Multidisciplinary Approaches to Cancer Symposium

Who, How, When?
Personalized Pathology for Genomics Classification in Lung Cancer

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Disclosures

- I do not have any relevant financial relationships.

This presentation and/or comments will provide a balanced, non-promotional, and evidence-based approach to all diagnostic, therapeutic and/or research related content.

Cultural Linguistic Competency (CLC) & Implicit Bias (IB)

STATE LAW:

The California legislature has passed Assembly Bill (AB) 1195, which states that as of July 1, 2006, all Category 1 CME activities that relate to patient care must include a cultural diversity/linguistics component. It has also passed AB 241, which states that as of January 1, 2022, all continuing education courses for a physician and surgeon **must** contain curriculum that includes specified instruction in the understanding of implicit bias in medical treatment.

The cultural and linguistic competency (CLC) and implicit bias (IB) definitions reiterate how patients' diverse backgrounds may impact their access to care.

EXEMPTION:

Business and Professions Code 2190.1 exempts activities which are dedicated solely to research or other issues that do not contain a direct patient care component.

This presentation is dedicated solely to research or other issues that do not contain a direct patient care component.

What's biomarker testing

Molecular genomic and cytogenomics analysis for specific gene changes in the cancer cells that could mean certain targeted drugs might help treat the cancer.

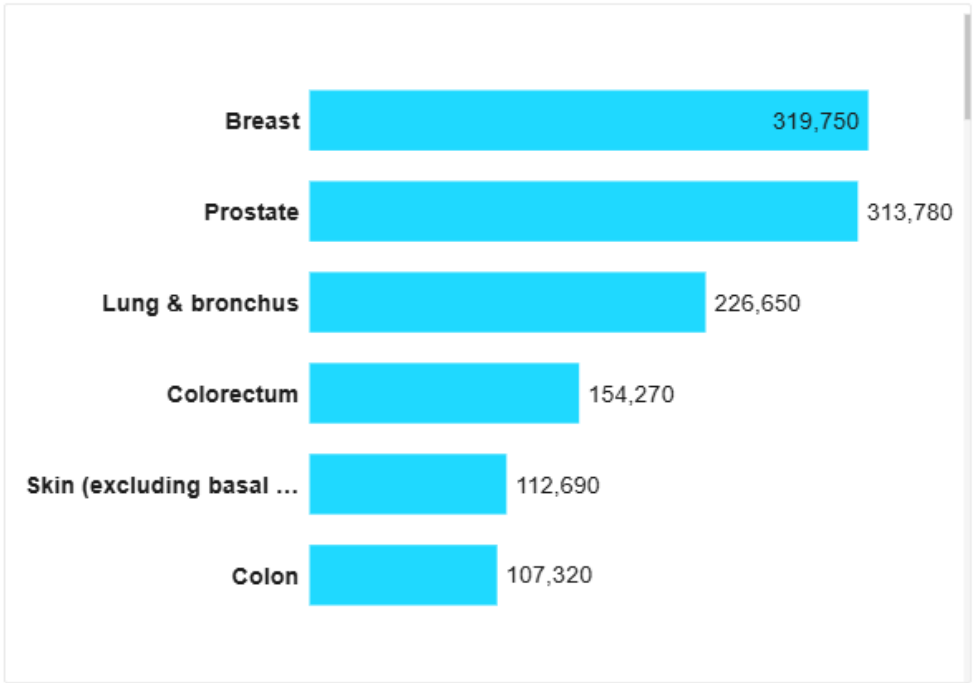
- **Immunohistochemistry study**
- **Cytogenetics and FISH analysis.** **(FISH is a technique that allows DNA sequences to be detected on metaphase chromosome or interphase nuclei from fixed cytogenetics samples)**
- **Targeted molecular assay (NGS, sanger, RT-PCR or PCR)**
- **Whole Genome array (OncoScan & CytoScan)**
- **Whole Genome Sequencing**

The American Cancer Society's estimates for cancer in the United States for 2025

2025 Estimated New Cancer Cases

Cases by Cancer Type

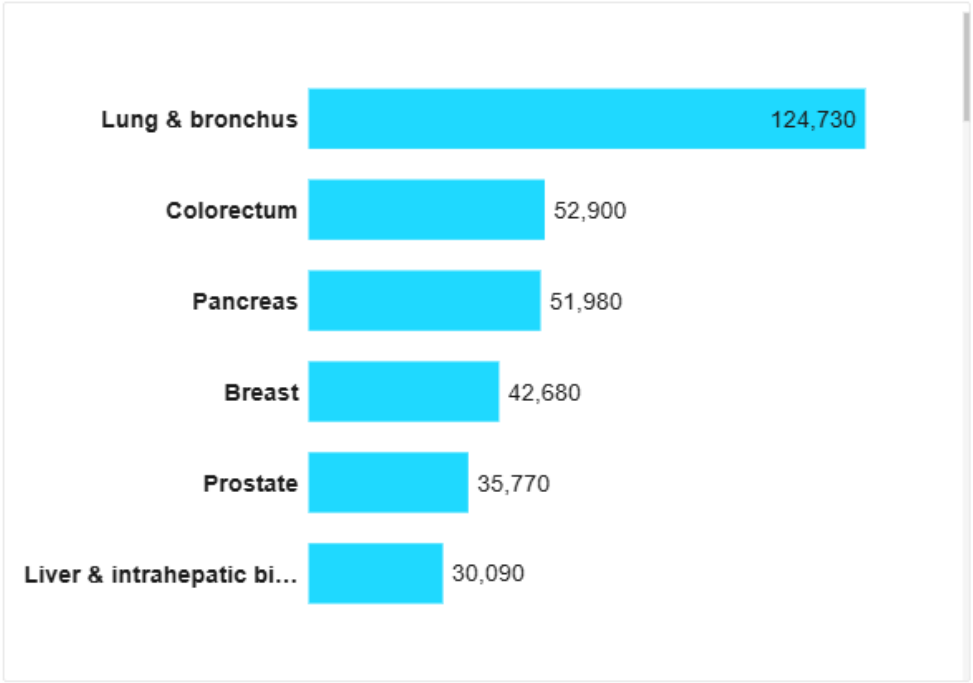
View by: Sex: Sexes combined | Cancer Type: All



2025 Estimated Cancer Deaths

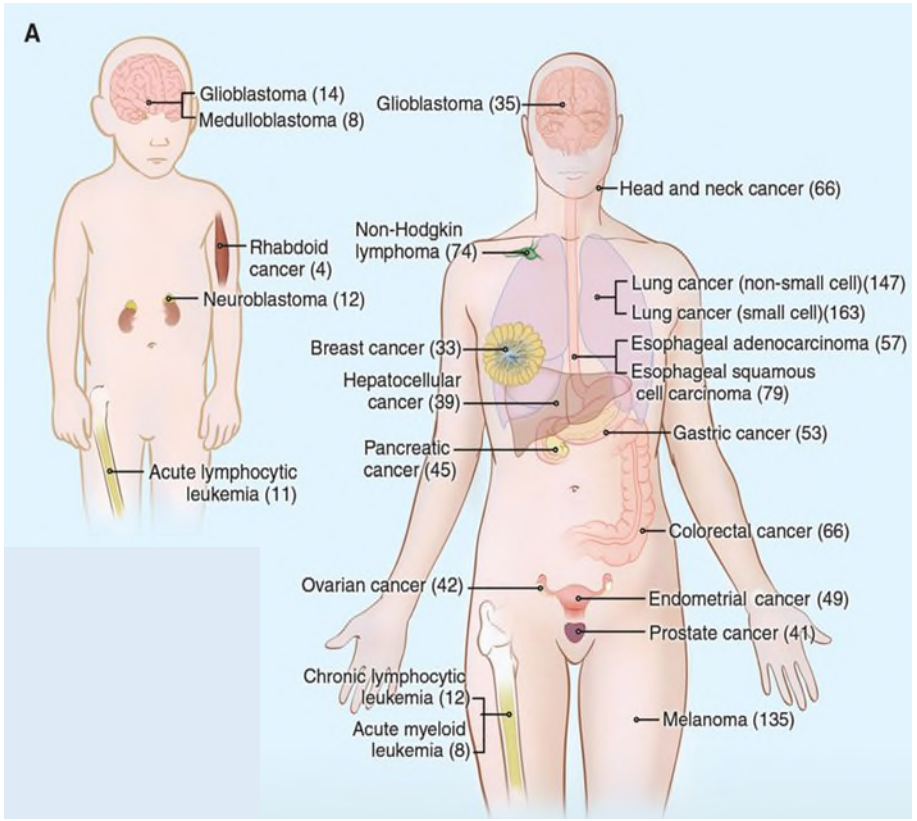
Deaths by Cancer Type

View by: Sex: Sexes combined | Cancer Type: All



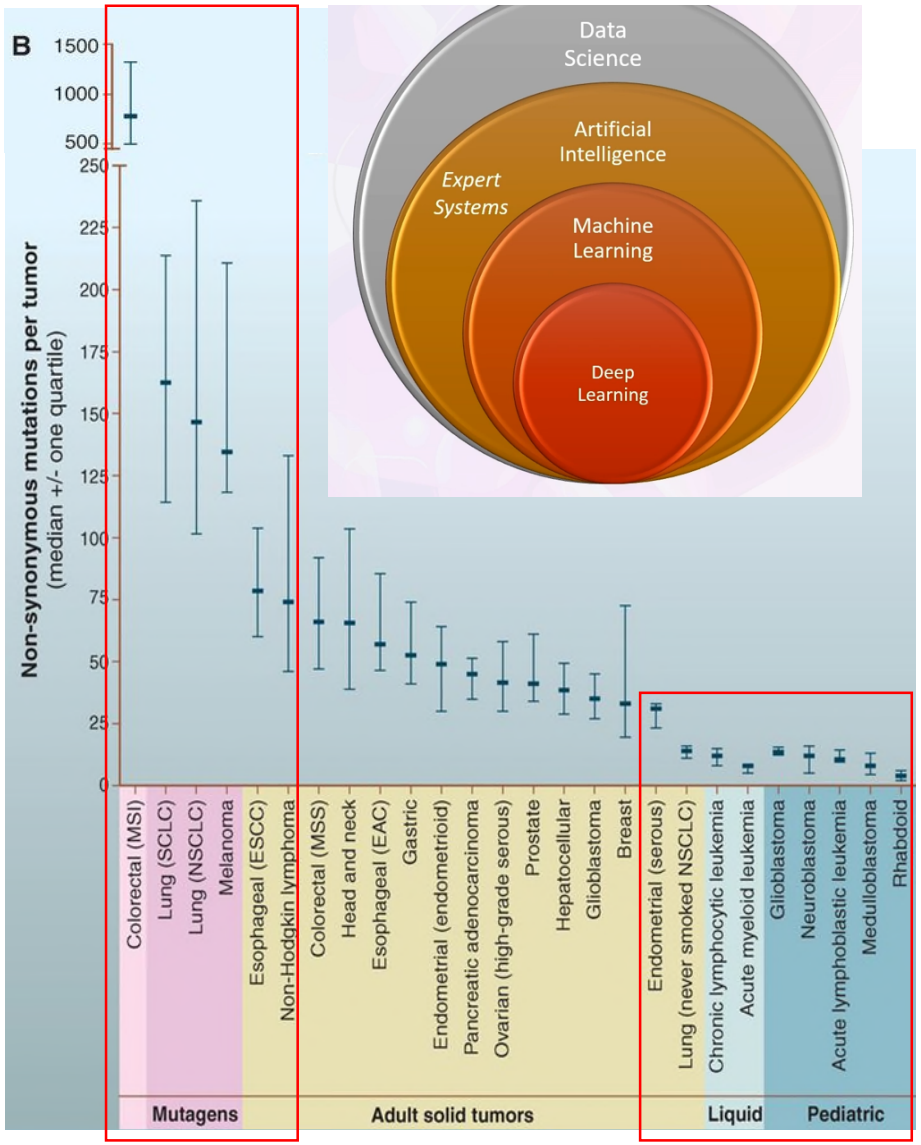
https://www.cancer.org/cancer/lung-cancer/about/key-statistics.html

Genomic Landscapes of Common Human Cancers



Average 33-66 genes mutated

- >90% missense mutations
- 5-8% nonsense changes
- <2-5% splice site or UTR'or fusions



Bert Vogelstein et al. Science 2013;339:1546-1558

Who Should be tested?

- Advanced stage lung adenocarcinoma (stages IIIB and IV)

- By morphology:

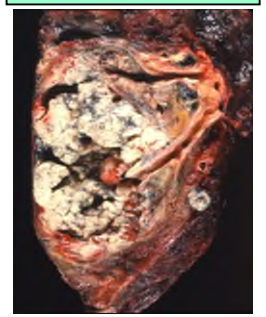
- Adenocarcinoma or any tumors with adenocarcinoma component

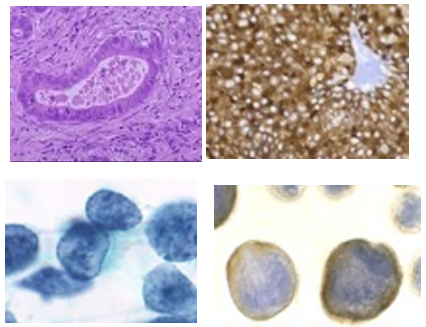
- Other biopsies with suspicious of presence of adenocarcinoma component

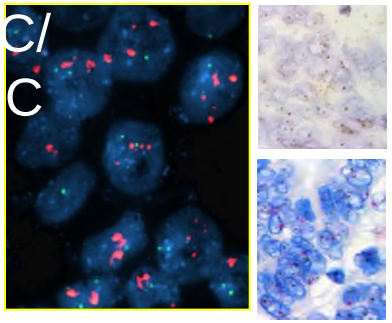
- Squamous cell carcinoma, when clinically indicated such as younger patient or never smokers who have higher possibility of having oncogenic drivers

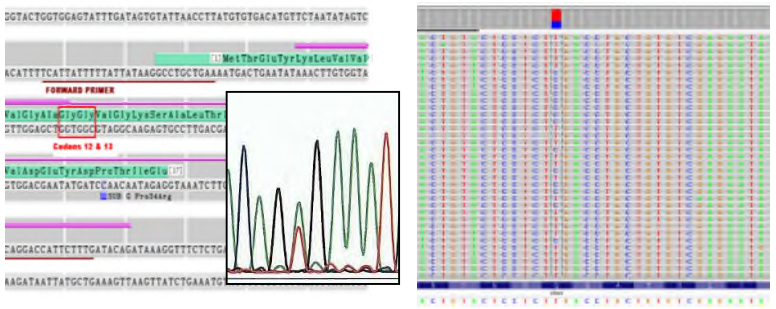
Modern Pathology
Phenotype and Genotype are Complementary

Tissue pathology → **Molecular pathology**





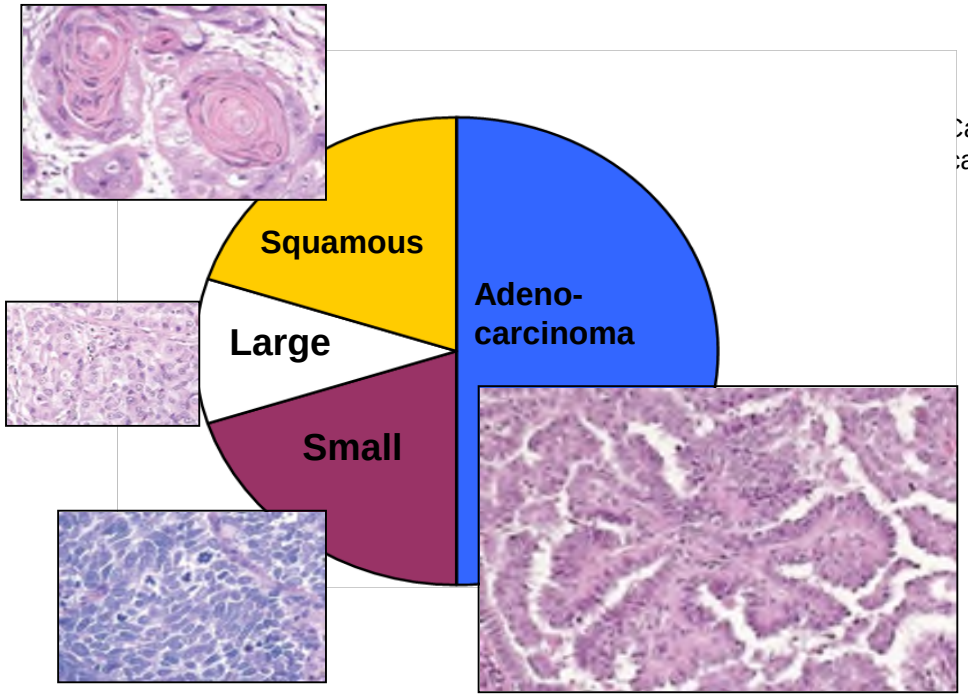




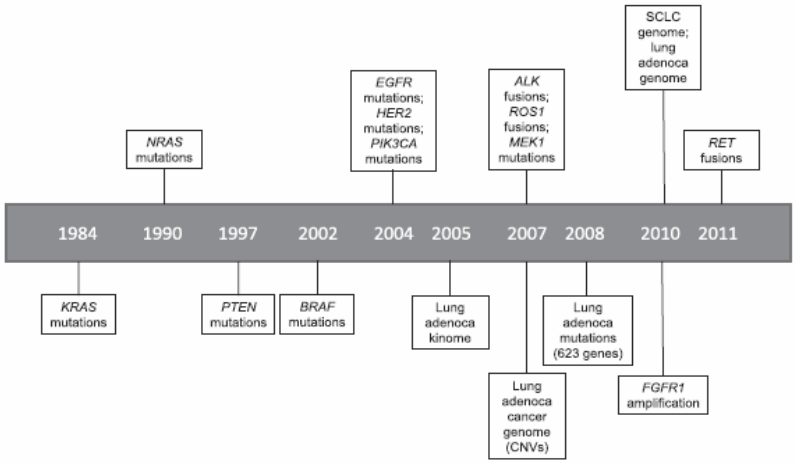
24 hrs	Tissue collection/Fixation → Biopsy
1-2 working days (except IHC)	Fixation/Tissue Processing → Pathologists review and report → Pathology
10 working days	Molecular Testing → Molecular testing
	Final report with tumor histology and molecular results

Slide courtesy of Dr. Sanja Dacic, Yale Cancer Center

Traditional View of Lung Cancers

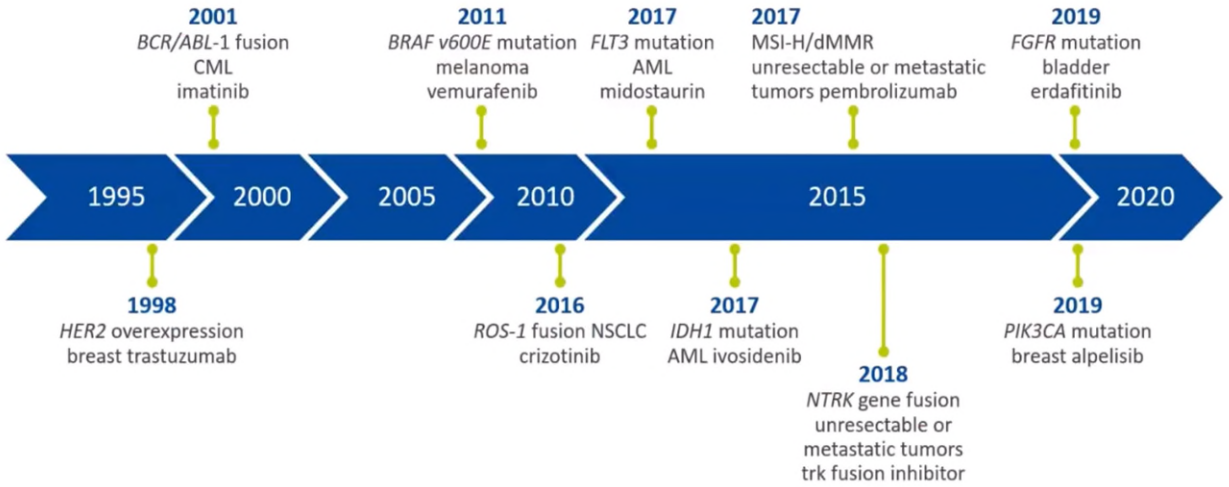


cancer: Most
cancer



Levy et al. Genome Research 22:2201, 2012

Evolution of target therapies

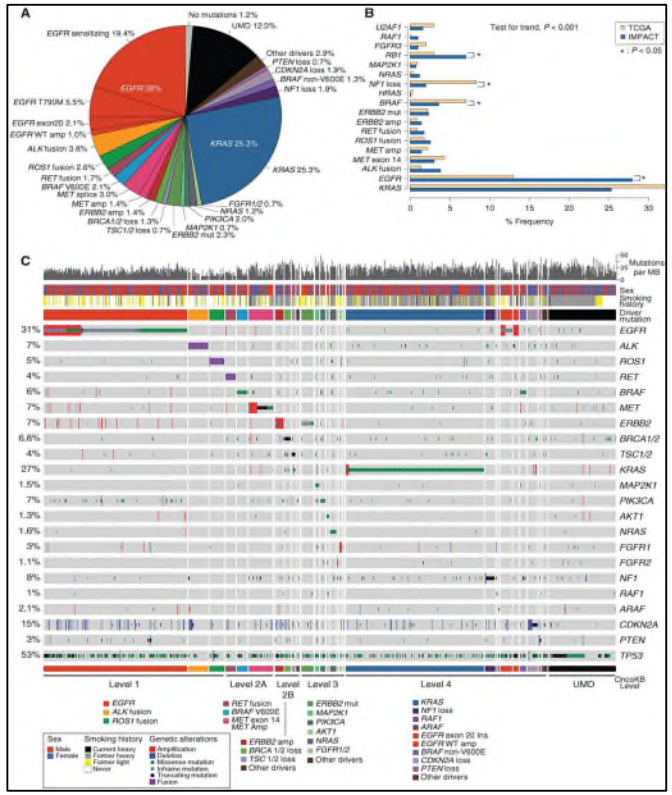


***KRAS* G12C and *EGFR* make up ~ 75% of all actionable driver mutations in NSCLC** (Analysis of AACR Genie v8 2022)

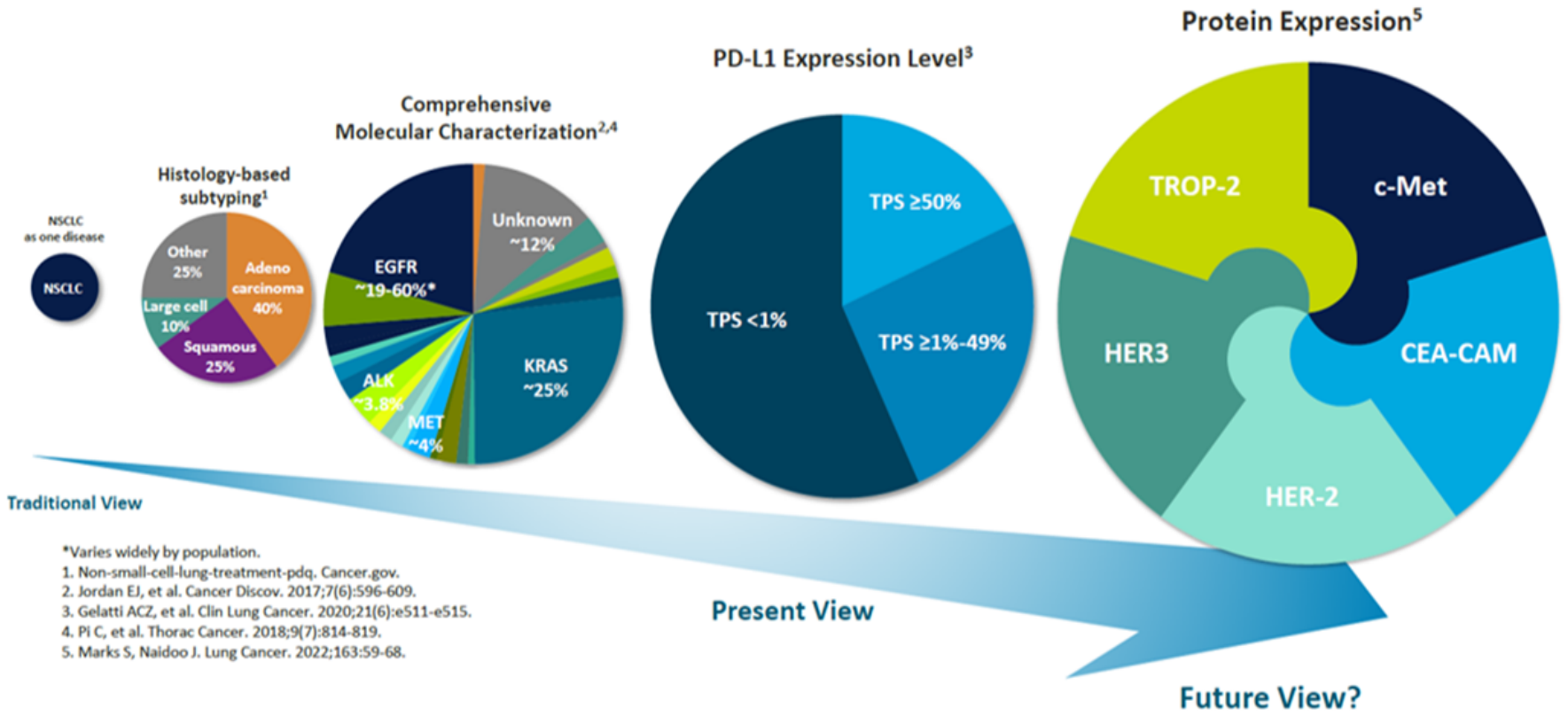
Molecular Classification of Lung Cancers

Prospective Comprehensive Molecular Characterization of Lung Adenocarcinomas for Efficient Patient Matching to Approved and Emerging Therapies

Emmet J. Jordan; Hyunjae R. Kim; Maria E. Arcila; David Barron; Debyani Chakravarty; JianJiong Gao; Matthew T. Chang; Andy Ni; Ritika Kundra; Philip Jonsson; Gowtham Jayakumaran; Sizhi Paul Gao; Hannah C. Johnsen; Aphrothiti J. Hanrahan; Ahmet Zehir; Natasha Rekhtman; Michelle S. Ginsberg; Bob T. Li; Helena A. Yu; Paul K. Paik; Alexander Drilon; Matthew D. Hellmann; Dalicia N. Reales; Ryma Benayed; Valerie W. Rusch; Mark G. Kris; Jamie E. Chaft; José Baselga; Barry S. Taylor; Nikolaus Schultz; Charles M. Rudin; David M. Hyman; Michael F. Berger; David B. Solit; Marc Ladanyi; Gregory J. Riely



Current and Future View of Lung Cancers: Many opportunities for personalized approach in treatment.



*Varies widely by population.

1. Non-small-cell-lung-treatment-pdq. Cancer.gov.
2. Jordan EJ, et al. Cancer Discov. 2017;7(6):596-609.
3. Gelatti ACZ, et al. Clin Lung Cancer. 2020;21(6):e511-e515.
4. Pi C, et al. Thorac Cancer. 2018;9(7):814-819.
5. Marks S, Naidoo J. Lung Cancer. 2022;163:59-68.

Modified courtesy of Ignacio I. Wistuba, MD, 2025

How to Test?

	Tissue-based NGS	ctDNA-based NGS (liquid biopsy)
Nature of procedure	Invasive, requires a biopsy	✓ Minimally invasive
Turnaround time	Longer	✓ Shorter (7 – 14 days)
Source of molecular alterations	Biopsied tissue	✓ Better captures intratumoral heterogeneity and clonal evolution
Sensitivity	✓ Higher sensitivity	Limited sensitivity, dependent on amount pf DNA shedded into bloodstream Negative results require confirmation by tissue-based testing
Concurrent PD-L1 testing	✓ Concurrent PD-L1 testing possible	Concurrent PD-L1 testing not possible
Testing for acquired resistance mechanism	May document histologic transformation	May detect various resistance mechanisms from multiple clones

- Not all tumors shed ctDNA and may have negative plasma result
  - Tumor size, location
  - Tumor vascularity, metastasis
  - Prior treatment
- How to handle a negative result on liquid biopsy with high suspicion of a resistance mechanism? **Test tissue!**

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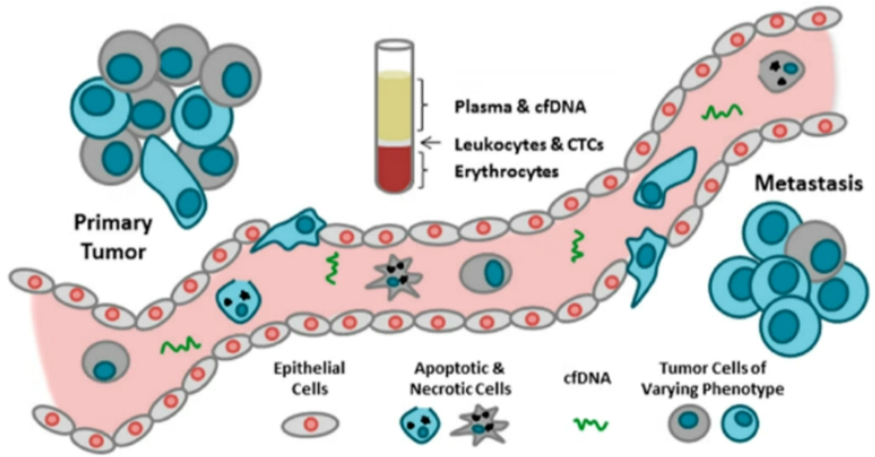
- Blood sample containing cell-free DNA from multiple sources, shed from tumor

1-5 mutant tumor DNA fragments in 10,000+ self DNA fragments*



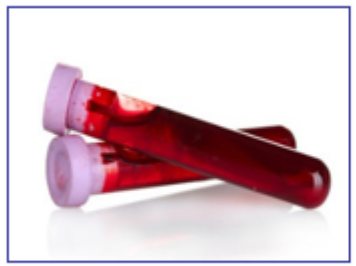
Lowes. Int J Mol Sci. 2016:17:E1505. Figure 1 of given citation is used in its original form under the terms and conditions of the Creative

Rolfo Et al. JTO.2021

City of Hope Practice: HopeSeq Comprehensive Assays Diagnostic Algorithm for Lung Cancer Diagnosis 2025

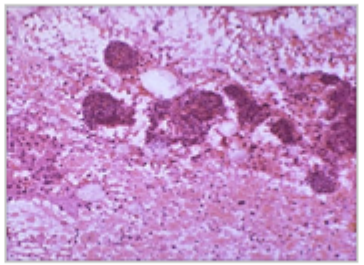
FFPE of the cytology cell block or core or resection biopsies or 40 ng of DNA and 40ng of RNA

cfDNA Testing (Liquid Biopsy)

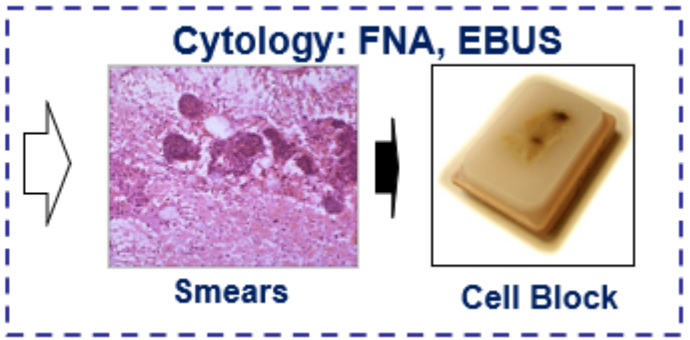


Blood

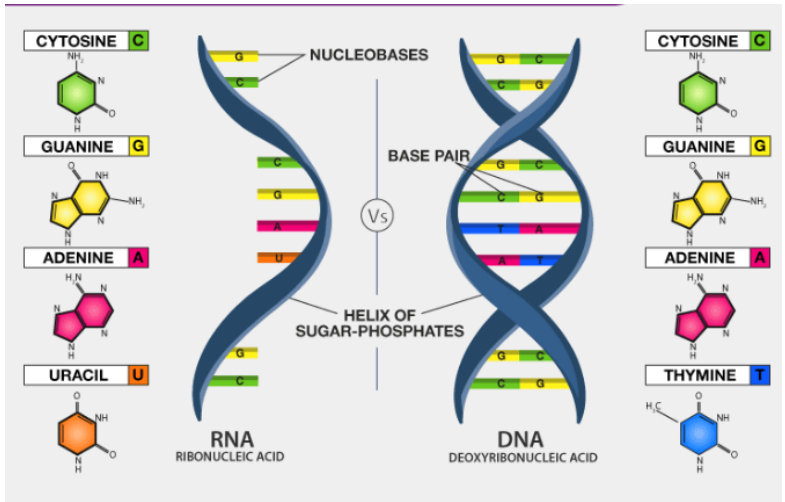
Biopsy



Cytology



Resection



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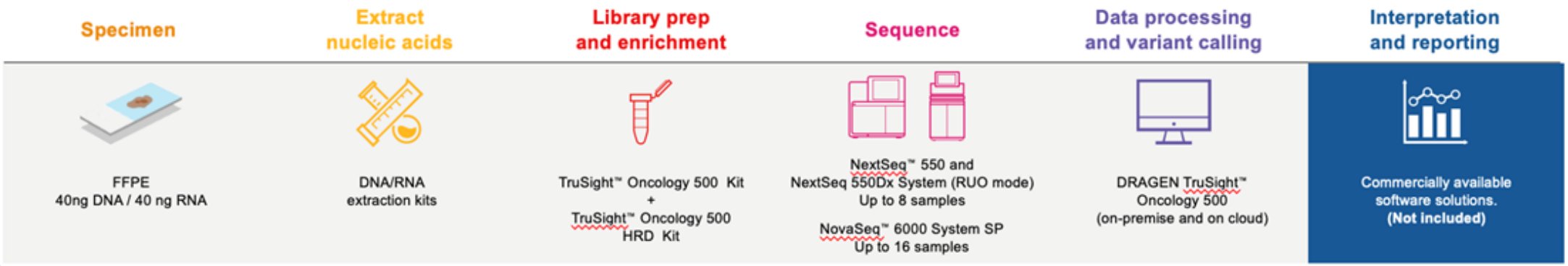
Comprehensive NGS assay with combined RNA and DNA Seq

- **Pre-Analytics Workflow** – Billing and authorization, Pathologist review, Order and circle best tumor area
- **Analytics Workflow (wet lab) –** RNA and DNA extraction and Sequencing
- **Post-Analytics workflow – Bioinformatics, Curation, and** Pathologists review and sign out



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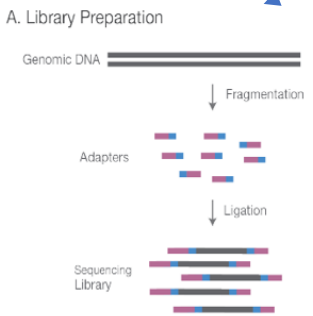
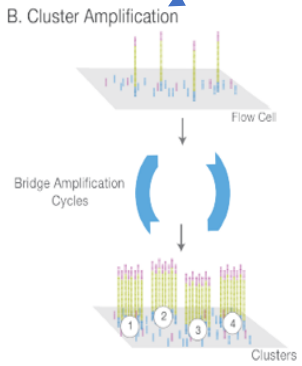
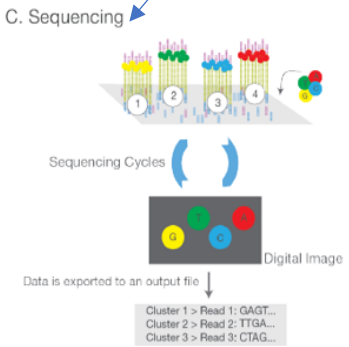
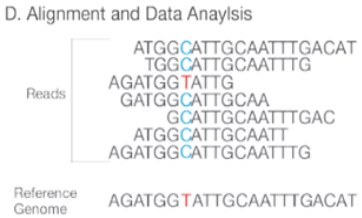
HopeSeq Comprehensive NGS assay workflow

Specimen	Extract nucleic acids	Library prep and enrichment	Sequence	Data processing and variant calling	Interpretation and reporting
FFPE 40ng DNA / 40 ng RNA	DNA/RNA extraction kits	TruSight™ Oncology 500 Kit + TruSight™ Oncology 500 HRD Kit	NextSeq™ 550 and NextSeq 550Dx System (RUO mode) Up to 8 samples NovaSeq™ 6000 System SP Up to 16 samples	DRAGEN TruSight™ Oncology 500 (on-premise and on cloud)	Commercially available software solutions. (Not included)









Sequencing Platform	Output	Software	Generates	Software	Generates	Software	Generates
NovaSeq	BCL	Dragen	TMB Score				
			MSI Score				
			CNV Fold Change				
			BAM	IGV	IGV Pileup		
			FASTQ	NextGene	PJT		NextGene Pileup
				CLC Bio	VCF	QCI	SNV
							MNV
							Indel
							Annotation
							Interpretation
							Clinical Trials
							Drugs

- DNA Alignment and Realignment
- Read Collapsing
- Indel Realignment and Read Stitching

M. Afkhami, MD unpublished

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HopeSeq Comprehensive NGS assay-COH

Variant analysis: DNA Sequencing

- Small Variant Calling
- Small Variant Filtering
- Copy Number Variant Calling
- Phased Variant Calling
- Variant Merging
- Annotation
- Tumor Mutational Burden
- Microsatellite Instability Status
- Contamination Detection

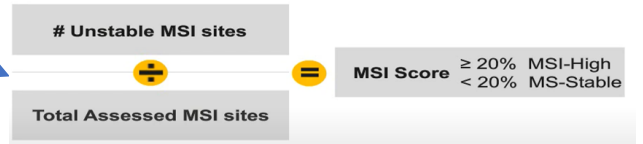
CNV deletion FC values: ≤ 0.6
CNV amplification FC values: ≥1.43
CNV normal range: >0.6 and <1.43
NovaSeq Dragen calculates fold changes for 500 genes based on individual cut off values and determines the AMP or LOSS.

$$TMB = \frac{\text{Total eligible variants (N)}}{\text{Total coding region} \geq 50X \text{ coverage (M)}}$$

TMB eligible variants included in the score determination:

- Variants in the coding region.
- Variant Frequency >= 5%.
- Coverage >= 50X.
- SNVs, INDELS (MNVs excluded).
- Nonsynonymous and synonymous variants.

TMB High: TMB score > 17
TMB Intermediate: TMB score > 5 and ≤ 17
TMB Low: TMB score ≤ 5



M. Afkhami, MD unpublished

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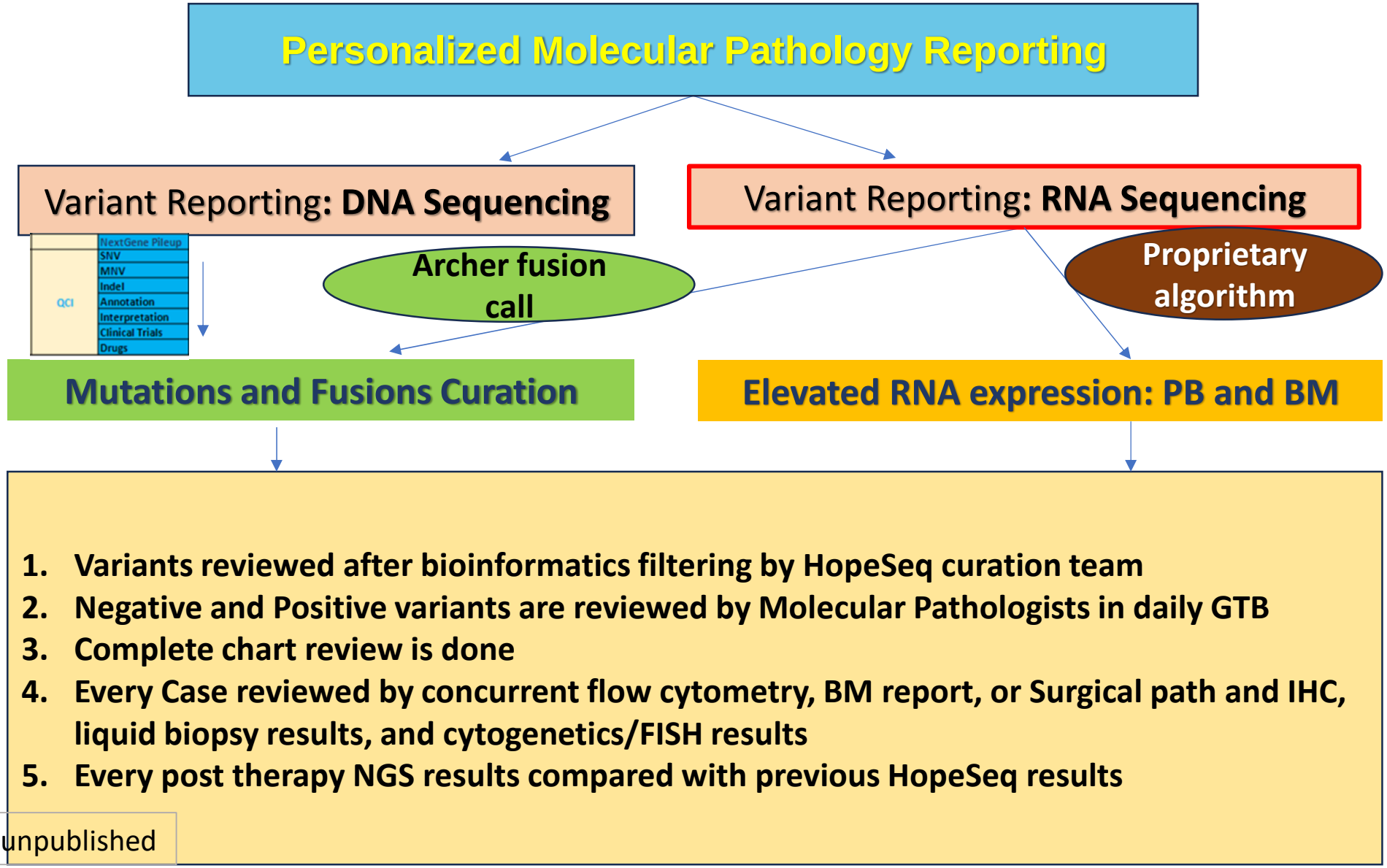
HopeSeq Comprehensive NGS assay-COH



M. Afkhami, MD unpublished

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How to Test? Predictive IHCs

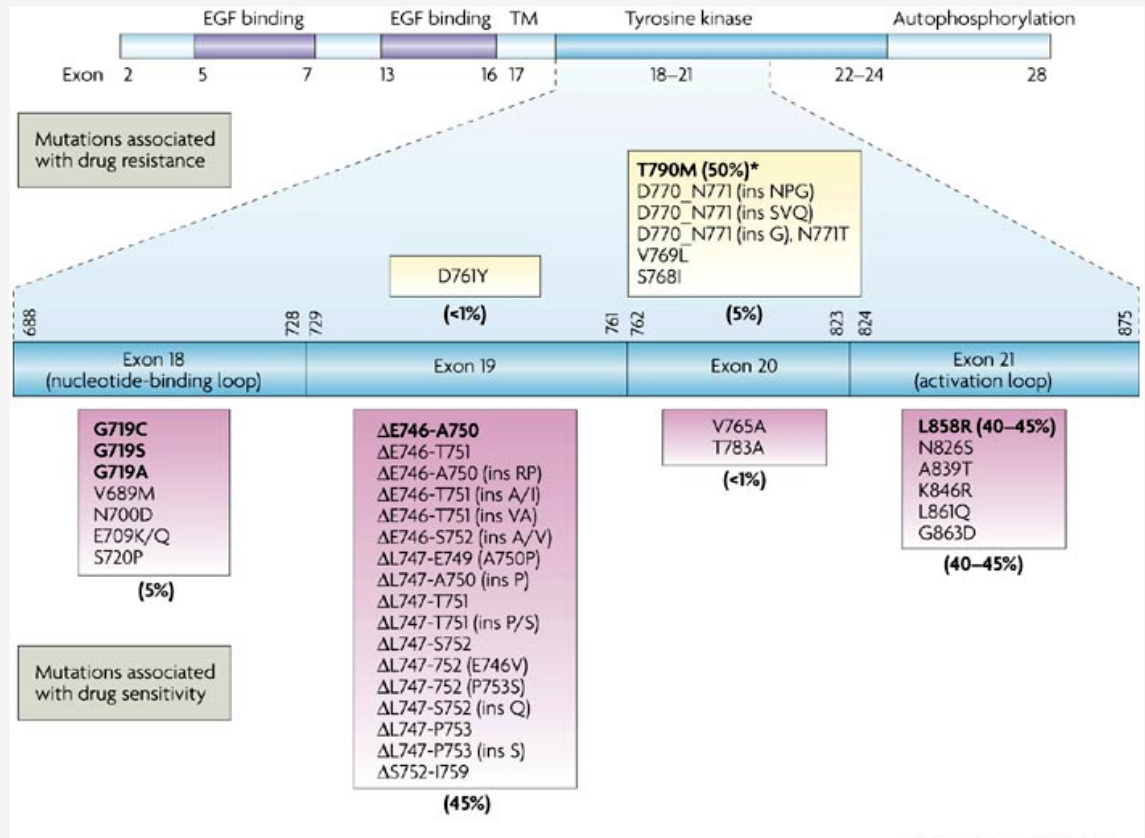
Targets	Clones	Sensitivity	Specificity	Recommendation
EGFR	EGFR-L858R EGFR-E746	70-90%	95-97%	Not recommended
ALK	D5F3	97-99%	98-100%	FDA-approved CDx assay
ROS1	D4D6	100%	92%	Useful for screening
BRAF1	VE1	90-97%	99-100%	May be useful
Pan-NTRK	EPR17341	95-97%	98-100%	More studies needed
MET (for *MET* ex14)	SP44	64-90%	47-83%	Not recommended
RET	EPR2871	87%	82%	More studies needed

	NGS[2-8]	DNA FISH[5,9-14]	IHC[4-6,8]
Strengths	• **Allows for efficient multiplex testing** with the ability to find *NTRK* gene fusions and identify multiple genomic targets • Comprehensive: **Can identify the exact fusion partner**	• Well suited to identifying fusions • There is utility in using FISH in diseases such as IFS, where the predominant driver for IFS is *ETV6-NTRK3*	• IHC used in a majority of labs • Research-use-only TRK antibodies • Ventana is commercially available; pan-TRK in vitro diagnostic under development
Considerations	• Large tissue sample required • Review and perform bioinformatic data analyses of prior NGS results to uncover *NTRK* gene fusions (provided panel included coverage)	• Not designed for multiplexing • In order to detect fusions at multiple locations (such as the 3 *NTRK* genes), multiple FISH tests would be needed • Must use break apart methodology to identify novel fusions	• Single-plex (additional genetic targets require additional samples) • Protein expression may not always indicate a fusion; confirmation of *NTRK* gene fusion via additional testing is required treatment
Turnaround Time	14 days (for the majority of labs)	1-14 days	1-14 days

Validation of a Targeted RNA Sequencing Assay for Kinase Fusion Detection in Solid Tumors

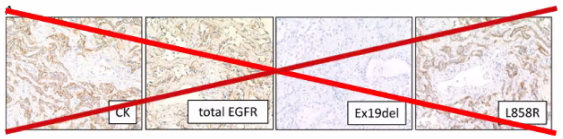
Julie W. Reeser,* Dorrelyn Martin,* Jharna Miya,* Esko A. Kautto,* Ezra Lyon,* Eliot Zhu,* Michele R. Wing,* Amy Smith,* Matthew Reeder,* Eric Samorodnitsky,* Hannah Parks,* Karan R. Naik,* Joseph Gozgit,† Nicholas Nowacki,† Kurtis D. Davies,‡ Marileila Varella-Garcia,‡ Lianbo Yu,¶ Aharon G. Freud,‖ Joshua Coleman,† Dara L. Aisner,† and Sameek Roychowdhury*†

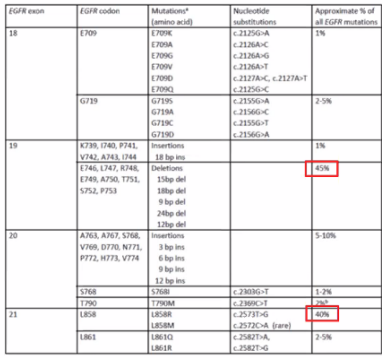
EGFR mutations



Testing for *EGFR* Mutations

- *EGFR* Tyrosine Kinase domain mutations (exons 18 to 21) = most reliable predictors of response to EGFR TKI
- Must be able to detect mutations in samples with 20% tumor purity
- NGS, Sanger, PCR all acceptable
- Methods not recommended:
  - FISH for EGFR amplification
  - Total EGFR expression by IHC
  - EGFR mutation-specific IHC



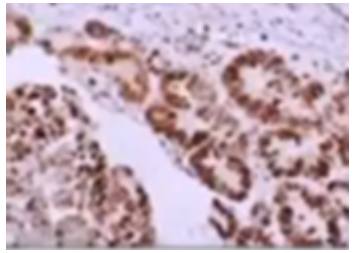


EGFR mutations enriched in
- Women
- East Asians
- Never smokers

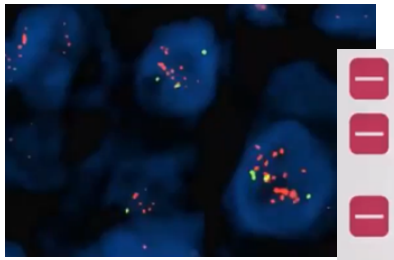
Mok et al. *NEJM*. 2009.

Fusion testing

- **Immunohistochemistry study**
  - **May be used as screening tool prior to confirming positive testing**
  - **Fast TAT**
  - **Low cost**
  - **Not sensitive or specific for most of the NTRK and RET fusions**



- **DNA Fluorescence in situ hybridization (FISH)**
  - **Not available for all partner detection**
  - **Costly**
  - **TAT 5-7 days**



- May require three sets of break-apart probes[2,3]
- May miss certain intra-chromosomal rearrangements (particularly *NTRK1*)
- Does not absolutely determine that an identified rearrangement represents a functional fusion

- **Next Generation Sequencing (NGS)**
  - **NGS is the preferable method in detection of fusions as it identifies the causative driver and partner in a single test saving in both TAT and cost**

	IHC	FISH	DNA NGS	RNA NGS
Pros	✓ Potential local implementation	✓ Potential local implementation	✓ Simultaneously get mutation information	✓ Obtain fusion partner information without intron coverage issues; **directly assess fusion expression**
Cons	– Significant false neg, pos except for ALK	– False neg, pos – Tissue utilization	– Poor coverage of some intronic areas due to repetitive sequences leads to reduced sensitivity	

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	ALK	*ROS1*	*RET*	*NTRK1,2,3*	*NRG1*	*FGFR1,2,3*
Prevalence	~5%	~1%	1-2%			<1%
Clinical features	Young, never to light smokers	Young, never to light smokers	Young, never to light smokers			
Common Testing Methods	RNAseq/ NGS, FISH, ALK-D5F3 IHC	RNA seq/NGS, FISH	RNA seq/NGS, FISH	RNA seq/NGS, FISH, Pan TRK IHC	RNA seq/NGS , FISH	RNA seq/NGS, FISH
FDA approved Therapies	Yes	Yes	Yes	Yes	Yes	Yes
Acquired resistance mechanism	Point mutations, G1202R	Point mutation G2032R	Point mutations, MET amplification	NK	NK	NK

ALK Fusions

- First generation
  - Crizotinib
- Second generation
  - Ceritinib
  - Alectinib
  - Brigatinib
- Third generation
  - Lorlatinib

Solomon, JCO 2024

ROS1 Fusions

- First generation
  - Crizotinib
  - Entrectinib
- Second generation
  - Repotrectinib

RET Fusions

- Selective inhibitors
  - Selpercatinib
  - Pralsetinib
- Phase III LIBRETTO 431
  - Selpercatinib vs 1L chemo/IO
    - RR 84% vs 65%
    - PFS 24.8m vs 11.2m (HR 0.46)

Efficacy of Selpercatinib in RET Fusion-Positive Non-Small-Cell Lung Cancer.
Drilon A et al. N Engl J Med. 2020 PMID: 32846060

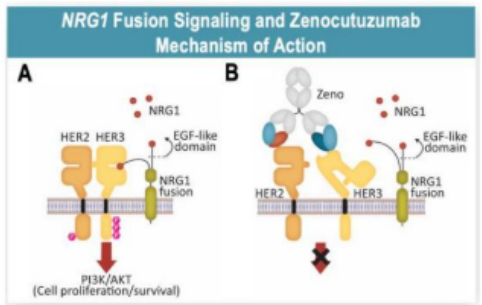
Selpercatinib in Patients With RET Fusion-Positive Non-Small-Cell Lung Cancer: Updated Safety and Efficacy From the Registrational LIBRETTO-001 Phase I/II Trial.
Drilon A et al. J Clin Oncol. 2023 PMID: 36122315

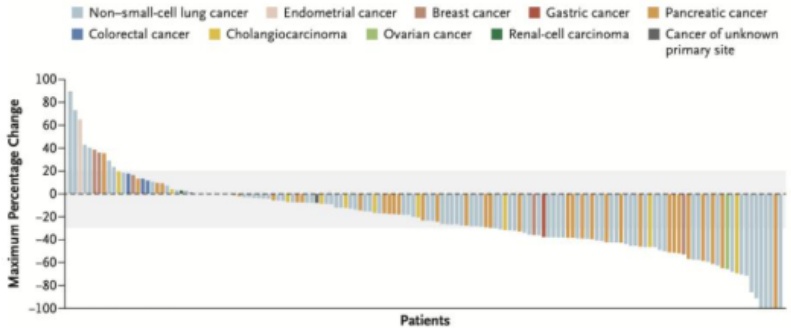
NTRK1,2,3 Fusions

- <1% of lung adenocarcinoma
- Common testing methods
  - NGS and FISH
- FDA approvals for all solid tumors harboring *NTRK* gene fusions
  - Larotrectinib (Nov 2018)
  - Entrectinib (Aug 2019)
- Second generation
  - Repotrectinib

NRG1 Fusions

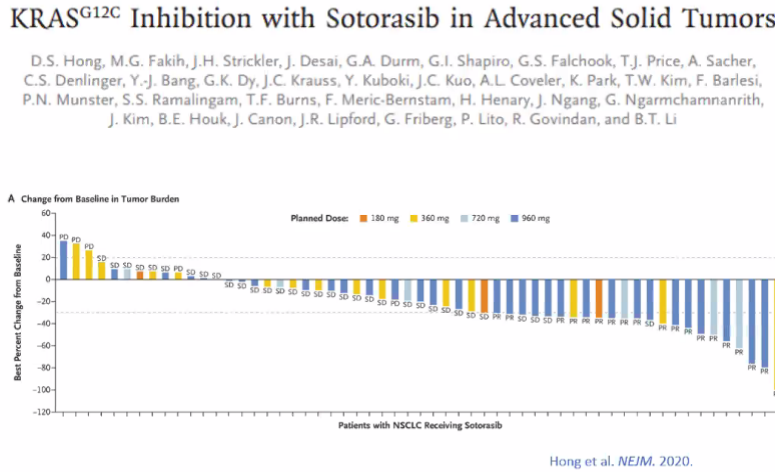
- NRG fusions present in <1% of NSCLC
- RNA-sequencing
- First approved agent
  - Zenocutuzumab
- Phase II eNRGy1 trial
  - Zenocutuzumab in NRG1+ tumors
  - RR 29%, DOR 11.1m, PFS 6.8m



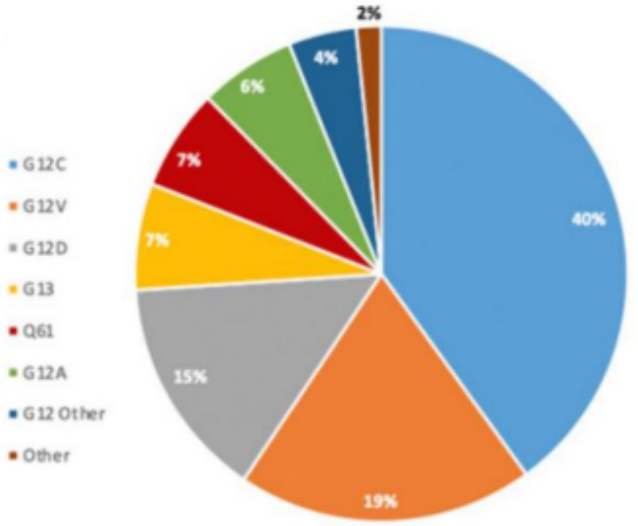


KRAS G12C Mutation

- 13% of lung adenocarcinoma
  - More common in former/current smokers
- Testing methods:
  - NGS, PCR
- Targeted therapies:
  - Sotorasib (FDA approval June 2021)
  - Adagrasib (FDA breakthrough Designation)



Hong et al. *NEJM*. 2020.



KRAS Categories	N
G12C	1,882
G12V	915
G12D	684
G13	327
Q61	313
G12A	298
G12 Other	210
Other	77
Total	4,706

KRAS G12C inhibitors for previously treated NSCLC

First generation

- Sotorasib
- Adagrasib

- Phase III CodeBreaK200
  - Sotorasib vs 2L docetaxel
  - PFS 5.6m vs 4.5m, HR 0.66
  - No significant difference in OS

Second generation inhibitor

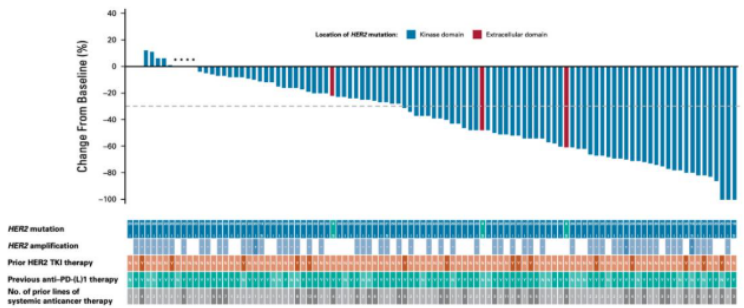
- Olomorasib, LOXO-RAS-20001 ph 1/2 trial
- NSCLC previously treated with KRAS G12Ci

MET exon 14 Mutations

- 3-4% of NSCLC
  - Adenocarcinoma,
  - Squamous cell carcinoma (rarely),
  - Sarcomatoid/pleomorphic carcinoma (9-22%)
- FDA-approved therapies:
  - Capmatinib (May 2020)
  - Tepotinib (Feb 2021)
- Testing methods:
  - DNA sequencing
  - RNA sequencing (confirms absence of exon 14)
  - MET IHC is not recommended

HER2 Mutations

- HER2 mutations present in ~2% of NSCLC
- First approved agent
  - Trastuzumab deruxtecan
- Phase II DESTINY-Lung0
  - T-DXd at 5.4mg/kg q3w
  - RR 49%, mDOR 16.8m

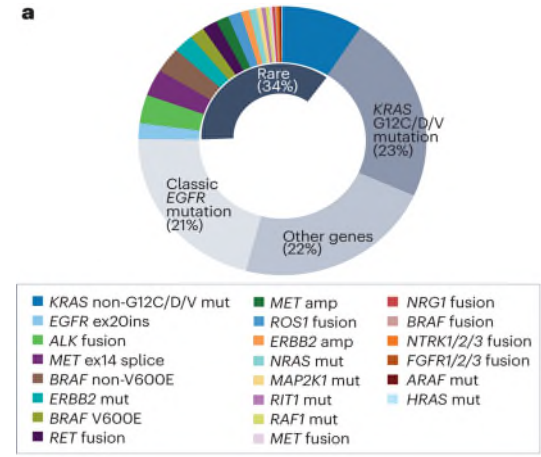


Janne, WCLC 2023; Goto, JCO 2023

BRAF V600E Mutation

- *BRAF* mutations seen in 2-3% of NSCLC
  - *BRAF* V600E seen in 1-2%
  - Strong association with smoking
- Dabrafenib + trametinib FDA approved for NSCLC harboring *BRAF* V600E (June 2017)
- Phase II PHAROS trial
  - Encorafenib + binimetinib

- **Less commonly recognized subtypes:**
  - *KRAS non-G12C, HRAS, NRAS, DDR2, LTK, RIT1, ARAF, non-BRAF^{V600E}, RAF1,* and *MAP2K1.*

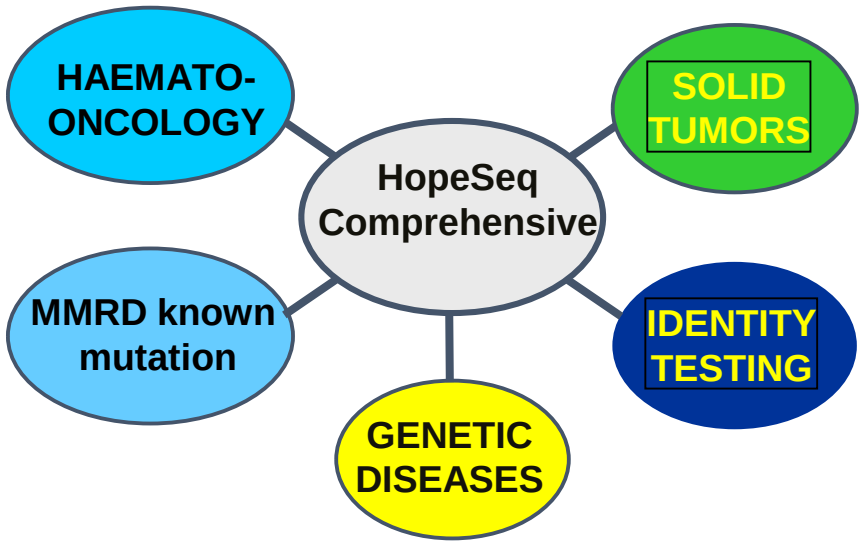


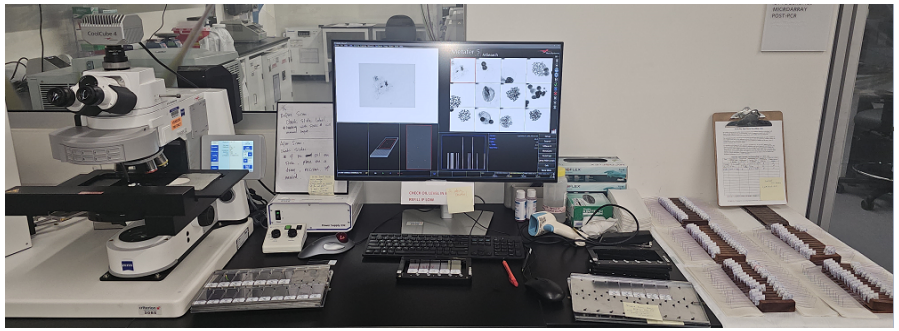
G. Harada et al, Nat Rev Clin Oncol, 2023

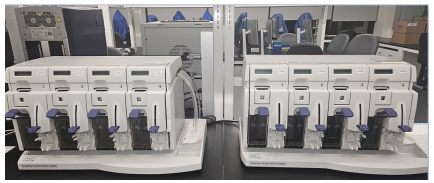
City of Hope

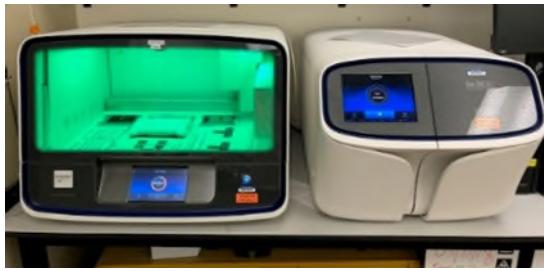
Molecular Pathology and Therapy Biomarker Division Technologies:

Clinical Molecular Genomics and Cytogenomics Laboratory with Annual volume 2024 of 35,000 Molecular and 15,000 Cytogenomics Tests





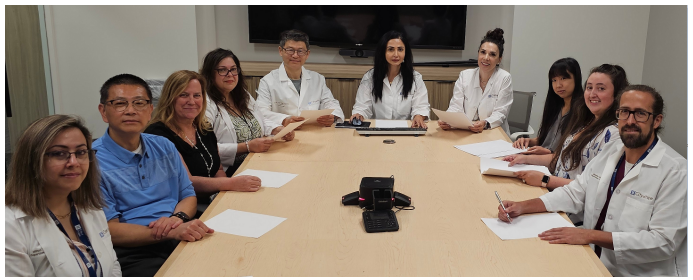


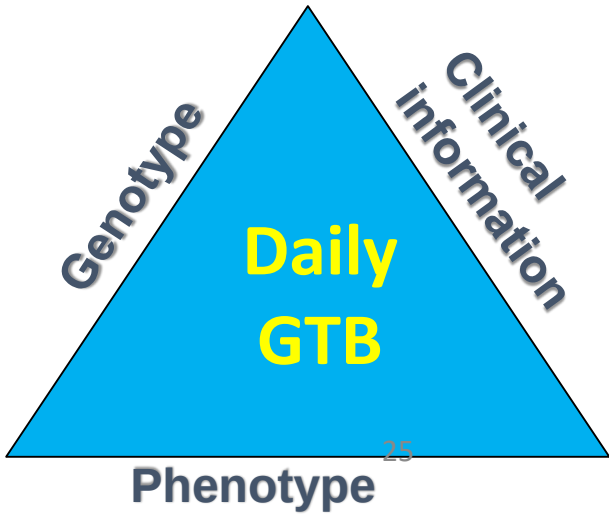


City of Hope

What's distinct City of hope NGS approach from others

- Personalized Genomic Report
- Daily Genomic Tumor Board (GTB)
- Accessibility to molecular and other pathologists by Text, EPIC, and Email
- Communication of plan for treatment or next testing plan during disease team and GTB
- Rapid Heme and Solid tumor panel with same DNA/RNA extraction
- Low tumor cellularity requirements for both DNA and RNA sequencing for Comprehensive NGS
- Fusion detection of genes included with any known and novel partners,~ >5000 rearrangements
- Immunohistochemistry (IHC) studies addition to the test, PD-L1, HER2, FOLR1, cMET, MTAP, CLND18, etc.
- High depth of coverage: Minimal residual disease detection
- Fast Turn Around Time





When to test?

- At the time of diagnosis for advance stage adenocarcinoma
- At time of recurrence or progression

- Testing of stages I,II,IIIA is encouraged (eg. ADURA trials: adjuvant Osimertinib following resection of EGFR-mutant early-stage tumors)

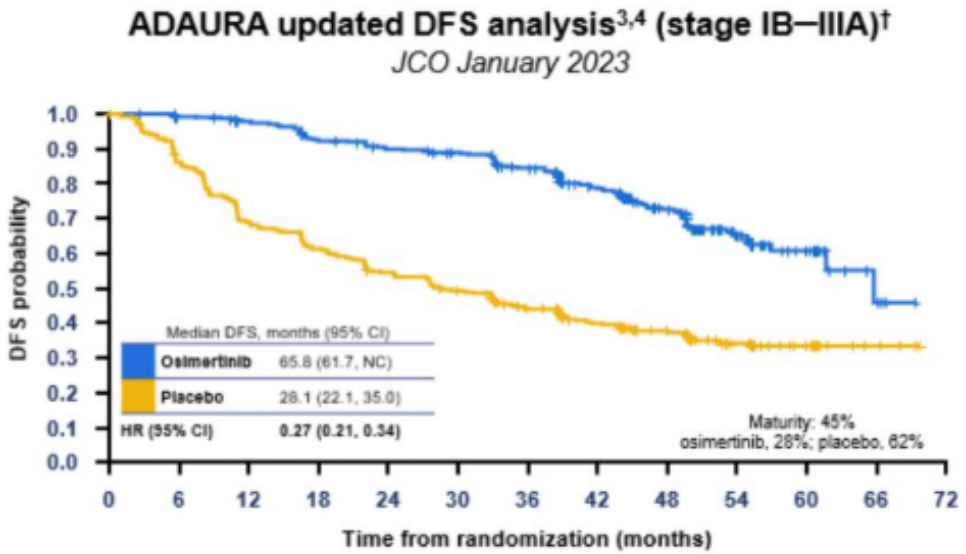
The NEW ENGLAND JOURNAL of MEDICINE

ESTABLISHED IN 1812 OCTOBER 29, 2020 VOL. 383 NO. 18

Osimertinib in Resected *EGFR*-Mutated Non–Small-Cell Lung Cancer

Yi-Long Wu, M.D., Masahiro Tsuboi, M.D., Jie He, M.D., Thomas John, Ph.D., Christian Grohe, M.D., Margarita Majem, M.D., Jonathan W. Goldman, M.D., Konstantin Laktionov, Ph.D., Sang-We Kim, M.D., Ph.D., Terufumi Kato, M.D., Huu-Vinh Vu, M.D., Ph.D., Shun Lu, M.D., Kye-Young Lee, M.D., Ph.D., Charuwan Akewanlop, M.D., Chong-Jen Yu, M.D., Ph.D., Filippo de Marinis, M.D., Laura Bonanno, M.D., Manuel Domine, M.D., Ph.D., Frances A. Shepherd, M.D., Lingmin Zeng, Ph.D., Rachel Hodge, M.Sc., Ajlan Atasoy, M.D., Yuri Rukazenkov, M.D., Ph.D., and Roy S. Herbst, M.D., Ph.D., for the ADAURA Investigators*

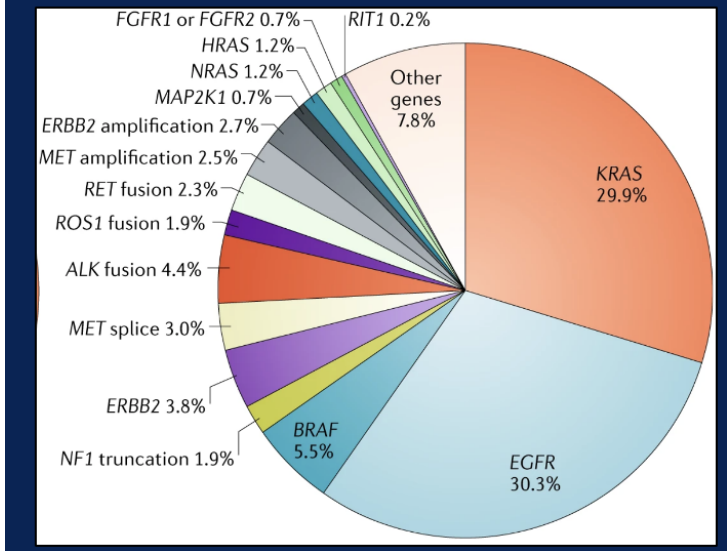
Wu et al. NEJM. 2020.



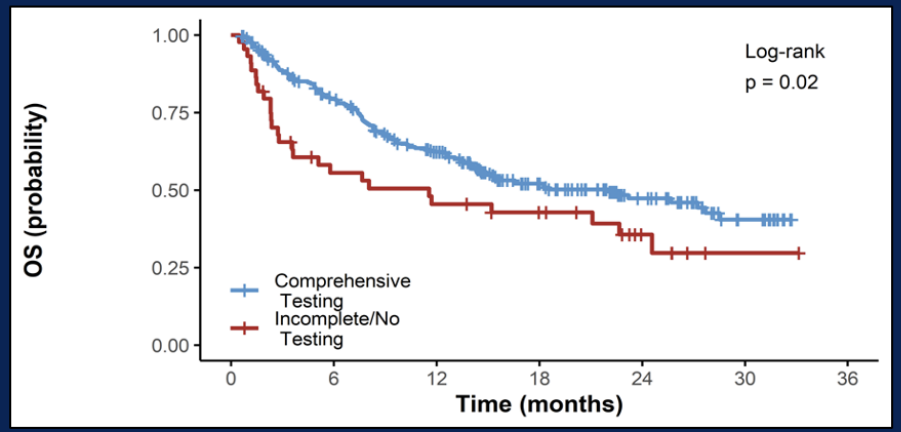
Herbst ASCO 2023

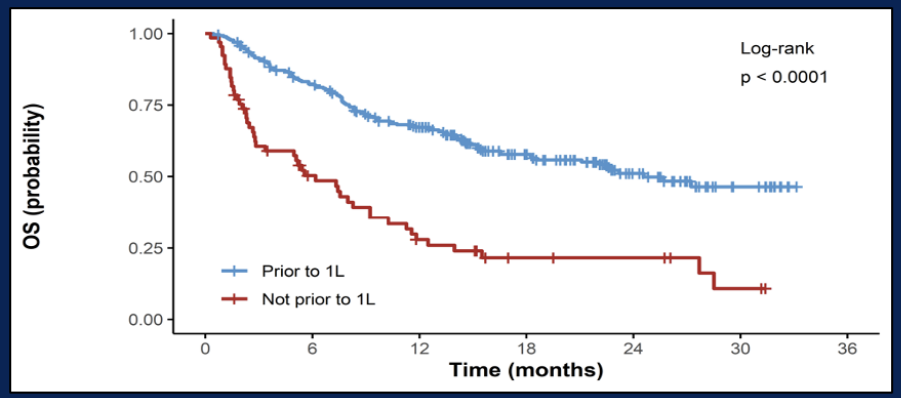
City of Hope

Personalized Therapy Relies on Comprehensive NGS, Timely Testing, and Delivery of Care

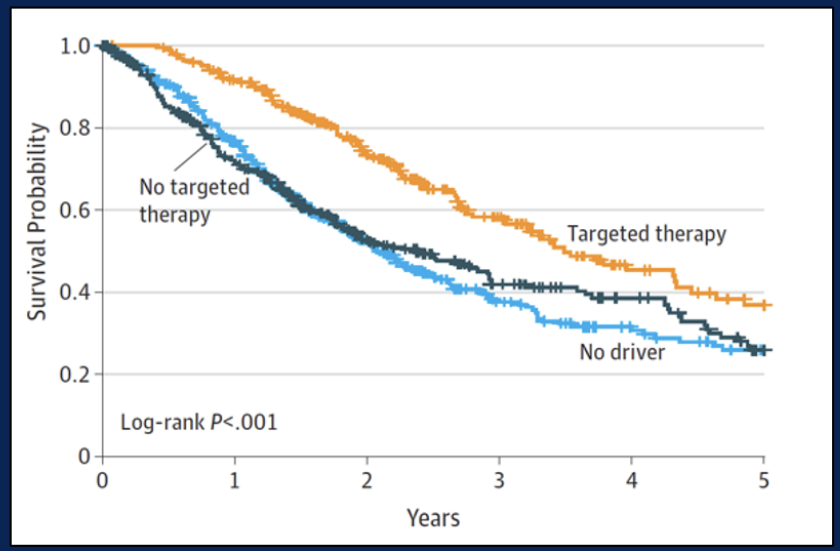


Actionable Genomic Alterations occur in ~ 50% of all Non-Sq NSCLC





Overall Survival is associated with Comprehensiveness AND Availability of NGS[1]



Survival benefit from targeted therapy is lost if targeted therapy is never delivered[2]

1. Aggarwal C et al. *JCO Precis Oncol*. 2023;7:e2300191.
2. Singal G et al. *JAMA*. 2019;321(14):1391-1399.

Future Direction: Digital Pathology and AI for Prediction of biomarkers and Therapy

- "third generation sequencing" – e.g. oxford nanopore
- Optical genomic mapping - e.g. Bionano
- Digital spatial profiling
- Digital imaging and machine learning
- Others…

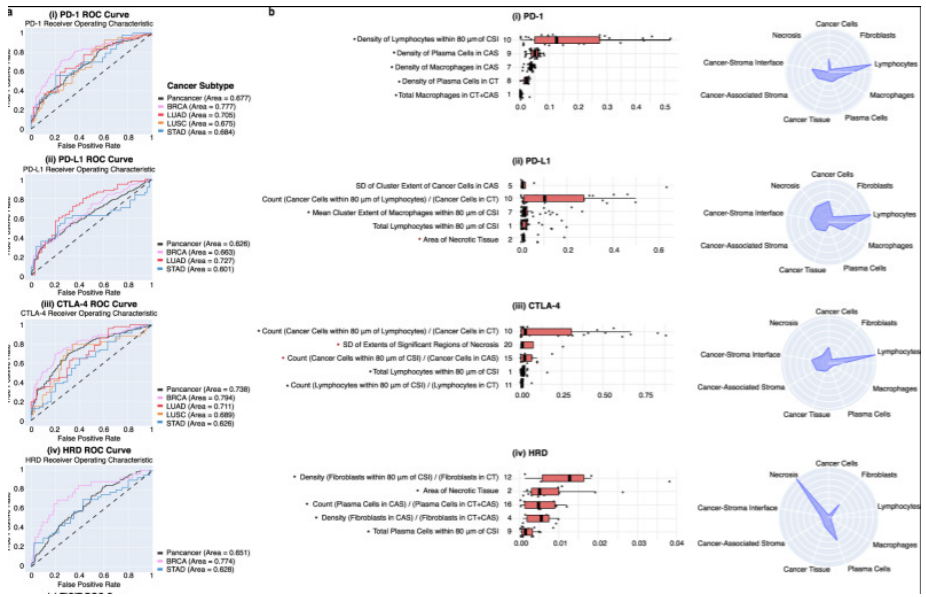
› Nat Commun. 2021 Mar 12;12(1):1613. doi: 10.1038/s41467-021-21896-9.

Human–interpretable image features derived from densely mapped cancer pathology slides predict diverse molecular phenotypes

James A Diao [# 1 2], Jason K Wang [# 1 2], Wan Fung Chui [# 1 2], Victoria Mountain [1], Sai Chowdary Gullapally [1], Ramprakash Srinivasan [1], Richard N Mitchell [2 3], Benjamin Glass [1], Sara Hoffman [1], Sudha K Rao [1], Chirag Maheshwari [1], Abhik Lahiri [1], Aaditya Prakash [1], Ryan McLoughlin [1], Jennifer K Kerner [1], Murray B Resnick [1 4], Michael C Montalto [1], Aditya Khosla [1], Ilan N Wapinski [1], Andrew H Beck [# 5], Hunter L Elliott [# 1], Amaro Taylor-Weiner [# 6]

Affiliations + expand

PMID: 33712588 PMCID: PMC7955068 DOI: 10.1038/s41467-021-21896-9



ARTICLE OPEN

Check for updates

Direct identification of *ALK* and *ROS1* fusions in non-small cell lung cancer from hematoxylin and eosin-stained slides using deep learning algorithms

Chen Mayer [1,4✉], Efrat Ofek [1,4], Danielle Even Fridrich [1], Yosse Nurit Paz-Yaacov [2] and Iris Barshack [1,3]

Review › Ann Oncol. 2024 Jan;35(1):29-65. doi: 10.1016/j.annonc.2023.10.125. Epub 2023 Oct 23.

Artificial intelligence for predictive biomarker discovery in immuno-oncology: a systematic review

A Prelaj [1], V Miskovic [2], M Zanitti [3], F Trovo [4], C Genova [5], G Viscardi [6], S E Rebuzzi [7], L Mazzeo [2], L Provenzano [8], S Kosta [3], M Favali [4], A Spagnoletti [8], L Castelo-Branco [9], J Dolezal [10], A T Pearson [10], G Lo Russo [8], C Proto [8], M Ganzinelli [8], C Giani [8], E Ambrosini [4], S Turajlic [11], L Au [12], M Koopman [13], S Delaloge [14], J N Kather [15], F de Braud [8], M C Garassino [10], G Pentheroudakis [16], C Spencer [17], A L G Pedrocchi [4]

Affiliations + expand

PMID: 37879443 DOI: 10.1016/j.annonc.2023.10.125

City of Hope