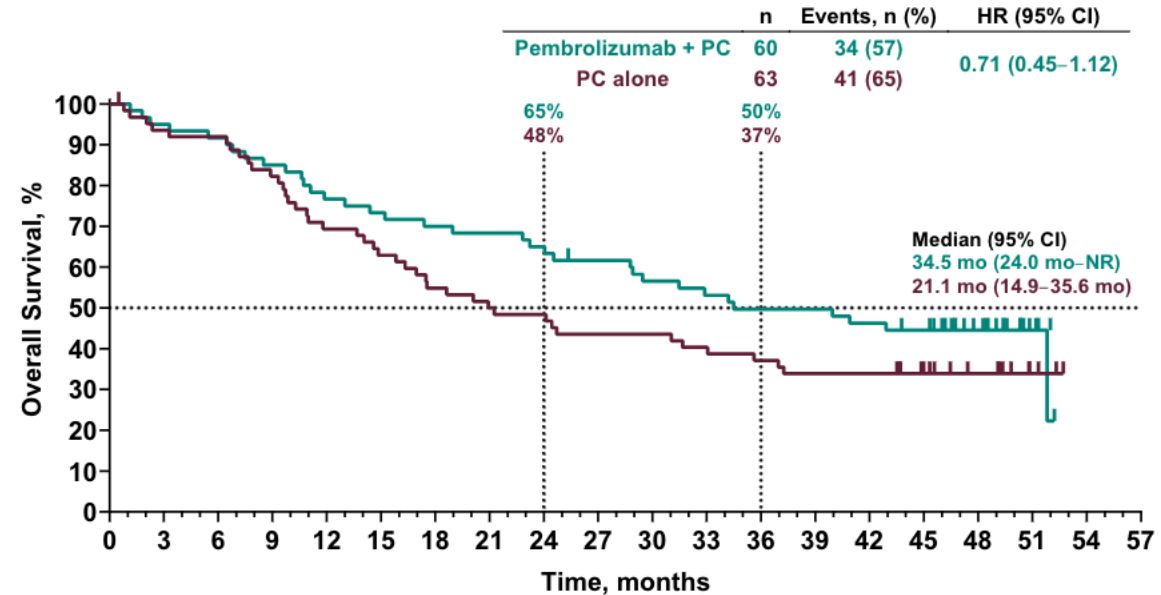


2001

Comparison of 4 platinum doublet regimens

Median survival for all 4, about 10 months

Three-year survival under 10%



2021

Comparison of platinum doublet with or without IO

Median survival for chemoIO is 3 years

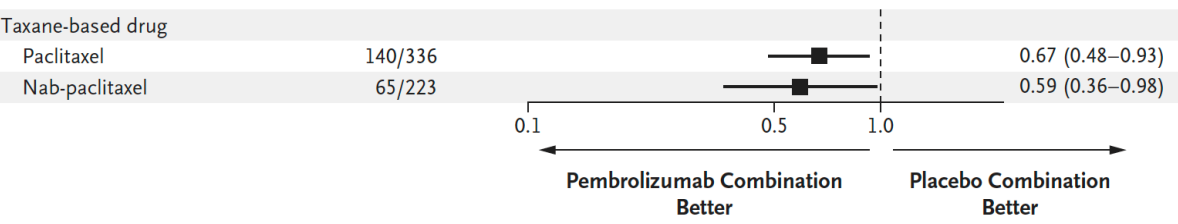
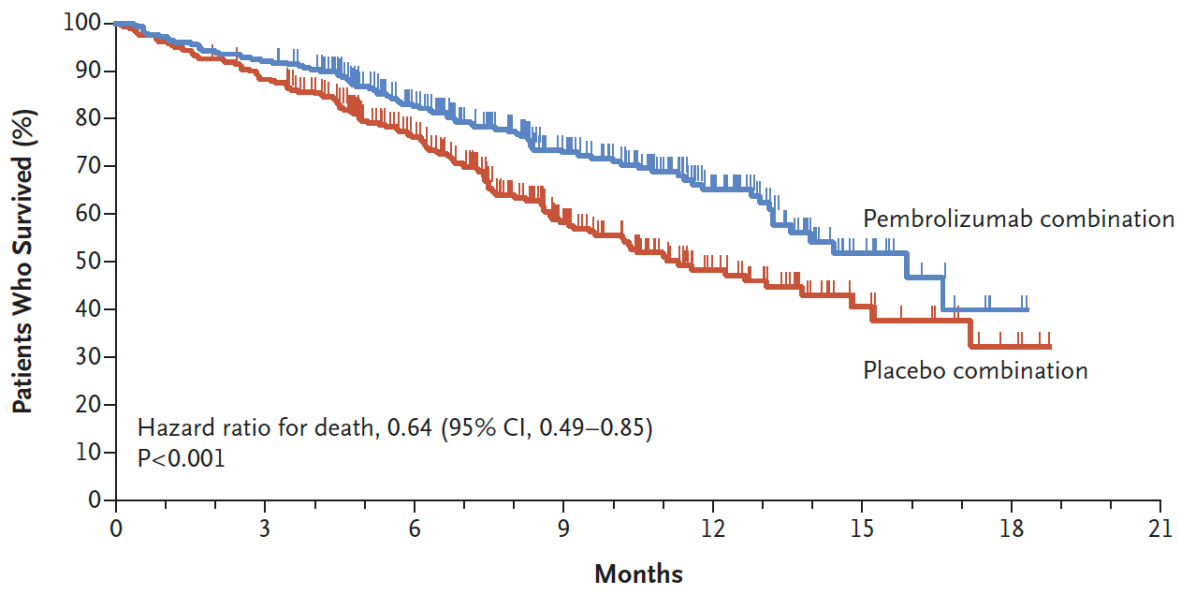
Long-term survival is about 40% (curves flatten out)

Note the group randomized to chemo alone gets IO later – even of these some can be rescued

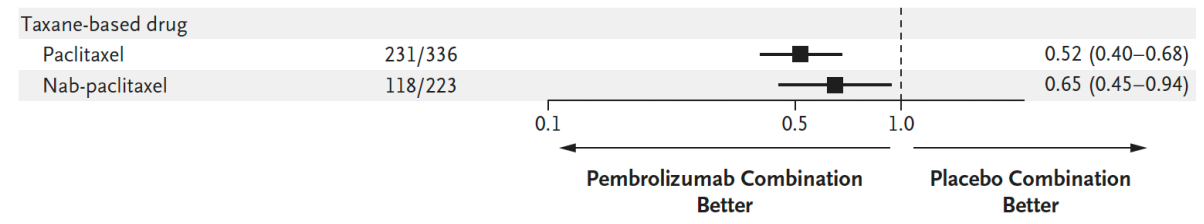
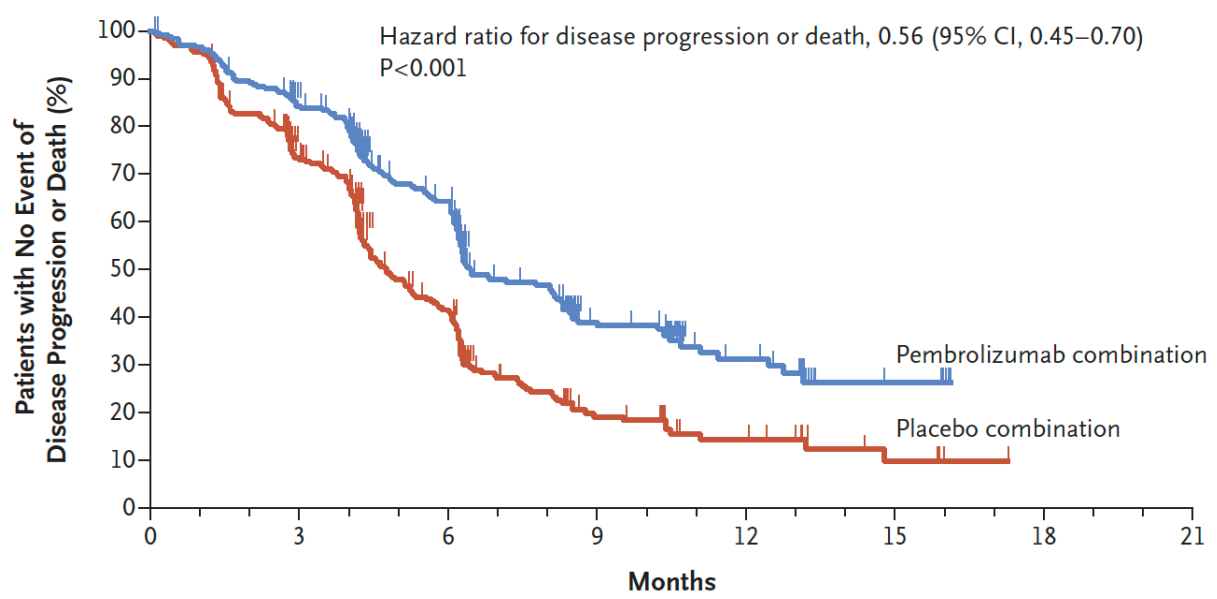
# Chemoimmunotherapy for squamous cell carcinoma

## Keynote 407: carboplatin (nab)-paclitaxel +/- pembrolizumab

Overall survival



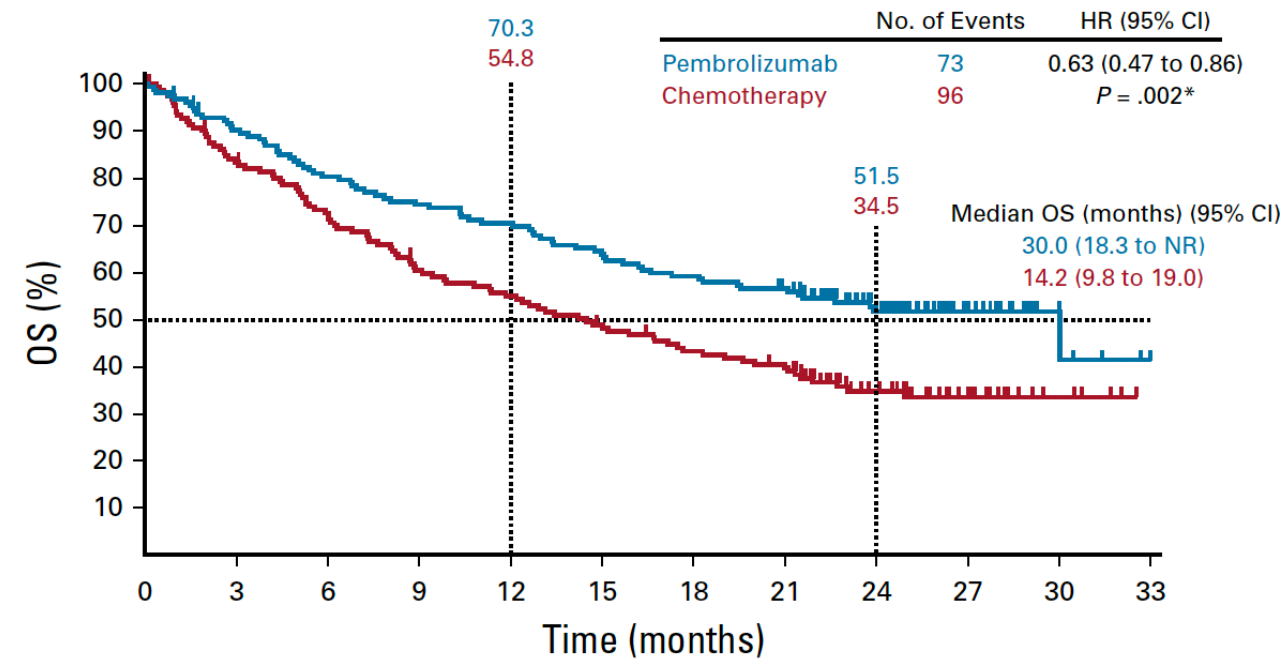
Progression-free survival





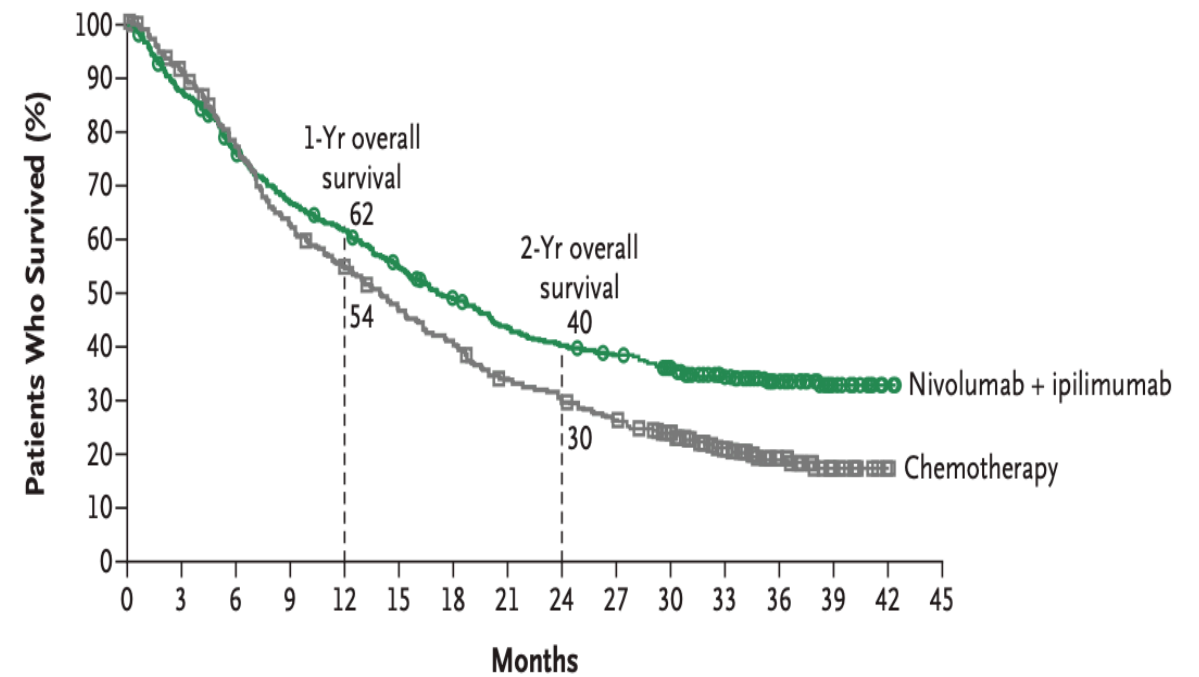
# “Chemo-free” options

## Keynote 604: PD-L1 $\geq 50\%$



Reck et al., *J Clin Oncol* 2019

## CheckMate 227: nivolumab and ipilimumab

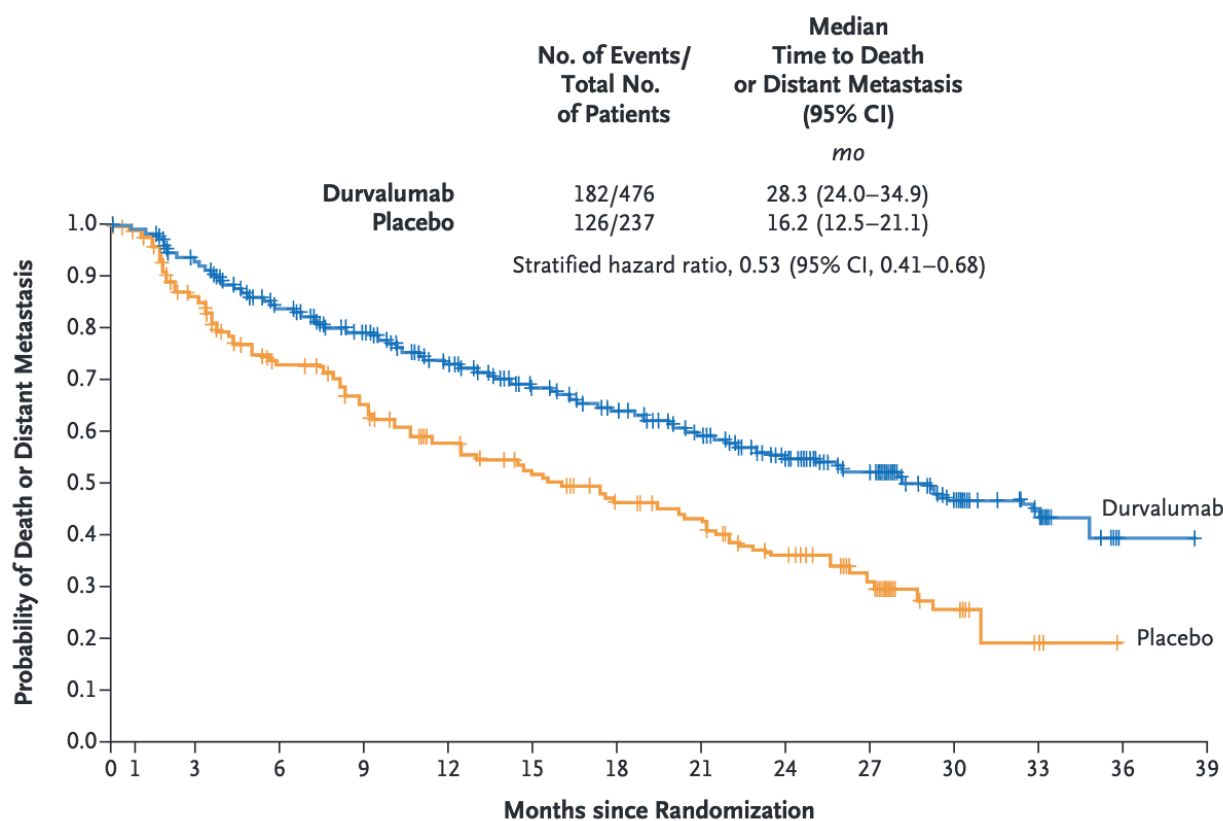


Hellmann et al, *N Engl J Med* 2019

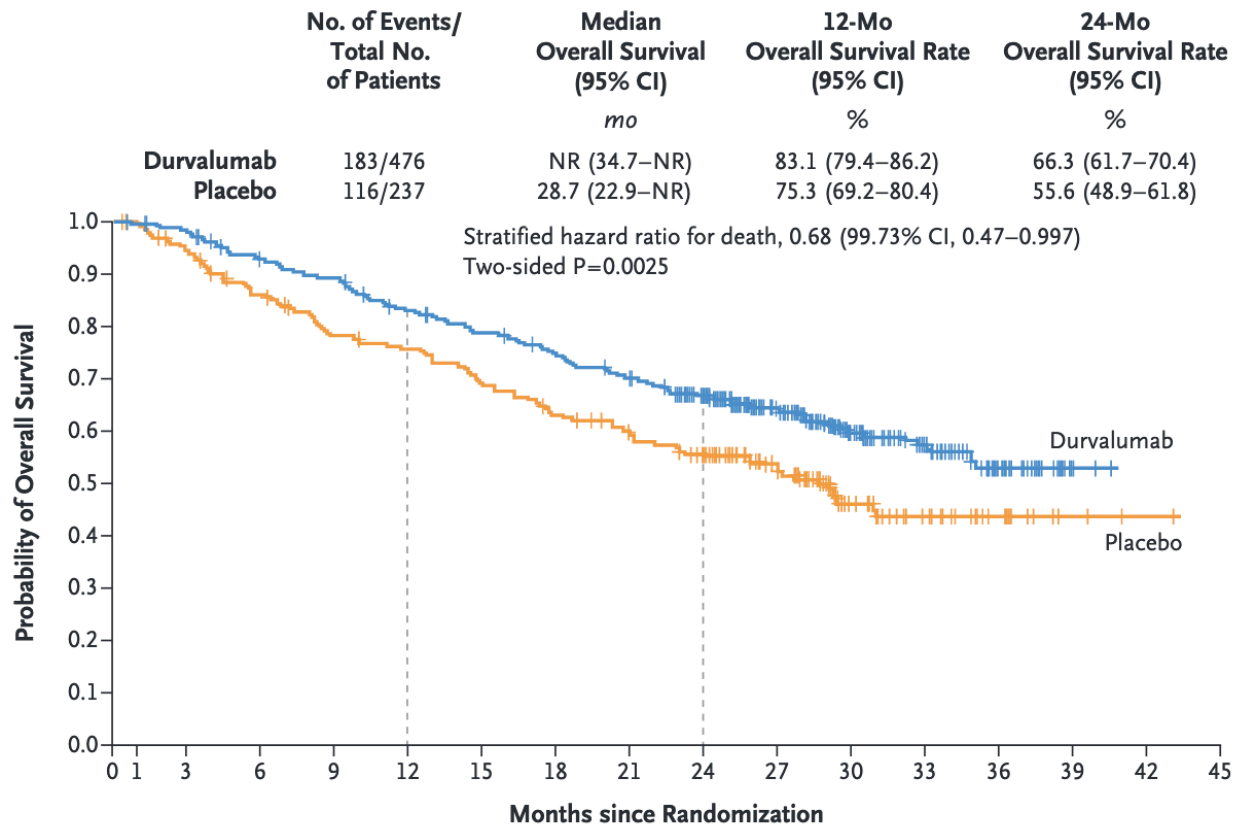
# Bringing immunotherapy to early stage disease: Durvalumab after chemoRT for stage III NSCLC

## PACIFIC

### Metastasis-free survival



### Overall survival

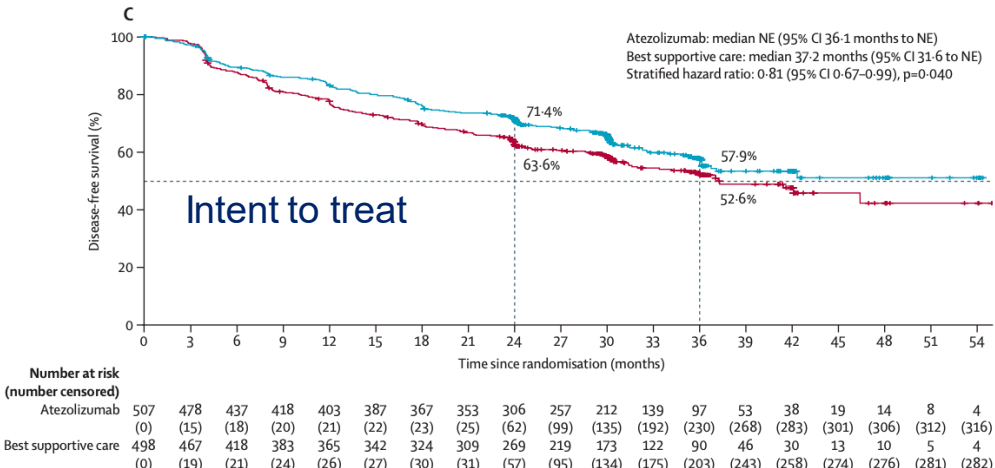
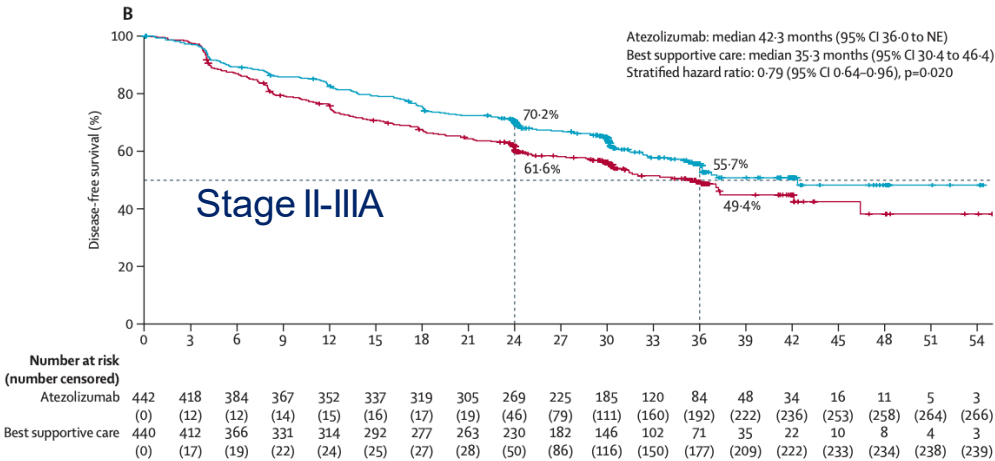
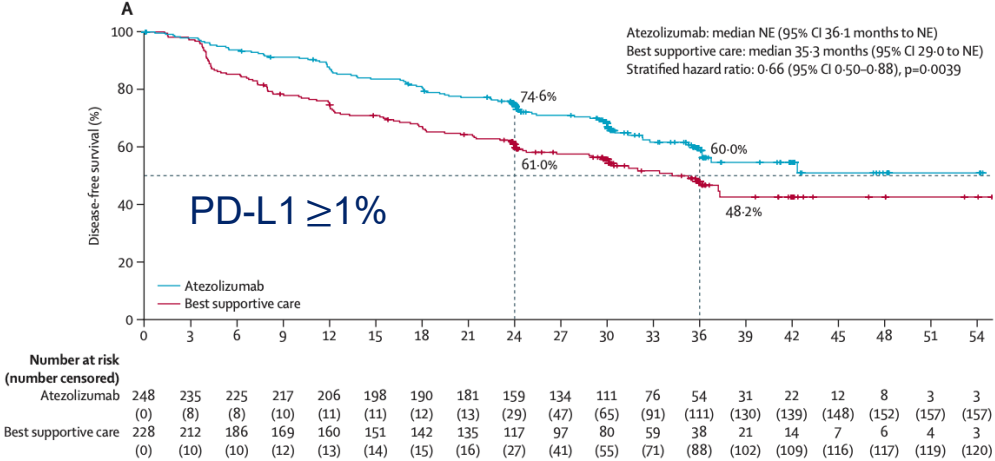
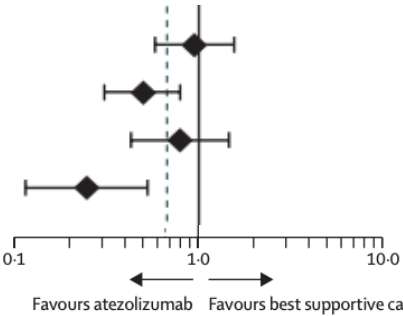


# Adjuvant (post-surgical) immunotherapy

## IMpower010: Adjuvant atezolizumab for stage IB– IIIA NSCLC

PD-L1 status by SP263

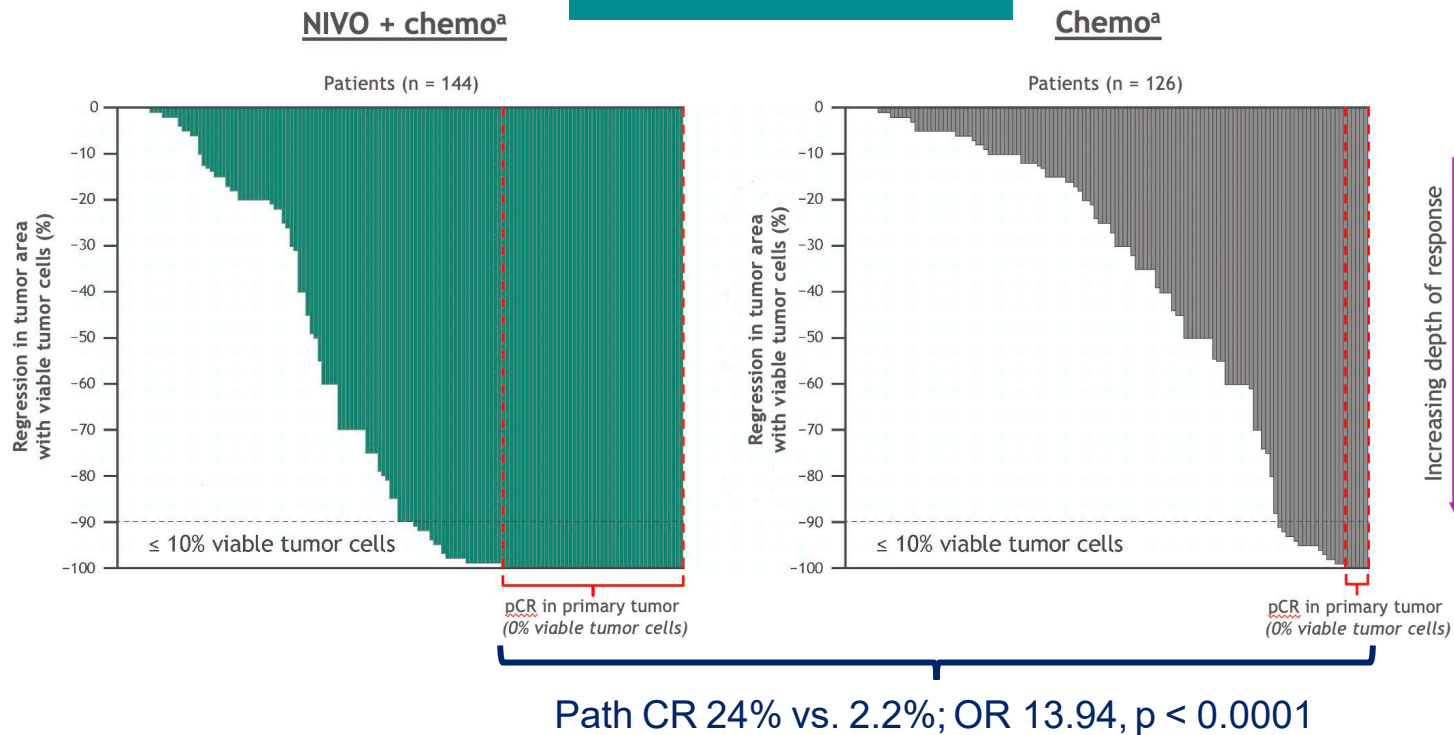
- TC <1%
- TC ≥1%
- TC 1-49%
- TC ≥50%



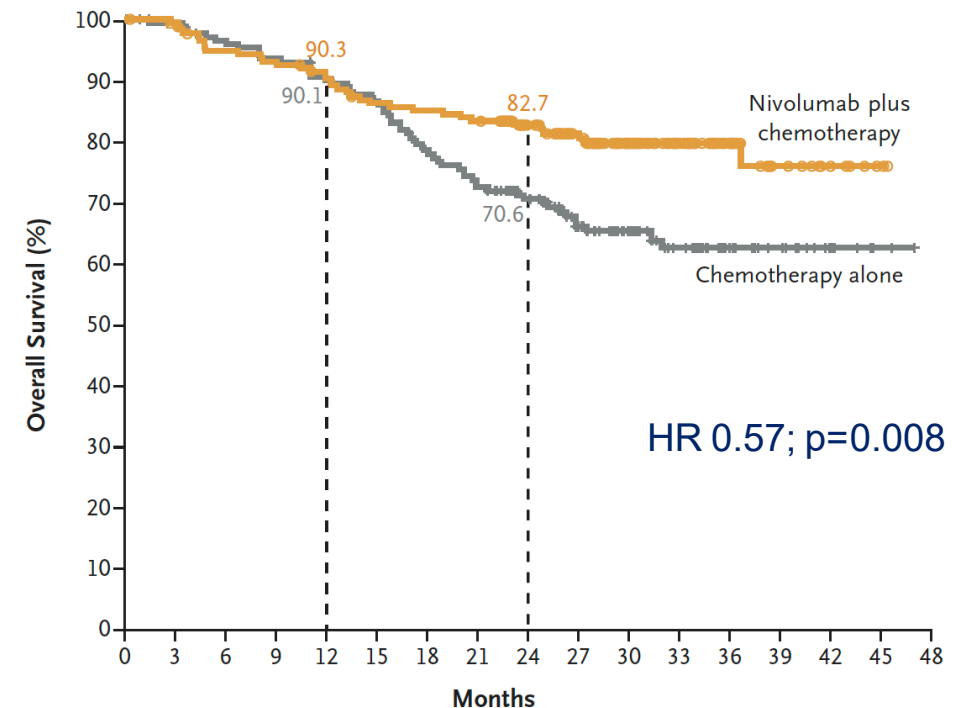
# Bringing immunotherapy before surgery: Neoadjuvant chemolO for NSCLC

CheckMate 816: Neoadjuvant platinum doublet +/- nivolumab

## Tumor reduction

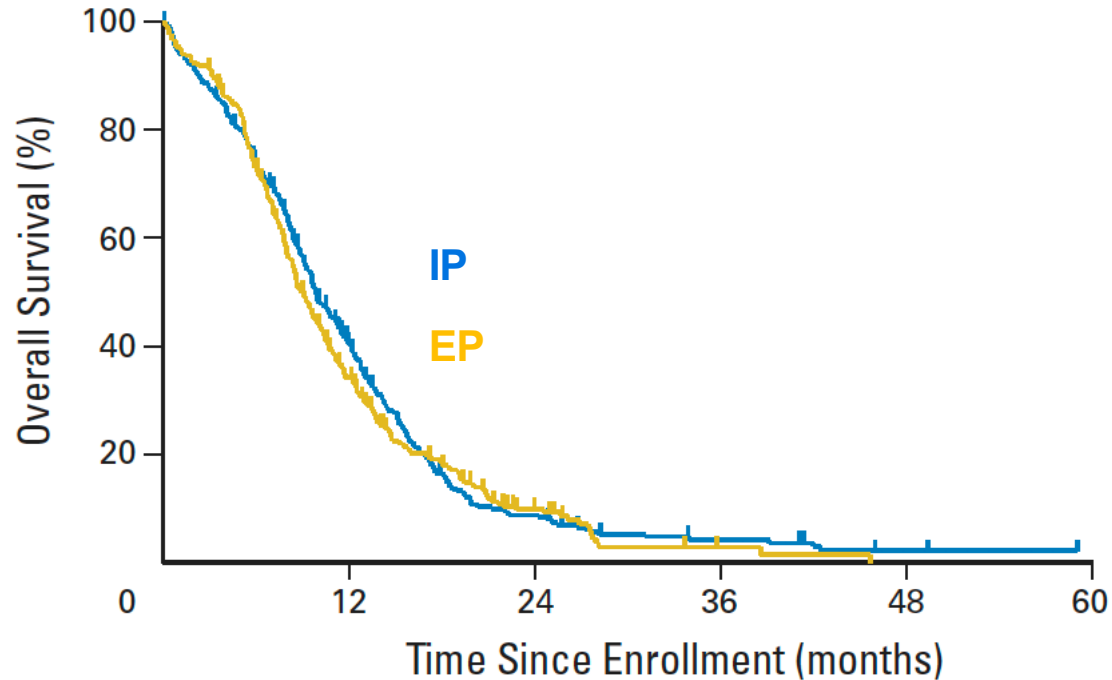


## Overall survival



Forde et al, *N Engl J Med* 2022

# Small cell lung cancer: where we were, where we are

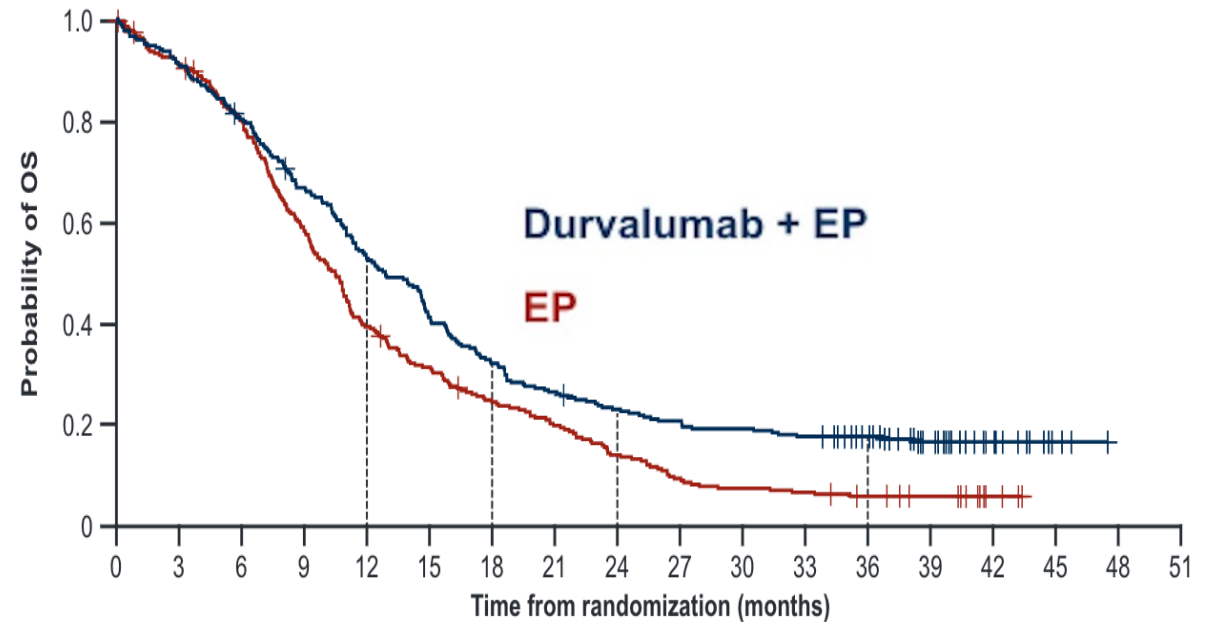


2009

Comparison of 2 platinum doublet regimens

Two-year survival under 10%

Essentially no long-term survivors



2021

Comparison of platinum doublet with or without IO

Two-year survival approximately 20%

Curves flatten out – 3-year survival will be similar to 2

Again evidence of salvage in the control arm – later IO

# Summary: first-line indications for immunotherapy in lung cancer

## Non-small cell lung cancer

Surgically resectable  
Neoadjuvant  
Adjuvant ✓  
✓  
Locally advanced  
Post-chemoRT  
*with chemoRT* ✓  
**X?**  
Metastatic ✓

## Small cell lung cancer

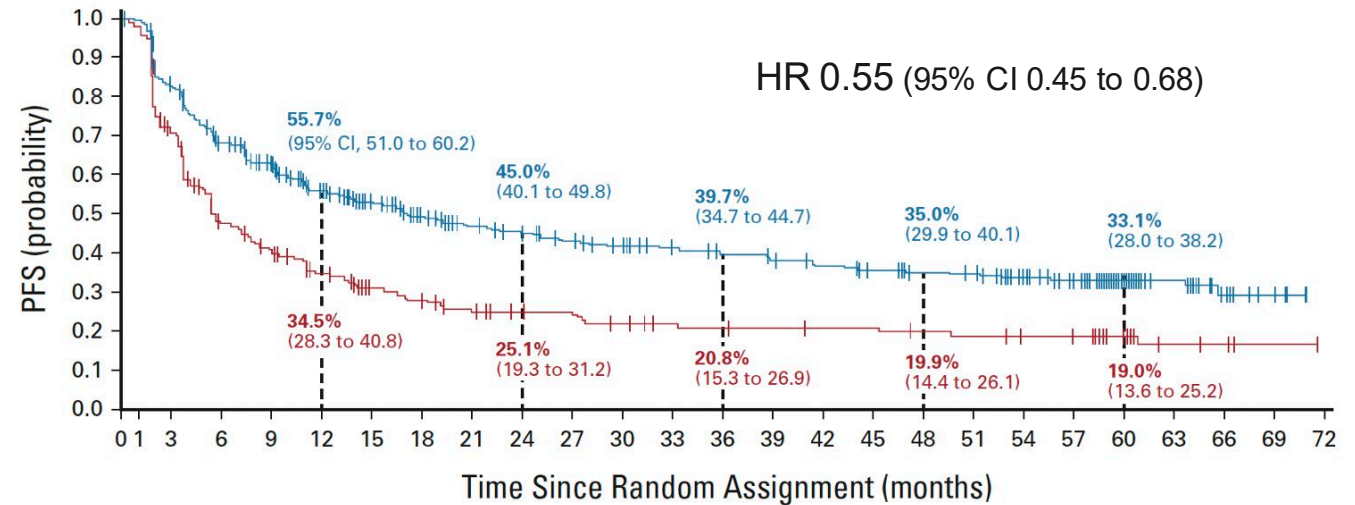
Extensive stage ✓  
Limited stage  
Post-chemoRT  
*with chemoRT* ✓  
?

Press reports only



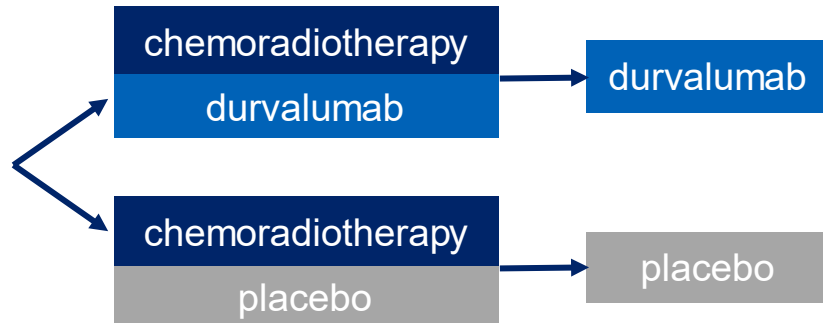
# Combining IO with radiation – negative interaction?

## PACIFIC



Spiegel et al., *J Clin Oncol* 2022

## PACIFIC-2



Uh-oh...

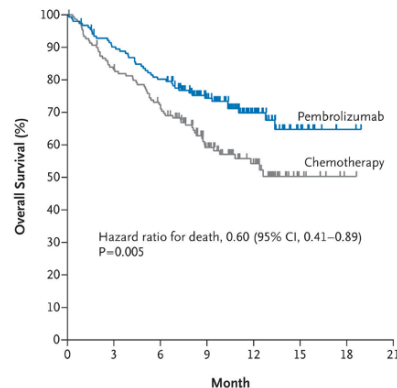
*Update on PACIFIC-2 Phase III trial of Imfinzi concurrently administered with platinum-based chemoradiotherapy in unresectable, Stage III non-small cell lung cancer*

PUBLISHED  
14 November 2023

# Developing precision medicine for immunotherapy

## KEYNOTE 024

Pembro vs Chemo  
in NSCLC  
with PD-L1 TPS  $\geq 50\%$



No. at Risk								
Pembrolizumab	154	136	121	82	39	11	2	0
Chemotherapy	151	123	106	64	34	7	1	0

If no targetable mutation, check PD-L1

PD-L1 TPS  $\geq 50\%$

Pembrolizumab  
Monotherapy

PD-L1 TPS  $< 50\%$

Pembrolizumab  
+ Chemotherapy

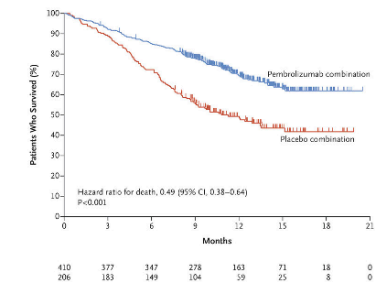
Upon development of  
resistance

?

Limited understanding  
of resistance

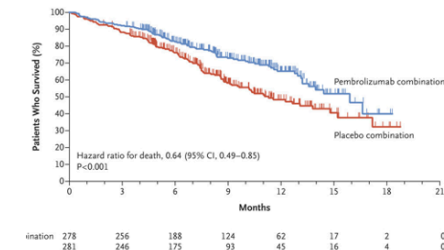
## KEYNOTE 189

Chemo +/- Pembro  
in Nonsquamous NSCLC  
with PD-L1 TPS 0-100%



## KEYNOTE 407

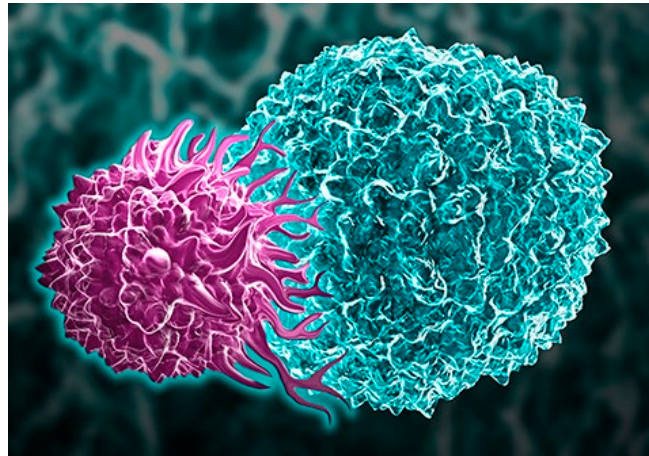
Chemo +/- Pembro  
in Squamous NSCLC with  
PD-L1 TPS 0-100%



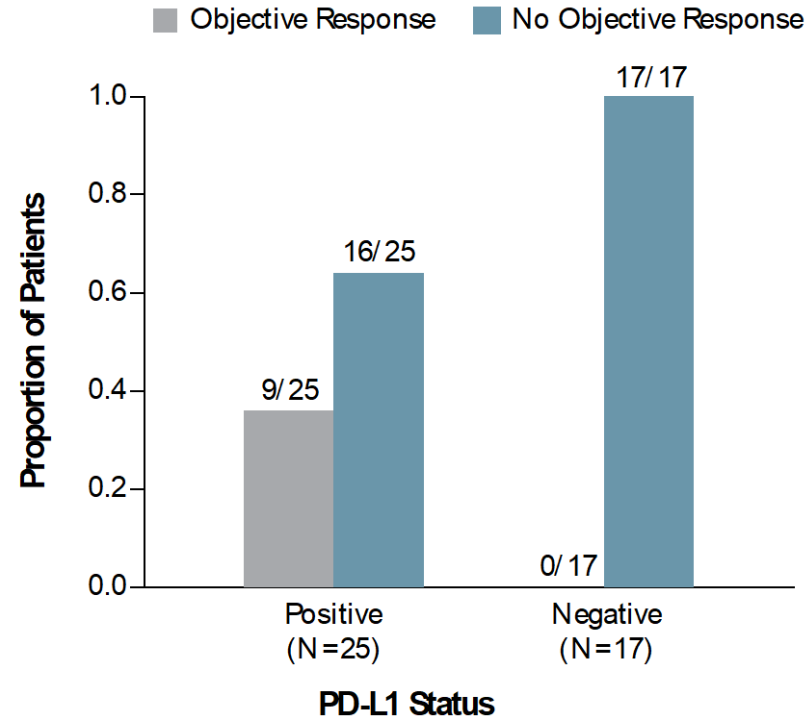
Reck M et al. *N Engl J Med* 2016;375:1823-1833.

Gandhi L, et al. *N Engl J Med* 2018;378:2078-2092.  
Paz-Ares L, et al. *N Engl J Med* 2018;379:2040-2051.

## The search for predictive biomarkers



# Biomarker 1.0: the target, PD-L1!

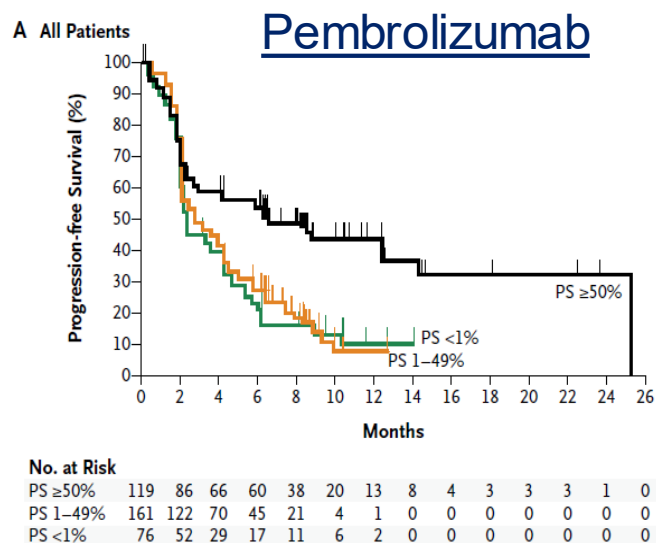


Association between Pretreatment Tumor PD-L1 Expression and Clinical Response

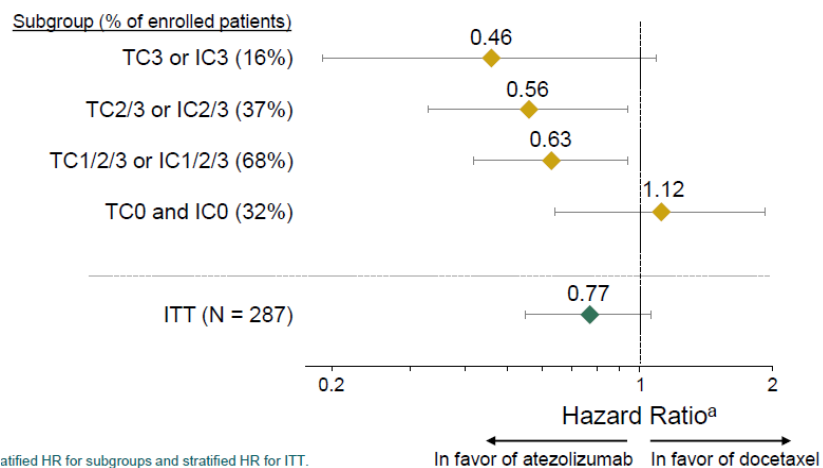
Response Status	PD-L1-Positive	PD-L1-Negative	Total
	number (percent)		
Objective response	9 (36)	0	9 (21)
No objective response	16 (64)	17 (100)	33 (79)
All	25	17	42

P=0.006 for association by Fisher's exact test

# PD-L1 positivity is associated with improved responses



## Atezolizumab in NSCLC



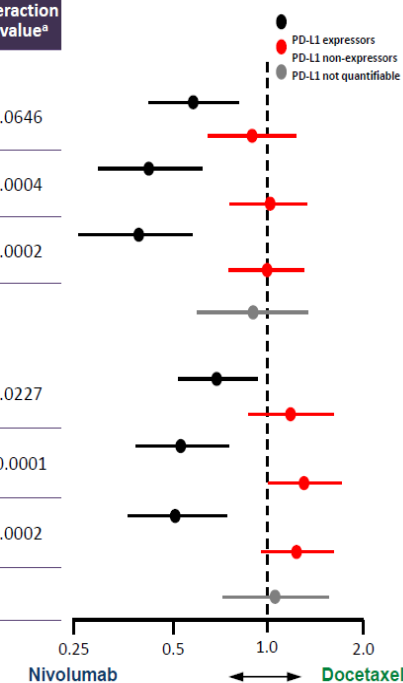
Stratified HR for subgroups and stratified HR for ITT.  
cut-off Jan 30, 2015.

## Nivolumab in Non-Squamous NSCLC

OS and PFS Hazard Ratios by Baseline PD-L1 Expression

PD-L1 expression level	Nivolumab n	Docetaxel n	Unstratified HR (95% CI)	Interaction P-value <sup>a</sup>
<b>OS</b>				
≥1%	123	123	0.59 (0.43, 0.82)	0.0646
<1%	108	101	0.90 (0.66, 1.24)	
≥5%	95	86	0.43 (0.30, 0.63)	0.0004
<5%	136	138	1.01 (0.77, 1.34)	
≥10%	86	79	0.40 (0.26, 0.59)	0.0002
<10%	145	145	1.00 (0.76, 1.31)	
Not quantifiable	61	66	0.91 (0.61, 1.35)	
<b>PFS</b>				
≥1%	123	123	0.70 (0.53, 0.94)	0.0227
<1%	108	101	1.19 (0.88, 1.61)	
≥5%	95	86	0.54 (0.39, 0.76)	<0.0001
<5%	136	138	1.31 (1.01, 1.71)	
≥10%	86	79	0.52 (0.37, 0.75)	0.0002
<10%	145	145	1.24 (0.96, 1.61)	
Not quantifiable	61	66	1.06 (0.73, 1.56)	

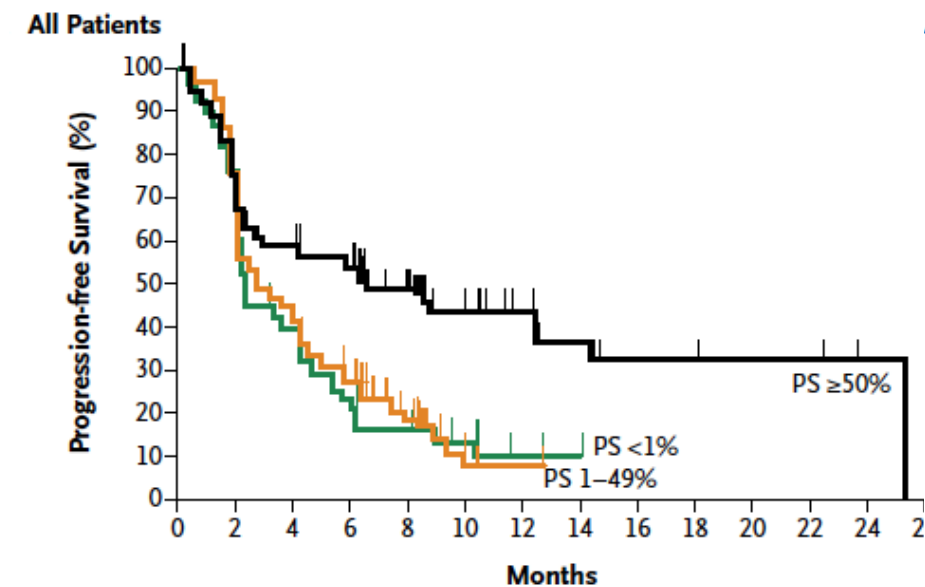
<sup>a</sup> Interaction p-value from Cox proportional hazard model with treatment, PD-L1 expression and treatment by PD-L1 expression interaction.



Garon et al, *NEJM* 2015  
Paz Ares, ASCO 2015  
Spira, ASCO 2015

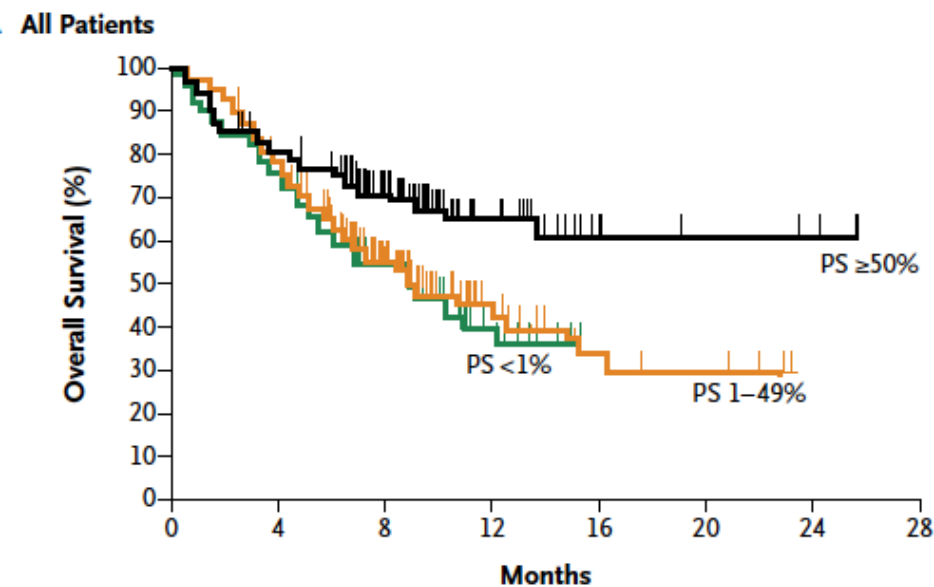
# Pembrolizumab in NSCLC – importance of PD-L1?

Progression-free survival



No. at Risk												
PS $\geq 50\%$	119	86	66	60	38	20	13	8	4	3	3	1
PS 1-49%	161	122	70	45	21	4	1	0	0	0	0	0
PS $< 1\%$	76	52	29	17	11	6	2	0	0	0	0	0

Overall survival



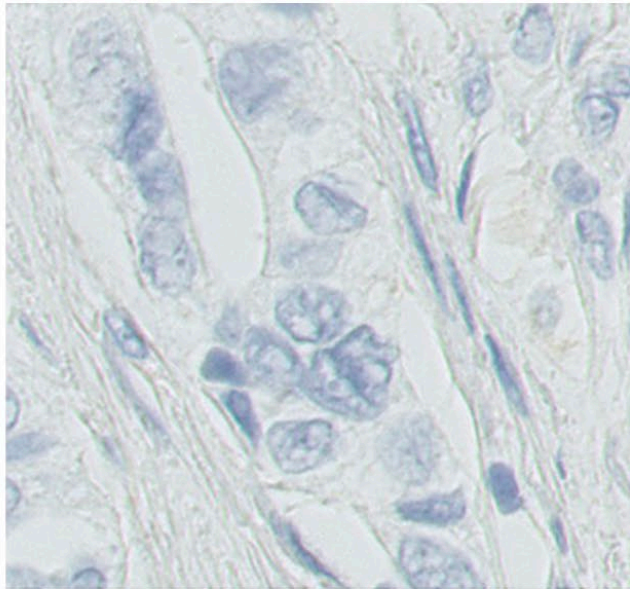
No. at Risk								
PS $\geq 50\%$	119	92	56	22	5	4	3	0
PS 1-49%	161	119	58	15	6	4	0	0
PS $< 1\%$	76	55	33	8	0	0	0	0



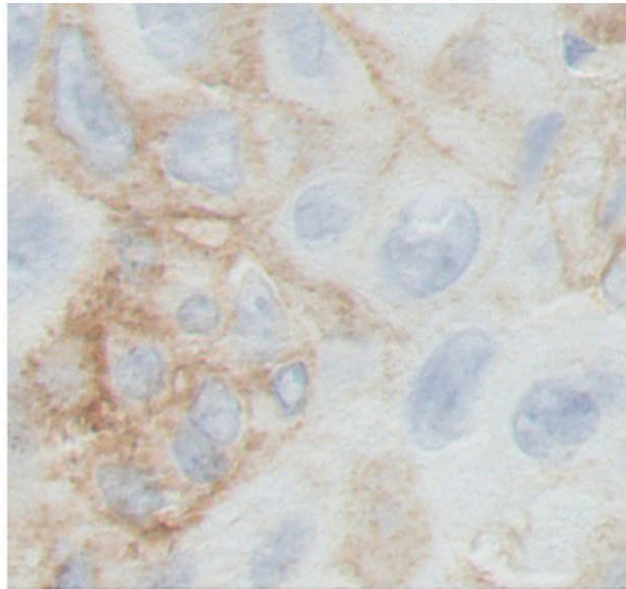
# PD-L1 as a predictive biomarker

## PD-L1 Tumor Proportion Score (TPS)

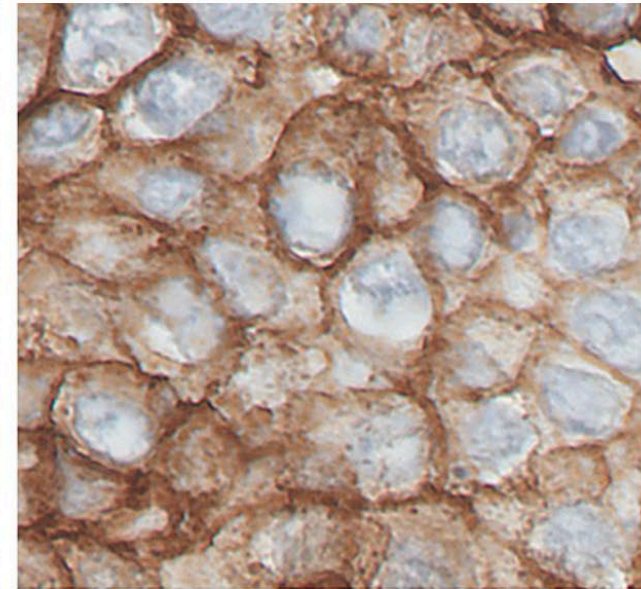
**<1%**



**1-49%**

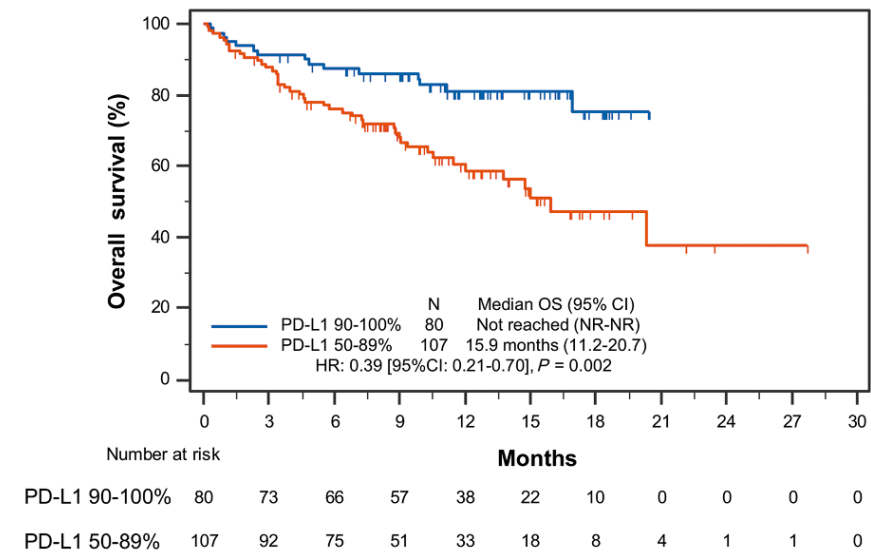
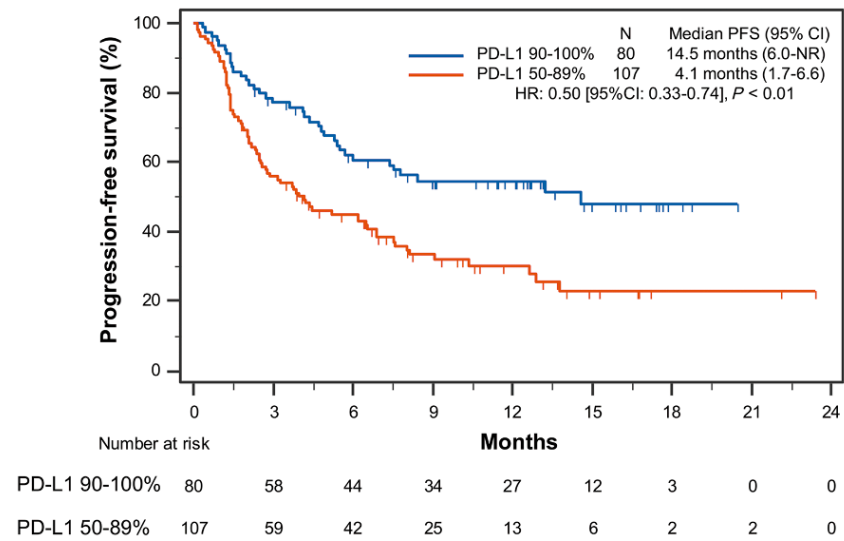
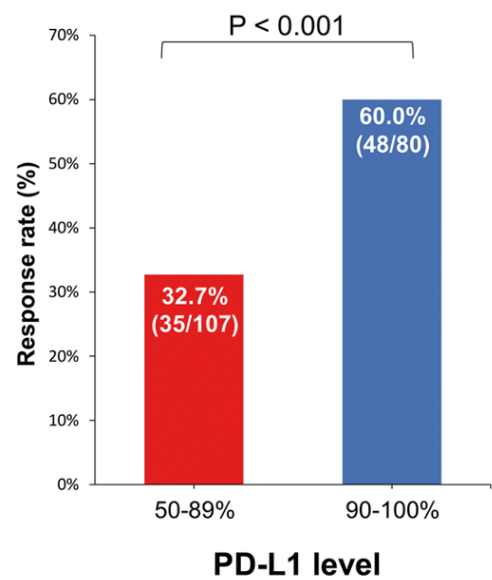


**≥50%**



*When the PD-L1 TPS is above 50%, are higher levels even better?*

# PD-L1 TPS 50-89% vs ≥ 90%



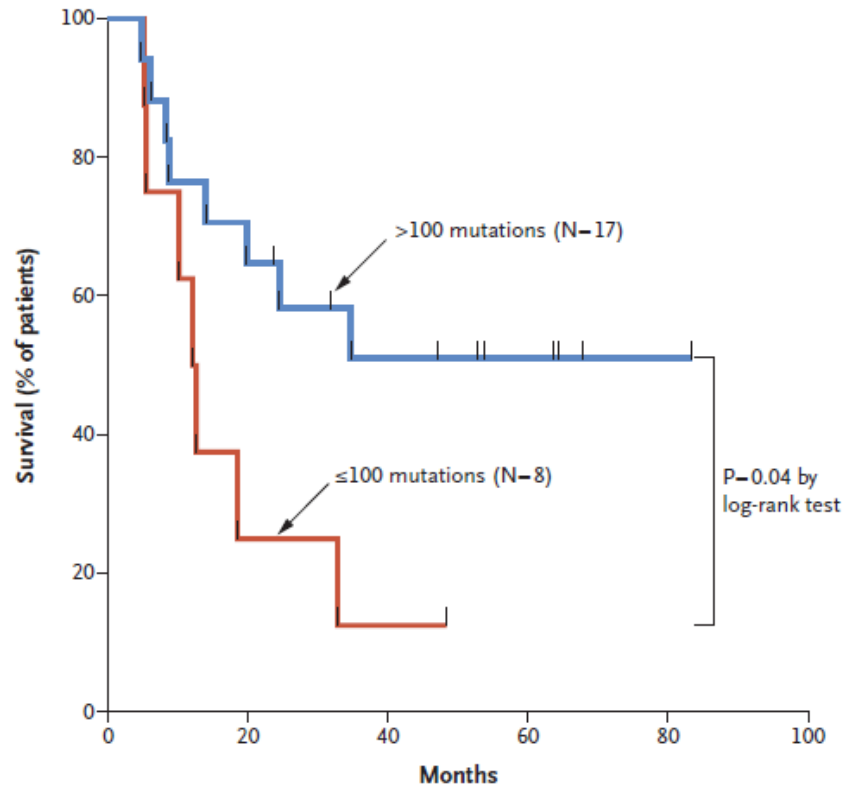
# What is the clinical application of PD-L1 testing?

PD-L1  $\neq$  EGFR

- PD-L1 is a dynamic marker
- PD-L1 is heterogeneously expressed in tumor tissue
- PD-L1 negative tumors can respond to checkpoint blockade
- Would not use PD-L1 status to exclude a patient from checkpoint blockade therapy, however, in the setting of multiple immunotherapeutic agents, this information may be used to shape clinical decisions

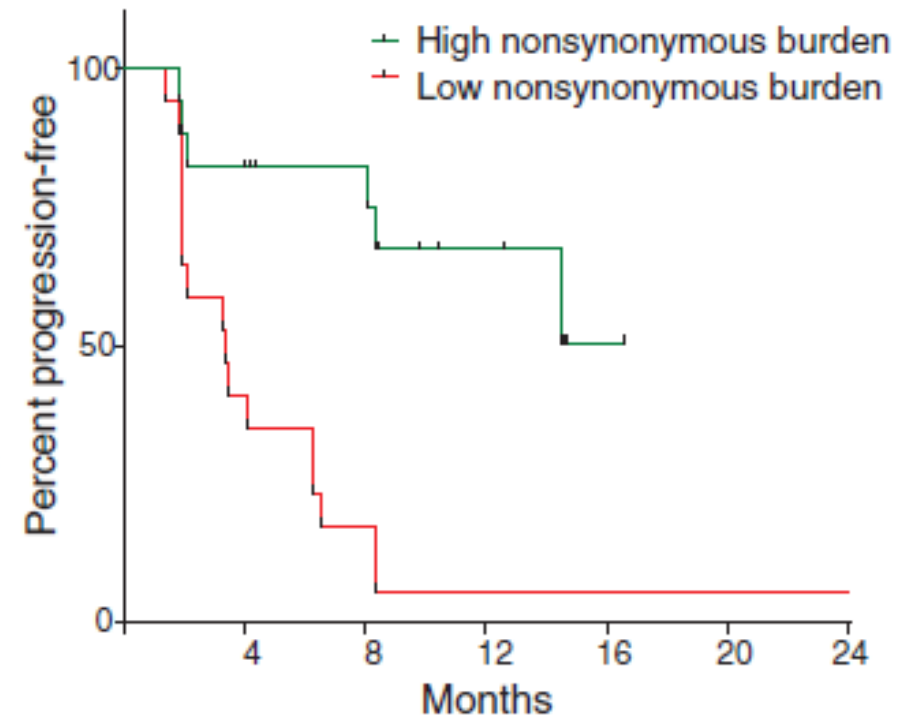
# Mutational burden as a predictive biomarker

Melanoma: ipilimumab



Snyder et al, *N Engl J Med* 2015

Lung CA: pembrolizumab



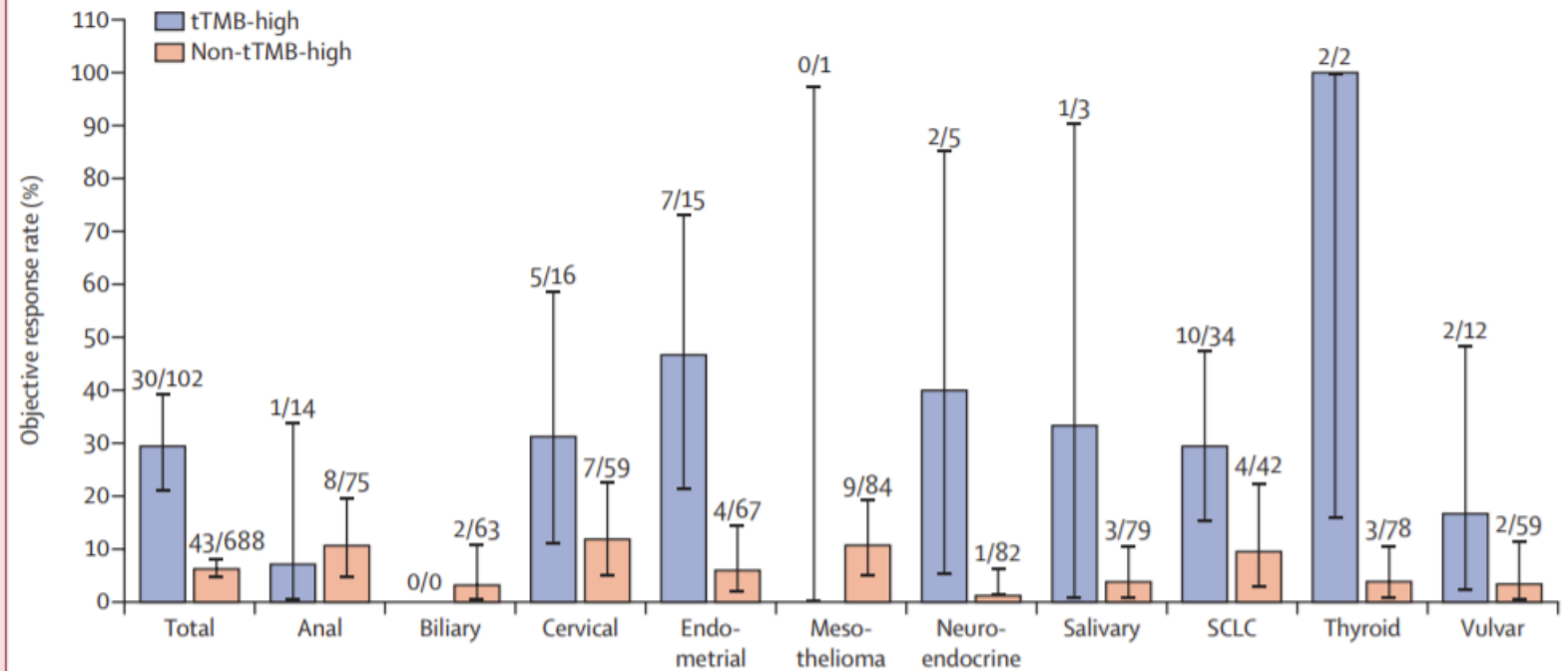
Rizvi et al, *Science* 2015

# Pembrolizumab in TMB-high cancers

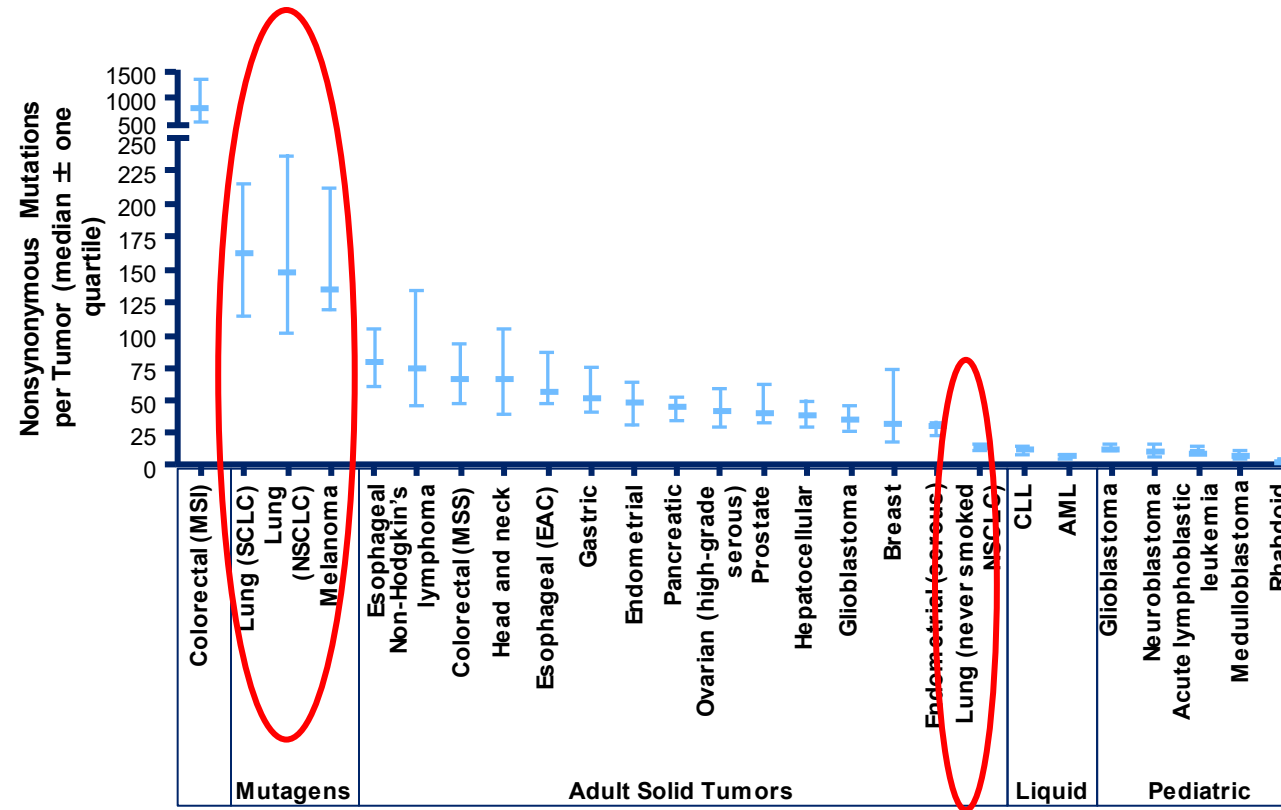
	tTMB-high (n=102)	tTMB-high (excluding MSI-H; n=81)*	Non-tTMB- high (n=688)
Best response			
Complete response	4 (4%)	3 (4%)	11 (2%)
Partial response	26 (25%)	20 (25%)	32 (5%)
Stable disease	14 (14%)	11 (14%)	227 (33%)
Non-complete response or non-progressive disease†	0	0	3 (<1%)
Progressive disease	48 (47%)	38 (47%)	349 (51%)
Not evaluable‡	1 (1%)	1 (1%)	13 (2%)
Not assessed§	9 (9%)	8 (10%)	53 (8%)
Objective response rate	29% (21–39)	28% (19–40)	6% (5–8)

Data are n (%) or % (95% CI). MSI-H=high microsatellite instability. RECIST=Response Evaluation Criteria in Solid Tumors. tTMB-high=high tissue tumour mutational burden. \*Excludes 14 patients who were MSI-high and seven additional patients who had missing MSI status. †Patients without measurable disease per central review at baseline who did not have a complete response or progressive disease. ‡Patients who did not have a post-baseline imaging assessment evaluable for response. §Patients who did not have post-baseline imaging.

**Table 2: Objective response (per RECIST version 1.1), assessed by independent central review in the efficacy population**

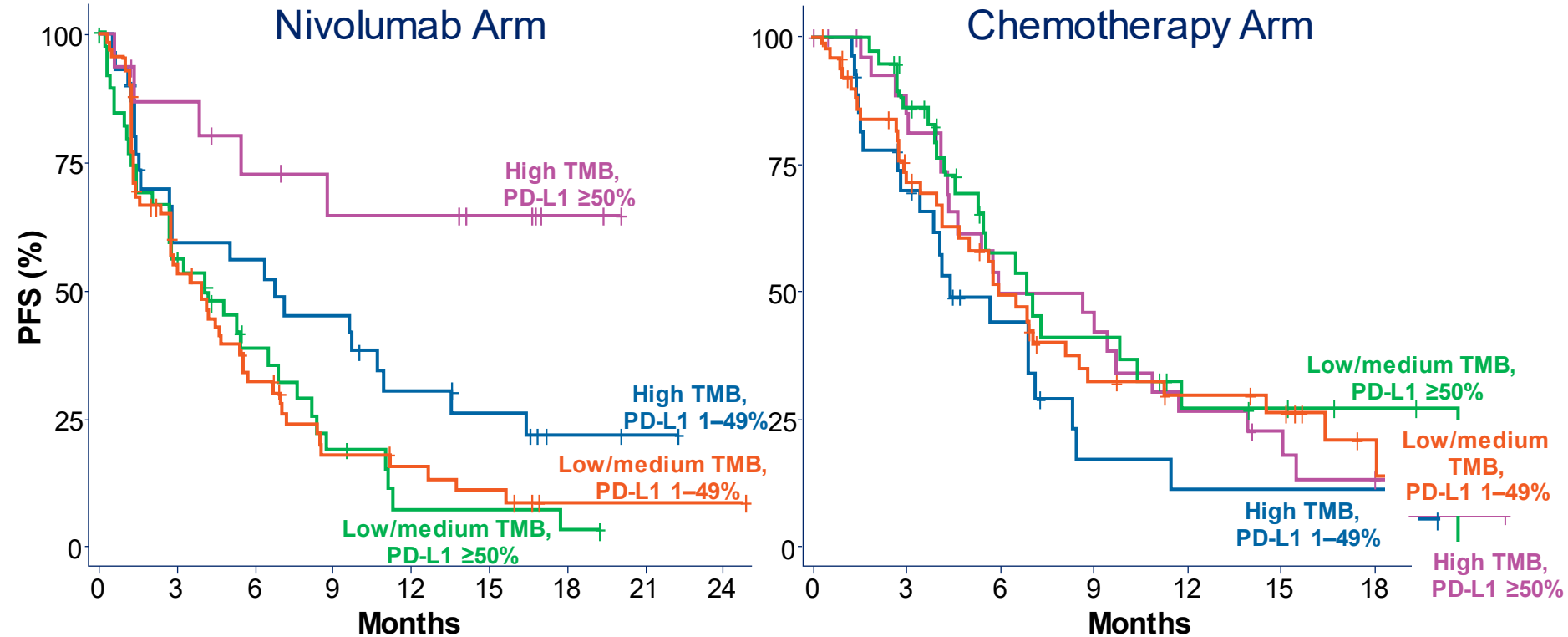


# PD-(L)1 blockade is more active in tumors with high mutation burden



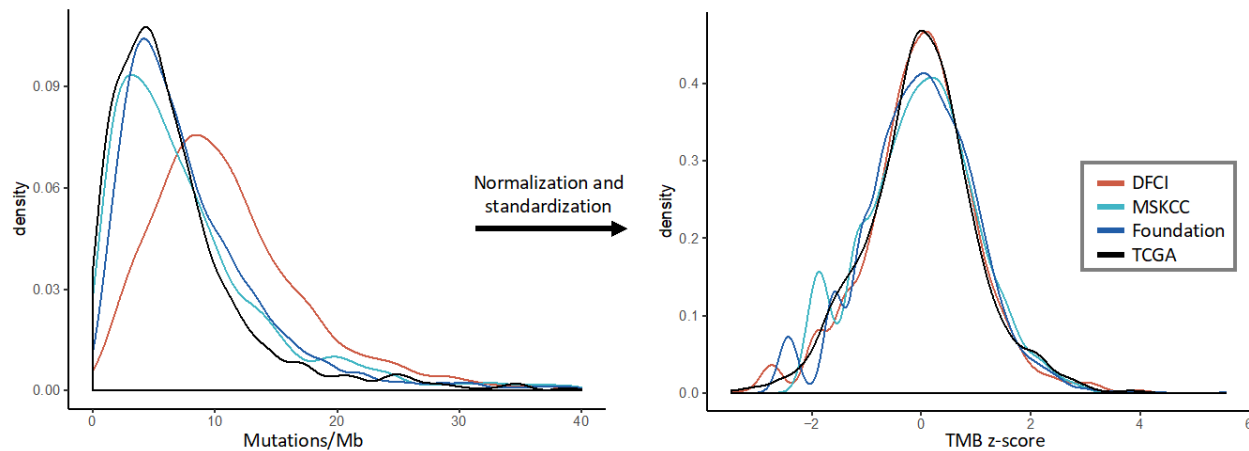


# Both PD-L1 and TMB influence response to checkpoint blockade



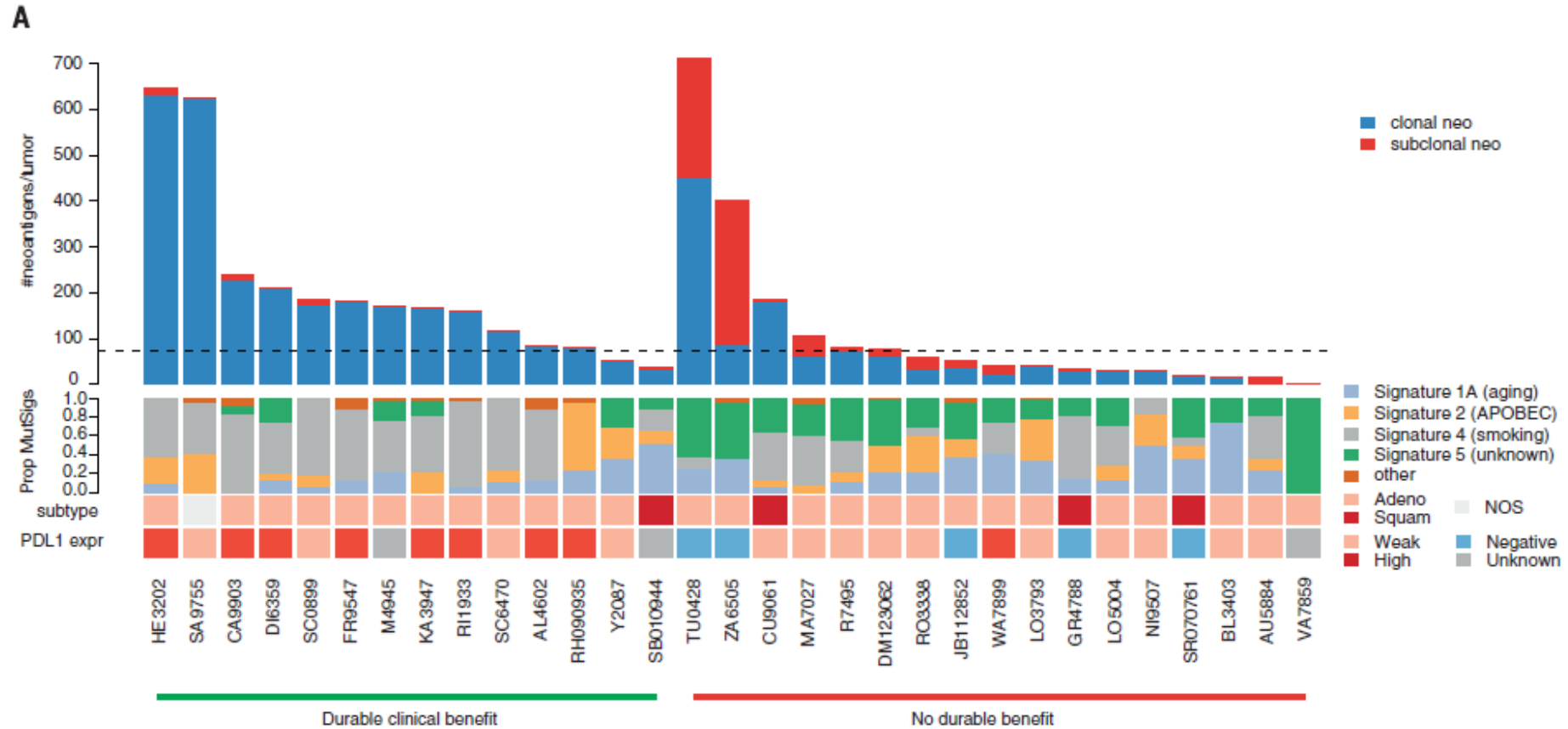
# Challenges with TMB

- Still not used routinely for treatment selection in NSCLC
- Limited access to published trial data
- Cohort sizes at any individual institution are relatively small
- Differences across platforms make it difficult to compare and combine data

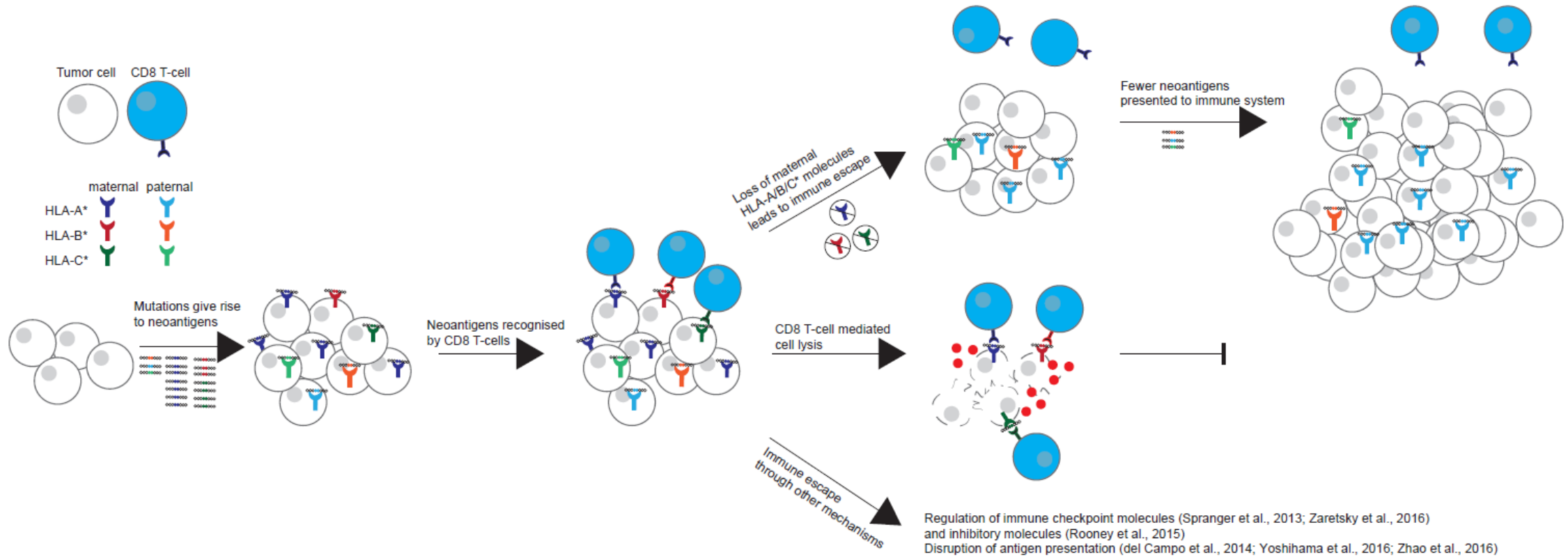


Percentile	TMB z-score	DFCI TMB	MSKCC TMB	Foundation TMB	TCGA TMB (mutation count)
10th	-1.04	4.81	2.27	2.83	1.84 (55)
20th	-0.47	7.22	3.89	4.45	3.35 (101)
30th	-0.24	8.42	4.78	5.30	4.18 (125)
40th	0.00	9.87	5.90	6.36	5.25 (158)
50th	0.17	11.07	6.89	7.27	6.10 (183)
60th	0.45	13.24	8.76	8.97	7.58 (228)
70th	0.70	15.47	10.82	10.80	9.41 (282)
80th	0.95	18.05	13.34	13.00	11.31 (339)
90th	1.38	23.49	19.10	17.90	15.43 (463)

# Importance of mutational clonality



# Immune editing through HLA loss of heterozygosity



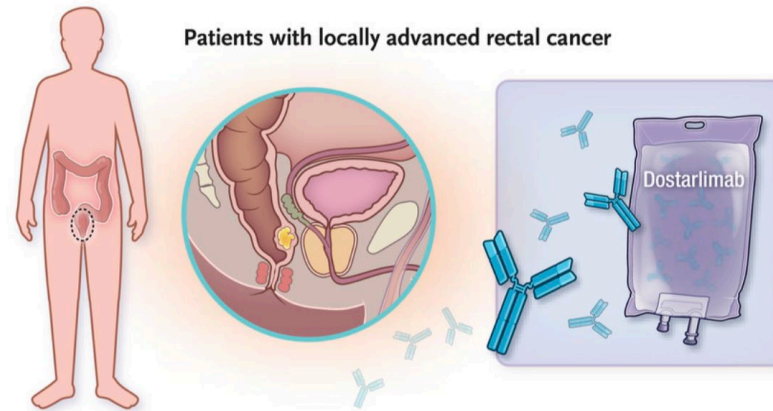
# At the extreme end of TMB... MRD rectal cancer

The NEW ENGLAND JOURNAL of MEDICINE

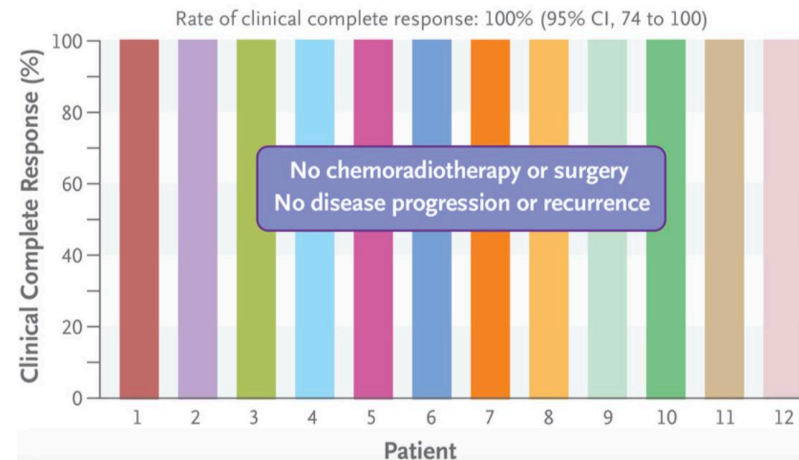
## RESEARCH SUMMARY

### PD-1 Blockade in Mismatch Repair–Deficient, Locally Advanced Rectal Cancer

Cercek A et al. DOI: 10.1056/NEJMoa2201445



#### Overall Response to Dostarlimab in 12 Patients



# Summary

CTLA-4 blockade is an effective treatment that confers a benefit in overall survival in patients with advanced melanoma

PD-1 (or PD-L1) blockade appears to have activity in melanoma, lung cancer, renal cancer, bladder cancer, head and neck cancer, ovarian cancer, and many other solid tumors

Unique kinetics of response, including delayed responses and long-term durability of responses are characteristic

Unique toxicities are managed with algorithms that employ immunosuppressive agents such as steroids

Further studies are needed to develop biomarkers for these agents and to understand which combinations are most promising





Memorial Sloan Kettering  
Cancer Center