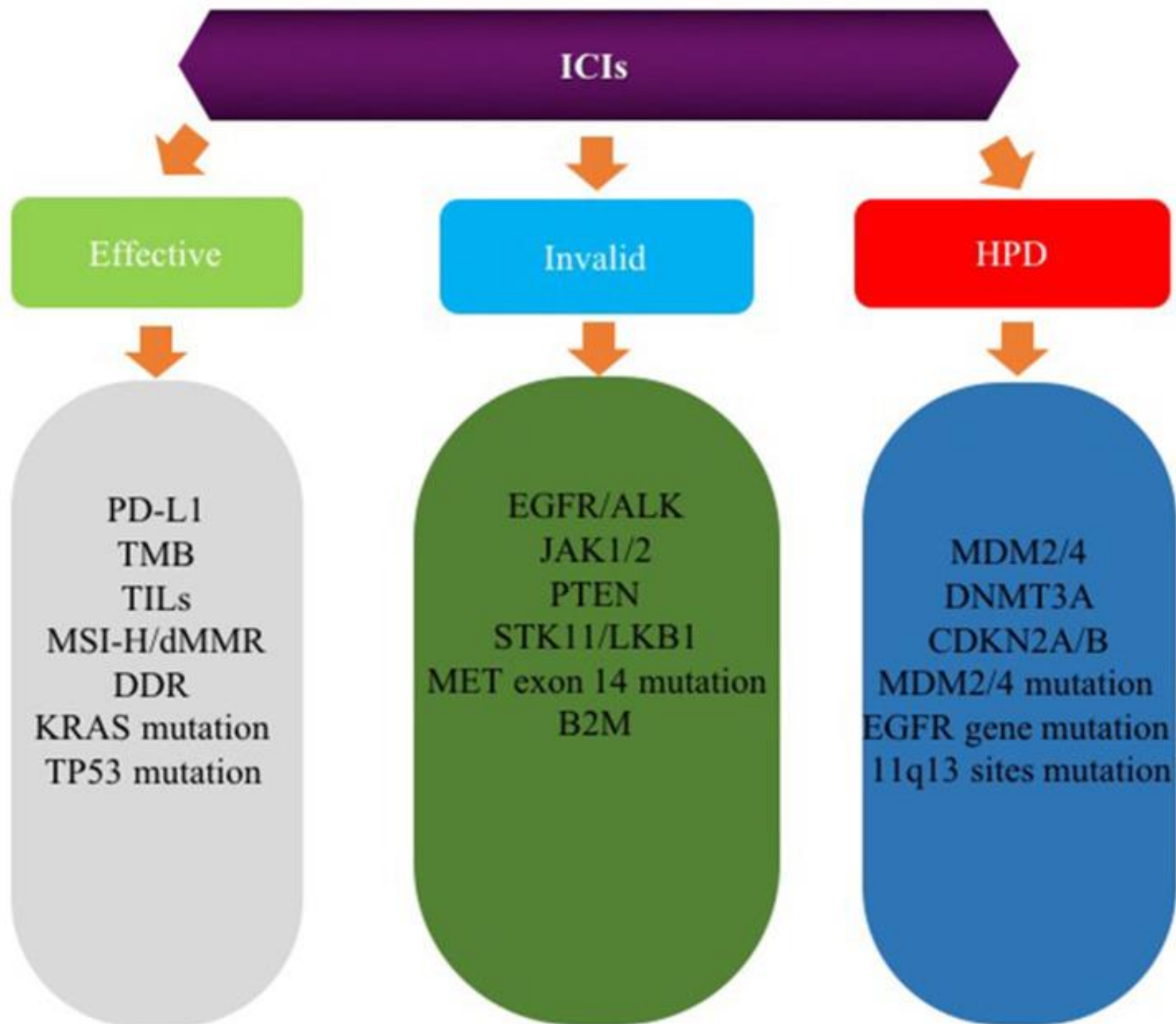


# ***Biomarkers for efficacy with immunotherapy*** **(“non -PDL1/MSI/TMB”)**

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# Tumor-infiltrating lymphocytes (TILs)

- In NSCLC, an abundance of TILs in primary tumor tissue has been associated with a more favorable prognosis.
- The abundance of TILs may also be used as a biomarker to predict the efficacy of PD-1/PD-L1 inhibitors.
- The proliferation of CD8<sup>+</sup> T cells has been directly associated with the shrinkage of tumors on imaging after ICI treatment. [1]
- In KEYNOTE-001, the number of CD8<sup>+</sup> T lymphocytes in the tumor parenchyma and margins of the baseline biopsy specimen correlated with Pembrolizumab response. [2]
- In those undergoing CTRT, Univariate and multivariate analyses demonstrated that CD8<sup>+</sup> TIL density was an independent and significant predictive factor for PFS and OS. [3]

## Prognostic Role of Tumor-Infiltrating Lymphocytes in Lung Cancer: a Meta-Analysis

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Changping Wu<sup>a</sup> Jingting Jiang<sup>a</sup>

**Conclusion:** This meta-analysis clarified that high level of CD8<sup>+</sup> and CD3<sup>+</sup> T cells infiltration in TS or TN, and high CD4<sup>+</sup> T lymphocytes infiltration in TS showed better OS in lung cancer patients, whereas high density of FOXP3<sup>+</sup> T cells infiltration in TS could be recognized as a negative prognostic factor.

*Nature*. 2014 November 27; 515(7528): 568–571. doi:10.1038/nature13954.

## PD-1 blockade induces responses by inhibiting adaptive immune resistance

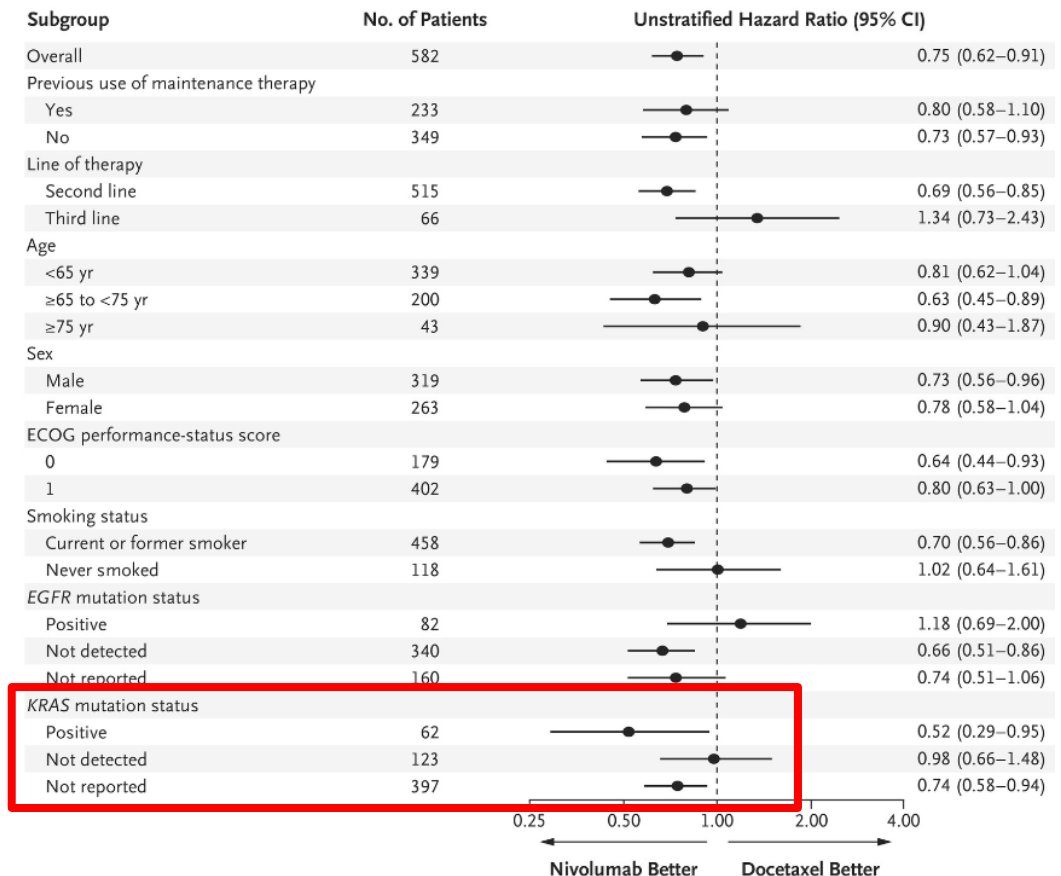
patients. Our findings indicate that tumour regression following therapeutic PD-1 blockade requires pre-existing CD8<sup>+</sup> T cells that are negatively regulated by PD-1/PD-L1 mediated adaptive immune resistance.

1. *Nature*. 2014;515:568–571.
2. *N Engl J Med*. 2015 May 21;372(21):2018-28
3. *Eur J Cancer*. 2016 Mar;55:7-14.

## KRAS mutations

- 15–20% of patients with NSCLC, particularly in smokers with lung adenocarcinoma
- KRAS mutations are implicated in tumor formation, proliferation, migration, diffusion and angiogenesis
- KRAS did not regulate and available data is variable regarding correlation with PD-L1 expression.

CheckMate-057 confirmed that patients with KRAS mutations benefited more from nivolumab compared with those without KRAS mutations



**Table 2. Atezolizumab Efficacy by Cohort and Mutation Status**

PD-L1 Status, Mutation Status, and Cohort		No. of Patients	ORR per IRF, No. (%; 95% CI) <sup>a</sup>		Median DOR per IRF, months (95% CI) <sup>a</sup>		Median PFS per IRF, months (95% CI) <sup>a</sup>		Median OS, months (95% CI)	
All treated patients (TC2/3 or IC2/3)										
Cohort										
1		139	30 (22; 15 to 29)		9.8 (5.6 to NE)		5.4 (3.0 to 6.9)		20.1 (20.1 to NE)	
2		268	52 (19; 15 to 25)		NE (8.3 to NE)		2.8 (1.5 to 3.9)		15.5 (12.3 to NE)	
3		252	45 (18; 13 to 23)		11.8 (6.9 to NE)		2.8 (2.7 to 3.0)		13.2 (10.3 to 17.5)	
PD-L1 TC3 or IC3 subgroup										
Cohort										
1		65	20 (31; 20 to 43)		10.0 (6.9 to NE)		5.6 (2.7 to 8.3)		NE (12.0 to NE)	
2		122	32 (26; 19 to 35)		NE (8.3 to NE)		4.0 (1.5 to 5.5)		15.1 (12.0 to NE)	
3		115	31 (27; 19 to 36)		7.2 (5.6 to NE)		4.1 (2.8 to 5.6)		17.5 (11.1 to NE)	
EGFR mutation status <sup>b</sup>										
Cohort			Mutant	WT	Mutant	WT	Mutant	WT	Mutant	WT
1 <sup>c</sup>		117	3 (23; 5 to 54)	20 (19; 12 to 28)	NE (5.6 to NE)	8.5 (5.6 to 12.3)	5.5 (2.6 to 8.3)	5.5 (3.0 to 6.9)	20.1 (NE to NE)	NE (15.5 to NE)
2 <sup>d</sup>		219	0 (0; 0 to 19)	43 (21; 16 to 28)	NE (NE to NE)	NE (8.3 to NE)	1.3 (1.2 to 1.6)	2.8 (1.4 to 4.0)	9.8 (6.8 to NE)	16.3 (13.6 to NE)
3 <sup>e</sup>		207	1 (7; 0 to 34)	35 (18; 13 to 24)	NE (NE to NE)	16.4 (6.9 to NE)	1.4 (1.3 to 2.9)	2.8 (2.6 to 3.7)	7.4 (3.4 to 12.7)	14.7 (11.0 to NE)
KRAS mutation status										
Cohort										
1 <sup>f</sup>		100	9 (27; 13 to 46)	11 (16; 8 to 27)	10.0 (6.9 to NE)	7.1 (5.2 to 12.3)	8.3 (1.6 to 12.7)	4.8 (2.8 to 6.9)	NE (NE to NE)	20.1 (14.1 to 20.1)
2 <sup>g</sup>		200	16 (32; 20 to 47)	24 (16; 11 to 23)	11.3 (6.9 to NE)	NE (8.3 to NE)	4.1 (2.6 to 7.1)	1.4 (1.4 to 2.8)	17.7 (13.7 to NE)	15.1 (12.1 to NE)
3 <sup>h</sup>		188	10 (19; 9 to 31)	24 (18; 12 to 25)	NE (NE to NE)	16.4 (5.7 to NE)	2.6 (1.4 to 2.8)	2.8 (1.9 to 3.0)	12.1 (6.9 to NE)	13.8 (10.6 to NE)
Atezolizumab updated efficacy analysis <sup>i</sup>										
			ORR per INV, No. (%; 95% CI) <sup>j</sup>				Median OS (95% CI)		12-Month OS Rate (95% CI)	
All Treated Patients (TC2/3 or IC2/3)										
Cohort										
1		138 <sup>k</sup>	35 (25; 18 to 33)				23.5 (18.1 to NE)		66.4 (58.1 to 74.6)	
2		269 <sup>k</sup>	53 (20; 15 to 25)				15.5 (12.3 to 19.3)		58.1 (52.1 to 64.1)	
3		252	50 (20; 15 to 25)				13.2 (10.3 to 17.5)		52.3 (46.1 to 58.6)	
PD-L1 TC3 or IC3 Subgroup										
Cohort										
1		65	22 (34; 23 to 47)				26.9 (12.0 to NE)		61.5 (49.0 to 74.0)	
2		122	32 (26; 19 to 35)				16.6 (12.0 to NE)		58.7 (49.8 to 67.6)	
3		115	36 (31; 23 to 41)				17.5 (11.1 to 21.4)		57.5 (48.4 to 66.6)	

NOTE. On the basis of a data cutoff of December 1, 2015.  
Abbreviations: DOR, duration of response; EGFR, epidermal growth factor receptor; INV, investigator; IRF, independent review facility; ORR, objective response rate; OS, overall survival; PFS, progression-free survival; NE, not estimable; TC2/3 or IC2/3 = TC or IC ≥ 5% PD-L1-expressing cells, respectively; TC3 or IC3 = TC ≥ 50% or IC ≥ 10% PD-L1-expressing cells, respectively; WT, wild type.  
<sup>a</sup>Assessed by IRF per Response Evaluation Criteria in Solid Tumors (RECIST) version 1.1.  
<sup>b</sup>Patients were considered EGFR mutant for the analysis if their tumor tested positive for at least one of the following mutations: exon 19 deletions or insertions, L858R, exon 20 insertion, G719X, L861Q, or S768I.  
Three patients with a T790M mutation were not included in this analysis; two of these patients also had an exon 19 deletion.  
<sup>c</sup>Number of patients tested: mutant (n = 13), WT (n = 104).  
<sup>d</sup>Number of patients tested: mutant (n = 18), WT (n = 201).  
<sup>e</sup>Number of patients tested: mutant (n = 14), WT (n = 193).  
<sup>f</sup>Number of patients tested: mutant (n = 33), WT (n = 67).  
<sup>g</sup>Number of patients tested: mutant (n = 50), WT (n = 150).  
<sup>h</sup>Number of patients tested: mutant (n = 54), WT (n = 134).  
<sup>i</sup>On the basis of an updated data cutoff of August 1, 2016; median duration of follow-up 22.5 months. Fewer than 50% of survival events had occurred at the time of data cutoff.  
<sup>j</sup>Assessed by INV per RECIST version 1.1.  
<sup>k</sup>One patient was mistakenly assigned to cohort 2 at the time of the August 1, 2016, data cutoff.

NOTE. On the basis of a data cutoff of December 1, 2015.

Abbreviations: DOR, duration of response; EGFR, epidermal growth factor receptor; INV, investigator; IRF, independent review facility; ORR, objective response rate; OS, overall survival; PFS, progression-free survival; NE, not estimable; TC2/3 or IC2/3 = TC or IC ≥ 5% PD-L1-expressing cells, respectively; TC3 or IC3 = TC ≥ 50% or IC ≥ 10% PD-L1-expressing cells, respectively; WT, wild type.

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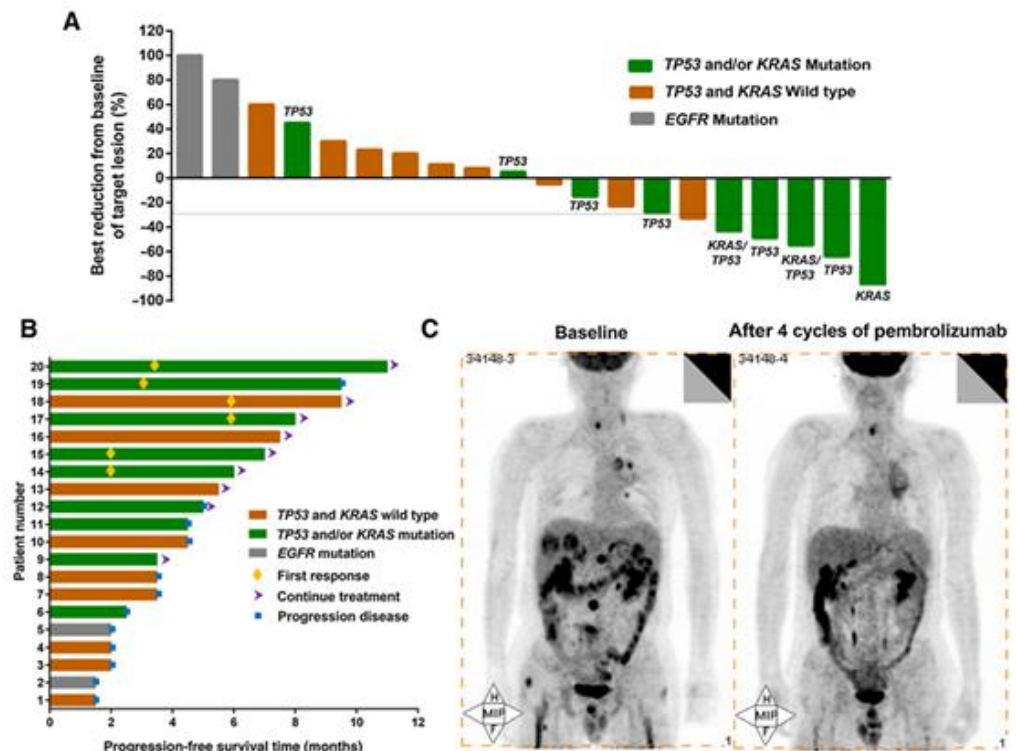
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The **BIRCH study** also reported that patients with advanced NSCLC with KRAS mutations receiving atezolizumab had better outcomes compared with those with wild-type KRAS

# TP53

- Mutation rate of TP53 was 39–46% in adenocarcinomas, 81% in squamous cell carcinomas and 68% in large-cell carcinomas.
- Dong *et al* performed an integrated analysis on the multiple-dimensional data types and reported that mutation of TP53 or KRAS increased the expression of PD-L1 and infiltration by CD8<sup>+</sup> T cells.
- The *TP53*/*KRAS* comutated subgroup manifested exclusive increased expression of PD-L1 and a highest proportion of *PD-L1*<sup>+</sup>/*CD8A*<sup>+</sup>





# Genes and signalling pathways associated with DNA damage repair (DDR)

- Mutations in these genes can result in genomic instability
- These mutations lead to an increase in the load of non-synonymous mutations and the number of TILs, making patients more sensitive to immunotherapy
- Mutation status of DDR was correlated with the level of TMB, and that patients with co-mutation may benefit more from immunotherapy.

<b>BER</b>	<i>OGG1</i>	Renal, breast and lung cancer
	<i>XRCC1</i>	Non-small cell lung cancer
<b>NER</b>	<i>ERCC1</i>	Lung and skin cancer, and glioma
	<i>XP</i>	Xeroderma pigmentosum predisposing to skin cancer. Also increased risk of bladder and lung cancer
<b>MMR</b>	<i>MSH2</i> ,	Lynch syndrome predisposing to colorectal cancer as well as endometrial, ovarian, stomach, hepatobiliary tract, upper urinary tract, brain and skin cancer
	<i>MLH1</i>	
<b>HRR</b>	<i>BRCA1</i>	Increased risk of breast, ovarian, prostate, pancreatic, as well as gastrointestinal and haematological cancer, and melanoma
	<i>BRCA2</i>	
	<i>FANC</i>	Group of proteins associated with Fanconi anaemia predisposing to squamous cell carcinomas of the head and neck and acute myeloid leukaemia (e.g. FANCA, FANCB)
<b>NHEJ</b>	<i>KU70</i>	Breast, colorectal and lung cancer
	<i>KU80</i>	Lung cancer
<b>Cell cycle checkpoints</b>	<i>ATM</i>	Ataxia-telangiectasia predisposing to leukaemia, breast and pancreatic cancer
	<i>ATR</i>	Leukaemia, lymphoma, gastric and endometrial cancer
<b>P53</b>		Li-Fraumeni syndrome

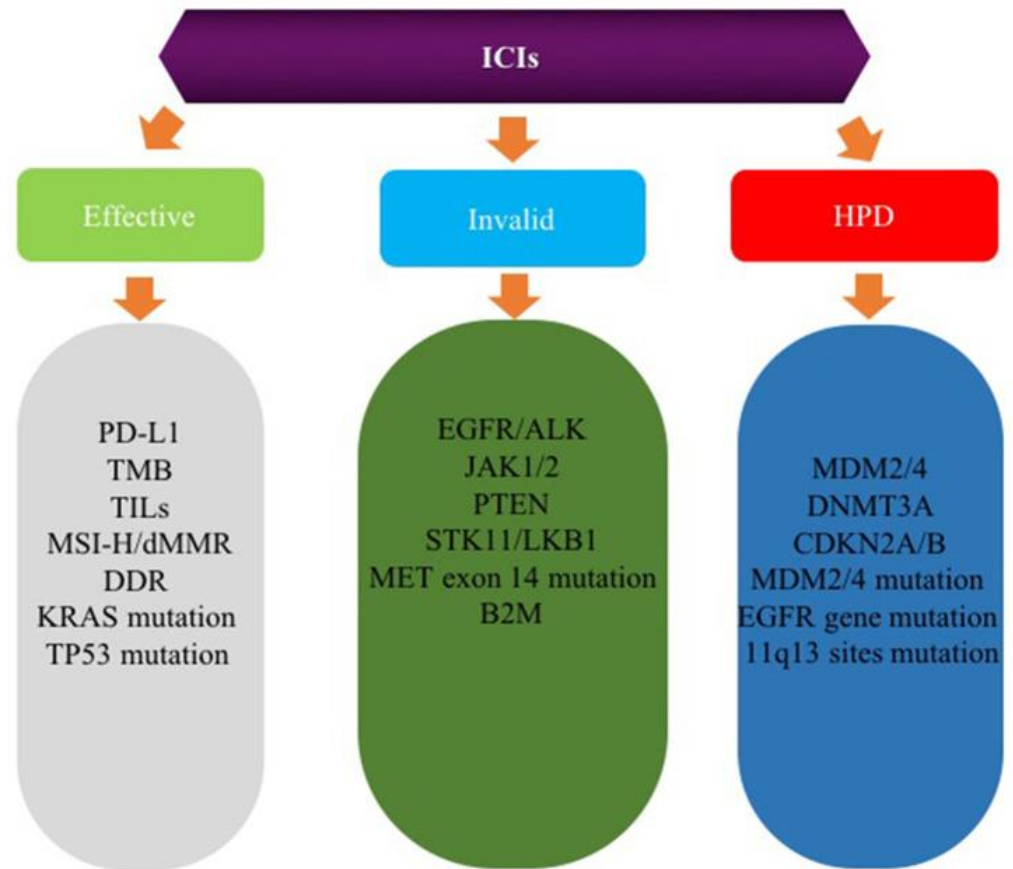
# Predictors of 'toxic' immunotherapy

- HPD, also known as the 'toxic' response.
- May occur in 10–16% in patients with NSCLC
- Clinical characteristics - age >65 years, number of baseline metastatic sites >2 or local recurrence. **(inconsistent at best to predict HPD)**
- Mouse double minute (**MDM**)2/4 amplification, DNA methyltransferase 3  $\alpha$  (**DNMT3A**) mutation and cyclin dependent kinase inhibitor 2A/2B (**CDKN2A/B**) deletion; **EGFR** and **11q13** mutations were strongly correlated with HPD



# Conclusions

- Biomarkers that **predict treatment responses**, and the development of **rational therapeutic combinations** could enhance the efficacy of immune checkpoint blockade.
- Need to devise a **decision-making algorithms** and **bio-score systems**, to better guide the application of immunotherapy in the clinical setting.



- *Thank YOU*