

# Genomic-Driven Precision Oncology with Next Generation Sequencing Testing

35<sup>th</sup> Annual Park City Anatomic Pathology Update February 6-10, 2022

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# Learning Objectives

1. Understand Comprehensive Genomic Profiling By NGS Testing.
2. Understand How Molecular Tumor Board Can Support Precision Oncology.
3. Review Newly FDA-Approved Oncologic Therapies In 2021.
4. A Case Study In Precision Oncology: NSCLC Patient With Brain Metastasis.

# TRADITIONAL MEDICINE vs. **PRECISION MEDICINE**

Traditionally, radiation, chemotherapy, and surgery were the only means by which doctors could treat cancer.  
With precision medicine, doctors use a patient's genes to uncover clues for treating the disease.

## RADIATION

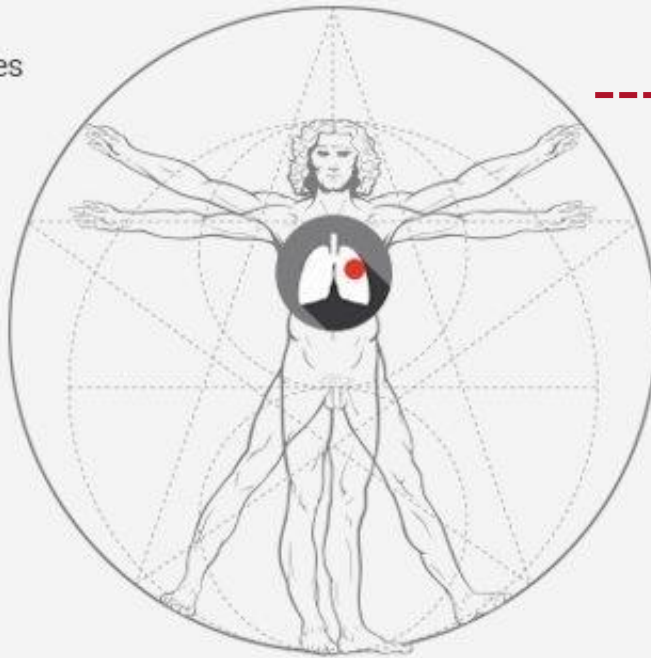
- High-energy particles damage or destroy cancer cells

## CHEMOTHERAPY

- Chemicals attack cancer

## SURGERY

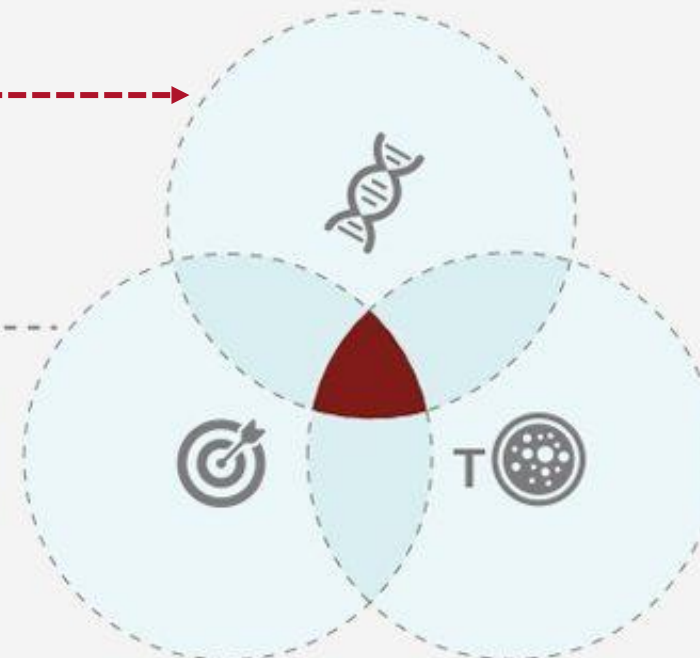
- Operate on part of the body to diagnose or treat cancer



NGS



Advanced  
Personalized  
Treatment



## GENETICS

- Gene sequencing
- Locate cancer-causing genes

## IMMUNOTHERAPY

- Identify ways to customize treatment
- Find ways to turn immune system on
- Personalize treatment with immune-activating drugs

## TARGETED THERAPIES

- Drugs turn specific genes on or off

+ TRADITIONAL THERAPIES

<https://healthmatters.nyp.org/precision-medicine/>

# Healthcare Professionals' Attitude Towards NGS Testing and Precision Cancer Medicine

- Largely positive but with some concerns.
- Lack of evidence and guidelines.
- Limited HCP knowledge about testing.
- Insurance coverage and cost to patient.
- Need for decision and implementation supports.



Journal of Oncology Practice®

Volume 15, Issue 6 297

*J. Vetsch, C.E. Wakefield and P. Techakesari et al./Seminars in Oncology 46 (2019) 291–303*



# Basics: Two Major Next Generation Sequencing Methods

Thermo Fischer  
(Amplicon/Emulsion Bead PCR)

Minority Market Share

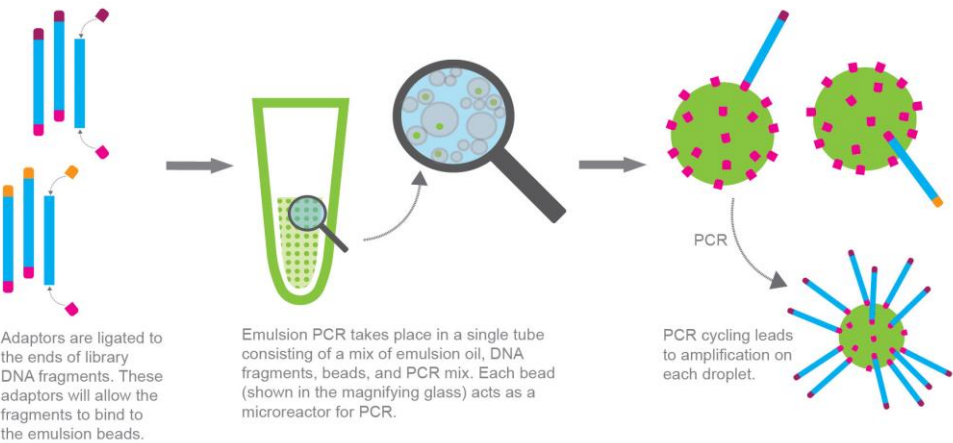
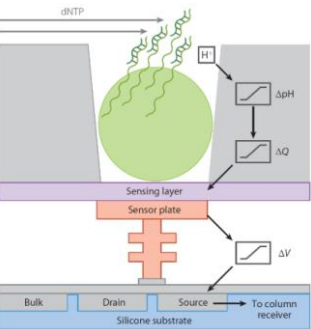


Figure 3. Conceptual illustration of emulsion PCR.



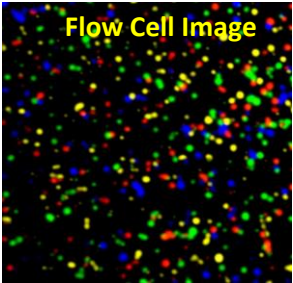
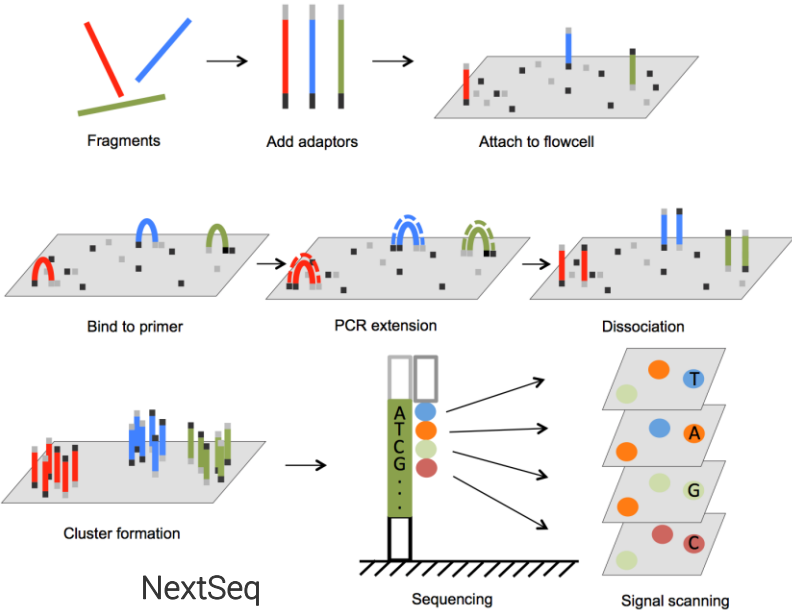
One Fragment

One Clonal Cluster

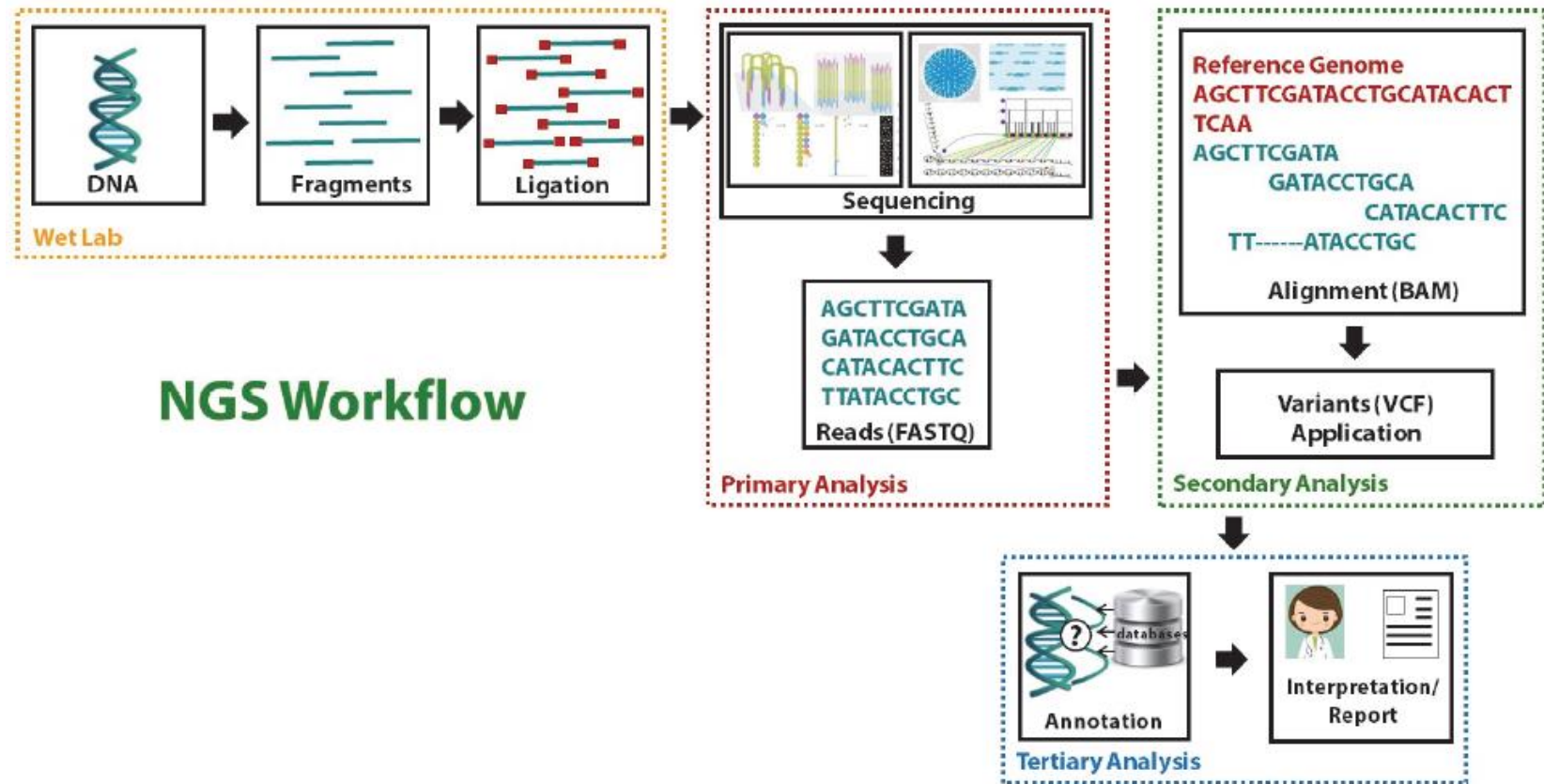
One Read

Illumina  
(Hybrid Capture/Flow Cell)

Majority Market Share  
~ 80-90%



# NGS Basics: Wet Bench to Bioinformatics



# NGS Basics: Potential Causes for False Negative Or False Positive Results



- Sample Issues

- Specimen adequacy
- Poor DNA Quality
- Pre-Processing

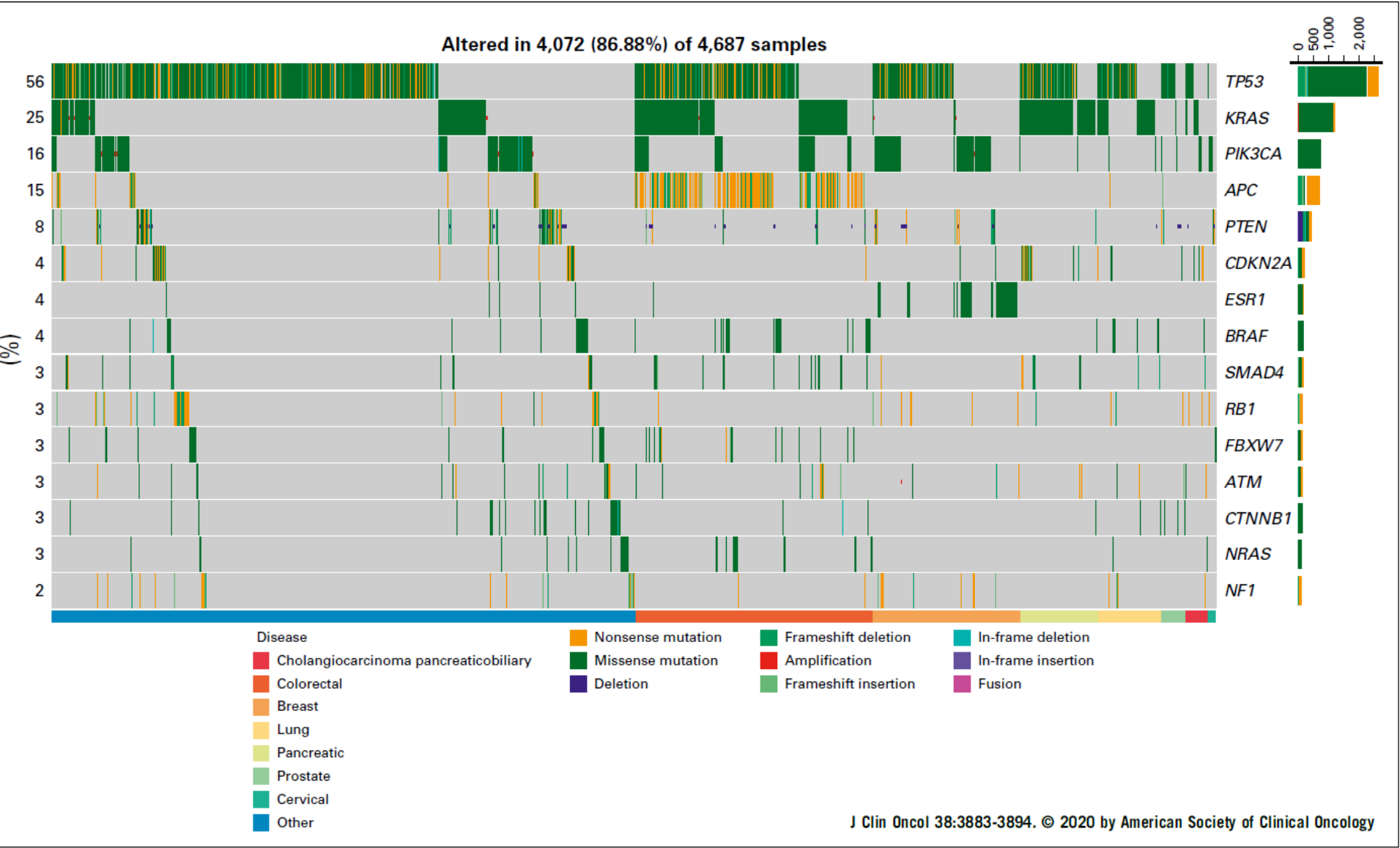
- Bioinformatics Issues

- Large deletions or insertions
- Complex or multi-nucleotide variants
- Difficult Regions
  - GC-bias
  - Homopolymers
  - Tandem repeats
  - Pseudogenes

- Interpretation Issues

- UpToDate Database
- Medical Expertise

# The National Cancer Institute Molecular Analysis for Therapy Choice (NCI-MATCH)



- Tumor biopsy specimens from 5,954 patients with refractory malignancies.
- 38% of patients had actionable mutations.
- All available investigational therapies known with evidence of efficacy in biomarker-defined populations.
- 18% were assigned to actively enrolling treatment arms.



# Understanding Comprehensive Tumor Profiling Report By NGS



## Executive Summary:

This is a 59-year-old male with advanced NSCLC. Multiple genomic alterations including activating EGFR and inactivating TP53 mutations were detected. So on.....

## Genomic Alterations Detected:

- 4-Tier Classification
- FDA-Approved Therapy

## Immunotherapy Biomarkers:

- Tumor Mutational Burden (TMB)
- Microsatellite Instability (MSI)

## Variants of Undetermined Significance (VUS):

- Uncertain Clinical Significance

# 4-TIER Somatic Variant Classification In Cancer (AMP, ASCO, CAP)

## SPECIAL ARTICLE

Standards and Guidelines for the Interpretation  
and Reporting of Sequence Variants in Cancer



*A Joint Consensus Recommendation of the Association for  
Molecular Pathology, American Society of Clinical Oncology,  
and College of American Pathologists*

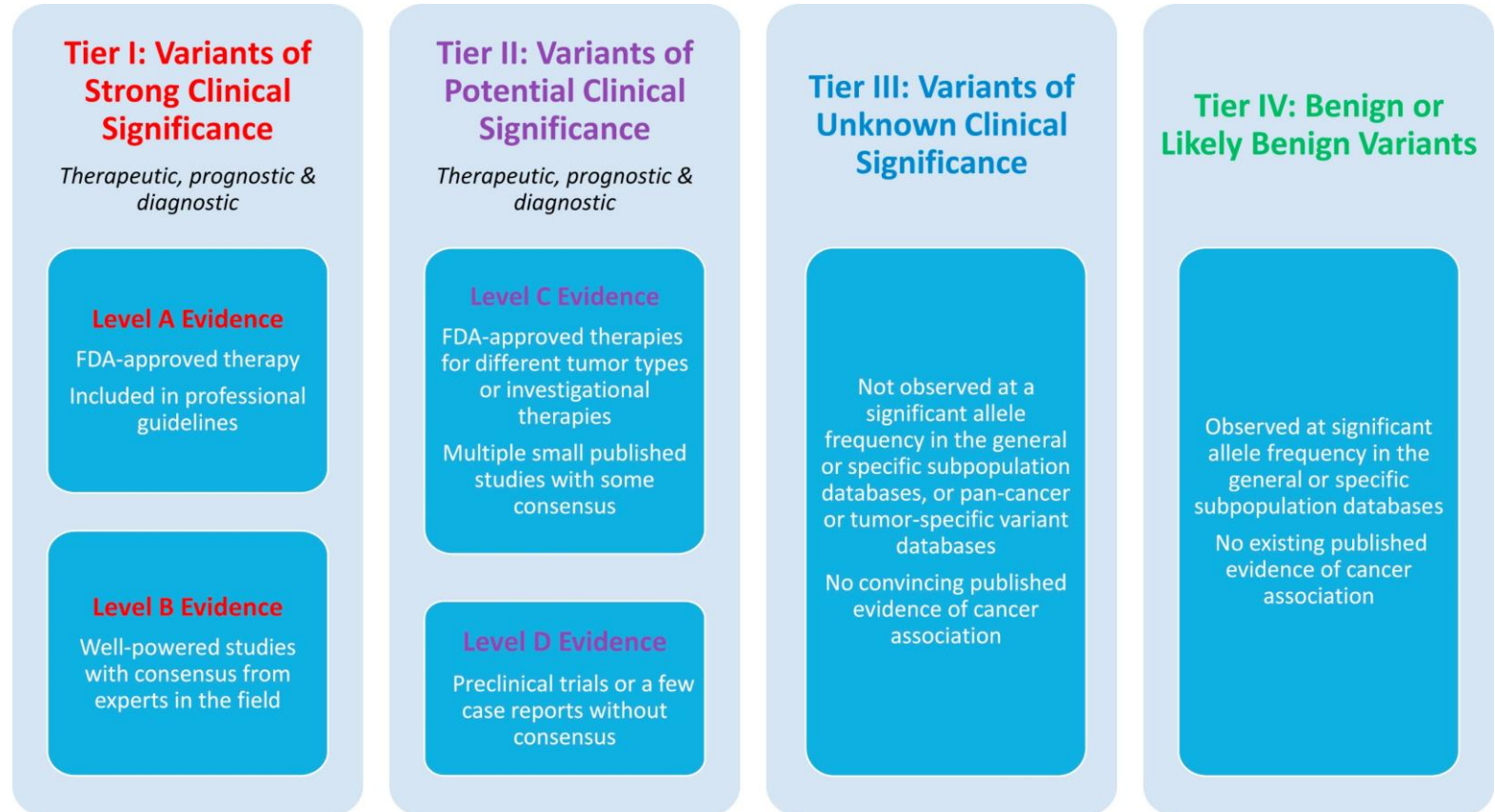
Marilyn M. Li,<sup>\*†</sup> Michael Datto,<sup>\*†</sup> Eric J. Duncavage,<sup>\*§</sup> Shashikant Kulkarni,<sup>\*¶</sup> Neal I. Lindeman,<sup>\*||</sup> Somak Roy,<sup>\*,\*\*</sup>  
Apostolia M. Tsimberidou,<sup>\*††</sup> Cindy L. Vnencak-Jones,<sup>\*‡‡</sup> Dayna J. Wolff,<sup>\*§§</sup> Anas Younes,<sup>\*¶¶</sup> and Marina N. Nikiforova<sup>\*,\*\*</sup>

### TIER 1 Example:

- Melanoma BRAF V600E
- Breast Cancer HER2 Amplification

### TIER 2 Example:

- NSCLC with “hotspot” PIK3CA mutations
- CRC with TP53 mutations



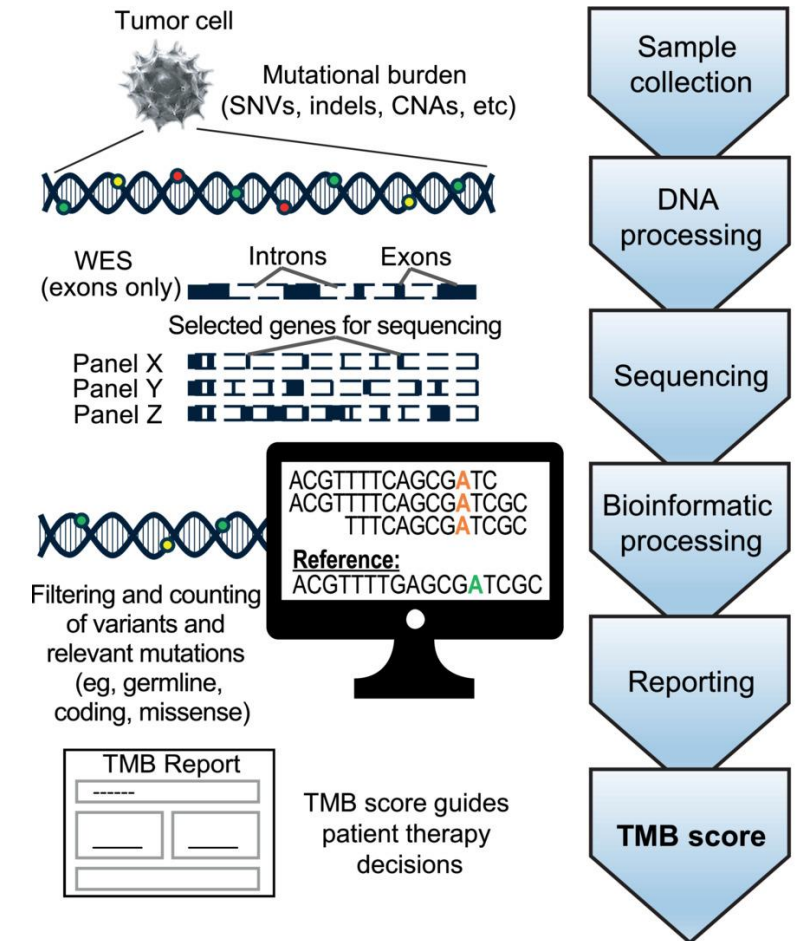
The Journal of Molecular Diagnostics, Vol. 19, No. 1, January 2017

# Tumor Mutational Burden (TMB)

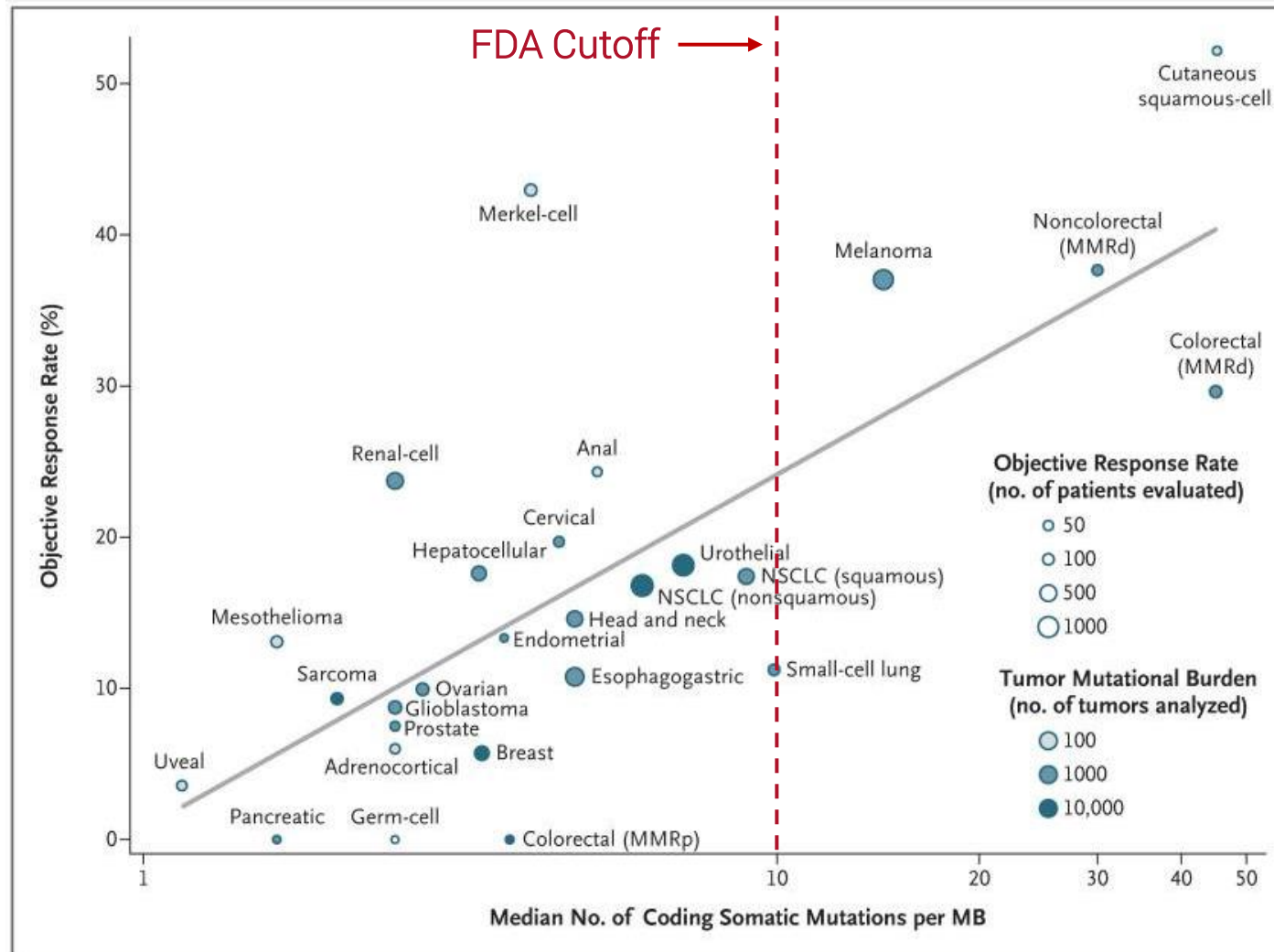
- Measurement of the number of mutations that exists in a tumor.

$$\text{TMB (mutations/Mb)} = \frac{\text{\# of non-synonymous somatic mutations}}{\text{Per mega-base in coding regions}}$$

- TMB is highly predictive of response to immunotherapy.
  - » FDA approval (2021) of pembrolizumab for TMB  $\geq 10$  in solid tumors.
- Lack of standardization regarding TMB across laboratories!



# TMB and IO Efficacy Varies Across The Tumor Types

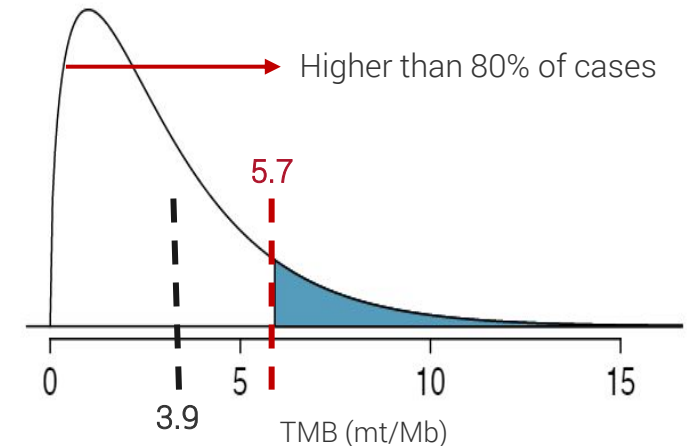


N Engl J Med. 2017 December 21; 377(25): 2500–2501



# Various Ways For Reporting TMB Back To Clinicians

- Scenario #1:
  - » The estimated tumor mutational burden (TBM) for this tumor is 5.7 mutations per megabase (mt/Mb).
- Scenario #2:
  - » TMB-Low: The estimated tumor mutational burden (TBM) for this tumor is 5.7 mutations per megabase (mt/Mb).
- Scenario #3:
  - » The estimated tumor mutational burden (TBM) for this tumor is 5.7 mutations per megabase (mt/Mb) which corresponds to 80<sup>th</sup> percentile in the patient's cancer cohort.
  - » The median TMB assessed by our laboratory for patient's cancer cohort is 3.9 mt/Mb.



# MSI: First FDA Approval Agnostic Of Cancer Sites

- Pembrolizumab (2017, Keytruda, Anti-PD1)
  - » 1<sup>st</sup> example of a tissue-agnostic FDA approval.
  - » Microsatellite instability-high (MSI-H) or mismatch repair deficient (dMMR) advanced solid tumors.
  - » Near 40% overall response rate (ORR) across 15 tumor types.
- MSI-H and dMMR Detection:
  - » Immunohistochemistry (Loss of MLH1, PMS2, MSH2, MSH6).
  - » Microsatellite instability by PCR.
  - » Microsatellite instability by NGS.

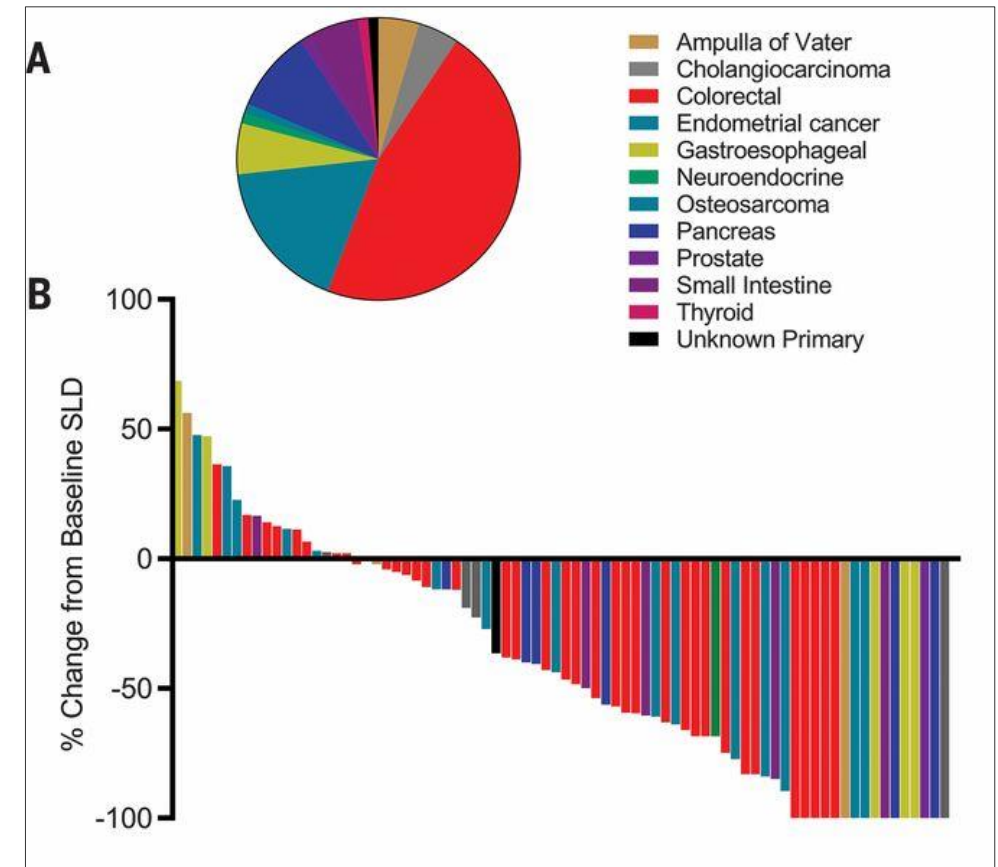
FDA NEWS RELEASE

## FDA approves first cancer treatment for any solid tumor with a specific genetic feature

[f Share](#) [t Tweet](#) [in LinkedIn](#) [✉ Email](#) [🖨 Print](#)

For Immediate Release: May 23, 2017

**Fig. 1. Patient survival and clinical response to pembrolizumab across 12 different tumor types with mismatch repair deficiency.**

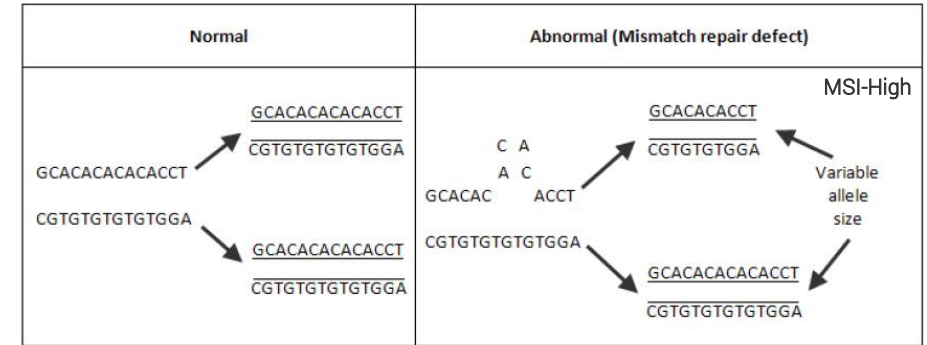


Dung T. Le et al. Science 2017;357:409-413

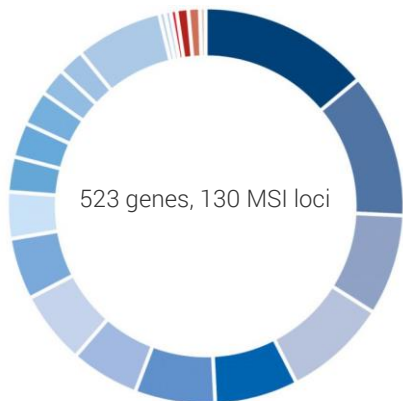
# MSI Status Determined By Next Generation Sequencing

- Microsatellites are DNA motifs (1-6 BP) repeating 5-50 times.
- During replication, slippage can cause gain or loss of repeats which are then corrected by MMR proteins.
- Examine microsatellite loci (100s-1000s).
  - » Using the capture gene sequences.
  - » Dedicated specific MSI markers.
  - » Establish “baseline” statistics.
  - » Interpret fraction (%) of unstable loci to infer MSI status.

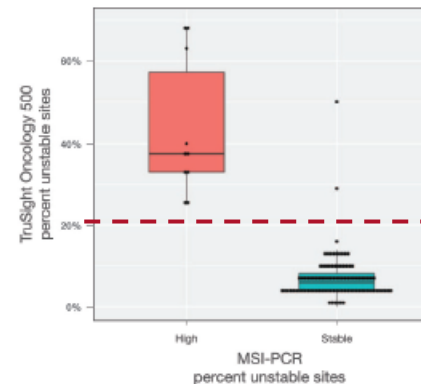
Microsatellite Replication



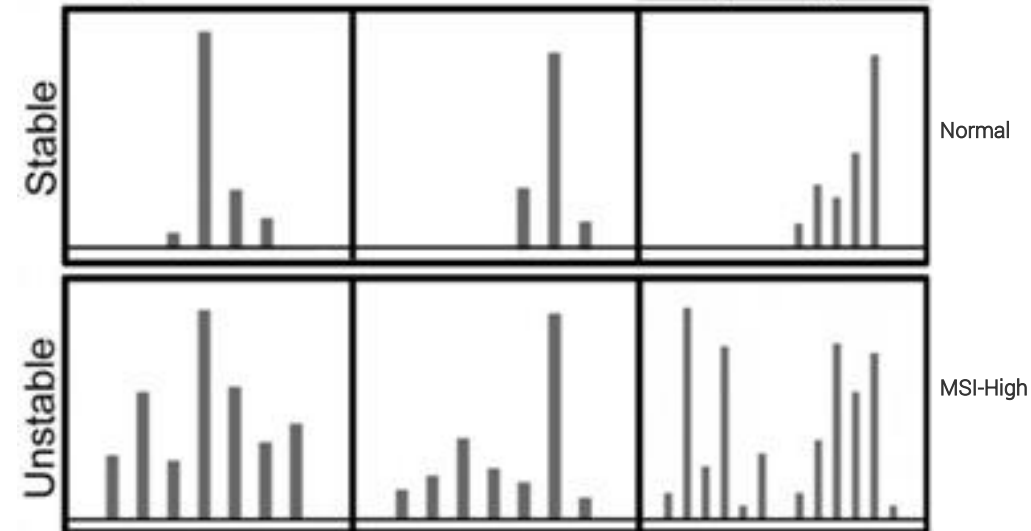
Comprehensive NGS Panel



MSI-High Cutoff



Representative NGS Virtual Electropherograms



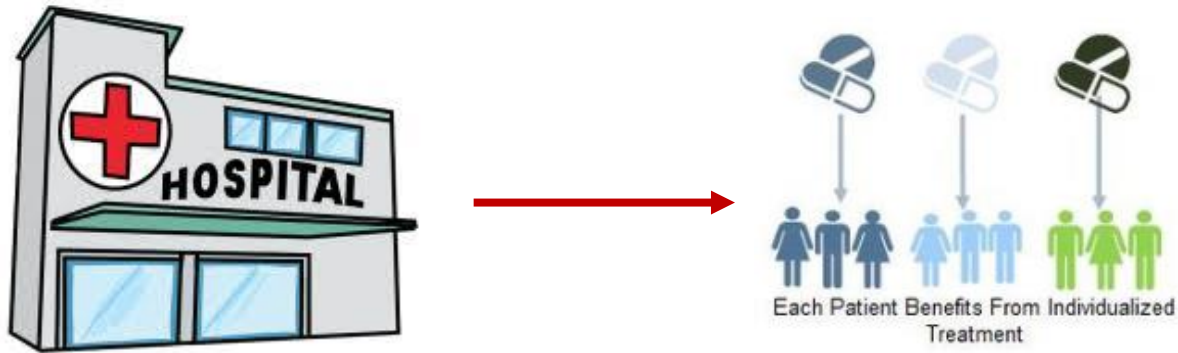


# Learning Objectives

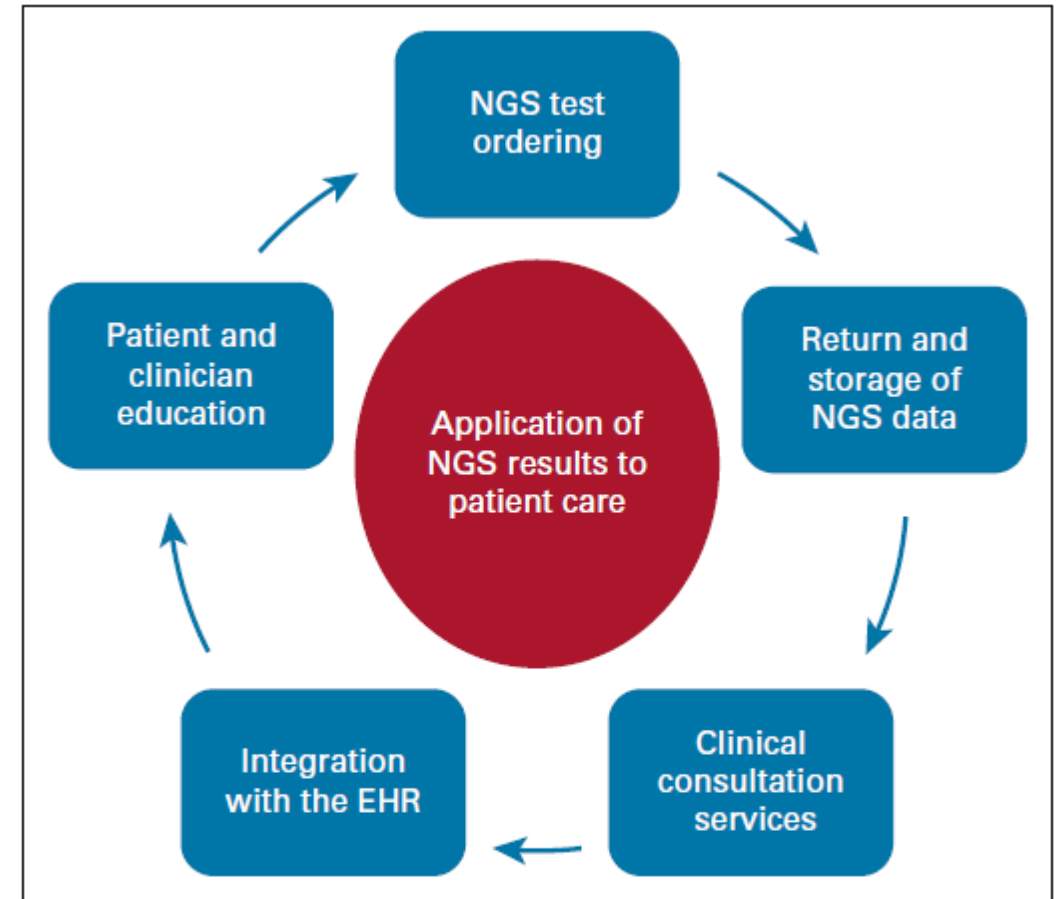
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# Integrating NGS Results Into Patient Care

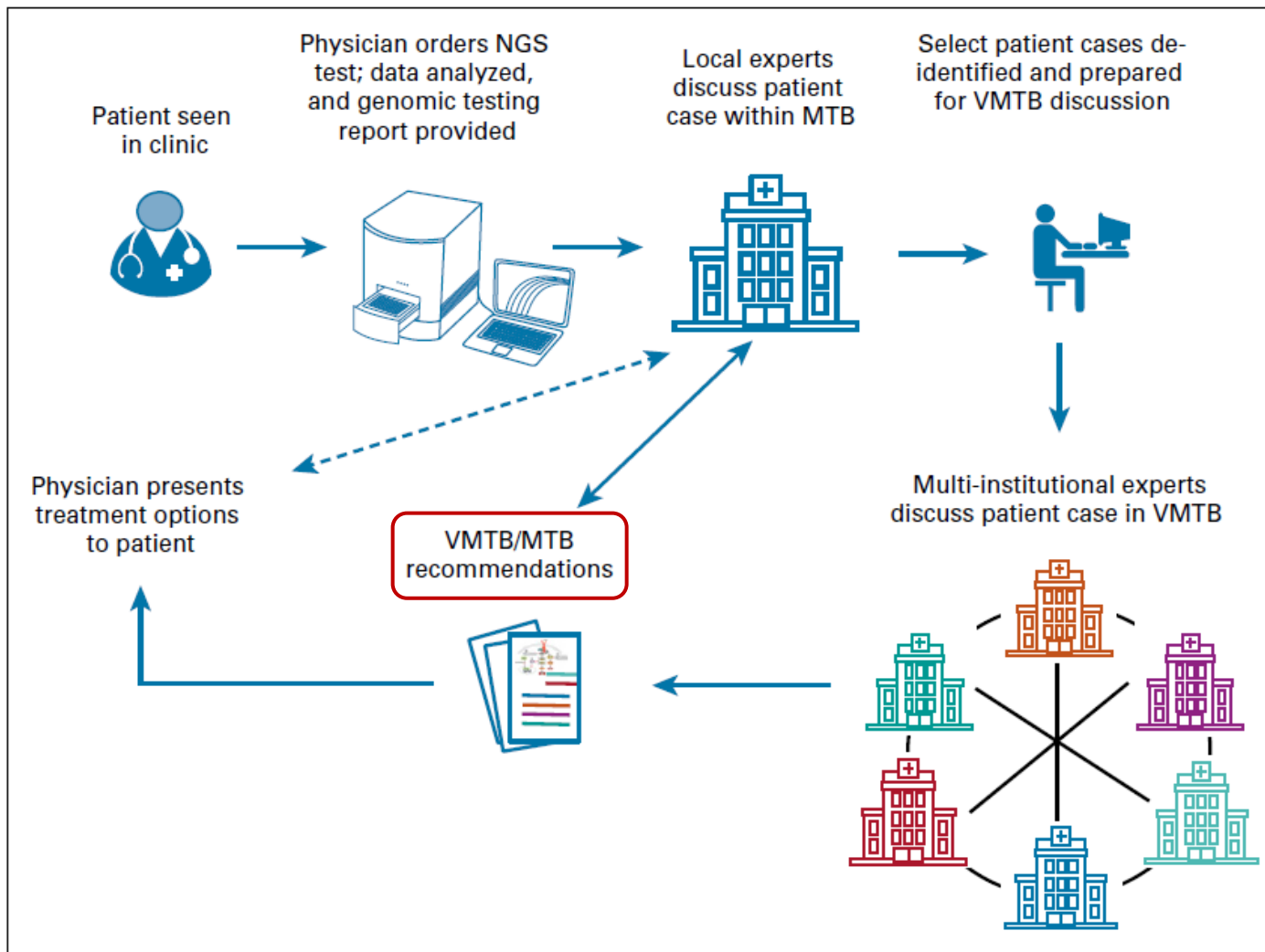


JCO Precis Oncol 5:884-895. © 2021 by American Society of Clinical Oncology



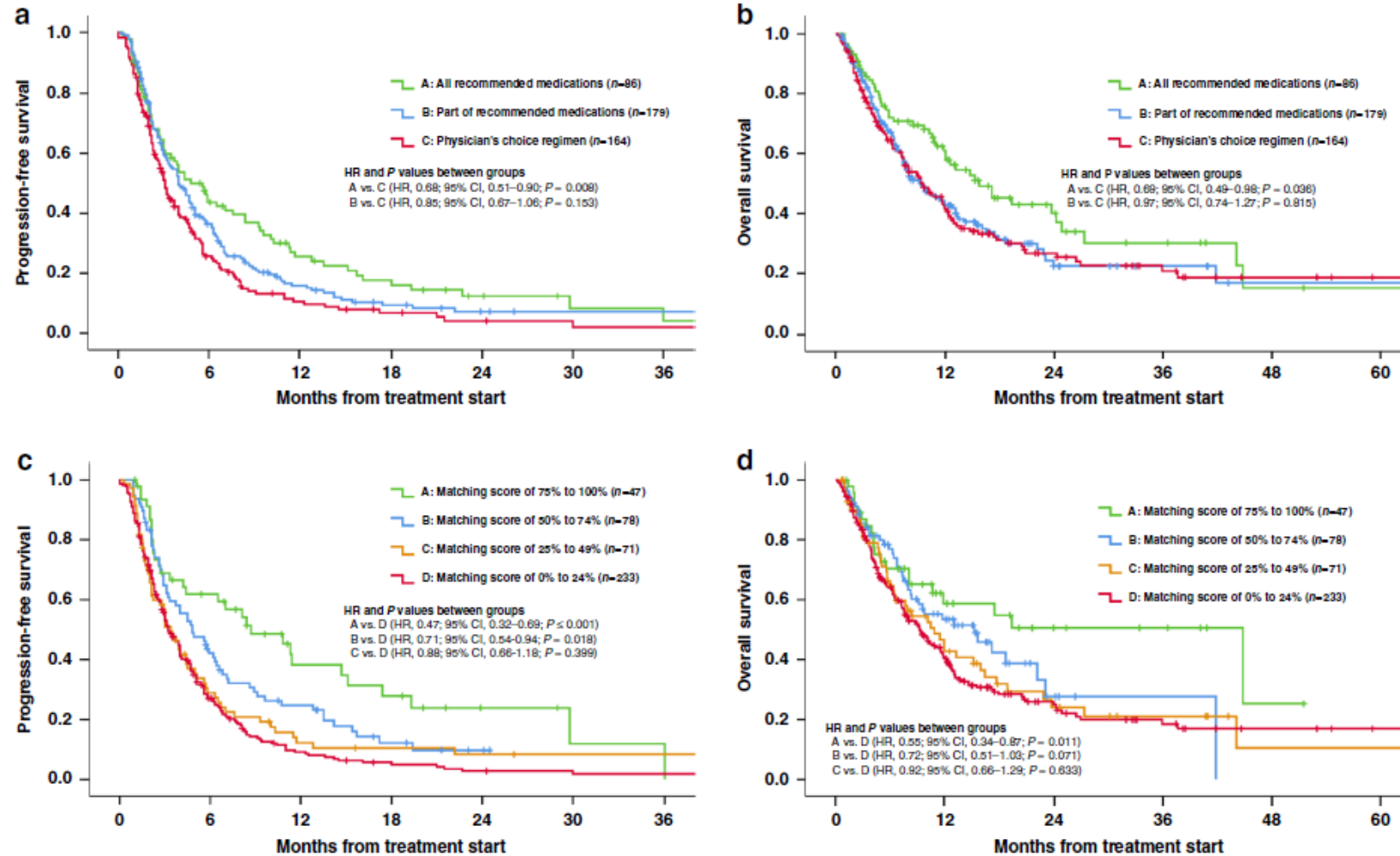
**FIG 1.** Key considerations for integrating somatic and germline NGS results into patient care. EHR, electronic health record; NGS, next-generation sequencing.

# Incorporation of Molecular Tumor Board



JCO Clin Cancer Inform 4:602-613. © 2020 by American Society of Clinical Oncology

# Molecular Tumor Board Improves Patient Outcomes

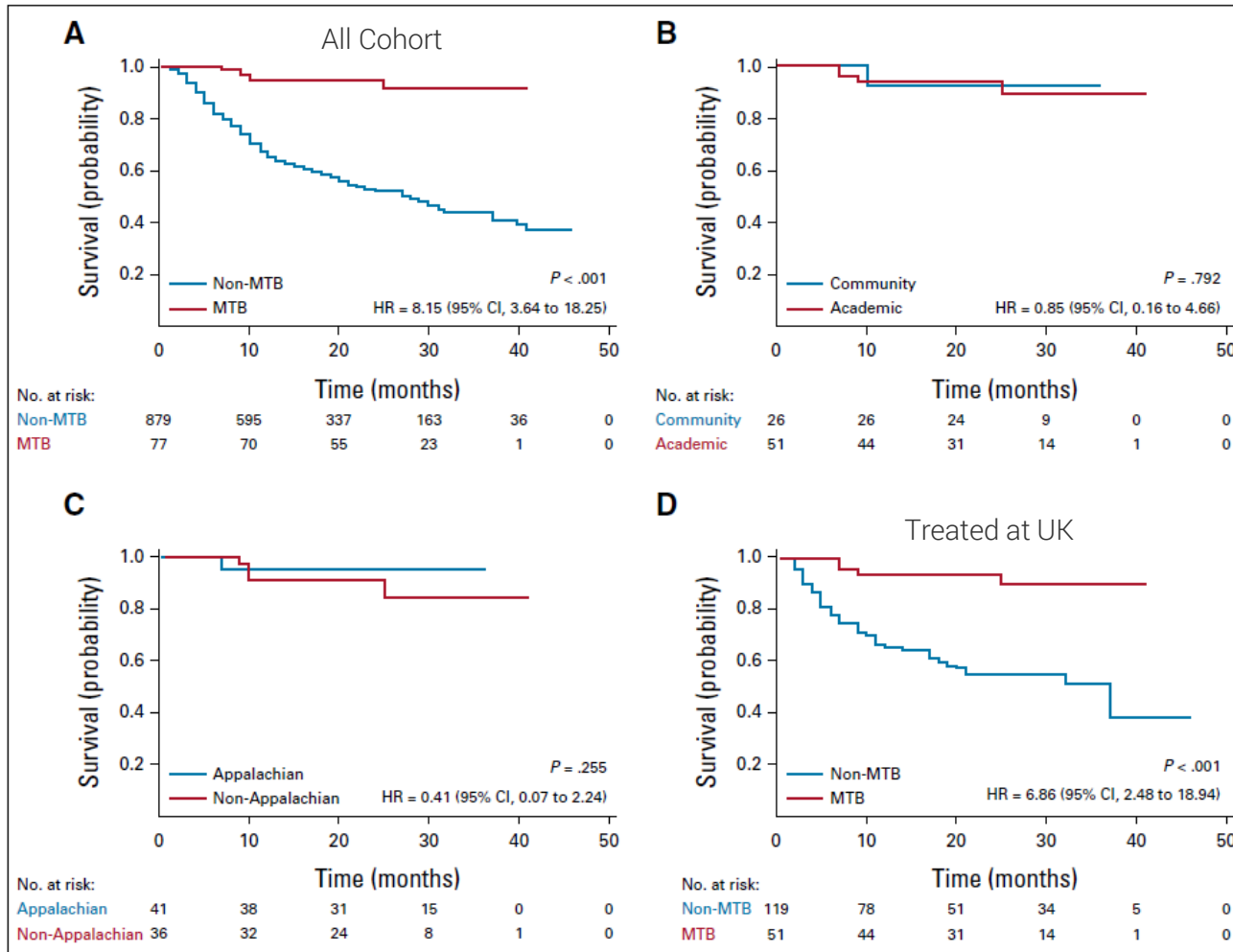


- Outcome of 715 patients with advanced cancer presented at MTB (Academic Medical Center).
- The goal of the MTB was to develop an N-of-One treatment plan.
- MTB-recommended regimens (versus physician choice) have significantly longer progression-free (PFS) and overall survival (OS), and are better matched to therapy.
- High matching score led to overall better clinical outcomes (PFS and OS).

Fig. 2 Progression-free survival and overall survival according to compliance with recommendation of Molecular Tumor Board and matching scores.

NATURE COMMUNICATIONS | (2020)11:4965 | <https://doi.org/10.1038/s41467-020-18613-3>

# Molecular Tumor Board Review Improves Overall Survival In NSCLC Patients



**FIG 2.** Kaplan-Meier plots depicting overall survival in patients on the basis of (A) all patients in cohort comparing MTB review versus no MTB review;

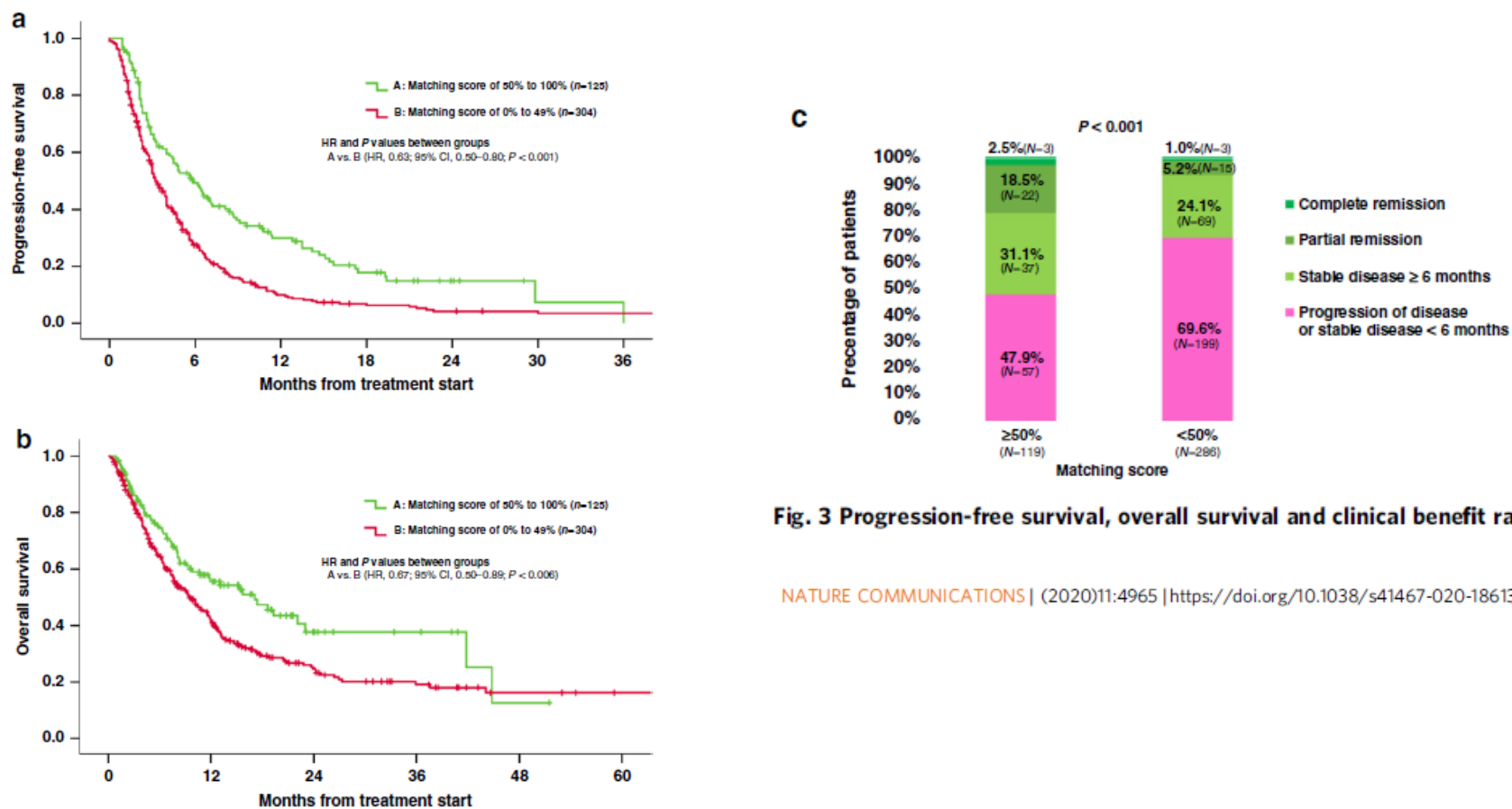
- A case-control study of Kentucky patients newly diagnosed with non-small-cell lung cancer between 2017 and 2019 (956 patients were included).
- Seventy-seven (8.1%) were reviewed by the MTB and classified as cases.
- The primary end point was the association between MTB review and overall patient survival.
- MTB review is an independent positive predictor of overall survival regardless of residence location.



# Matching Scores and Patient Outcome

**Matching score:** The number of pathogenic alterations targeted by drugs given divided by total number of pathogenic alterations.

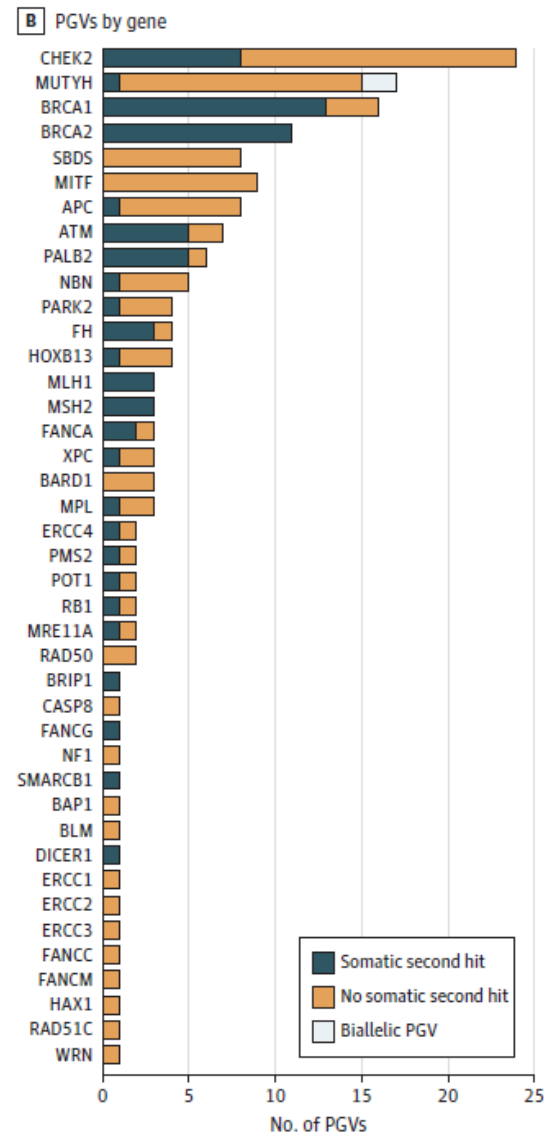
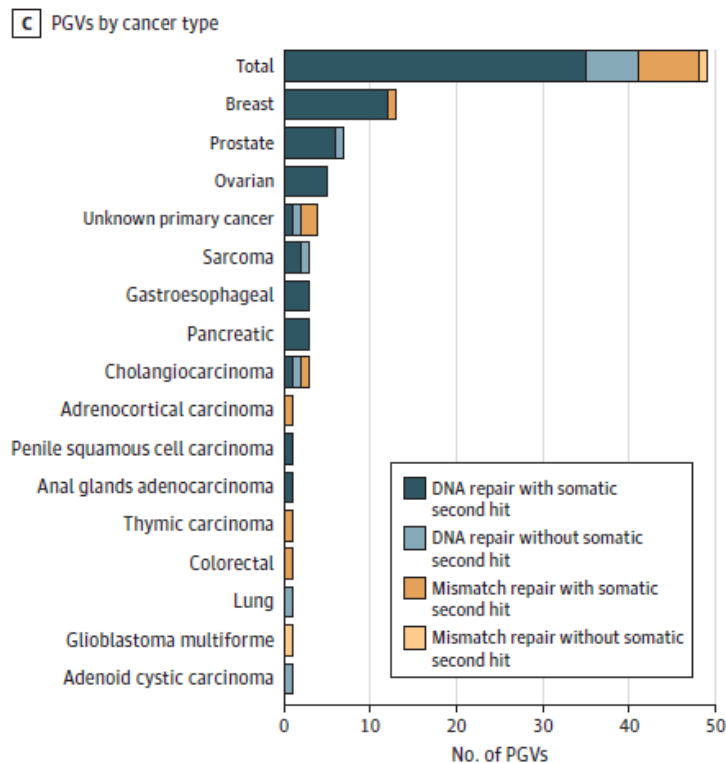
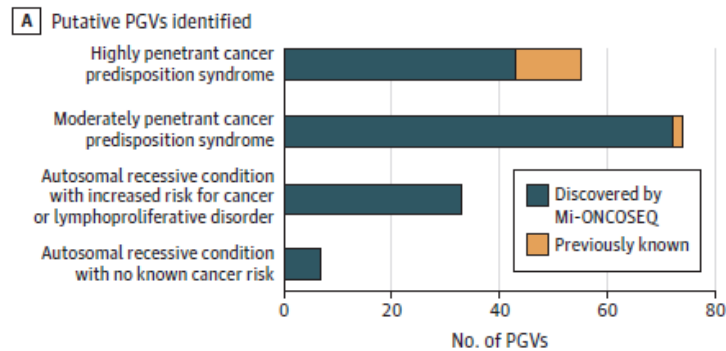
Example: Tumor has 8 pathogenic genomic alterations and the patient received two agents that targeted four alterations. Then, **Matching score** is 50% (4/8).



**Fig. 3 Progression-free survival, overall survival and clinical benefit rate**

NATURE COMMUNICATIONS | (2020)11:4965 | <https://doi.org/10.1038/s41467-020-18613-3>

# Pathogenic Germline Mutations Identified By NGS



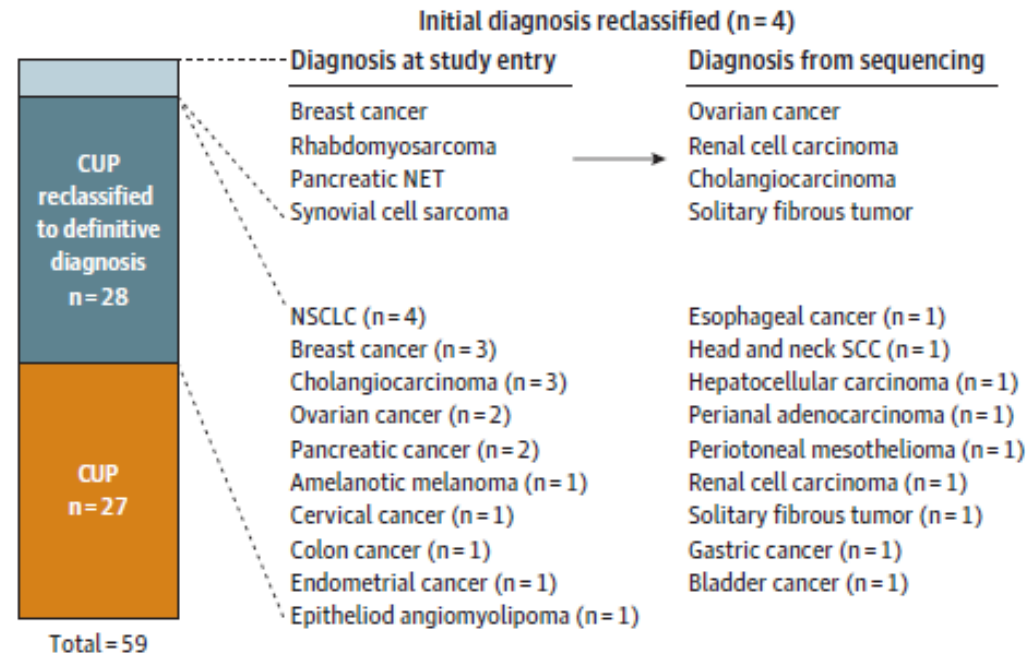
- 1138 patients in this cohort study underwent fresh tumor biopsy and blood sample collection for genomic profiling of paired tumor and normal DNA.
- Pathogenic germline variants (PGVs) were identified in 160 patients (15.8% of cohort), including 49 PGVs (4.8% of cohort) with therapeutic relevance.
- The high rate of therapeutically relevant PGVs identified across diverse cancer types supports a recommendation for directed germline testing in all patients with advanced cancer.
- When a pathogenic germline variant is suspected during tumor-only testing, the variant is recommended to be confirmed with a paired-normal sample according to the AMP-ASCO-CAP guidelines.

JAMA Oncol. 2021;7(4):525-533. doi:10.1001/jamaoncol.2020.7987

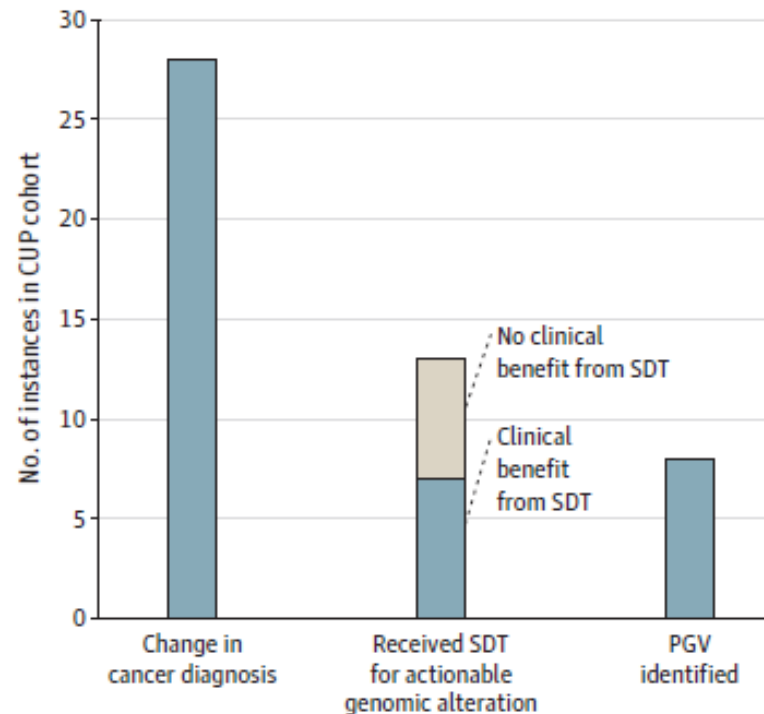
# Utility of NGS Testing For Patients With Cancer Of Unknown Primary (CUP)

**Figure 5. Cancers of Unknown Primary Origin in MET1000 Cohort**

**A** Classification of diagnoses



**B** Sequencing results



- Among 55 cases of cancer of unknown primary (CUP) origin sequenced, 28 (50.9%) were reclassified to a definitive diagnosis through RNA sequencing.
- An additional 4 cases with presumed known diagnoses at study entry were also reclassified.
- 13 patients (23.6%) received sequencing-directed therapy (SDT).
- Identification of a pathogenic germline variant (PGV) conferring increased cancer risk in 8 patients (14.5%).

JAMA Oncol. 2021;7(4):525-533. doi:10.1001/jamaoncol.2020.7987



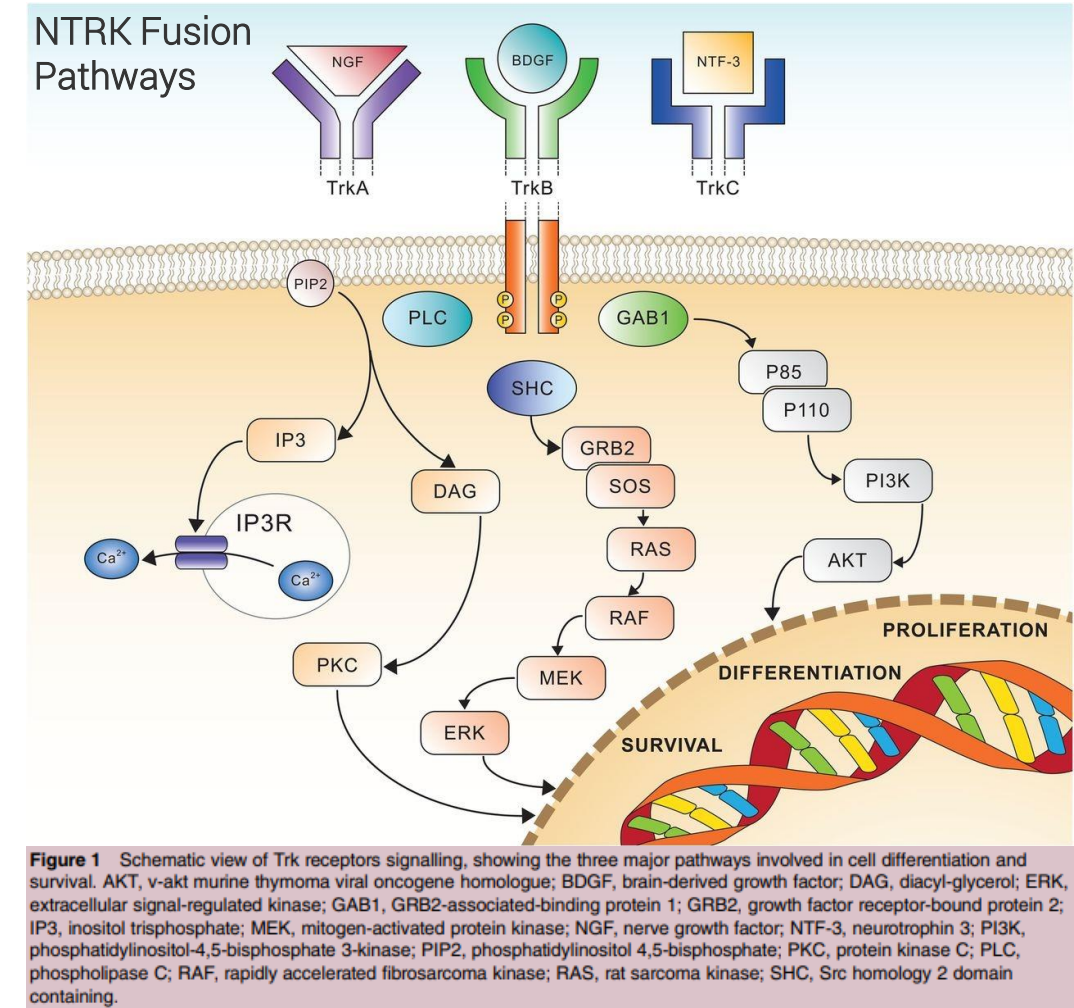
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# “New Era: Tissue-Agnostic” FDA-Approved Drugs

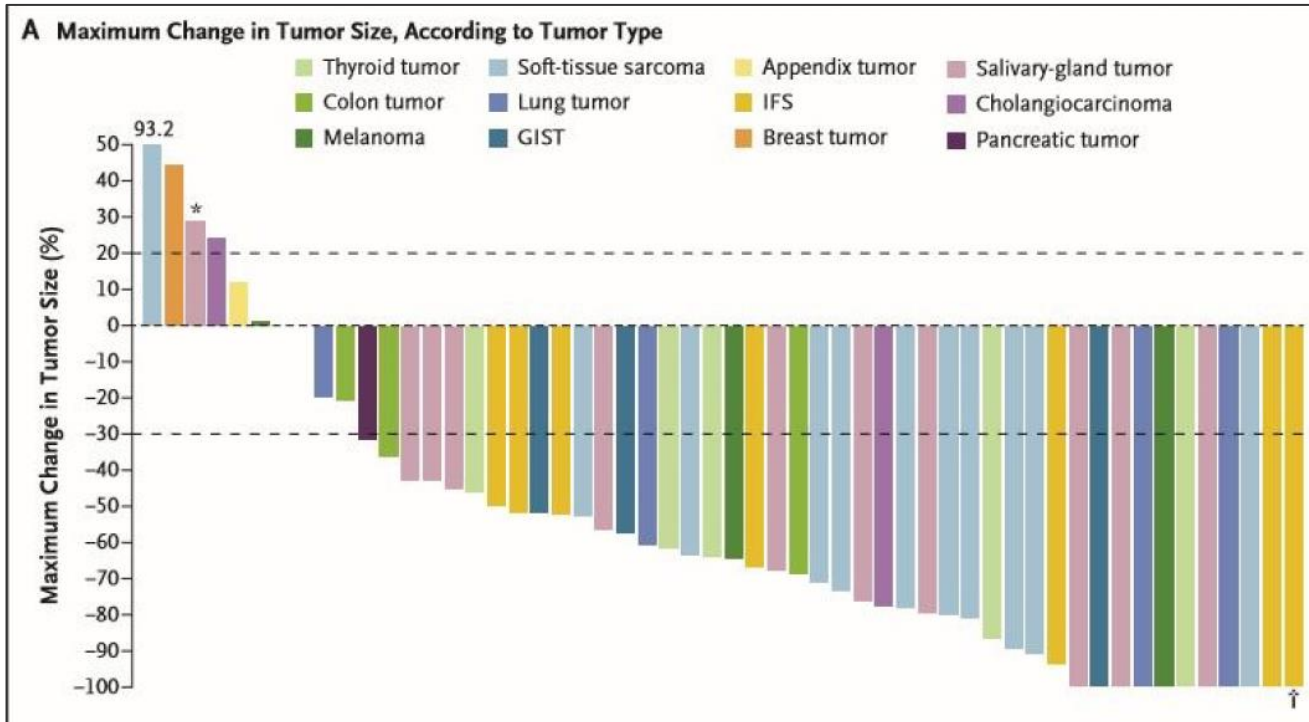
- **Pembrolizumab** (2017, Keytruda, Anti-PD-1)
  - » 1st example of a tissue-agnostic FDA approval.
  - » MSI-H and dMMR advanced solid tumors.
- **Larotrectinib** (2018, Loxo Oncology, NTRK Fusion Inhibitor)
  - » Adult and pediatric solid tumors w/ **NTRK gene fusions**.
  - » ORR was 75%, including 22% complete responses and 53% partial responses.
- **Entrectinib** (2019, Genentech, NTRK Fusion Inhibitor)
  - » Adult and pediatric solid tumors w/ **NTRK gene fusions**.
  - » ORR of 57.4% and a median duration of response of 10.4 months.
- **Pembrolizumab** (2020, Keytruda, Anti-PD-1)
  - » FDA approval of pembrolizumab for TMB  $\geq 10$  (mt/Mb) in advanced solid tumors.
- **Dostarlimab-gxly** (2021, Jemperli, Anti-PD-1)
  - » 2021 (April): For adult patients with mismatch repair deficient (dMMR) recurrent or advanced endometrial cancer.
  - » 2021 (Aug): For adult patients with mismatch repair deficient (dMMR) recurrent or advanced solid tumors.



Amatu A, et al. *ESMO Open* 2016;1:e000023. doi:10.1136/esmoopen-2015-000023

# Larotrectinib: Remarkable Efficacy

(2018, Loxo Oncology)



February 22, 2018

N Engl J Med 2018; 378:731-739

DOI: 10.1056/NEJMoa1714448

- First new targeted therapy developed in a tissue type-agnostic manner.
- For patients with TRK fusion cancer, larotrectinib is a new standard of care.
- Routine pan-cancer screening will be important to identify NTRK fusions.
- **Conclusion:** Larotrectinib demonstrated high antitumor activity regardless of tumor type, age, NTRK mutated gene (1,2 or 3) or NTRK fusion partner.

# Newly FDA Approved Agents In 2021

## Solid Tumors (10)

- **Sotorasiib**: NSCLC harboring KRAS G12C gene mutations.
- **Tepotinib**: Metastatic NSCLC harboring MET exon 14 skipping alterations.
- **Mobocertinib**: NSCLC harboring EGFR exon 20 insertion mutations.
- **Amivantamab-vmjw**: Metastatic NSCLC with EGFR exon 20 insertion mutation (a bi-specific antibody)
- **Tivozanib**: A kinase inhibitor (VEGFR) for renal cell carcinoma (RCC).
- **Dostarlimab-gxly**: Mismatch repair-deficient (dMMR) endometrial cancer and dMMR advanced solid tumors (Agnostic).
- **Infigratinib**: Cholangiocarcinoma harboring FGFR2 gene fusion.
- **Enfortumab vedotin-ejfv**: Antibody-drug conjugate for metastatic urothelial cancer.
- **Tisotumab vedotin-tftv**: Antibody-drug conjugate for metastatic cervical cancer.
- **Belzutifan**: A HIF inhibitor for VHL-associated RCC, hemangioblastoma or pNET (Agnostic).

## Heme Tumors (5)

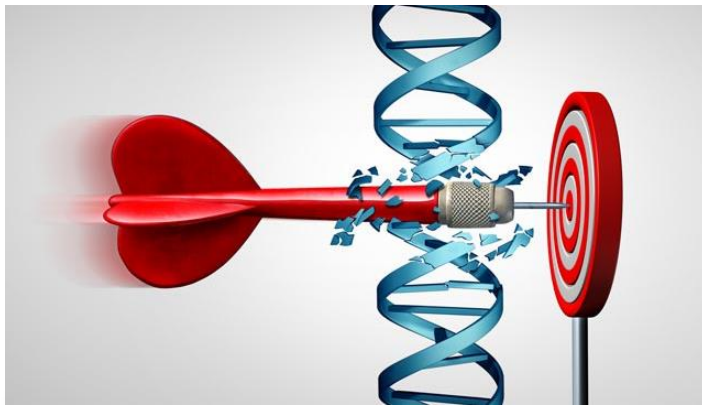
- **Lisocabtagene maraleucel**: Large B-cell lymphoma (CART-T).
- **Loncastuximab tesirine-lpyl**: Antibody-drug conjugate, large B-cell lymphoma
- **Umbralisib**: relapsed marginal zone lymphoma (MZL) and follicular lymphoma (FL).
- **Melphalan flufenamide**: Relapsed multiple myeloma.
- **Idecabtagene vicleucel**: Relapsed multiple myeloma (CART-T).

## PLUS, Over 25 New Indications For Existing Drugs!!!!!!

- Many Immunotherapy Agents (**Atezolizumab, Nivolumab, Pembrolizumab, etc.**)
- **Ivosidenib**: IDH1-mutated cholangiocarcinoma.
- **Abemaciclib**: First CDK 4/6 inhibitor, adjuvant treatment of breast cancer.

# NSCLC Had The Most FDA Approved Agents In 2021

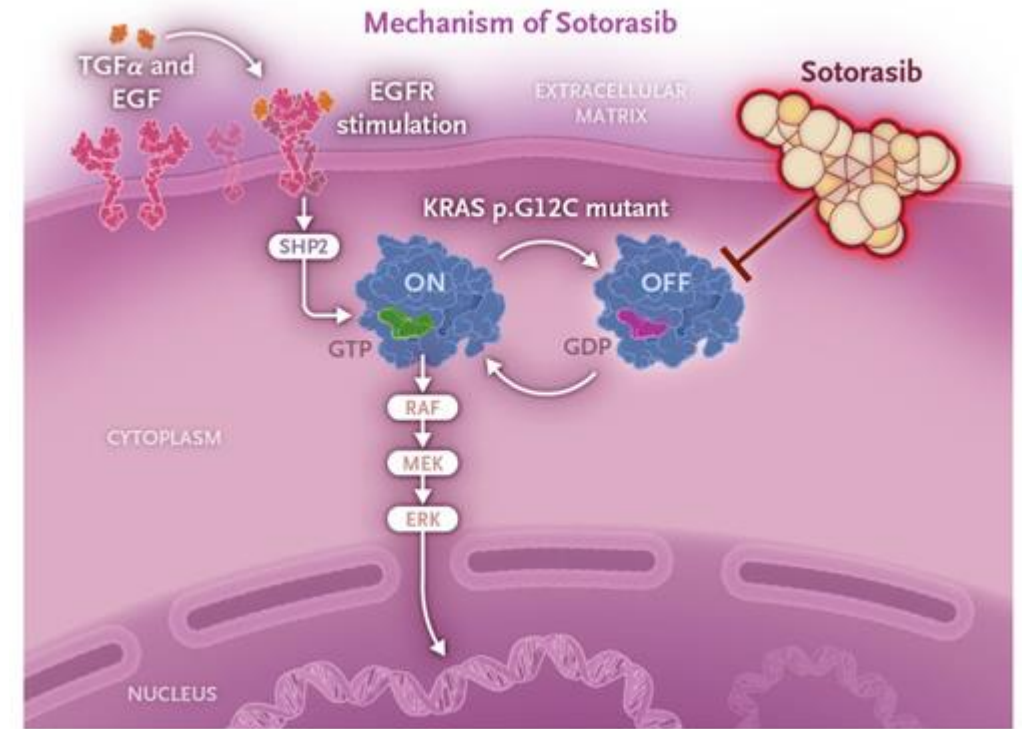
- **Sotorasiib**: NSCLC harboring KRAS G12C gene mutations.
- **Tepotinib**: Metastatic NSCLC harboring MET exon 14 skipping alterations.
- **Mobocertinib**: NSCLC harboring EGFR exon 20 insertion mutations.
- **Amivantamab-vmjw**: Metastatic NSCLC with EGFR exon 20 insertion mutation.





# First KRAS<sup>G12C</sup> Inhibitor Sotorasib (AMG-510)

- Accelerated FDA approval on May 28, 2021.
- KRAS G12C seen ~13% NSCLC and ~3% CRC.
- Mutations of KRAS favor the GTP-bound conformational active state and leads to constitutive activation.
- **Sotorasib** is a first-in-class, potent and highly selective small-molecule inhibitor of KRAS G12C that locks it in an inactive GDP-bound state (not active against other KRAS mutant forms).
- Routine testing of KRAS gene is important to identify patients who may benefit from KRAS inhibitors.

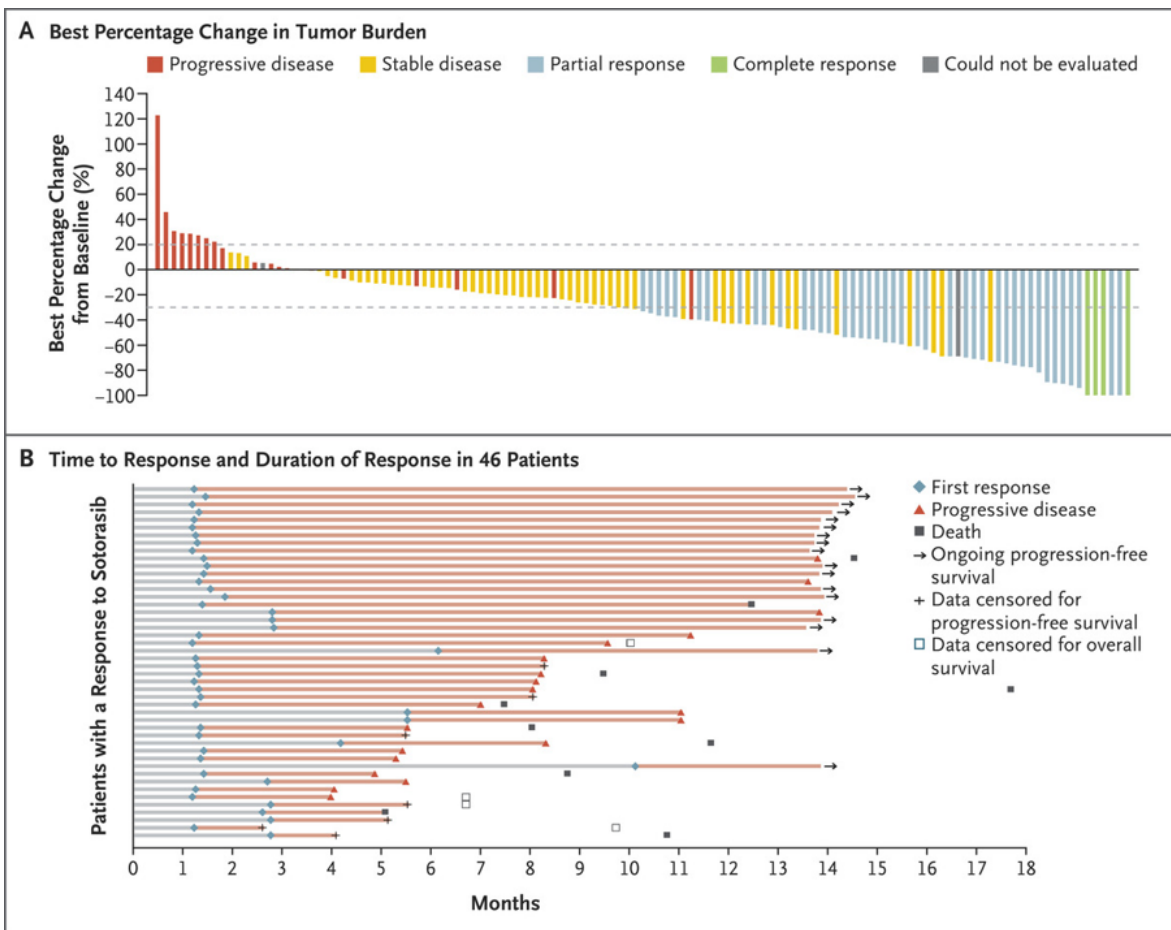


N ENGL J MED 384;25 NEJM.ORG JUNE 24, 2021

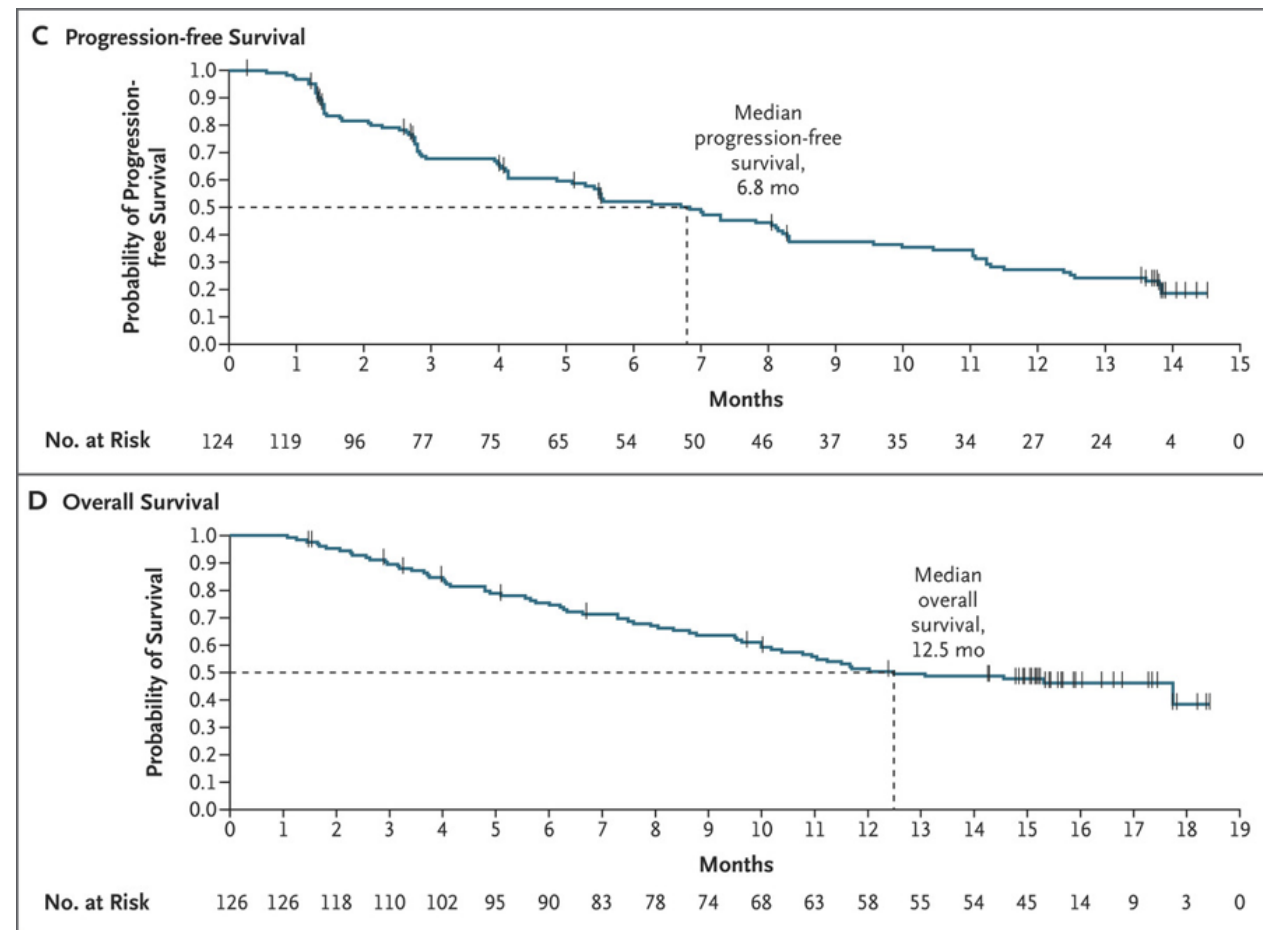


# NSCLC Patients: Efficacy of Sotorasib Therapy

N ENGL J MED 384;25 NEJM.ORG JUNE 24, 2021



- Overall response rate of ~ 37%, with 80% disease control.
- Duration of response of >11 months.

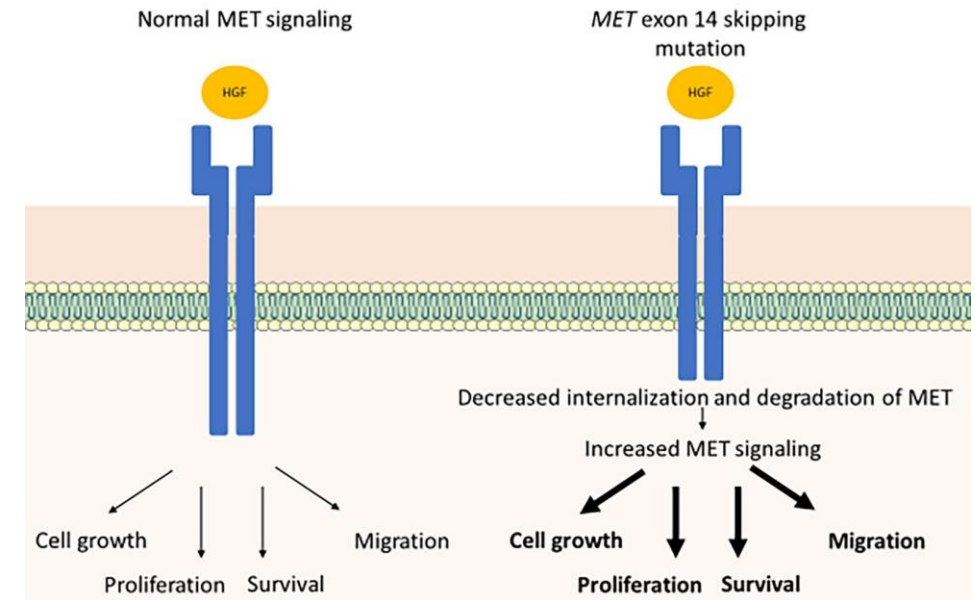


- Median overall survival of 12.5 months in NSCLC.

# Tepotinib in NSCLC with MET Exon 14 Skipping Mutations

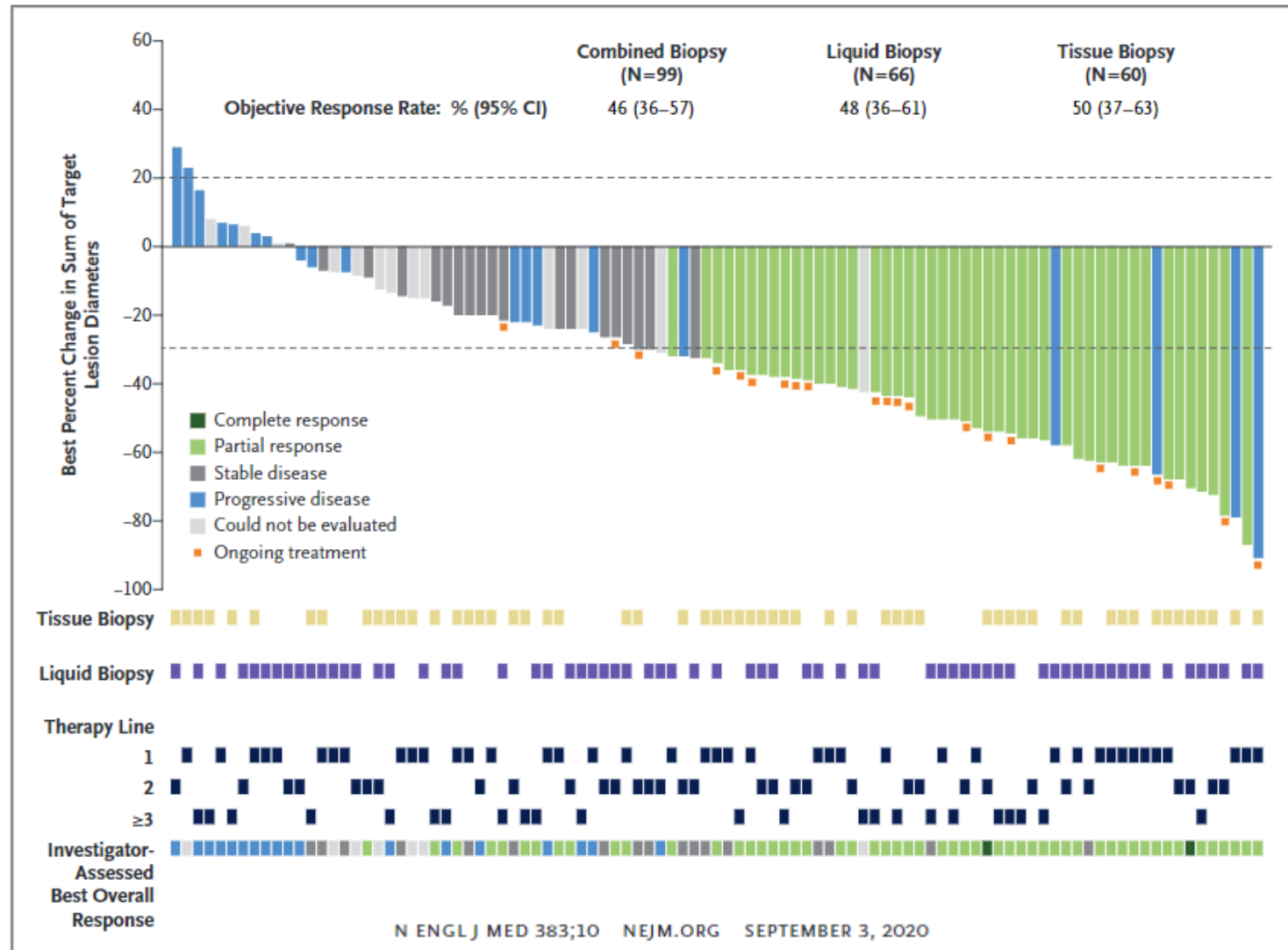
- Accelerated FDA approval (February 2021).
- METex14 skipping mutation, 3-4% of NSCLC.
- These alterations spatially disrupt distinct splicing sites at the acceptor or donor site flanking MET exon 14 which leads to “exon 14 skipping.”
- This leads to impaired MET ubiquitination, decreased MET turnover, and increased signaling.
- **Tepotinib** showed substantial antitumor activity in approximately half the patients with advanced NSCLC with a MET exon 14 skipping mutation.

Fig. 1 Schematic representation of the effect of *MET*ex14 on MET stability and signaling.



Cancer Treatment Reviews 95 (2021) 102173

# Tepotinib in NSCLC with MET Exon 14 Skipping Mutations



- Tepotinib
  - » FDA Approval in 2021
  - » NSCLC with METex14
  - » Response rate was 46%
  - » 11.1 months duration of response
  - » Less side-effect profile
- Capamatinib
  - » FDA Approval in 2020
  - » NSCLC with METex14
  - » Encouraging activity in brain metastasis
- Otherwise, both drugs are similarly efficacious.

# First Two EGFR Exon 20 Inhibitors Approved in 2021

## Amivantamab

- Previously FDA approved EGFR TKIs have minimal activity for EGFRex20ins-positive mNSCLC.
- **Amivantamab** is a bi-specific antibody with “2 heads” one targeting EGFR and one MET (RR of 40%).
- Amivantamab has demonstrated preliminary activity in EGFR TKI-resistant tumors driven by EGFR secondary mutations (T790M and/or C797S) or new MET amplification.
- May not penetrate blood-brain-barrier as well as TKIs.
- Adverse events: Infusion reaction.

Journal of Clinical Oncology 39, no. 30 (October 20, 2021) 3391-3402.

## Mobocertinib

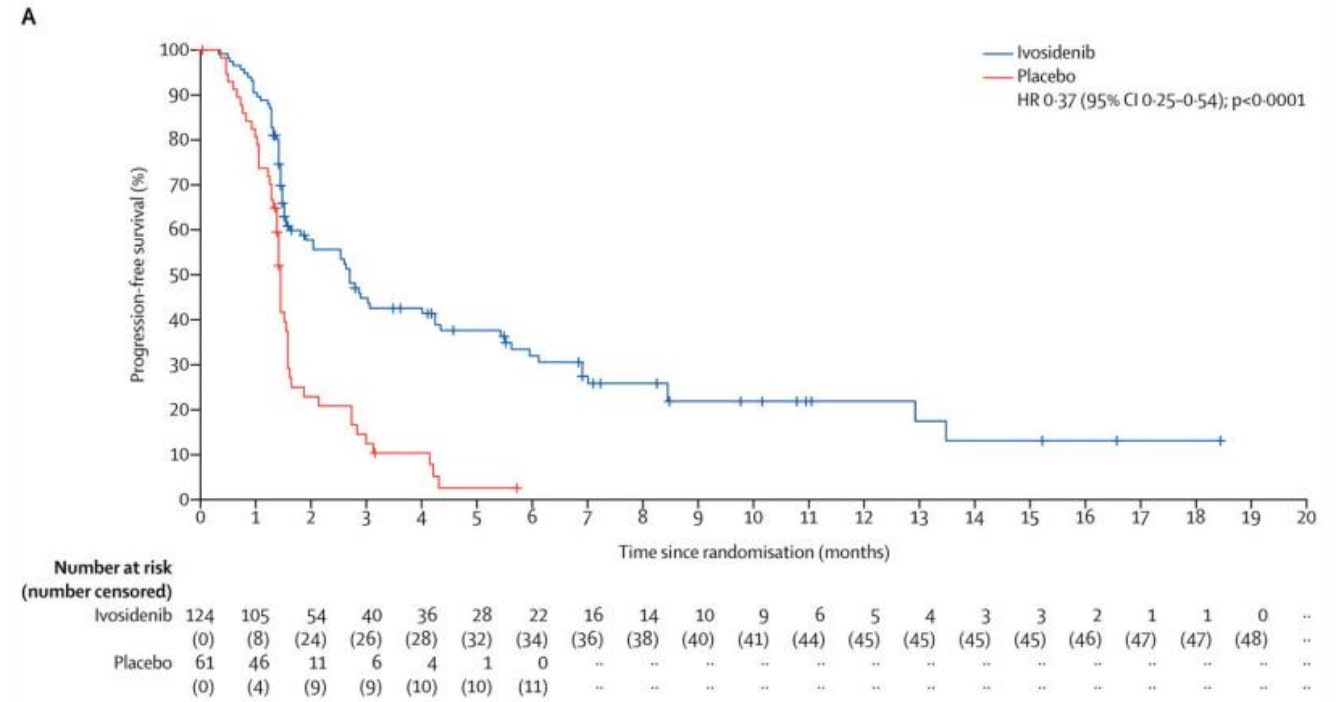
- Previously FDA approved EGFR TKIs have minimal activity for EGFRex20ins-positive mNSCLC.
- **Mobocertinib**, a first-in-class, potent, oral, irreversible TKI designed to selectively target in-frame EGFRex20ins mutations in NSCLC (RR of 28%).
- A small molecule irreversible TKI which covalently binds cysteine 797 of EGFR active site.
- C797S-containing mutant can confer resistance to Mobocertinib.
- Adverse events: Gastrointestinal, skin rash, prolongs QTC

JAMA Oncol. 2021;7(12):e214761.  
doi:10.1001/jamaoncol.2021.4761.

	1 <sup>st</sup> Generation	2 <sup>nd</sup> Generation	3 <sup>rd</sup> Generation	EGFRex20ins	EGFRex20ins
EGFR TKIs	Gefitinib, Erlotinib	Afatinib, Dacomitinib	Osimertinib	Amivantamab	Mobocertinib
Acquired Resistance	T790M	T790M	C797S	?	C797S

# New Indication: Ivosidenib (Tibsovo™) in Cholangiocarcinoma

- IDH1 mutations occur in ~13% of pts with intrahepatic cholangiocarcinoma.
- **Ivosidenib** targeted inhibitor of mutated IDH1 approved for patients with newly diagnosed acute myeloid leukaemia.
- FDA approved a new indication for Ivosidenib (August 2021).
- PFS was significantly improved with ivosidenib compared with placebo, and ivosidenib was well tolerated.
- This study shows the clinical benefit of targeting IDH1 mutations in advanced, IDH1-mutant cholangiocarcinoma.
- Notable for drug efficacy crossing boundaries between hematologic-solid tumor malignancies (in this case-AML and cholangiocarcinoma).

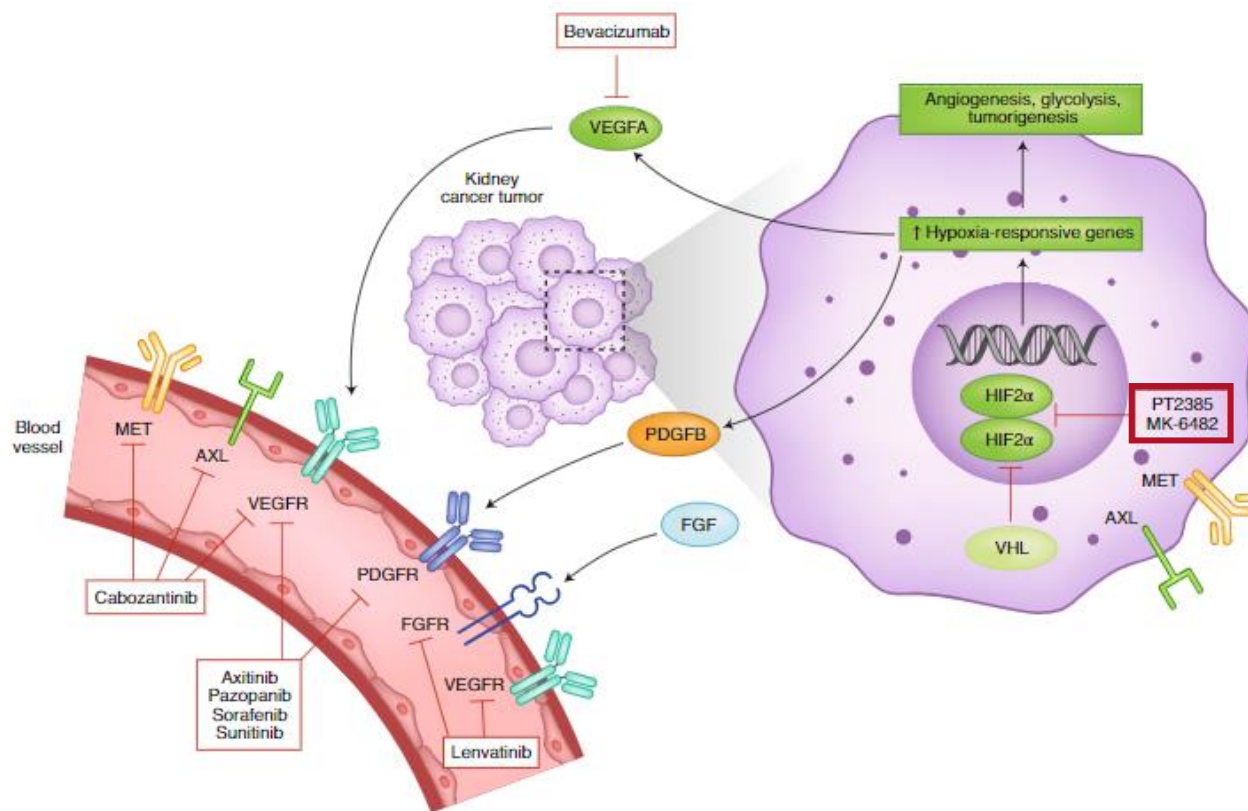


*Lancet Oncol.* 2020 June ; 21(6): 796–807. doi:10.1016/S1470-2045(20)30157-1.



# First HIF-2 $\alpha$ Inhibitor Approval For Cancers Associated with VHL Disease

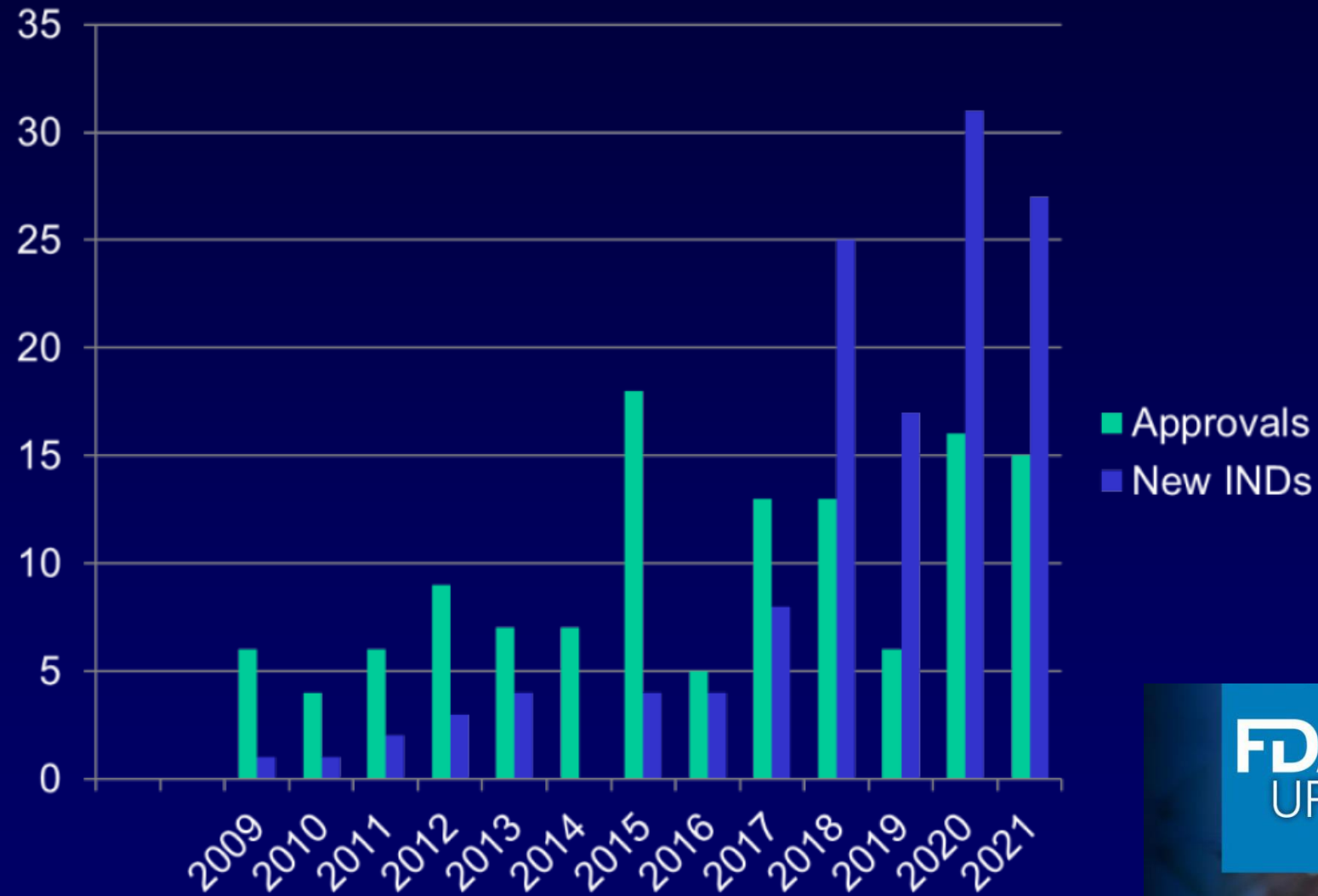
- Von Hippel-Lindau Syndrome is a hereditary cancer syndrome characterized by the development of multiple vascular tumors.
- Inactivation of VHL leads to aberrant stabilization and accumulation of HIF-2 $\alpha$ , which drives tumor growth.
- **Belzutifan** is a first-in-class FDA-approved HIF-2 $\alpha$  inhibitor for VHL-associated RCC, hemangioblastoma or pNET.
- Belzutifan prevents heterodimerization of HIF-2 $\alpha$  and downstream activation of transcription.
- Example of agnostic FDA approval.



**Fig. 1** | HIF-2 $\alpha$  inhibitors as novel inhibitors of the HIF2-VEGF-VEGFR pathway.

NATURE MEDICINE | VOL 26 | OCTOBER 2020 | 1519-1530 | [www.nature.com/naturemedicine](http://www.nature.com/naturemedicine)

# Trends in New Drug Approval



**FDA**  
UPDATE





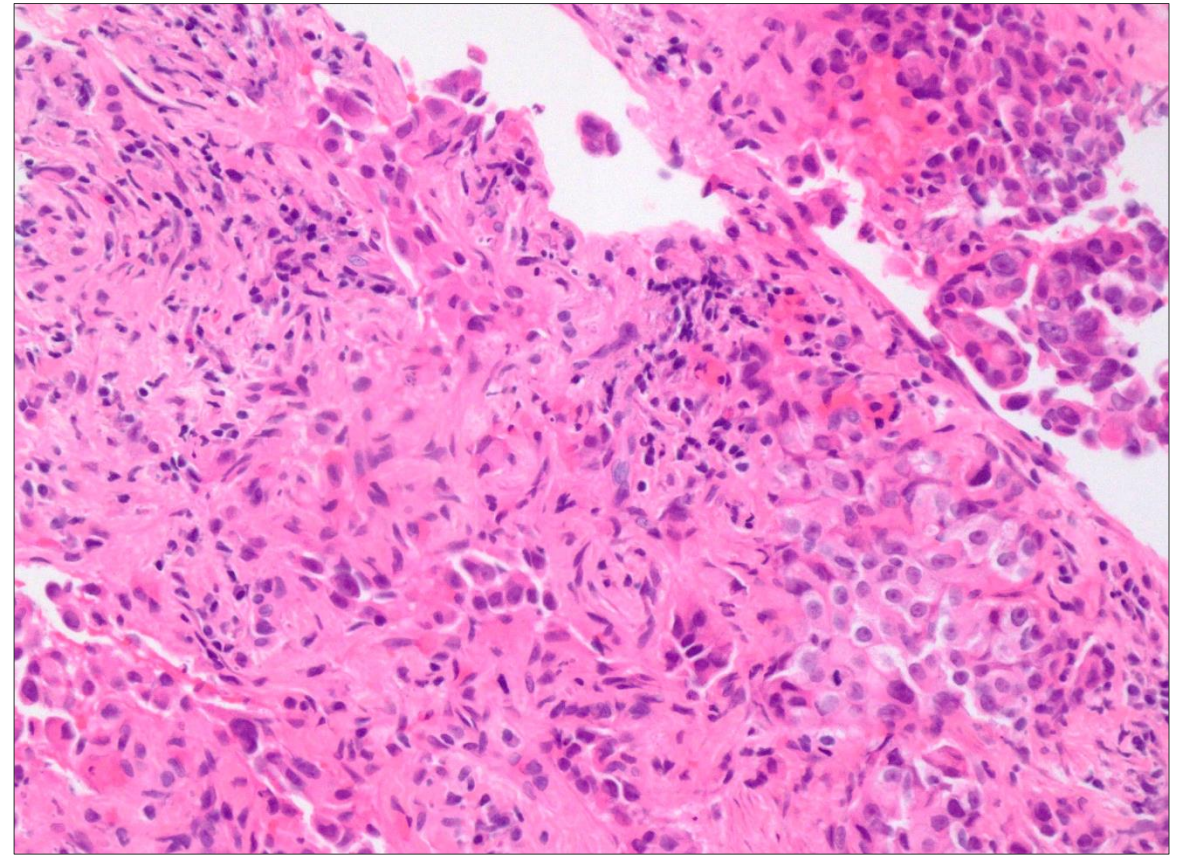
# Learning Objectives

1. Understand Comprehensive Genomic Profiling By NGS Testing.
2. Understand How Molecular Tumor Board Can Support Precision Oncology.
3. Review Newly FDA-Approved Oncologic Therapies In 2021.
4. A Case Study In Precision Oncology: NSCLC Patient With Brain Metastasis.



# Case: 49-year-old male, Stage-4 NSCLC

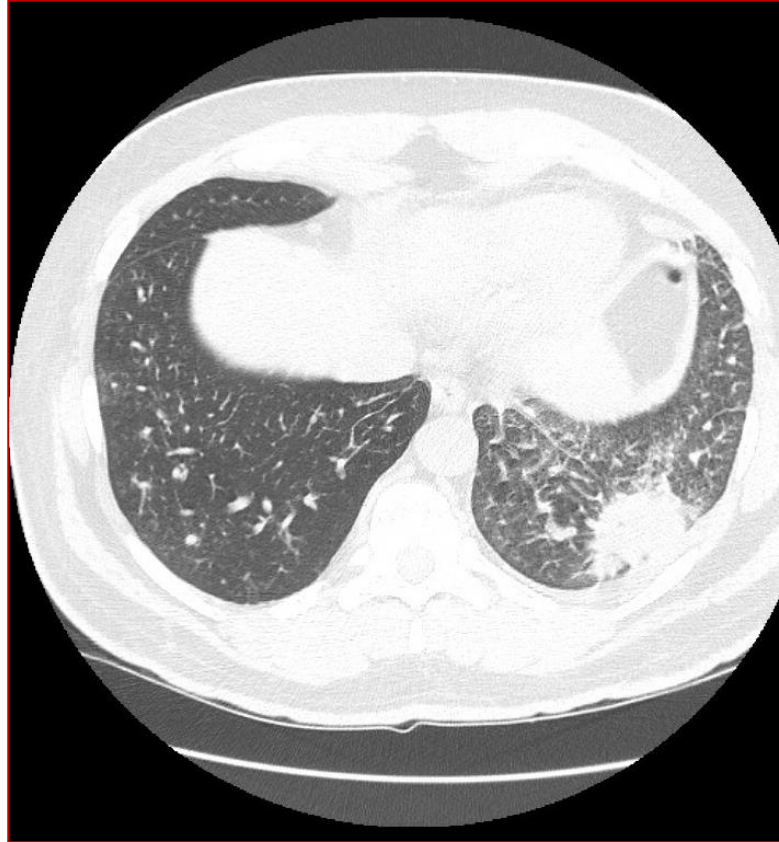
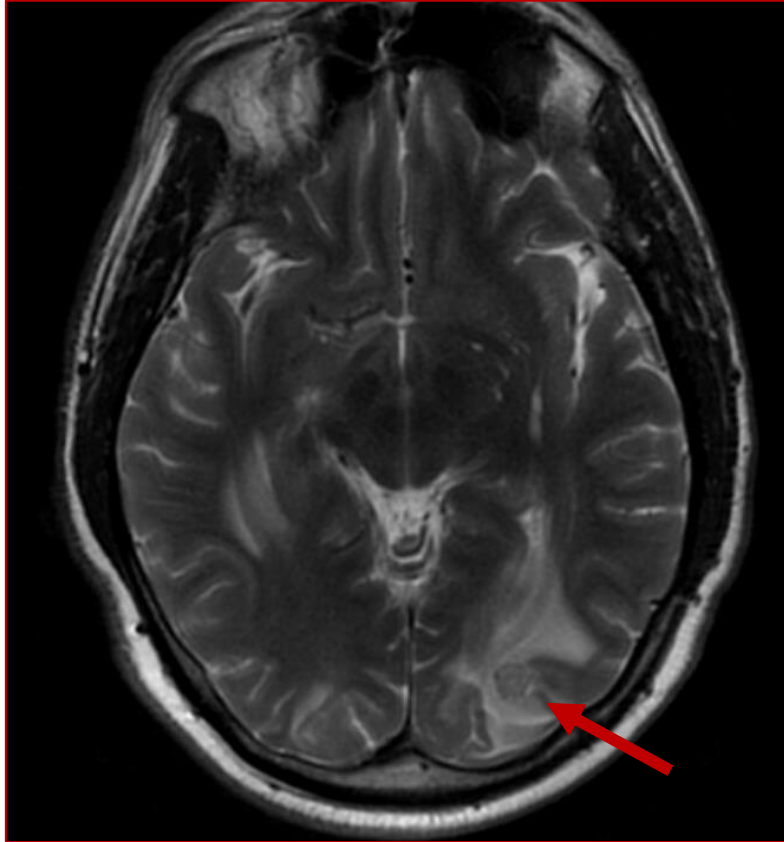
- **March 2019**- Chief complaint of cough (OSH)
- CT- pulmonary mass, LAD
- MRI- Mets to brain and axial skeleton
- Biopsy- Invasive moderately differentiated adenocarcinoma with squamoid features
- Neg EGFR (Sanger), Neg BRAF (PCR)
- ALK and ROS1 FISH: N/A
- PD-L1: 80%
- **April 2019**- Referred to Tertiary Academic Hospital
- Supraclavicular LN Biopsy
- NGS tumor profiling (DNA/RNA)



Supraclavicular LN Biopsy

[JCO Precis Oncol.](#) 2021 Nov;5:88-92. doi: 10.1200/PO.20.00296.

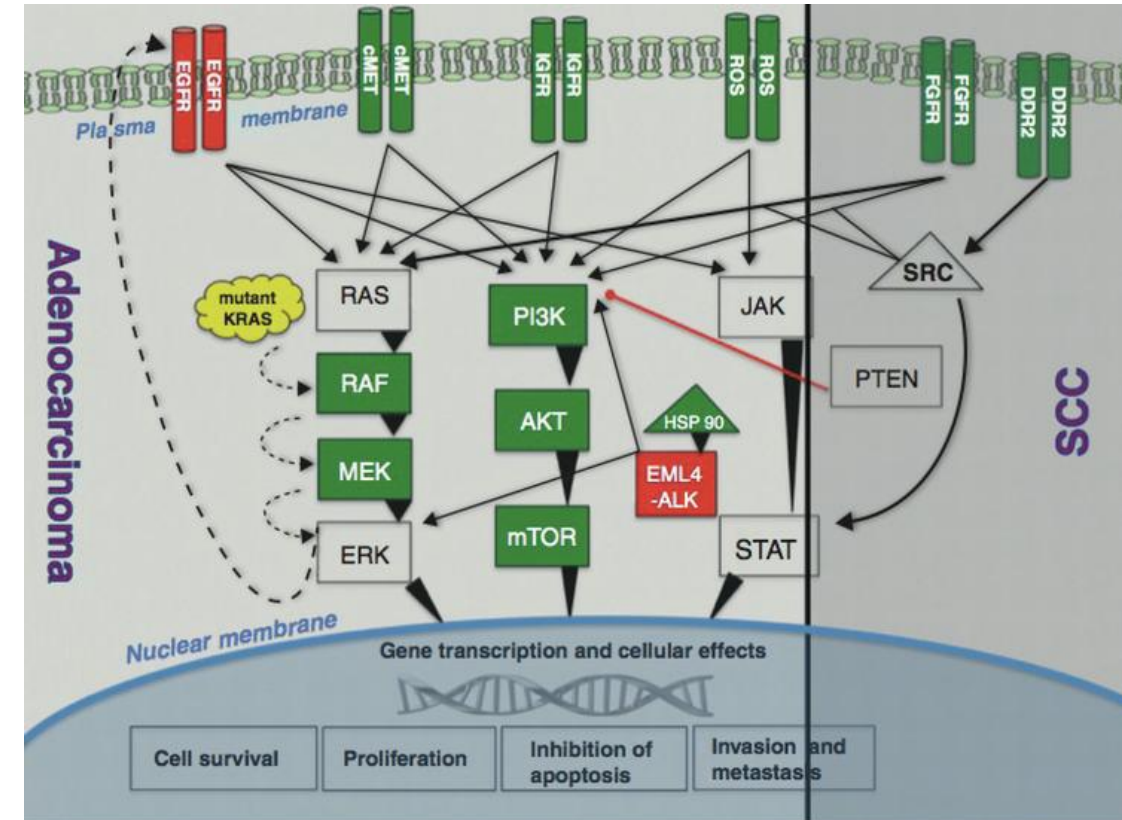
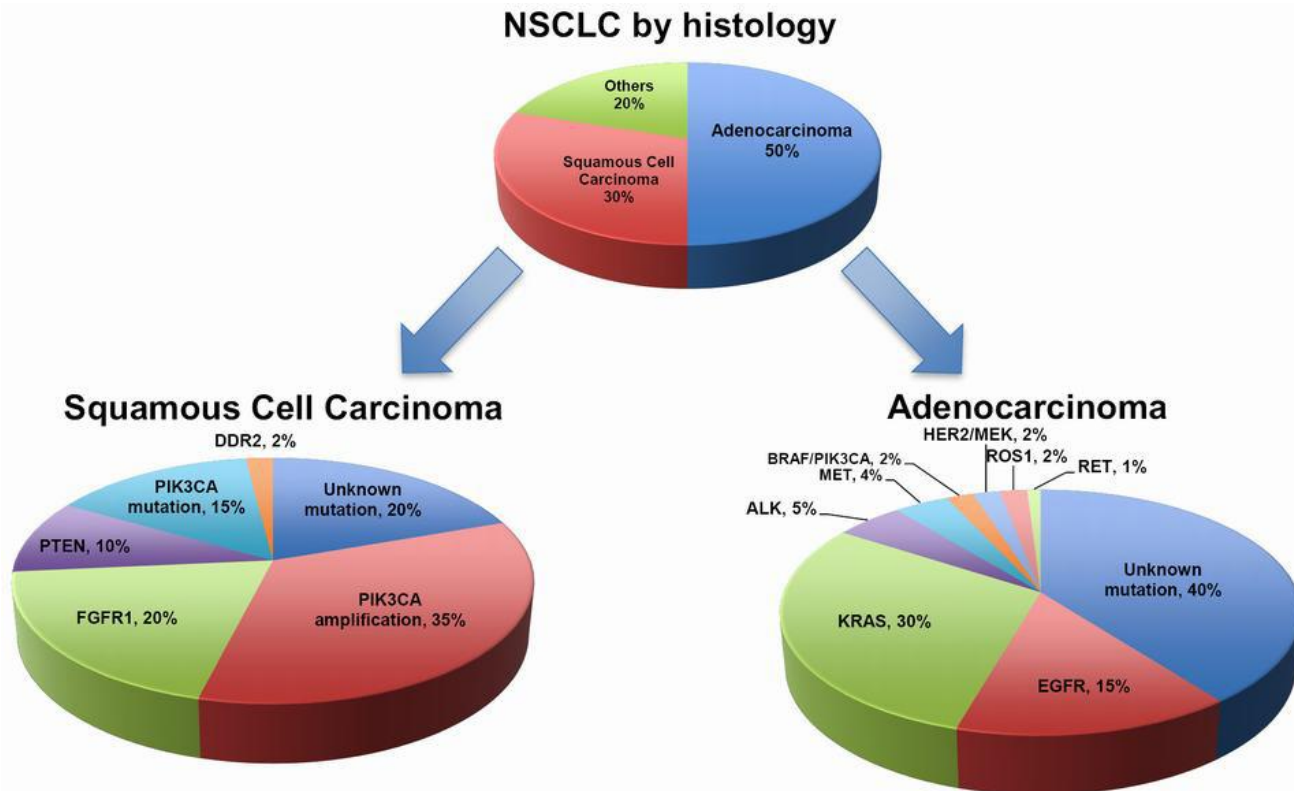
## MRI and CT on March 2019



JCO Precis Oncol. 2021 Nov;5:88-92. doi: 10.1200/PO.20.00296.



# NSCLC Mutational Landscape and Pathways



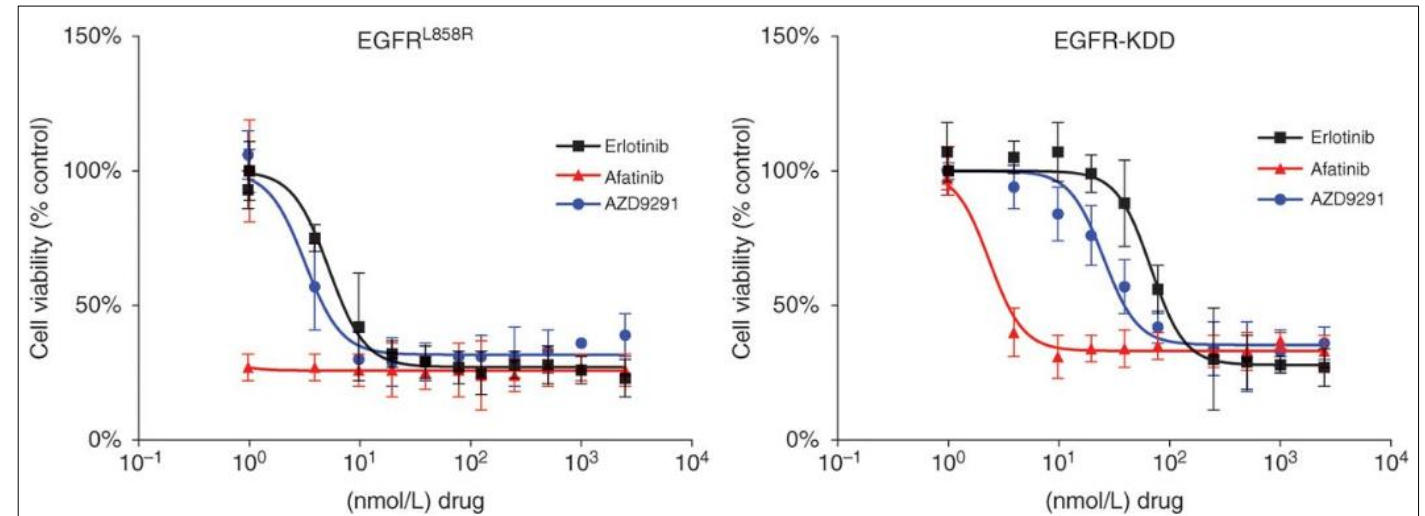
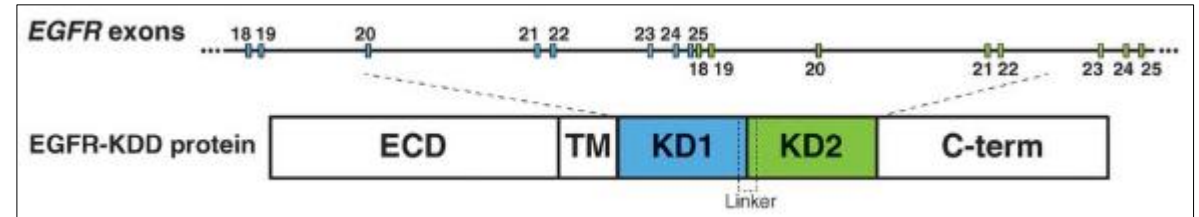
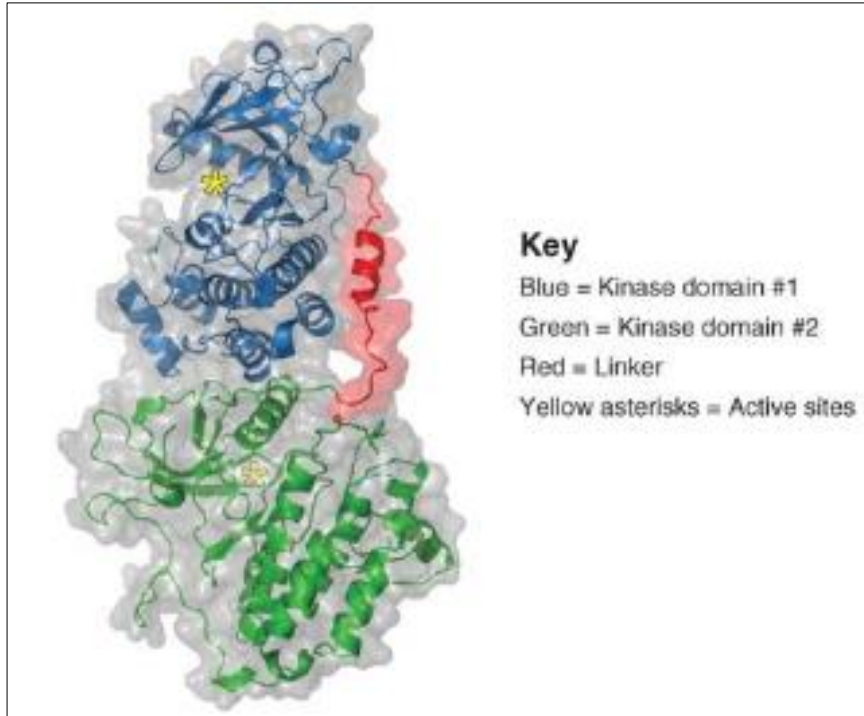
• Vol 4, No 1 (February 2015) Targeted therapy for non-small cell lung cancer: current standards and the promise of the future

# Comprehensive NGS Tumor Profiling\* (April 2019)

RESULT SUMMARY						
Variant Detected	FDA Approved Therapy Within Indication	FDA Approved Therapy Outside Indication	Resistance to Therapies	NCCN Guidelines	Clinical Trial Opportunity	TMB
<b>EGFR Exon 18 to 25 Kinase Domain Duplication</b>	Osimertinib, Erlotinib, Afatinib, Gefitinib	No	No	Yes - see variant details below	Yes - see below	3 Muts/Mb

\*161 Gene Panel: SNVs, Indels, CNV, Fusions

# EGFR Kinase Domain Duplication



<https://cancerdiscovery.aacrjournals.org/content/5/11/1155>

AZD9291 (Osimertinib)



## CLINICAL PRESENTATION

## HISTOLOGIC SUBTYPE<sup>a</sup>

## TESTING<sup>hh</sup>

## TESTING RESULTS<sup>hh</sup>

Advanced  
or  
metastatic  
Disease

- Establish histologic subtype<sup>a</sup> with adequate tissue for molecular testing (consider rebiopsy<sup>gg</sup> if appropriate)
- Smoking cessation counseling
- Integrate palliative care<sup>c</sup> ([See NCCN Guidelines for Palliative Care](#))

- Adenocarcinoma
- Large cell
- NSCLC not otherwise specified (NOS)

- Molecular testing
  - ▶ **EGFR mutation testing (category 1)**
  - ▶ **ALK testing (category 1)**
  - ▶ **ROS1 testing**
  - ▶ **BRAF testing**
  - ▶ Testing should be conducted as part of broad molecular profiling<sup>ii,jj</sup>
- PD-L1 testing (category 1)

Squamous cell carcinoma

- Molecular testing
  - ▶ Consider **EGFR mutation and ALK testing<sup>kk</sup>** in never smokers or small biopsy specimens, or mixed histology<sup>ll</sup>
  - ▶ Consider **ROS1 and BRAF testing** in small biopsy specimens or mixed histology
  - ▶ Testing should be conducted as part of broad molecular profiling<sup>ii,jj</sup>
- PD-L1 testing (category 1)

**Sensitizing EGFR mutation positive** ([see NSCL-18](#))

- ▶ **ALK positive** ([see NSCL-21](#))
- ▶ **ROS1 positive** ([see NSCL-24](#))
- ▶ **BRAF V600E positive** ([see NSCL-25](#))
- ▶ **PD-L1 ≥1% and EGFR, ALK negative or unknown** ([see NSCL-27](#))
- ▶ **EGFR, ALK, ROS1, BRAF negative or unknown, PD-L1 <1% or unknown** ([see NSCL-28](#))

- ▶ **Sensitizing EGFR mutation positive** ([see NSCL-18](#))
- ▶ **ALK positive** ([see NSCL-21](#))
- ▶ **ROS1 positive** ([see NSCL-24](#))
- ▶ **BRAF V600E positive** ([see NSCL-25](#))
- ▶ **PD-L1 ≥1% and EGFR, ALK negative or unknown** ([see NSCL-27](#))
- ▶ **EGFR, ALK, ROS1, BRAF, negative or unknown, PD-L1 <1% or unknown** ([see NSCL-29](#))

<sup>a</sup>See [Principles of Pathologic Review \(NSCL-A\)](#).

<sup>c</sup>Temel JS, Greer JA, Muzikansky A, et al. Early palliative care for patients with metastatic non-small-cell lung cancer. *N Engl J Med* 2010;363:733-742.

<sup>gg</sup>If repeat biopsy is not feasible, plasma testing should be considered.

<sup>hh</sup>See [Principles of Molecular and Biomarker Analysis \(NSCL-G\)](#).

<sup>ii</sup>The NCCN NSCLC Guidelines Panel strongly advises broader molecular profiling with the goal of identifying rare driver mutations for which effective drugs may already be available, or to appropriately counsel patients regarding the availability of clinical trials. Broad molecular profiling is a key component of the improvement of care of patients with NSCLC. [See Emerging Biomarkers to Identify Patients for Therapies \(NSCL-H\)](#).

<sup>jj</sup>Testing should include the neurotrophic receptor tyrosine kinase (*NTRK*) gene fusion; if positive, see [NSCL-26](#).

<sup>kk</sup>In patients with squamous cell carcinoma, the observed incidence of *EGFR* mutations is 2.7% with a confidence that the true incidence of mutations is less than 3.6%. This frequency of *EGFR* mutations does not justify routine testing of all tumor specimens. Forbes SA, Bhama G, Bamford S, et al. The catalogue of somatic mutations in cancer (COSMIC). *Curr Protoc Hum Genet* 2008;chapter 10:unit 10.11.

<sup>ll</sup>Paik PK, Varghese AM, Sima CS, et al. Response to erlotinib in patients with *EGFR* mutant advanced non-small cell lung cancers with a squamous or squamous-like component. *Mol Cancer Ther* 2012;11:2535-2540.

Note: All recommendations are category 2A unless otherwise indicated.  
Clinical Trials: NCCN believes that the best management of any patient with cancer is in a clinical trial. Participation in clinical trials is especially encouraged.

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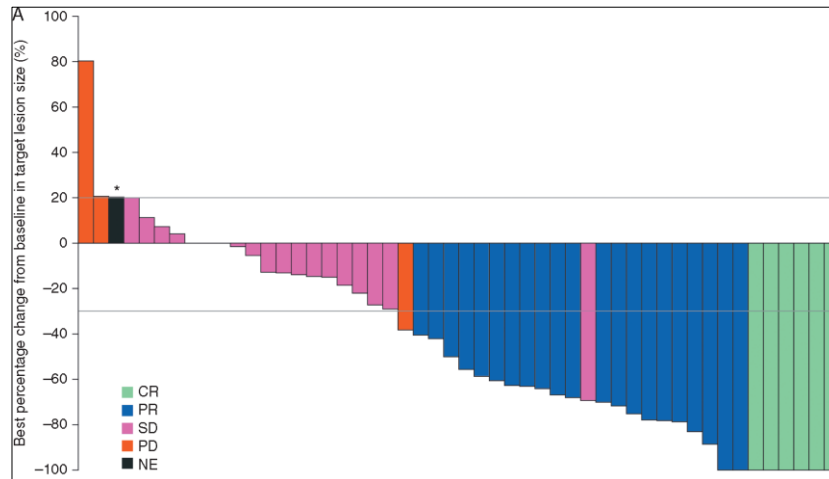
# Pooled Analysis of 2 Phase II Studies

Annals of Oncology, Volume 29, Issue 3, March 2018, Pages 687–693

Central nervous system response to osimertinib

Patients evaluable for CNS response ( $n = 50$ )

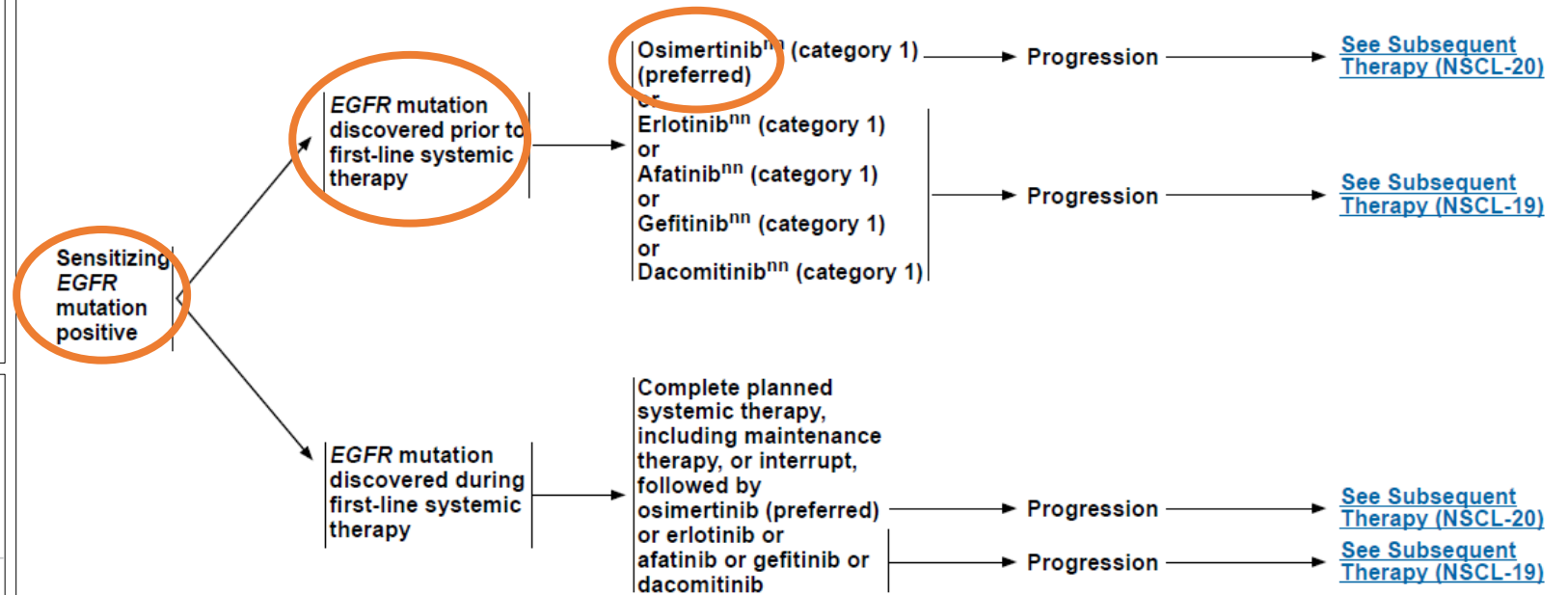
CNS ORR <sup>a</sup> , (95% CI)	54% (39% to 68%)
Complete response, $n$ (%)	6 (12)
Partial response, $n$ (%)	21 (42)
Stable disease $\geq 6$ weeks, $n$ (%)	19 (38)
Progressive disease, $n$ (%)	3 (6)
Not evaluable, $n$ (%)	1 (2)



Patient Started on Tagrisso 80 mg daily (April 2019).

SENSITIZING EGFR MUTATION POSITIVE<sup>hh</sup>

FIRST-LINE THERAPY<sup>mm</sup>



<sup>hh</sup>See Principles of Molecular and Biomarker Analysis (NSCL-G).

<sup>mm</sup>See Targeted Therapy for Advanced or Metastatic Disease (NSCL-I).

<sup>nn</sup>For performance status 0-4.

Note: All recommendations are category 2A unless otherwise indicated.

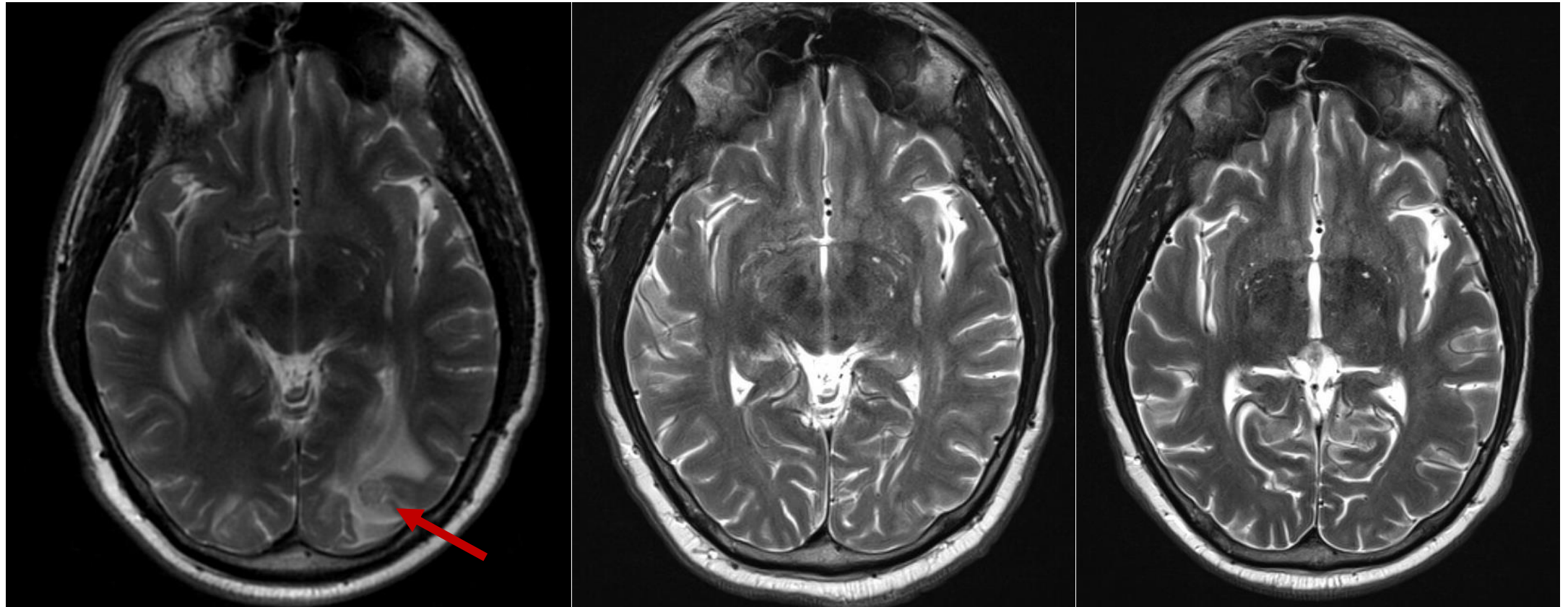
Clinical Trials: NCCN believes that the best management of any patient with cancer is in a clinical trial. Participation in clinical trials is especially encouraged.

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NSCL-18



# Brain: Repeat Imaging



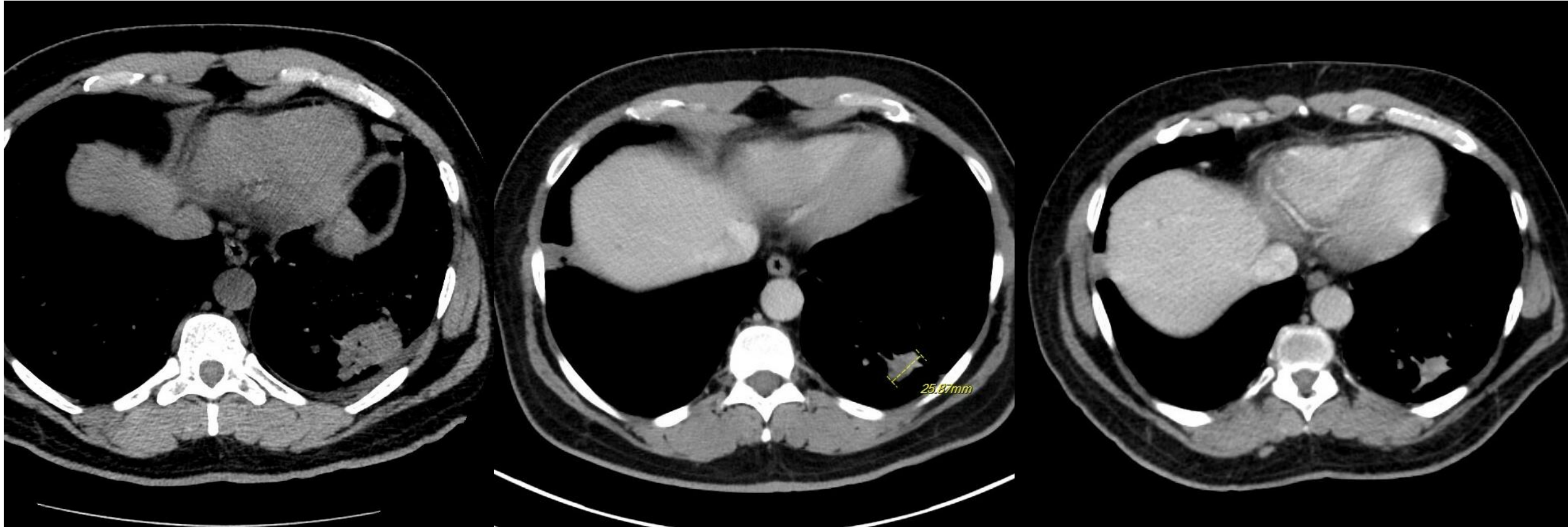
**March 2019**

**August 2019**

**May 2020**

[JCO Precis Oncol. 2021 Nov;5:88-92. doi: 10.1200/PO.20.00296.](#)

# Lung: Repeat Imaging



March 2019

August 2019

September 2019

[JCO Precis Oncol. 2021 Nov;5:88-92. doi: 10.1200/PO.20.00296.](#)



# Past

# Present and Future

**"All the News That's Fit to Print"**

## The New York Times

Late Edition  
New York: Today, afternoon thunderstorms; high 65. Tonight, showers; end low 67. Tomorrow, partly cloudy with showers; high 70. Yesterday, high 66, low 74. Weather map, page 10.

VOL. CXLIX . . . No. 51,412 Copyright © 1998 The New York Times NEW YORK, TUESDAY, JUNE 27, 2000 \$1 beyond the greater New York metropolitan area. 75 CENTS

### Genetic Code of Human Life Is Cracked by Scientists

#### JUSTICES REAFFIRM MIRANDA RULE, 7-2; A PART OF 'CULTURE'

By LINDA GREENHOUSE

WASHINGTON, June 26 — The Supreme Court reaffirmed the Miranda decision today by a 7-to-2 vote that erased a shadow over one of the most famous rulings of modern times and acknowledged that the Miranda warnings "have become part of our national culture."

The court said in an opinion by Chief Justice William B. Rehnquist that because the 1966 Miranda decision "announced a constitutional rule" a statute by which Congress had sought to overrule the decision was itself unconstitutional.

Miranda had appeared to be in jeopardy both because of that long-ignored but recently rediscovered law, by which Congress had tried to overrule Miranda 32 years ago, and because of the court's perceived hostility to the original decision.

The chief justice said, though, that the 1968 law, which replaced the Miranda warnings with a case-by-case test of whether a confession was voluntary, could be upheld only if the Supreme Court decided to overturn Miranda. But with Miranda having

Justices Antonio Scalia and Clarence Thomas cast the dissenting votes.

The decision overturned a ruling last year by the federal appeals court in Richmond, Va., which held that Congress was entitled to the last word because Miranda's presumption that a confession was not voluntary unless preceded by the warnings was not required by the Constitution.

The decision today — only 14 pages long — Chief Justice Rehnquist's opinionally spare style — brought an abrupt end to one of the oddest episodes in the court's recent history, an intense and strangely delayed re-litigation of a previous generation's battle over the rights of criminal suspects. Miranda v. Arizona was a landmark of the Warren Court, and Chief Justice Rehnquist, despite his record as an early and intemperate critic of the decision, evidently did not want his reputation to be an imprint of his own tenure.

There was considerable drama in the courtroom today as the chief justice announced that his second ob-

**The Book of Life**  
The three billion base pairs ...  
... of the intertwining double helix of DNA ...  
... that make up the set of chromosomes in our cells, have been sequenced.

BASE PAIRS  
Runge between the strands of the double helix  
A adenine  
C cytosine  
G guanine  
T thymine

**Science Times**  
An opinion issued  
■ Putting the genome to work.  
■ Some information has already paid research dividends.  
■ Two research methods now results.  
■ From Mendel to helix to genome.  
■ More articles, charts and photos of the genome effort.

Francis S. Collins, head of the Human Genome Project, left, with J. Craig Venter, head of Celera Genomics, after the announcement yesterday that they had finished the first survey of the human genome.

**A SHARED SUCCESS**  
2 Rivals' Announcement Marks New Medical Era, Risks and All  
By NICHOLAS WADE  
WASHINGTON, June 26 — In an achievement that represents a pinnacle of human self-knowledge, two rival groups of scientists met today that they had deciphered the hereditary script, the set of instructions that defines the human organism.

"Today we are learning the language in which God created life," President Clinton said at a White House ceremony attended by members of the two teams, Dr. James D. Watson, codiscoverer of the structure of DNA, and, via satellite, Prime Minister Tony Blair of Britain. (Excerpt, Page D-1.)

The teams' leaders, Dr. J. Craig Venter, president of Celera Genomics, and Dr. Francis S. Collins, director of the National Human Genome Research Institute, praised each other's contributions and signaled a spirit of cooperation from now on, even though the two efforts will remain firmly independent.

The human genome, the secret script that has now been deciphered, consists of two sets of 23 pairs of DNA.



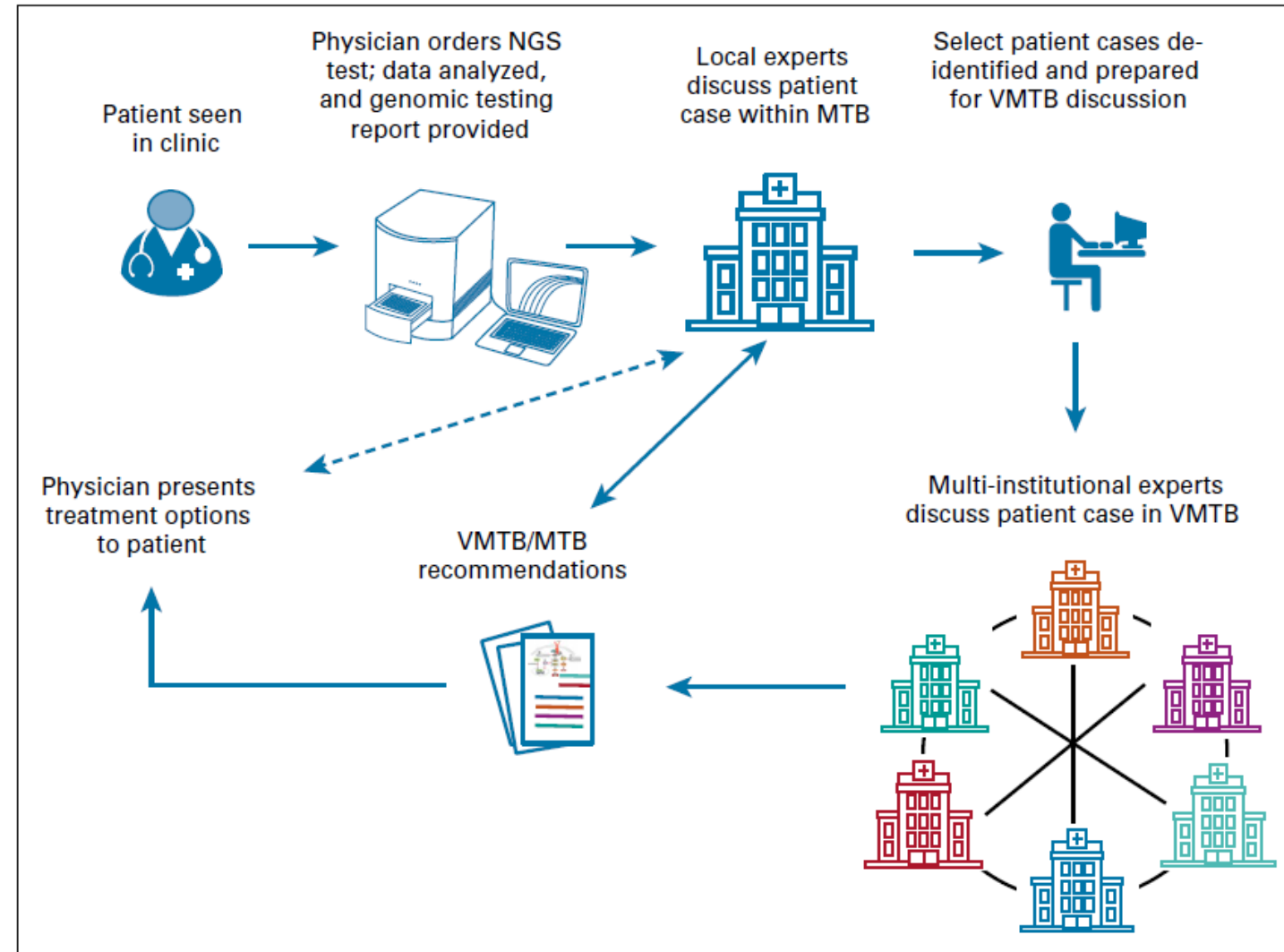
## THE PRECISION MEDICINE INITIATIVE

The time is right because of:

- Sequencing of the human genome
- Improved technologies for biomedical analysis
- New tools for using large datasets

**FACT SHEET: President Obama's Precision Medicine Initiative**

Building on President Obama's announcement in his State of the Union Address, today the Administration is unveiling details about the Precision Medicine Initiative, a bold new research effort to revolutionize how we improve health and treat disease. Launched with a \$215 million investment in the President's 2016 Budget, the Precision Medicine Initiative will pioneer a new model of patient-powered research that promises to accelerate biomedical discoveries and provide clinicians with new tools, knowledge, and therapies to select which treatments will work best for which patients.



# Thank You: Any Questions?



*ARUP is a nonprofit enterprise of the University of Utah and its Department of Pathology.*