

# Importance of NGS testing for STK11 and KEAP1 mutation and impact on treatment selection

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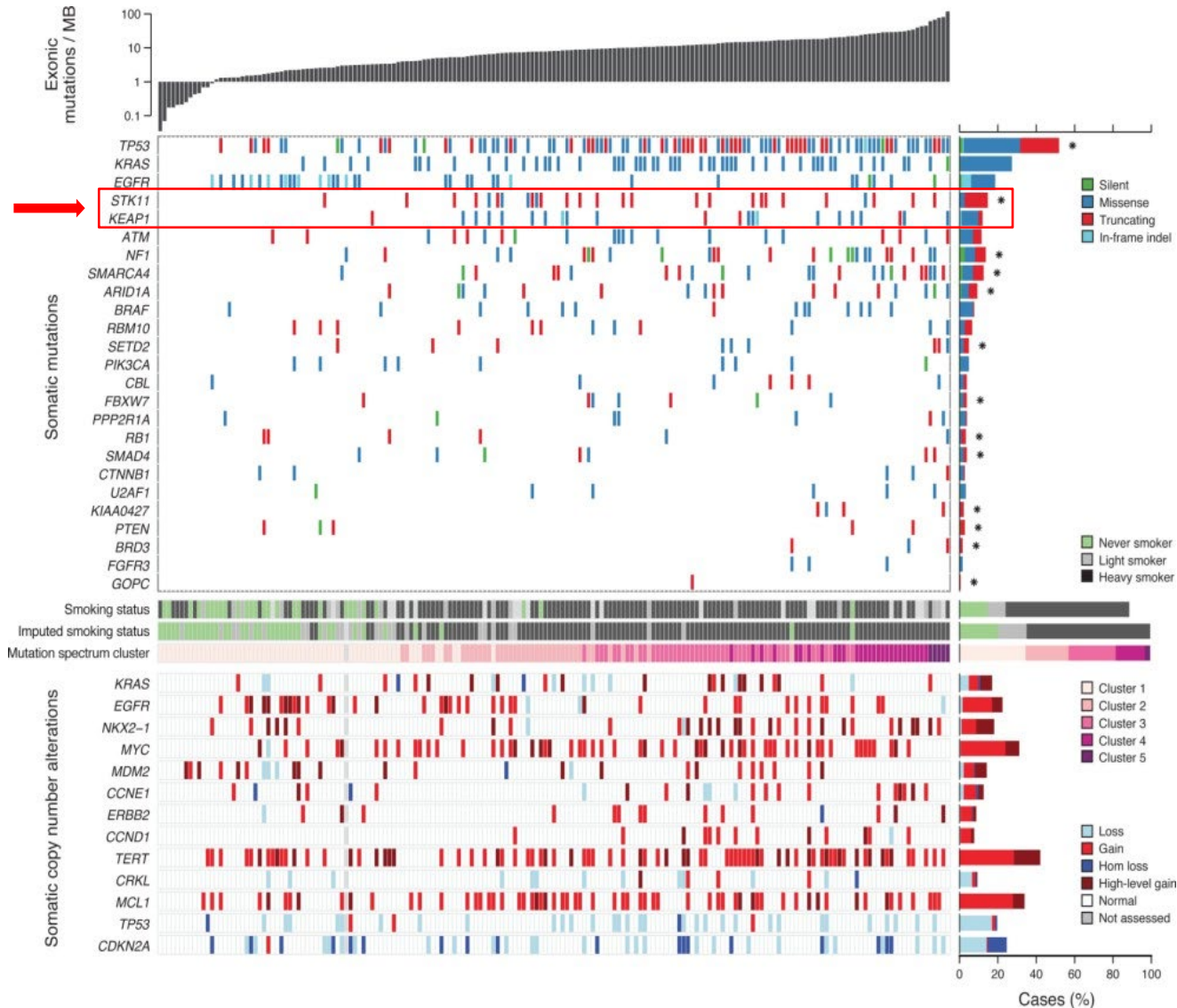


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# Disclosures

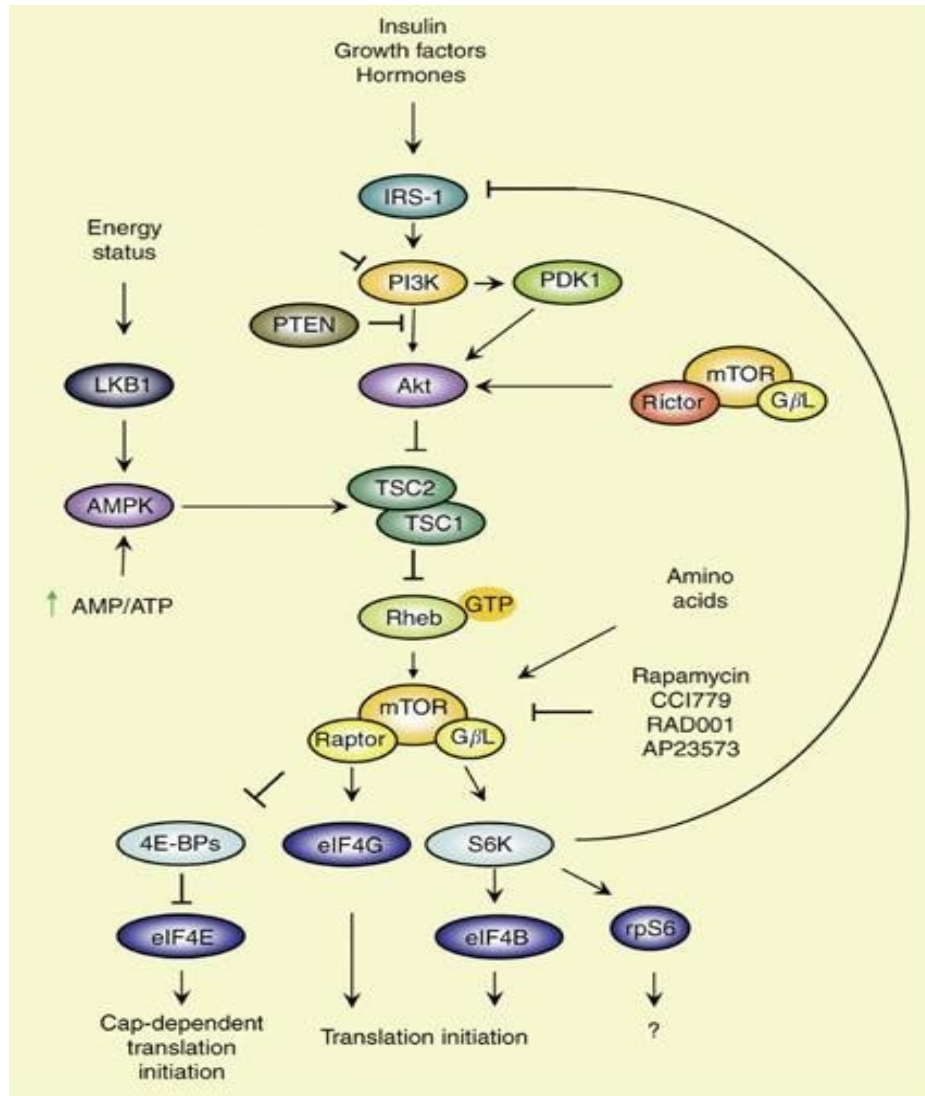
- Advisory board/Consultant: Amgen, Regeneron, AstraZeneca, AbbVie  
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Lilly, Johnson and Johnson
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# Lung cancer is genomically heterogeneous



- **STK11 and KEAP1 are the 2<sup>nd</sup> and 3<sup>rd</sup> most common TSG mutations** in lung adenocarcinoma (30%), also found in adenosquamous and squamous (KEAP1) carcinoma
- More frequently coexist with **KRAS** and **TP53** mutations, and **high TMB** but is rarely found with **EGFR** mutations
- More frequently found in **smokers**
- More frequently in **Caucasians** compared to Asian lung cancer patients

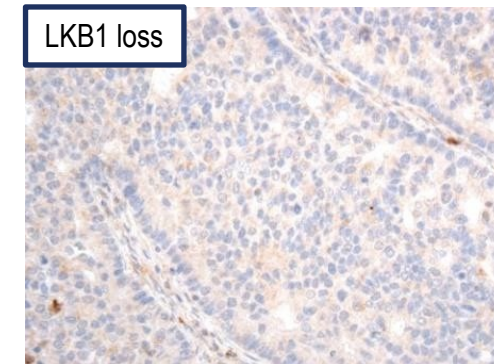
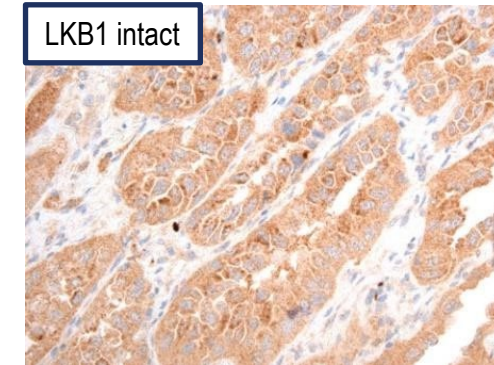
# LKB1 (Liver Kinase B1)/STK11 (Serine-Threonine Kinase 11)



- Tumor suppressor gene
  - Control of cell polarity, growth and proliferation based on cell energetic levels
- Negative prognostic factor
  - Related with more aggressive phenotype and worse survival
- Potential predictive marker
  - Resistance to ICI therapy
  - Sensitivity to mTORi
- No validated functionality test in the clinic!
  - Complexity of mutations

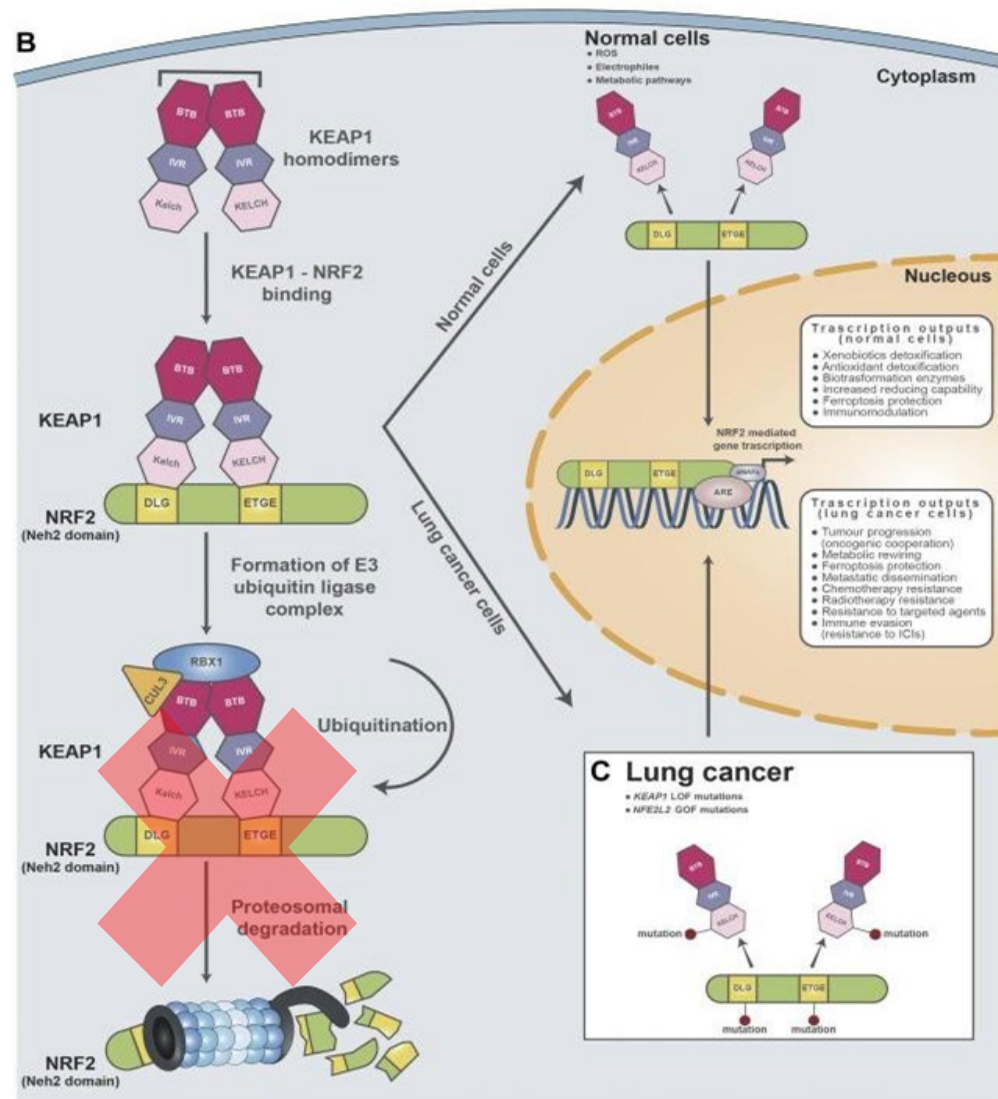
# STK11/LKB1 diagnostic test in the clinic is challenging

Method	Pros	Cons
NGS	Comprehensive, information on the type of mutation	Cost, no activity assessment, false positive or negative results (e.g., promoter hypermethylation)
IHC	Rapid, cost efficient, mutation agnostic	Equivocal or false negative results, no information on the type of mutation



LKB1 (clone Ley37D/G6) IHC 400x

# KEAP1-NRF2 axis is crucial for cellular homeostasis, enabling cells to tolerate oxidative and metabolic stress, and xenobiotics

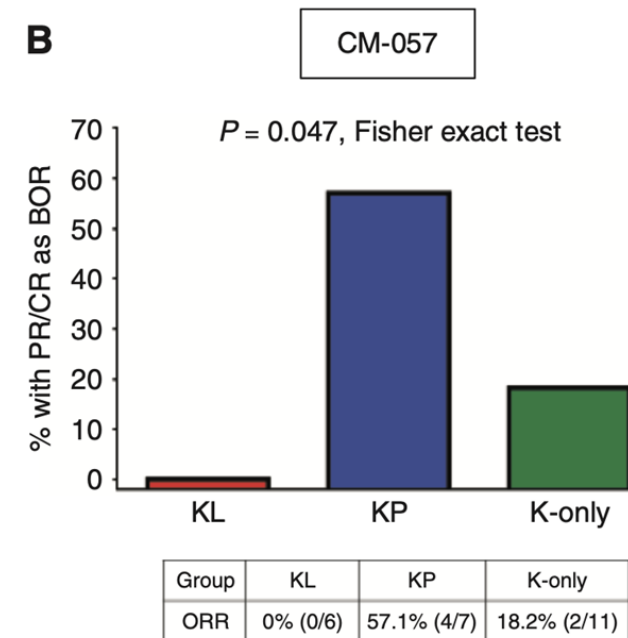
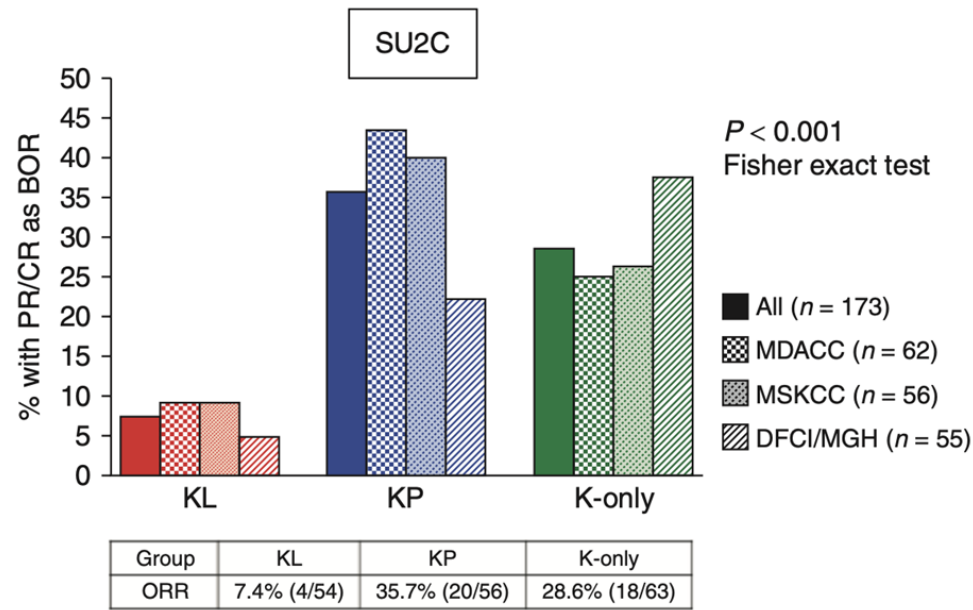
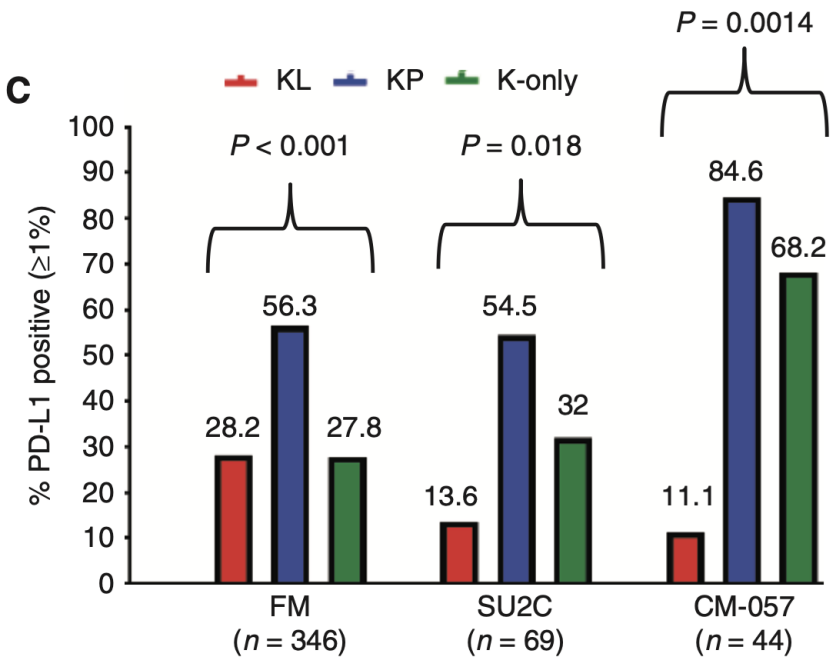


1. *KEAP1* mutations lead to the release and constitutive activation of NRF2, promoting cellular resistance to oxidative stress, proliferation, and metabolic reprogramming
2. *KEAP1* mutations are scattered throughout the whole gene length, and approximately one-third of them are **stop-gain variants**. **LOH** and **epigenetic silencing** have also been described.

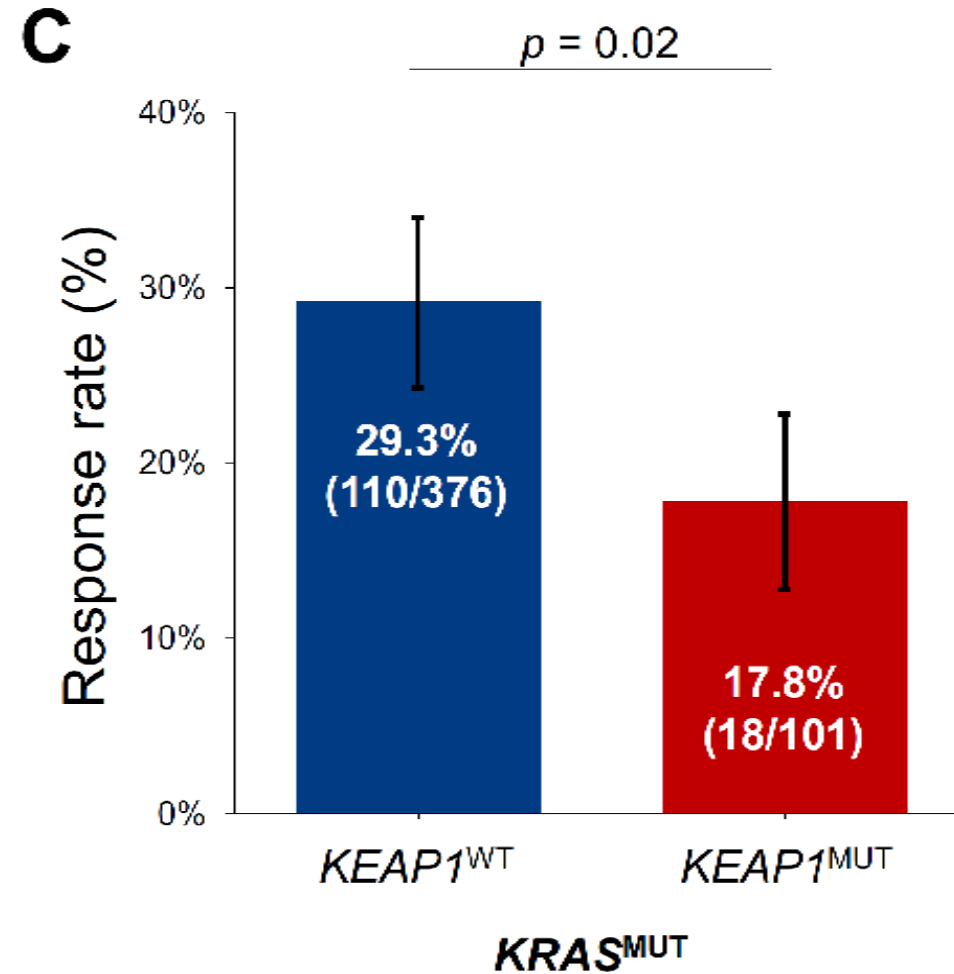
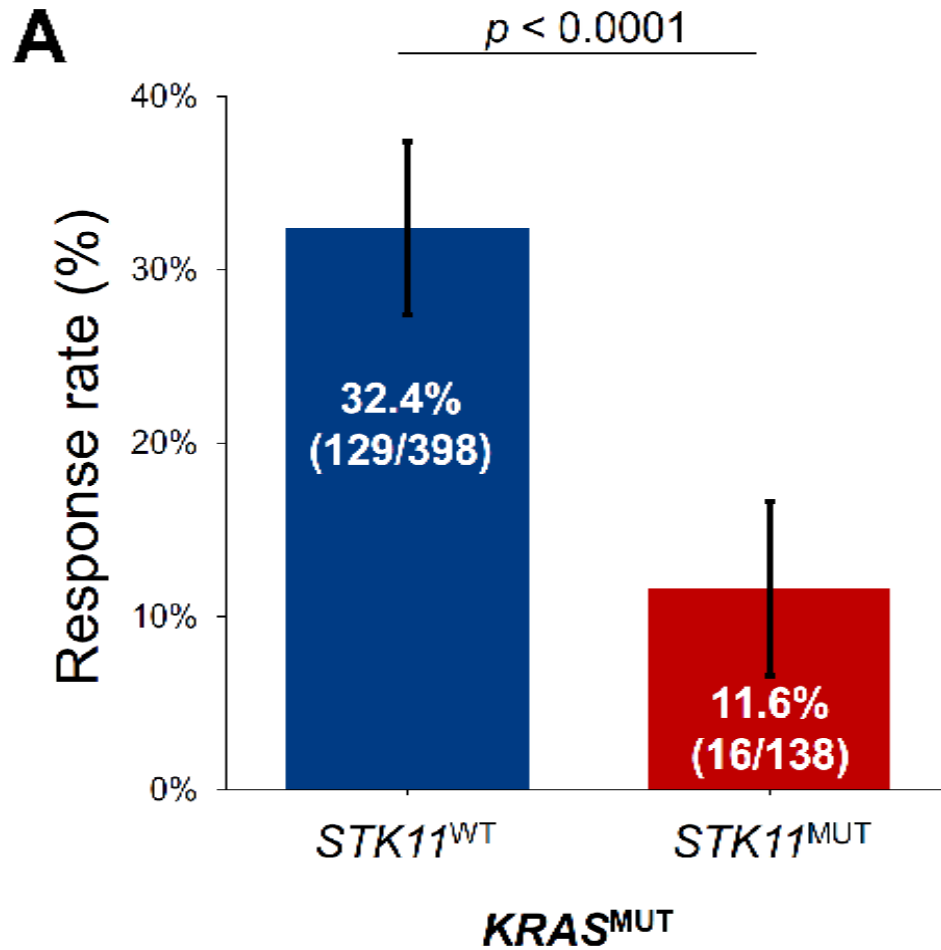
# KEAP1/Nrf2 diagnostic test in the clinic is challenging

Method	Pros	Cons
NGS	Comprehensive, information on the type of mutation	Cost, no activity assessment, false positive or negative results (e.g., promoter hypermethylation)
IHC	Rapid, cost efficient, mutation agnostic	KEAP1 protein is often still expressed even when mutated, making IHC a poor surrogate.
RNA-seq, RT-qPCR (NQO1, GCLC etc.)	Rapid, mutation agnostic	Not clinically available and not validated

# STK11 drives primary resistance to PD-(L)1 blockade

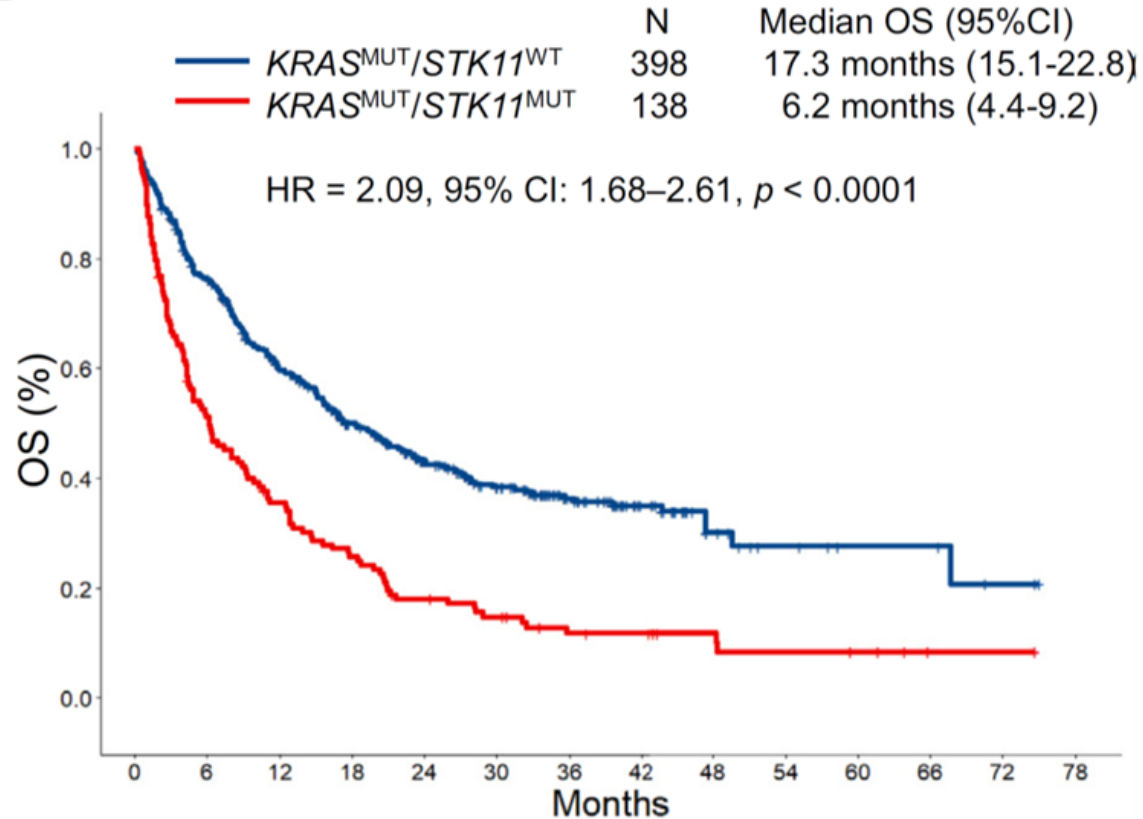


# Impact of *KEAP1*/*STK11* mutations on PD-(L)1 monotherapy efficacy in NSCLC

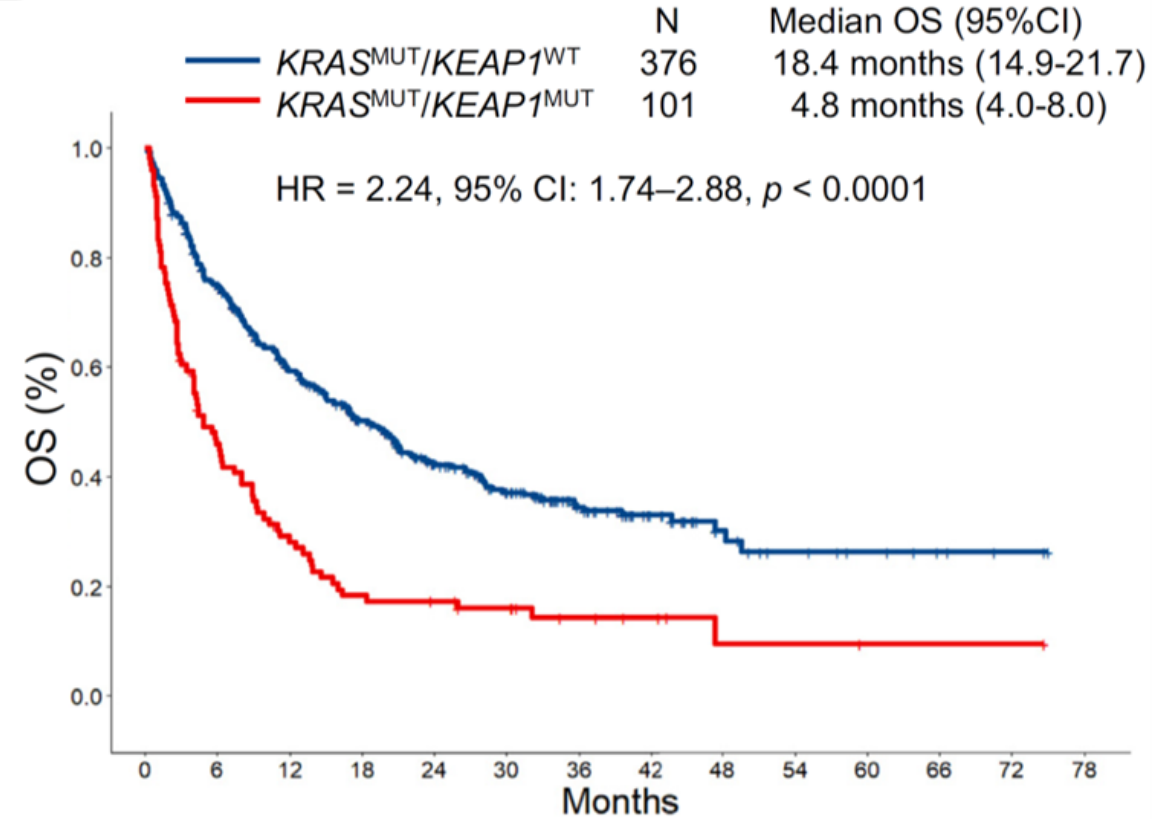


# Impact of *KEAP1*/*STK11* mutations on PD-(L)1 monotherapy efficacy in NSCLC

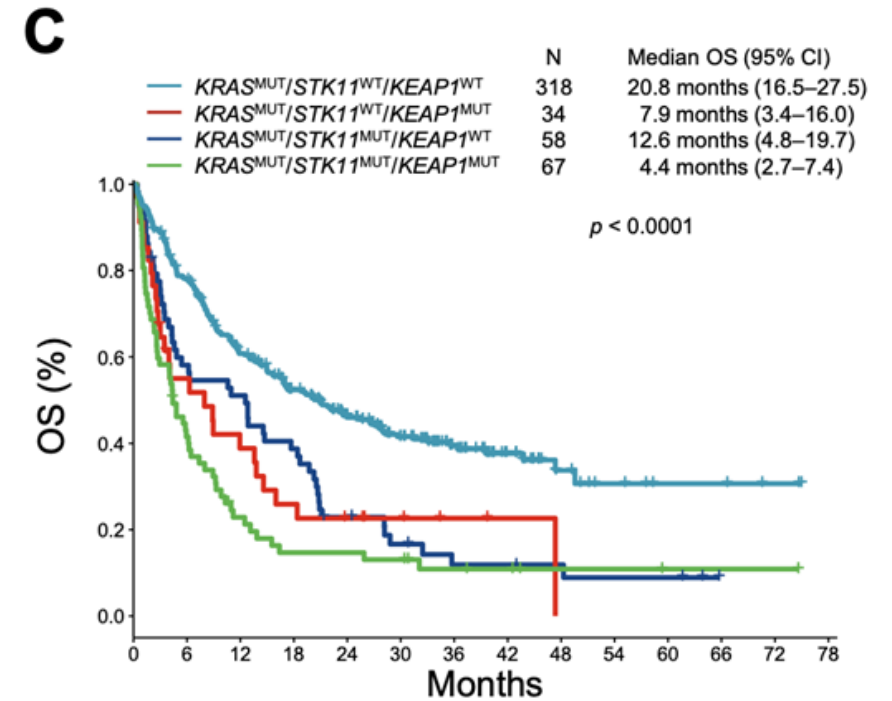
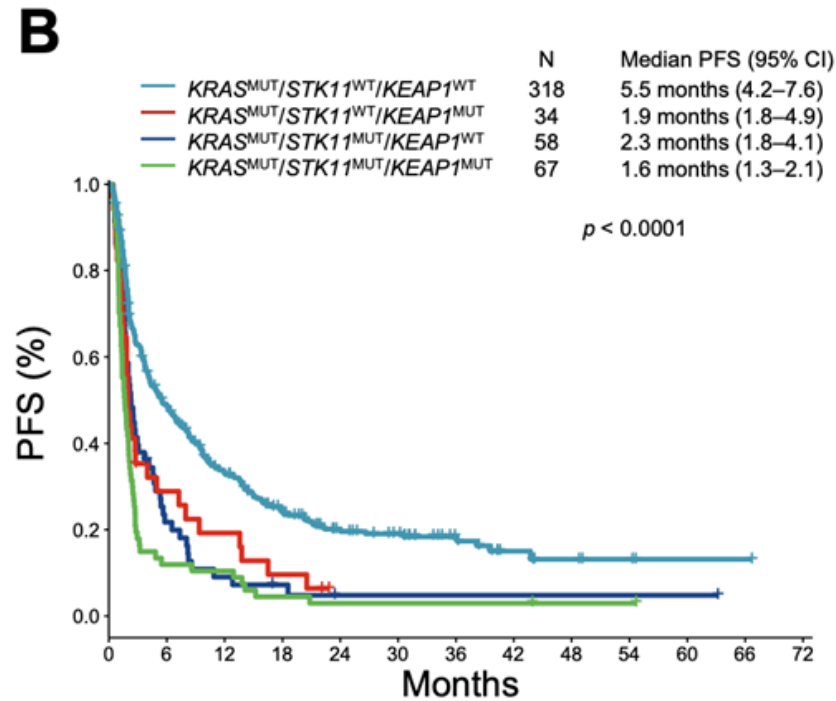
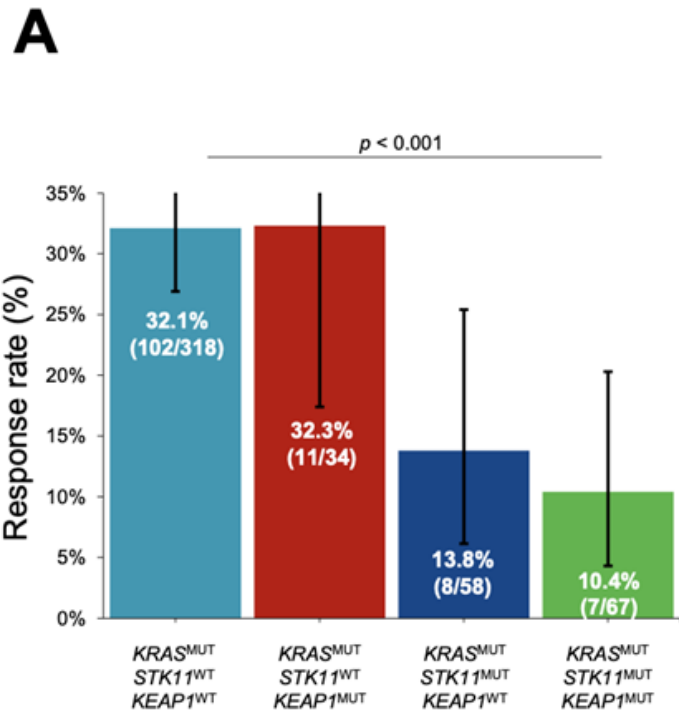
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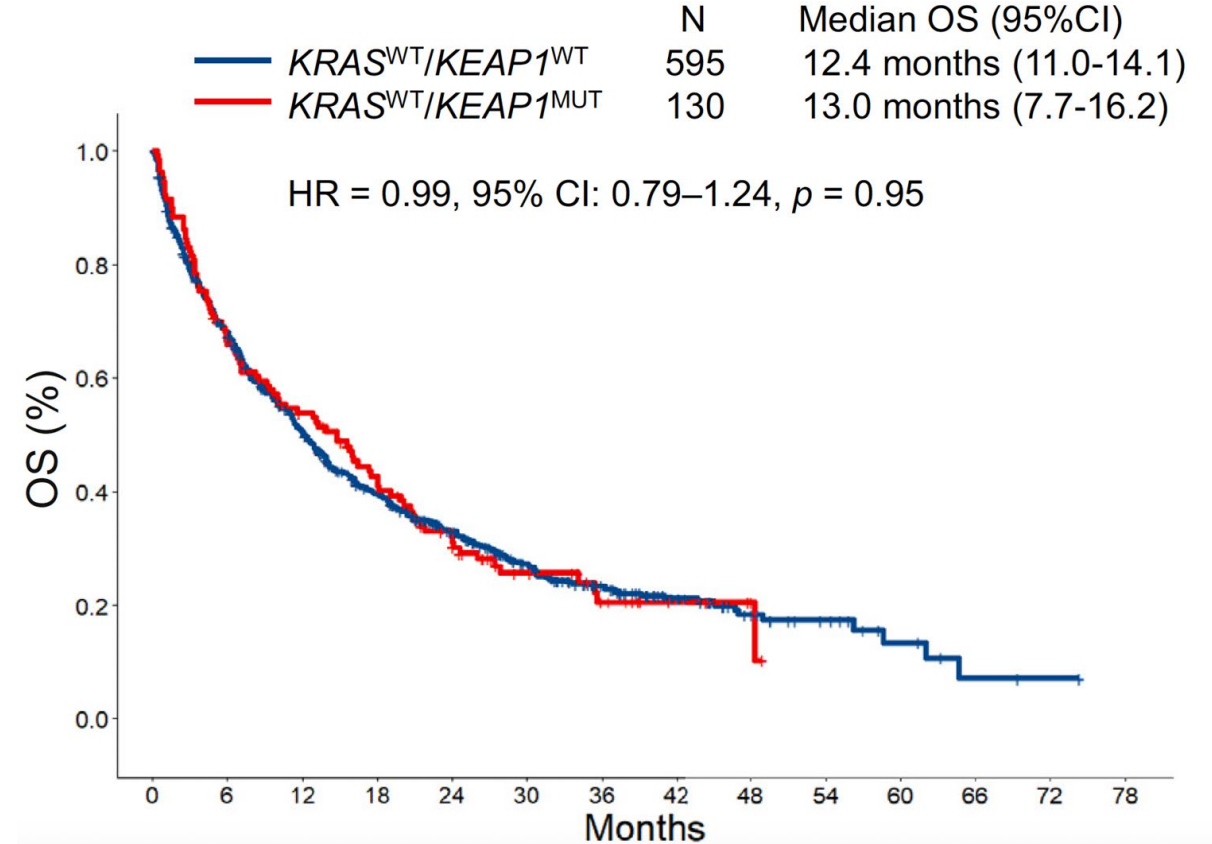
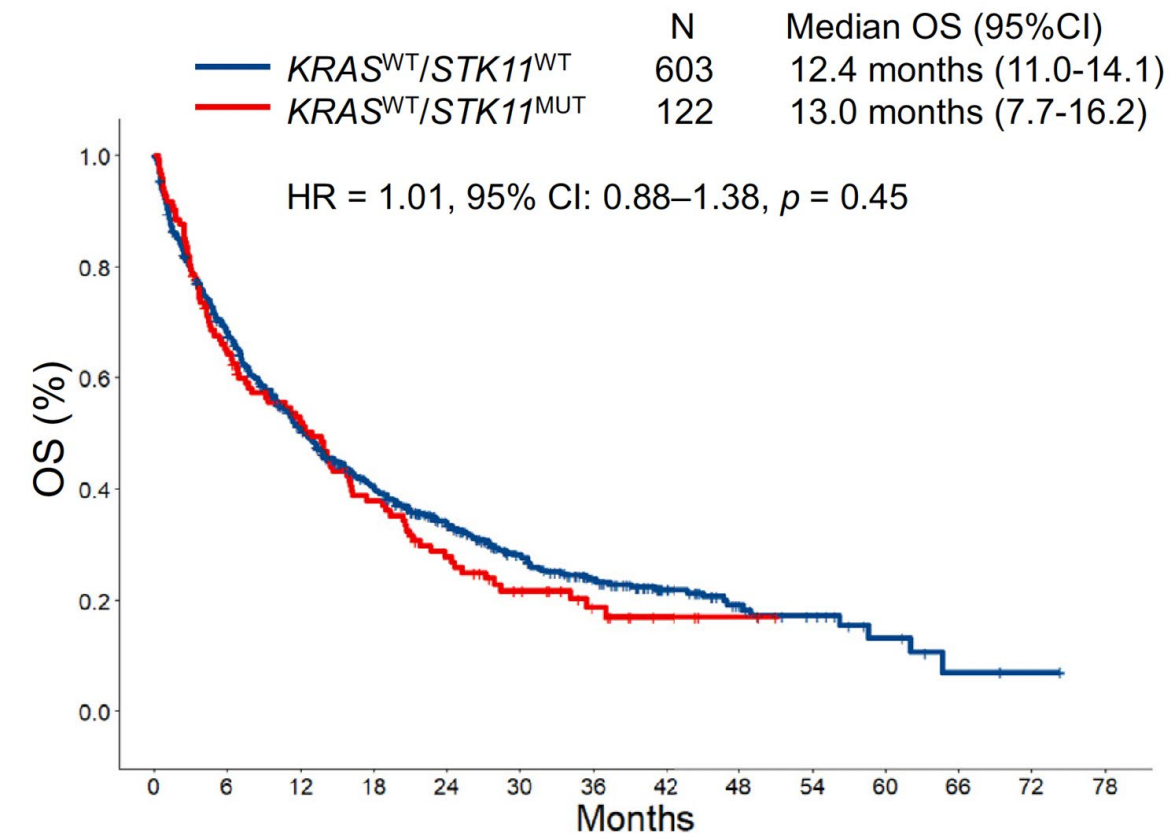
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# Triple mutant are very resistant to PD-(L)1 monotherapy

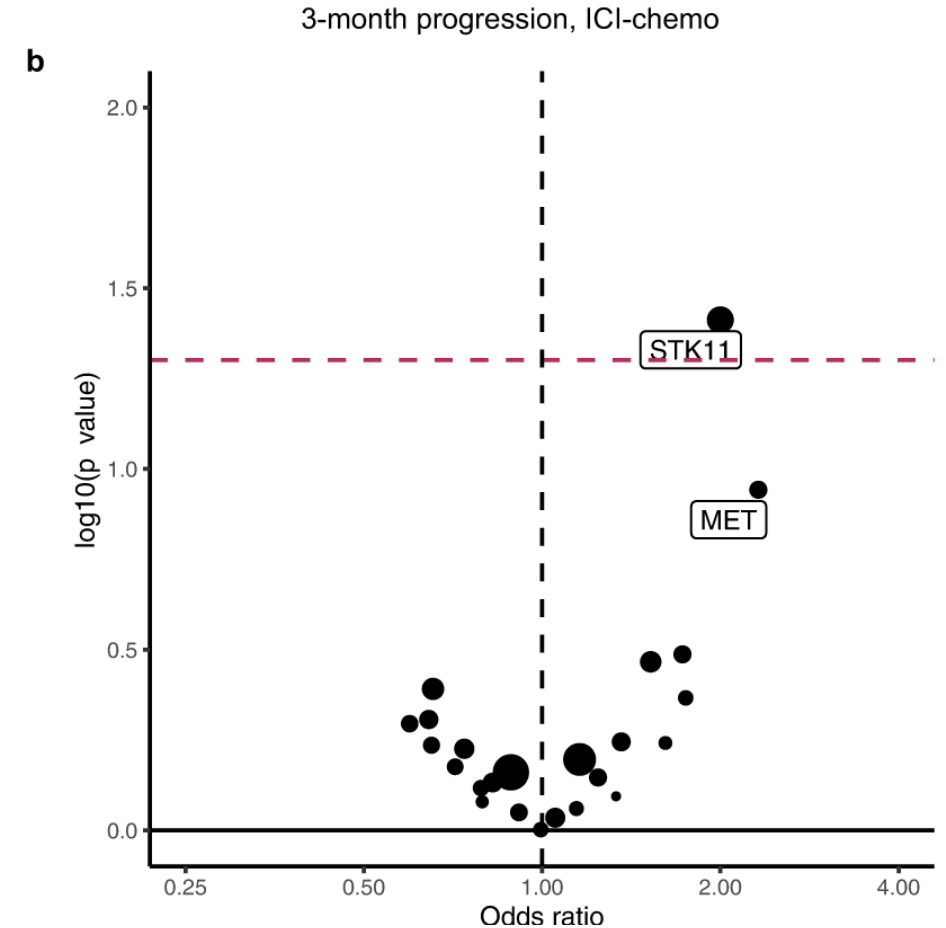
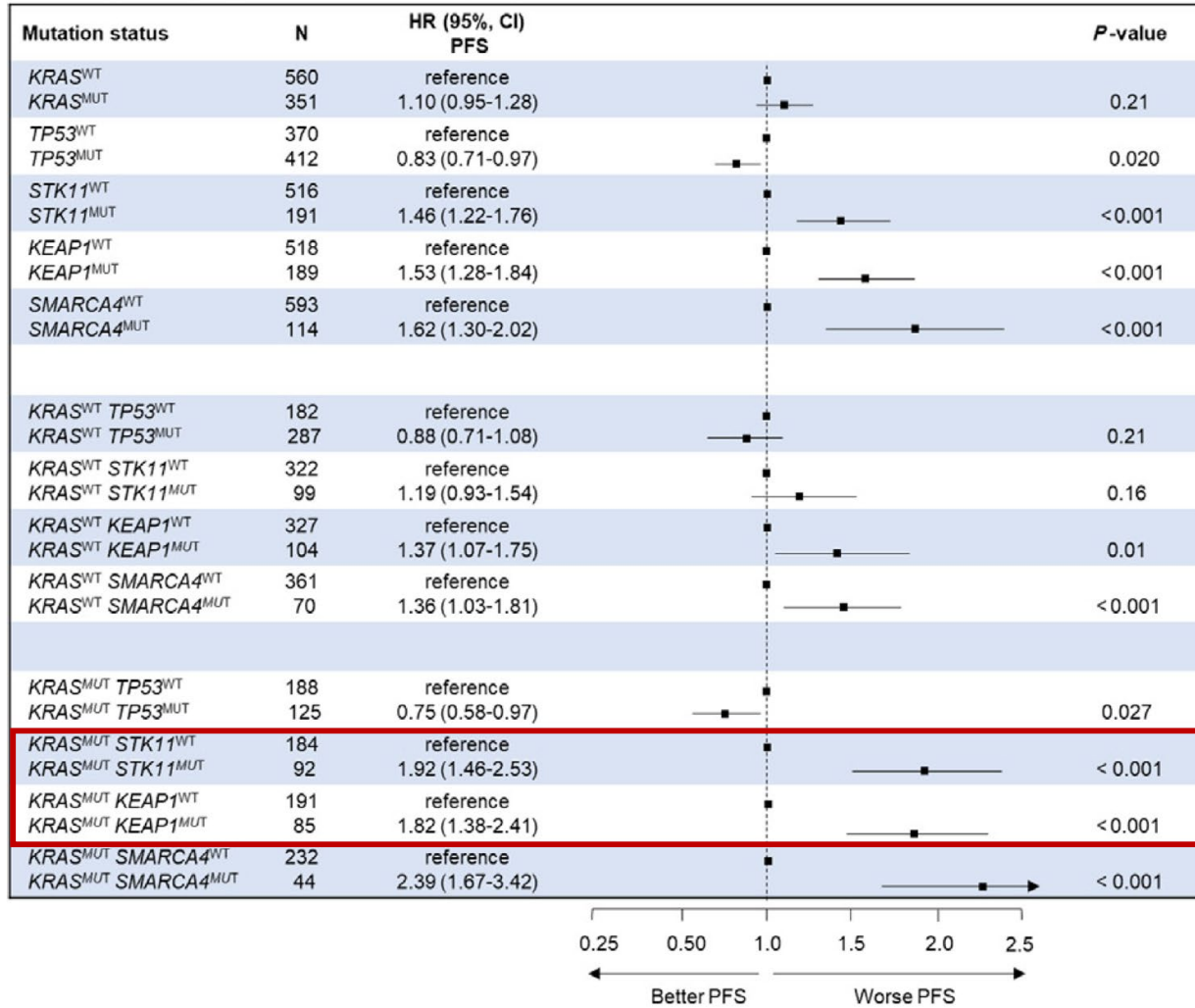


# STK11/KEAP1 mutations are not associated with ICI efficacy in KRAS WT NSCLC



# Impact of *KEAP1*/*STK11* mutations on chemo-immunotherapy efficacy in NSCLC

Forest-plot for progression-free survival (PFS)



# CTLA4 blockade for STK11 and KEAP1 mutant NSCLC

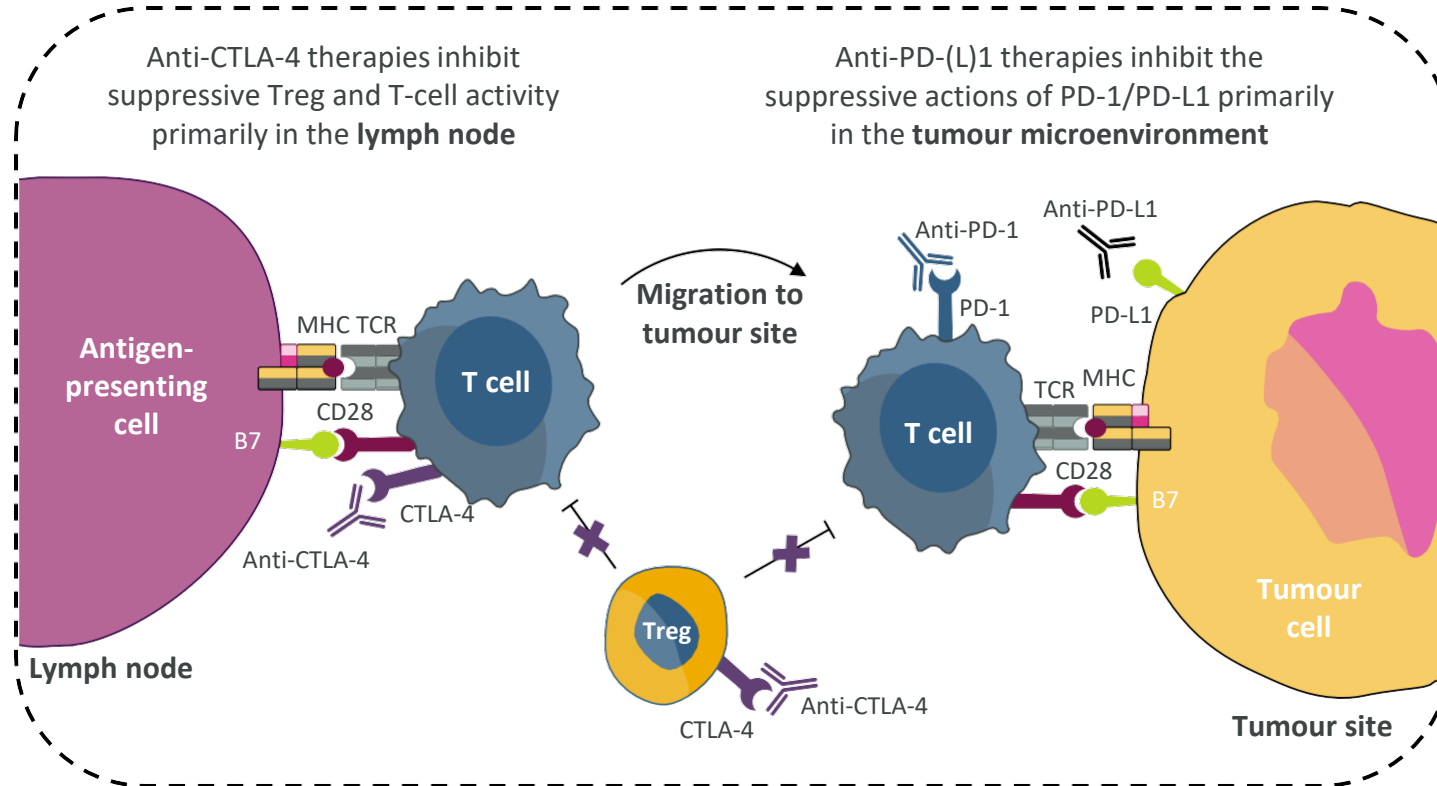


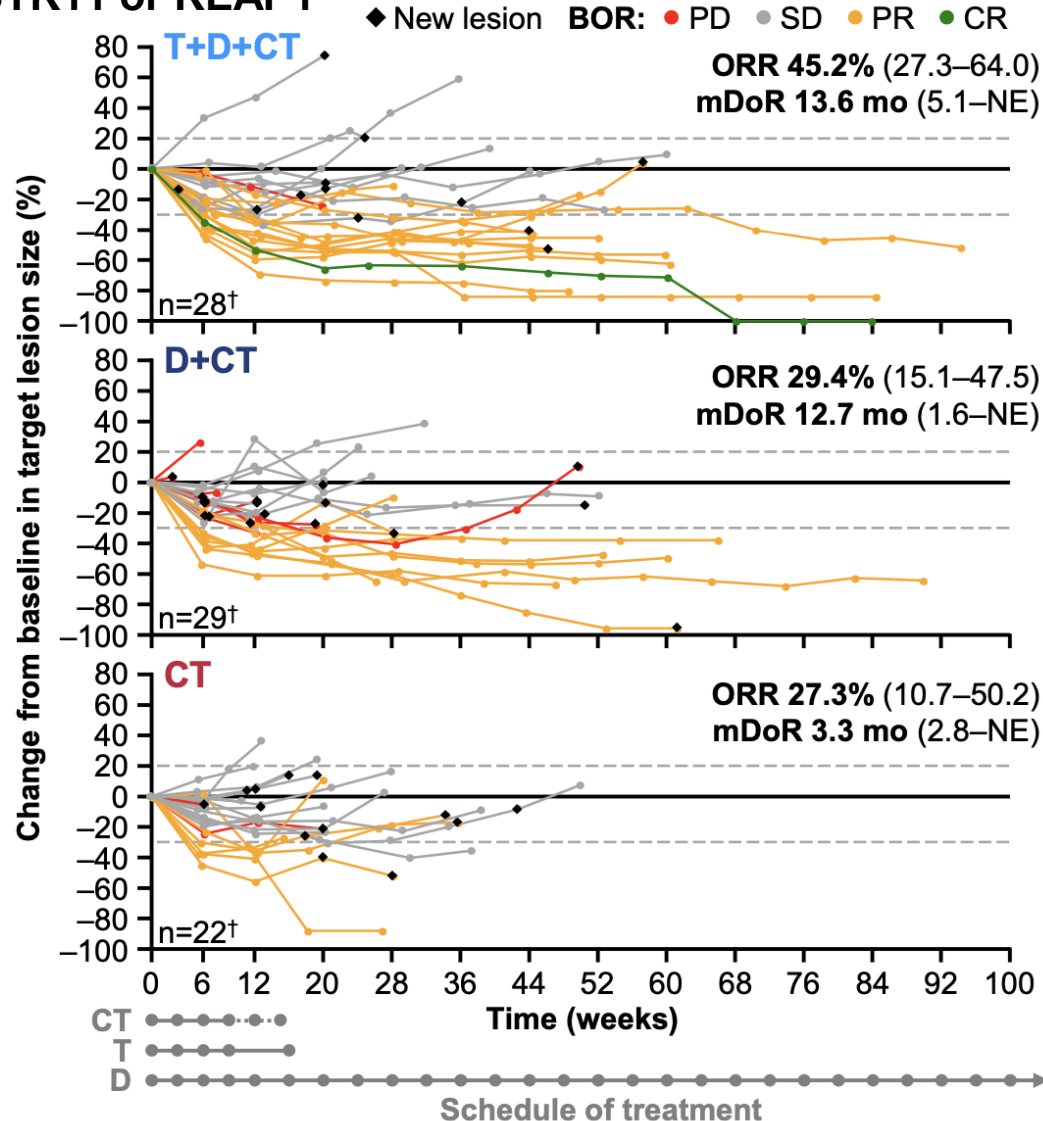
Image adapted from Buchbinder EI & Desai A. *Am J Clin Oncol* 2016;39:98–106<sup>1</sup>

CD28, cluster of differentiation 28; CTLA-4, cytotoxic T-lymphocyte-associated antigen-4; MHC, major histocompatibility complex; PD-1, programmed cell death 1; PD-(L)1, programmed cell death-(ligand) 1; TCR, T-cell receptor; Treg, regulatory T cells

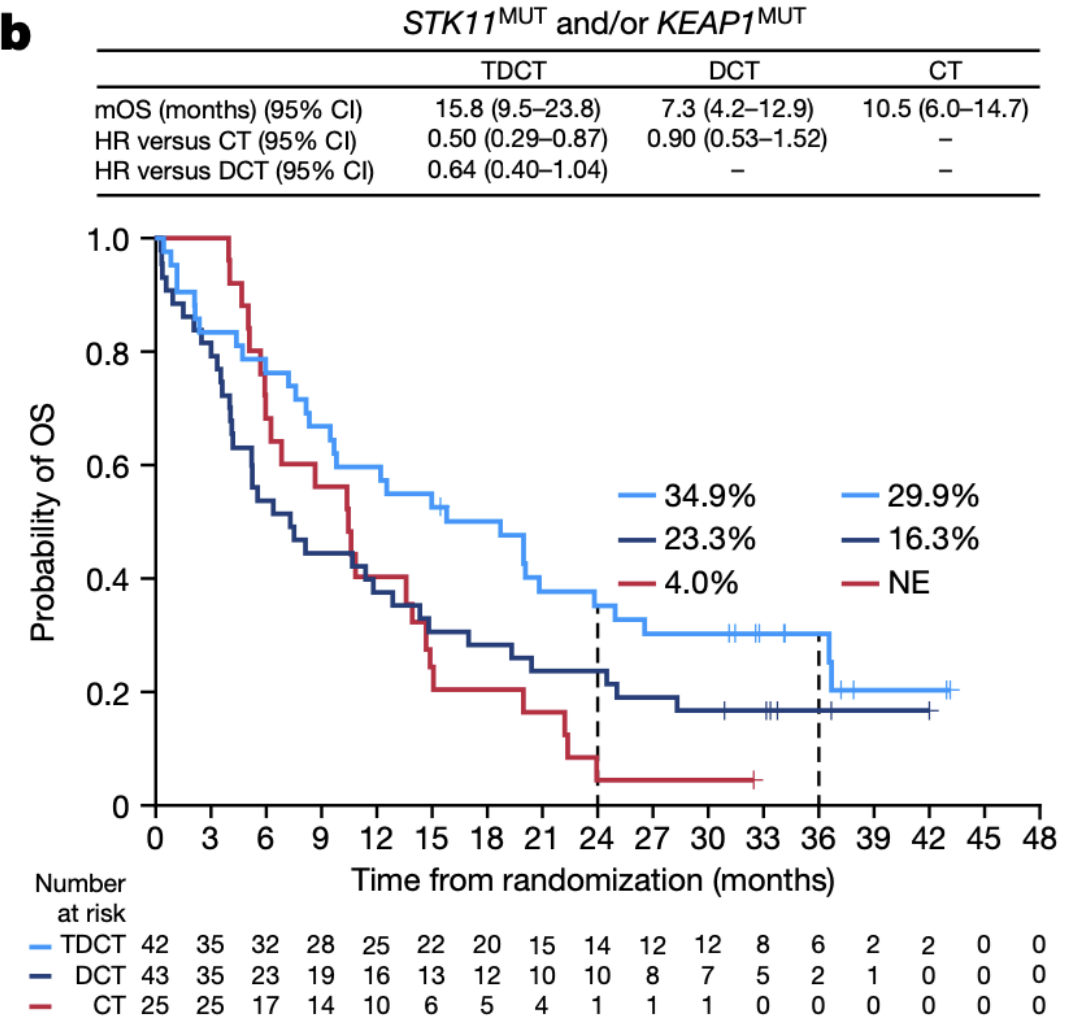
1. Buchbinder EI & Desai A. *Am J Clin Oncol* 2016;39:98–106; 2. Khan SK *et al. Clin Immunol* 2011;138:85–96; 3. Stewart R *et al. Cancer Immunol Res* 2015;3:1052–62

# CTLA4 blockade may reduce KEAP1/STK11-related resistance to PD-(L)1 inhibitors

## STK11 or KEAP1

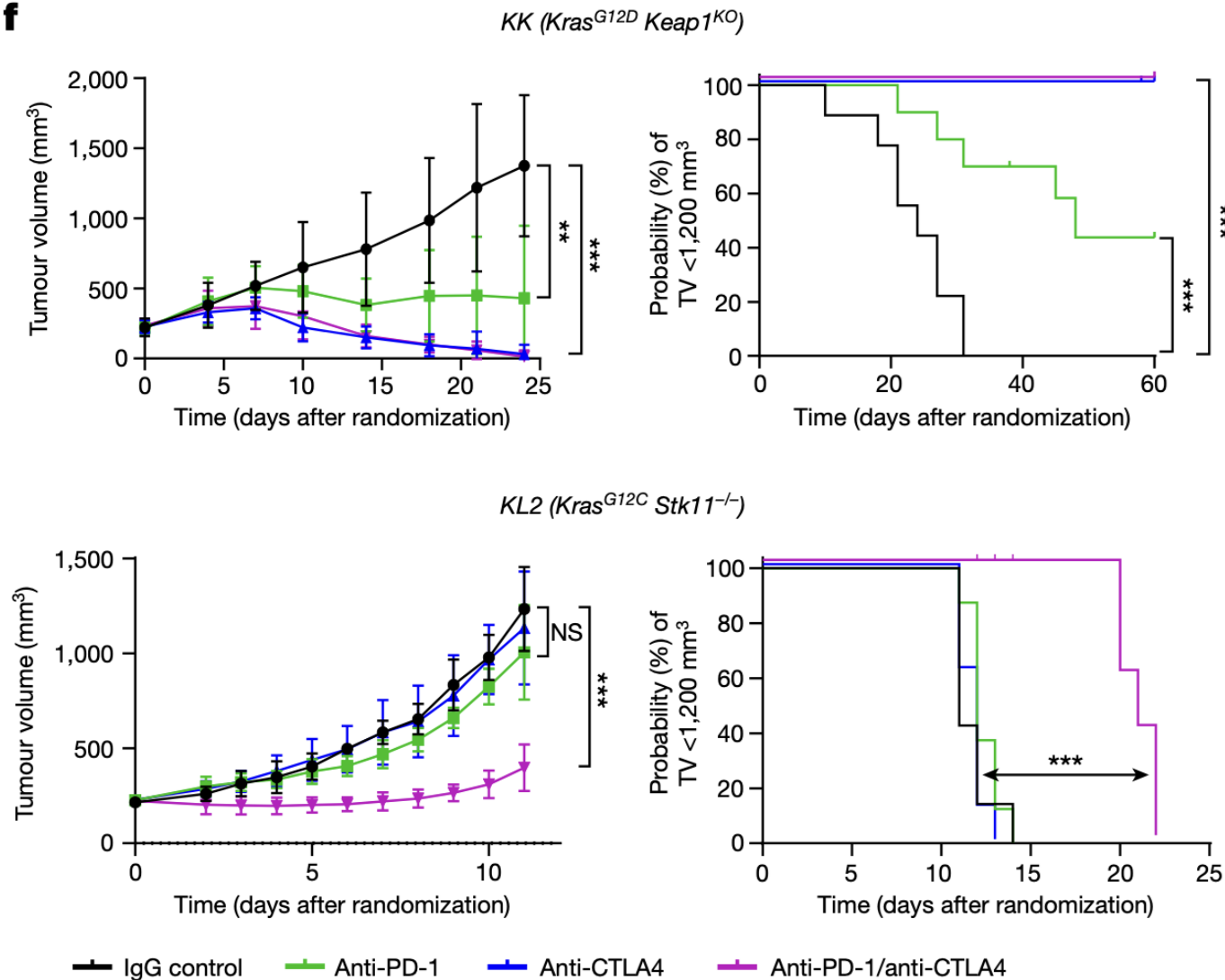


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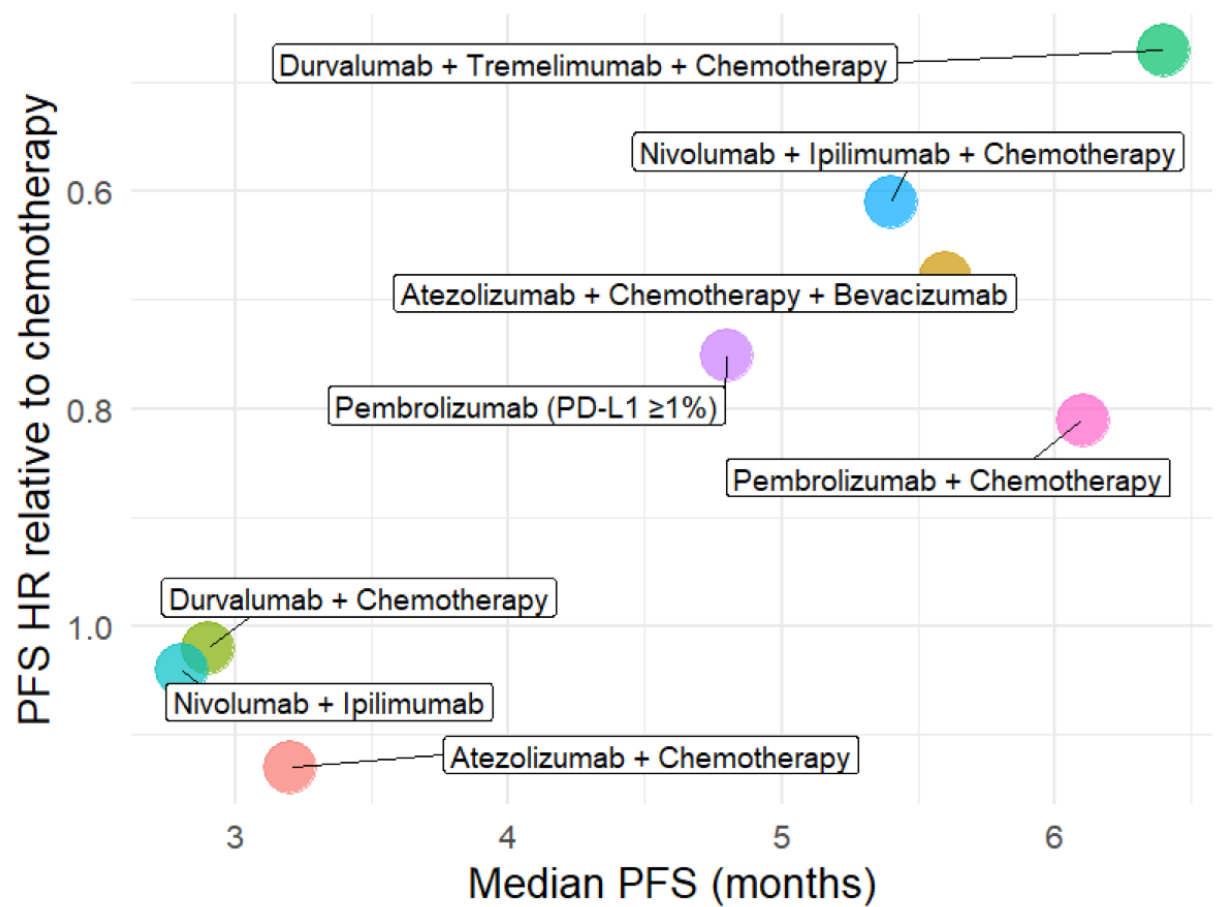
# CTLA4 blockade reduces KEAP1/STK11-related resistance to PD-(L)1 inhibitors in syngenic models in vivo

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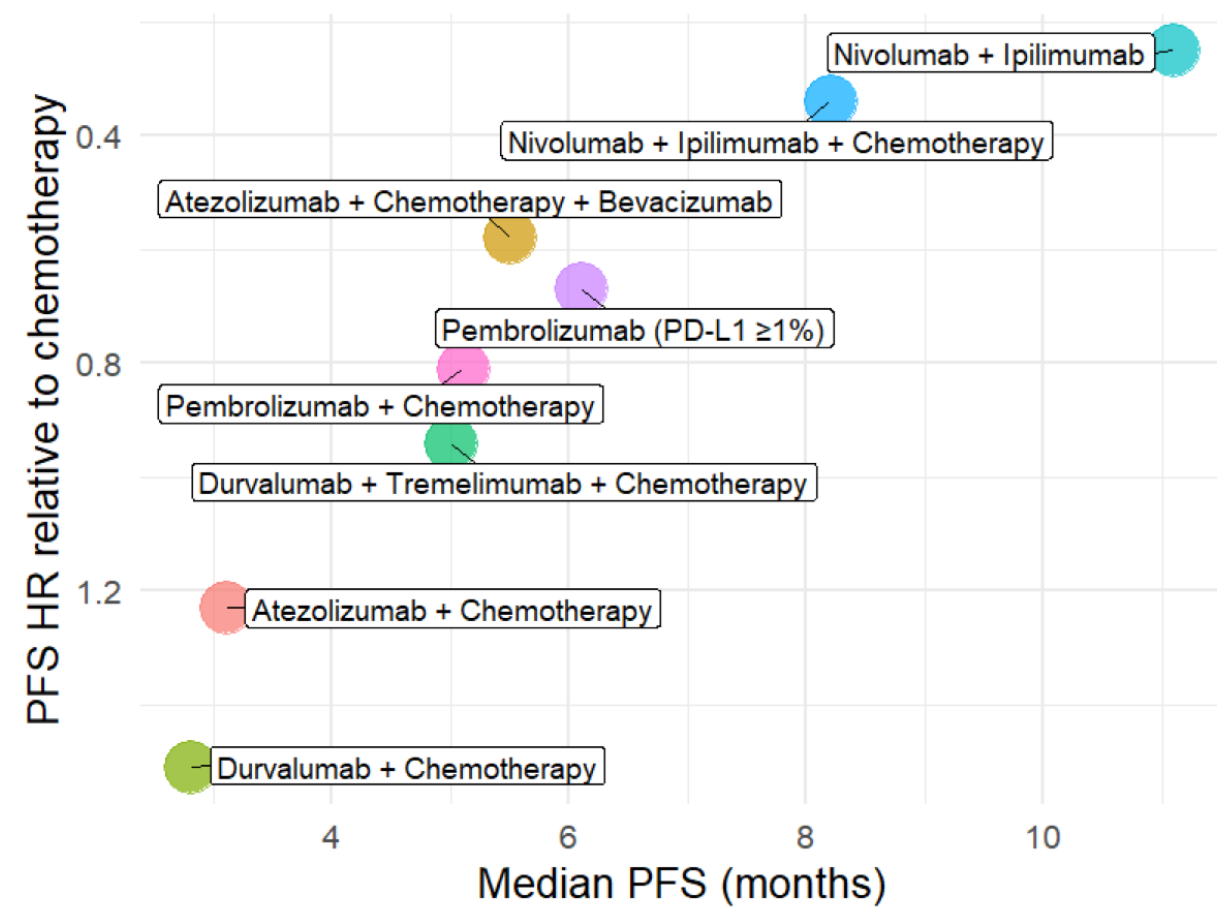


# Optimal treatment strategy for co-mutations?

*STK11* mutant NSCLC



*KEAP1* mutant NSCLC

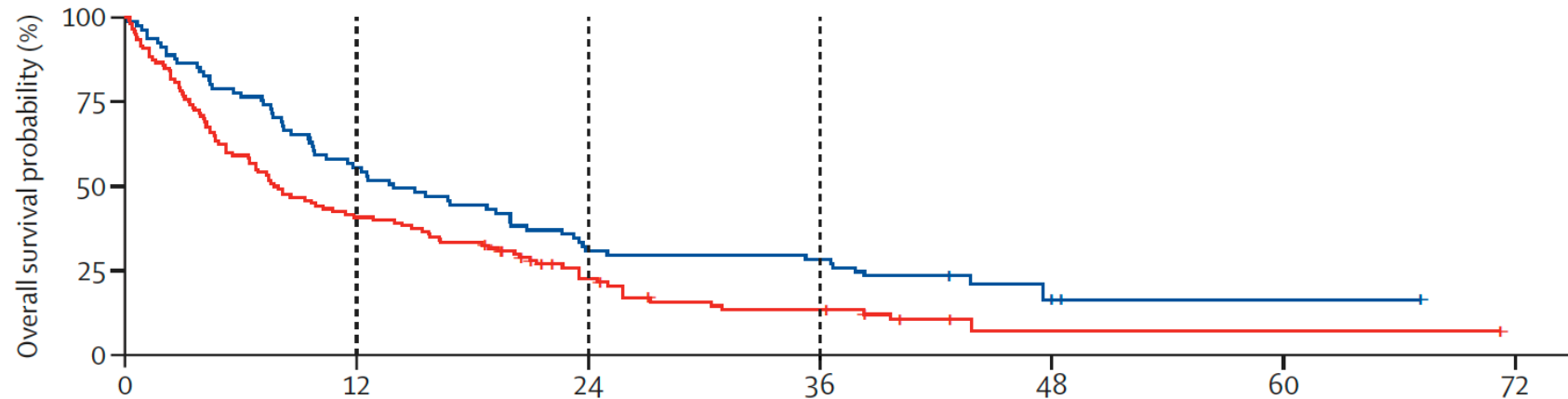


# Pooled analysis of 6 randomized clinical trials reporting outcomes in STK11 mutant NSCLC

A STK11 mutated

	Reconstructed events/patients	Median overall survival, months (95% CI)	1-year overall survival, rate (95% CI)	2-year overall survival, rate (95% CI)	3-year overall survival, rate (95% CI)
Dual CTLA-4 and PD-L1 or PD-1 blockade	65/81	13.9 (9.8–20.8)	55.6% (45.7–67.5)	30.9% (22.3–42.8)	28.4% (20.1–40.1)
Single PD-L1 or PD-1 blockade	102/120	7.8 (6.4–12.9)	40.8% (32.9–50.7)	22.7% (16.1–32.0)	13.4% (8.1–22.2)

HR 0.67; 95% CI 0.49–0.91; p=0.012



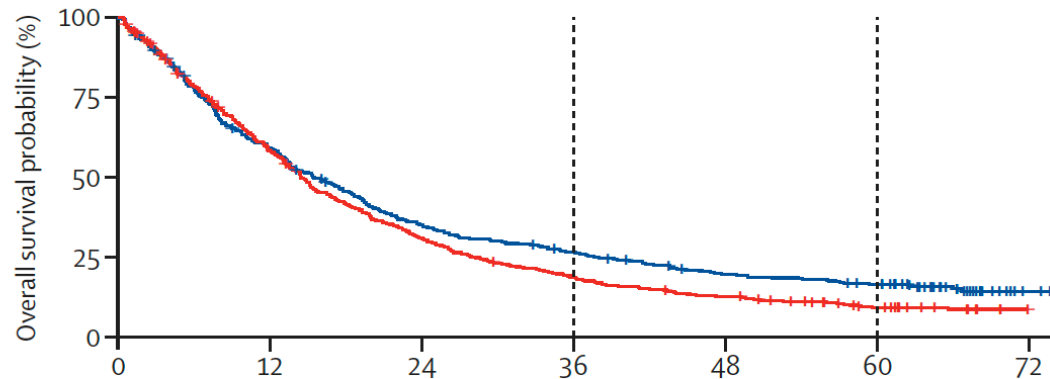
	0	12	24	36	48	60	72
Dual CTLA-4 and PD-L1 or PD-1 blockade	81 (0)	45 (0)	25 (0)	23 (0)	7 (9)	4 (12)	0 (16)
Single PD-L1 or PD-1 blockade	120 (0)	49 (0)	21 (8)	11 (10)	2 (16)	2 (16)	0 (18)

# Pooled analysis of 6 randomized clinical trials reporting outcomes in PD-L1 negative vs positive NSCLC

**A** PD-L1 TPS <1%

	Reconstructed events/patients	Median overall survival, months (95% CI)	3-year overall survival, rate (95% CI)	5-year overall survival, rate (95% CI)
Dual CTLA-4 and PD-L1 or PD-1 blockade	367/447	15.5 (13.6–18.5)	26.8% (22.9–31.3)	16.6% (13.4–20.6)
Single PD-L1 or PD-1 blockade	452/512	14.5 (13.4–15.9)	18.7% (15.5–22.4)	9.3% (7.0–12.3)

HR 0.85; 95% CI 0.74–0.98; p=0.021



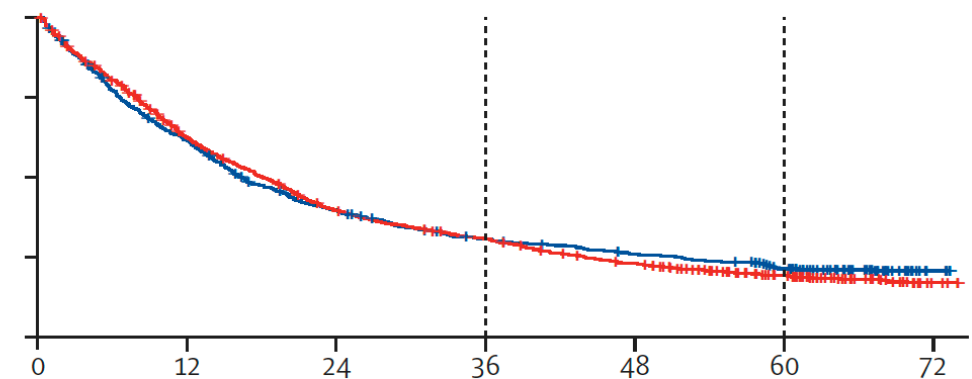
Number at risk (censored)

	0	12	24	36	48	60	72
Dual CTLA-4 and PD-L1 or PD-1 blockade	447 (0)	260 (7)	152 (10)	114 (12)	81 (16)	61 (23)	3 (77)
Single PD-L1 or PD-1 blockade	512 (0)	292 (11)	155 (12)	92 (13)	62 (14)	36 (25)	1 (59)

**B** PD-L1 TPS ≥1%

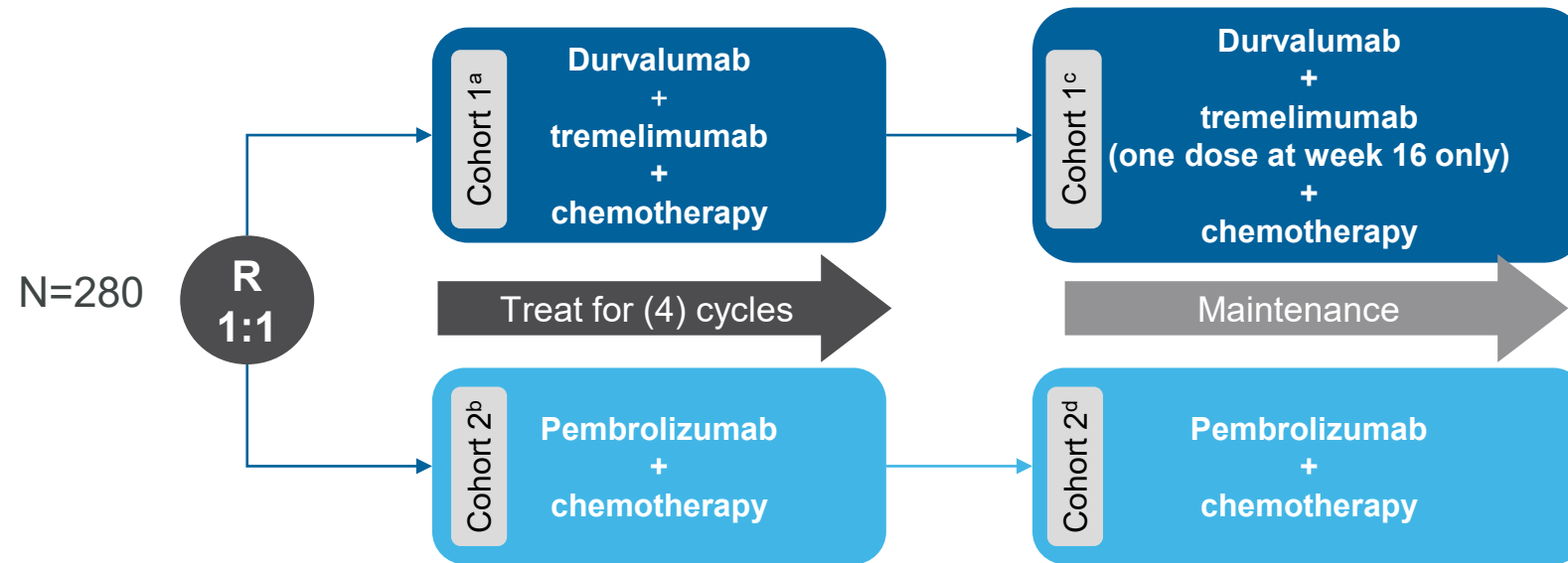
	Reconstructed events/patients	Median overall survival, months (95% CI)	3-year overall survival, rate (95% CI)	5-year overall survival, rate (95% CI)
Dual CTLA-4 and PD-L1 or PD-1 blockade	629/813	16.5 (15.0–18.9)	30.8% (27.8–34.2)	21.5% (18.8–24.6)
Single PD-L1 or PD-1 blockade	844/1056	18.1 (16.6–19.8)	30.9% (28.2–33.8)	19.3% (17.0–21.9)

HR 0.97; 95% CI 0.88–1.08; p=0.60



	0	12	24	36	48	60	72
Dual CTLA-4 and PD-L1 or PD-1 blockade	813 (0)	496 (7)	317 (12)	239 (19)	199 (23)	155 (32)	6 (178)
Single PD-L1 or PD-1 blockade	1056 (0)	646 (17)	406 (21)	313 (25)	230 (31)	160 (66)	5 (207)

# TRITON: randomized phase III clinical trial comparing POSEIDON vs KN189 in STK11/KEAP1 mutant NSCLC



## Primary endpoints

- OS

## Key secondary endpoints

- PFS
- ORR, DoR
- Safety/Tolerability

## Exploratory endpoint

- OS and PFS in patients with KRAS or KEAP1

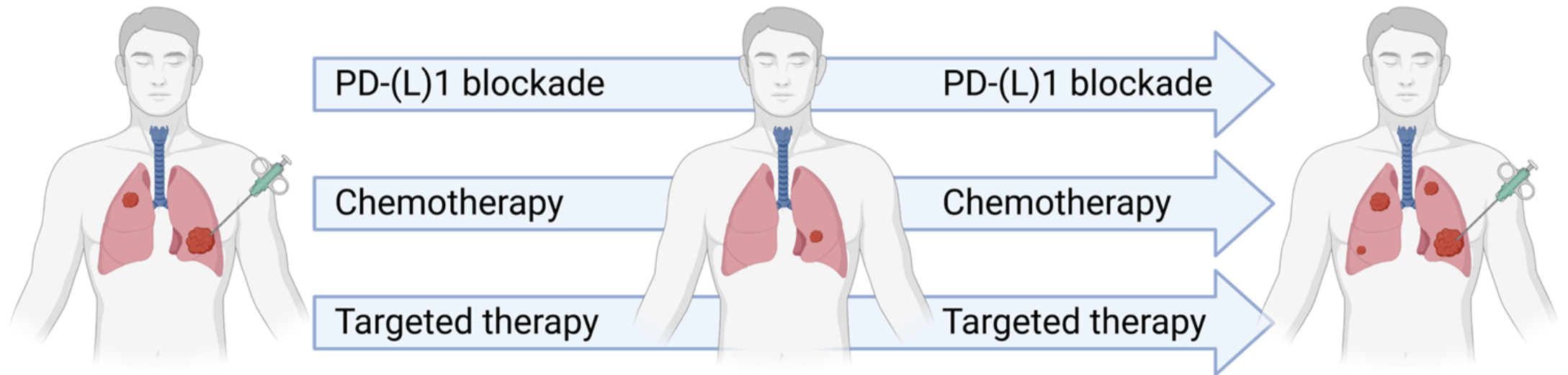
## Patient population

- Metastatic nonsquamous NSCLC
- No prior systemic treatment for metastatic disease
- **KRAS, STK11, and/or KEAP1 alterations**
- No EGFR or ALK alterations
- ECOG PS 0 or 1
- Mandatory tissue requirement

## Post Analysis

- PD-L1 expression
- Comutations
- Smoking history

# Understanding of acquired resistance to ICI in NSCLC: DFCI



Pre-treatment tumor sample

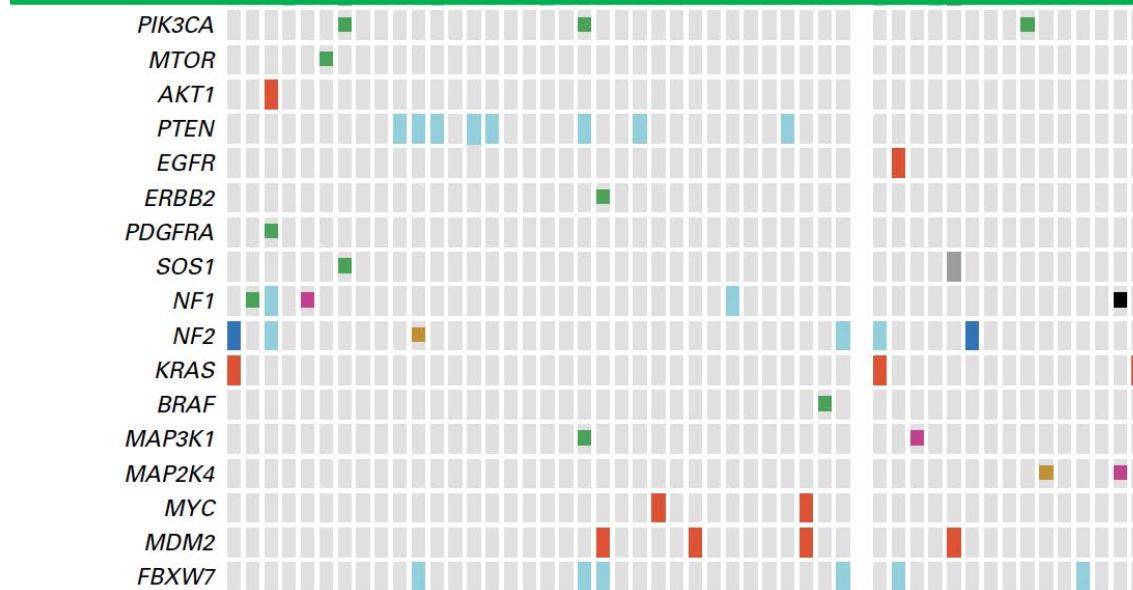
Treatment effect

Acquired resistance tumor sample

Analysis	PD-(L)1 blockade (N=82)	Chemotherapy (N=32)	Targeted therapy (N=89)
• Tumor genomic profiling	N=79	N=30	N=89
• Digital pathology	N=16	N=5	N=11
• Multiplexed immunofluorescence	N=6	N=0	N=0
• HLA class I immunohistochemistry	N=8	N=7	N=9

# Acquired mutations and copy number changes after ICI

**TSG**  
**Immune metabolism**



Acquired mutation

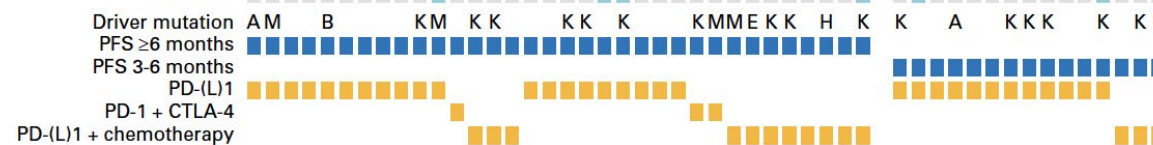
- Missense
- Nonsense
- Insertion/deletion
- Splice site
- Not assessed

Acquired copy-number alteration

- Heterozygous deletion
- Homozygous deletion
- Amplification

Baseline driver mutation

- K KRAS
- A ALK
- M MET
- E EGFR
- H HER2
- B BRAF

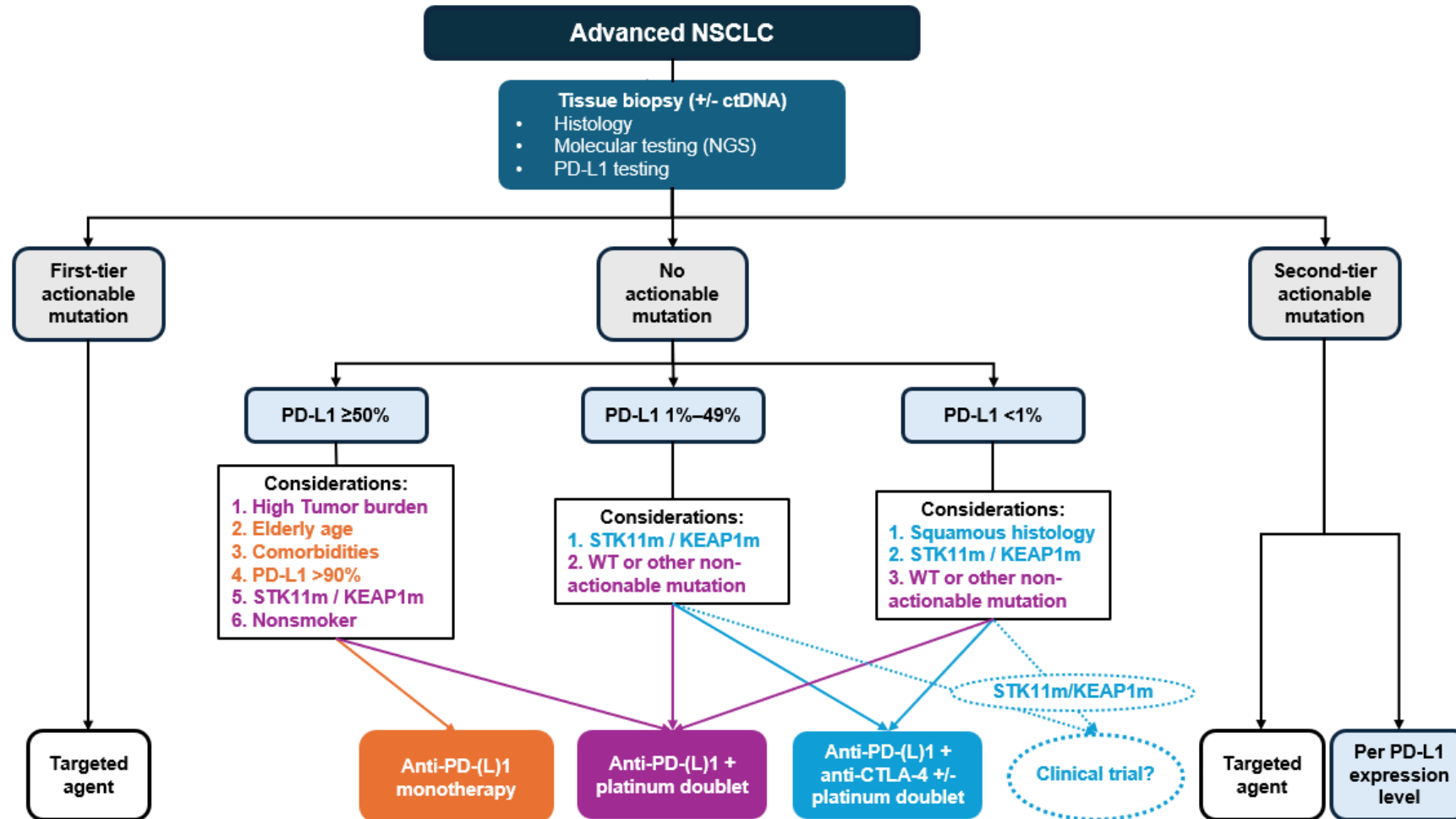


**Immune checkpoint**  
**Antigen presentation**

# Are we testing for STK11 and KEAP1?

	Assay	Company	STK11	KRAS	KEAP1	Sample type
Decentralized (in-house) assays	TruSight Oncology 500 <sup>1</sup>	Illumina	+	+	+	FFPE
	TruSight Oncology 500 High-Throughput <sup>1</sup>	Illumina	+	+	+	FFPE
	TruSight Oncology 500 ctDNA assay v2 <sup>2</sup>	Illumina	+	+	+	ctDNA
	TruSight Tumor 170 <sup>3</sup>	Illumina	+	+	-	FFPE
	AmpliSeq Focus <sup>4</sup>	Illumina	-	+	-	FFPE
	AmpliSeq Comprehensive Panel <sup>5</sup>	Illumina	+	+	-	FFPE
	OncoPrint™ Focus Assay <sup>6</sup>	ThermoFisher	-	+	-	FFPE
	OncoPrint™ Comprehensive Assay <sup>7</sup>	Thermo Fisher	+	+	-	FFPE
	OncoPrint™ Precision Assay <sup>8</sup>	Thermo Fisher	-	+	-	FFPE
	OncoPrint™ Dx Target Test <sup>9</sup>	Thermo Fisher	-	+	-	FFPE
Centralized (outsourced)	Archer™ FUSIONPlex™ Lung v2 Panel <sup>10</sup>	Integrated DNA Technologies	-	+	-	FFPE
	AmoyDx® HANDLE Classic NGS Panel <sup>11</sup>	Amoy Diagnostics	+	+	+	FFPE
	Guardant360® CDx <sup>12</sup>	Guardant Health	+	+	-	ctDNA
	FoundationOne® CDx <sup>13</sup>	Foundation Medicine	+	+	+	FFPE
	FoundationOne® Liquid CDx <sup>14</sup>	Foundation Medicine	+	+	+	ctDNA
	Caris	Caris Life	+	+	+	FFPE
	TEMPUS	TEMPUS	+	+	+	FFPE

# Current guidelines and pathways do not include STK11 and KEAP1



# Take home messages

- STK11 and KEAP1 are tumor suppressor genes involved in maintaining metabolic homeostasis under normal conditions. In non–small cell lung cancer, their inactivation contributes to tumor initiation, progression, and metastasis.
- Mutations in both STK11 and KEAP1 occur more commonly in smokers and carry distinct clinical implications depending on concurrent alterations in genes such as TP53 and KRAS.
- These mutations confer resistance to immune checkpoint inhibitors and are associated with an immune-cold or immune-depleted tumor microenvironment.
- Therapeutic strategies to overcome the immunosuppressive phenotype of STK11- and KEAP1-mutant NSCLC are currently under investigation and dual PD-(L)1 blockade + CTLA-4 inhibition has the potential to abrogate resistance.

# Acknowledgements

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