

Novel Frontiers in the Use of cDNA in Oncology

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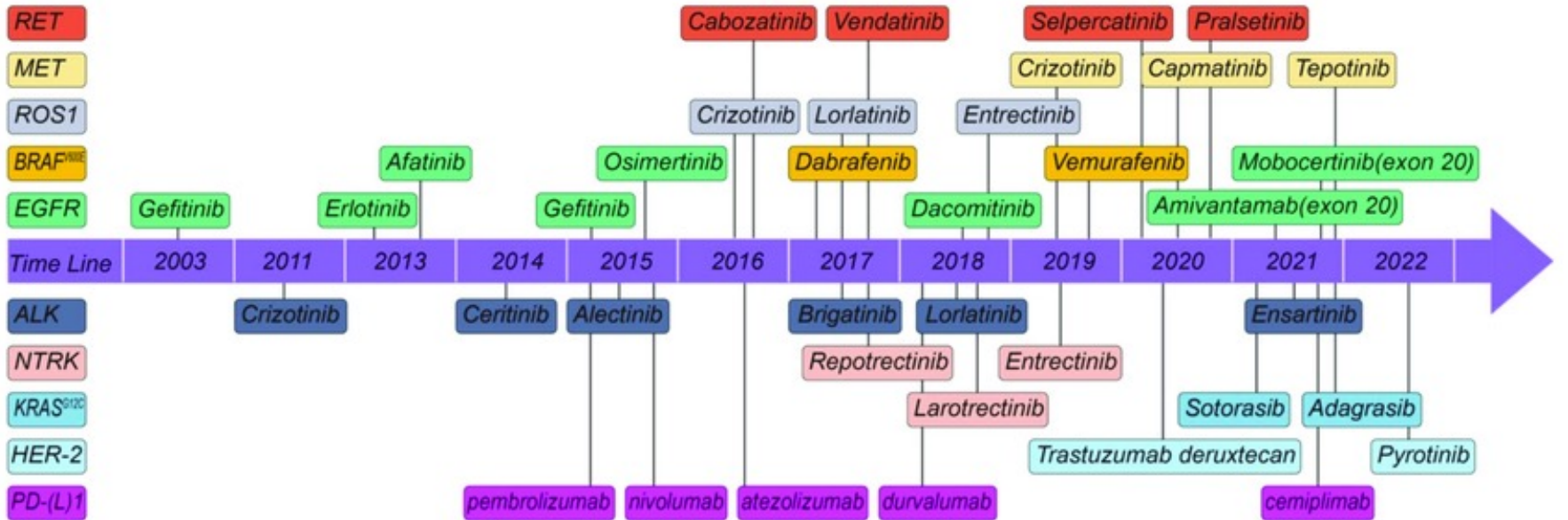


**Mount
Sinai**

*Tisch Cancer
Center*

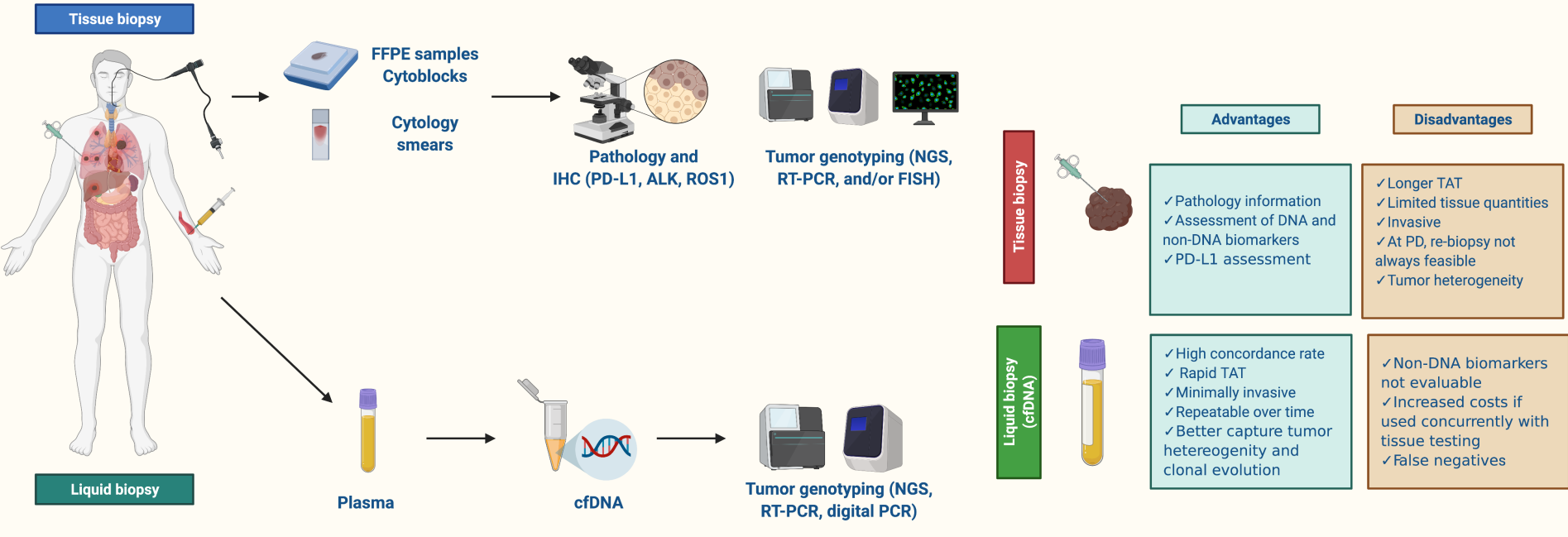


Updates in Cancer Therapies | *A Review of the 2023 ASCO & ESMO Annual Meetings*

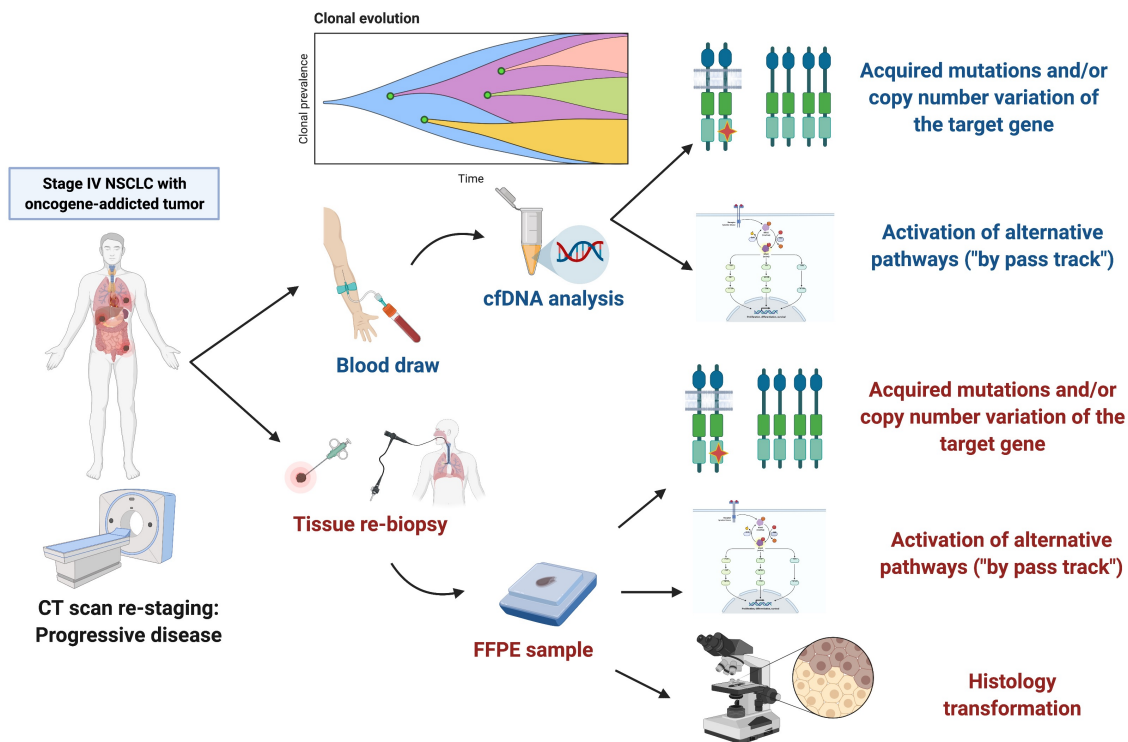


Gou et al, Cells 2022, 11, 3200

Tissue vs. Liquid biopsy



Identifying the mechanisms of acquired resistance: Tissue vs. Liquid biopsy



Main liquid biopsy techniques used



NGS-based approaches:

- ✓ High sensitivity
- ✓ Multiplex
- ✓ Gene rearrangements
- ✓ Gene amplifications



PCR-based approaches:

- ✓ Variable sensitivity
- ✓ Single gene testing
- ✓ Only for mutations

Main techniques used for tumor tissue



NGS-based approaches:

- ✓ High sensitivity
- ✓ Multiplex
- ✓ Gene rearrangements
- ✓ Gene amplifications



FISH:

- ✓ Gene rearrangements & amplifications



PCR-based approaches:

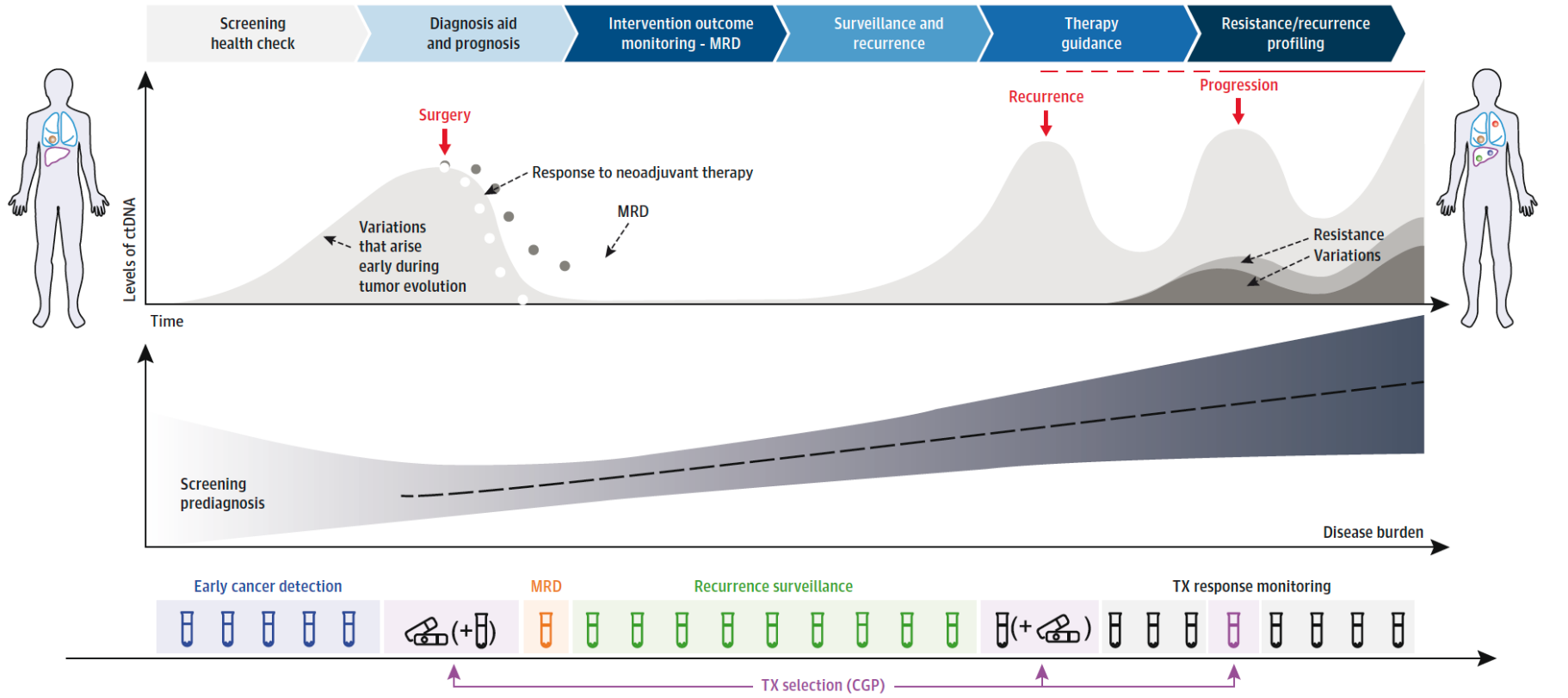
- ✓ Variable sensitivity
- ✓ Single/Multiplex gene testing
- ✓ Only for mutations



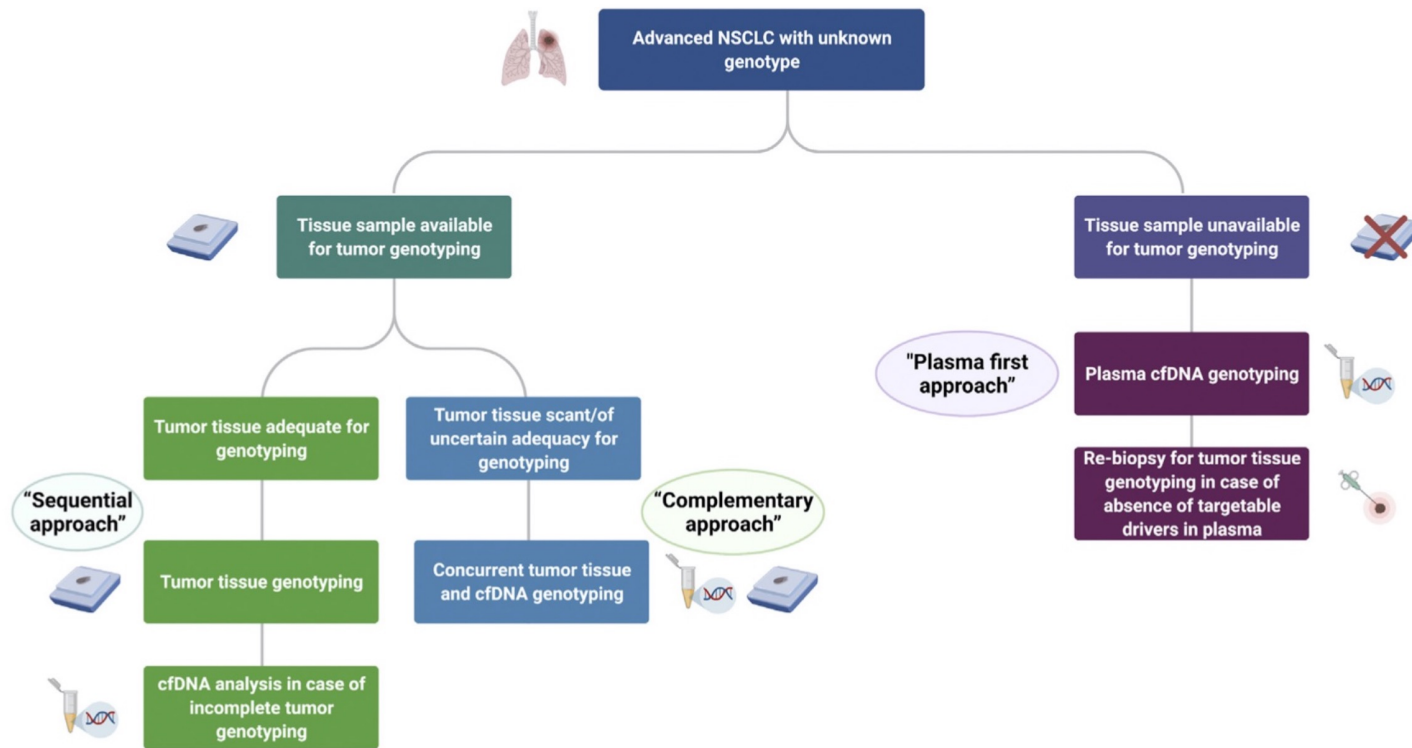
IHC:

- ✓ Protein expression

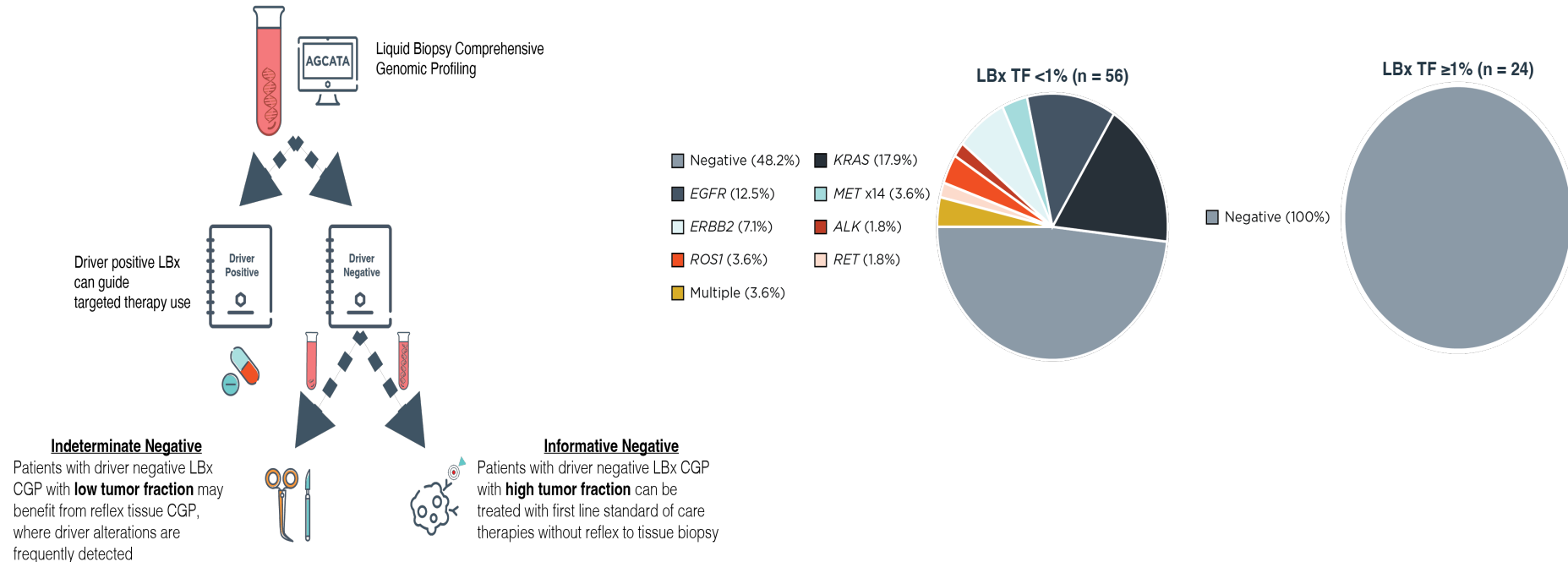
Liquid biopsy during lung cancer patient journey



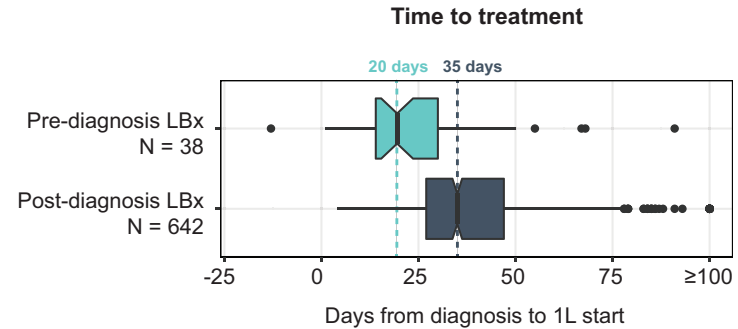
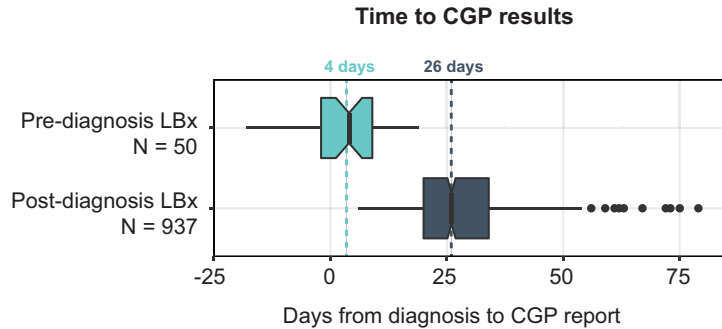
Why is important the approach we use in liquid biopsy?



Measurement of ctDNA Tumor Fraction Identifies Informative Negative Liquid Biopsy Results with Reduced Value of and Need for Tissue Confirmation



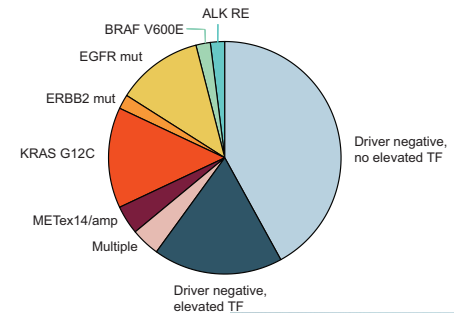
Liquid biopsy of lung cancer prior to pathological diagnosis is associated with shorter time to treatment



Average time from diagnosis to 1L for pre-diagnosis LBx orders (N = 38) was **20 days** compared to **35 days** for post-diagnosis LBx orders (N = 642) ($p < 0.001$).

Abbreviated time to CGP result return and faster therapy initiation

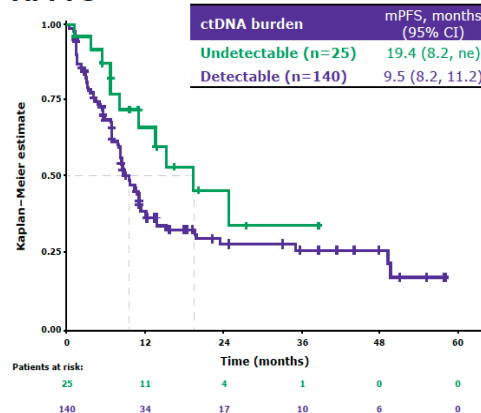
36% of early LBx samples were positive for an actionable NCCN driver



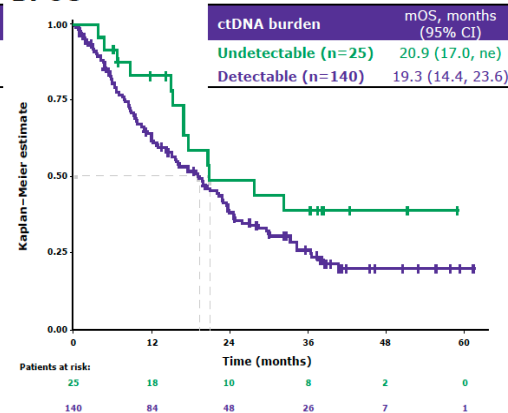
Liquid biopsies (LBx) and tissue biopsies (TBx) for identifying *MET* exon 14 skipping (*MET*ex14) in advanced NSCLC: Analyses from the Phase II VISION study of tepotinib

IRC	1L		+2L	
	T+/L- (n=52)	T+/L+ (n=42)	T+/L- (n=54)	T+/L+ (n=32)
ORR, % (95% CI)	57.7 (43.2, 71.3)	64.3 (48.0, 78.4)	44.4 (30.9, 58.6)	53.1 (34.7, 70.9)
mDOR, months (95% CI)	ne (10.4, ne)	19.4 (7.6, ne)	12.6 (5.1, 20.8)	9.9 (4.4, 15.4)
mPFS, months (95% CI)	22.1 (14.8, ne)	12.1 (7.8, 49.7)	13.8 (8.2, 24.9)	8.2 (5.5, 13.7)
mOS, months (95% CI)	32.7 (15.3, ne)	28.5 (14.2, ne)	20.8 (15.6, 32.5)	19.8 (10.0, 26.5)

A. PFS



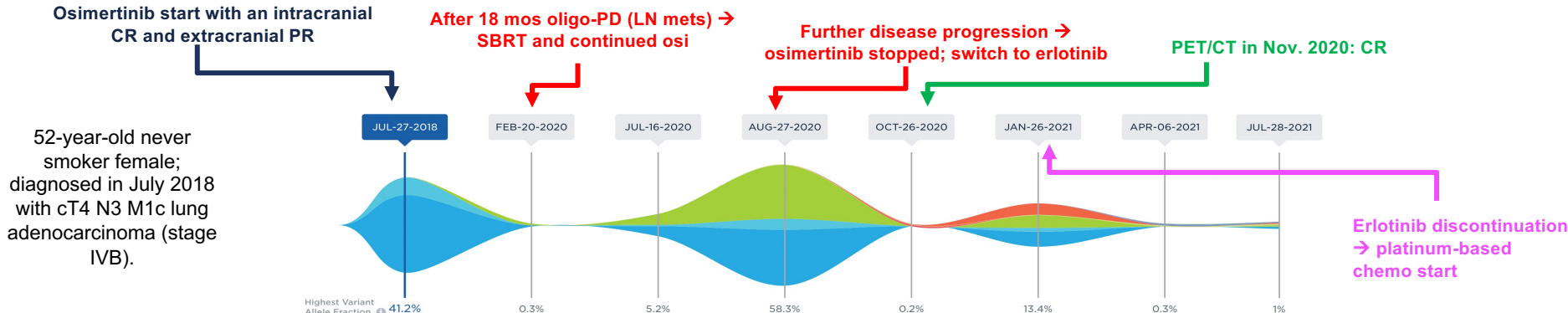
B. OS



Tepotinib had robust, durable activity in 1L and +2L, with a more favorable treatment outcome when *MET*ex14 skipping was undetectable in blood (L-)

- TBx and LBx are both suitable and complementary for detecting *MET*ex14 skipping, but LBx may select patients with a worse prognosis, potentially due to greater disease burden

Liquid biopsy can capture the dynamic evolution of resistance mechanisms to EGFR TKIs

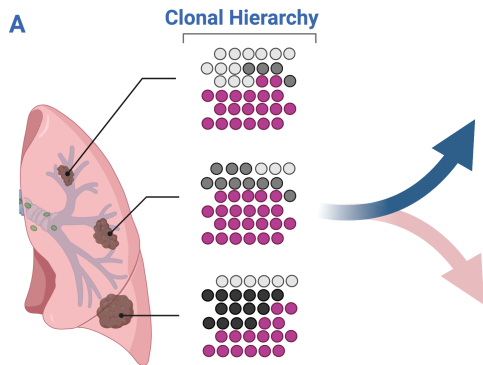


52-year-old never smoker female; diagnosed in July 2018 with cT4 N3 M1c lung adenocarcinoma (stage IVB).

Genetic Alteration	% cfDNA or amplification							
<i>EGFR</i> E746_A750del	41.2%	0.2%	4.7%	58.3%	ND	13.4%	ND	1%
<i>EGFR</i> C797S	ND	0.3%	5.2%	55.6%	ND	10.7%	ND	0.7%
<i>ARID1A</i> Q456Q	ND	ND	ND	0.2%	ND	0.2%	0.3%	0.6%
<i>EGFR</i> T790M	ND	ND	ND	ND	ND	9.6%	ND	0.4%
<i>TP53</i> C275Y	ND	ND	ND	ND	ND	ND	0.1%	0.2%
<i>ARID1A</i> F1728F	ND	ND	ND	ND	ND	ND	0.3%	0.2%
<i>TP53</i> S127F	6.5%	ND	0.4%	7.6%	ND	2.6%	ND	0.2%
<i>BRAF</i> Amplification	2.2%	ND	ND	ND	ND	ND	ND	ND
<i>CDK6</i> Amplification	2.2%	ND	ND	ND	ND	ND	ND	ND
<i>EGFR</i> Amplification	3.4%	ND	ND	4.2%	ND	ND	ND	ND
<i>NTRK2</i> L699L	-	-	-	-	0.2%	ND	ND	-
<i>EGFR</i> N338N	ND	ND	ND	ND	0.1%	ND	ND	ND
<i>FGFR1</i> V795I	ND	ND	ND	ND	ND	ND	0.1%	ND

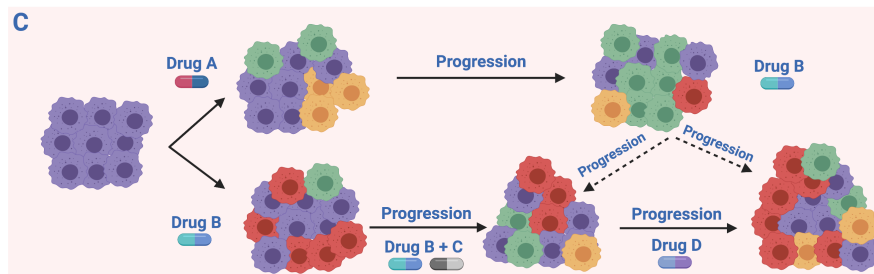
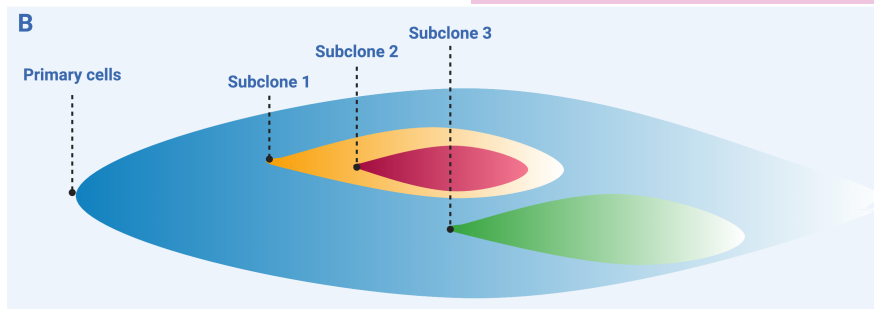
Acquired resistance is a dynamic process

Mechanisms of acquired resistance might be heterogeneous and multiple mechanisms can simultaneously occur in the same patient, reflecting the clonal heterogeneity of the tumor



Tracking the clonal evolution of the tumor over time might allow the implementation of tailored therapeutic approaches

The clonal evolution of the tumor under the selective pressure of anticancer therapies



Treatment Timeline

Acquired Resistance Is Oncogene and Drug Agnostic

Resistance Mechanisms	MET	EGFR/HER2/HER3	AXL	IGF1-R	FGFR 1/2/3	NTRK 1/2/3	KIT	RAS (KRAS, NRAS)	BRAF	MAP2K1
	EGFR	EGFR	EGFR	ALK	EGFR	EGFR	ALK	EGFR	EGFR	ALK
	ALK	ALK	ALK				ROS1	ALK	ALK	BRAF
Therapeutic Targets	NTRK	ROS1	RET					NTRK	NTRK	NTRK
		RET	BRAF					ROS1		
		BRAF						RET		

TUMOR TYPE: Lung adenocarcinoma COUNTRY CODE: TW REPORT DATE: 28 July 2021 ORDER TEST #: ORD-147554-01

PATIENT: _____

DISEASE: Lung adenocarcinoma

NAME: _____

DATE OF BIRTH: _____

SEX: _____

MEDICAL RECORD #: _____

PHYSICIAN: _____

ORDERING PHYSICIAN: Su, Wu-Chou

SPECIMEN: _____

DATE OF COLLECTION: 19 July 2021

SEQUENCING DEPTH (2000X): _____

Biomarker Findings
 Blood Tumor Mutational Burden - 3 Muts/Mb
 Microsatellite status - MSI-High Not Detected
 Tumor Fraction - 25%

Genomic Findings	VAF (%)
EGFR L858R	20
EGFR T790M	15
EGFR amplification	NA
TP53 Q192*	4
BRCA2	1
DNMT3A	1.5

9 Therapies with Clinical Benefit 4 Therapies with Lack of Response 20 Clinical Trials

A hypermutable phenotype caused by defective DNA mismatch repair

The total number of somatic variations per coding area of a tumor genome

Tumor fraction can be an indicator of the robustness of the report

The number of times each DNA fragment is read during sequencing; the smaller the panel, the greater the depth

The approximate percentage of ctDNA present in a ctDNA sample; take into consideration when interpreting VAFs

Follow-up germline testing may be required to distinguish between germline and somatic findings; considered more likely to be germline if VAF approximately 50% (the low VAF represented here suggests a subclonal somatic mutation)*

SNVs A single nucleotide change in DNA

InDels Insertion and/or deletion of nucleotides into/from DNA

CNAs Increase or loss in the number of copies of a particular gene

REs Movement of DNA sequences across the genome that may lead to gene fusions

BIOMARKER FINDINGS

Blood Tumor Mutational Burden-3 Muts/Mb

10 Trials

Microsatellite status: MSI-high not detected

Tumor fraction, 25%

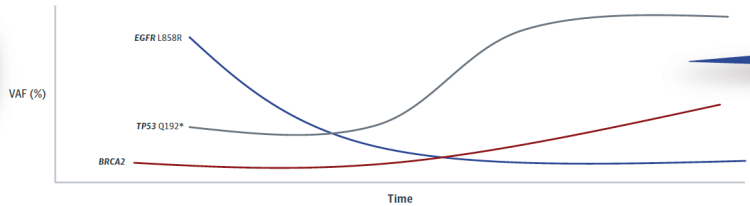
MSI-High not detected.
No evidence of MSI in this sample

Tumor fraction is an estimate of the percentage of ctDNA present in a ctDNA sample based on observed aneuploid instability.

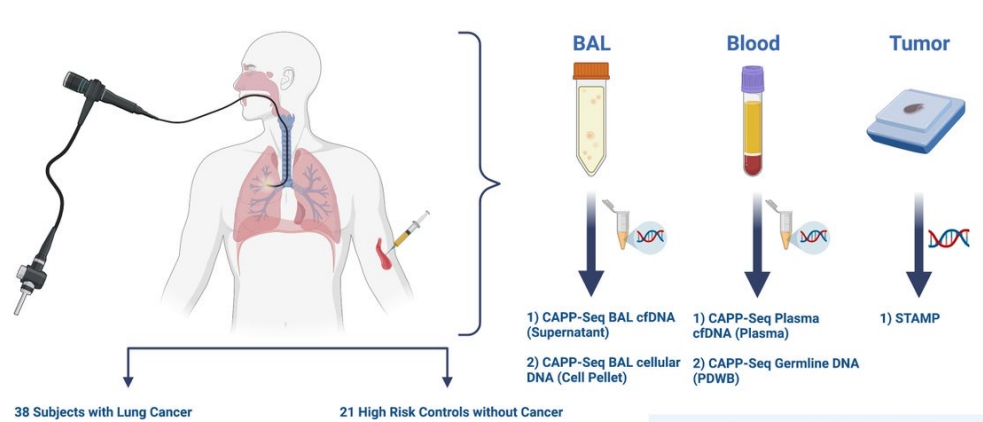
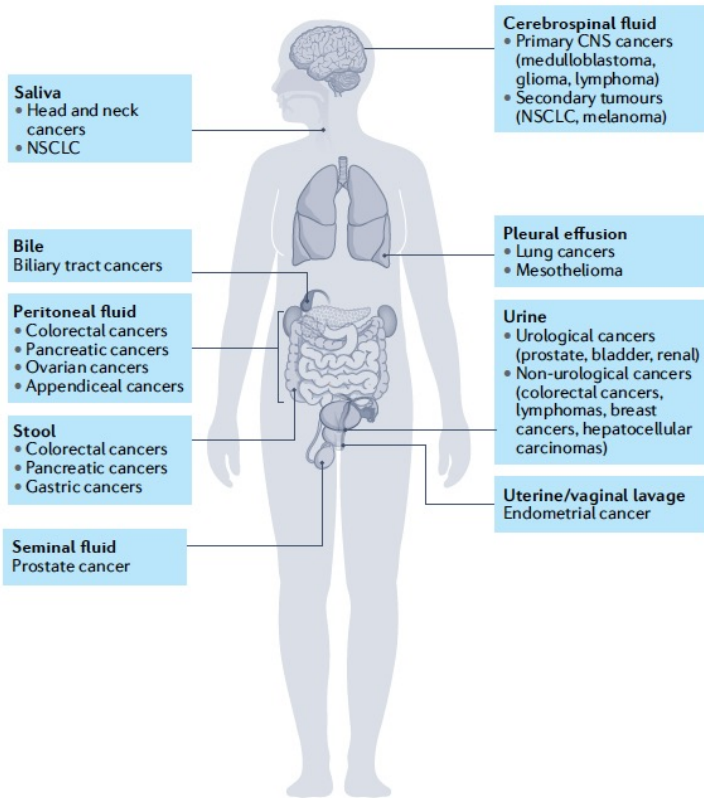
Some ctDNA reports will have therapy recommendations for patients based on the genomic findings

CHIP: an age-related source of biological noise, due to hematopoietic cell variations that can falsely appear as ctDNA variations

BREADTH OF COVERAGE
 The number of genes sequenced (all reports will usually have a full list of genes sequenced; the more genes covered, the lower the depth)



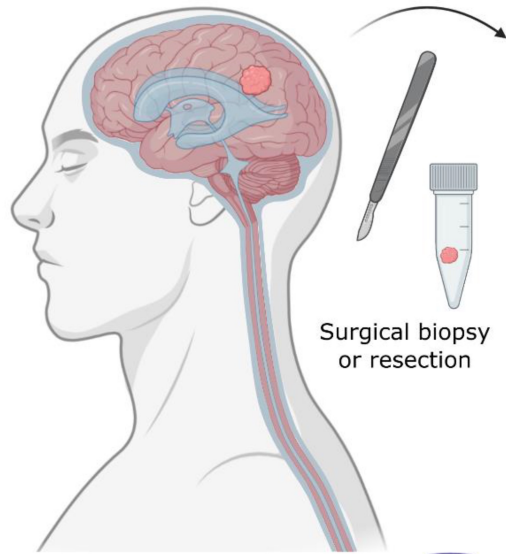
Non-blood sources for liquid biopsy



Hybrid-capture, targeted deep sequencing of lung cancer mutational burden in cell-free BAL fluid identifies more tumor-derived mutations with increased allele frequencies compared with plasma cell-free DNA.

Rolfo, Malapelle, Russo, *Cancer Res* (2022) 82 (16): 2826–2828

Nair et al (M. Diehn) *Cancer Res* 2022;82:2838–47



Solid biopsy (tumour specimen)

Advantages

Allow histological diagnosis

Limitations

Very invasive and risky procedure

Sometimes not feasible due to tumour anatomical location

Not representative of tumour heterogeneity
Static snapshot

Surgical biopsy
or resection

Liquid biopsy (CSF ctDNA)

Advantages

Less-invasive and easier to obtain than a tumour biopsy

CSF obtained as SOC for some patients

Concordance with tissue characterisation

Representative of intratumour and interlesion heterogeneity

Longitudinal real-time monitoring

Limitations

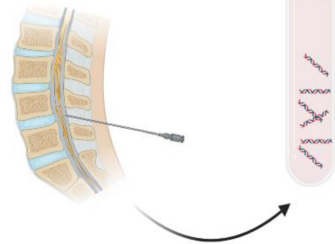
No histological characterisation

Lack of standardisation

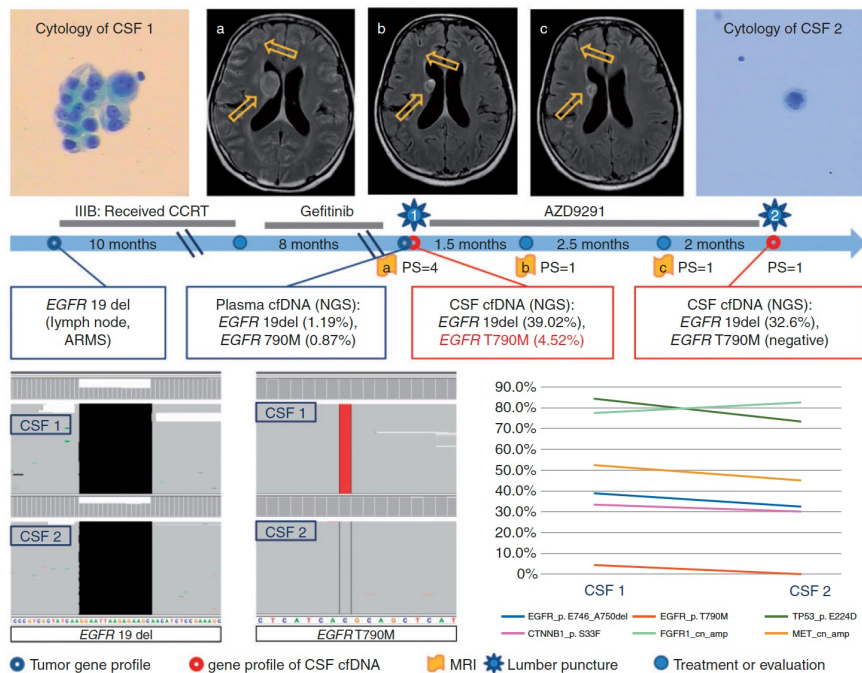
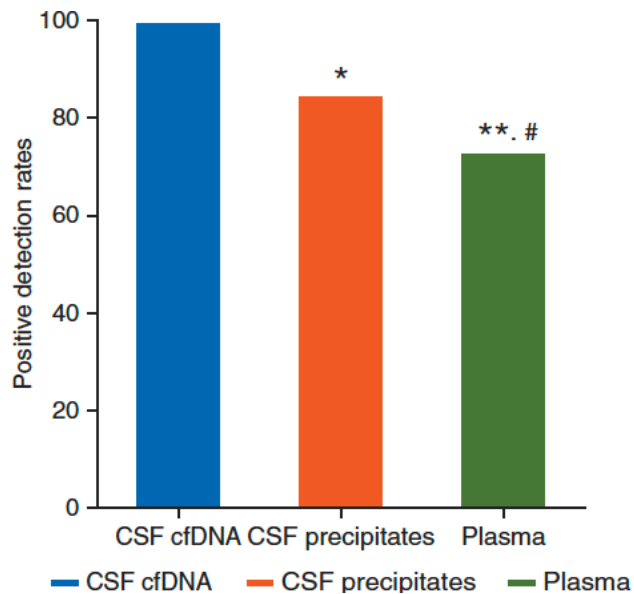
Contraindications for lumbar puncture

Limited sensitivity

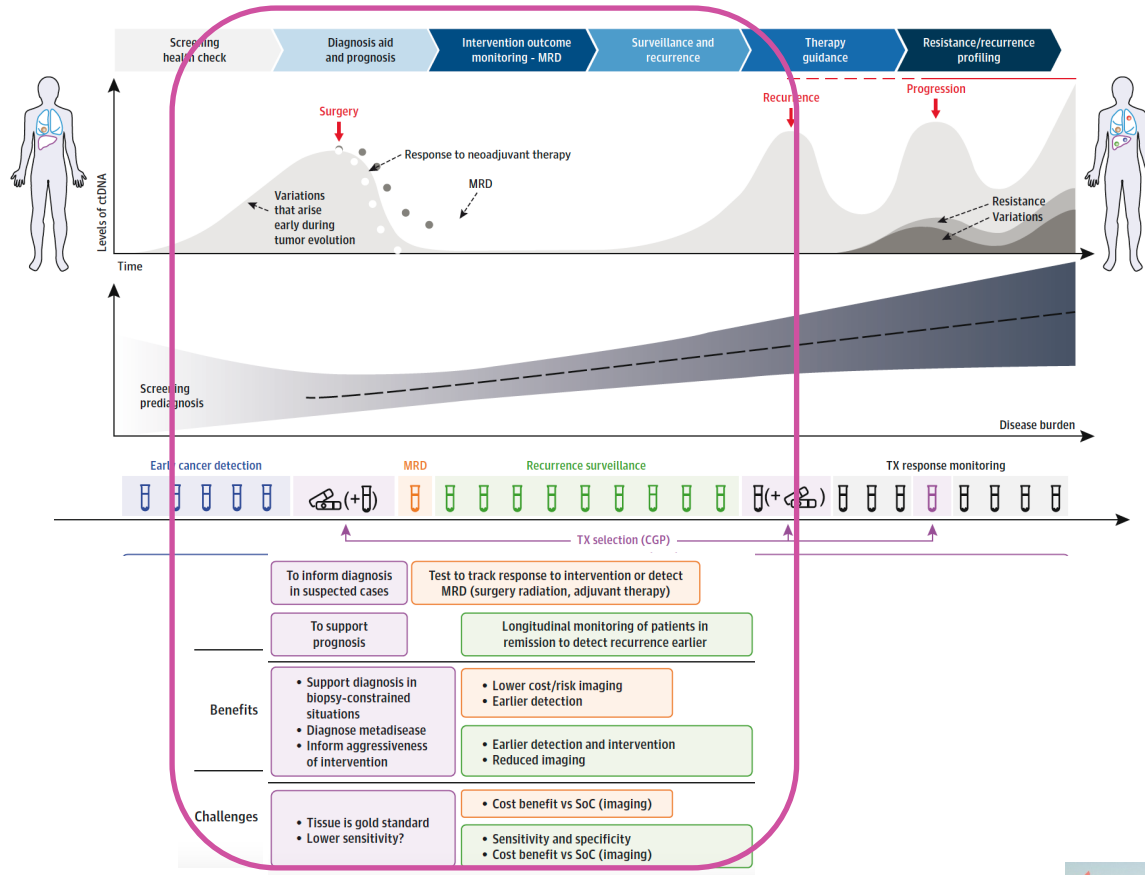
Lumbar puncture



CSF for EGFR mutations detection in patients with leptomeningeal metastases



Liquid biopsy during lung cancer patient journey



Retrospective Data From ~900 NSCLC Patients demonstrate that pre- and post-treatment MRD is a strongly prognostic biomarker

Study	N	Stage	Treatment(s)	ctDNA assay
Chaudhuri <i>Cancer Discov</i> 2017	37	IB-IIIIB	RT and/or surgery +/- chemo	CAPP-Seq
Abbosh <i>Nature</i> 2017	24	IA-IIIIB	Surgery +/- chemo	Natera
Chen <i>CCR</i> 2019	25	I-III	Surgery +/- chemo	cSMART
Moding <i>Cancer Discov</i> 2020	48	IIB-IIIIB	chemoRT +/- IO	CAPP-Seq
Abbosh <i>AACR</i> 2020	88	I-III	Surgery +/- chemo	ArcherDx
Zviran <i>Nat Med</i> 2020	22	I-III	Surgery +/- chemo	MRDetect
Waldeck <i>Mol Oncol</i> 2021	16	IA-IIIIB	Surgery +/- chemo, RT	Custom NGS
Xia <i>CCR</i> 2021	329	I-III	Surgery +/- chemo	Custom NGS
Gale <i>Ann Oncol</i> 2022	59	I-III	RT and/or surgery +/- chemo	Inivata
Zhang <i>Cancer Discov</i> 2022	245	I-III	Surgery +/- chemo, IO, TKI	Custom NGS

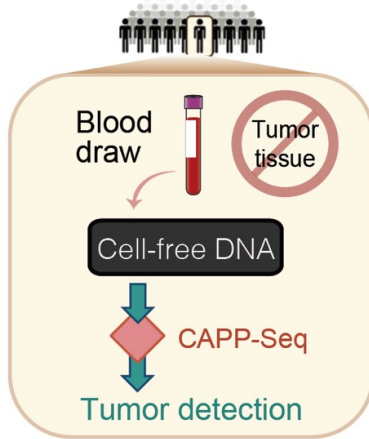
***Several studies including different population, treatment and assays

Slide Courtesy Dr. Natasha Leighl

Christian Rolfo, Mount Sinai, NY

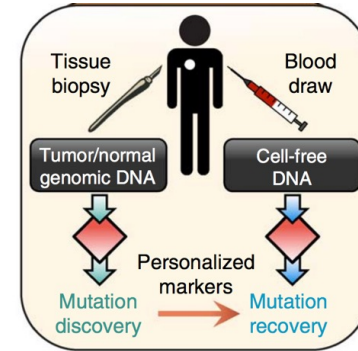
Different types of ctDNA MRD Assays

Tumor-naive



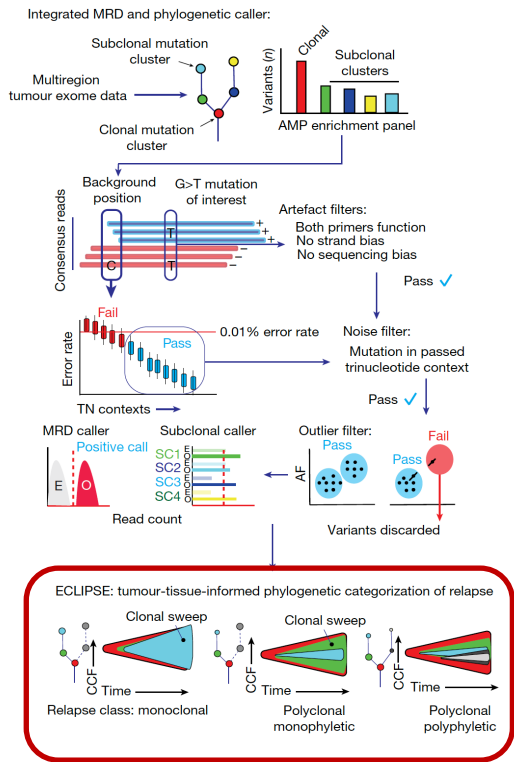
- Genotyping with no knowledge of tumor mutations (“off the shelf”)
- Faster, less expensive
- Limit of detection ~0.1%

Tumor-informed

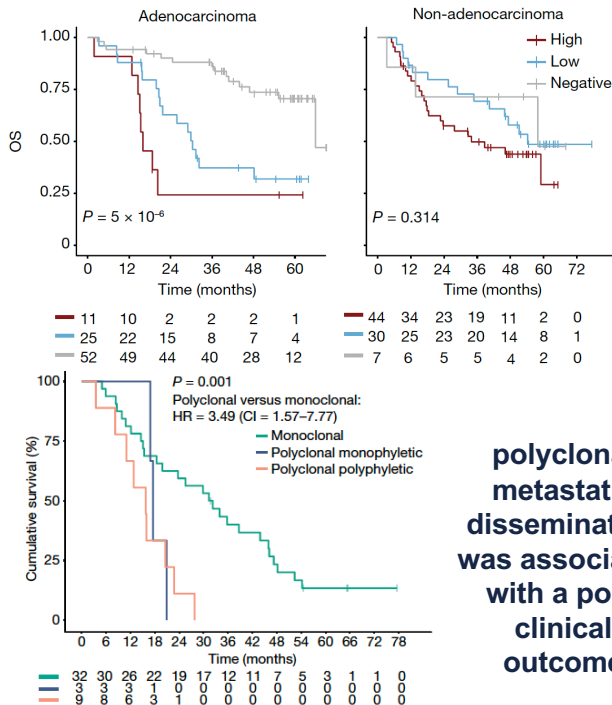


- Tracking multiple known mutations (bespoke or personalized)
- Requires tumor tissue, time, \$\$
- Limit of detection ~0.01%

Tracking early lung cancer metastatic dissemination in TRACERx using ctDNA (WES)

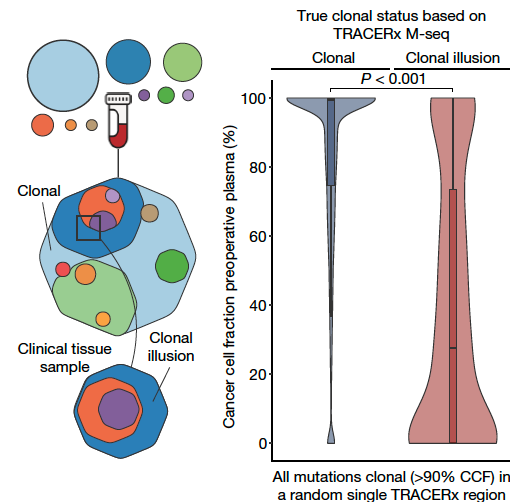


ctDNA can identify MRD and predict survival



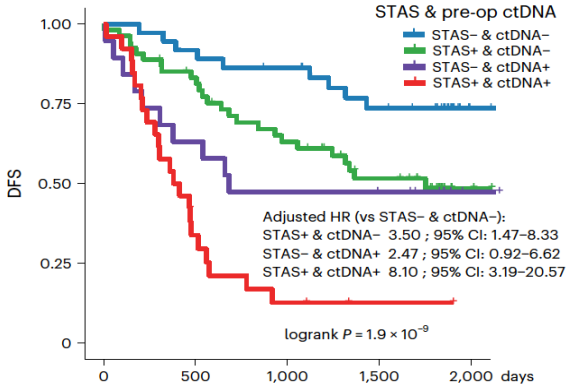
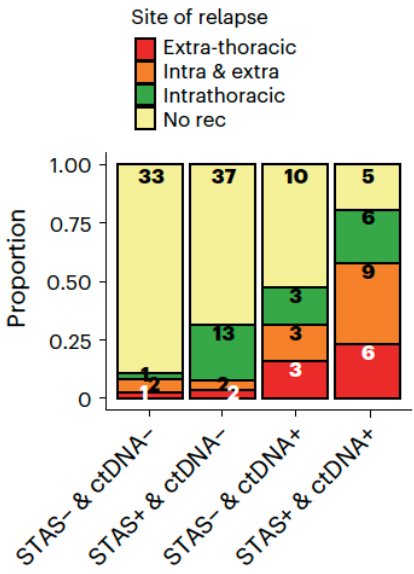
polyclonal metastatic dissemination was associated with a poor clinical outcome

LB can overcome sampling bias from a single tissue sample



Integration of liquid biopsy and pathology: The TRACERx study

STAS: Spread Through Air Spaces

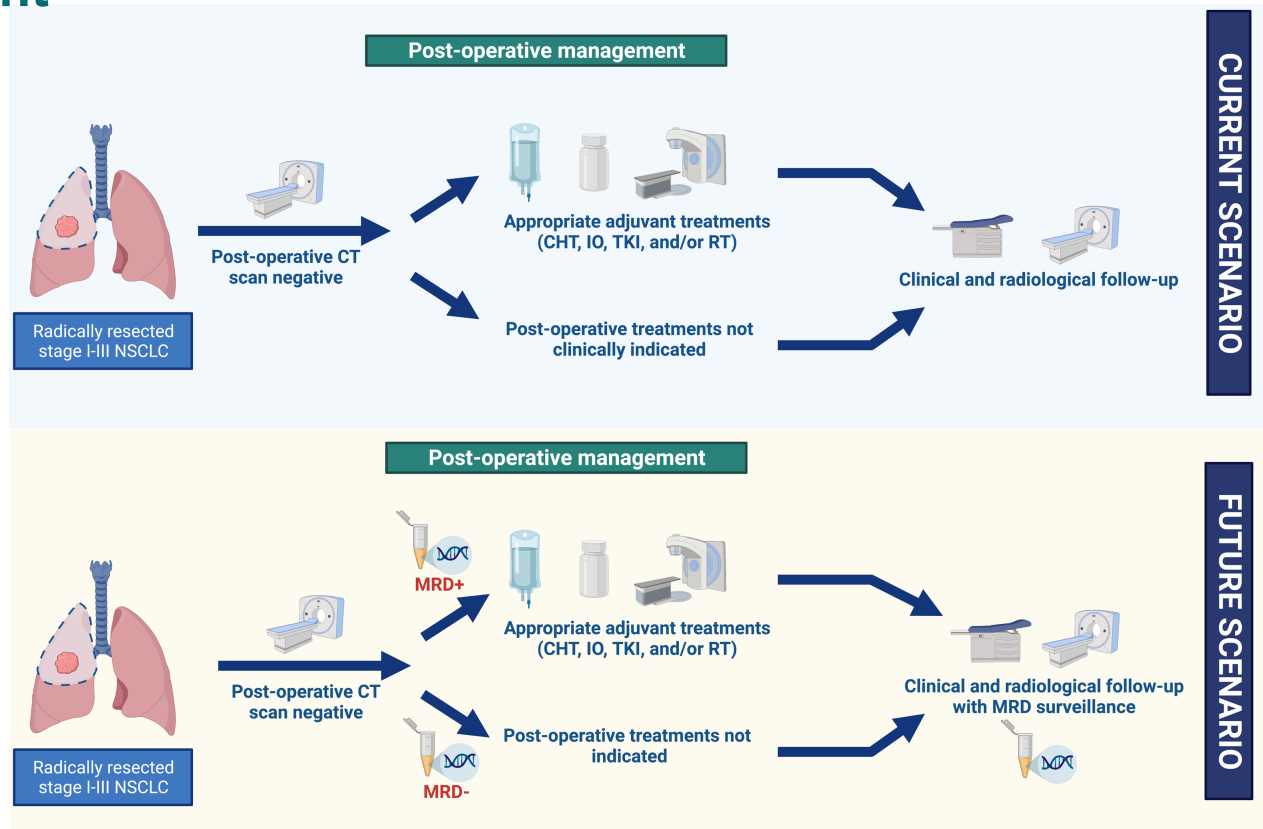


	STAS- & ctDNA-	STAS+ & ctDNA-	STAS- & ctDNA+	STAS+ & ctDNA+
STAS- & ctDNA-	37	33	30	23
STAS+ & ctDNA-	54	43	31	21
STAS- & ctDNA+	19	12	9	8
STAS+ & ctDNA+	26	8	3	1

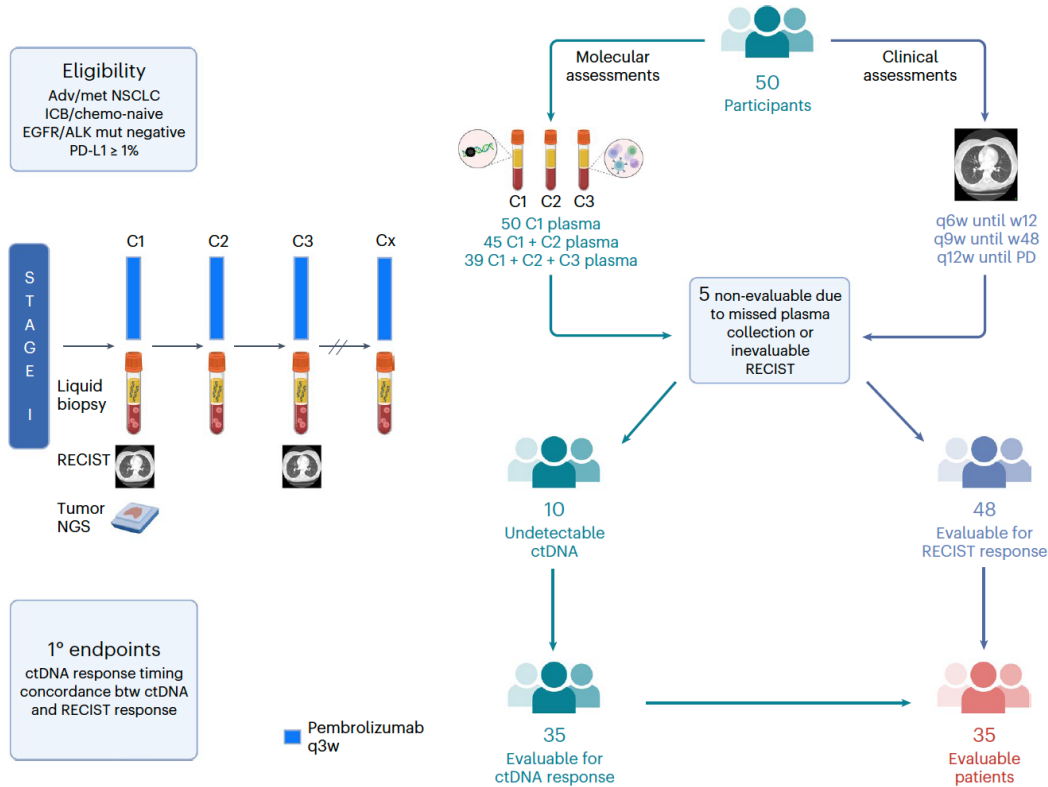
High-grade patterns	Micropapillary	Solid/cribriform
Pathological features	STAS+	Necrosis+ High Ki-67
Genomic features	High clonal diversity (lack of large recent clonal expansion)	Pre-op ctDNA+ High CIN Low clonal diversity (presence of large recent clonal expansion)
Relapse site	Intra-thoracic	Extra-thoracic

“...These data provide insights into the relationship between LUAD morphology, the underlying evolutionary genomic landscape, and clinical and anatomical relapse risk...”

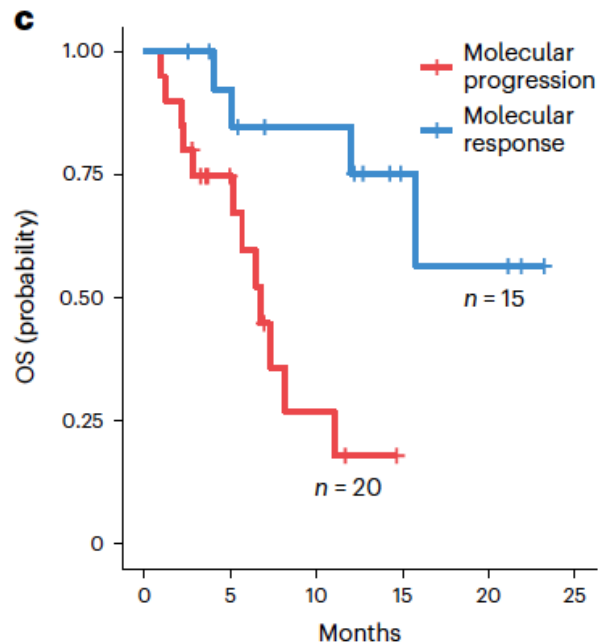
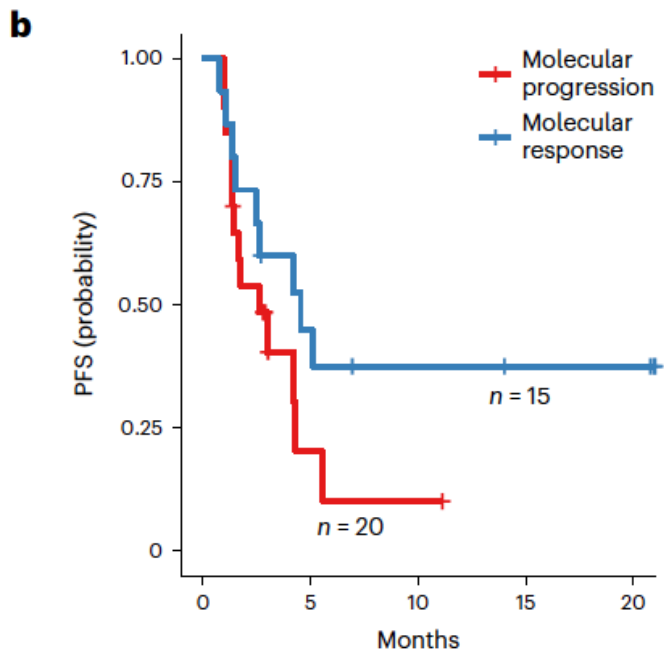
Liquid biopsy can potentially revolutionize post-operative management



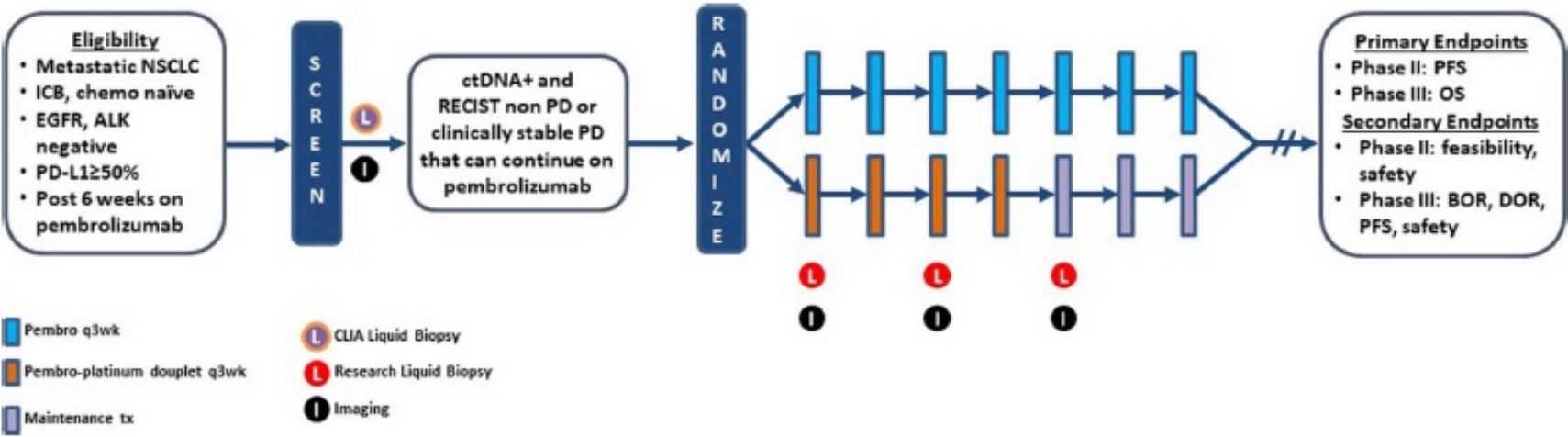
BR.36 study design



Molecular response and IO outcomes



Trial schema for the interventional second stage of the BR.36 study.



ADMIRO Trial

Principal investigators: Besse & Remon

- Stage II NSCLC (8th TNM)
- ECOG PS 0-1
- EGFR-negative
- PET-CT and brain MRI/CT

Surgery

Tumour uninformed assay

Primary endpoint: DFS at 2 years (ctDNA-guided versus pathologic-guided)

Secondary endpoint:

- DFS ctDNA positive versus negative in ctDNA guided arm
- MRD-free interval in ctDNA negative
- Overall survival

Stratification:

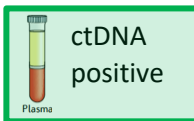
- Histology: squamous versus non-squamous
- Nodal status: N0 versus N1
- Site

+14 to +60 days

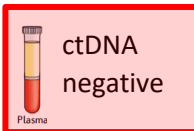
ctDNA
post-surgery
(14–42 days)

R
1:1

ctDNA
guided



ctDNA
positive

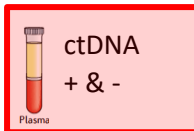


ctDNA
negative

Adjuvant CT,
4 cycles, q3w
+/- ICB according to
SoC

Observation

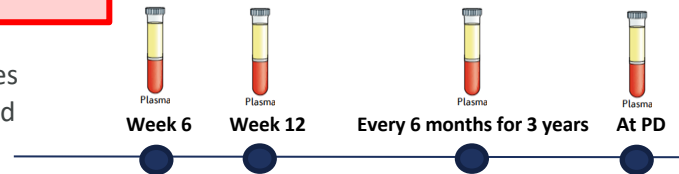
Pathologic
guided



ctDNA
+ & -

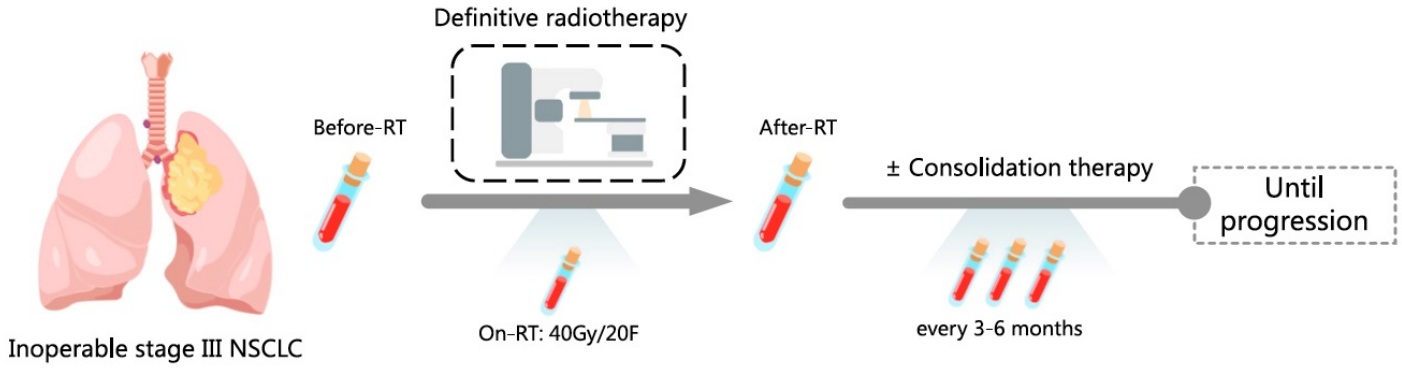
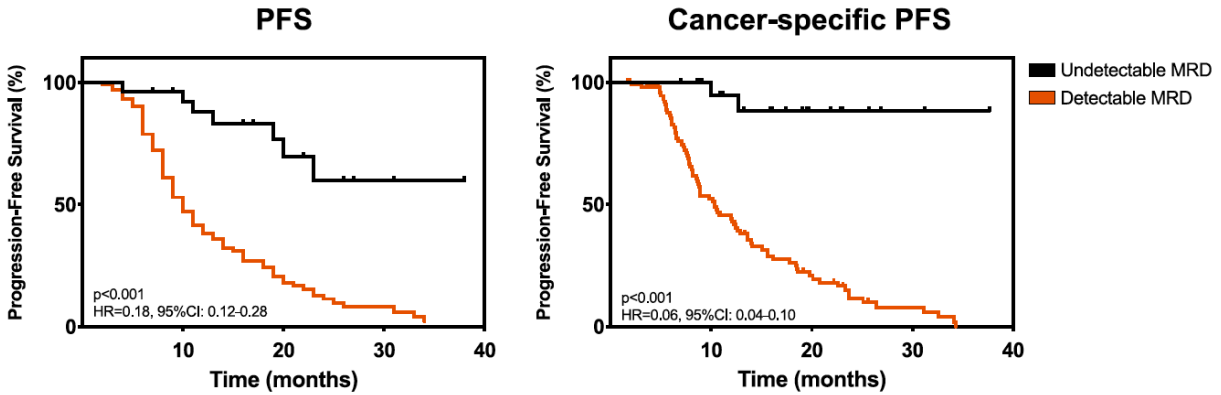
Standard management

These blood samples
will be collected and
stored

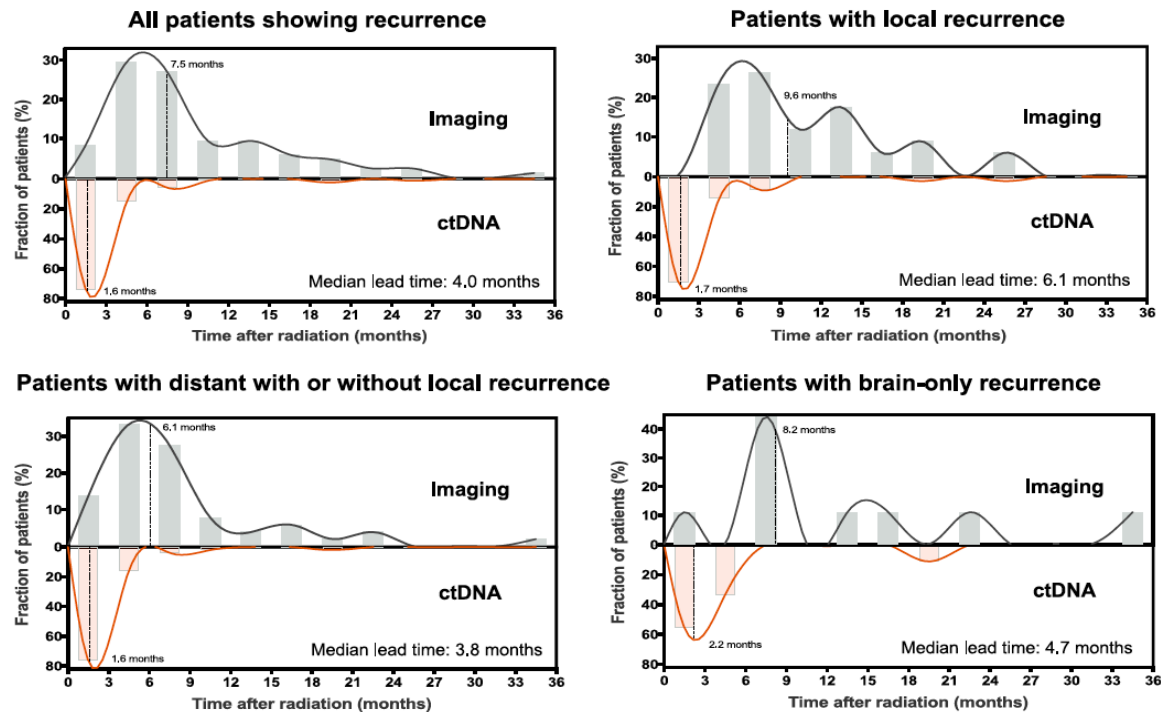


Information provided by Dr Natasha Leighl and Dr Jordi Remon.

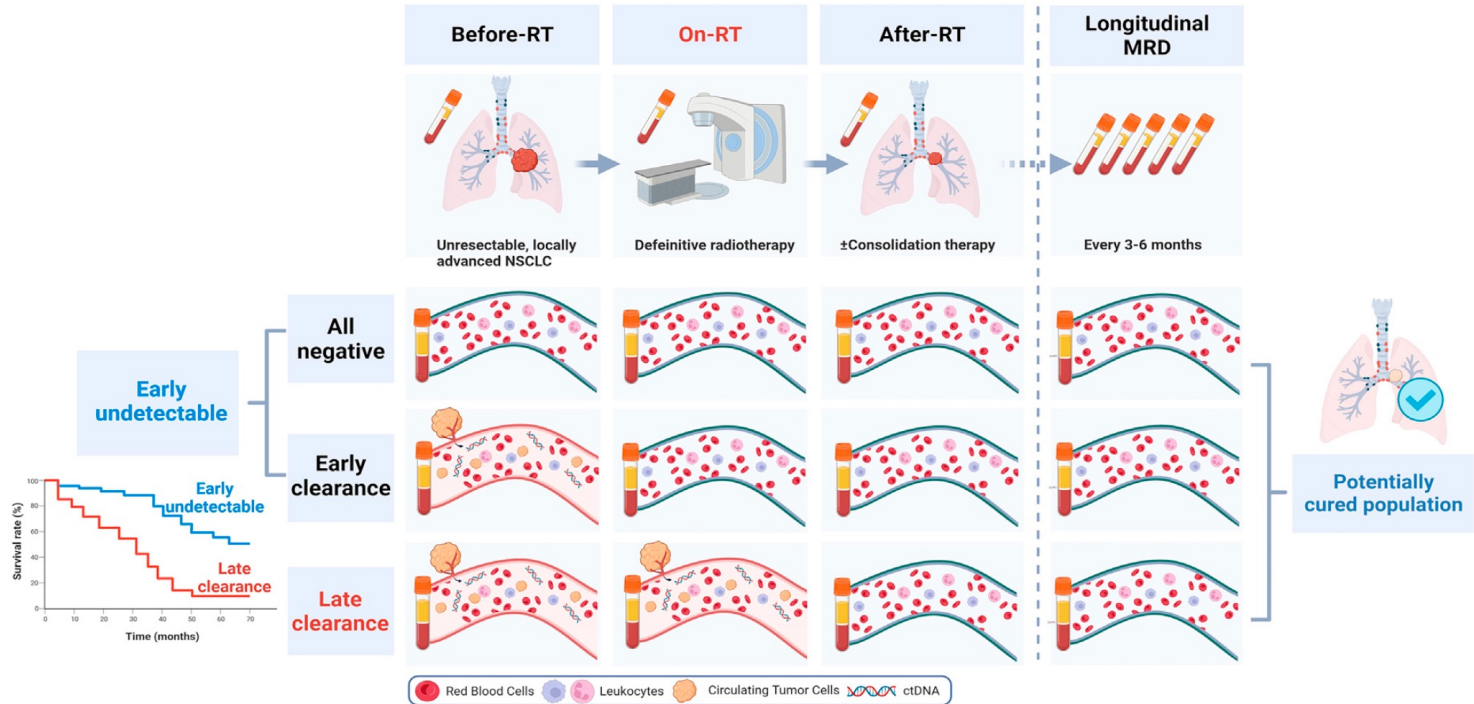
Dynamic circulating tumor DNA during chemoradiotherapy predicts clinical outcomes for LA-NSCLC patients



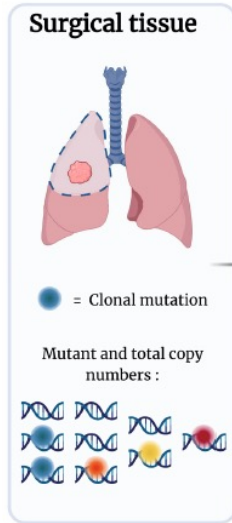
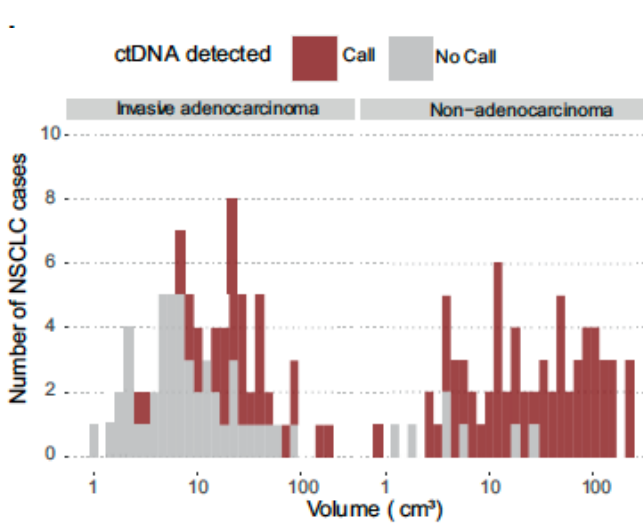
Longitudinal MRD detection rate of patients with different progression patterns



The growing significance of longitudinal MRD in NSCLC clinical practice



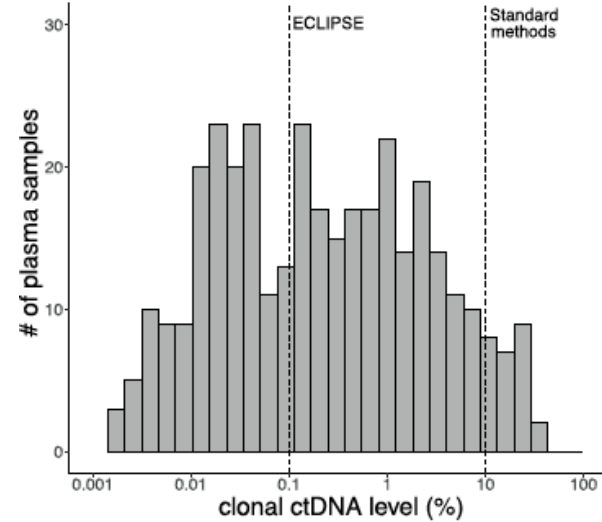
Detecting MRD via Subclonal Populations and AI



ECLIPSE

(Extraction of Clonality from Lliquid bioPSy)

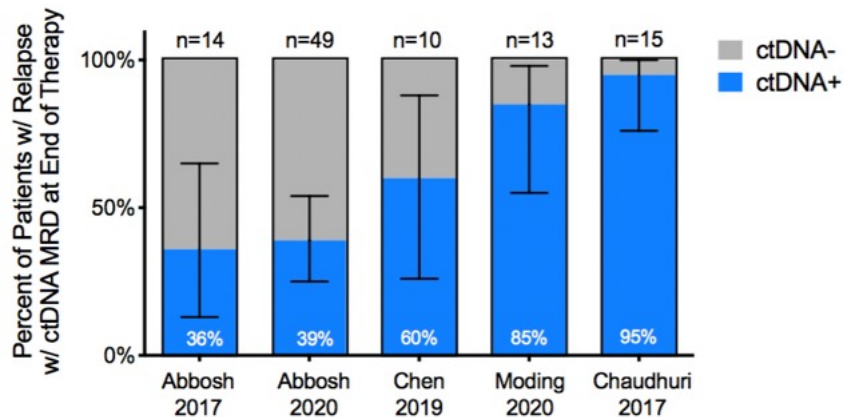
- Background de-noising
- Sample purity calculation
- Clone quality filtering
- High confidence clone detection
- Cancer Cell Fraction (CCF) estimates
- CCF power calculations



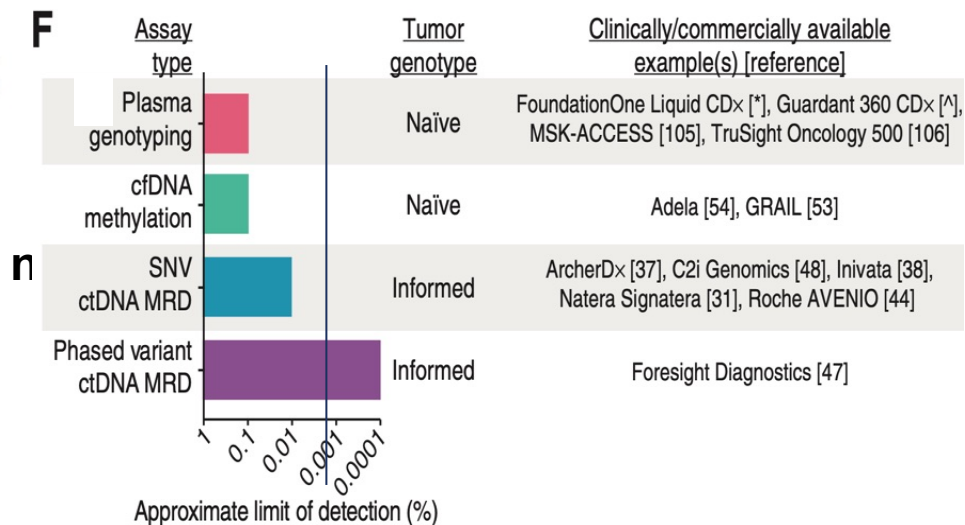
Abbosh C, et al. *Nature*. 2023;616:553–562.

Slide Courtesy of Dr. Natasha Leigh

Sensitivity of MRD Assay: A Challenge



Summary of assay types, tumour genotyping requirements and approximate LODs²



Take Home Message

- Liquid Biopsy is a perfect tool for monitoring in advance disease and MRD
- Integrating liquid biopsy in clinical trials is a necessity
- Real time monitoring in patients with high risk of recurrence requires improved technology in liquid biopsy

Thanks!



ISLB

INTERNATIONAL SOCIETY
OF LIQUID BIOPSY

#ISLB24



See You at

ISLB 2024

in Chicago, USA!

