

Novel Frontiers in the Use of ctDNA in Oncology

Updates in Cancer Therapies: An ASCO/ESMO Review

October 2022

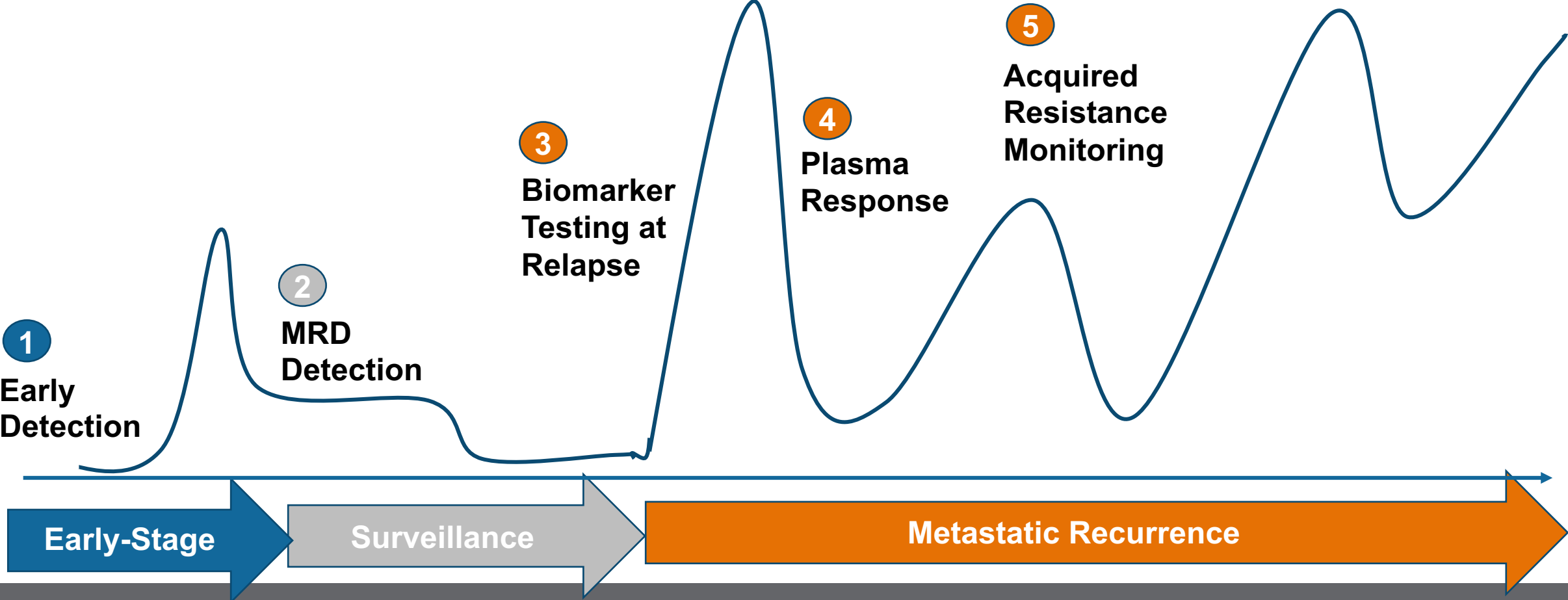
Julia Rotow, MD

Lowie Center for Thoracic Oncology, Dana-Farber Cancer Institute



Dana-Farber
Cancer Institute

Cell-free DNA Across Many Phases of Disease



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

Pellini B and Chaudhuri A. *J Clin Oncol*. 2022

2022 ASCO
ANNUAL MEETING

AASCO22

Presented by:
Shuna Pellini, MD
Assistant Member, Department of Thoracic Oncology, Moffitt Cancer Center

Content of this presentation is the property of the author, licensed by ASCO. Permission required for reuse.

ASCO
AMERICAN SOCIETY OF
CLINICAL ONCOLOGY
KNOWLEDGE CONQUERS CANCER

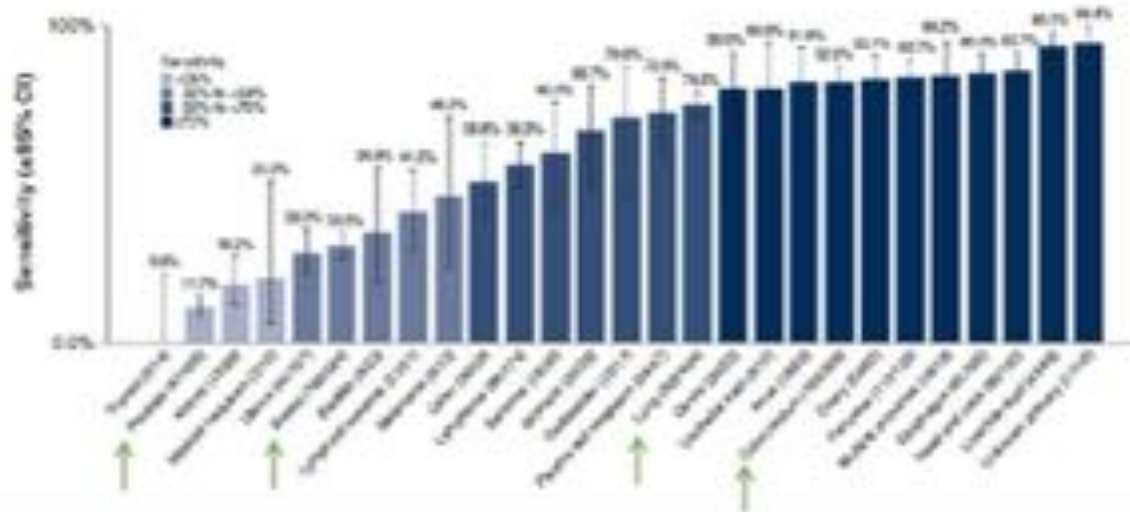
Content of this presentation is the property of the author, licensed by ASCO. Permission required for reuse.

ctDNA methylation for early cancer detection

	Cancer	Non-cancer	Total
	2823	1254	4077
Test positive	1453	6	1459
Test negative	1370	1248	2618
	Sensitivity = 1453/2823 51.5% (49.6%-53.3%)	Specificity = 1248/1254 99.5% (99.0%-99.8%)	

Two-sided 95% Wilson confidence intervals were calculated.

Targeted methylation assay
Tumor-naïve

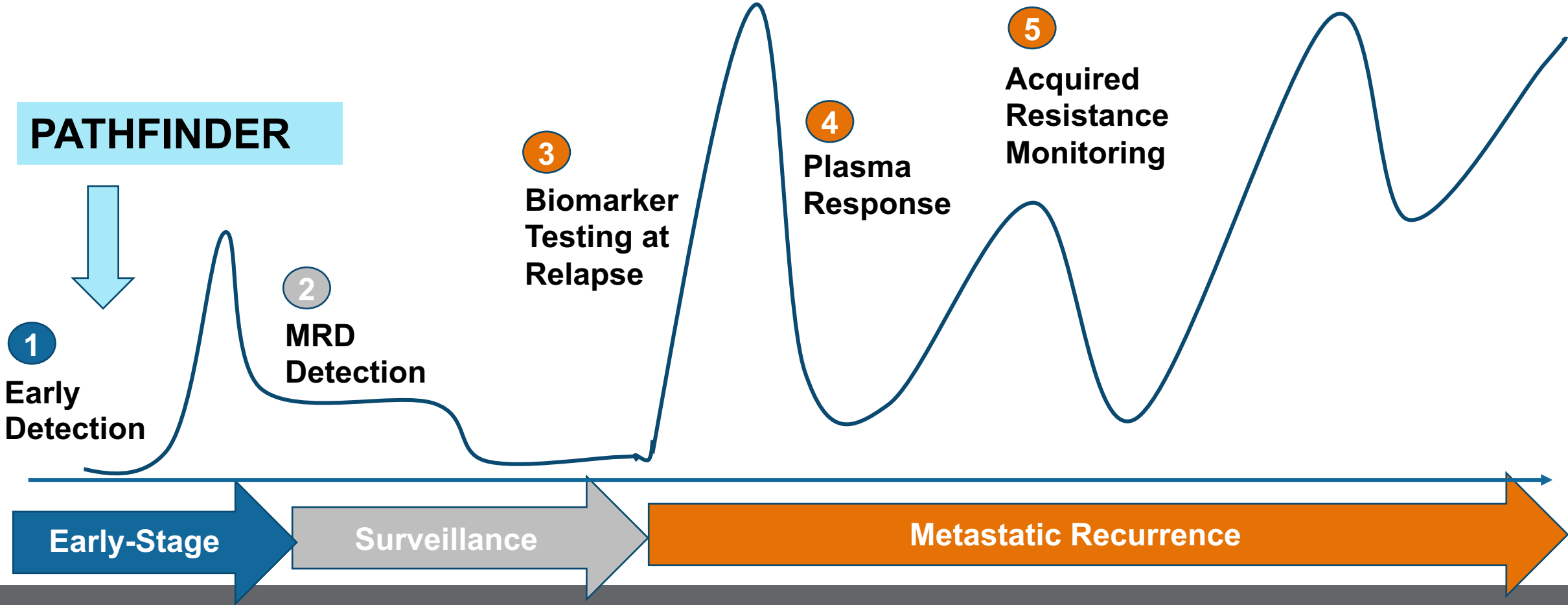


Sensitivity varies with cancer type, histology, and stage

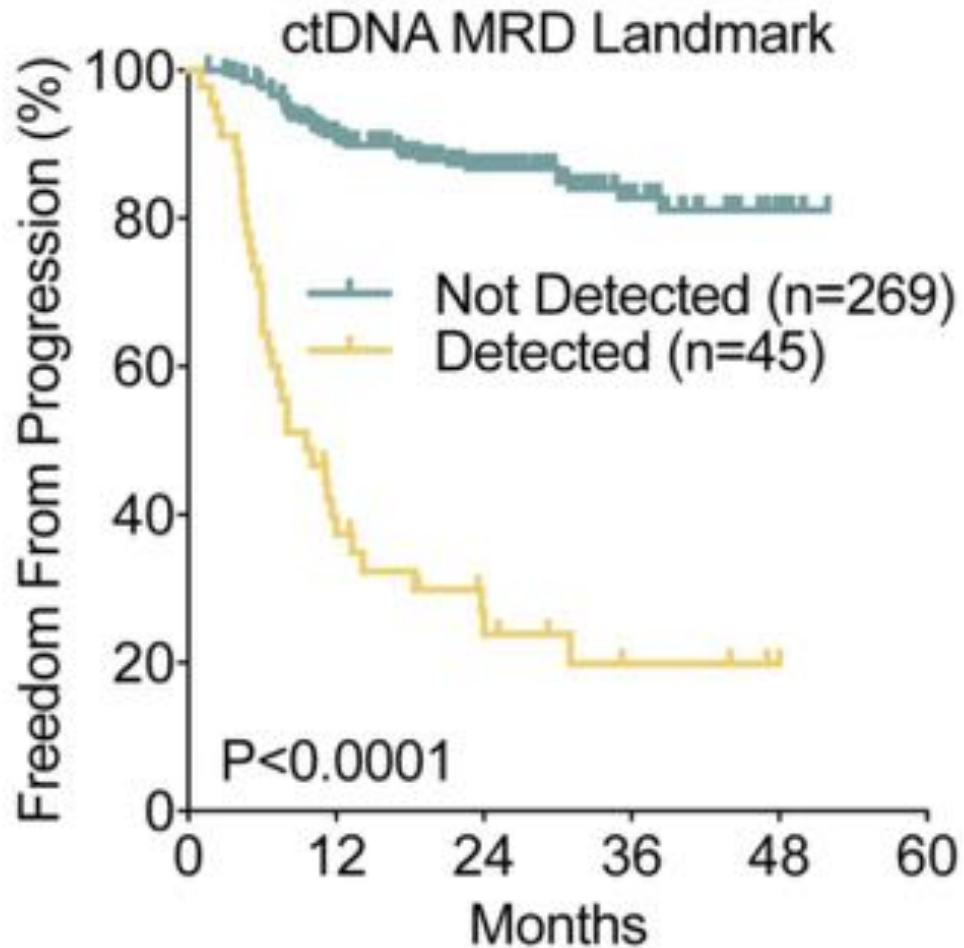
Klein EA et al. Ann Oncol. 2021

Cell-free DNA Across Many Phases of Disease

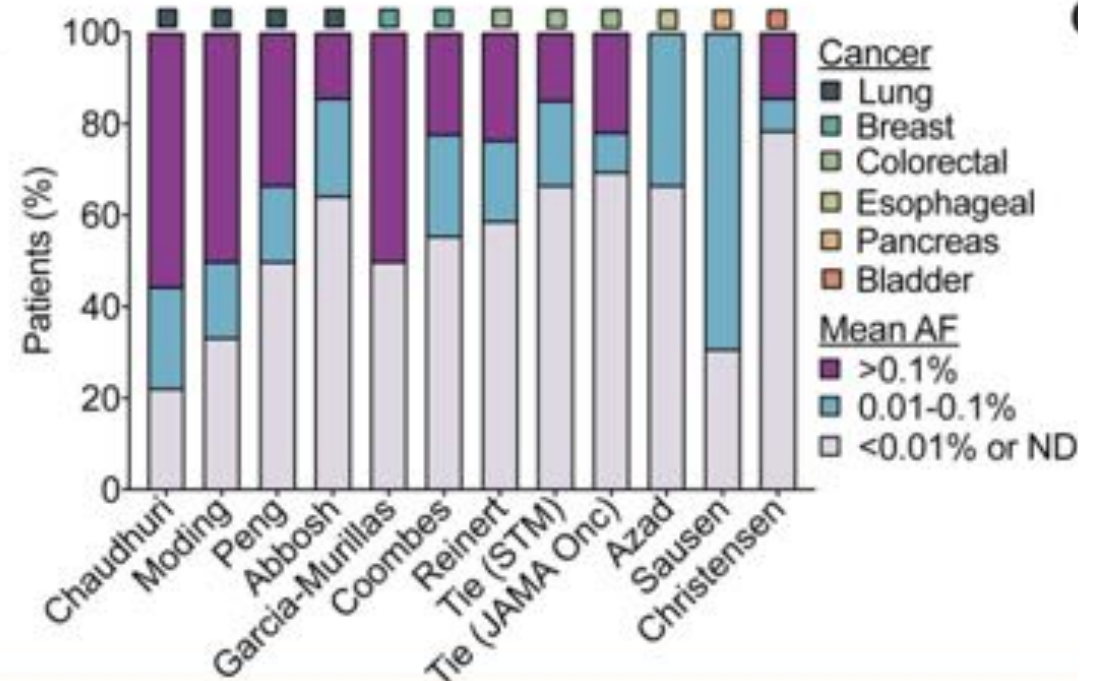
PATHFINDER



Pooled MRD Analysis – Solid Tumors



What degree of sensitivity is needed to declare a patient MRD negative? To modify therapy based on a MRD negative status?

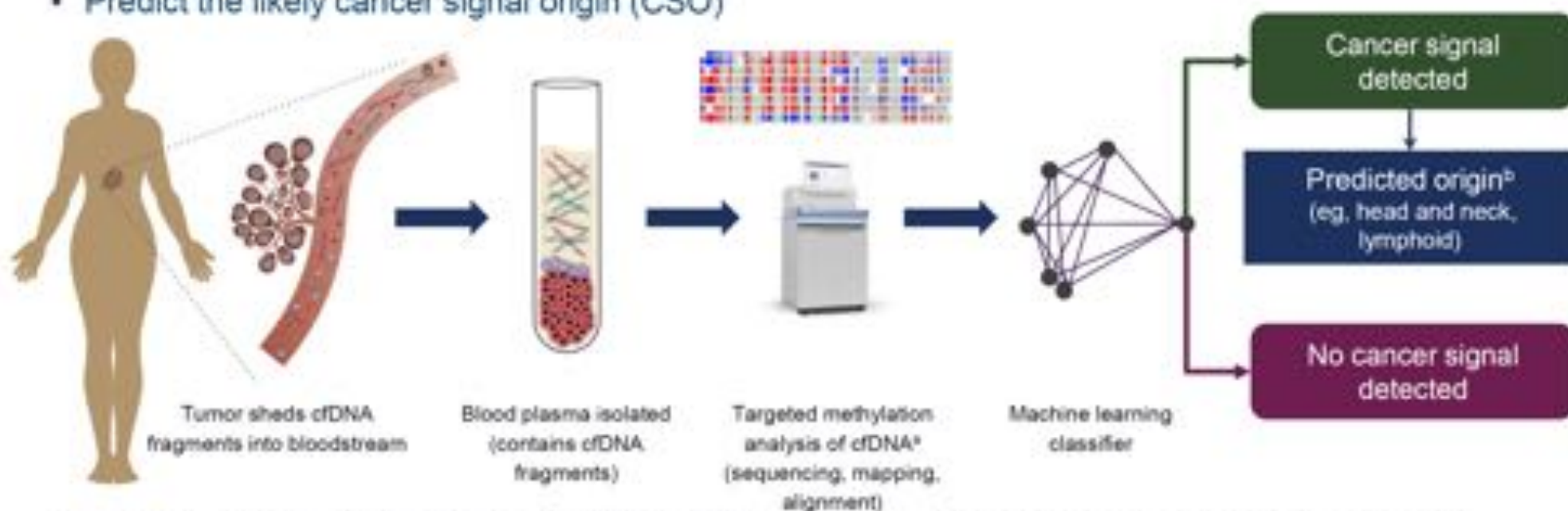


Modig et al. Cancer Discovery. 2021;11(12):2968-86.

Background: Multi-Cancer Early Detection (MCED) Blood Assays

MCED testing uses a targeted methylation, next-generation sequencing (NGS)-based assay to:

- Detect and analyze cfDNA in the bloodstream
- Deploy machine learning to detect a cancer signal
- Predict the likely cancer signal origin (CSO)



cfDNA, cell-free DNA. ^aIsulite treatment, targeted probes pull out fragments matching regions of interest. ^bFor a detected signal, the MCED test predicts 1-2 cancer signal origins (CSO) that can be either an anatomic site (eg. colorectal) or a cellular lineage (eg. lymphoid). Adapted from Liu MC, et al. Ann Oncol. 2020;31(8):745-750. PMID: 33506768

PATHFINDER Eligibility Criteria

Inclusion:

- Adults ≥ 50 years who were eligible for either:
 - With Additional Risk Cohort
 - Without Additional Risk Cohort
- Eligibility for With Additional Risk Cohort:
 - Lifetime history of smoking at least 100 cigarettes
 - Hereditary cancer predisposition^a
 - A history of cancer with no treatment for >3 years^b
- Eligibility for Without Additional Risk Cohort:
 - None of the above risk factors

^aGenetic cancer predisposition, hereditary cancer syndrome, or meeting criteria for germline testing based on NCCN guidelines.

^bPersonal history of invasive or hematologic malignancy, with definitive treatment completed >3 years prior to enrollment. Adjuvant hormonal therapy for breast cancer.



Deb Schrag, MD, MPH

Content of this presentation

Exclusion:

- Clinical suspicion of malignancy
- Undergoing diagnostic evaluation for malignancy
- History of invasive or hematologic malignancy diagnosed <3 years before enrollment
- Definitive treatment for invasive or hematologic malignancy <3 years before enrollment^b

Primary Objective: Understand extent of diagnostic testing to achieve diagnostic resolution

-Time to resolution

-Number and type of tests

Participant Characteristics

	With Additional Risk ^a n = 3,681	Without Additional Risk n = 2,940	Total N = 6,621
Age ^b , in years, mean (SD)	64.7 (8.7)	61.6 (8.1)	63.4 (8.6)
Female	65%	62%	63%
White, Non-Hispanic	93%	89%	92%
College Degree or Higher	59%	71%	65%
Up to Date With Standard Cancer Screening Prior to MCED Testing			
Colorectal Cancer ^c	91%	92%	92%
Breast Cancer ^d	78%	83%	80%

^aPrevious history of cancer, smoking, and hereditary risk.

^bParticipants >85 were eligible to participate, but to protect confidentiality, 85 years was the maximum age recorded and used in calculations for participants ≥85 years of age.

^cParticipants ≤75 years old, up to date with USPSTF colorectal cancer screening recommendations (n=4888 total eligible with complete information).

^dWomen 50-74 years old up to date with breast cancer screening recommendations (USPSTF, MRI, or ultrasound; n=3547 total eligible with complete information).



Deb Schrag, MD, MPH

Content of this presentation is copyright and responsibility of the author. Permission is required for re-use.

Fraction of Patients with Positive Signal

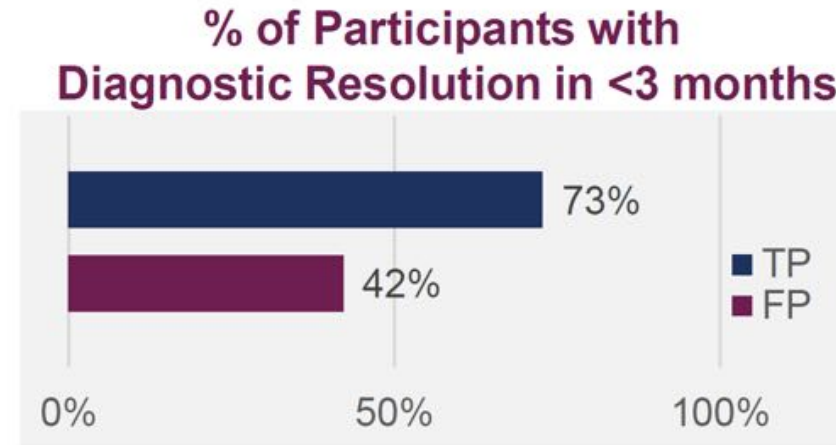
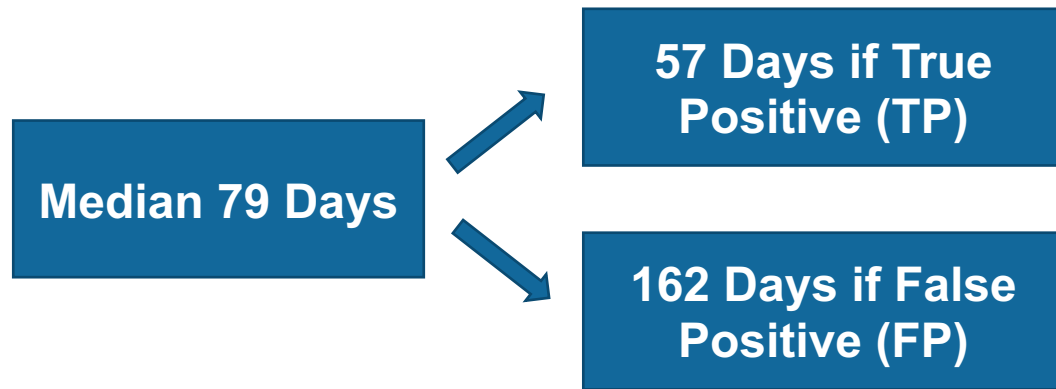
	With Additional Risk^a n = 3,681	Without Additional Risk n = 2,940	Total N = 6,621
Signal Detected	1.5%	1.2%	1.4%
No Signal Detected	98.5%	98.8%	98.6%

N=6621 analyzed

Schrag et al. ESMO 2022. #9030

Primary Objective: Achieving Diagnostic Resolution

Time Required to Achieve a Diagnostic Resolution



Extent of Testing to Achieve a Diagnostic Resolution

Imaging Procedure 92% (similar TP and FP)

Any Invasive Procedure: 82% TP 30% FP

Schrag et al. ESMO 2022. #9030

Secondary Objective: Accuracy of Predicted Cancer Origin

Test Performance: Ability to Predict Origin of Malignancy

	TP	FP	Total
Participants, n	35	57	92
Determinate predicted origin	34	53	87
Indeterminate predicted origin	1	4	5

Predicted Origin Accuracy	
First Predicted Origin,^a n	29/34 ^b
% (95% CI)	85.3 (69.9-93.6)
First or Second Predicted Origin,^{a,c} n	33/34 ^b
% (95% CI)	97.1 (85.1-99.8)

- The predicted origin helped to direct diagnostic workups

CI, confidence interval.

^aFor a detected signal, the MCEID test predicts cancer signal origins (CSO) that can be either an anatomic site (eg, colorectal) or a cellular lineage (eg, lymphoid).

^bExcludes 1 participant with indeterminate origin prediction from the true positive per study protocol.

^cProportion of first or second origin correctly predicted among true-positive participants.

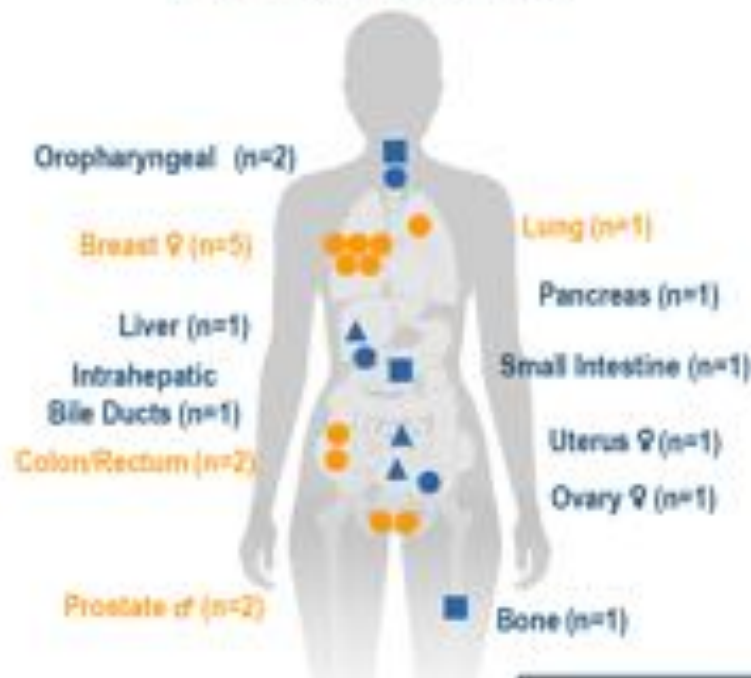


Deb Schrag, MD, MPH

Content of this presentation is copyright and responsibility of the author. Permission is required for re-use.

Cancers Diagnosed After a True Positive MCED Signal

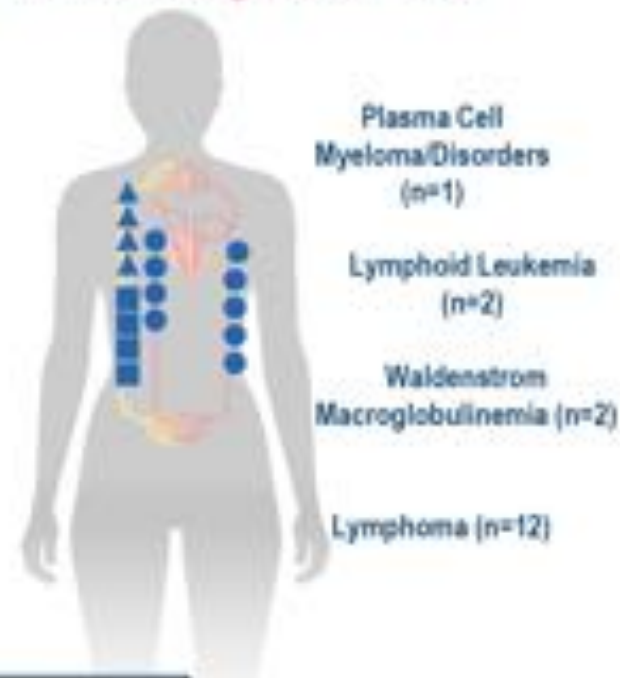
18 people diagnosed with Solid Tumors



35 people were diagnosed with 36 cancers

- 24 in high-risk cohort
- 11 in not-high-risk cohort
- 7 recurrent cancers
- 14 early-stage cancers
- 26 cancers lacking standard screening

17 People diagnosed with Hematologic Cancers



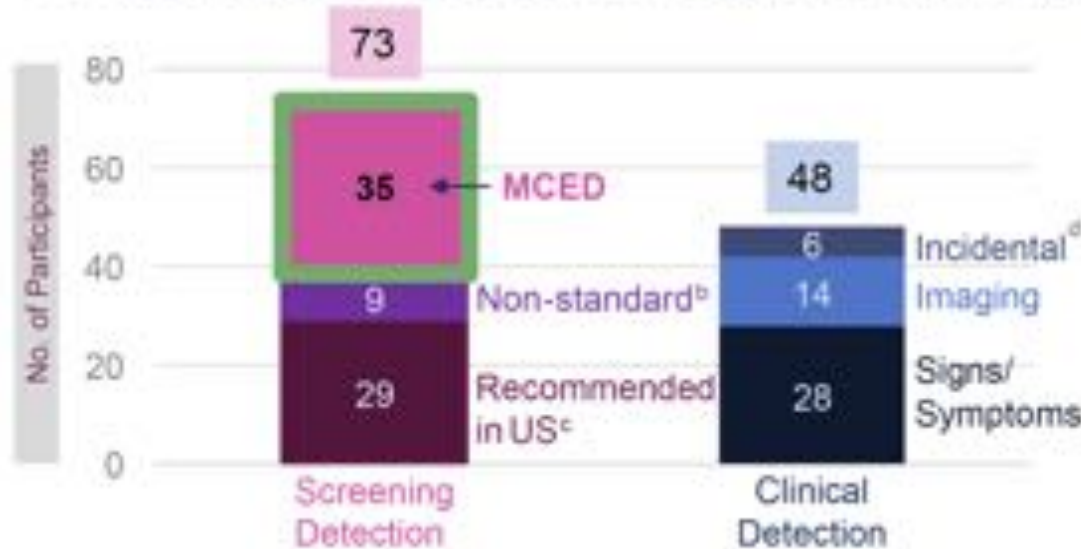
AJCC Staging: ▲ Stage I ■ Stage II ● Stage III/IV/No Stage/Recurrent

Available Screening: **USPSTF cancer screening** or No standard screening

Cancers Identified Within One Year of MCED Testing

Participants with Cancers Detected by Either Screening or Clinical Findings

121 participants had a cancer diagnosis within 1 year



- 35/121 (29%) had cancer diagnosed and positive MCED

Number needed to screen to detect one cancer: 189

MCED, multi-cancer early detection

^aBased on participants with cancer status assessment at the end of the study.

^b3 thyroid and 6 melanoma

^cBreast, cervical, colorectal, lung, and prostate cancer

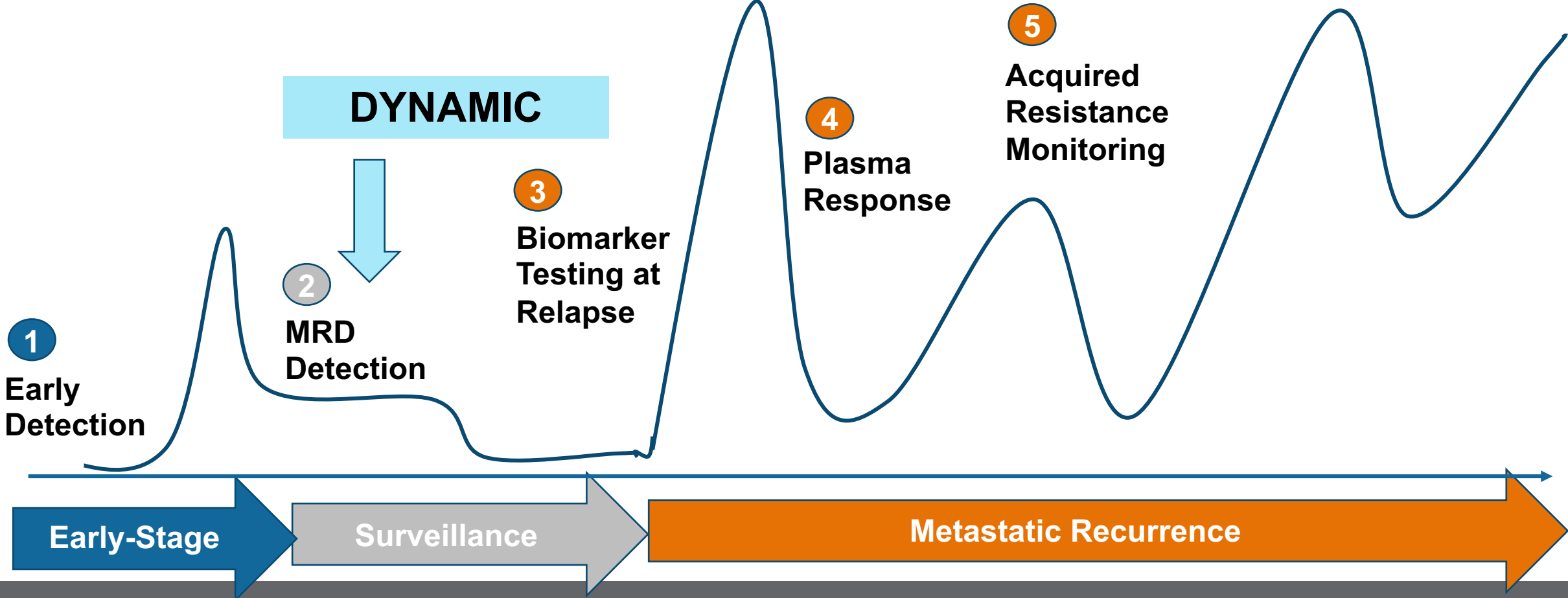
^d1 incidental radiology finding, 1 incidental finding on routine physical exam, 2 changed lab values, 1 surveillance of prior cancer, 1 follow-up after MGUS diagnosis



Deb Schrag, MD, MPH

Content of this presentation is copyright and responsibility of the author. Permission is required for re-use.

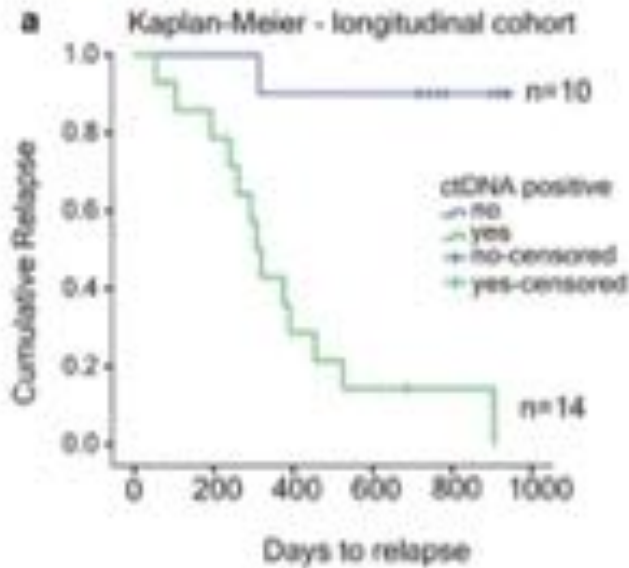
Cell-free DNA Across Many Phases of Disease



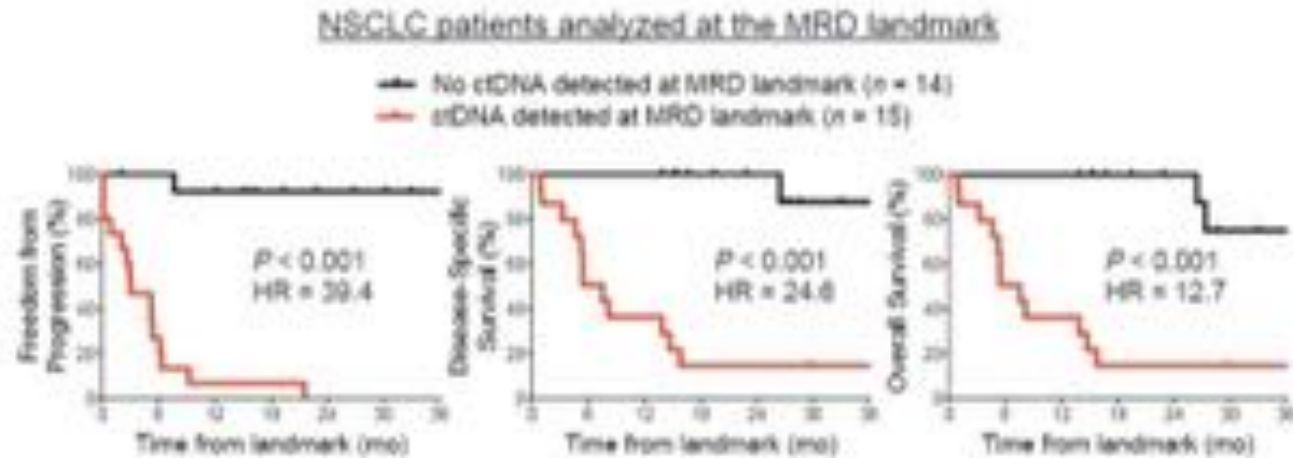
ctDNA can detect minimal residual disease (MRD) and it is a prognostic biomarker

18

Stages I-III NSCLC
Tumor-informed assay



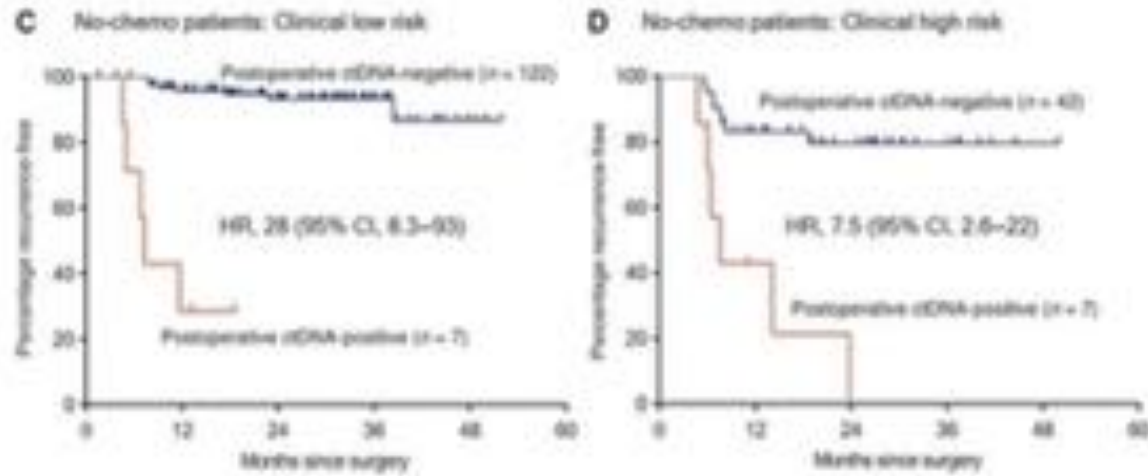
Stages I-III NSCLC
Tumor-naïve assay (CAPP-Seq)



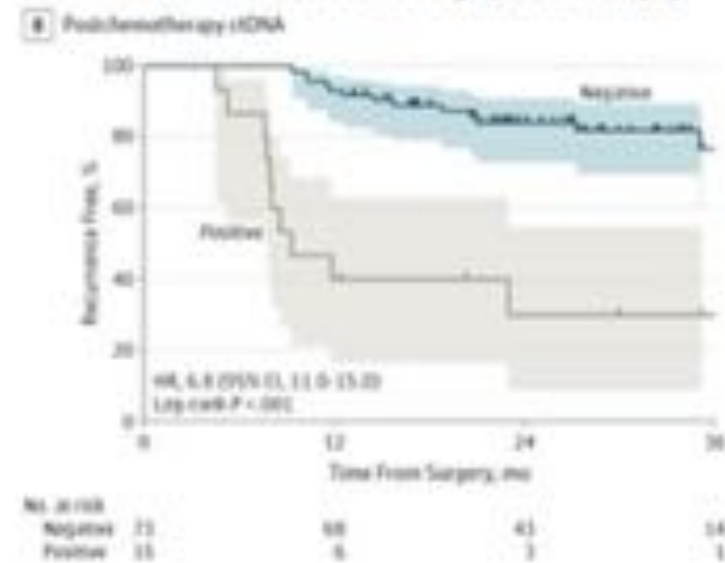
Abbosh C et al. *Nature*. 2017
 Chaudhuri A et al. *Cancer Discov*. 2017

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

Stage II CRC Tumor-informed assay (Safe-SeqS)



Stage III CRC Tumor-informed assay (Safe-SeqS)



Tie J et al. *Sci Transl Med*. 2016
Tie J et al. *JAMA Oncol*. 2019

DYNAMIC Study: Using ctDNA to Guide Adjuvant Chemotherapy In Stage II Colon Cancer

Can adjuvant chemotherapy be optimized for stage II disease?

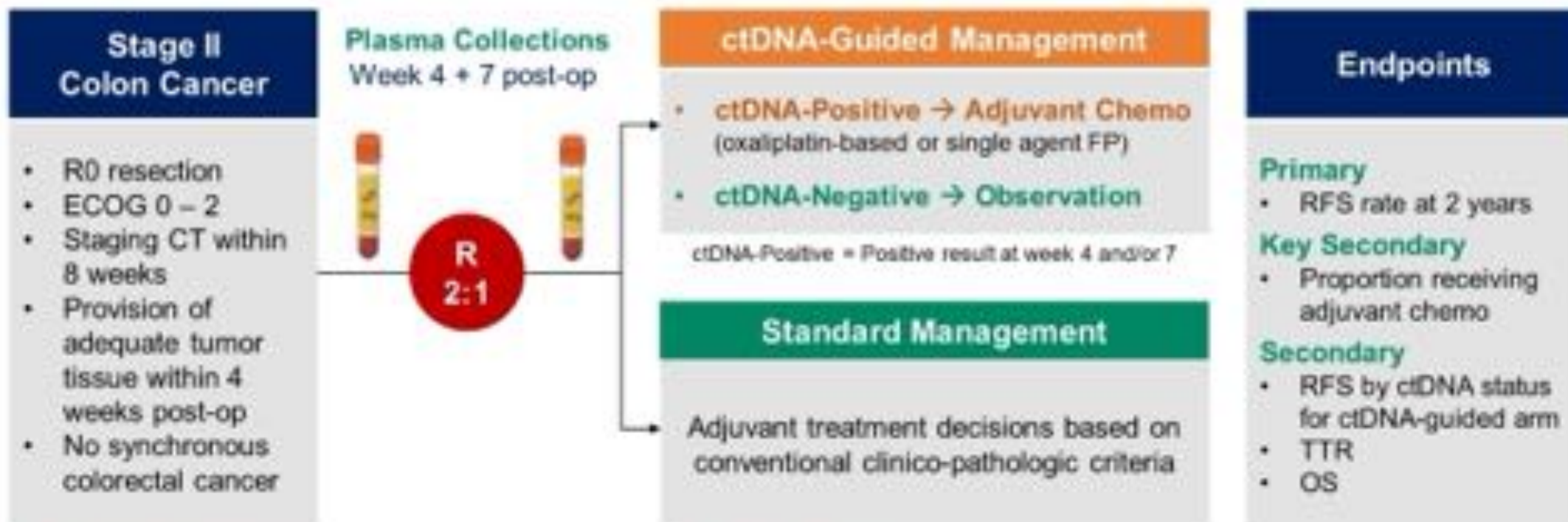
- Many will be cured by surgery alone (<5% survival benefit)
- Variability in use of adjuvant chemotherapy for stage II colon cancer
- Adjuvant chemotherapy to be considered if with high-risk features



DYNAMIC: Can a tumor-informed ctDNA-guided approach safely reduce use of adjuvant chemotherapy?

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

2022 ASCO
ANNUAL MEETING

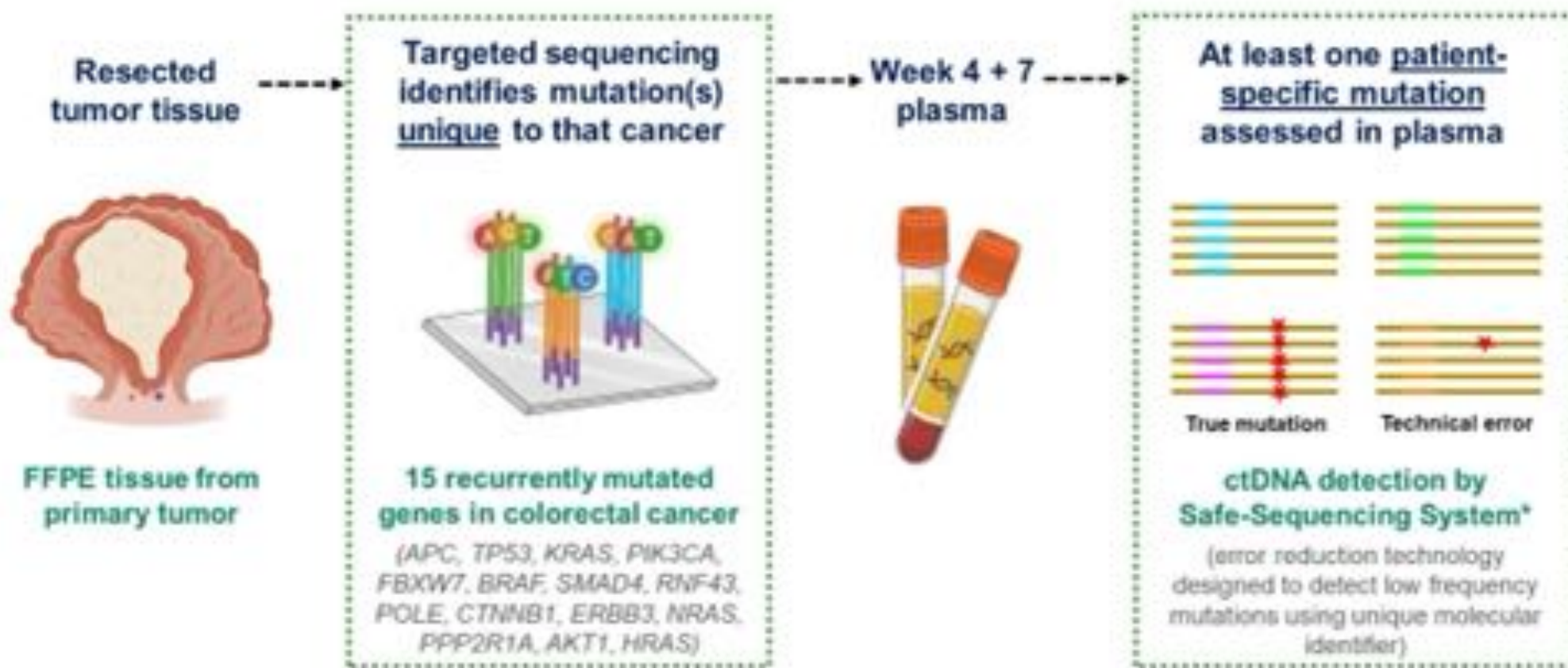
#ASCO22

PRESENTED BY
Jeanne Tie

Content of this presentation is the property of the
author. Shared by ASCO. Permission required for reuse.

ASCO
AMERICAN SOCIETY OF
CLINICAL ONCOLOGY
KNOWLEDGE CONQUERS CANCER

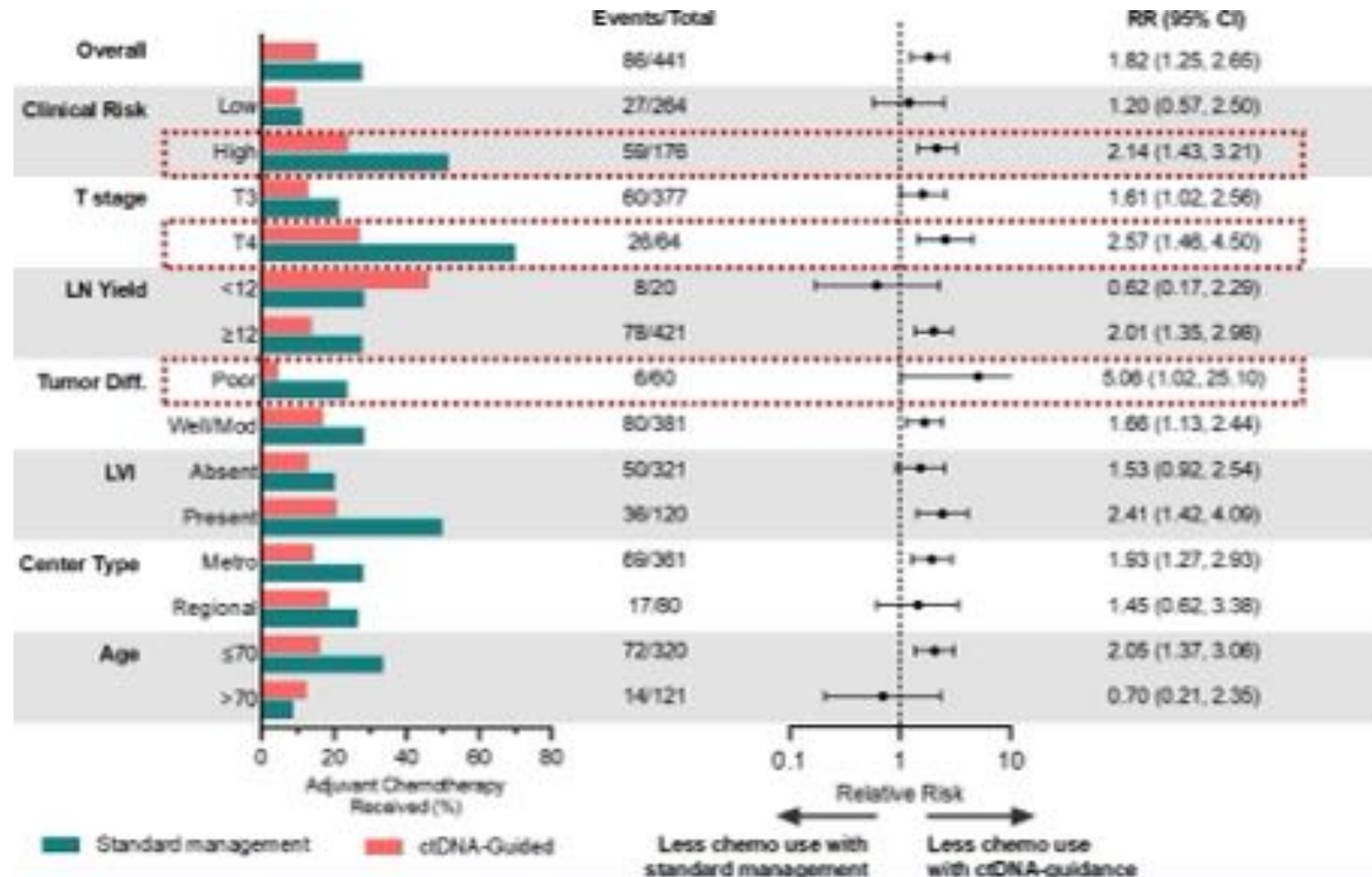
ctDNA Analysis: Tumor-Informed Personalized Approach



*Kinde et al. Proc Natl Acad Sci U S A. 2011;108(23):9530-5

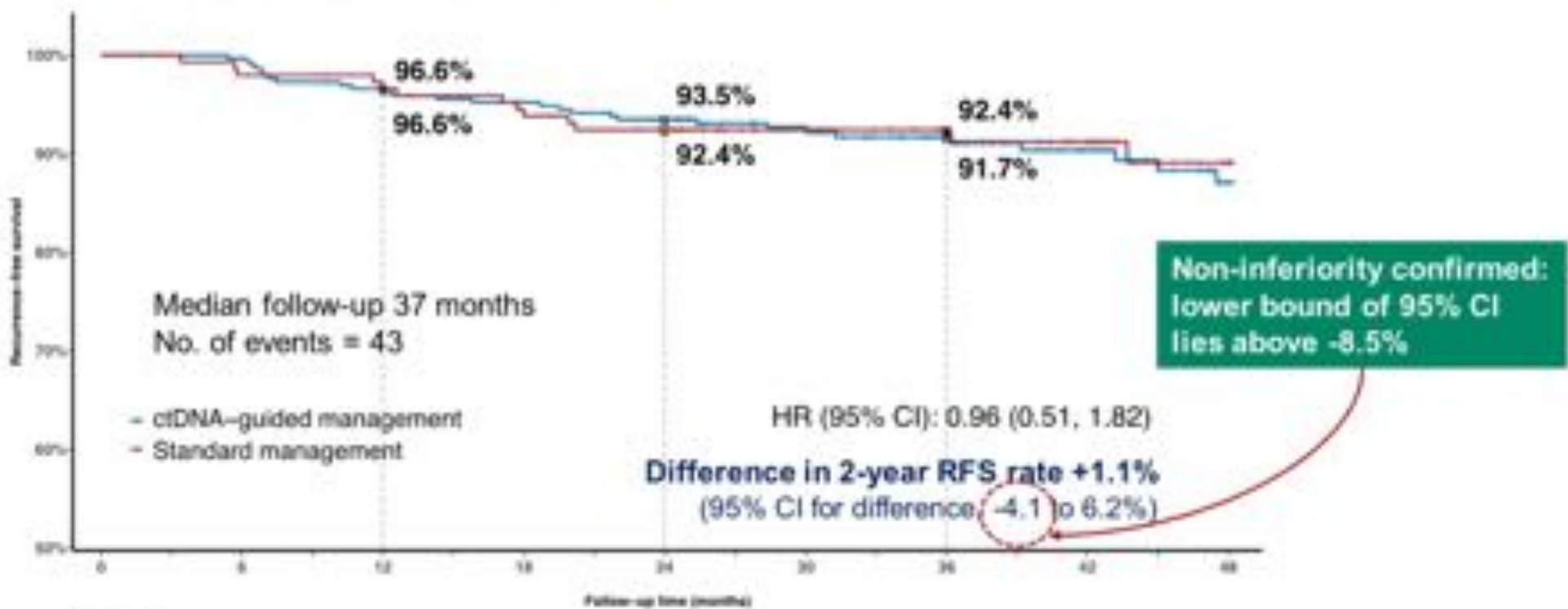
Adjuvant Chemotherapy Delivery

	ctDNA N = 294	Standard N = 147	P- value
Adjuvant Chemo Received n (%)	45 (15%)	41 (28%)	0.0017
Chemo Regimen			
Oxaliplatin-Based	62%	10%	<0.0001
Single Agent			
Fluoropyrimidine	38%	90%	



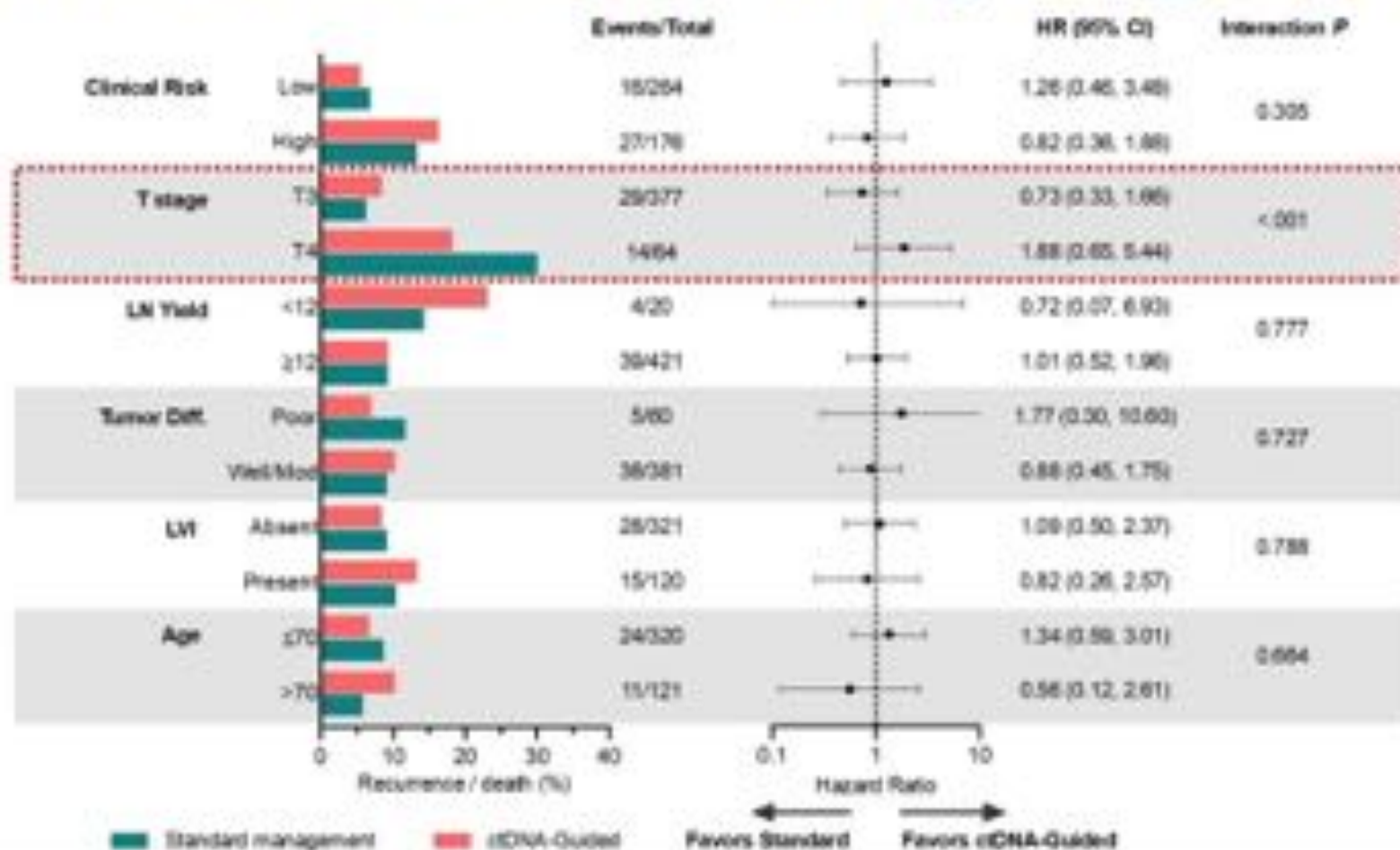
Tie et al. ASCO 2022. #LBA100

Recurrence-Free Survival



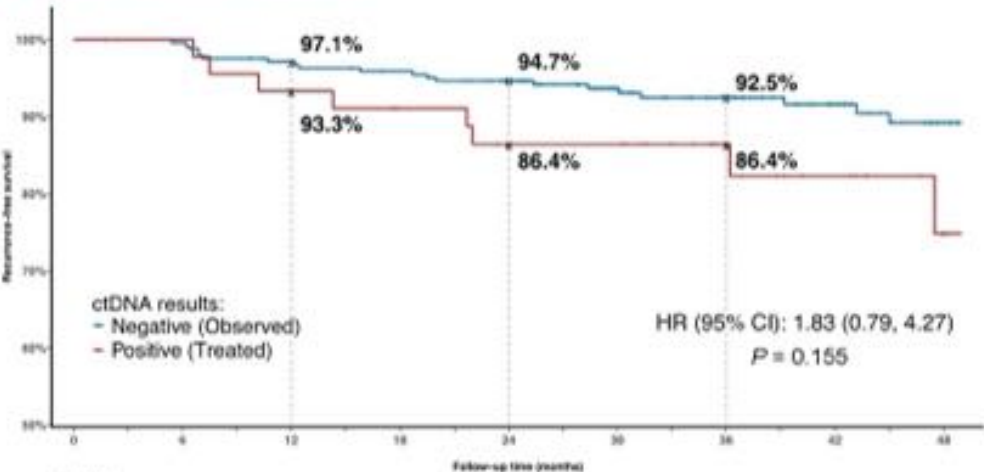
	0	6	12	18	24	30	36	42	48
ctDNA-guided	294	292	281	273	259	207	155	109	64
Standard	147	144	142	136	128	97	78	57	33

Recurrence-Free Survival in Key Subgroups



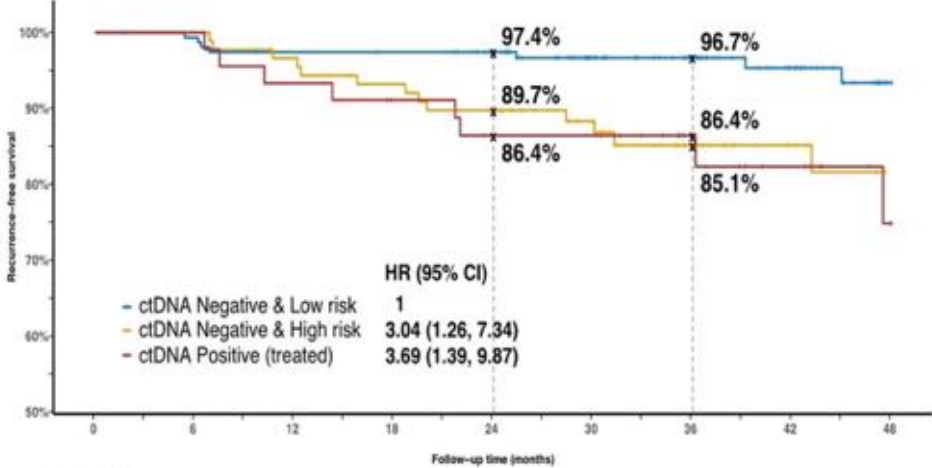
ctDNA Status and Recurrence-Free Survival

ctDNA Negative vs Positive



	0	6	12	18	24	30	36	42	48
ctDNA-Negative	346	244	236	231	220	160	131	93	55
ctDNA-Positive	45	45	42	39	36	36	22	16	9

ctDNA and Clinical Risk



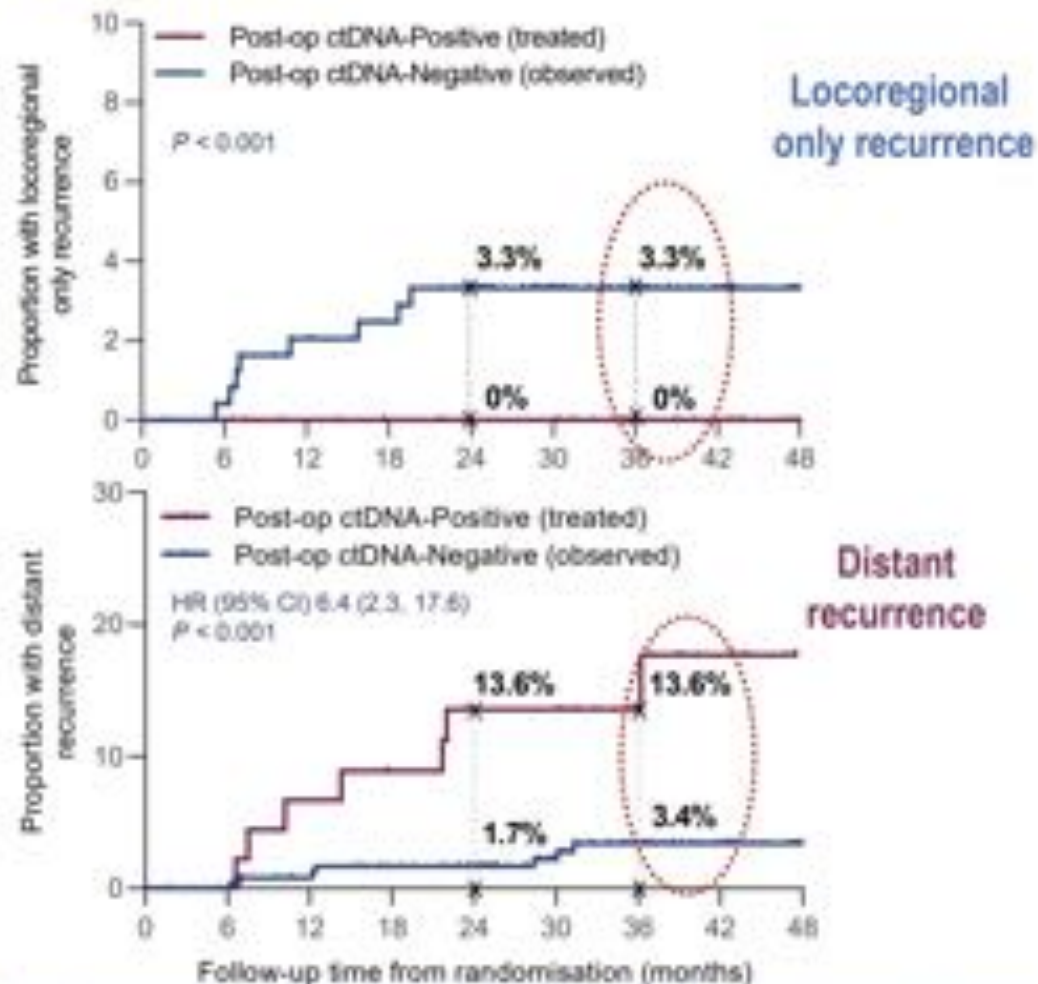
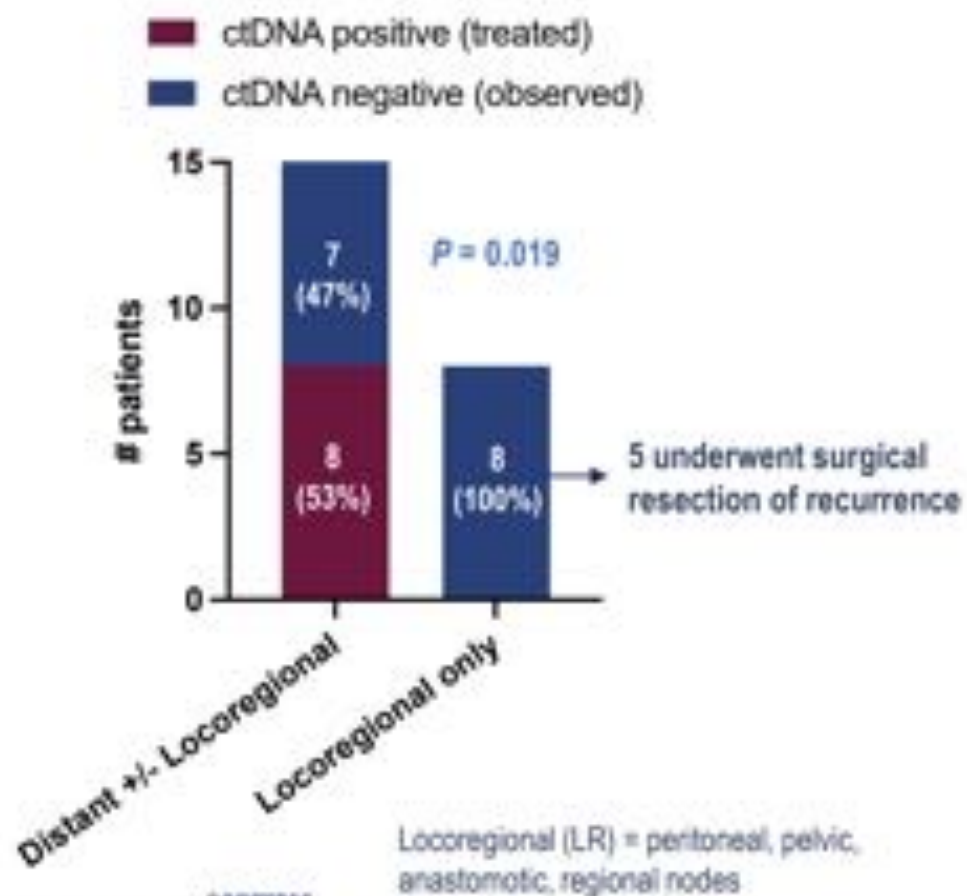
	0	6	12	18	24	30	36	42	48
ctDNA Negative & Low risk	156	154	150	149	142	109	80	64	34
ctDNA Negative & High risk	89	88	85	81	77	60	41	29	21
ctDNA Positive (treated)	45	45	42	39	36	36	22	16	9

Tie et al. ASCO 2022. #LBA100

Summary

- **For patients with stage II colon cancer, a ctDNA-guided approach (treating only patients with a positive ctDNA after surgery) compared to standard-of-care**
 - Substantially reduced the proportion receiving adjuvant chemotherapy (28% → 15%)
 - Did not compromise recurrence-free survival (2-year RFS: 93.5% vs 92.4%)
- **Patients with a positive ctDNA after surgery may derive RFS benefit from adjuvant chemotherapy**
 - Favorable 3-year RFS in patients treated with adjuvant chemotherapy (86.4%) versus low RFS in historical series (< 20%) if untreated
 - Ongoing trials (e.g., COBRA, CIRCULATE, CIRCULATE-PRODIGE) will provide further guidance regarding the optimal use of ctDNA-informed management
- **ctDNA-negative patients have a low recurrence risk without adjuvant chemotherapy**
 - 3-year RFS 92.5% (clinical low risk: 96.7%; T3: 94.2%)

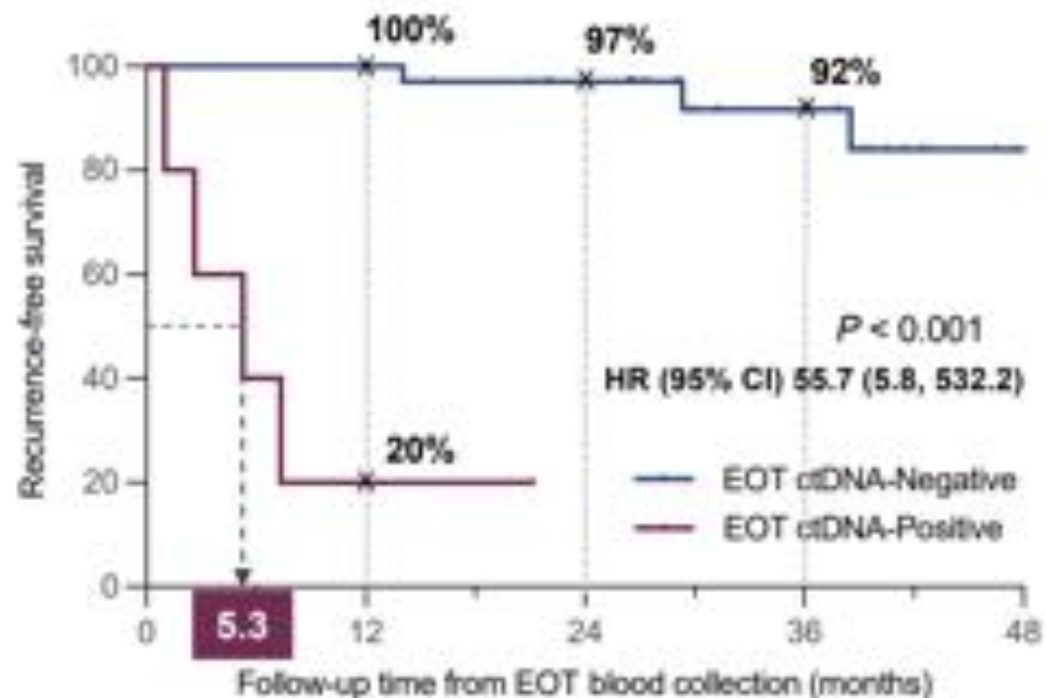
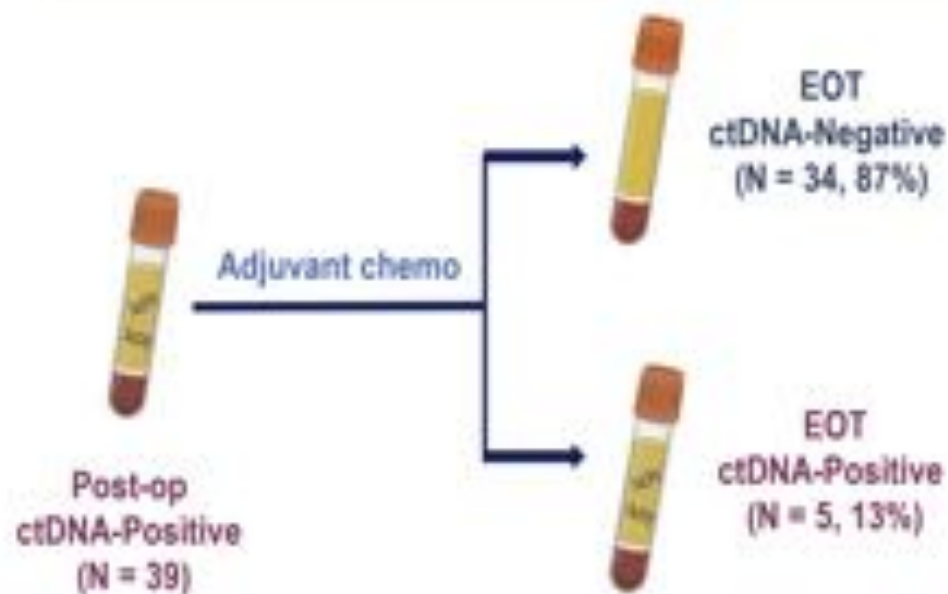
Post-op ctDNA and Sites of Recurrence



Content of this presentation is copyright and responsibility of the author. Permission is required for re-use

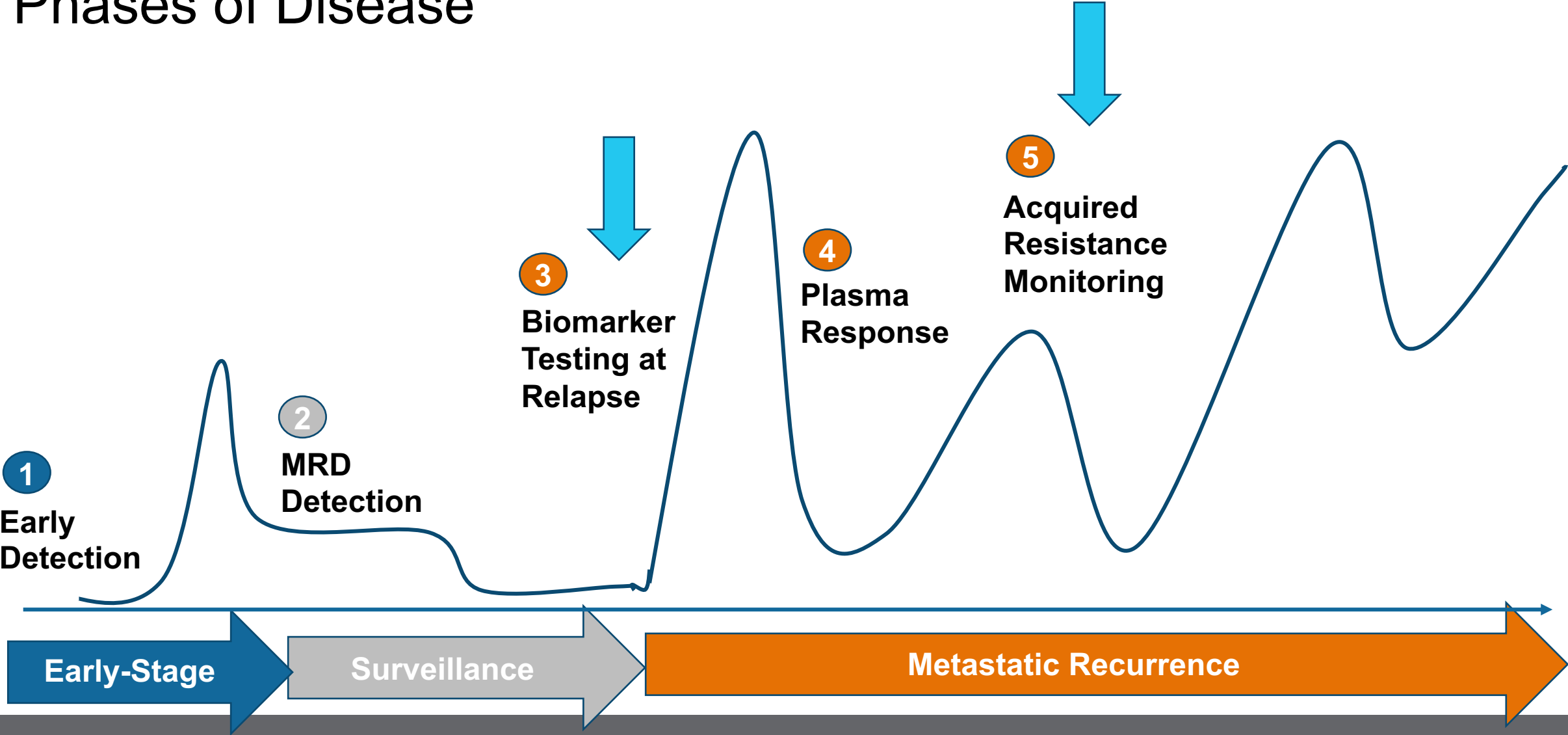
Post-op ctDNA-Positive: End-of-Treatment ctDNA and RFS

End-of-treatment (EOT) ctDNA collected in 39 of 44 post-op ctDNA-positive patients treated with adjuvant chemotherapy



	0	12	24	36	48
ctDNA-Negative	34	34	29	15	4
ctDNA-Positive	5	2	1	1	1

Cell-free DNA Across Many Phases of Disease



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

Table 1. Comparison of tumor versus ctDNA results for the guideline-recommended biomarkers in newly diagnosed metastatic NSCLC with FDA-approved therapies. EGFR was 10 deletion and US181, ALK fusion, ROS1 fusion, and BRAF V600E

		True +	True -	True not assessed	True (95)	Total		
EGFR (10 del)	ctDNA +	9	0	0	1	10	Sensitivity	90.0%
	ctDNA -	4	221	0	25	245	PPV	100.0%
	ctDNA TND	0	0	1	1	1	Specificity	100.0%
	ctDNA cancelled	0	0	1	0	1	NPV	99.0%
	Total	23	221	2	27	282	Concordance	99.2%
EGFR L858R	ctDNA +	7	0	0	1	8	Sensitivity	100.0%
	ctDNA -	1	211	0	24	237	PPV	100.0%
	ctDNA TND	0	0	1	1	1	Specificity	100.0%
	ctDNA cancelled	0	0	1	0	1	NPV	99.9%
	Total	10	211	2	27	282	Concordance	99.6%
ALK fusion (rearr)	ctDNA +	5	0	0	1	6	Sensitivity	83.3%
	ctDNA -	3	207	27	25	282	PPV	100.0%
	ctDNA TND	1	0	2	0	3	Specificity	100.0%
	ctDNA cancelled	0	1	0	0	1	NPV	99.0%
	Total	9	208	29	26	282	Concordance	99.6%
ALK fusion (unrearr)	ctDNA +	4	0	0	1	5	Sensitivity	71.4%
	ctDNA -	2	207	27	25	282	PPV	100.0%
	ctDNA TND	1	0	2	0	3	Specificity	100.0%
	ctDNA cancelled	0	1	0	0	1	NPV	99.0%
	Total	7	208	29	26	282	Concordance	99.6%
ROS1 fusion	ctDNA +	0	0	0	0	0	Sensitivity	-
	ctDNA -	2	101	25	20	288	PPV	-
	ctDNA TND	0	1	5	1	7	Specificity	100.0%
	ctDNA cancelled	0	1	0	0	1	NPV	99.7%
	Total	2	103	30	21	282	Concordance	99.7%
BRAF V600E mutation	ctDNA +	2	0	0	0	2	Sensitivity	100.0%
	ctDNA -	0	80	12	0	92	PPV	100.0%
	ctDNA TND	0	5	0	0	5	Specificity	100.0%
	ctDNA cancelled	0	0	1	0	1	NPV	100.0%
	Total	2	85	12	0	102	Concordance	100.0%

NOTE: Overall concordance across all four genes was greater than 99.2%, with a PPV of 100%. With continuous assay improvements, one ctDNA result originally reported as a false-negative for ALK fusion was identified as positive.

Stage IV NSCLC
Tumor-naïve assay
(Guardant 360)

Leigh N et al. Clin Cancer Res. 2019

cfDNA for symptomatic patients hospitalized with a new diagnosis of lung cancer

METHODS

PATIENT ENROLLMENT
 30 patients were enrolled from December 2021 to August 2022. Overall population received liquid biopsy, only 20 patients performed also conventional biopsy

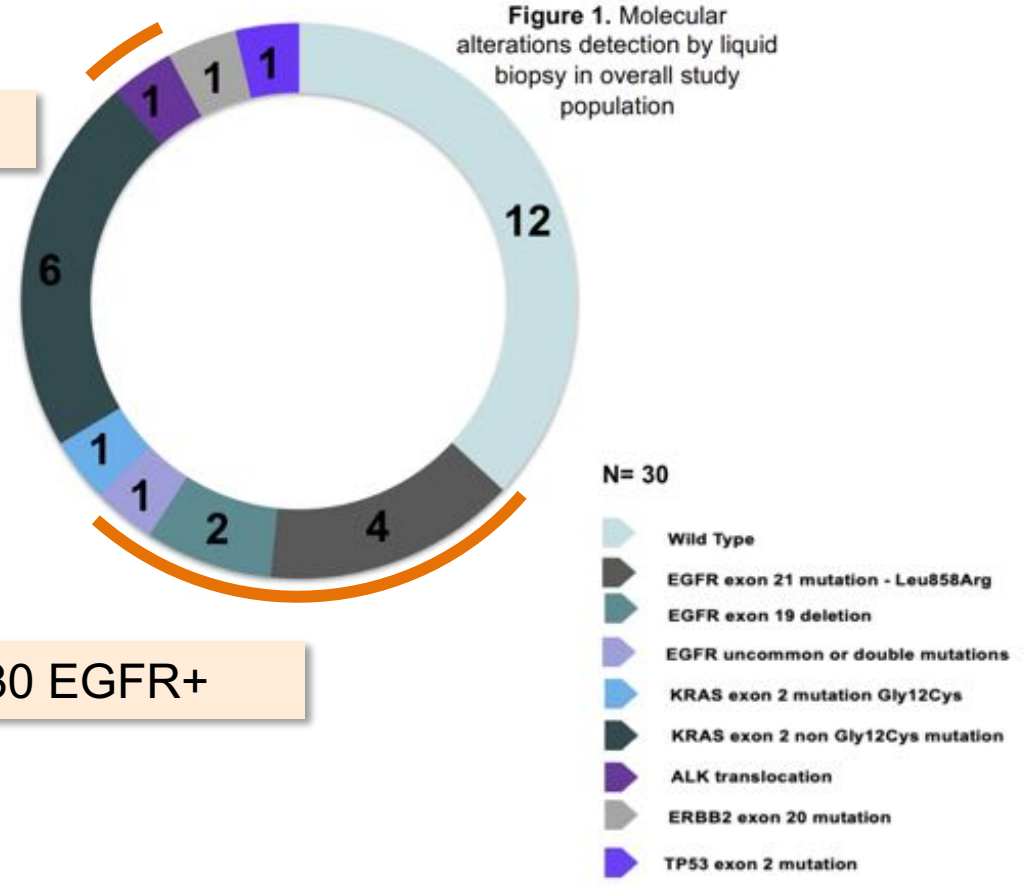


PLASMA COLLECTION
 For each patient plasma sample was collected at time of diagnosis, for patients with any molecular alterations, plasma sample was collected also at time of first reevaluation after starting treatment and at time of disease progression

DEMOGRAPHIC AND CLINICAL PATIENT'S CHARACTERISTICS AT DIAGNOSIS	
Median age – yrs	73
Sex- n	14 M
	16 F
Smoking status - n	8 Current smoker
	11 Former smoker
	11 Never smoker
Performance status (ECOG)	12 PS ECOG 1
	6 PS ECOG 2
	12 PS ECOG 3
Disease stage	28 stage IV
	2 stage III
First Symptoms	11 Dyspnoea
	8 Pain
	4 Cough/Haemoptysis
	7 Other

1/30 ALK+

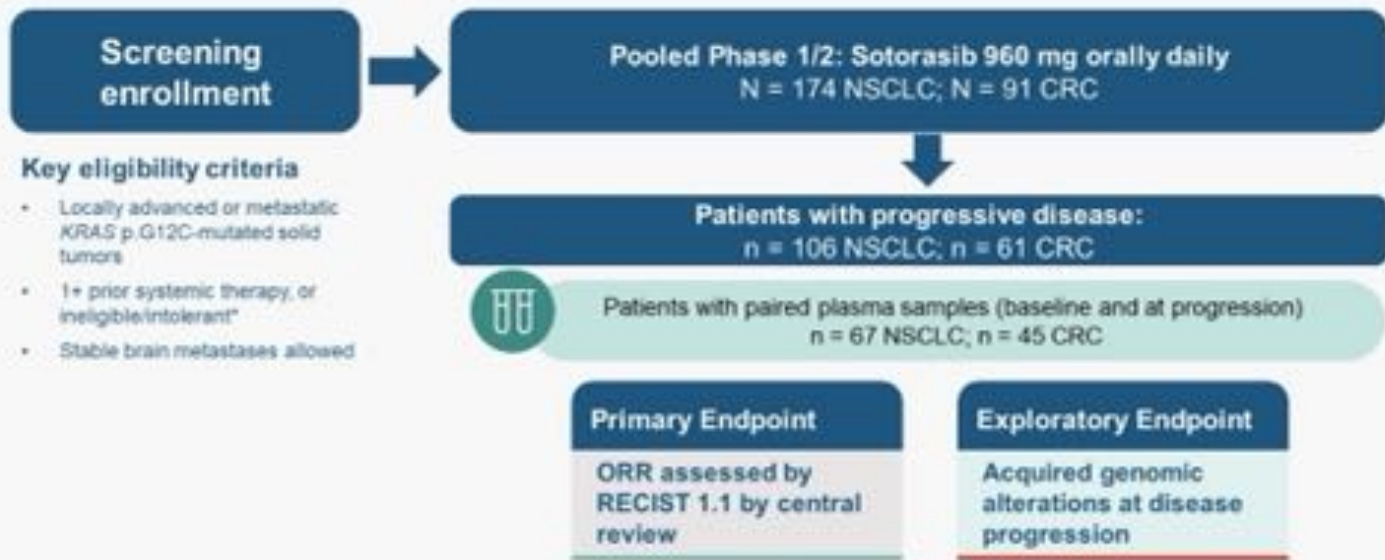
7/30 EGFR+



Median time (days) from assay to result
 Liquid Biopsy 11 days
 Conventional Biopsy 20 days

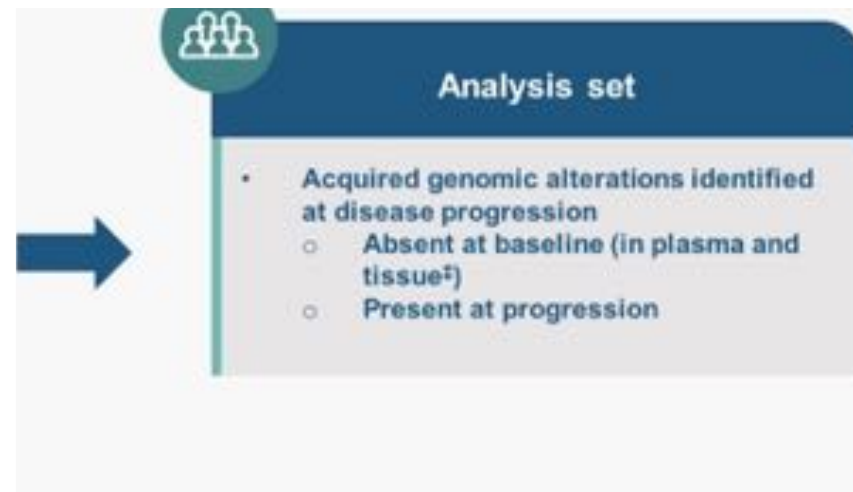
Parisi et al. ESMO 2022. #1099P

CodeBreak 100 Study Schema



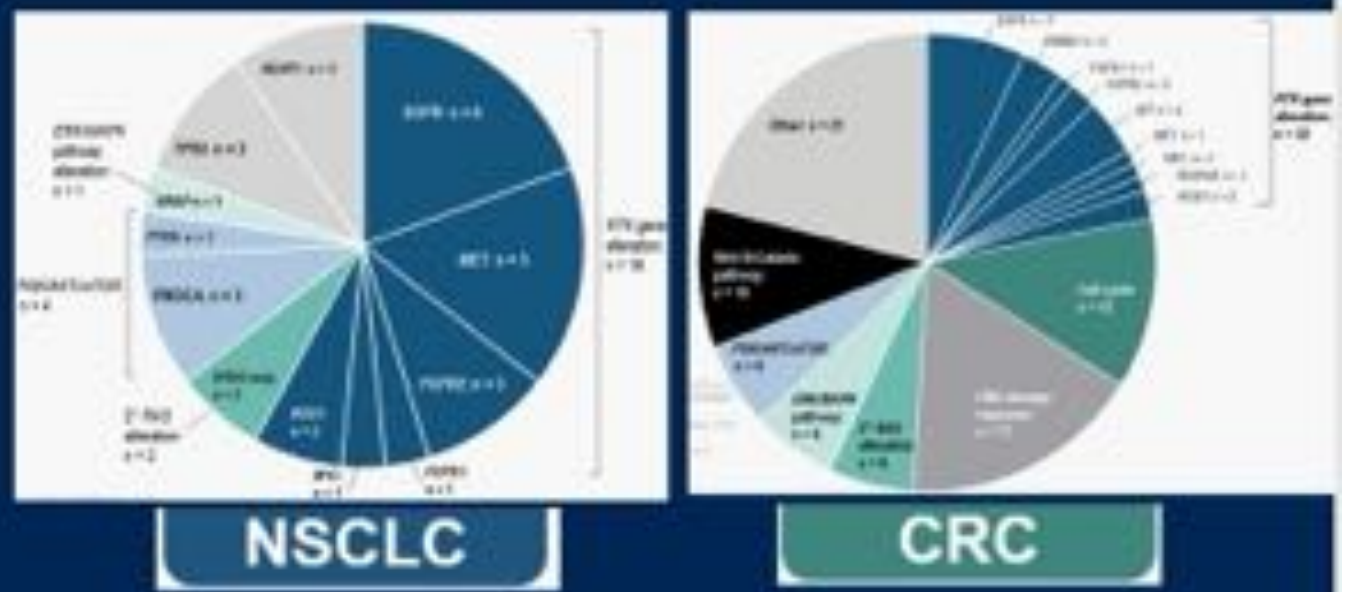
Presented by Bob Li. ASCO 2022.

cfDNA Assays

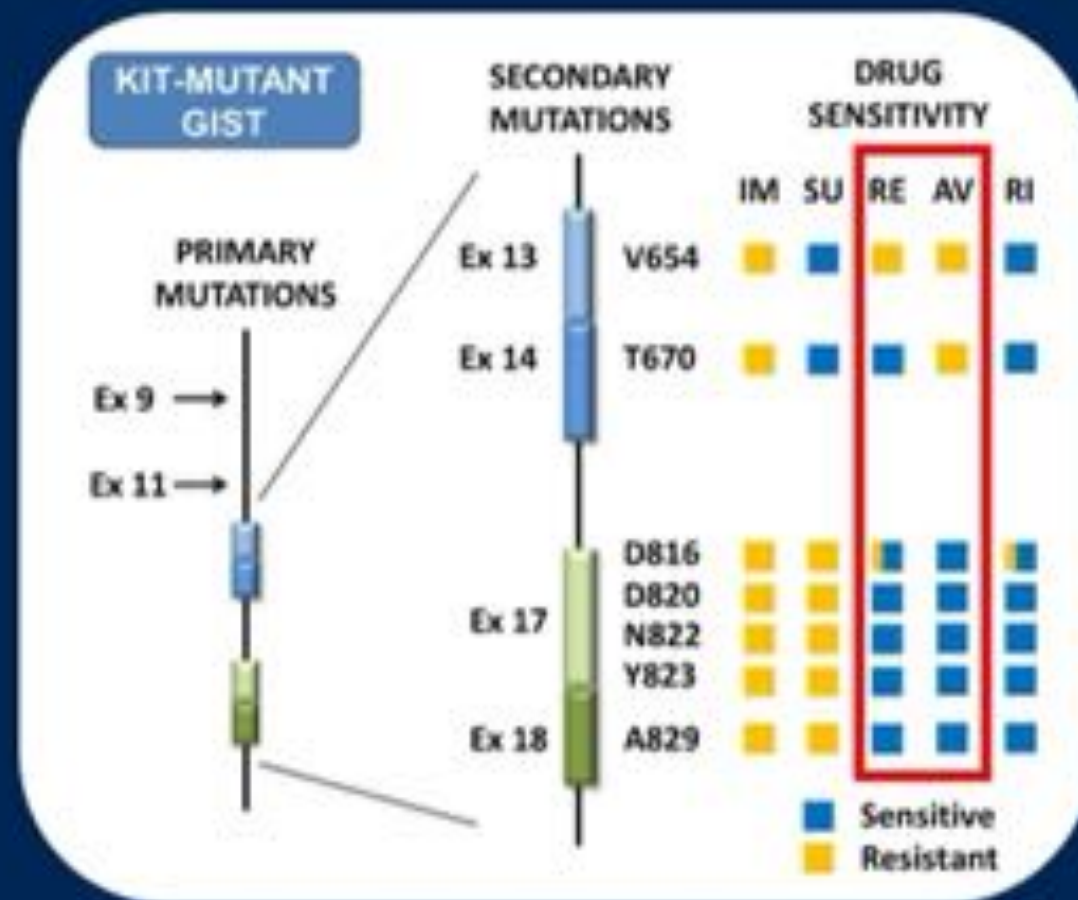
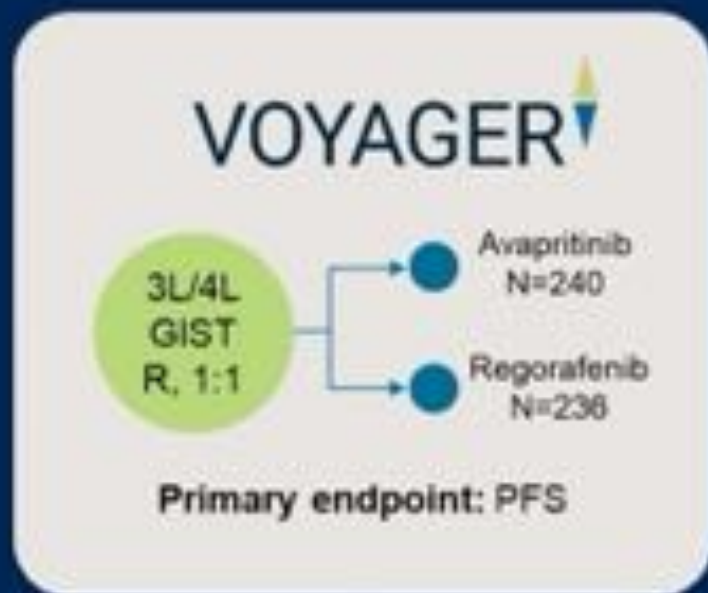


Largest evaluation of acquired resistance to sotorasib in *KRAS* p.G12C-mutated NSCLC and CRC: plasma biomarker analysis of CodeBreakK 100 Li et al.

- In both NSCLC and CRC patients, acquired resistance as detected by ctDNA was heterogenous
- Despite this, many mutations were in genes that have targeted therapies, particularly in RTKs
- This could lead to clinical utility studies combining sotorasib with other inhibitors.



Background VOYAGER phase III clinical trial



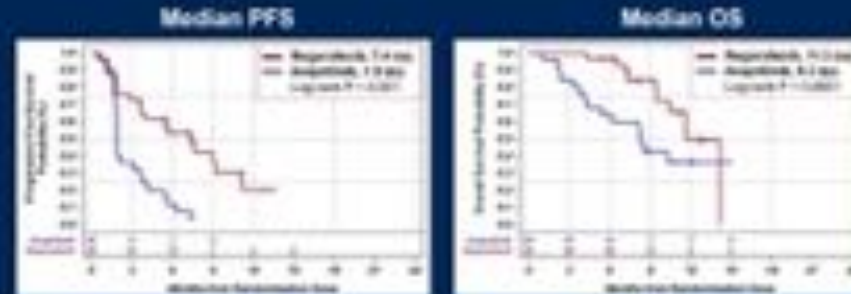
Circulating tumor DNA (ctDNA) analyses of the phase III VOYAGER trial: KIT mutational landscape and outcomes in patients with advanced gastrointestinal stromal tumor (GIST)

César Serrano et al.

- ctDNA sequencing correlates with outcomes in pretreated GIST. Identification of ATP binding pocket mutations in KIT negatively correlates with avapritinib activity.
- The multikinase inhibitory nature of regorafenib may be relevant for its clinical activity regardless the type of KIT secondary mutation by plasma.
- Potential clinical utility of selecting more targeted therapy in the absence of mutation

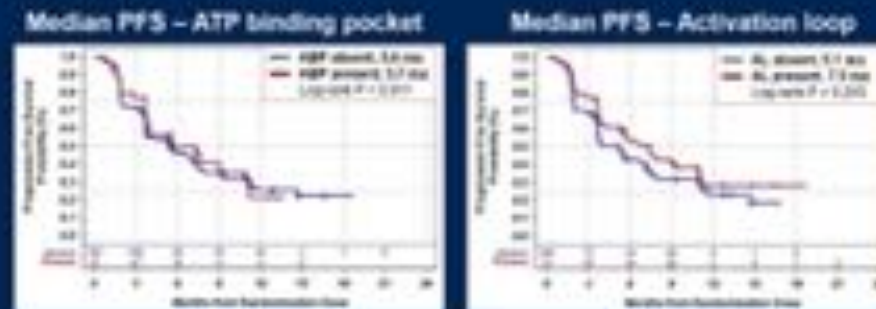
ctDNA mutations & outcomes: ATP-binding pocket

Shorter mPFS and mOS in patients with ctDNA+ ATP binding pocket mutations treated with AVAPRITINIB v. REGORAFENIB

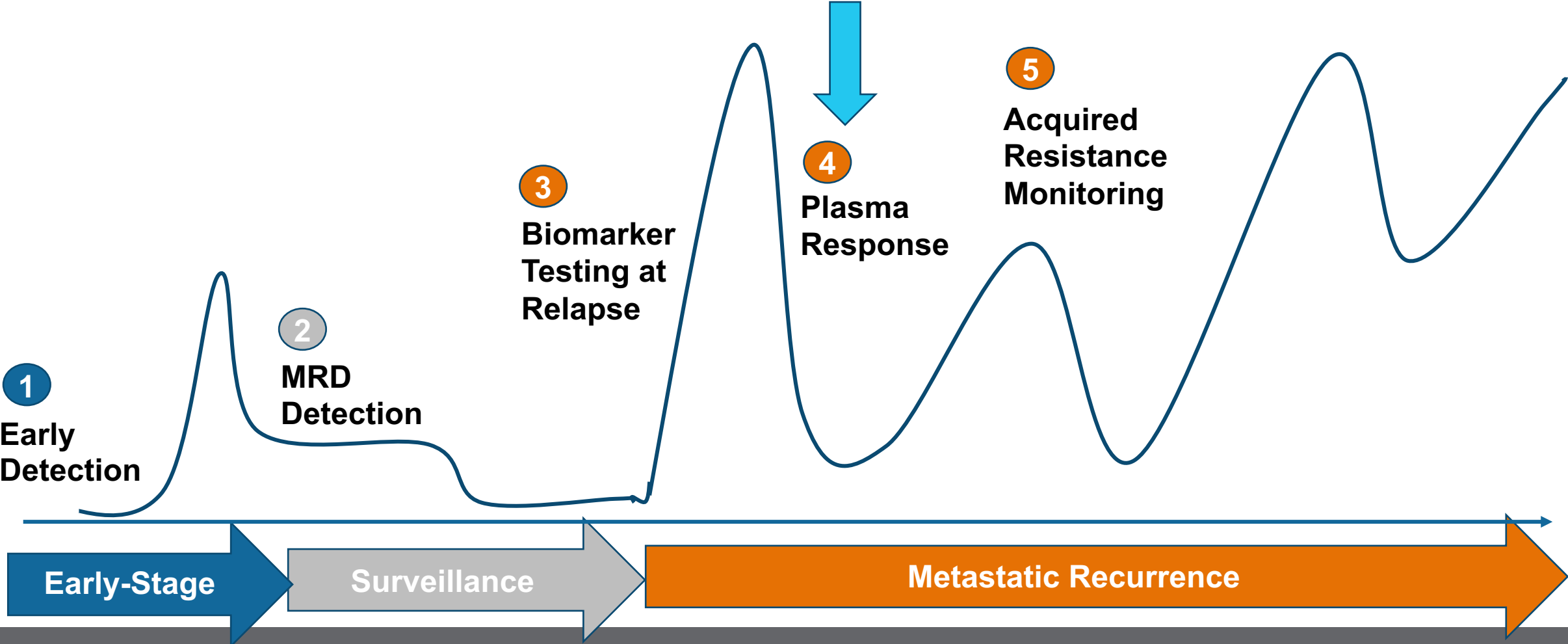


ctDNA mutations & outcomes: Regorafenib

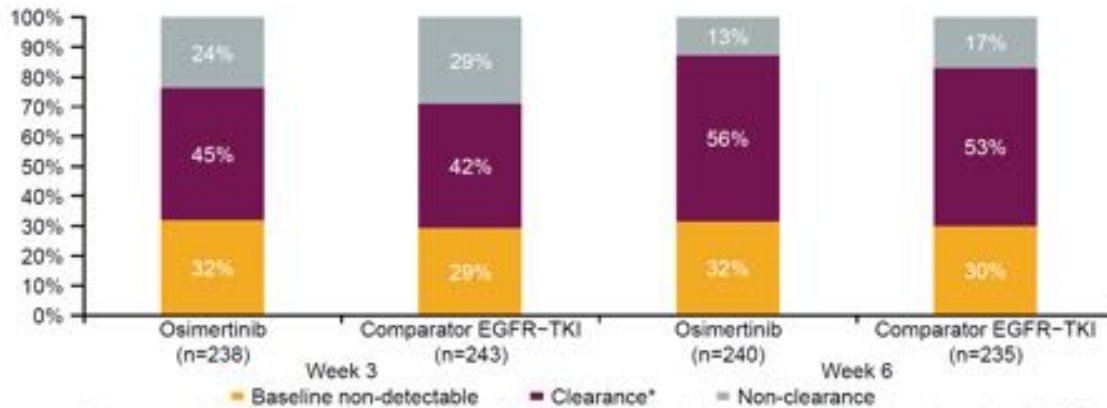
REGORAFENIB showed similar activity regardless KIT mutational status and the location of KIT mutation



Cell-free DNA Across Many Phases of Disease



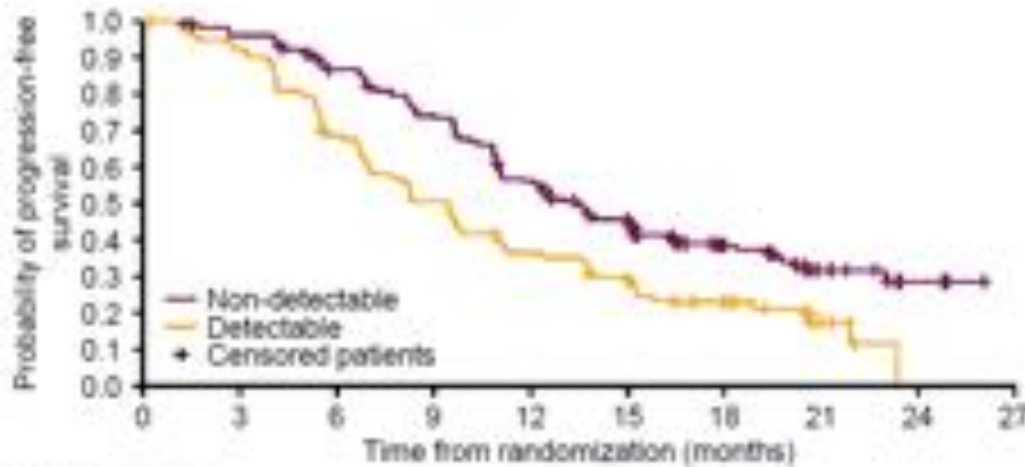
How often does the EGFRm clear from the plasma?



At 6 weeks osimertinib treatment

- 13% undetectable at baseline
- 56% convert to negative
- 32% remain detectable

Impact of positive week 3 plasma EGFR on PFS?



Plasma EGFR positive at 3 weeks

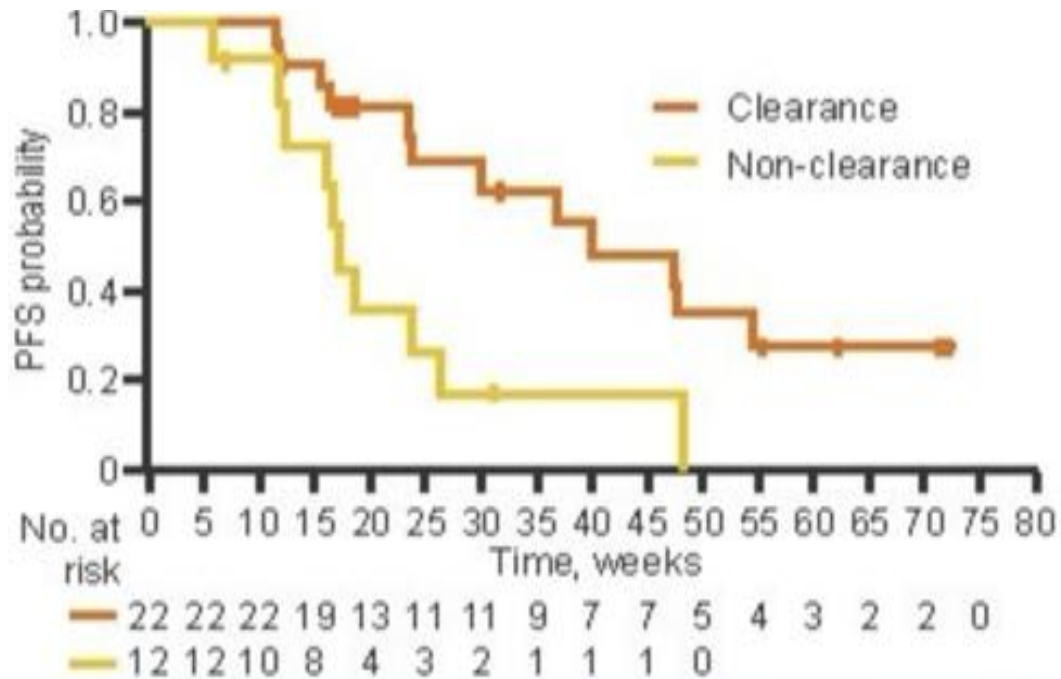
PFS 9.5 vs 13.5 months (HR 0.57, 0.4-0.7)

Plasma EGFR positive at 6 weeks

PFS 8.2 vs 13.5 months (HR 0.51, 0.4-0.7)

Zhou et al. ASCO 2019. Abstract #9020

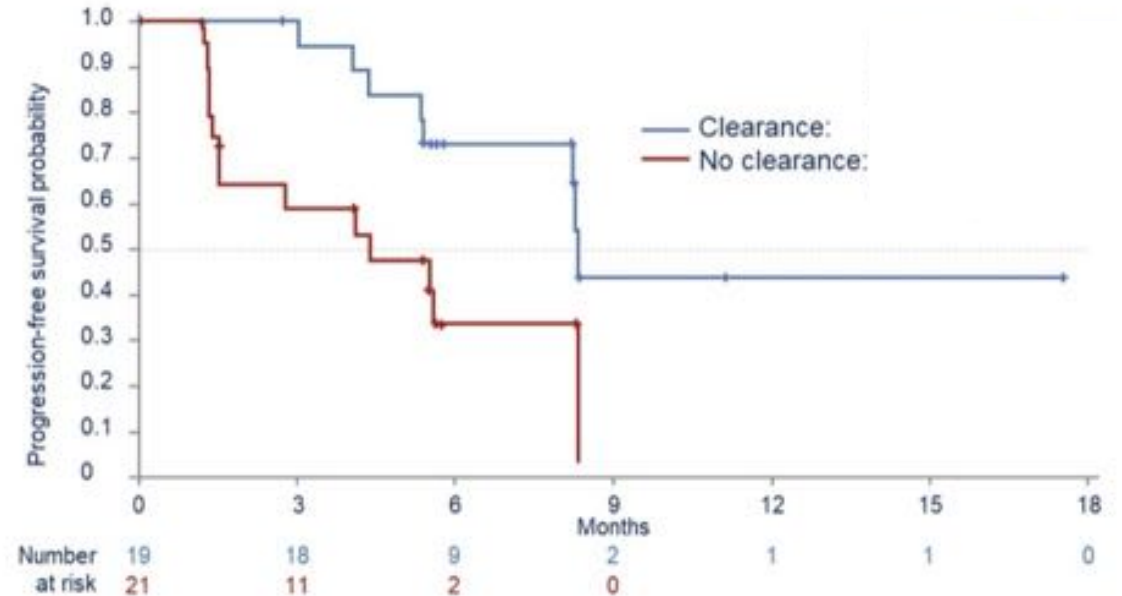
TATTON Savolitinib + Osimertinib for MET+ EGFR TKI Resistance



CfDNA status at cycle 3 or 4

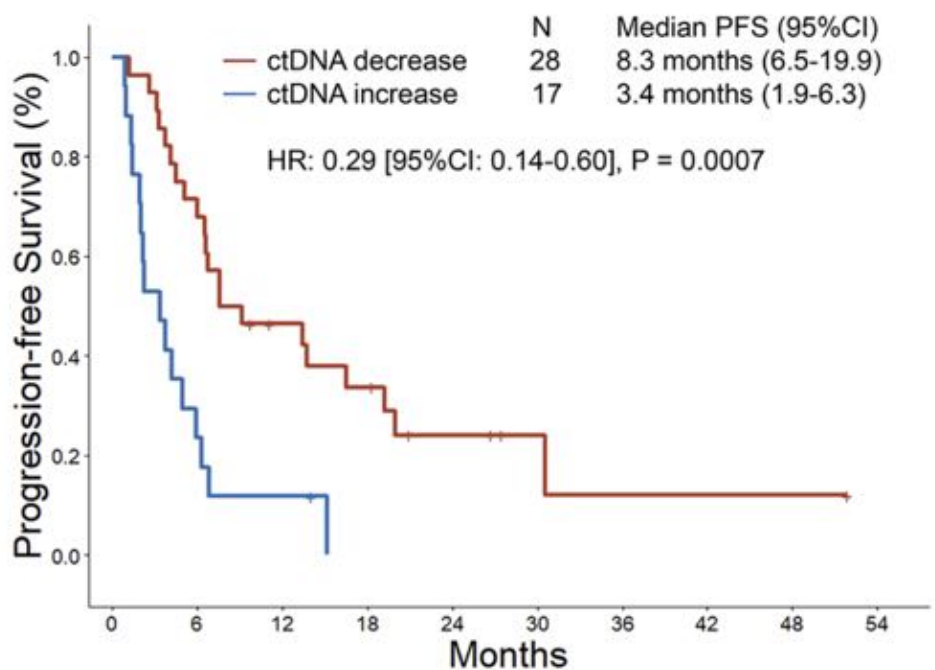
PFS 3.9 vs 9.1 months
(HR 0.34, 0.14-0.81)

U3 1402-A-U102: HER3-ADC for EGFR TKI resistance



CfDNA status at week 3/6

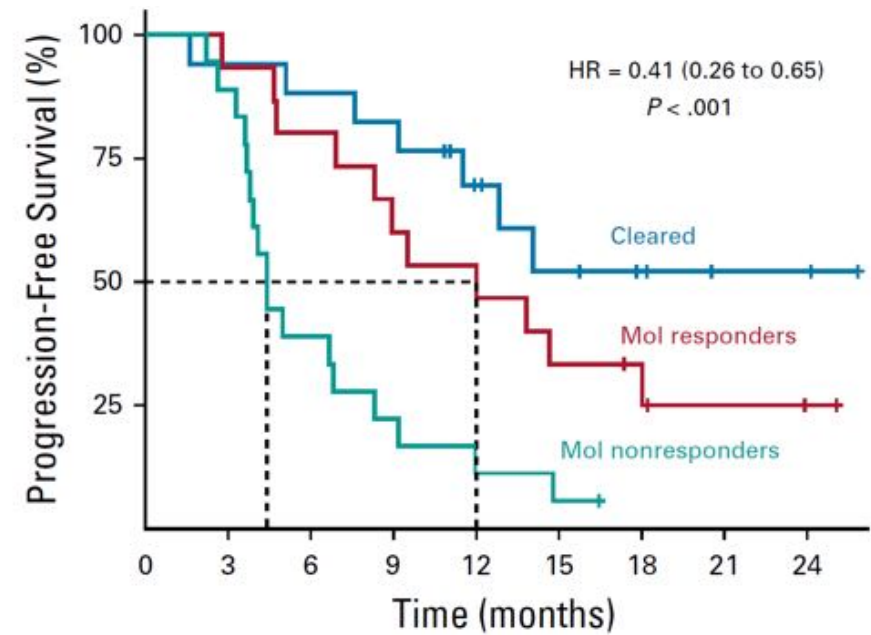
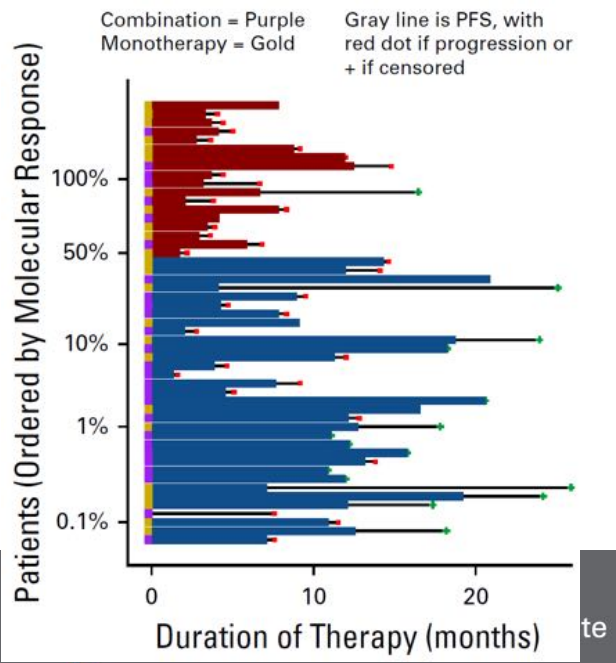
PFS 4.4 vs 8.3 months
(HR 0.33, 0.13-0.81)



Early cfDNA Trends Predict Survival Outcomes on ICI Therapy

cfDNA status 1st follow up (mean 21 days):
8.3 vs 3.4 months (HR 0.29, 0.14-0.60)

Ricciuti et al. BMJ. 2021;9:3001504



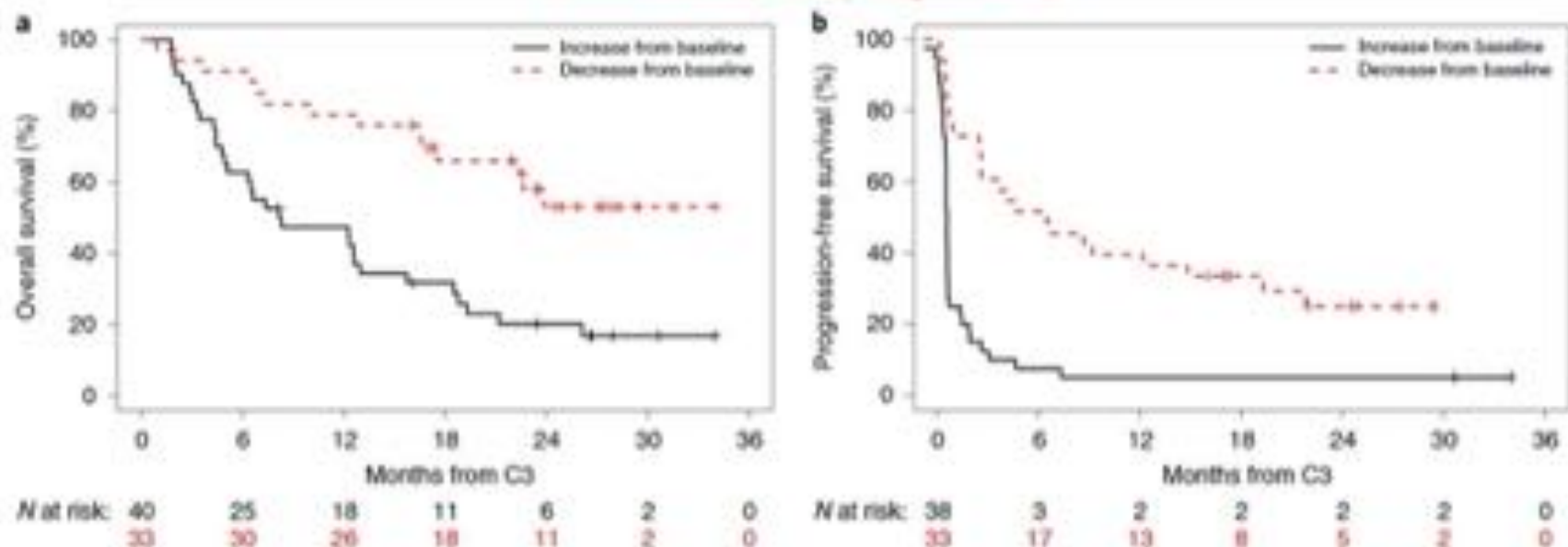
cfDNA status at 9 weeks:

12.8 vs 4.4 months
HR 0.20 (0.08-0.50)

Thompson et al. JCO Precis Oncol. 2021;5.

ctDNA decrease during pembrolizumab treatment is associated with favorable response to therapy and with better outcomes

Advanced HNSCC, TNBC, HGSOC, Melanoma, MST
Tumor-informed assay (Signatera™)



HNSCC, head and neck squamous cell carcinoma; TNBC, triple negative breast cancer; HGSOC, high-grade serous ovarian cancer; MST, mixed solid tumors

Bratman SV et al. *Nat Cancer*. 2020

Summary

- cfDNA offers a tool to improve cancer therapy across disease stages, from early detection to management of acquired resistance in the metastatic setting
- Plasma MRD status may inform selection of high-risk patients for adjuvant systemic therapy in stage II colon cancer
- Plasma clearance can predict for treatment benefit in the early and advanced stage setting
- Rapid identification of actionable biomarkers via ctDNA may allow for more effective personalized treatment strategies.