

ctDNA in medical oncology: Clinical and Research Applications

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Disclosures:



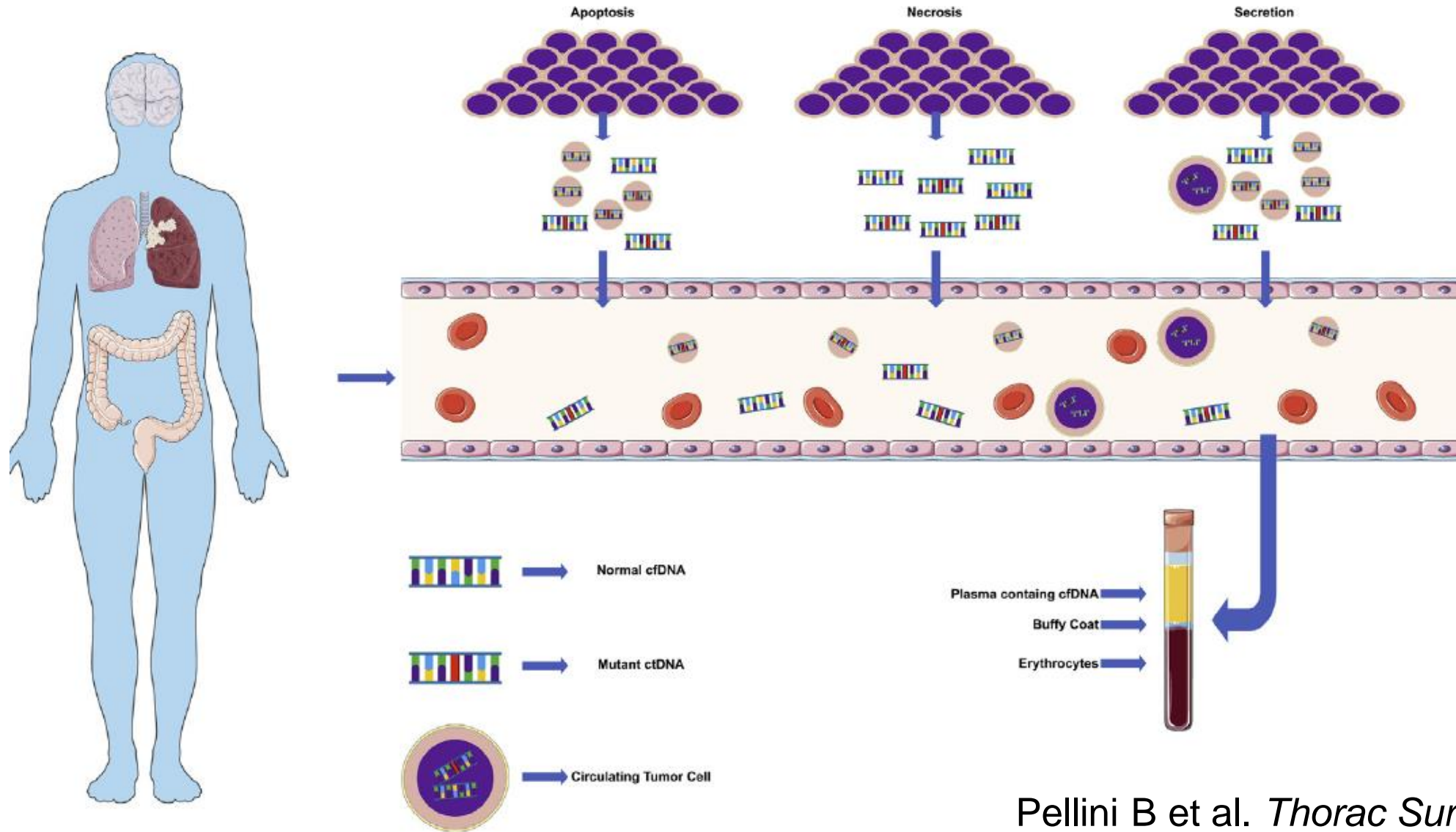
- Research support: Bristol Myers Squibb Foundation/the Robert A. Winn Diversity in Clinical Trials Awards Program (institution), George Edgecomb Society (institution), NIH/NCI 1R21CA259215-01A1 (institution), Bristol Myers Squibb (institution)
- Advisory Board/Consultant: : AstraZeneca, Guardant Health, Regeneron, Illumina, Foundation Medicine, AH Merus, BMS
- Speaker Honoraria: MJH Life Science, Merck, Foundation Medicine, BioAscend, PlaytoKnow AG, Grupo Pardini, GBOT

Outline

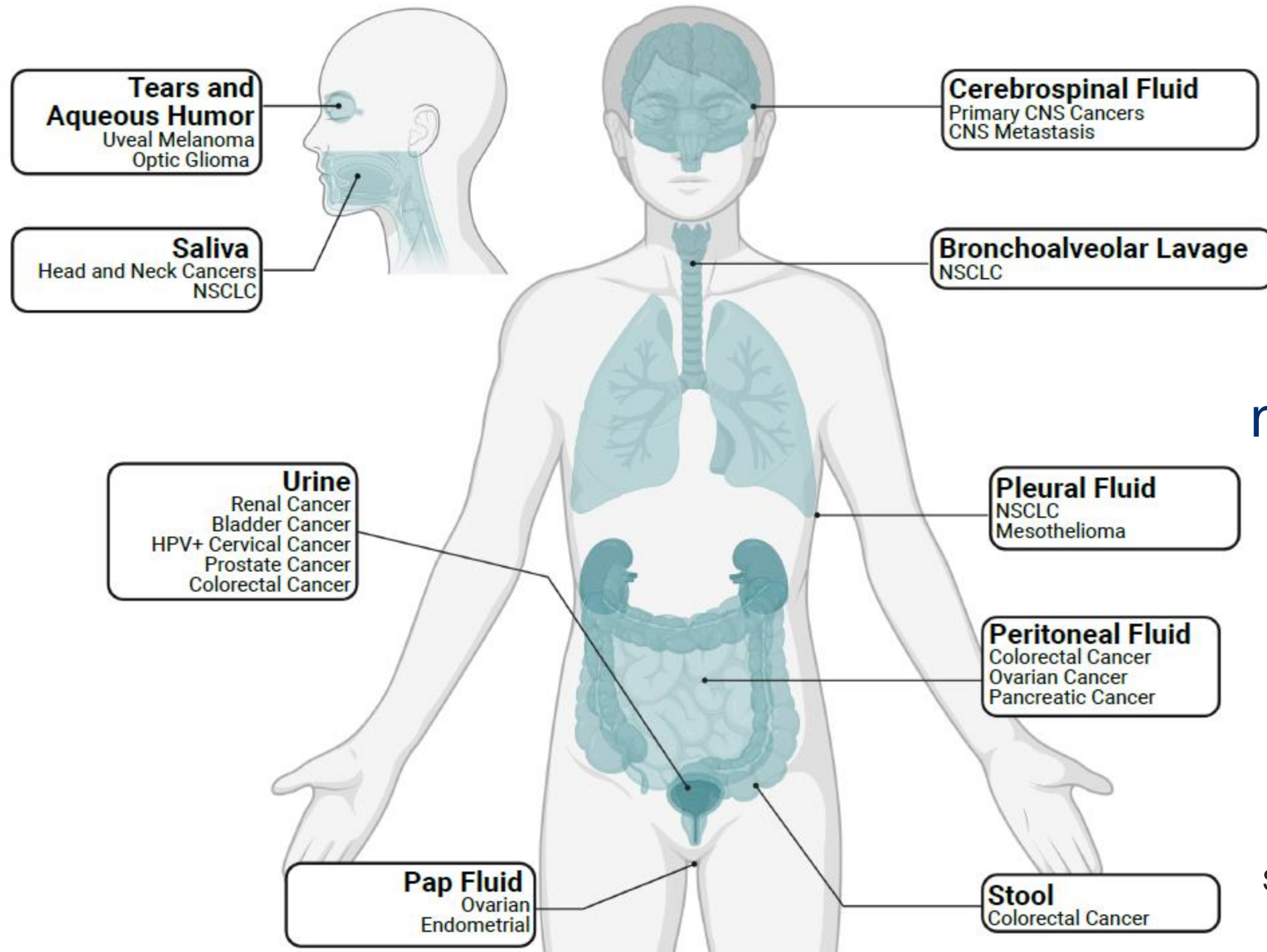


- ctDNA definition & sources of ctDNA
- ctDNA genotyping
- Tumor-informed vs. tumor-naïve assays
- ctDNA applications in oncology:
 - Molecular profiling
 - Treatment Monitoring
 - Minimal residual disease (MRD) detection

Tumor-derived fragments of nucleic acids identified in the blood are called circulating tumor DNA (ctDNA)



Pellini B et al. *Thorac Surg Clin.* 2020



Tumor-derived nucleic acids can be found in different biospecimens

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Plasma genotyping



Test	Limit of detection (% ctDNA)	Advantages	Limitations
Allele-specific PCR	~0.1-1%	<ul style="list-style-type: none"> • Ease of use • Lower cost 	<ul style="list-style-type: none"> • Lower sensitivity • Only tests small number of genomic positions
Digital PCR	~0.01%	<ul style="list-style-type: none"> • High sensitivity 	<ul style="list-style-type: none"> • Only tests small number of genomic positions
Hybrid capture-based NGS	~0.001-0.5%	<ul style="list-style-type: none"> • High sensitivity • No need for personalization 	<ul style="list-style-type: none"> • Less comprehensive than WES and WGS
WGS	~10%	<ul style="list-style-type: none"> • Broadly applicable • Entire genome is interrogated 	<ul style="list-style-type: none"> • Expensive • Low sensitivity • Mostly limited to SCNA detection
WES	~5%	<ul style="list-style-type: none"> • Broadly applicable • Entire exome is interrogated 	<ul style="list-style-type: none"> • Expensive • Low sensitivity

SCNA, somatic copy number alteration; NGS, next generation sequencing; WGS, whole genome sequencing; WES, whole exome sequencing

Outline



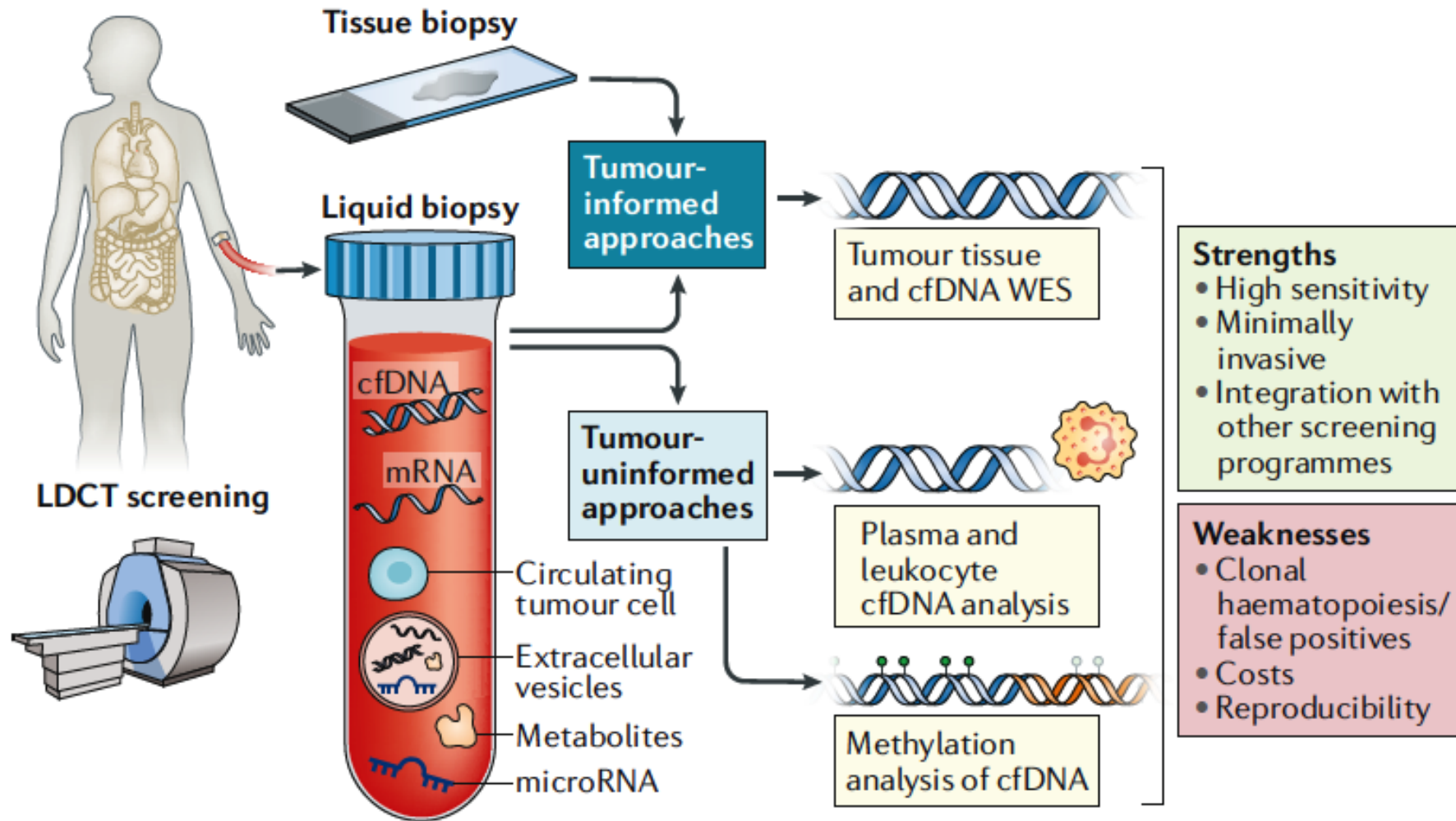
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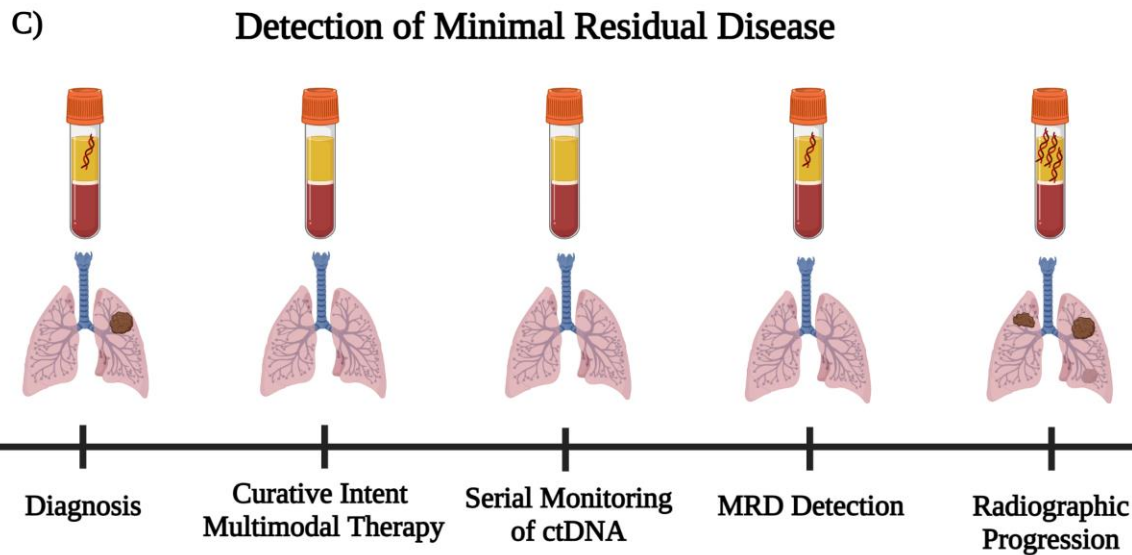
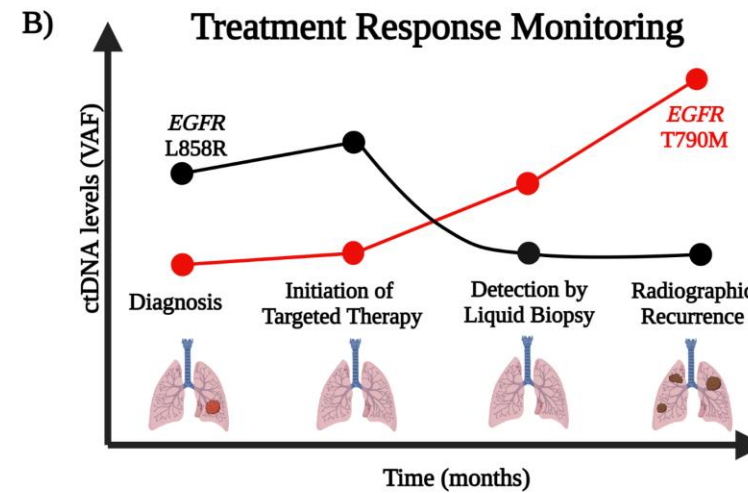
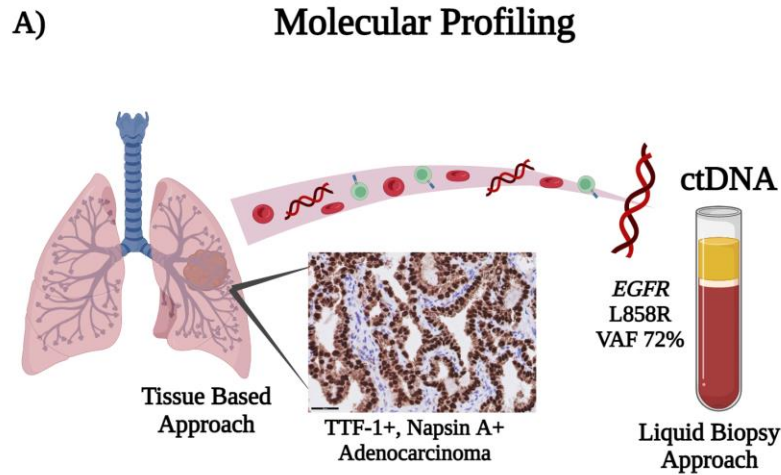
Tumor-informed vs. tumor-naïve assays

Tumor-Informed	Tumor-naïve
Requires tissue biopsy	No need for biopsy
Personalized assay	Off the shelf assay
Longer turnaround time	Shorter turnaround time
Does not account for tumor heterogeneity	Can detect clonal variants that emerge during follow-up
Potential for better sensitivity and specificity	Variable sensitivity and specificity

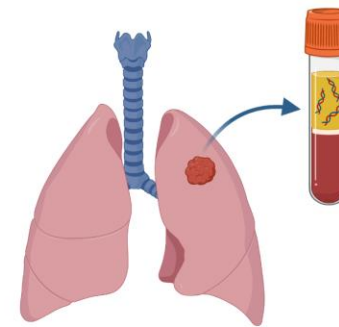
Challenges for ctDNA use in oncology



ctDNA applications in oncology



D) Early Cancer Detection



Outline



- ctDNA definition & sources of ctDNA
- ctDNA genotyping
- Tumor-informed vs. tumor-naïve assays
- ctDNA applications in oncology:
 - **Molecular profiling**
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ctDNA sequencing has high sensitivity and specificity to identify actionable genomic alterations

Table 3. Comparison of tissue versus cfDNA results for the guideline-recommended biomarkers in newly diagnosed metastatic NSCLC with FDA-approved therapies, *EGFR* exon 19 deletion and L858R, *ALK* fusion, *ROS1* fusion, and *BRAF* V600E

		Tissue +	Tissue -	Tissue not assessed	Tissue QNS	Total		
<i>EGFR</i> exon 19 del	cfDNA+	18	0	0	1	19	Sensitivity	81.8%
	cfDNA-	4	201	19	25	249	PPV	100.0%
	cfDNA TND	0	11	1	1	13	Specificity	100.0%
	cfDNA cancelled	0	0	1	0	1	NPV	98.0%
	Total	22	212	21	27	282	Concordance	98.2%
<i>EGFR</i> L858R	cfDNA+	9	0	0	2	11	Sensitivity	90.0%
	cfDNA-	1	213	19	24	257	PPV	100.0%
	cfDNA TND	0	11	1	1	13	Specificity	100.0%
	cfDNA cancelled	0	0	1	0	1	NPV	99.5%
	Total	10	224	21	27	282	Concordance	99.6%
<i>ALK</i> fusion (original)	cfDNA+	5	0	0	1	6	Sensitivity	62.5%
	cfDNA-	3	207	27	25	262	PPV	100.0%
	cfDNA TND	1	10	2	0	13	Specificity	100.0%
	cfDNA cancelled	0	1	0	0	0	NPV	98.6%
	Total	9	218	29	26	282	Concordance	98.6%
<i>ALK</i> fusion (reanalysis)	cfDNA+	6	0	0	1	7	Sensitivity	75.0%
	cfDNA-	2	207	27	25	261	PPV	100.0%
	cfDNA TND	1	10	2	0	13	Specificity	100.0%
	cfDNA cancelled	0	1	0	0	1	NPV	99.0%
	Total	9	218	29	26	282	Concordance	99.1%
<i>ROS1</i> fusion	cfDNA+	0	0	0	0	0	Sensitivity	-
	cfDNA-	2	151	85	30	268	PPV	-
	cfDNA TND	0	7	5	1	13	Specificity	100.0%
	cfDNA cancelled	0	1	0	0	1	NPV	98.7%
	Total	2	159	90	31	282	Concordance	98.7%
<i>BRAF</i> V600E mutation	cfDNA+	2	0	0	0	2	Sensitivity	100.0%
	cfDNA-	0	90	158	18	266	PPV	100.0%
	cfDNA TND	0	5	8	0	13	Specificity	100.0%
	cfDNA cancelled	0	0	1	0	1	NPV	100.0%
	Total	2	95	167	18	282	Concordance	100.0%

NOTE: Overall concordance across all four genes was greater than 98.2%, with a PPV of 100%. With continuous assay improvements, one cfDNA result originally reported as a false-negative for *ALK* fusion was identified as positive.

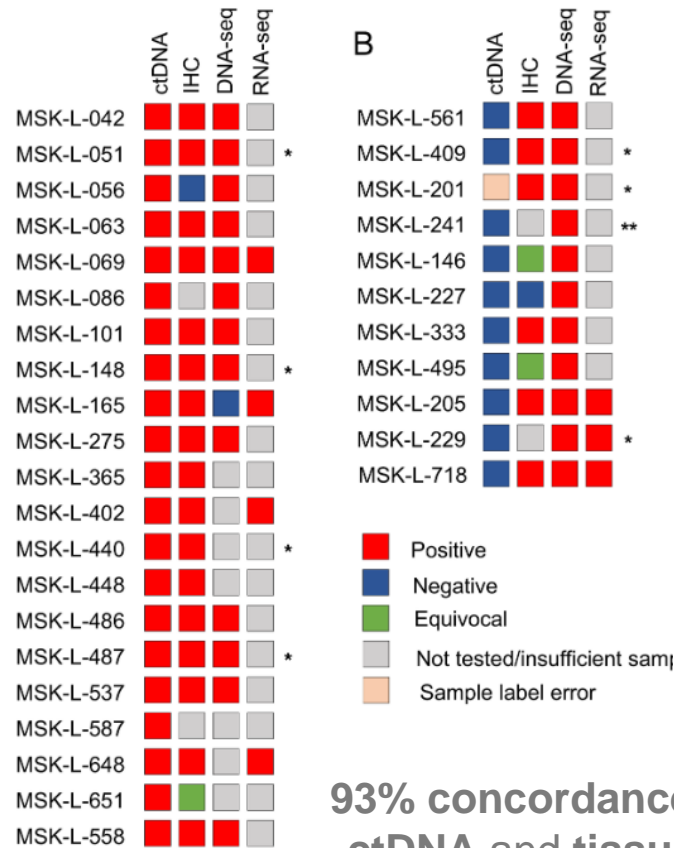
Stage IV NSCLC
Tumor-naïve assay
(Guardant 360)

Leighl N et al. *Clin Cancer Res.* 2019

ctDNA sequencing has high sensitivity and specificity to identify actionable genomic alterations

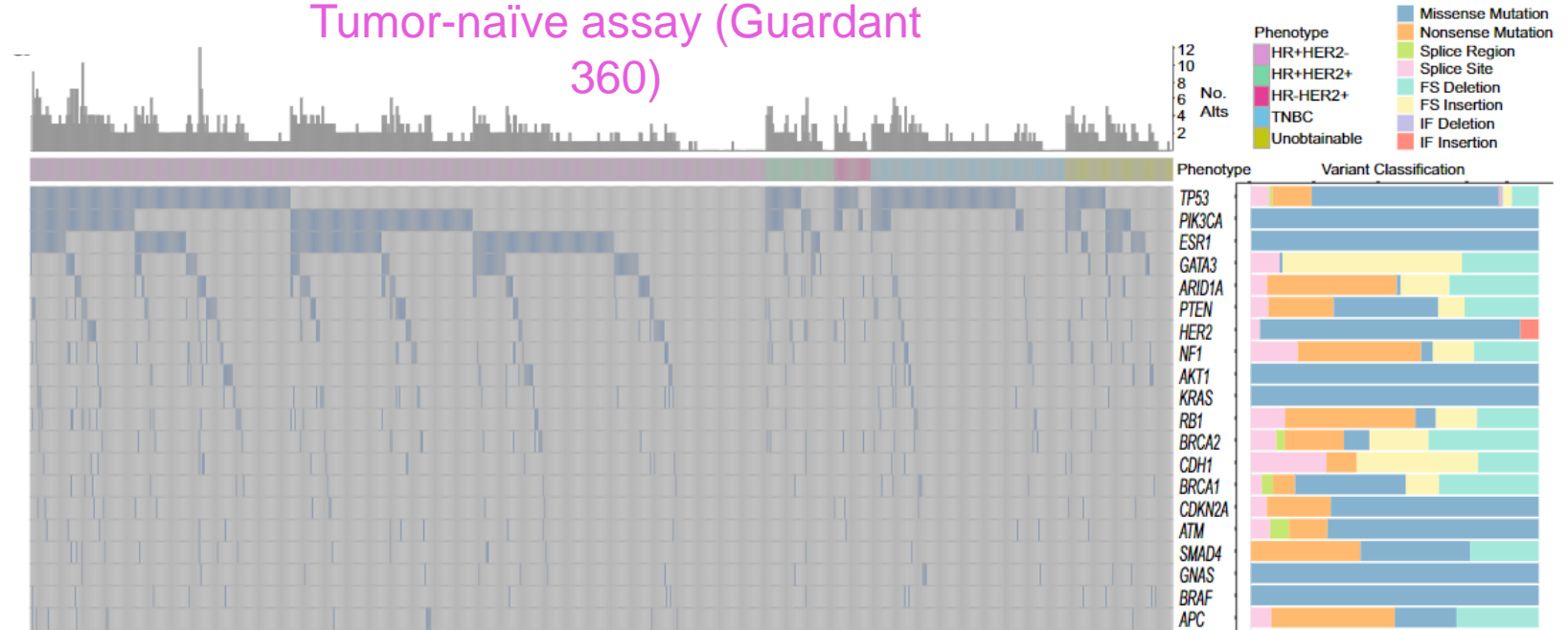
Stage IV NSCLC

Tumor-naïve assay (Resolution Bioscience)



93% concordance between ctDNA and tissue NGS to detect **ALK** fusions

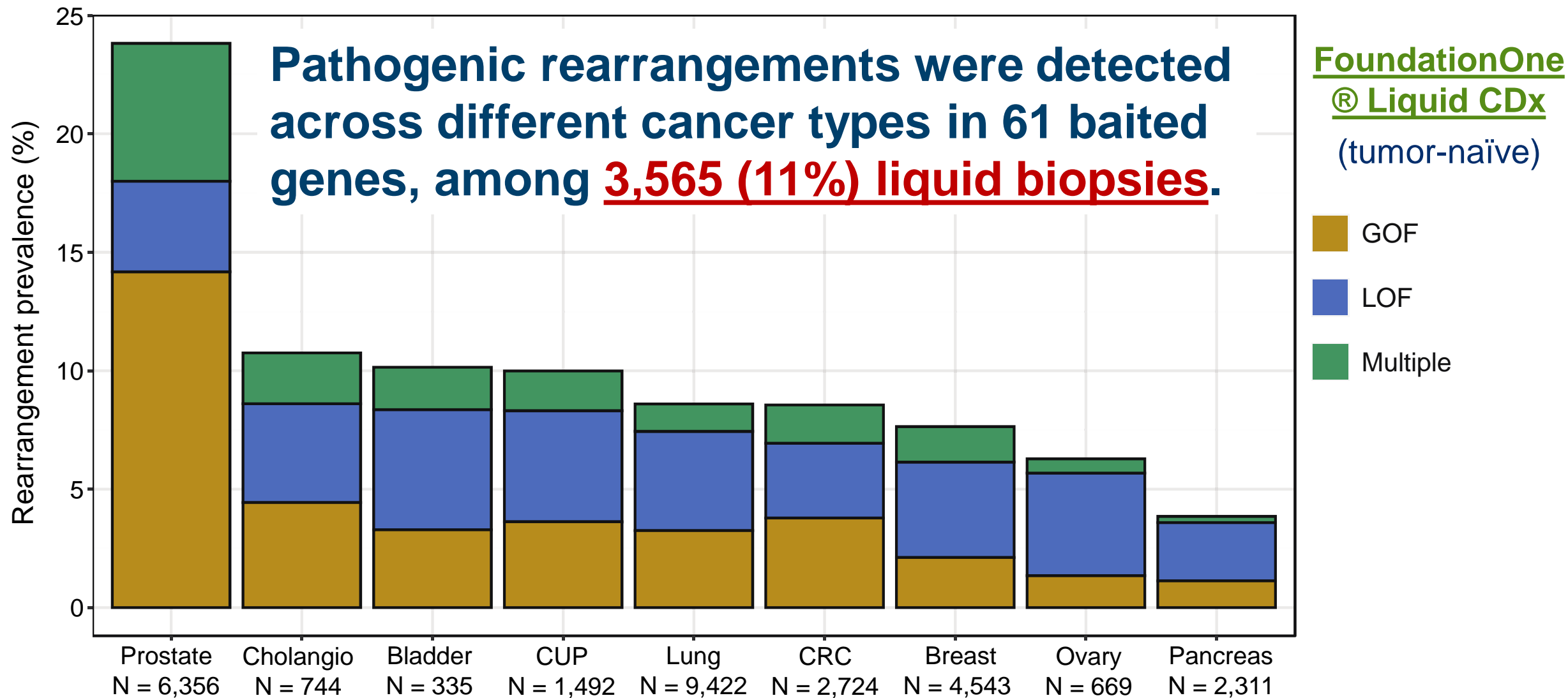
Advanced Breast Cancer
Tumor-naïve assay (Guardant 360)



92% of 800 patients were found to have at least one ctDNA alteration

Mondaca S et al. *Lung Cancer*. 2021
Kingston B et al. *Nat Commun*. 2021

Gene rearrangements can be detected using ctDNA





Research Use

Outline



- ctDNA definition & sources of ctDNA
- ctDNA genotyping
- Tumor-informed vs. tumor-naïve assays
- ctDNA applications in oncology:
 - Molecular profiling
 - **Treatment Monitoring**
 - Minimal residual disease (MRD) detection

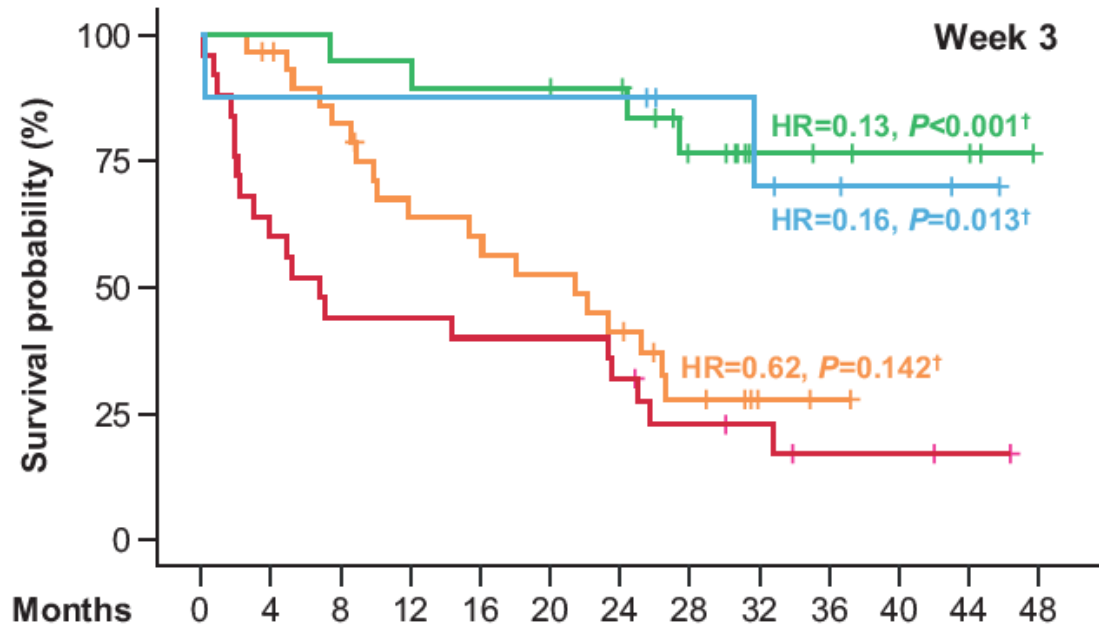
ctDNA decrease $\geq 90\%$ at week 3 or 9 during cemiplimab treatment is associated with improved OS



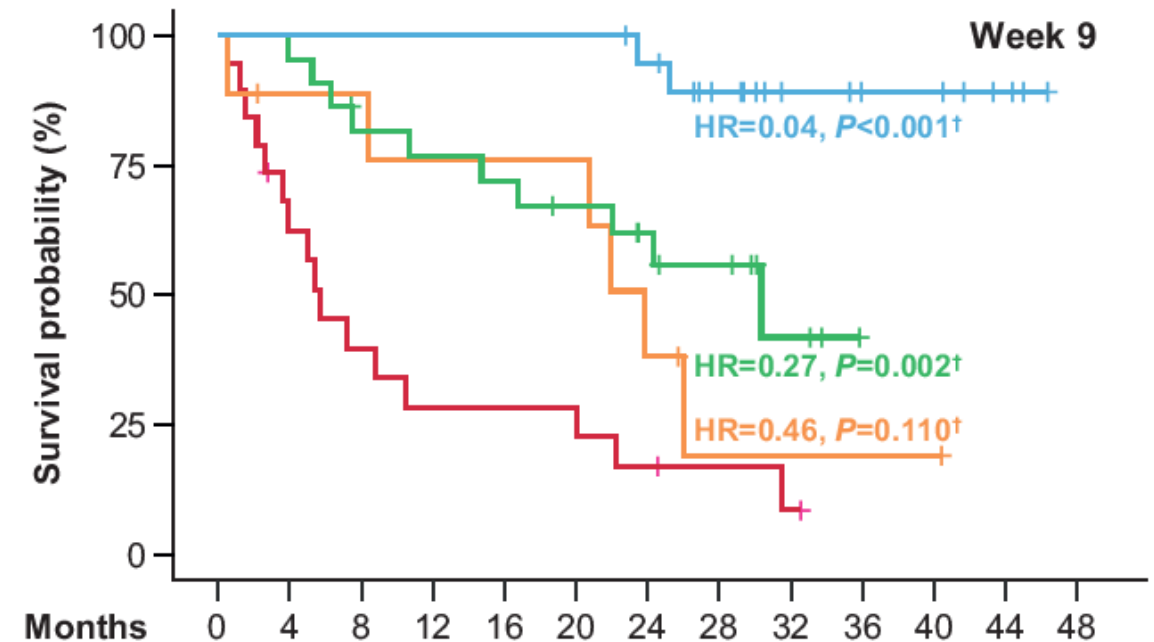
Advanced NSCLC

Tumor-informed assay (Signatera™ & FoundationOne Tracker)

Cemiplimab



Cemiplimab



ctDNA percent decrease from baseline

N=82

- Increase (n=25)
- Decrease ($\geq 90\%$; n=19)
- Decrease ($< 90\%$; n=30)
- Clearance (100%; n=8)

ctDNA percent decrease from baseline

N=70

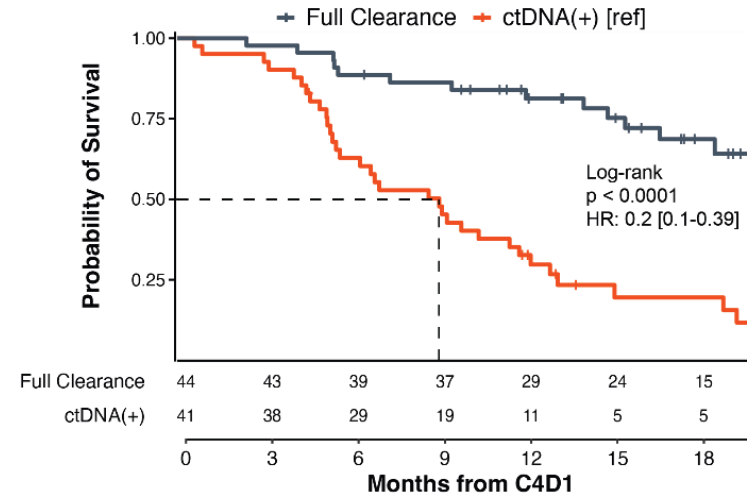
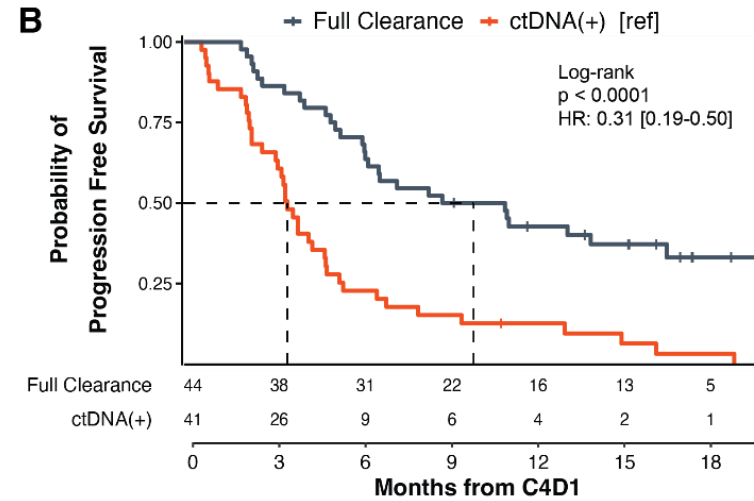
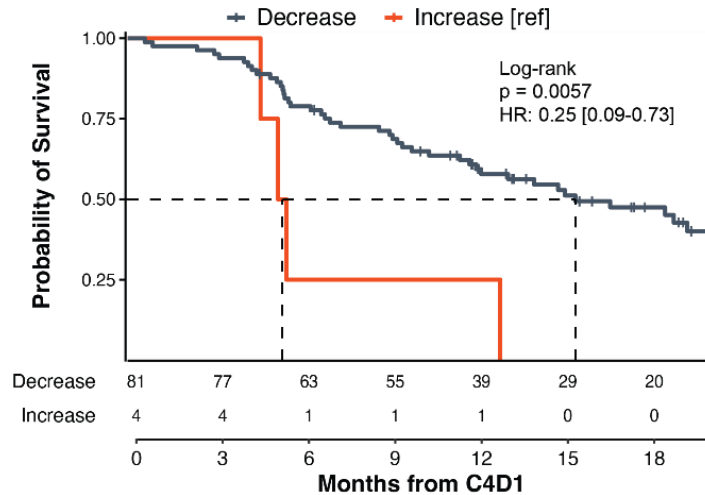
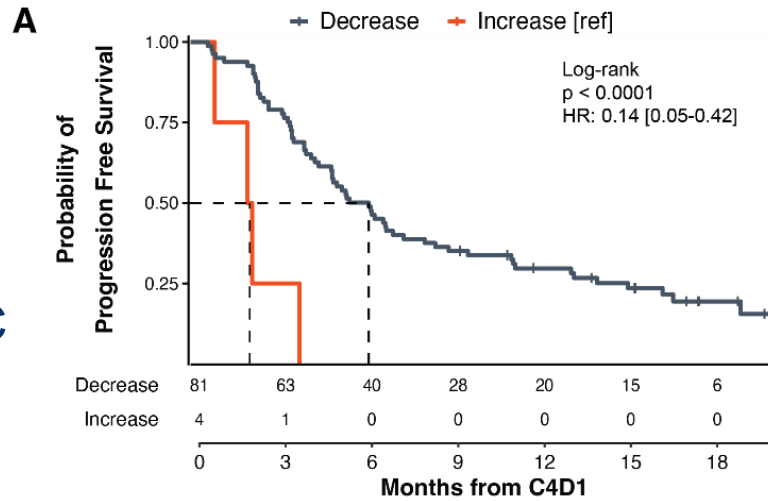
- Increase (n=19)
- Decrease ($\geq 90\%$; n=22)
- Decrease ($< 90\%$; n=9)
- Clearance (100%; n=20)

Vokes N et al. 2023 ASCO Annual Meeting.

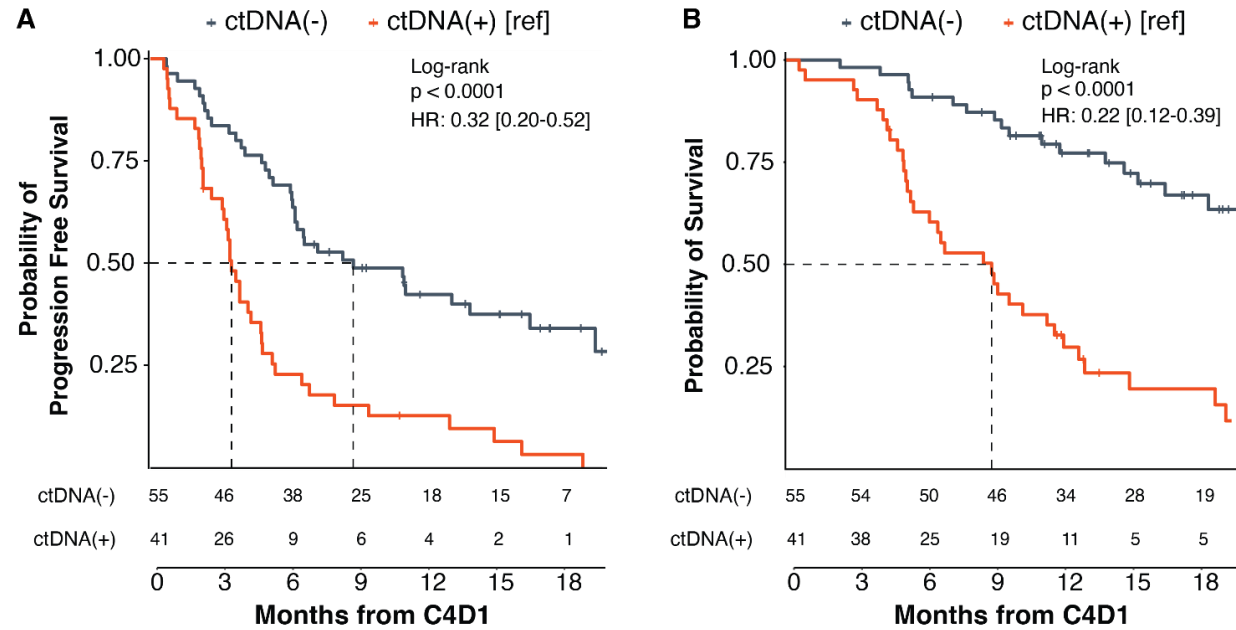
Circulating Tumor DNA Monitoring on Chemo-immunotherapy Informs Outcomes in Advanced Non-Small Cell Lung Cancer



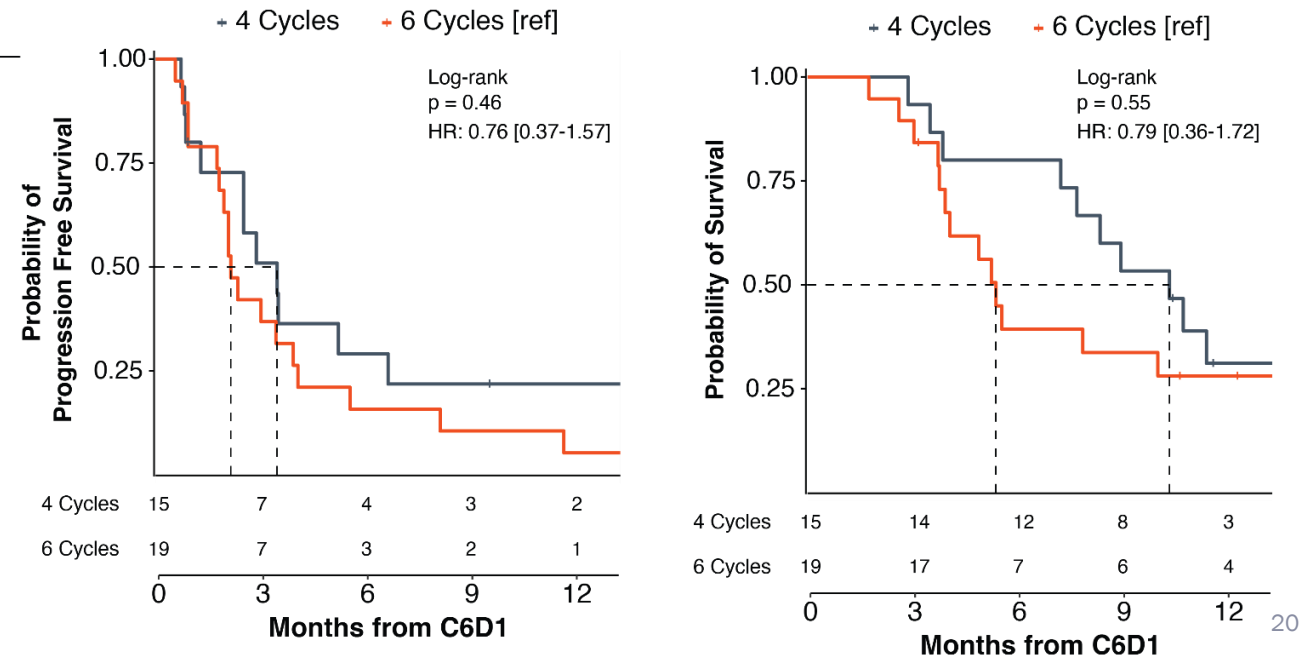
Advanced NSCLC
Tumor-informed
assay
(FoundationOne
Tracker)



ctDNA detection on chemolO can risk stratify patients prior to IO maintenance start, even without baseline ctDNA analysis



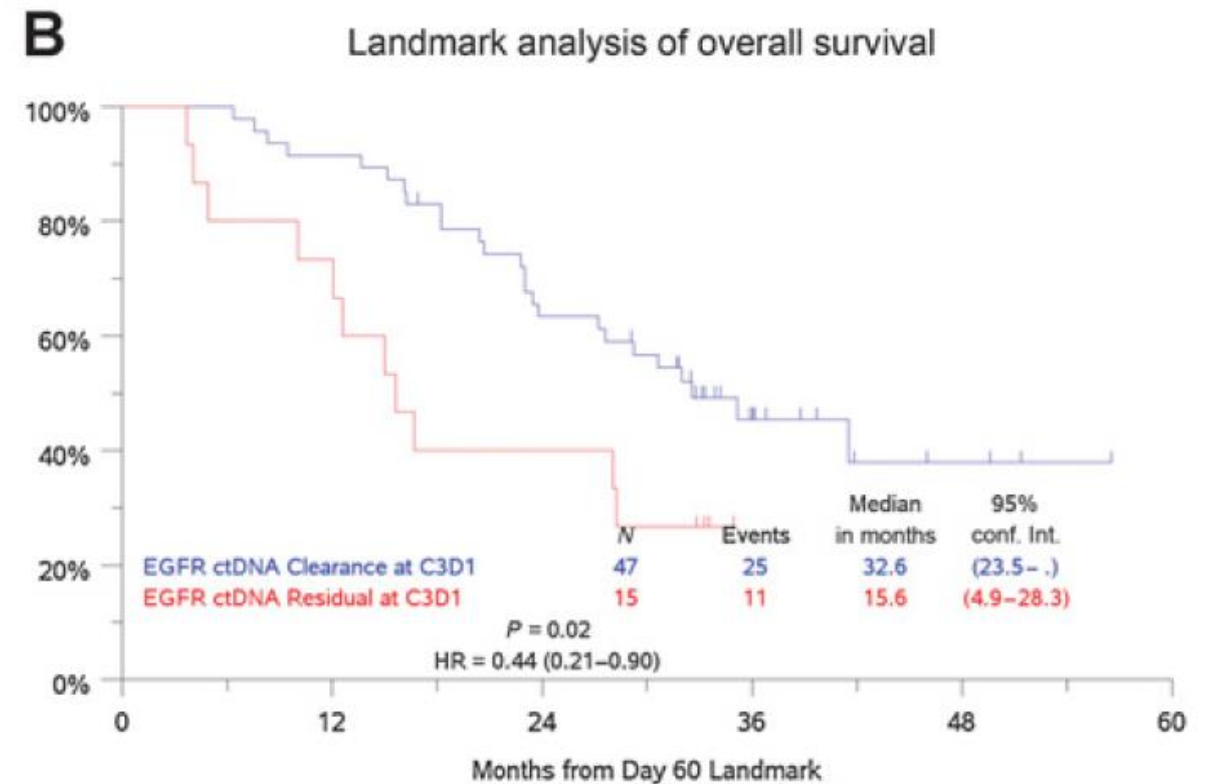
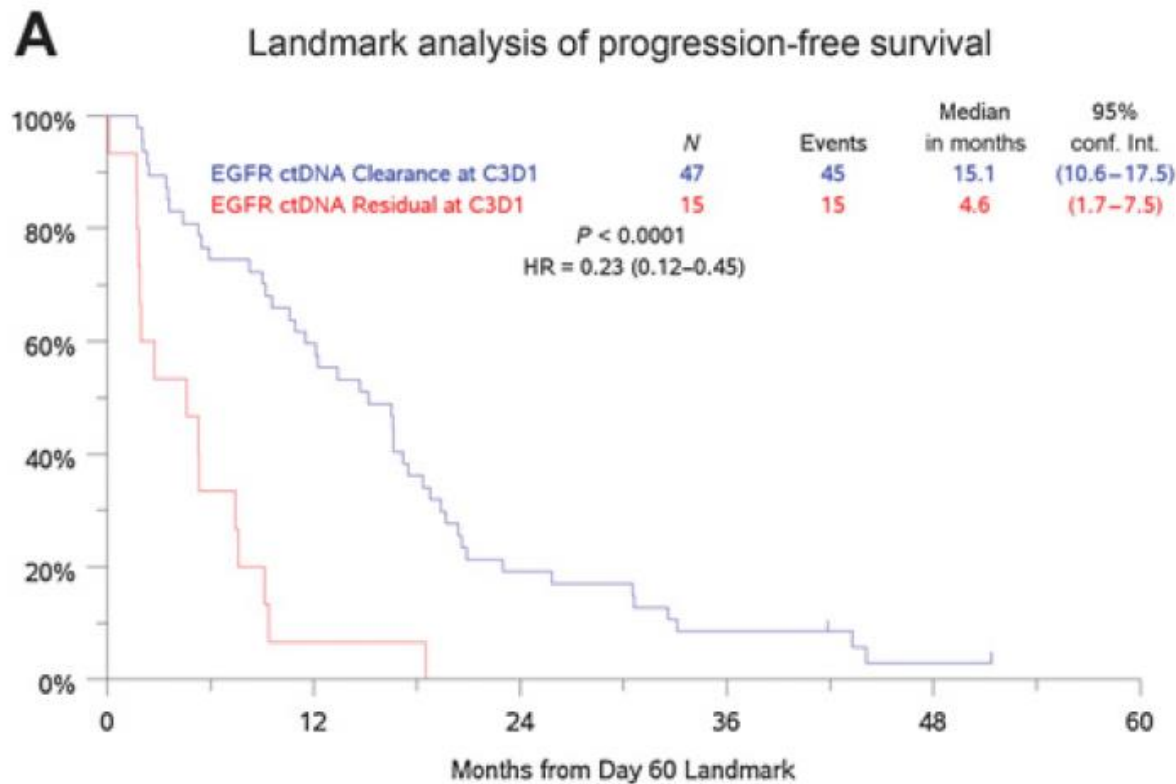
Additional cycles of induction therapy are not associated with improved outcomes in patients with ctDNA detection at C4D1



Patients with undetectable *EGFR* 8 weeks after treatment start had better PFS and OS



Stage IV NSCLC
Tumor-naïve assay
(Guardant 360)

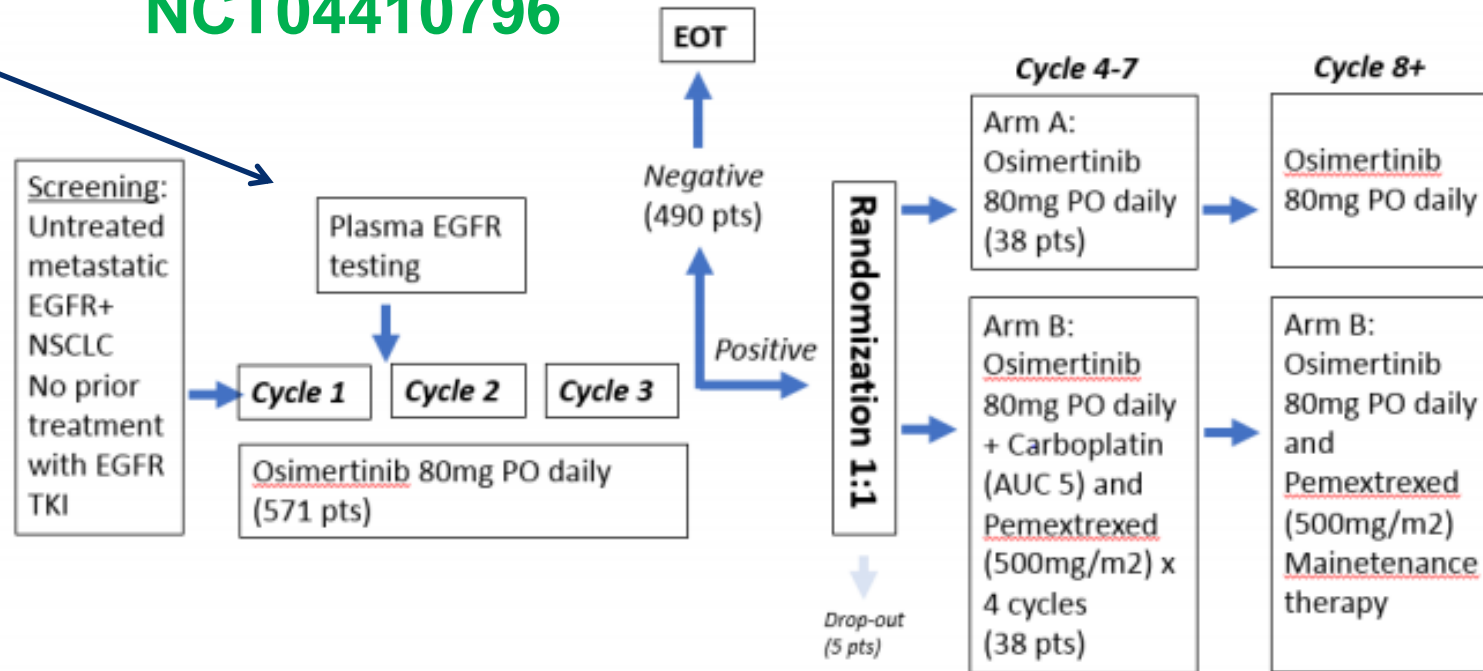




Treatment escalation based on ctDNA detection is under investigation for patients with *EGFR* mutations

3 weeks into therapy

NCT04410796



Treatment plan: All patients will receive osimertinib 80mg orally daily. Patients enrolled in Arm B will receive Carboplatin (AUC 5 IV q 3 weeks) and Pemetrexed (500mg/m² IV q 3 weeks) for a total of 4 cycles followed by pemetrexed maintenance from cycle 8 onwards.

Total enrollment: Approximately 571 patients will be screened. 80 will be eligible for randomization and treatment consent. 76 will be randomized.

Time to completion: 5 years

National Study PI: Helena Yu, MD (MSKCC); Moffitt PI: Bruna Pellini, MD

Outline

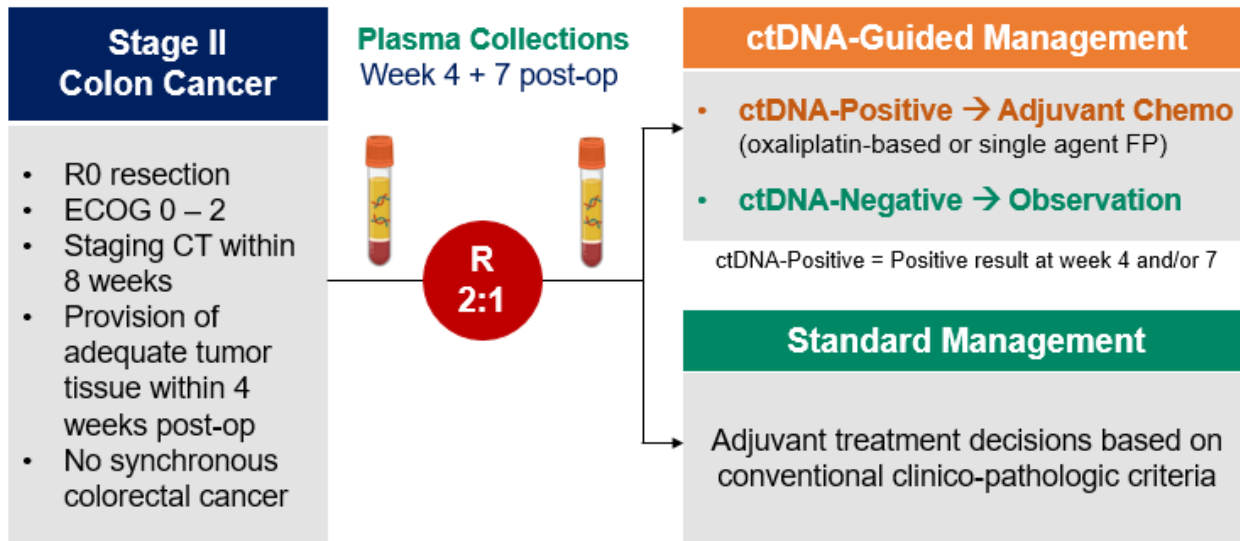


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The DYNAMIC study demonstrated that a **ctDNA-guided approach** for patients with **stage II CRC** (treating only patients with a positive ctDNA after surgery) **did not compromise RFS** compared to standard-of-care

DYNAMIC Study Design

ACTRN12615000381583



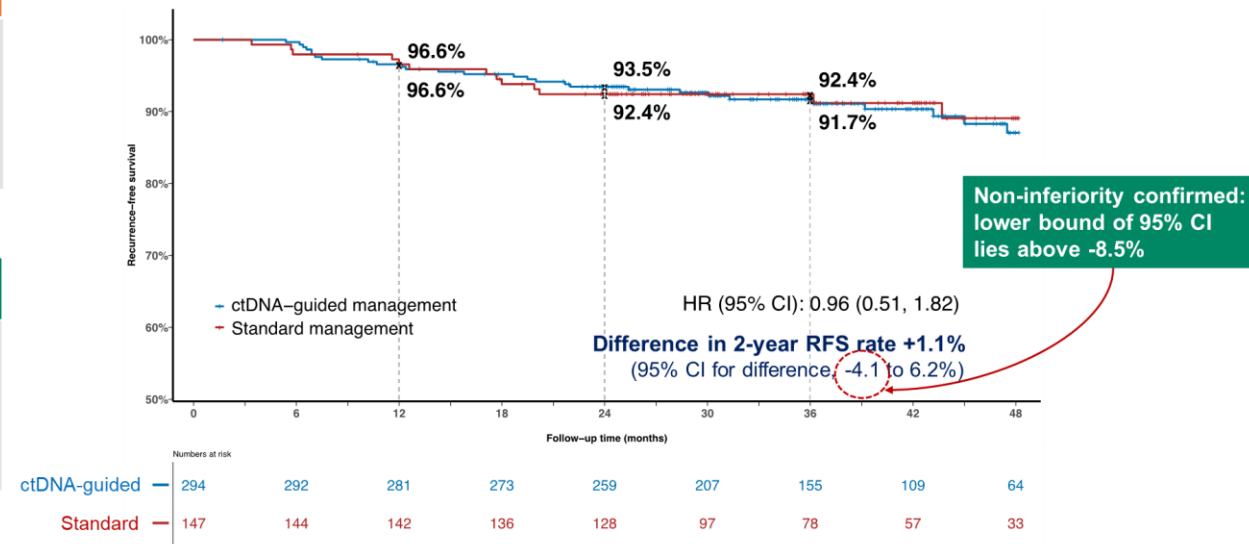
Stratification Factors

- T stage (T3 vs T4)
- Type of participating center (metropolitan vs regional)

Surveillance:

- CEA → 3-monthly for 24M, then 6-monthly for 36M
- CT C/A/P → 6-monthly for 24M, then at 36M

Recurrence-Free Survival



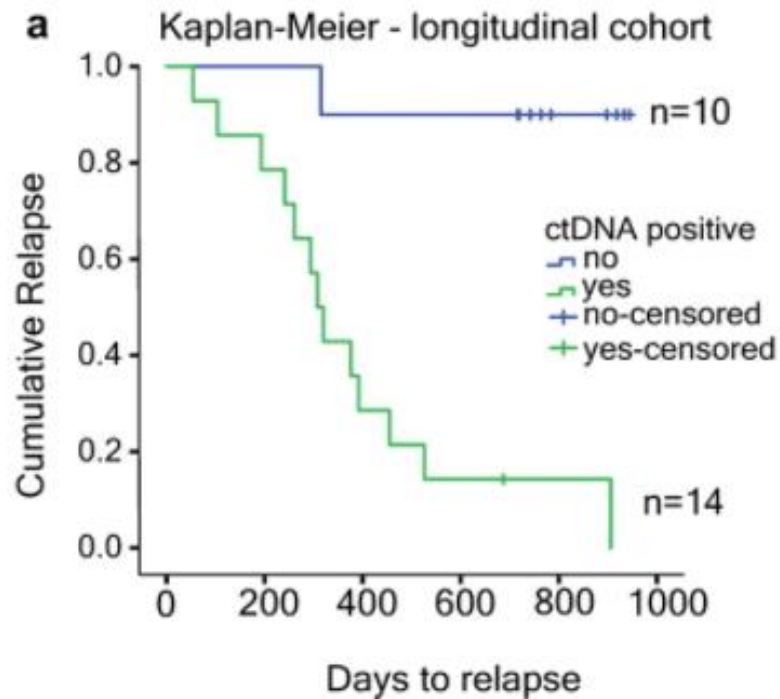
This approach substantially **reduced** the proportion receiving **adjuvant chemotherapy** (**28% → 15%**)

ctDNA can detect minimal residual disease (MRD) and it is a prognostic biomarker



Stages I-III NSCLC

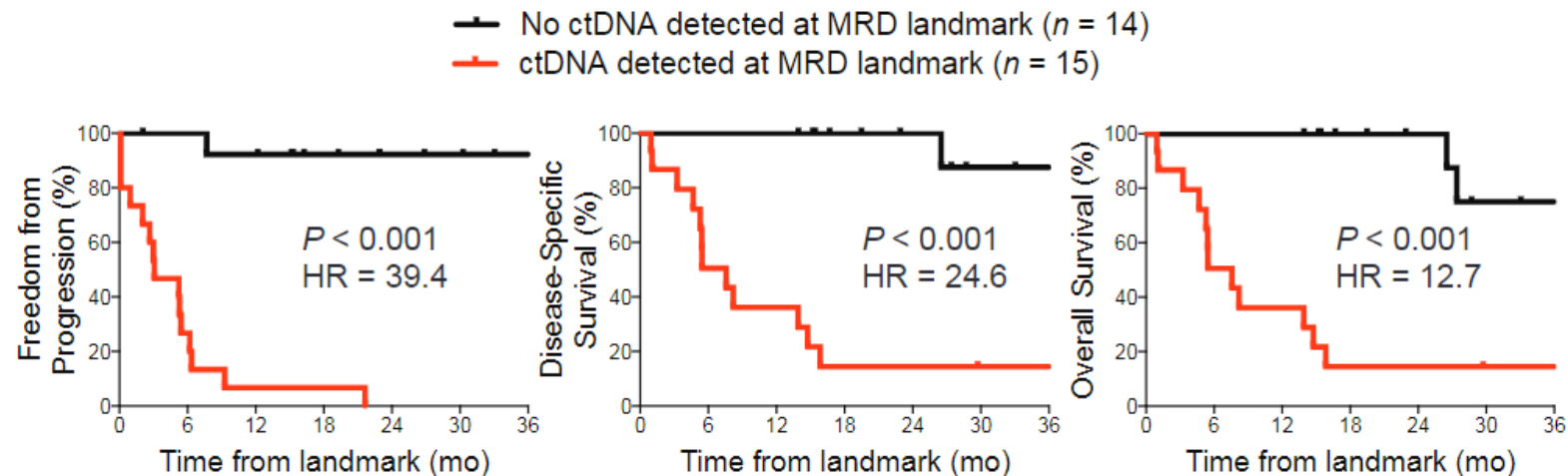
Tumor-informed assay
(Signatera™)



Stages I-III NSCLC

Tumor-naïve assay
(CAPP-Seq)

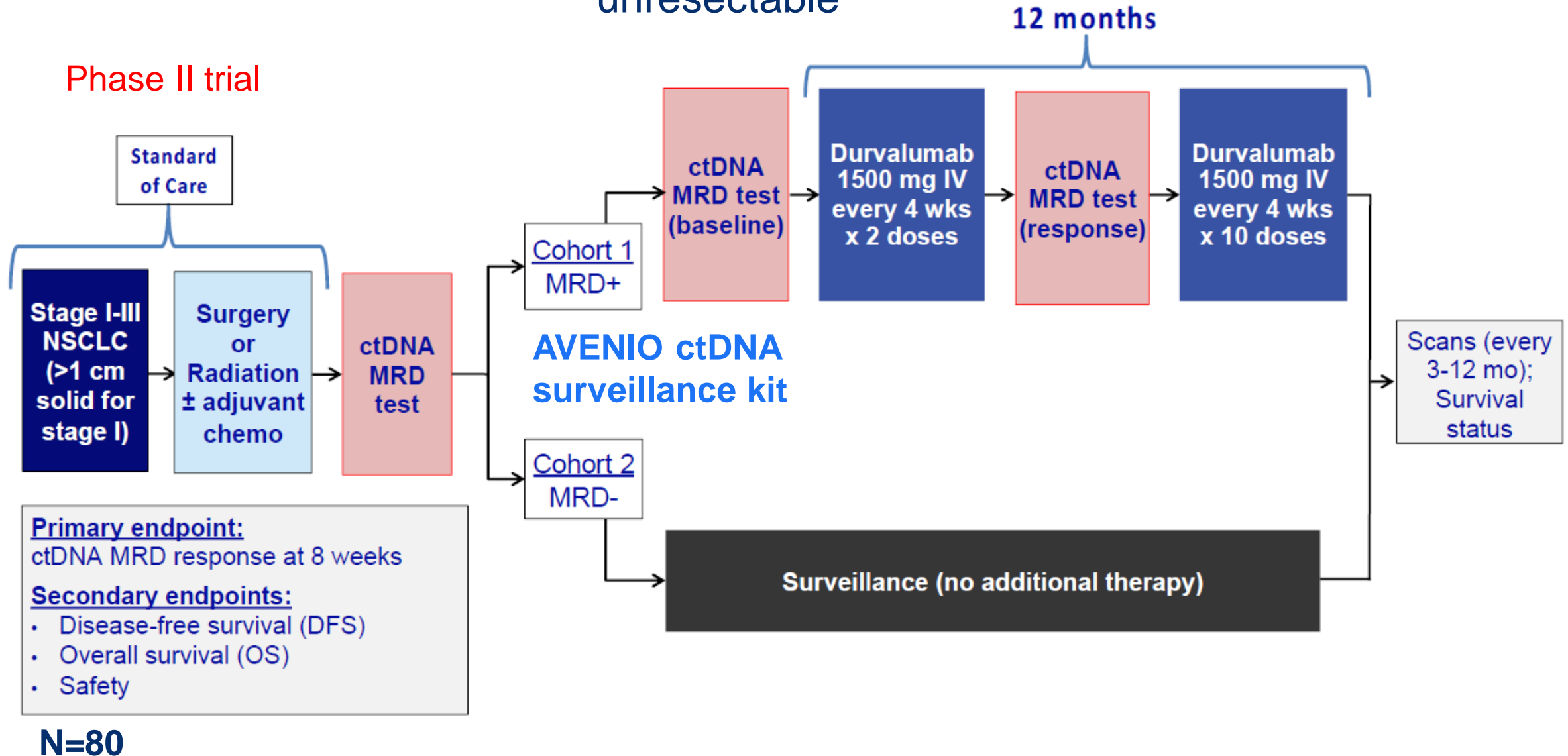
NSCLC patients analyzed at the MRD landmark



Abbosh C et al. *Nature*. 2017

Chaudhuri A et al. *Cancer Discov*. 2017

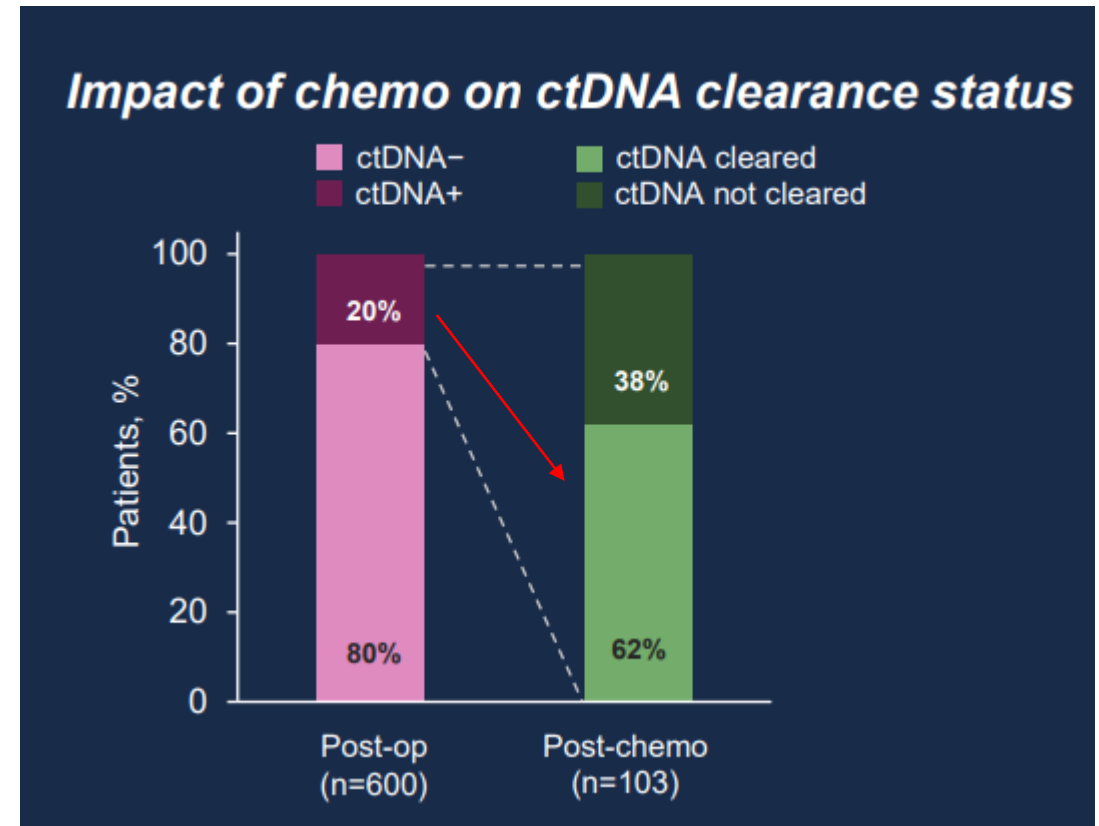
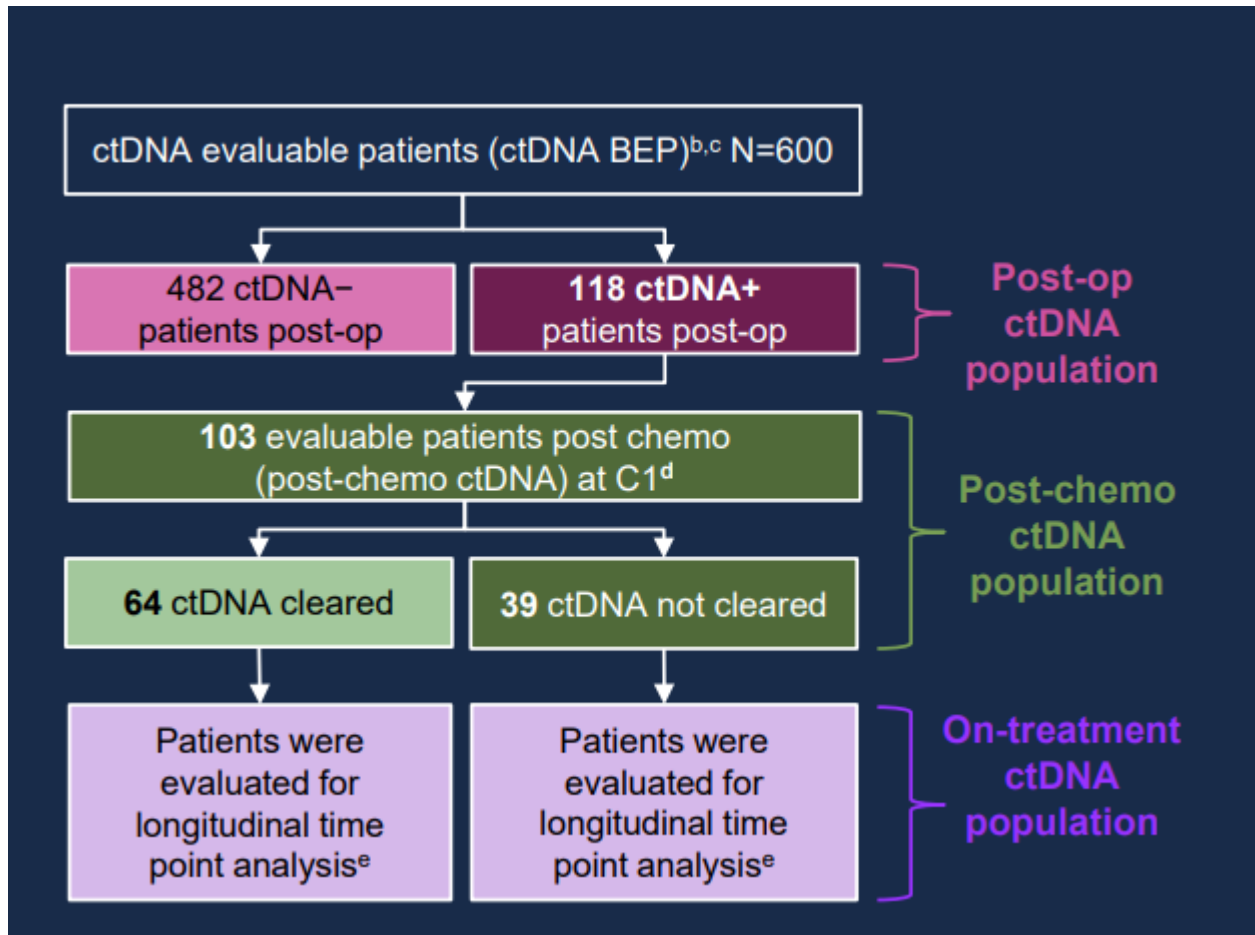
Prospective ctDNA MRD trial for patients with NSCLC stages I-III resectable & unresectable



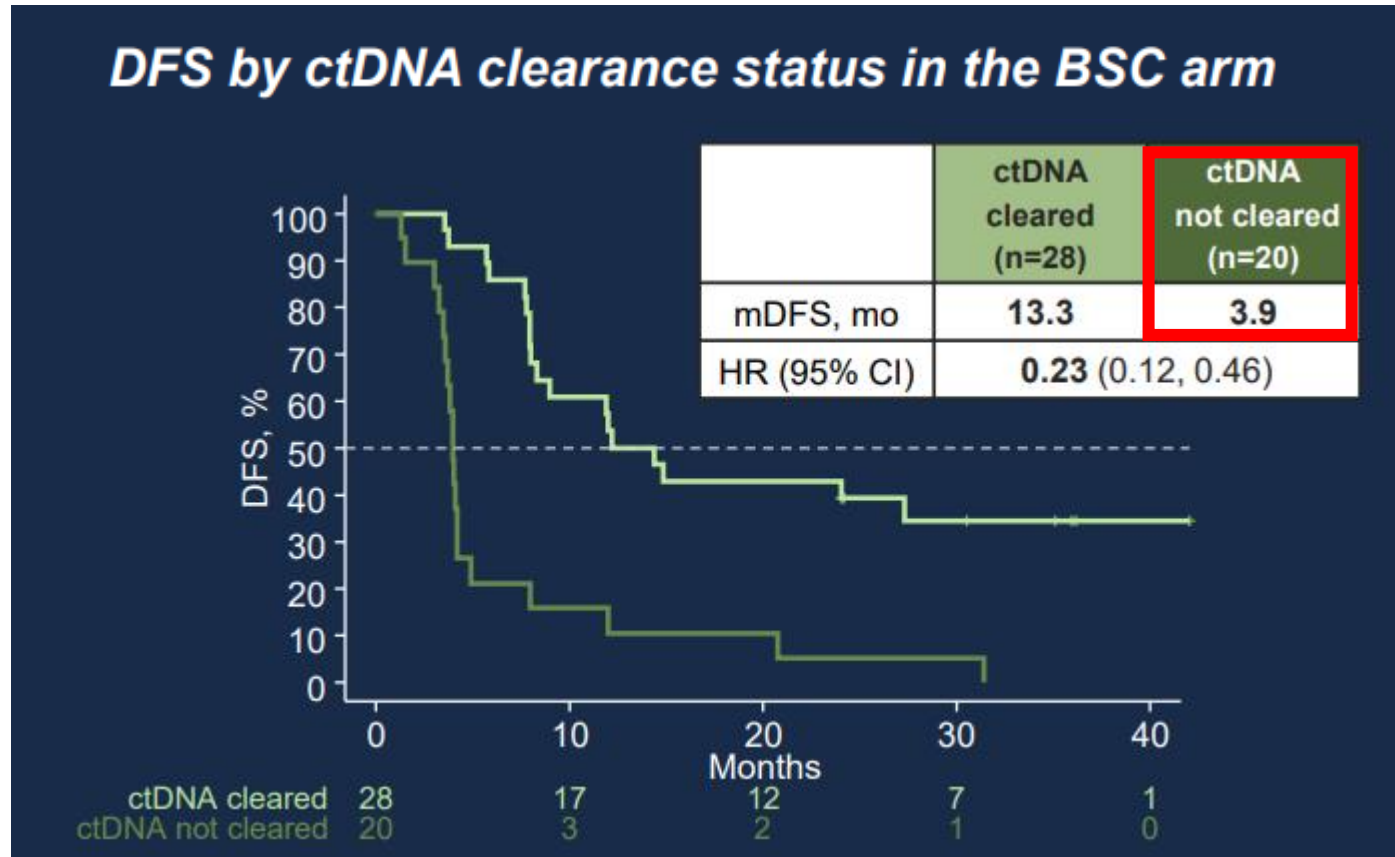
IMpower010: ctDNA Status in Patients With Resected NSCLC Who Received Adjuvant Chemotherapy Followed by Atezolizumab or Best Supportive Care



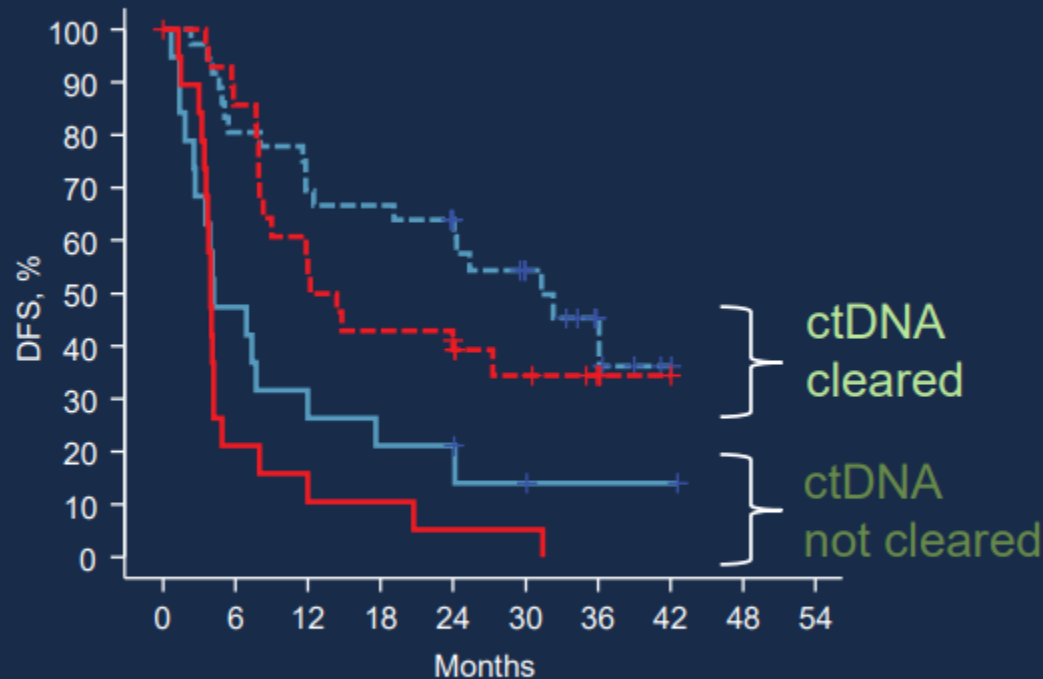
Adjuvant chemotherapy cleared ctDNA in ~62% of patients



IMpower-010: patients with detectable ctDNA MRD after adjuvant chemotherapy have worse prognosis



IMpower-010: data suggests adjuvant atezolizumab delays conversion to ctDNA +



Atezo, ctDNA cleared	36	35	29	28	25	24	24	23	21	17	12	10	5	2	1	0	0	0	0
Atezo, ctDNA not cleared	19	13	9	6	5	5	4	4	4	2	2	1	1	1	1	0	0	0	0
BSC, ctDNA cleared	28	28	24	18	15	12	12	12	12	8	7	6	4	1	1	0	0	0	0
BSC, ctDNA not cleared	20	16	4	3	2	2	2	1	1	1	1	0	0	0	0	0	0	0	0

Post-Chemo clearance status

ctDNA cleared	Atezo (n=36)	BSC (n=28)
mDFS, mo	31.3	13.3
HR (95% CI)	0.7 (0.37, 1.34)	

ctDNA not cleared	Atezo (n=19)	BSC (n=20)
mDFS, mo	4.2	3.9
HR (95% CI)	0.67 (0.34, 1.32)	

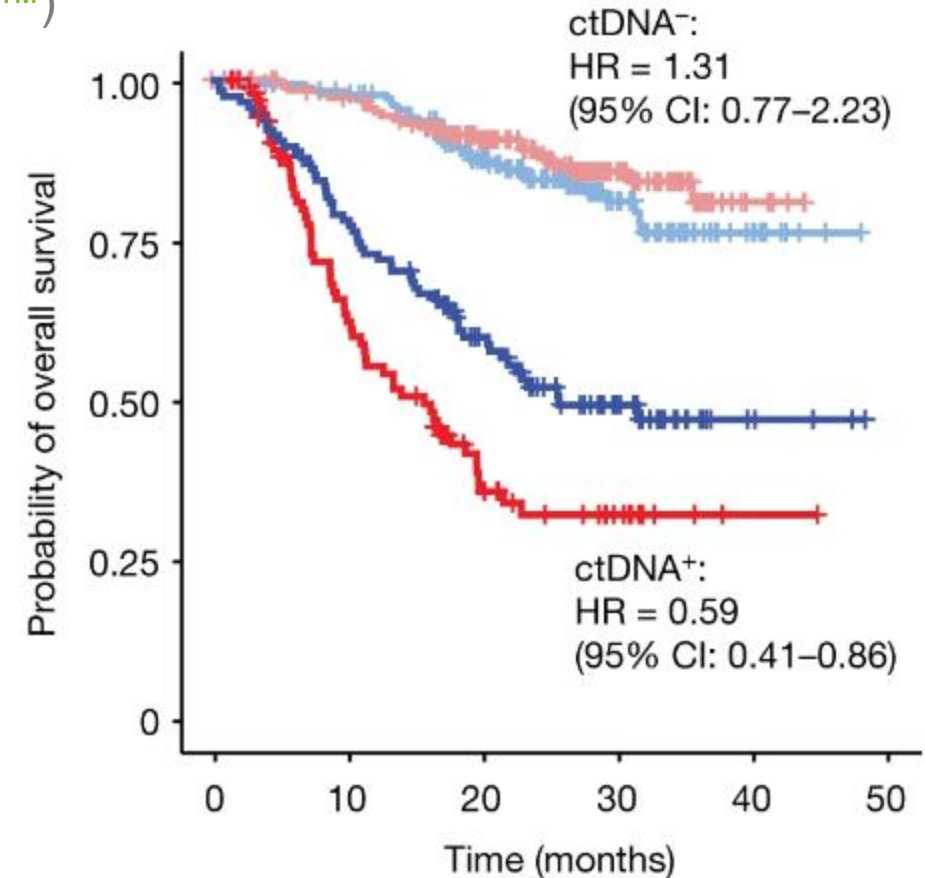
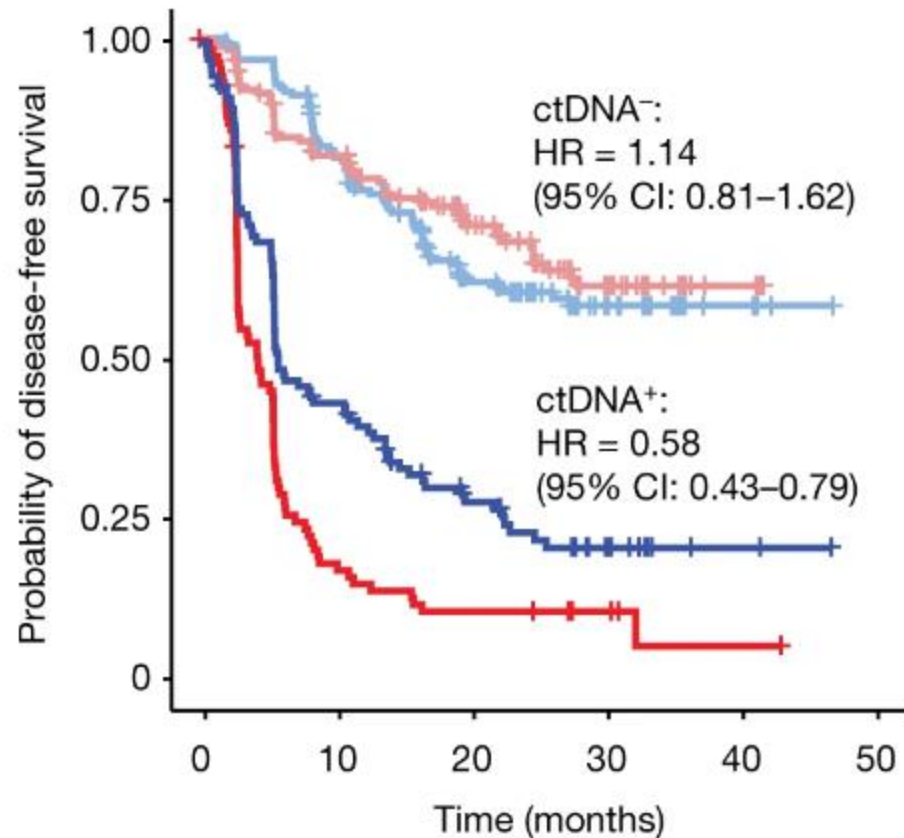
Patients with ctDNA MRD+ after surgery have better DFS and OS with adjuvant atezolizumab



Operable muscle-invasive urothelial cancer

Tumor-informed assay

(Signatera™)

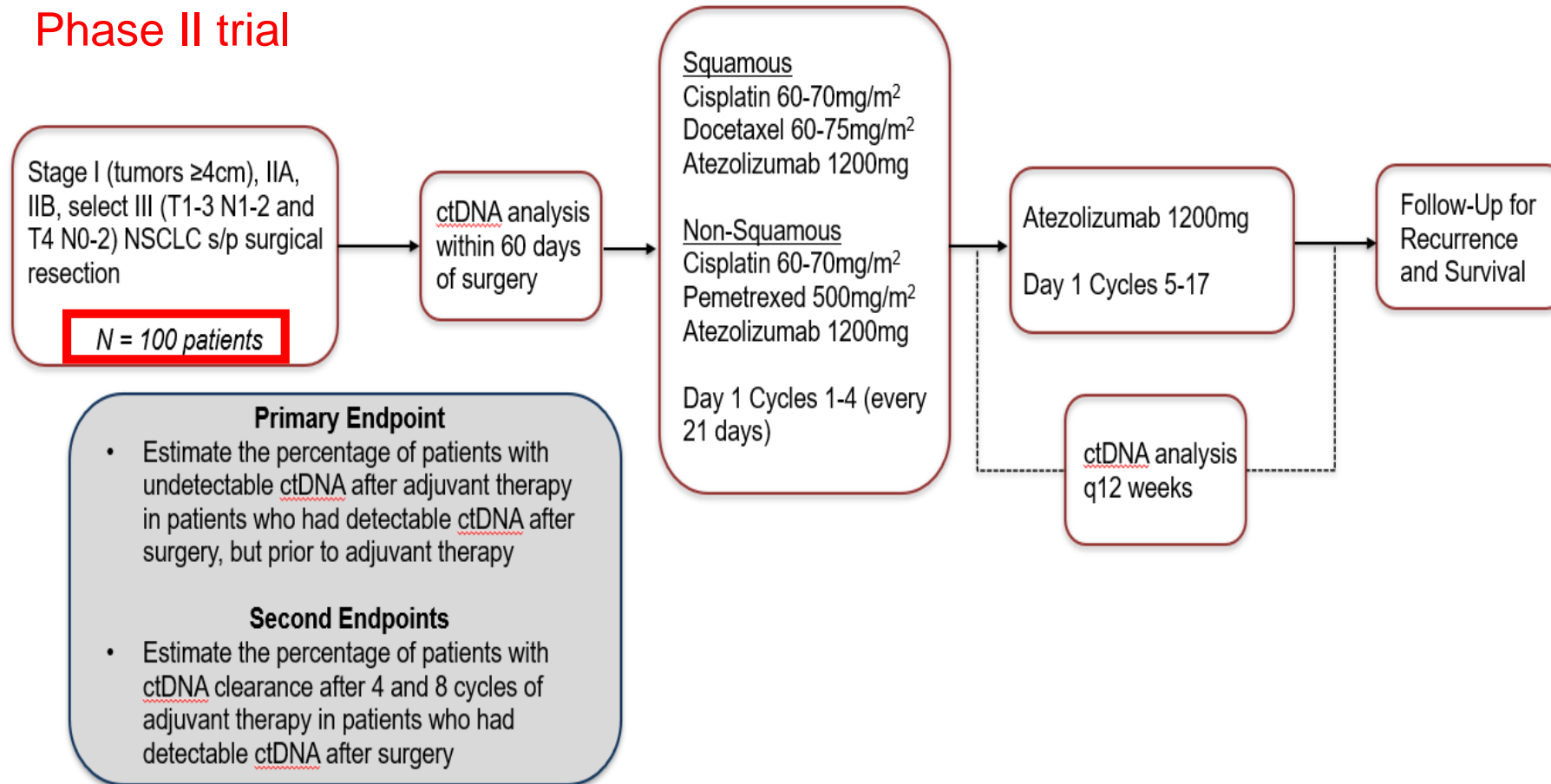


Prospective ctDNA MRD trial for patients with resectable NSCLC stages I-III



BTCRC LUN19-396

Phase II trial

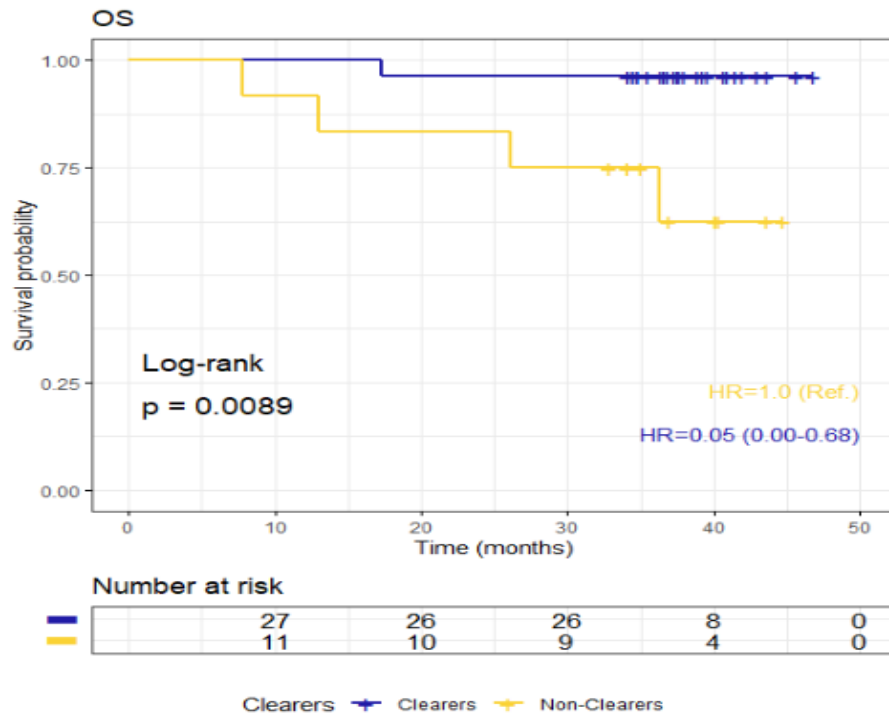


Slide adapted from G. Durm at 2023 Hawaii Lung Cancer Summit.

ctDNA clearance after neoadjuvant chemotherapy correlates with clinical outcomes

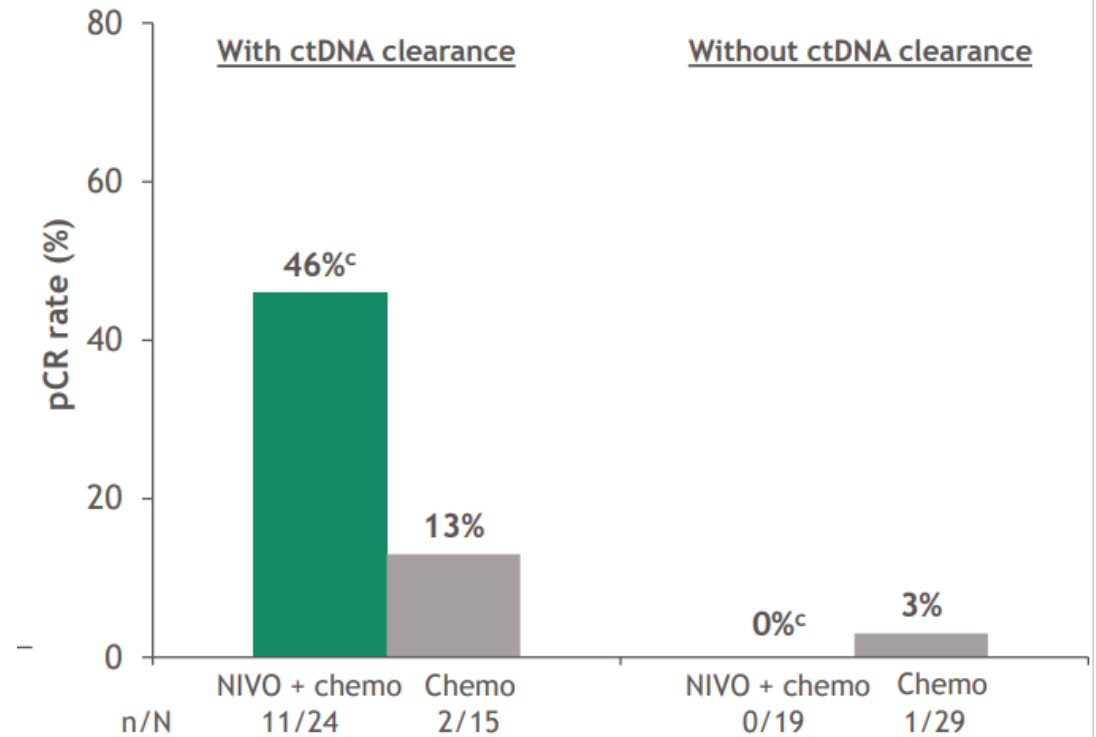


NADIM



CM816

ctDNA clearance and pCR rates



ctDNA clearance at the end of neoadjuvant treatment was associated with improved OS

Romero A et al. *J Thorac Oncol.* 2021:OA20.02
 Forde P et al. *Cancer Res.* 2021: CT003



Take home points

- ctDNA can be used for **molecular profiling** in patients with **advanced solid tumors** to guide **therapeutic decisions**
- ctDNA can **identify patients** with **advanced NSCLC** who are **responding to therapy (molecular response)** at an early timepoint
- ctDNA can **detect MRD** and it is a strong **prognostic biomarker**
- Ongoing **trials will inform if clinical decision-making can be guided by ctDNA** and if that improves patients' outcomes

Thank you!



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