

Marqueurs prédictifs en immunothérapie : indications actuelles et perspectives

Julien Adam, MD PhD

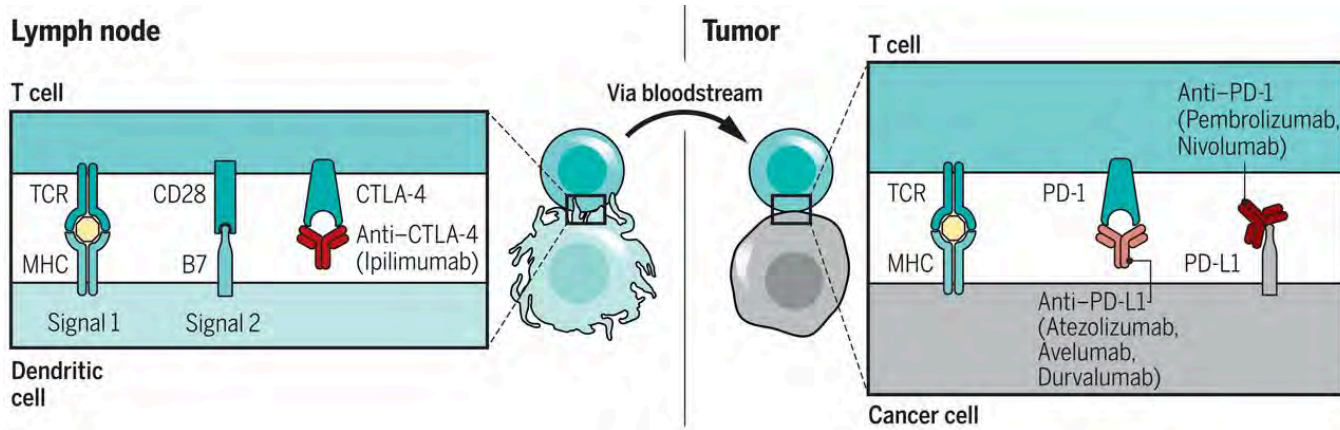
Department of Biology and Pathology

INSERM U981 & U1186

Gustave Roussy Cancer Center

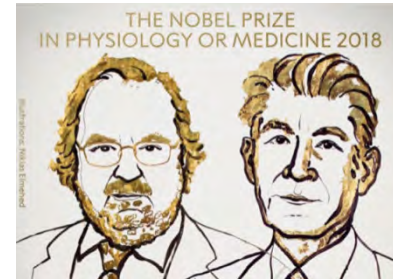
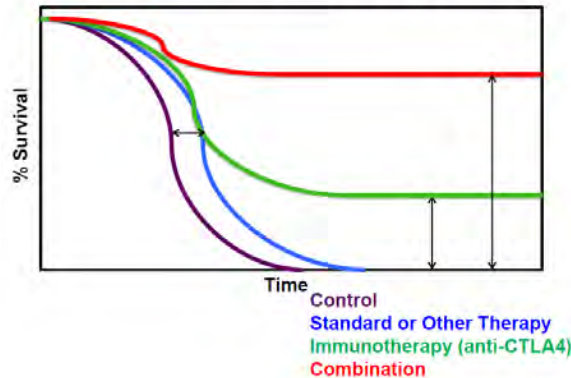
Grand Paris, France

Immunothérapie par blocage de checkpoints immunitaires



Ribas & Wolchok, Science 2018

Improving Survival with Combination Therapy

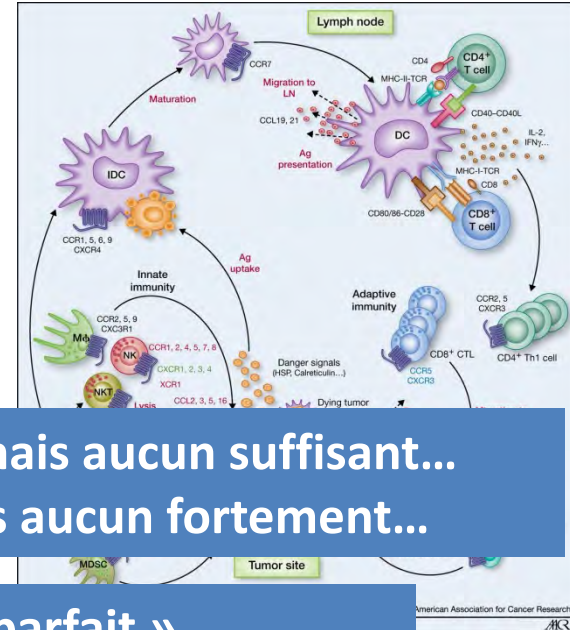
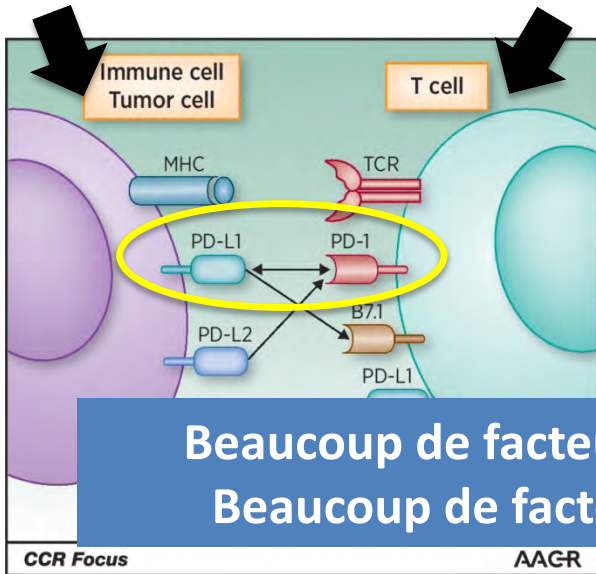


Revenir à la biologie...

Des cellules présentatrices d'antigènes PD-L1+

Des lymphocytes T spécifiques PD-1+

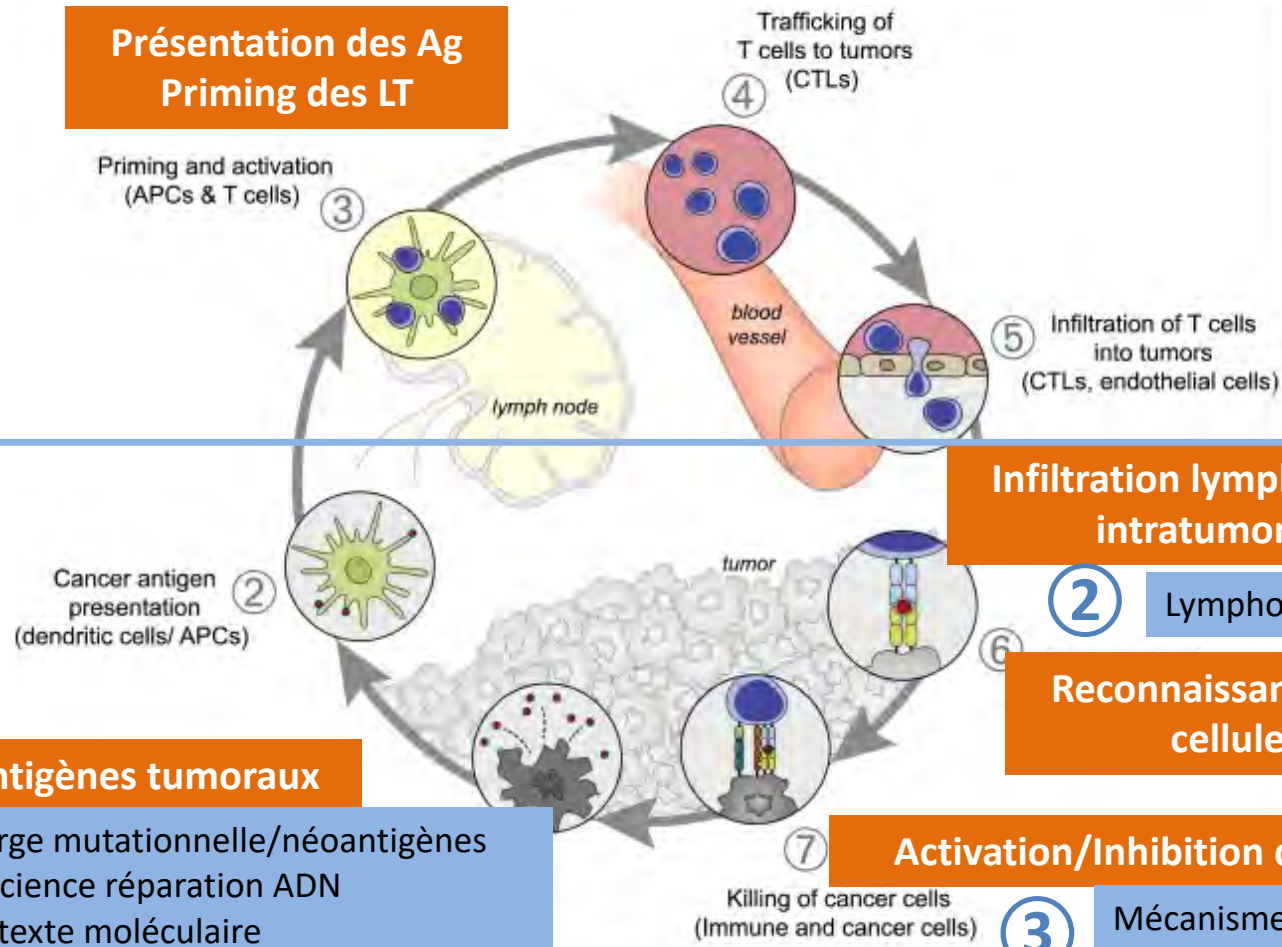
Dans un environnement complexe...



Beaucoup de facteurs nécessaires, mais aucun suffisant...
Beaucoup de facteurs corrélés mais aucun fortement...

Pas de biomarqueur « parfait »
Valeur prédictive positive ou négative ?

Présentation des Ag Priming des LT



Infiltration lymphocytaire intratumorale

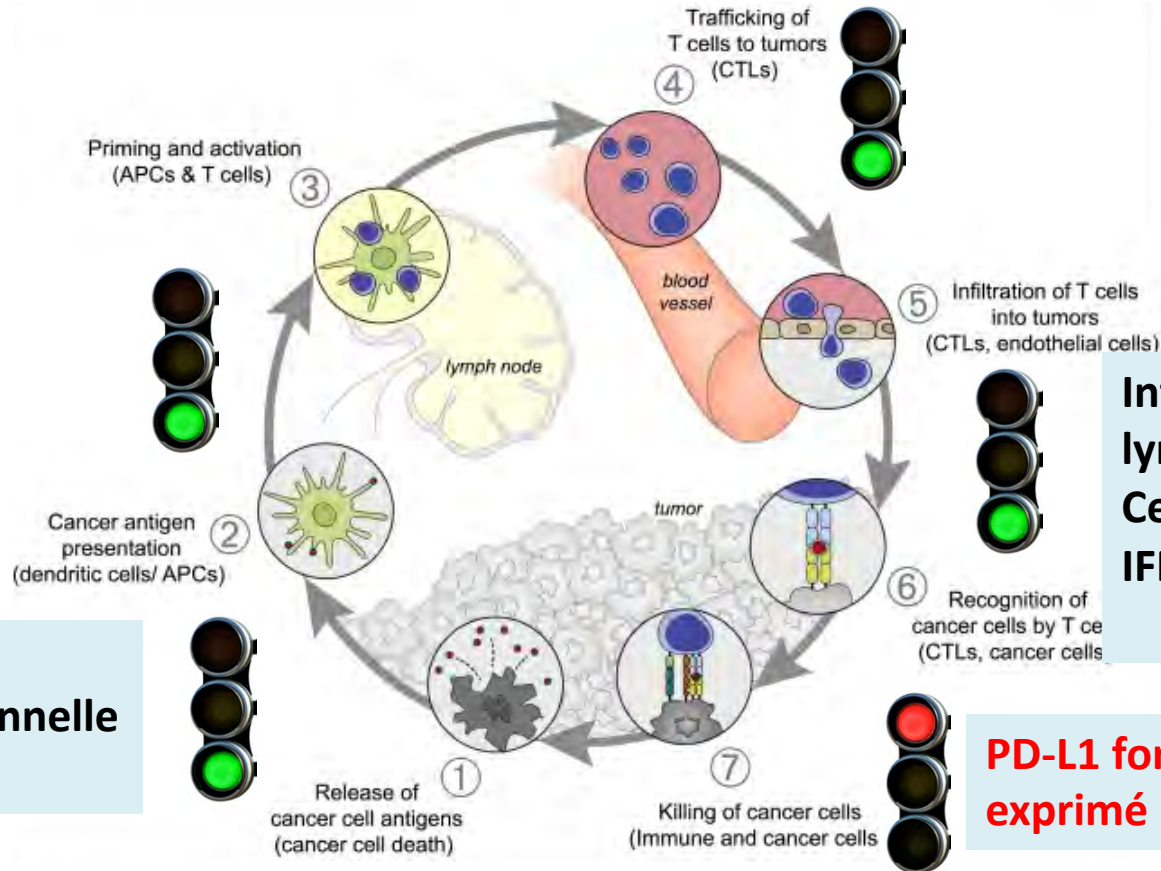
② Lymphocytes (in situ / ARN)

Reconnaissance des antigènes / cellules tumorales

Activation/Inhibition du LT

③ Mécanismes d'échappement à la réponse immunitaire (dont PD-L1)

Cas de figure « idéal » pour l'efficacité des anti-PD1/L1



Charge mutationnelle élevée

Infiltration lymphocytaire élevée
Cellules T effectrices
IFN gamma

PD-L1 fortement exprimé

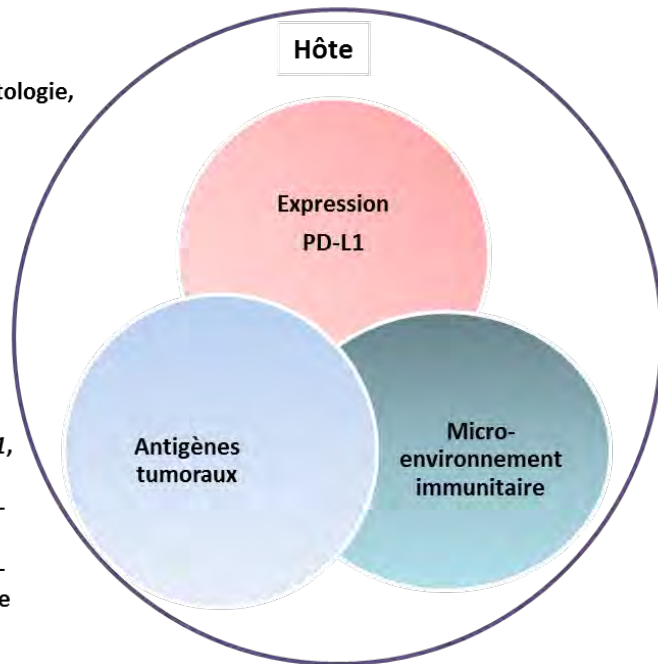
Panorama des biomarqueurs des anti-PD-1/L1

Caractéristiques de l'hôte

- Cliniques : âge, sexe, PS, histologie, tabagisme
- Microbiome
- Génétique constitutionnelle

Antigènes tumoraux

- Mutations *EGFR*, *KRAS*, *LKB1*, p53 mutations, *ALK+*, *JAK/STAT*, amplifications PD-L1
- TMB, MSI-High/dMMR, néo-antigènes, clonalité tumorale



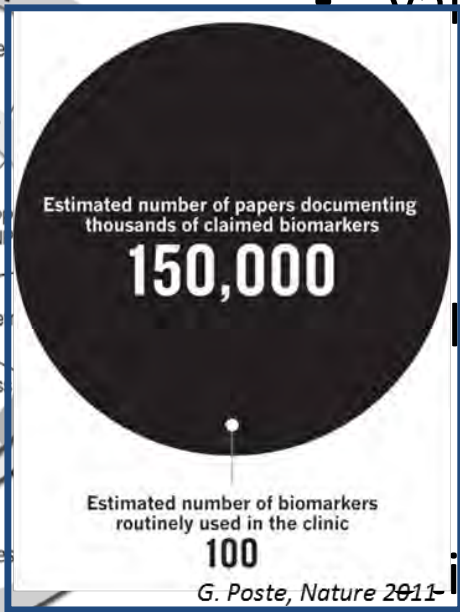
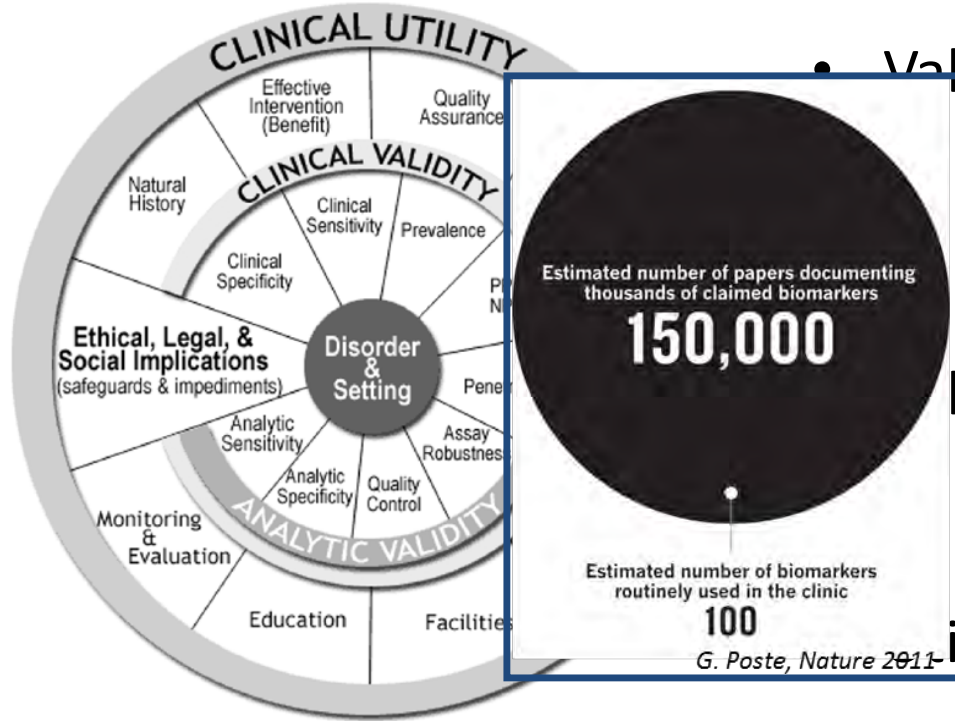
PD-L1 expression

- Expression protéique ou mRNA
- Cellules tumorales ou Cellules immunitaires

Micro-environnement immunitaire

- Tumeur « hot » ou « cold » (désert immunitaire ou immun exclu)
- CD8+T cell (infiltration et fonctionnalité)
- Voies signalisation de Interféron gamma
- Tregs, MDSCs, CD IDO+
- TIM3, LAG3, TIGIT (facteurs d'épuisement)
- Signature transcriptomique
- Clonalité TCR

Comment s'y retrouver ?



- Validation analytique

Standardisation, robustesse

Adapté aux conditions cliniques

Coût, délai d'analyse

Validation clinique

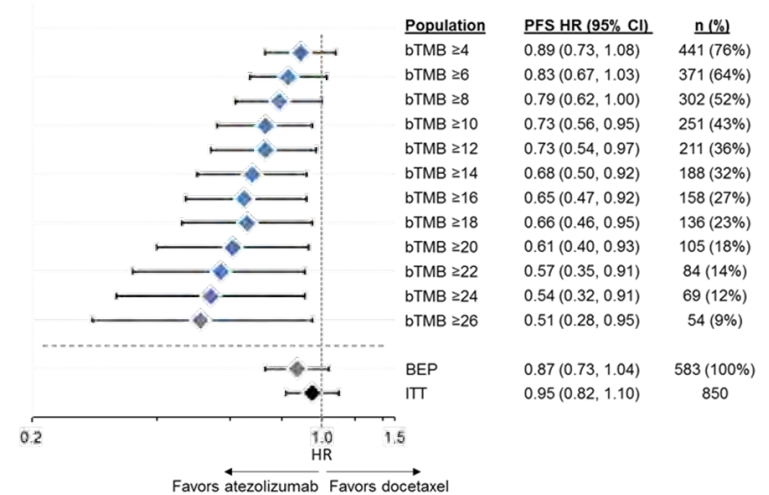
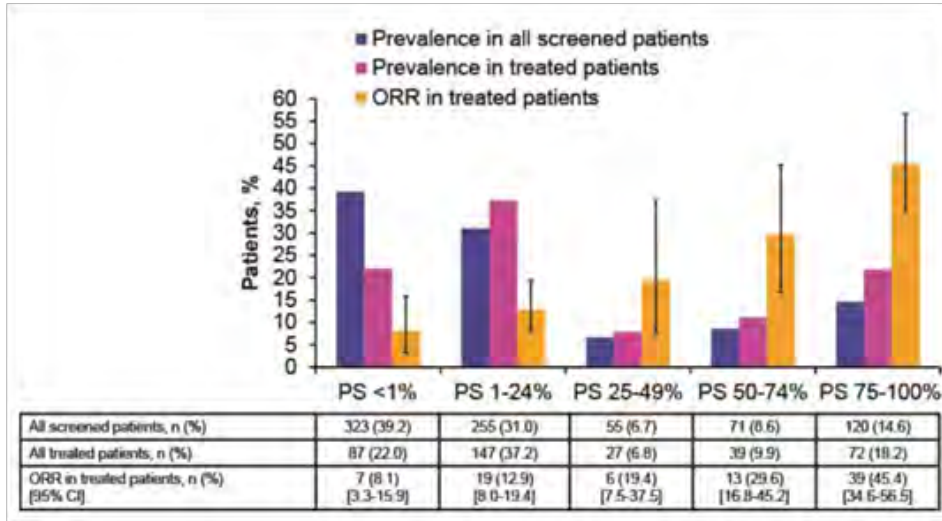
Méthodologie adéquate

Pronostique versus prédictif

Utilité clinique

– Guide la prise en charge

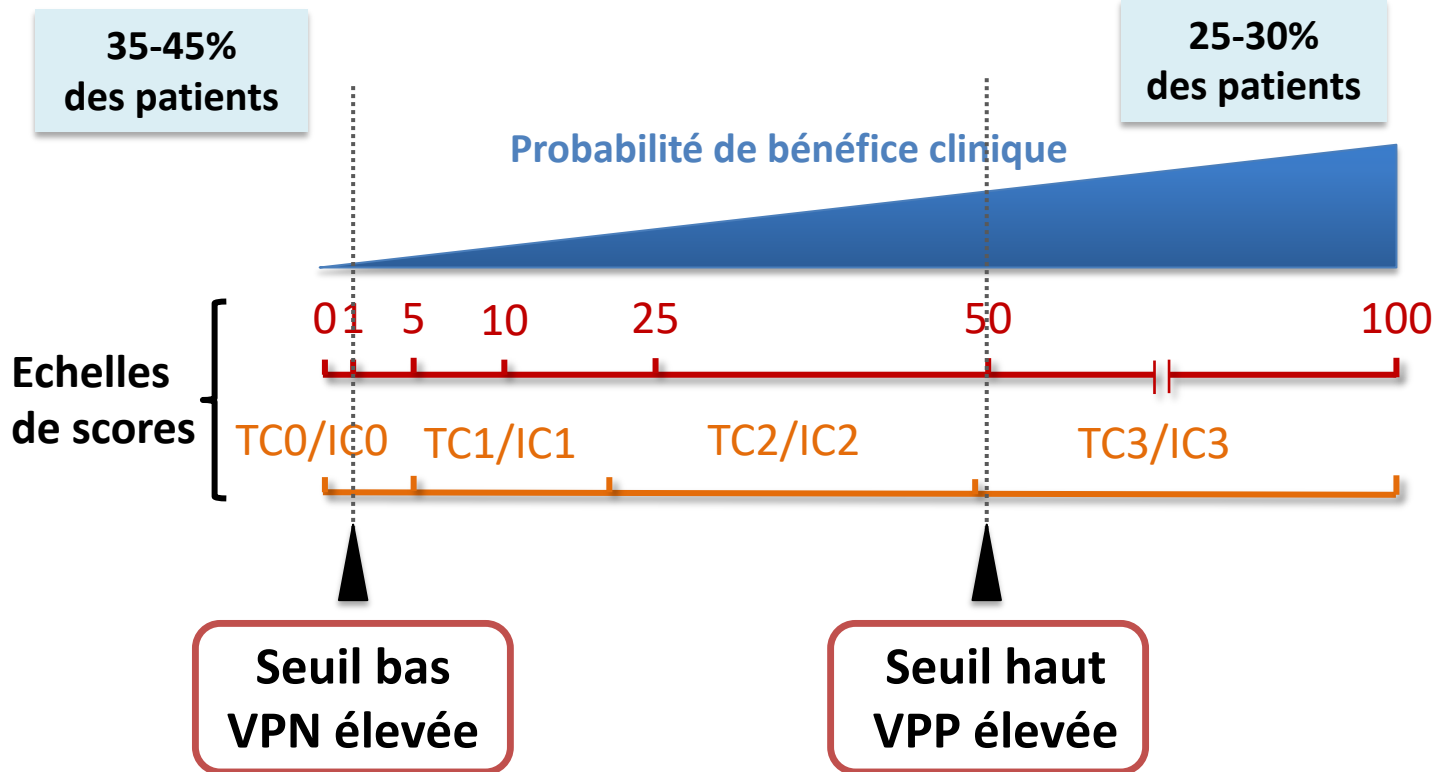
Des biomarqueurs « continus »



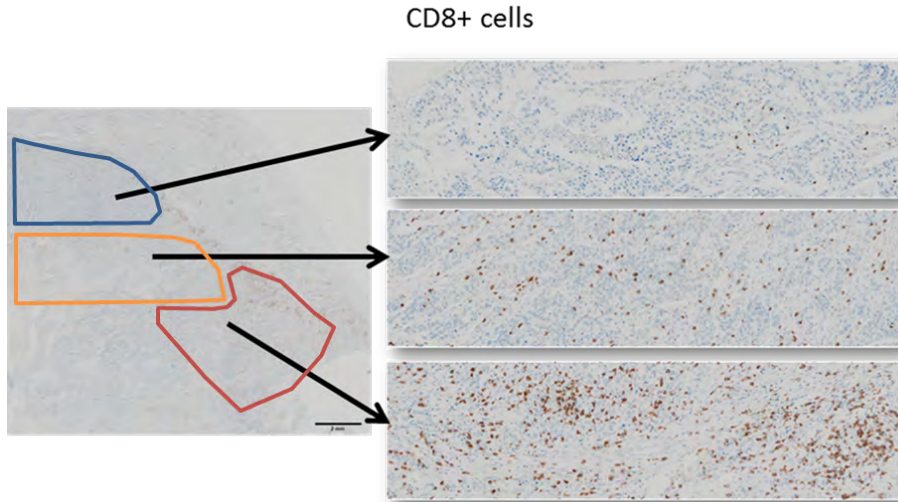
Gandara et al., ESMO 2017

Comment définir les seuils (essais cliniques) ?

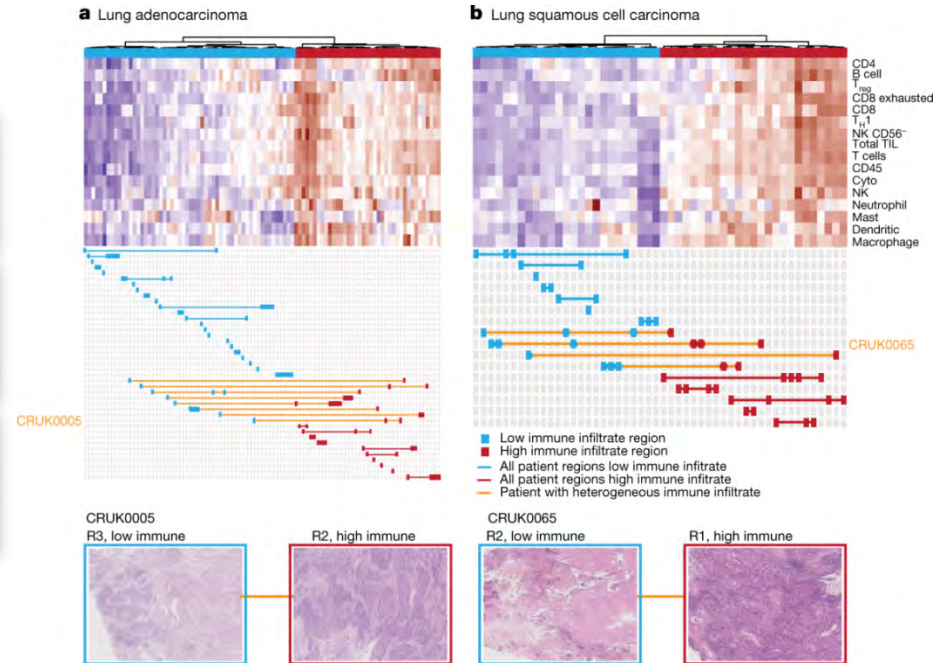
PD-L1 : un biomarqueur continu



Des biomarqueurs hétérogènes

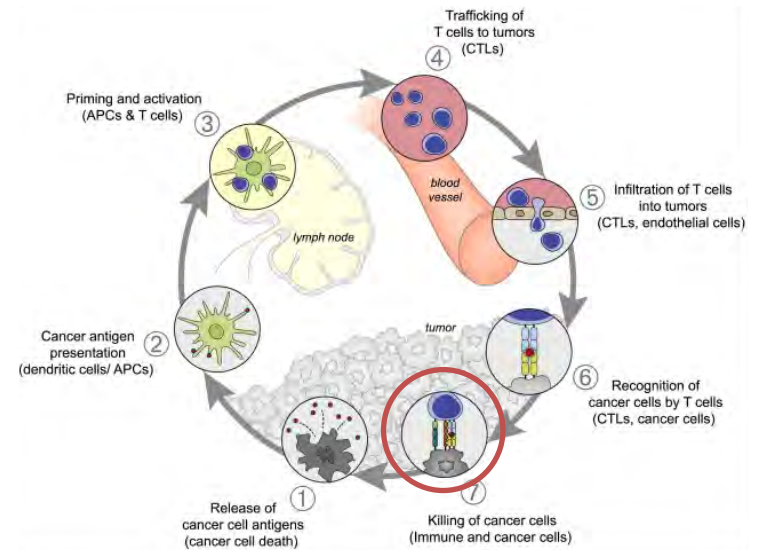


Dans l'espace
Dans le temps

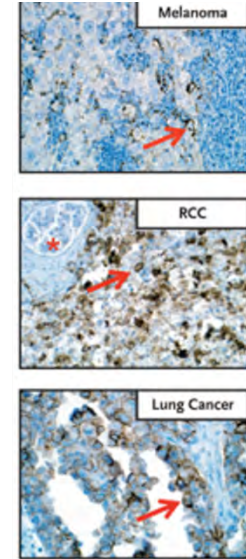
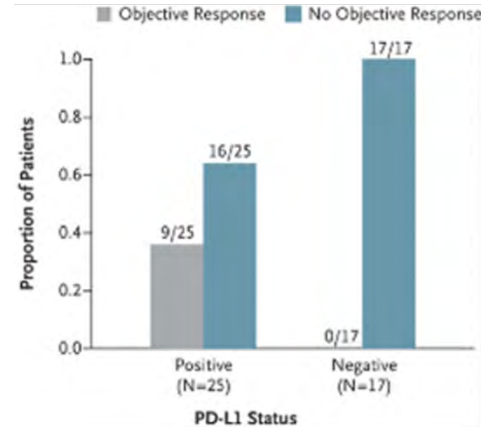
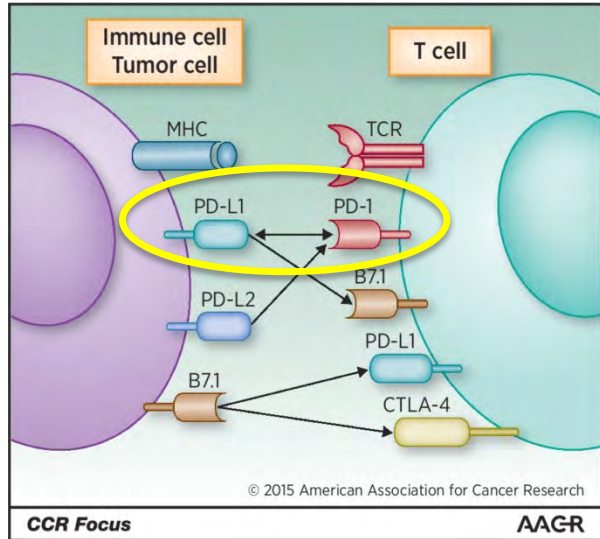


Hétérogénéité associée à des
facteurs moléculaires

PD-L1 comme biomarqueur dans les CPNPC



Au début de l'histoire...



Treatment: nivolumab, IHC clone 5H1
Topalian et al., NEJM, 2012

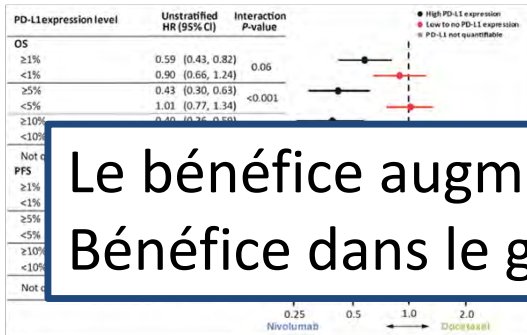
IHC PD-L1 IHC:

- Disponible universellement, rapide, peu cher
- Évaluée dans tous les essais cliniques

Expression de PD-L1 et bénéfice des anti-PD1/L1 dans les CPNPC métastatiques

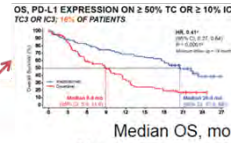
CheckMate 057

Nivolumab (carcinomes non épidermoïdes)



OAK

Atezolizumab



KEYNOTE-048

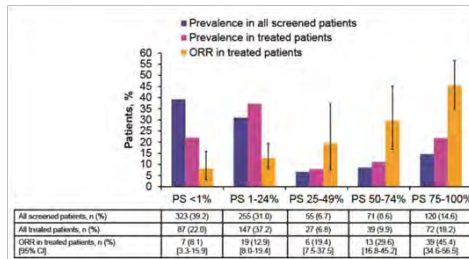
TPS ≥ 50 %

	Evt.	HR (IC _{95%})	p
Pembrolizumab	157	0.69	0.0003
Chimiothérapie	199	0.56-0.85	

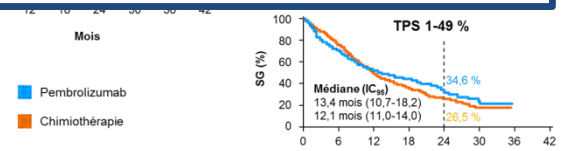
Le bénéfice augmente avec l'expression de PD-L1 (valeur continue)
Bénéfice dans le groupe PD-L1 <1% (variable selon études)

KEYNOTE-001

Pembrolizumab



Hazard Ratio^a
In favor of atezolizumab | In favor of docetaxel

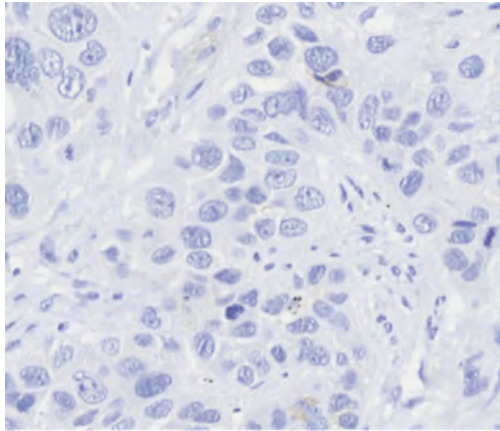


- PD-L1 ≥1% HR=0.81
- PD-L1 ≥20% HR=0.77
- PD-L1 ≥50% HR=0.69

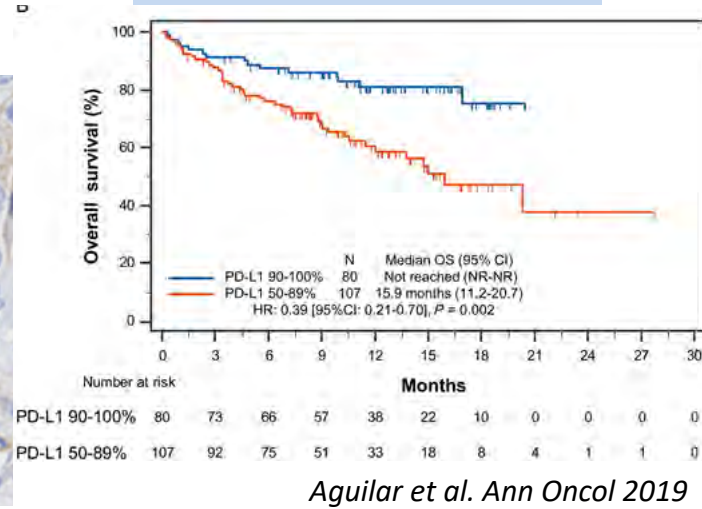
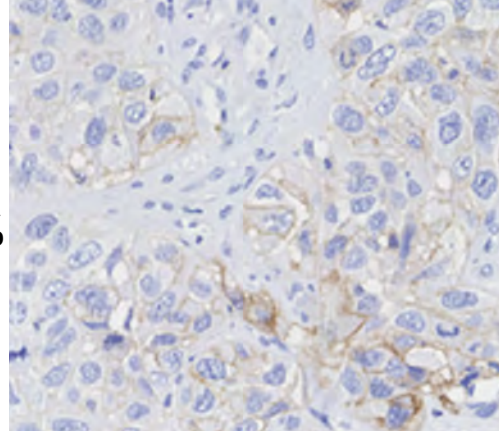
Nivolumab: Borghaei et al., NEJM 2015
Pembrolizumab: Garon et al., NEJM 2015
Atezolizumab: Rittmeyer et al., Lancet 2016

Continuum biologique et clinique

35-45% des CPNPC



1%



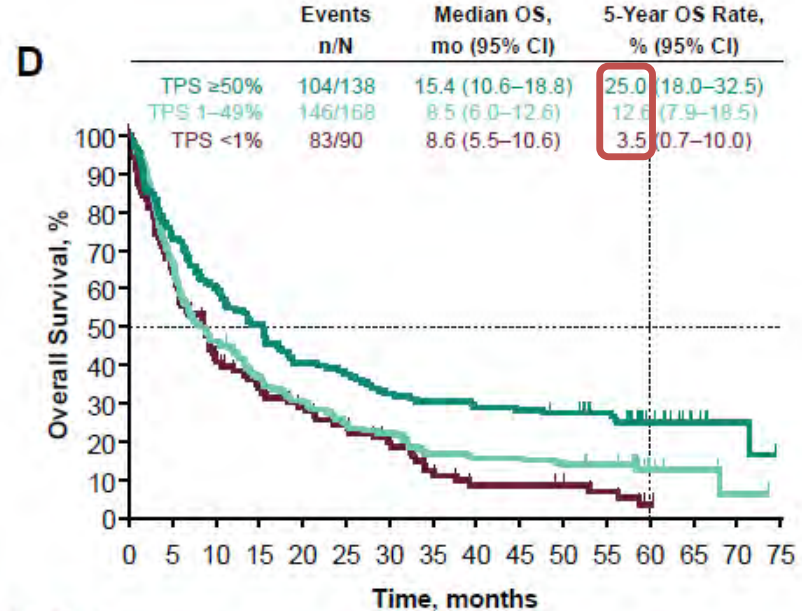
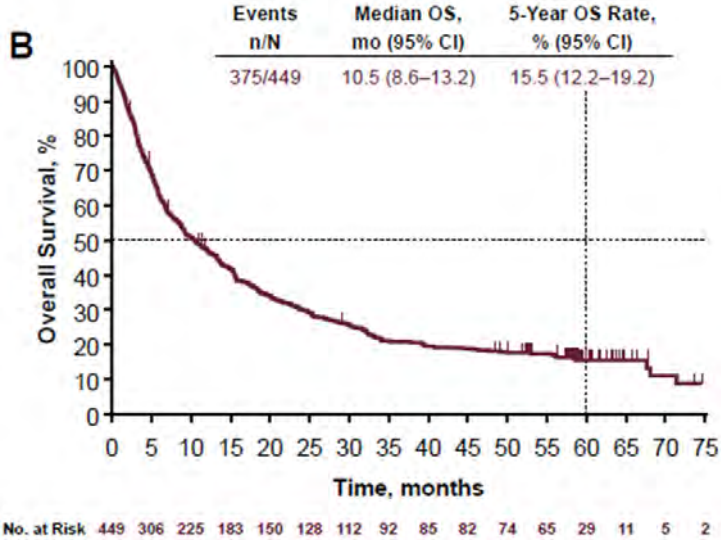
KEYNOTE 042
(pembrolizumab 1L mNSCLC)
Mok et al. Lancet 2019

PD-L1 $\geq 1\%$ HR=0.81

PD-L1 $\geq 20\%$ HR=0.77

PD-L1 $\geq 50\%$ HR=0.69

PD-L1 et bénéfice à long terme



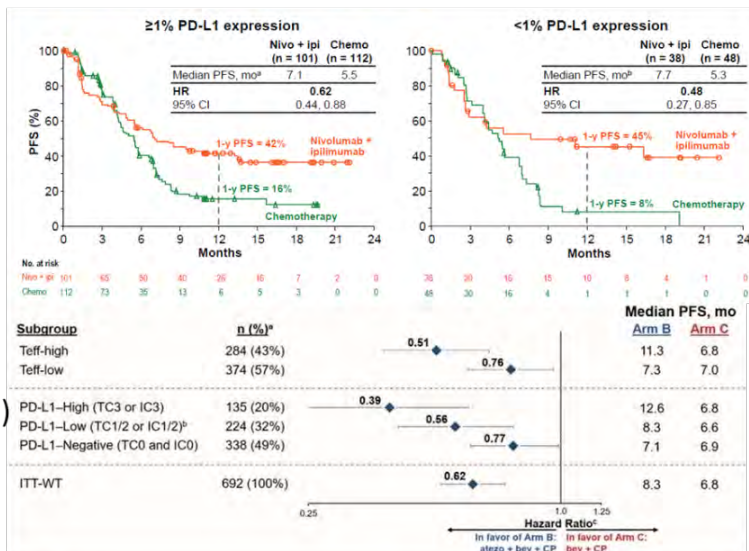
Pembrolizumab, CPNCP métastatique après traitement par chimiothérapie à base de platine

PD-L1 et combinaisons de traitements

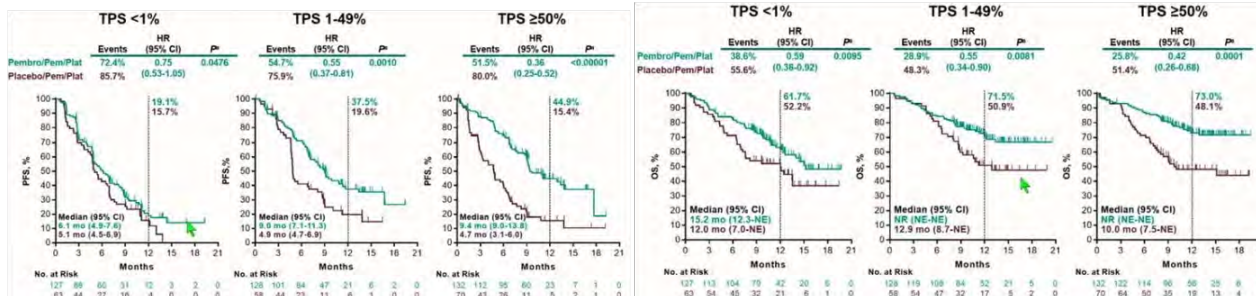
CM-227
(Nivolumab+
ipilimumab)

IM-150
(Atezo+bev+CP)

KN-189 (Pembro+CP)



Population: TMB
≥10 mut/Mb



Pourquoi PD-L1 ne suffit pas ?

L'information n'est pas exhaustive

- L'expression par les TC peut être pertinente ou non*
- Pas de prise en compte de l'expression par les IC**

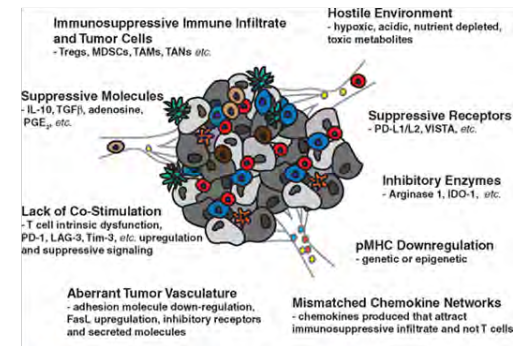
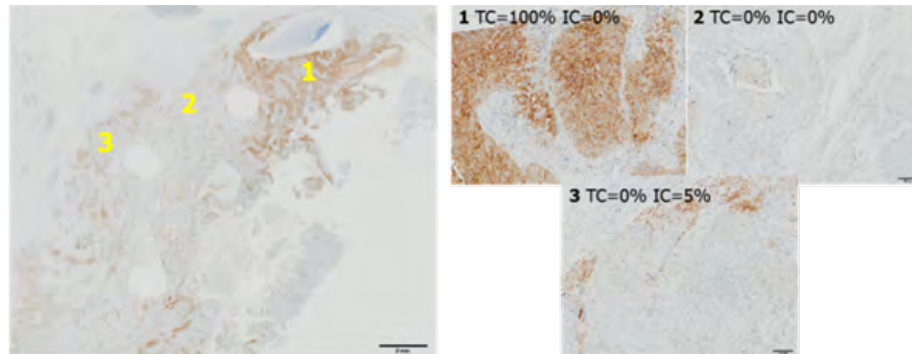
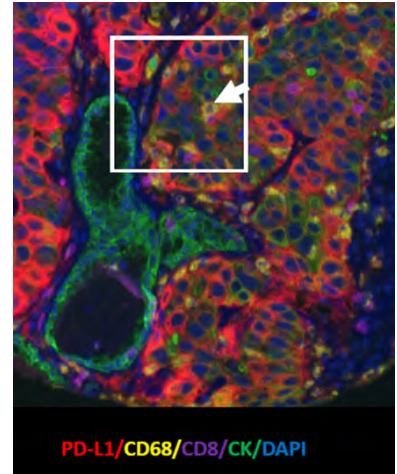
Le prélèvement tissulaire n'est pas représentatif

- Hétérogénéité tumorale*/**

D'autres informations sont manquantes

- Autres voies d'immunosuppression**

* Faux positifs, ** Faux négatifs



Implémentation pratique de PD-L1

Traitement	Clone	Epitope	Detection	Seuils de positivité
Nivolumab	28-8 Dako	EC	EnVision FLEX	TC : $\geq 1\%$, $\geq 5\%$, $\geq 10\%$
Pembrolizumab	22C3 Dako	EC	EnVision FLEX	TC : $\geq 1\%$, $\geq 50\%$
Durvalumab	SP263 Ventana	IC	OptiView	TC : $\geq 25\%$
Atezolizumab	SP142 ventana	IC	OptiView + amplification	TC : $\geq 1\%$, $\geq 5\%$, $\geq 50\%$ IC : $\geq 1\%$, $\geq 5\%$, $\geq 10\%$

Dako PD-L1 28-8 pharmDx for AS Linker 48
Dako PD-L1 22C3 pharmDx for AS Linker 48

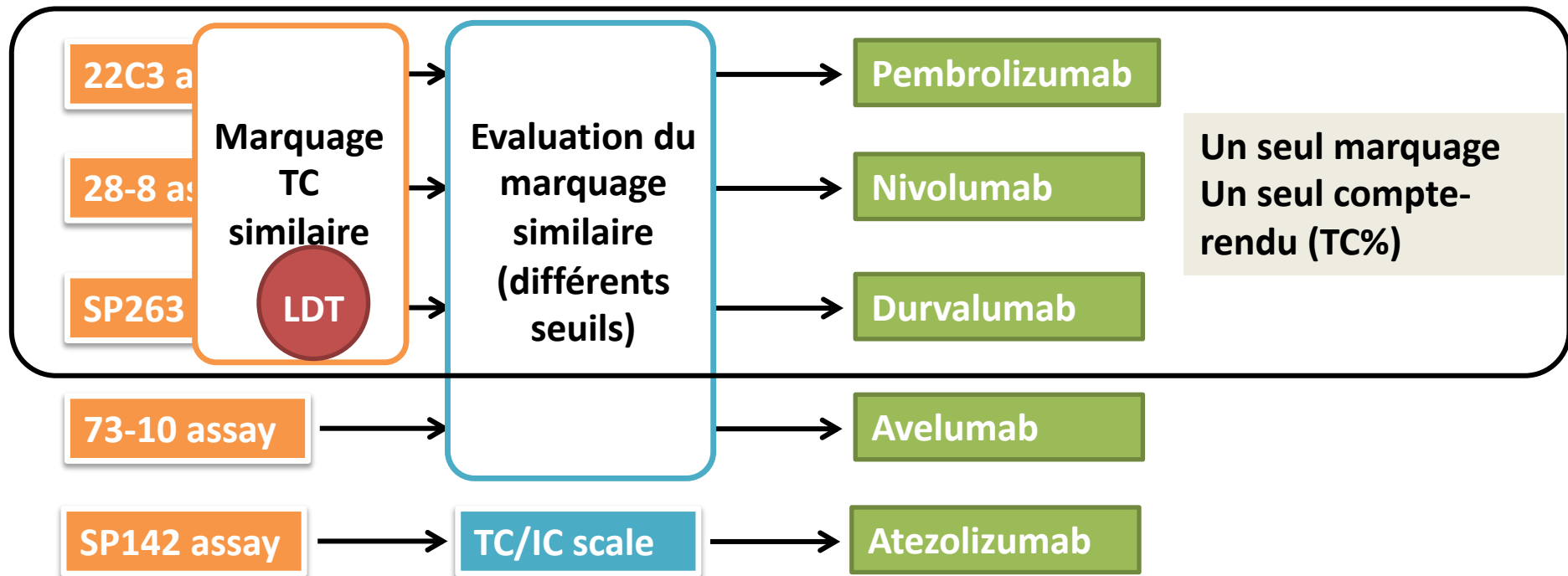


Ventana SP142 IHC Assay
Ventana SP263 IHC assay



- **Problématiques :**
- Comparaison des tests, harmonisation et utilisation de tests maison (coût)
- Reproductibilité de l'évaluation par le pathologiste
- Anticipation et travail en réseau

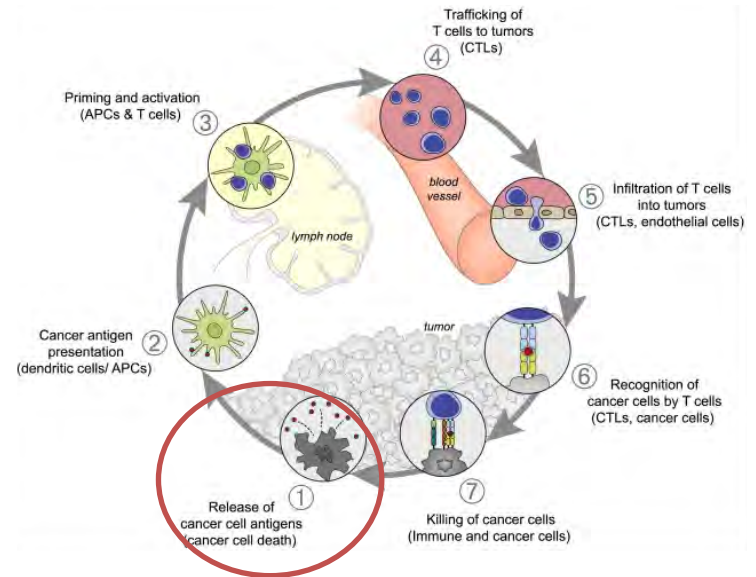
Harmonisation du testing PD-L1 dans les CPNPC



Peut-on faire mieux avec PD-L1 ?

- Prise en compte des cellules immunitaires : pas réaliste
- Analyse d'image : améliore la reproductibilité mais corrélation à la clinique à démontrer
- PD-L1 circulant, CTC : peu convaincant...
- ARN : corrélié/intégré à des signatures d'expression

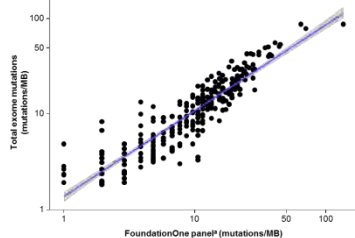
(Néo)antigènes et charge mutationnelle



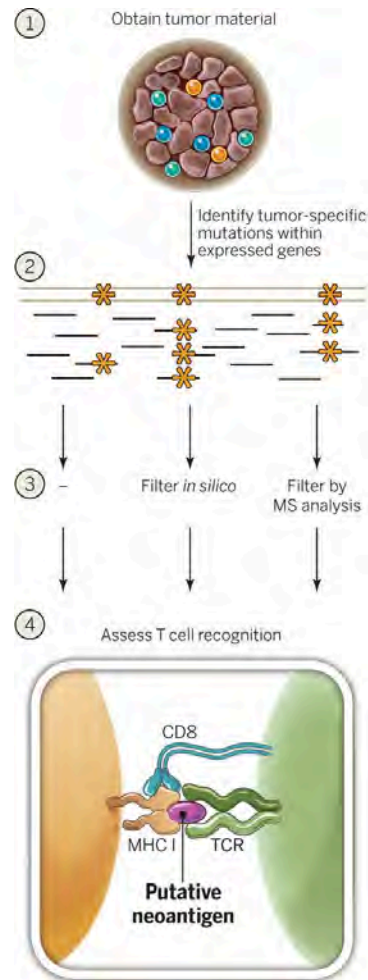
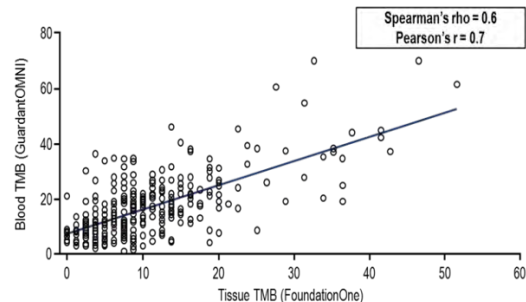
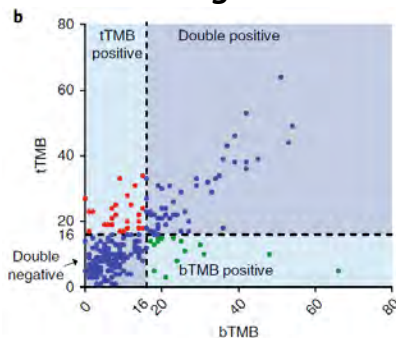
Charge mutationnelle

- Evaluer l'immunogénicité « potentielle »
 - Pas d'évaluation directe des néoantigènes
- Hétérogénéité tumorale limitée
- WES (référence) ou panels NGS (>1 Mb)
- Différentes méthodes d'analyse bioinformatique
- ADN tissulaire ou ADN circulant

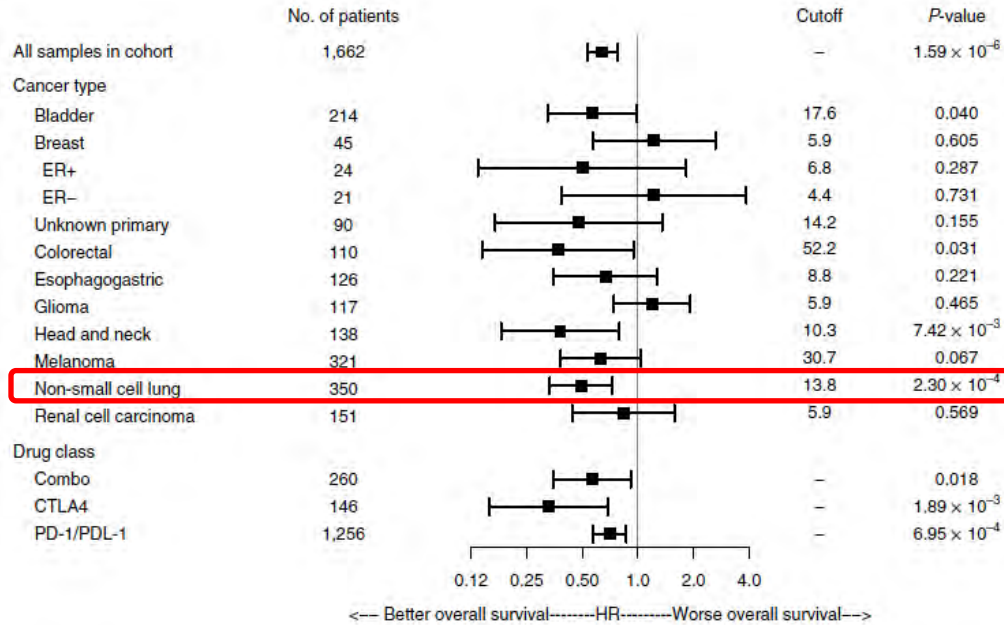
WES vs. gene panel



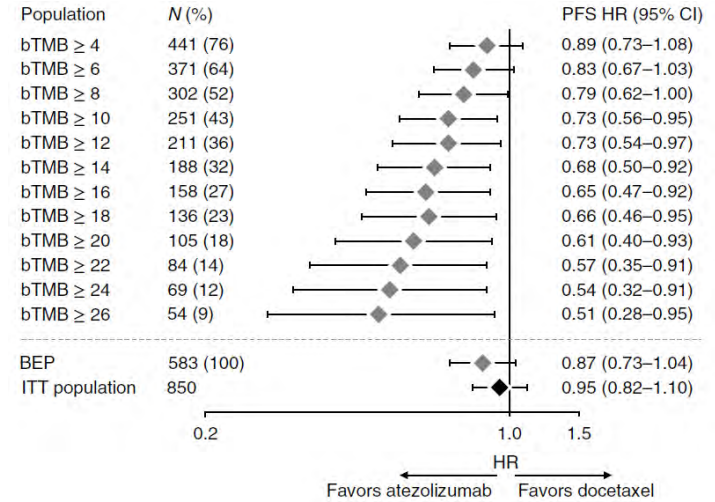
Tissu vs. sang



Charge mutationnelle



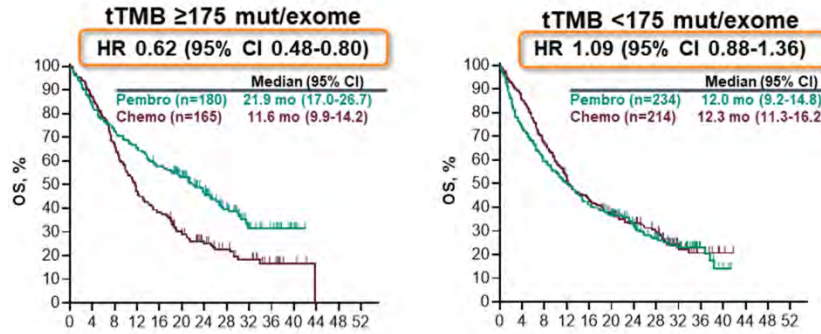
Samstein et al. Nature Genetics, 2019



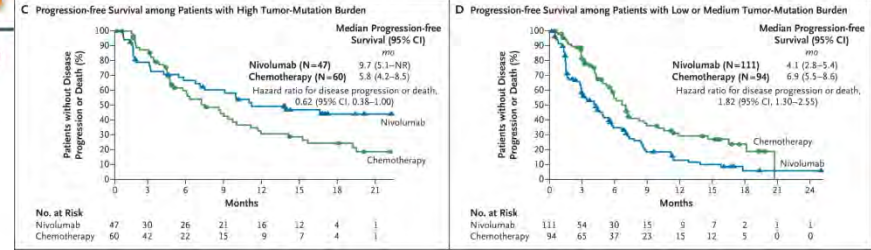
Gandara et al. Nat Med 2018

Charge mutationnelle et monothérapie anti-PD(L)1

Tissu

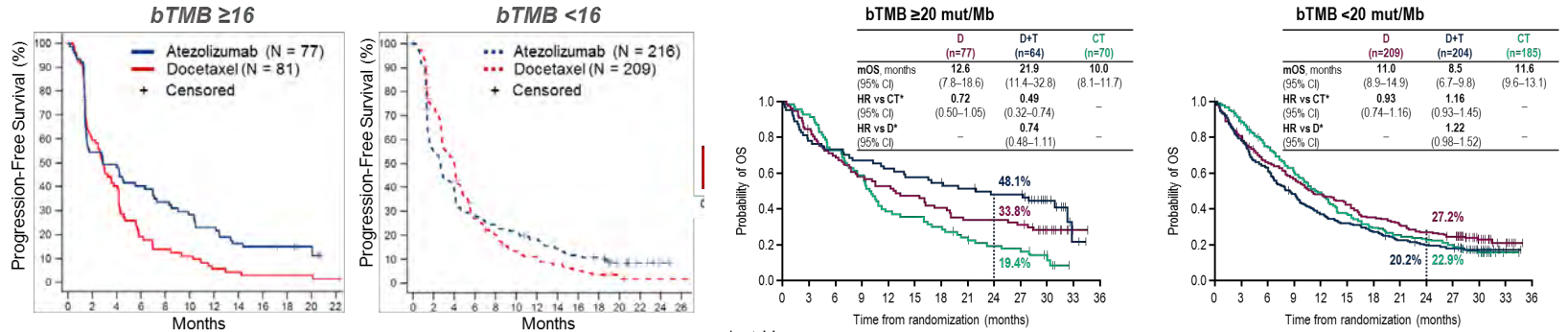


KEYNOTE-042 (Herbst et al., ESMO 2019)



CheckMate-026 (Carbone et al., NEJM 2017)

Sang



OAK (Gandara et al., Nat Med 2018) Interaction P = 0.036

MYSTIC (Peters et al., AACR 2019)

Validation prospective

B-F1RST: Study design



Patients with stage IIIb-IVa^a locally advanced or metastatic NSCLC (any histology; N = 152^b)

Atezolizumab 1200 mg IV q3w

Until PD, unacceptable toxicity or loss of clinical benefit

Inclusion Criteria

- Measurable disease per RECIST v1.1
- ECOG PS of 0 or 1
- Immunotherapy naïve
- PD-L1 unselected
- Provision of bloods

Exclusion Criteria

- Sensitizing EGFR mutations or ALK rearrangements
- Active brain metastases requiring treatment

Primary analysis

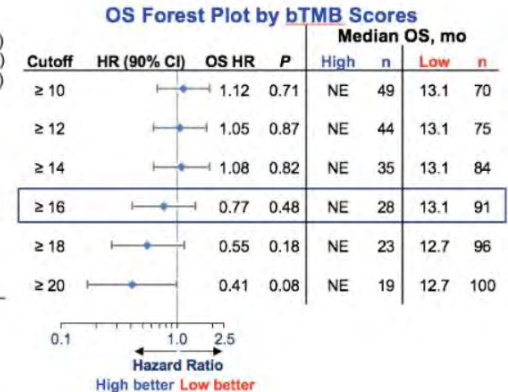
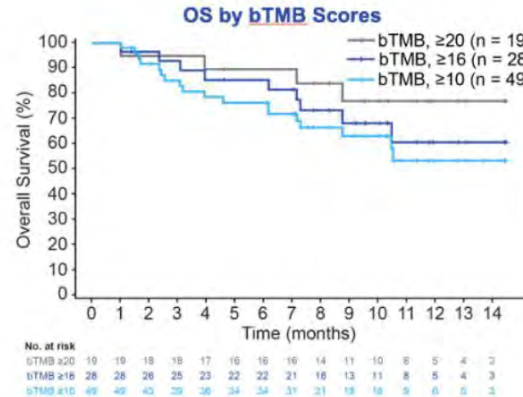
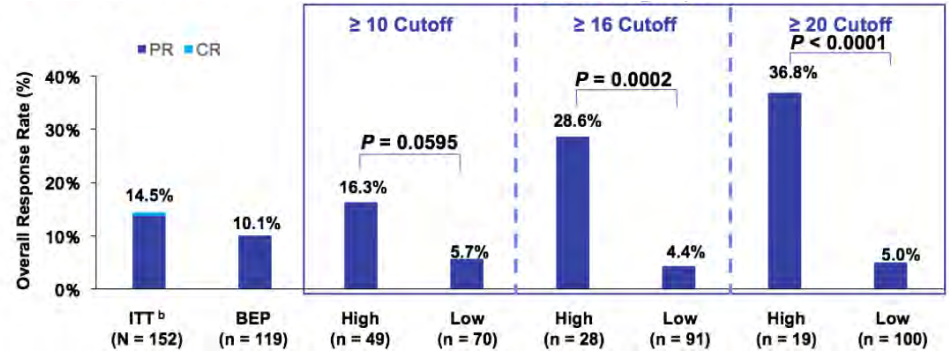
- All enrolled patients with at least 6 months of follow-up
- Prespecified bTMB biomarker cutoff of 16

Co-Primary Endpoints

- Efficacy endpoint: INV-assessed ORR per RECIST v1.1
- Biomarker endpoint: INV-assessed PFS per RECIST v1.1

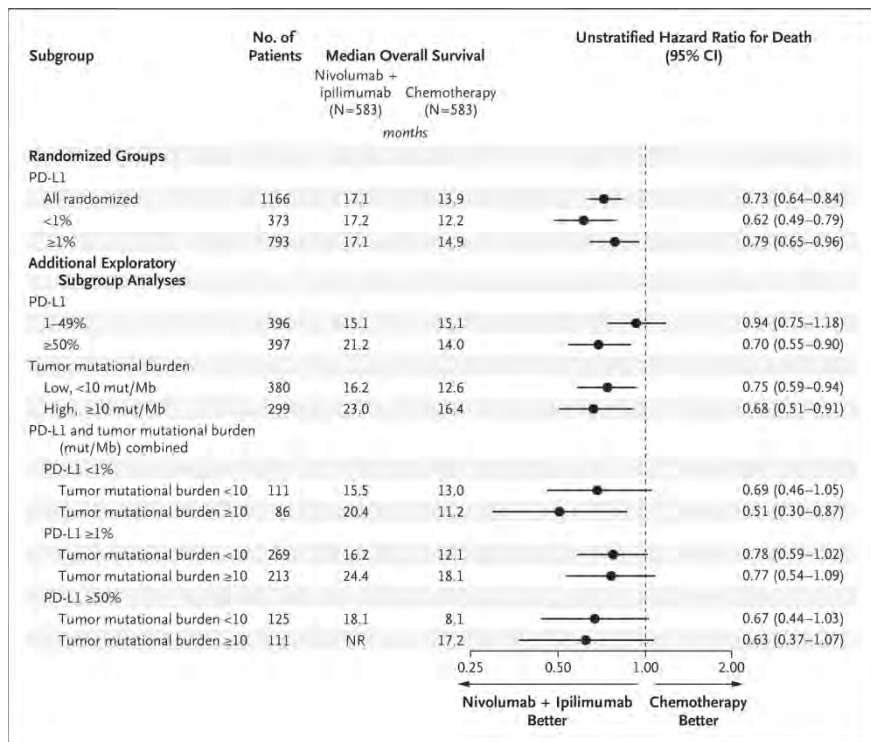
Secondary Objectives

- Safety and assessment of efficacy by INV-assessed DOR, OS

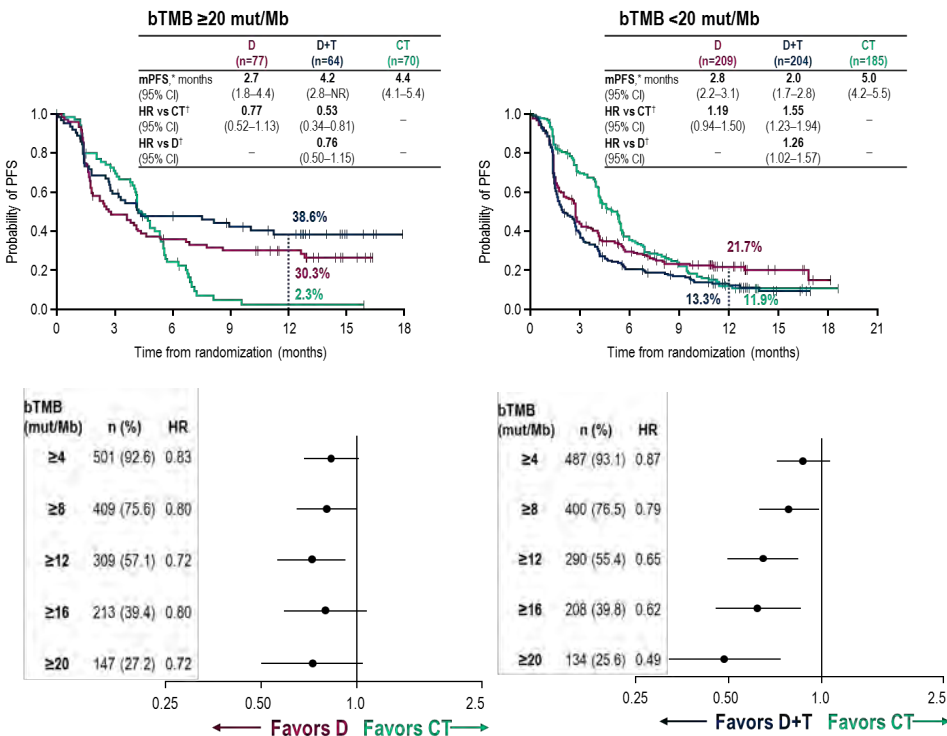


Charge mutationnelle et combinaison anti-PD(L)1 + anti-CTLA4

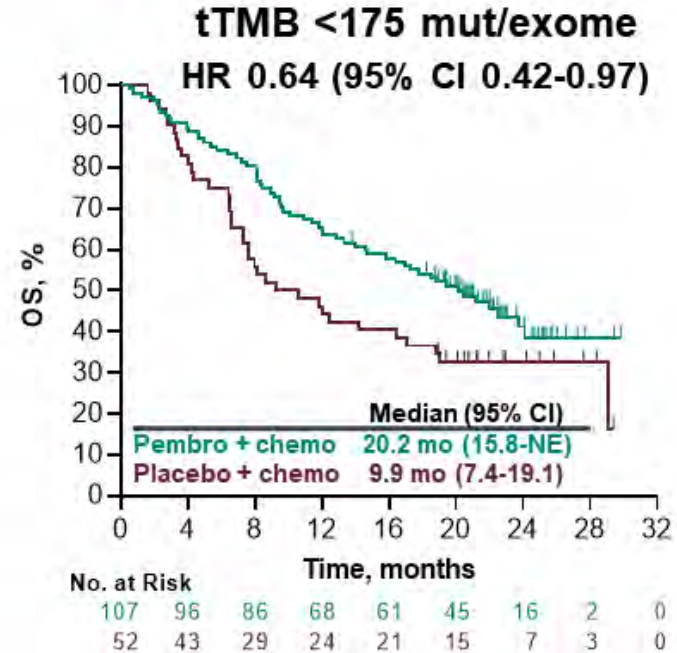
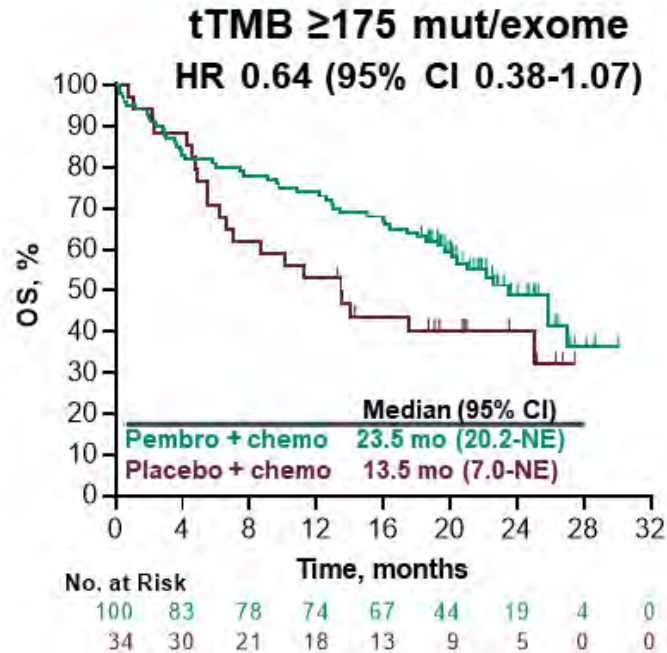
Nivolumab + ipilimumab



Durvalumab + tremelimumab



Charge mutationnelle et combinaison anti-PD1 + chimiothérapie

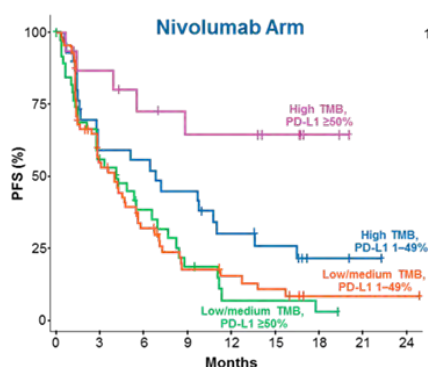
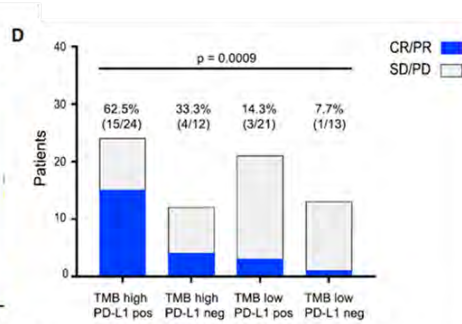
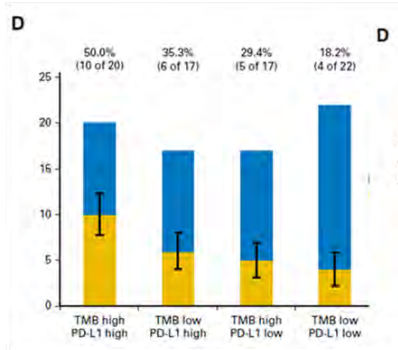
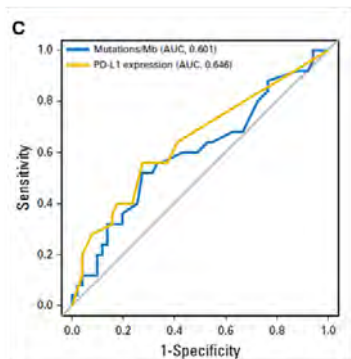


Data cutoff date: Sep 21, 2018.

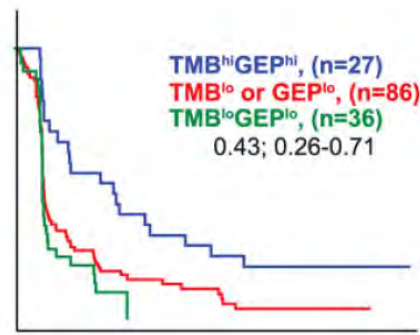
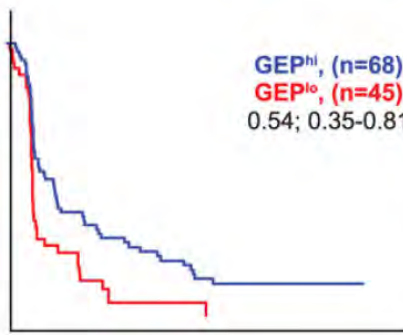
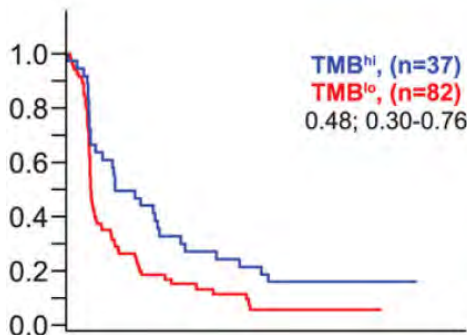
Paz Ares et al. ESMO 2019

Charge mutationnelle + ...

PD-L1

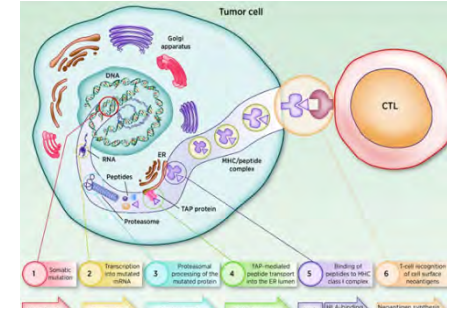


Signature
ARN

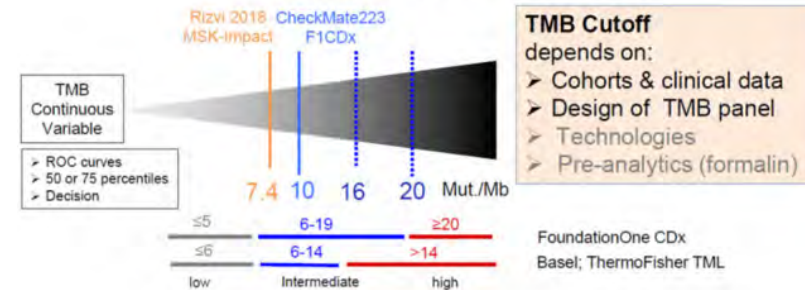


Charge mutationnelle : limitations

- Biologiques :
 - Biomarqueur indirect
 - Tous les mécanismes antigéniques ne sont pas évalués (insertions/délétions)
 - Multiples processus biologiques en « aval »
- Harmonisation de méthodes nécessaire
- Seuils multiples pour la décision clinique
- Validation clinique (analyses exploratoires principalement) et utilité actuelle ?
- Sang (ADNtc détectable ?) ou tissu ?
- Contexte : évolution des capacités de NGS



The threshold issue

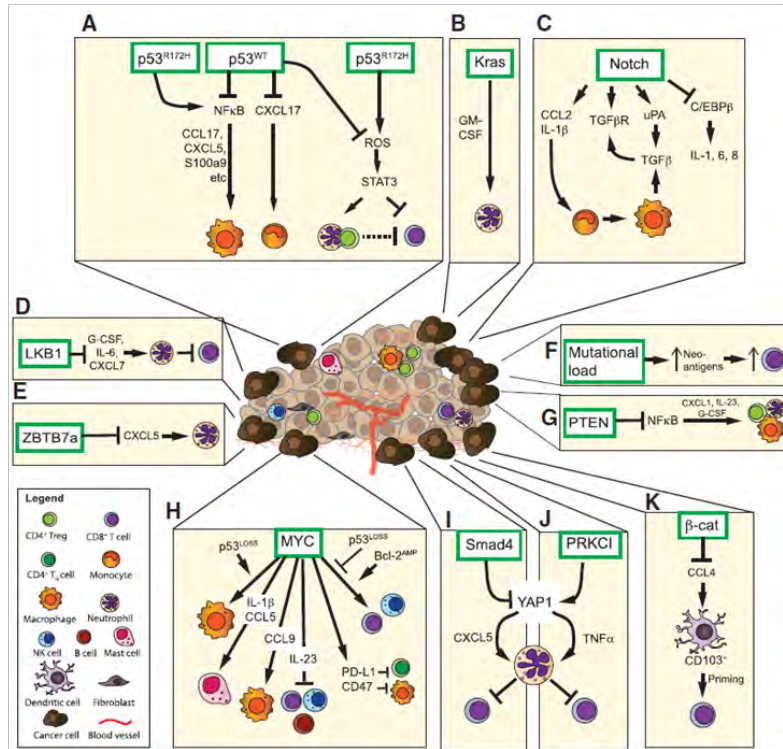


Caractéristiques moléculaires des tumeurs

Cancer-Cell-Intrinsic Mechanisms Shaping the Tumor Immune Landscape

Max D. Wellenstein¹ and Karin E. de Visser^{1,*}

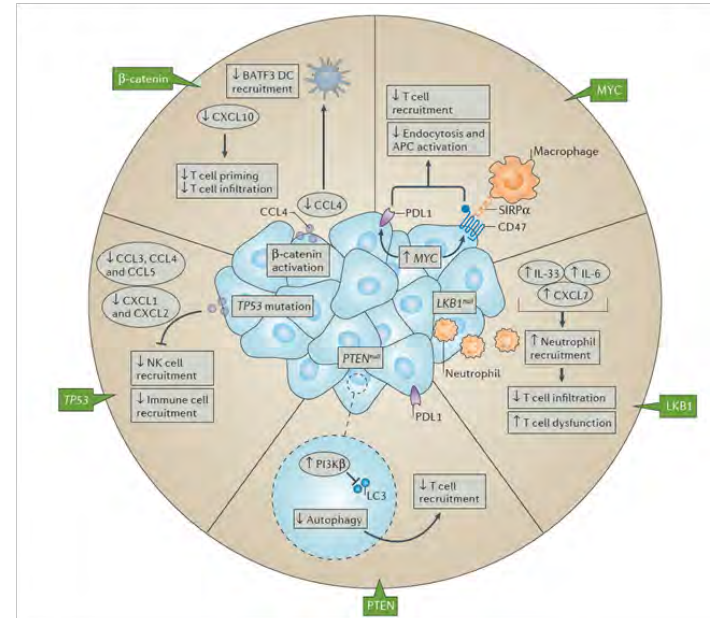
¹Division of Tumor Biology & Immunology, Oncode Institute, Netherlands Cancer Institute, 1066 CX Amsterdam, the Netherlands



Immunity, 2018

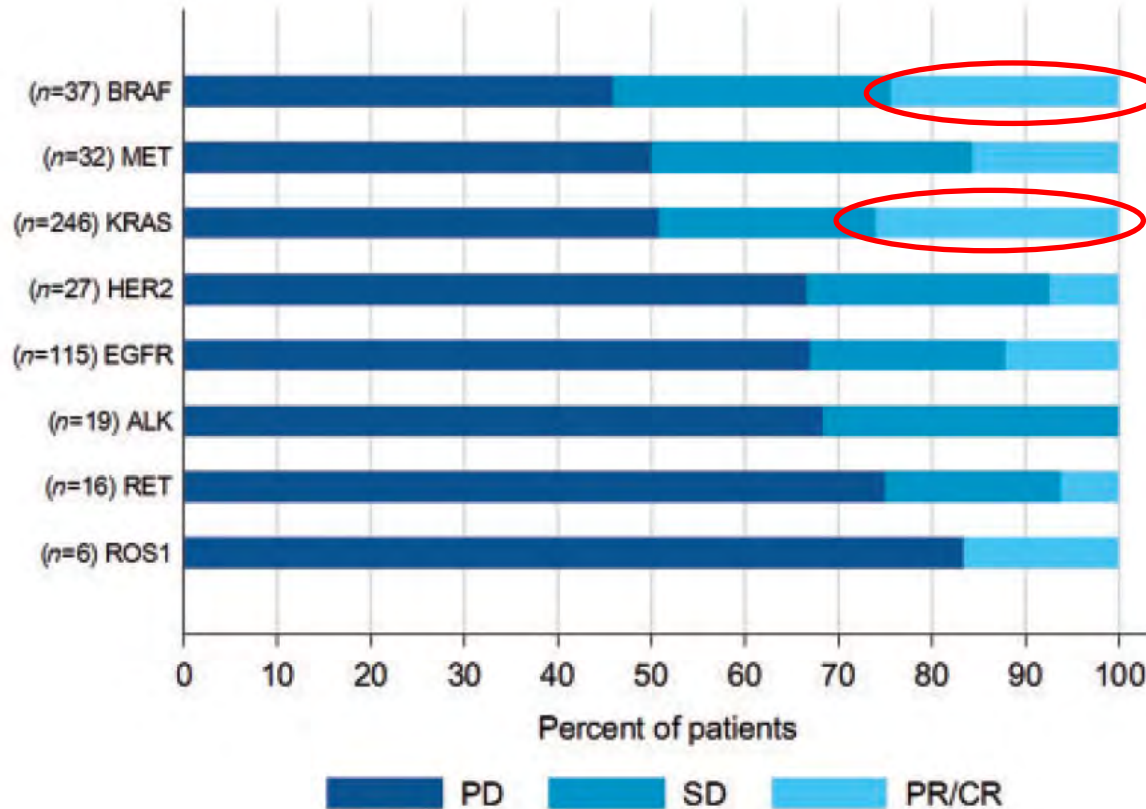
Impact of oncogenic pathways on evasion of antitumour immune responses

Stefani Spranger¹ and Thomas F. Gajewski^{2,3}



Nature Reviews Cancer, 2018

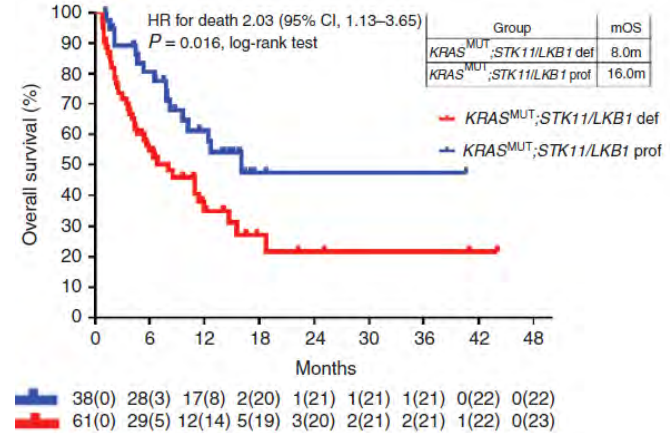
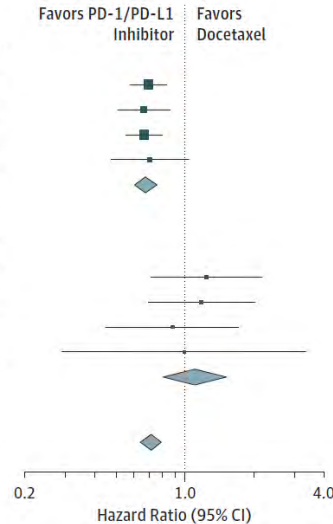
Addictions oncogéniques et réponses aux anti-PD(L)1



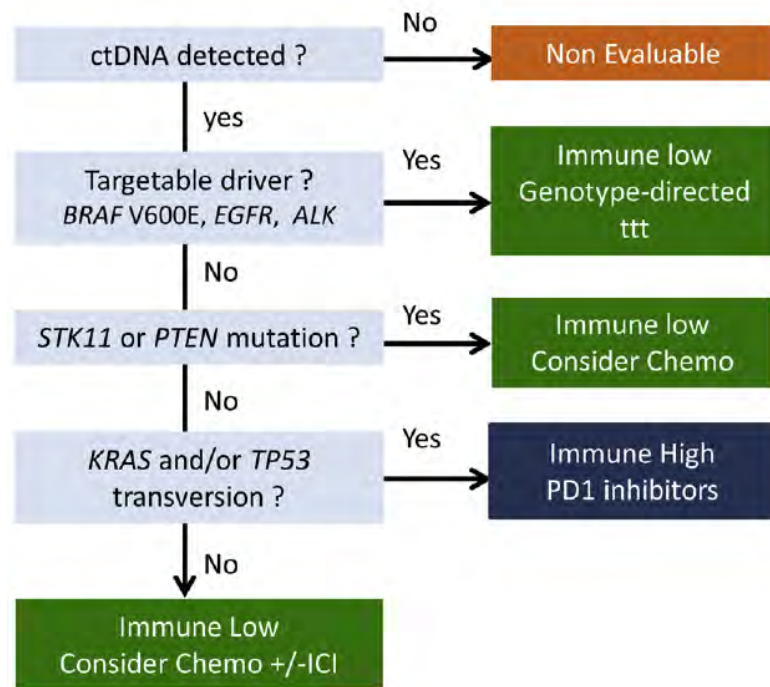
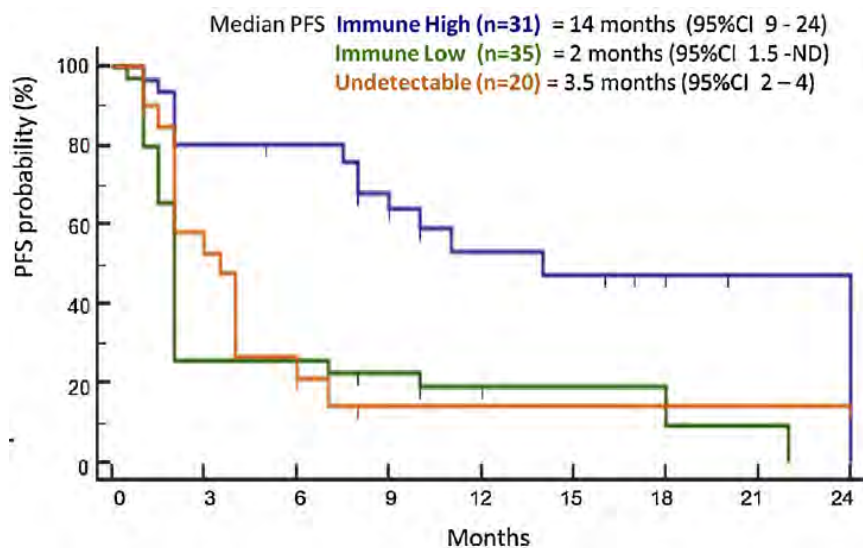
Altérations moléculaires et réponse aux anti-PD(L)1 (CPNPC)

- Associés négativement : *EGFR* mut, *KRAS/STK11* comut (VPN forte)
- Associés positivement: *BRAF* mut non-V600, *KRAS/TP53* comut (VPP modérée)

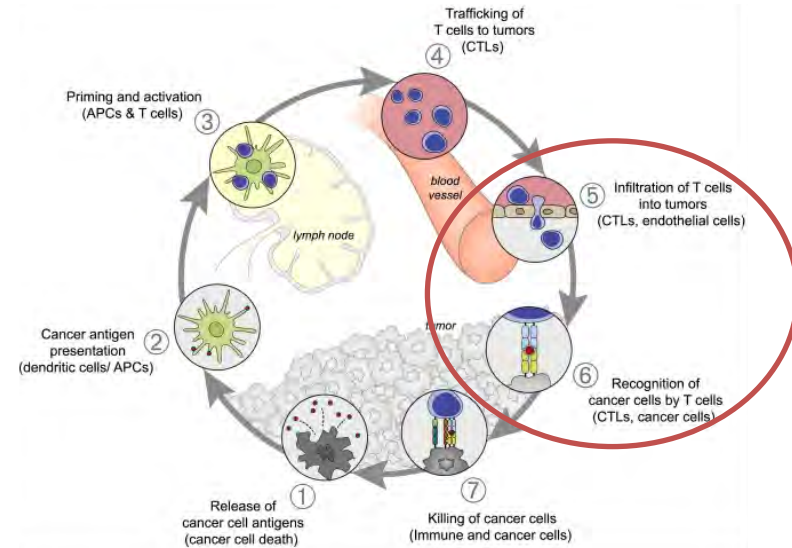
Trial	Hazard Ratio (95% CI)
EGFR wild-type	
OAK	0.69 (0.57-0.83)
CheckMate 057	0.66 (0.51-0.85)
Keynote 010	0.66 (0.55-0.79)
POPLAR	0.70 (0.47-1.04)
Subtotal	0.67 (0.60-0.75)
Heterogeneity: $\chi^2_3 = 0.18, P = .98; I^2 = 0\%$	
Test for overall effect: $z = 6.94 (P < .001)$	
EGFR mutated	
OAK	1.24 (0.71-2.18)
CheckMate 057	1.18 (0.69-2.02)
Keynote 010	0.88 (0.45-1.72)
POPLAR	0.99 (0.29-3.40)
Subtotal	1.11 (0.80-1.53)
Heterogeneity: $\chi^2_3 = 0.69, P = .88; I^2 = 0\%$	
Test for overall effect: $z = 0.61 (P = .54)$	
Total	0.71 (0.64-0.79)
Heterogeneity: $\chi^2_3 = 8.90, P = .26; I^2 = 21\%$	
Test for overall effect: $z = 6.37 (P < .001)$	
Test for subgroup differences: $\chi^2 = 8.03, P = .005; I^2 = 87.6\%$	



Altérations moléculaires : ADN plasmatisque

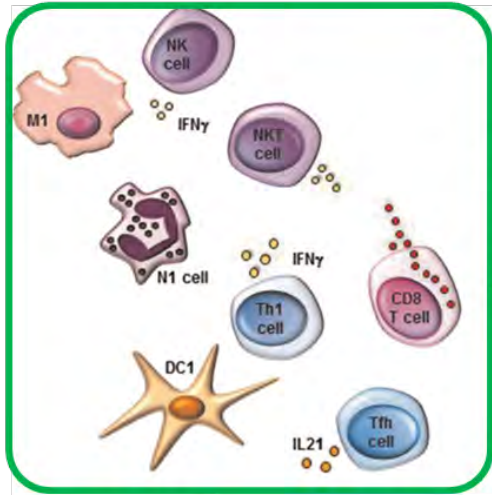


Microenvironnement immunitaire intra-tumoral

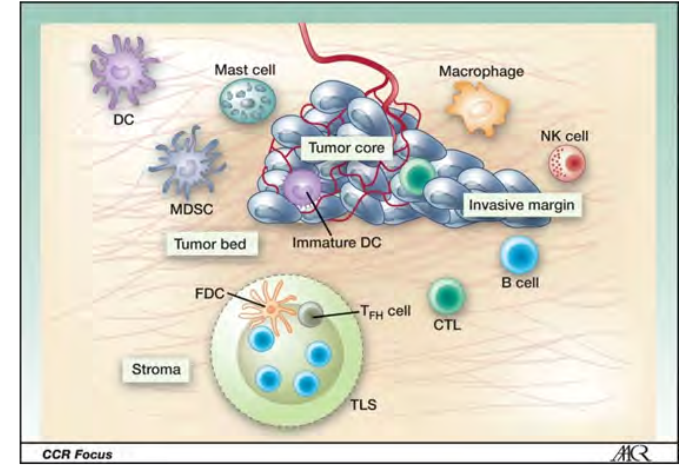
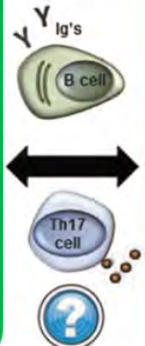
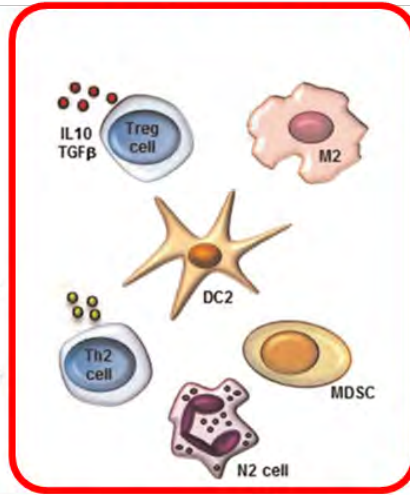


Réponse immunitaire intra-tumorale

Elimination

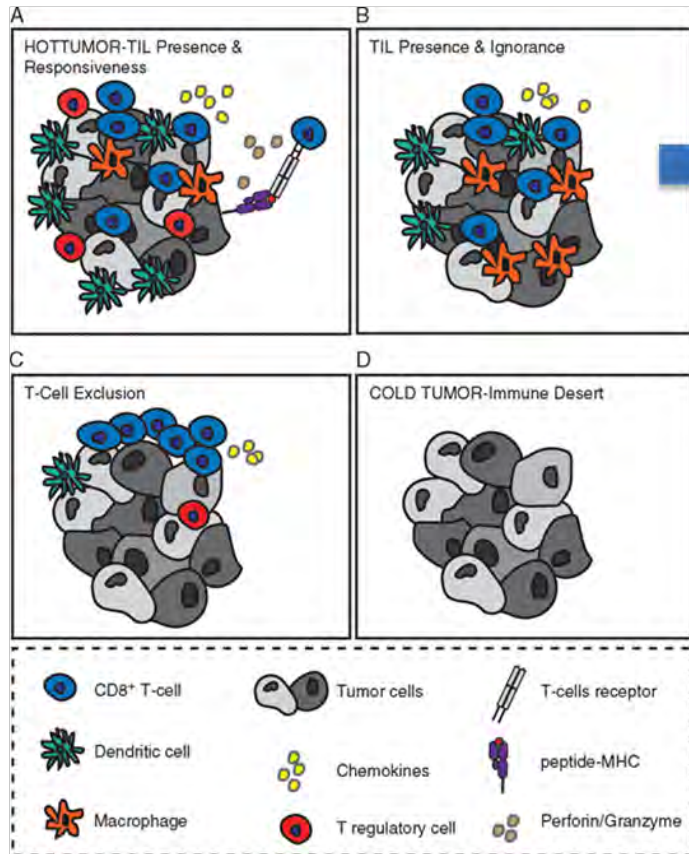


Echappement

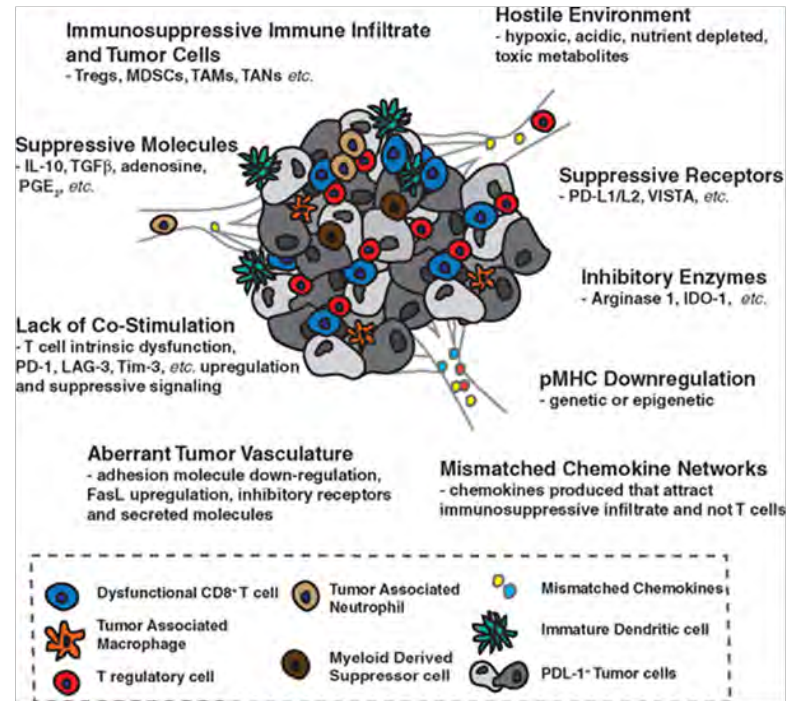


Salgado et al., Ann Oncol 2014

Presence of T-cell inflammation



Characterization of immune escape mechanisms



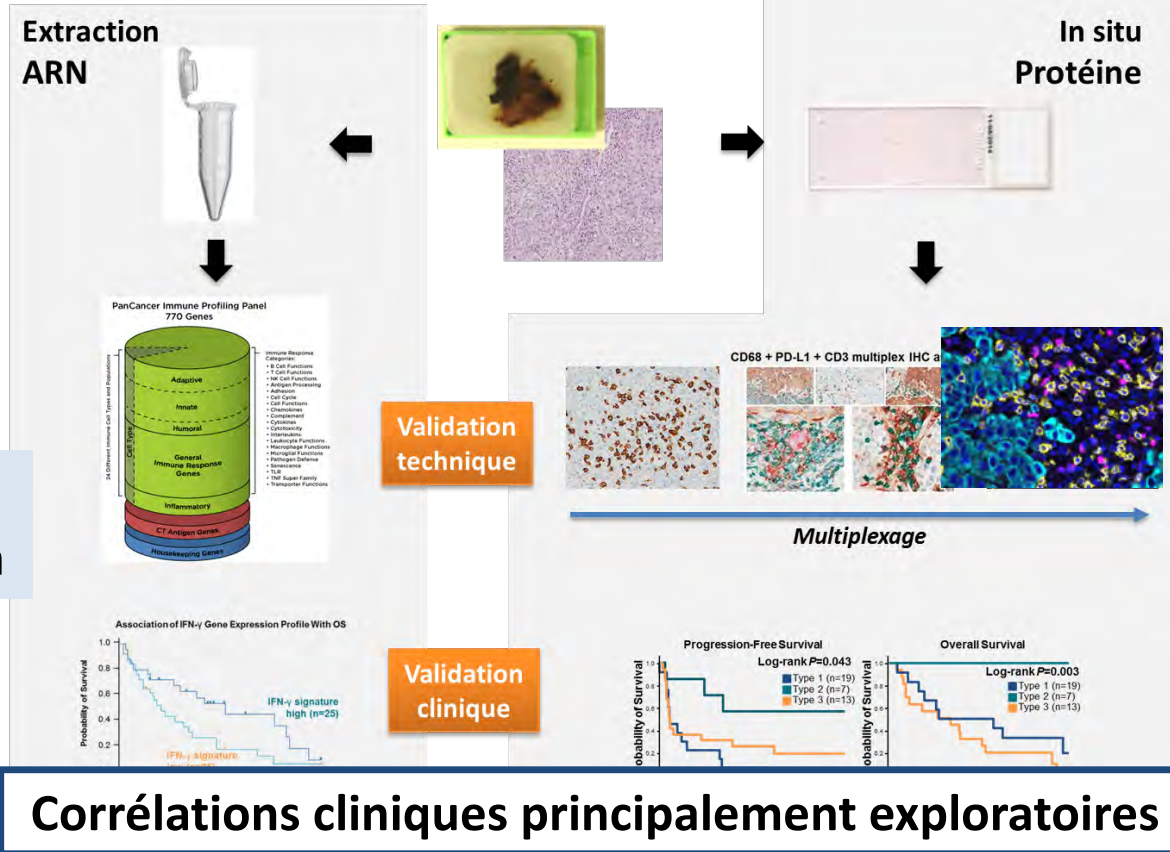
Méthodes

ARN

RNAseq
(complet ou
panel)
Nanostring

Signatures d'expression

Th1
Cellules Teff
IFNgamma
...



Protéine

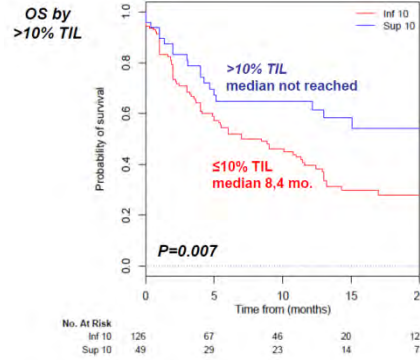
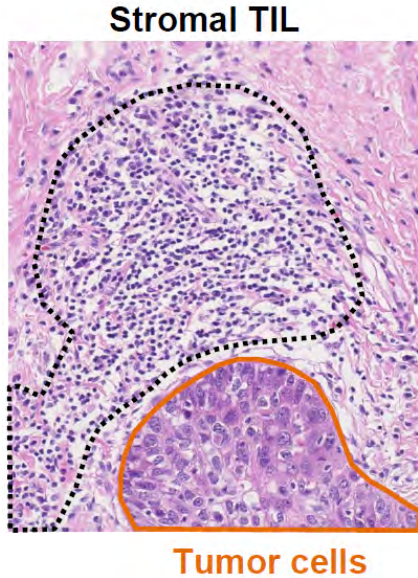
IHC, F-IHC
IMC

Phénotypage de cellules

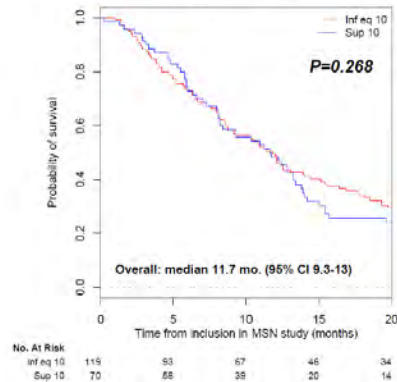
Corrélations cliniques principalement exploratoires

Morphologie : TIL

Immunotherapy



Chemotherapy

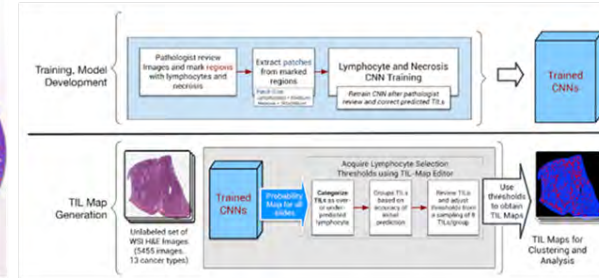


Mezquita et al. WCLC 2019

Cell Reports

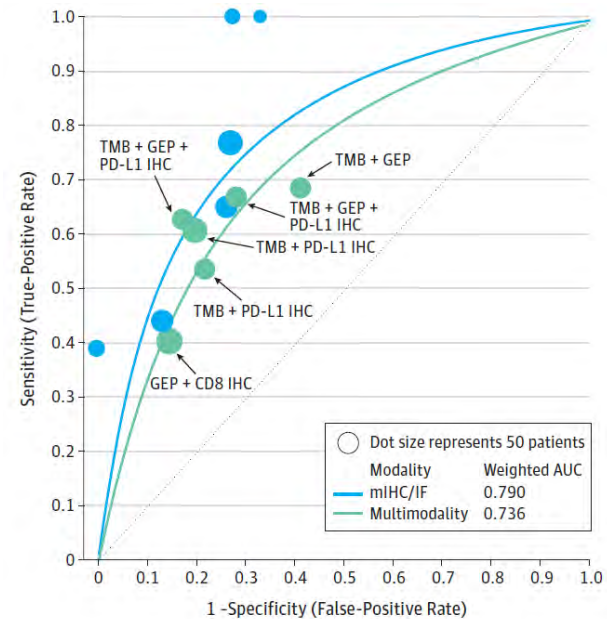
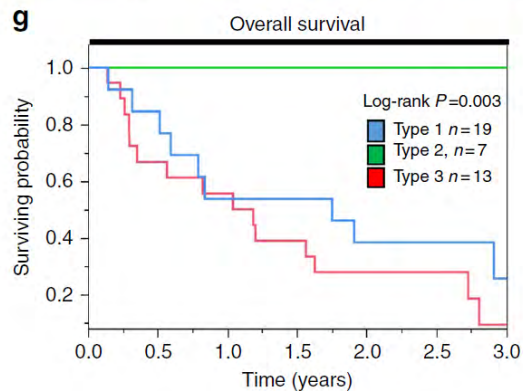
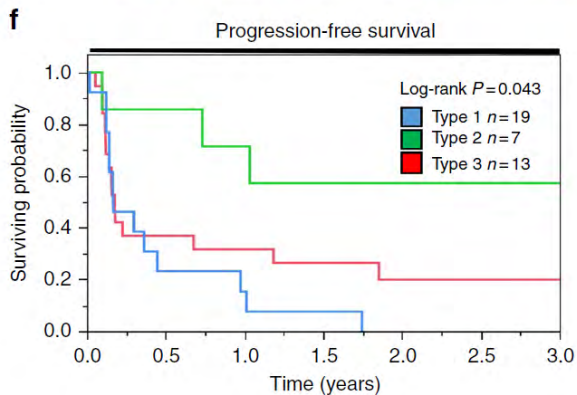
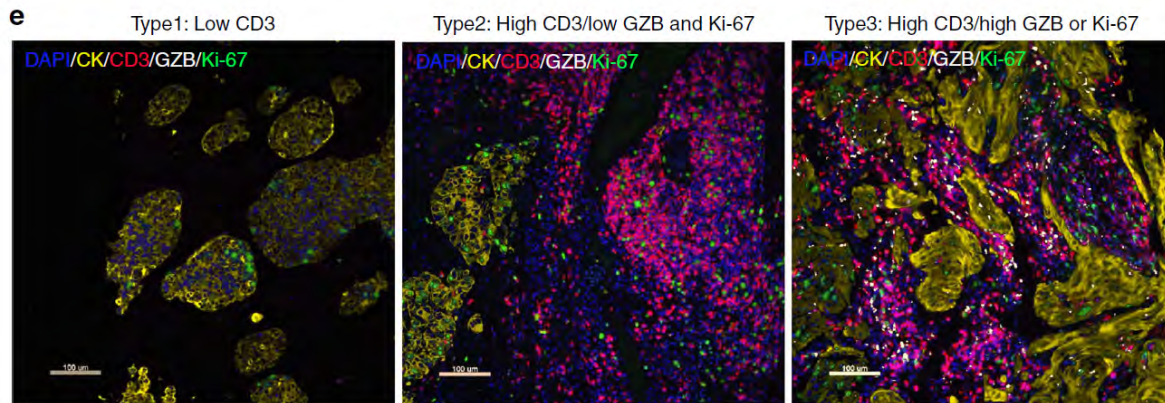
Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images

Joel Saltz,^{1,*} Rajarsi Gupta,^{1,4} Le Hou,² Tahsin Kurc,¹ Pankaj Singh,³ Vu Nguyen,² Dimitris Samaras,² Kenneth R. Shroyer,⁴ Tianhao Zhao,⁴ Rebecca Batista,⁴ John Van Amam,² The Cancer Genome Atlas Research Network, Ilya Shmulevich,⁵ Arvind U.K. Rao,^{3,7} Alexander J. Lazar,⁸ Ashish Sharma,⁹ and Vesteinn Thorsinn^{6,10,*}



Saltz et al., Cell Reports 2017

Phénotypage in situ (F-IHC multiplex)



Signatures ARN : IFN γ , Teff, Th1,...

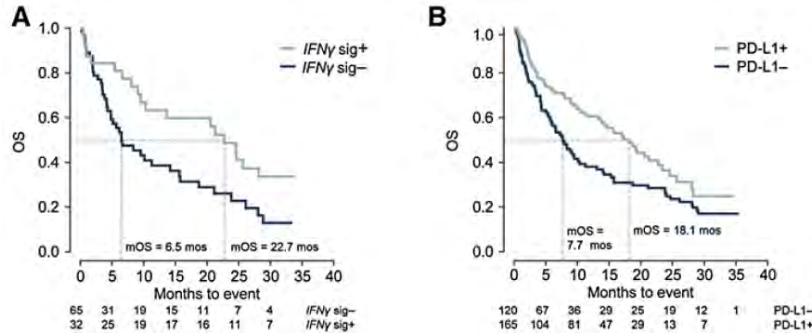


Table 5. Concordance between tumor IFN γ gene signature and PD-L1 status in NSCLC and urothelial cancer patients

NSCLC	IFN γ sig ⁺ mOS (n)	IFN γ sig ⁻ mOS (n)
PD-L1 ⁺ , mOS (n)	23 mo (19)	6 mo (18)
PD-L1 ⁻ , mOS (n)	25 mo (11)	7 mo (43)

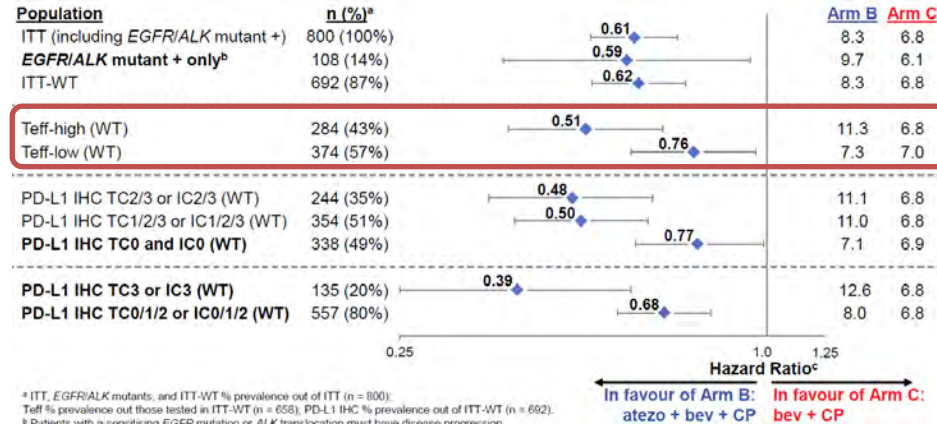
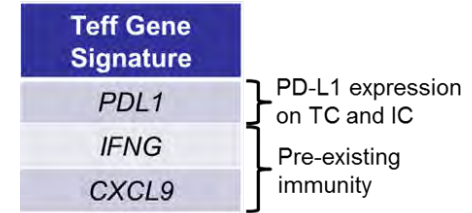
Fisher's exact test for count data; $P = 0.003$; OR = 4.1.

UC ^a	IFN γ sig ⁺ mPFS (n)	IFN γ sig ⁻ mPFS (n)
PD-L1 ⁺ , mPFS (n)	NR (14)	NR (11)
PD-L1 ⁻ , mPFS (n)	NR (1)	NR (16)

NOTE: Fisher's exact test for count data; $P = 0.001$; OR = 19.0.

Abbreviations: mPFS, median progression-free survival; NR, median not reached; UC, urothelial carcinoma.

^aUC OS data are not fully mature for subgroup analysis.



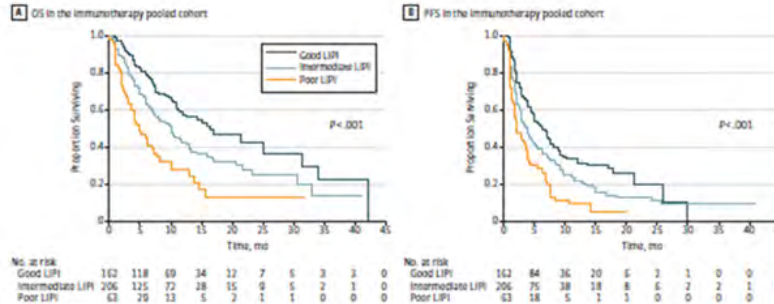
Infiltration immunitaire intratumorale

- Beaucoup de technique différentes :
 - Identifie-t-on les même tumeurs ?
- Validation clinique restreinte (analyses exploratoires)
- Limitations :
 - Hétérogénéité tumorale et représentativité des prélèvements
 - Valeur pronostique
 - Corrélation aux paramètres moléculaires
- Données complexes (nombre de paramètre, paramètres spatiaux) : champ d'application pour l'IA+++

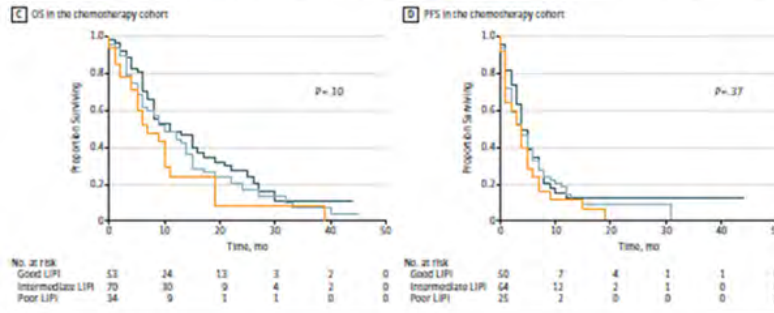
Marqueurs sanguins ? Paramètres biologiques

LIPI score: Derived neutrophils/(leukocytes minus neutrophils) ratio (dNLR) and lactate dehydrogenase (LDH) levels

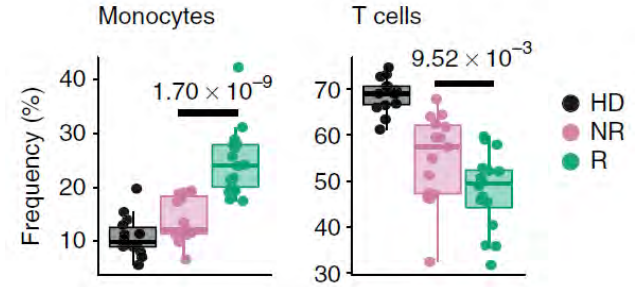
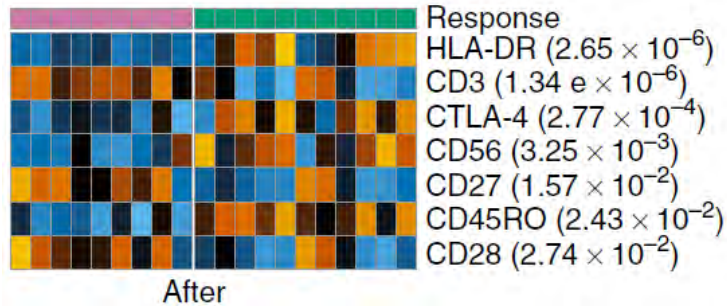
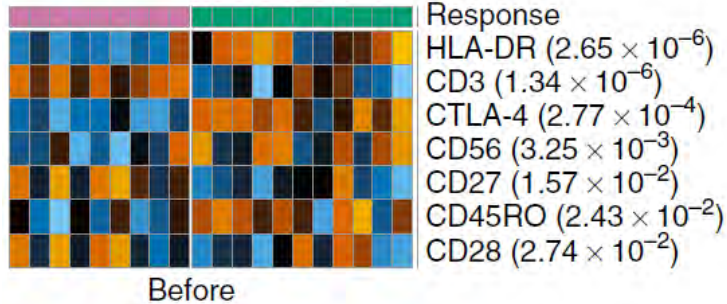
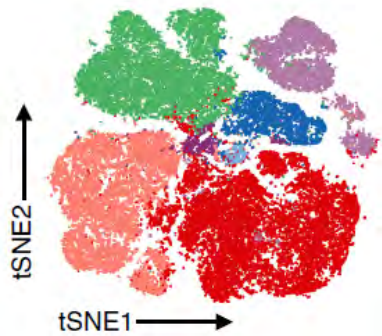
Immunothérapie



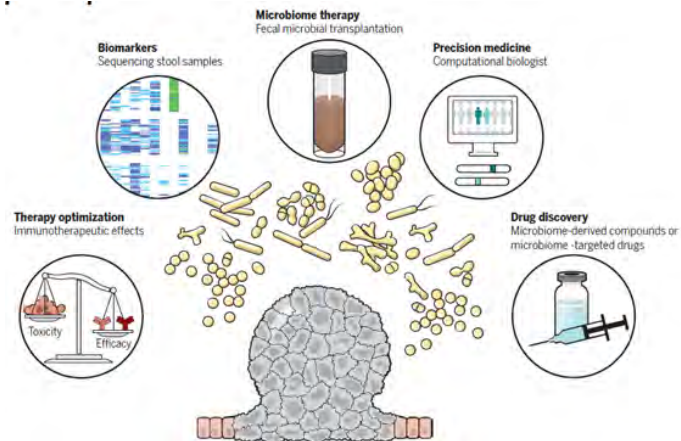
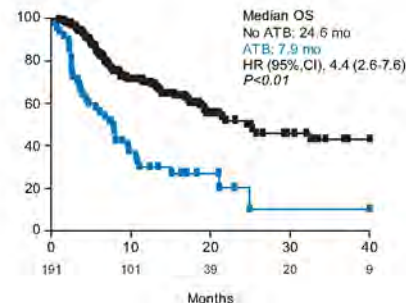
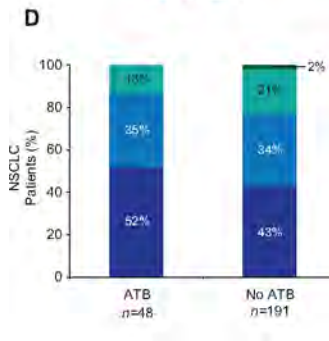
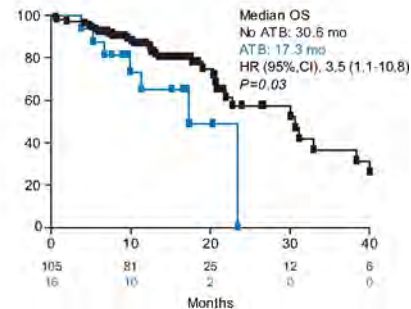
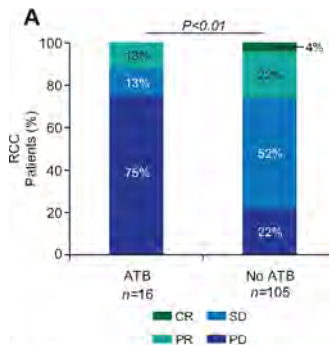
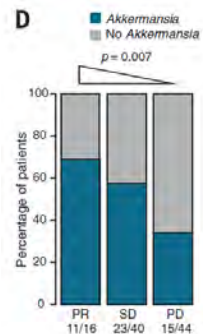
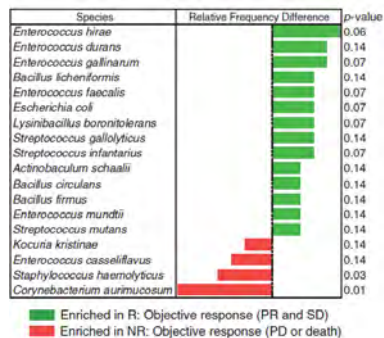
Chimiothérapie



Marqueurs sanguins ? Cellules circulantes

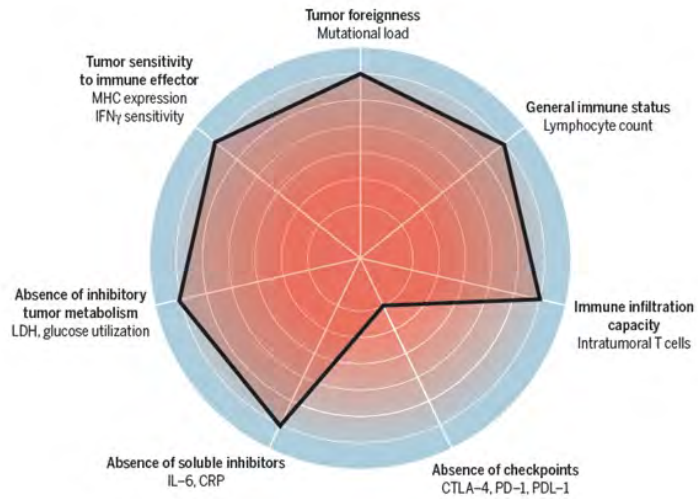


Microbiote intestinal

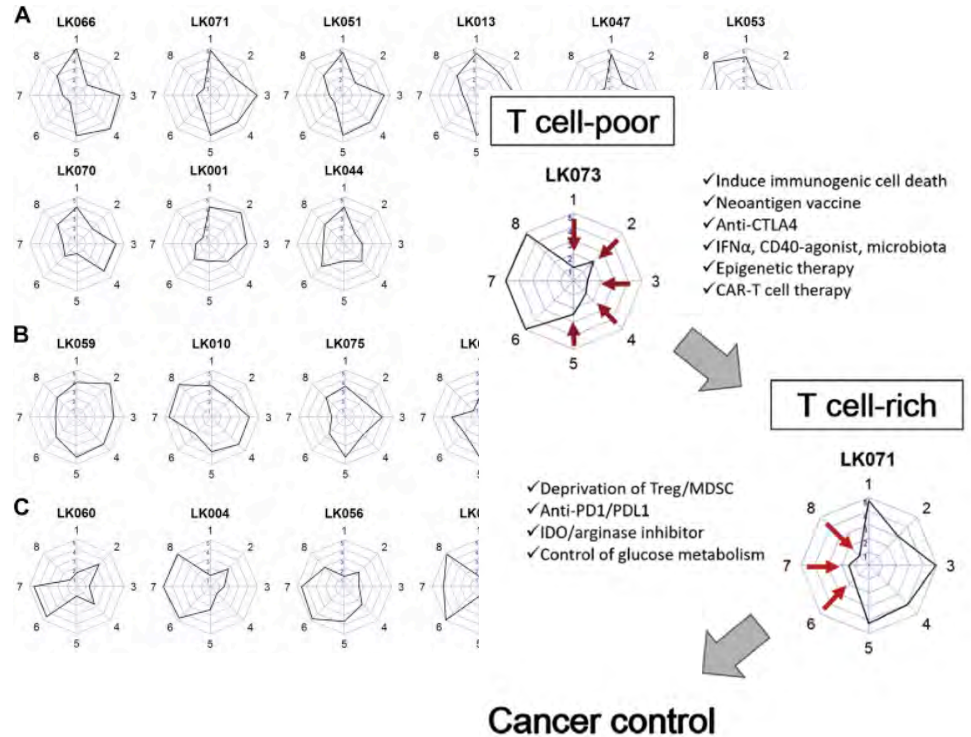


Combiner les biomarqueurs ?

« Cancer immunogram »

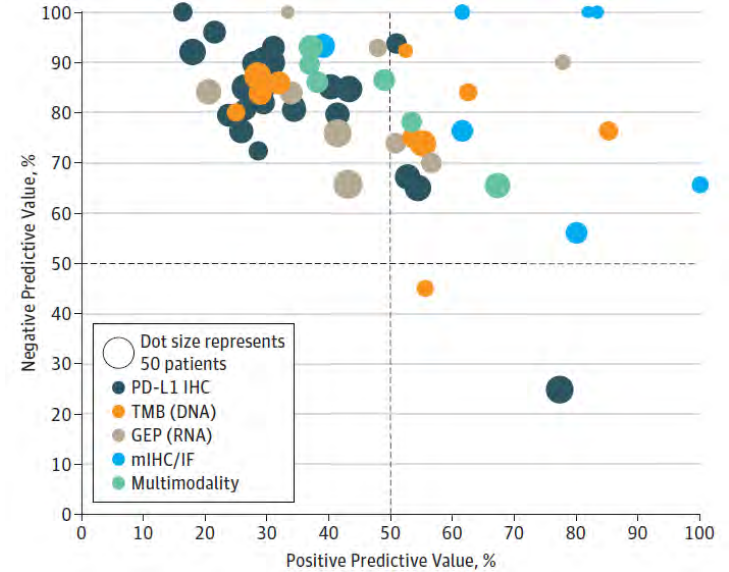
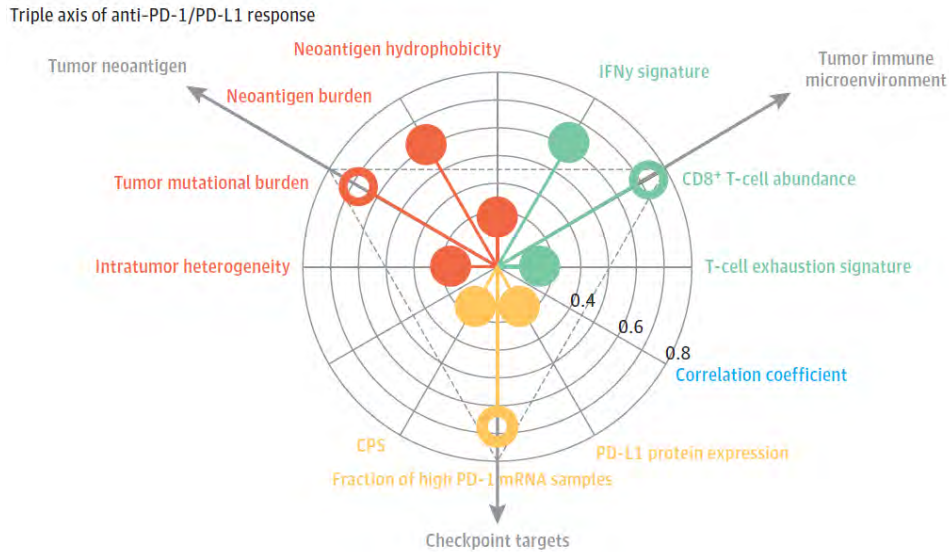


Blank et al. Science 2016



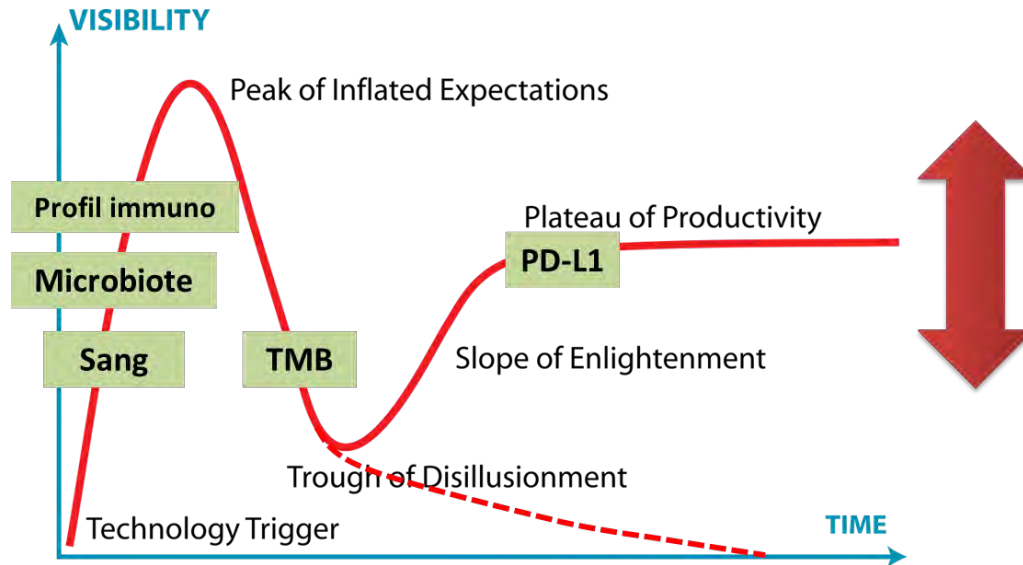
Karasaki et al., J Thor Oncol 2017

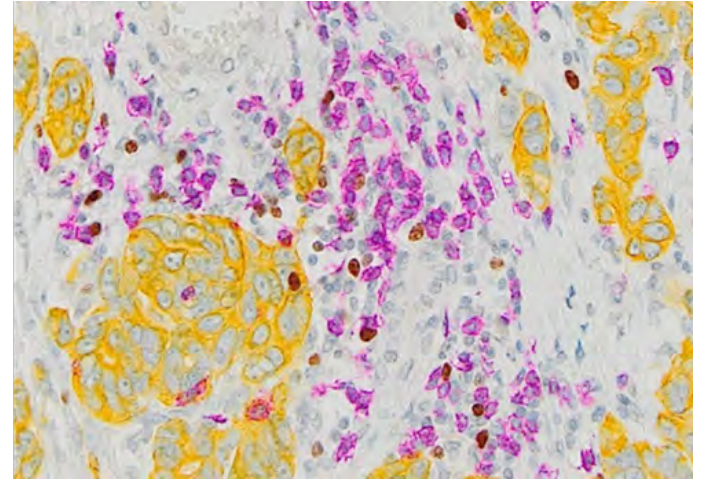
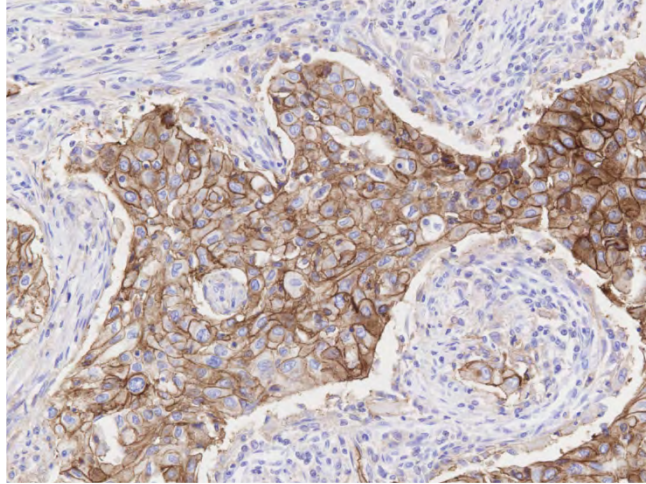
Combiner les biomarqueurs ?



Conclusions

- Biomarqueurs imparfaits
- Intégration des données
- Analyses exploratoires \Rightarrow validation prospective





Merci pour votre attention

julien.adam@gustaveroussy.fr

