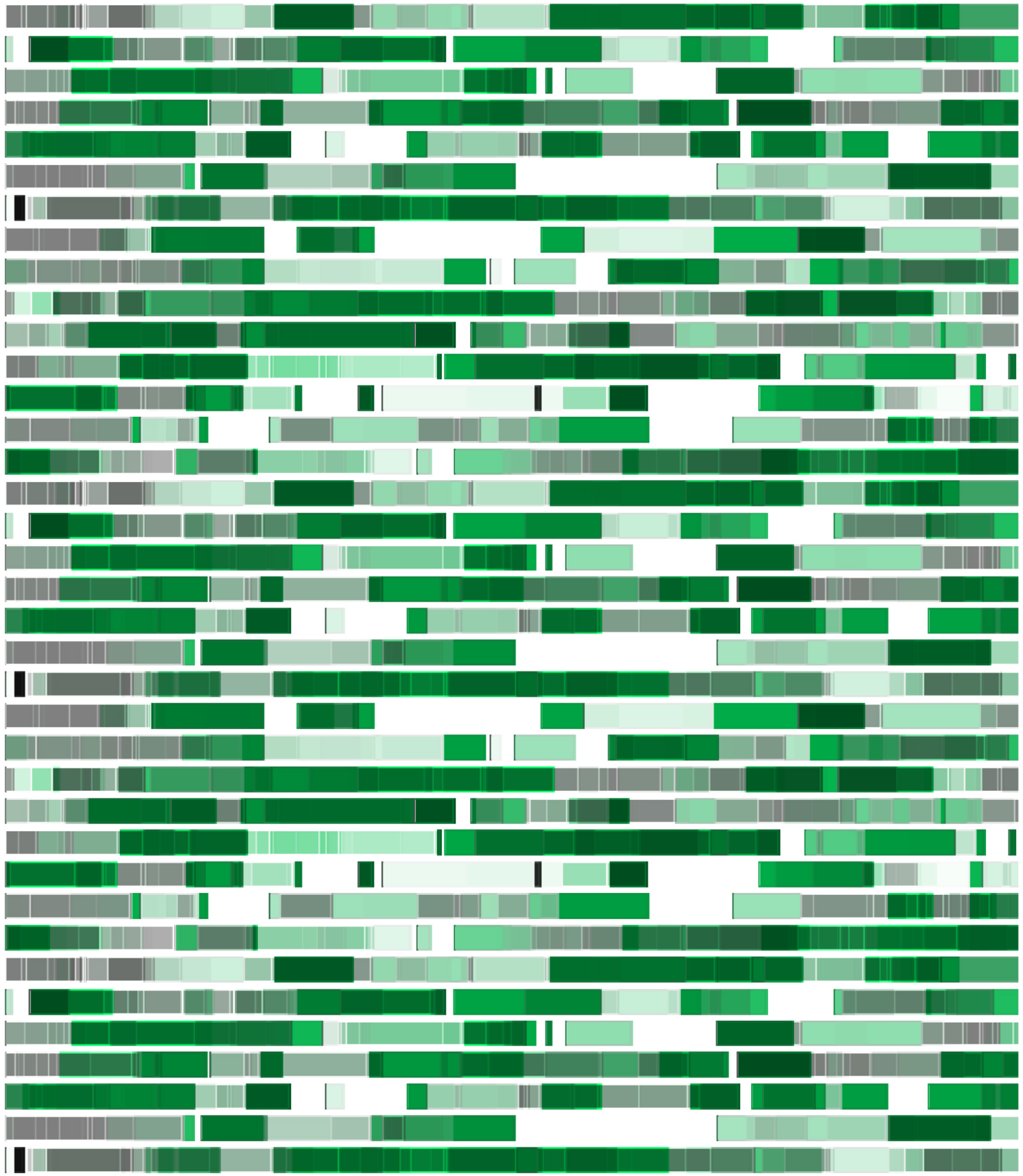
III JORNADA TRASLACIONAL DE ONCOLOGÍA DE PRECISIÓN:

A TRAVÉS DE LAS VÍAS DE SEÑALIZACIÓN
SEVILLA, 12 Y 13 DE FEBRERO DE 2026

TEST NO INVASIVO EN SANGRE PARA BIOPSIA LÍQUIDA

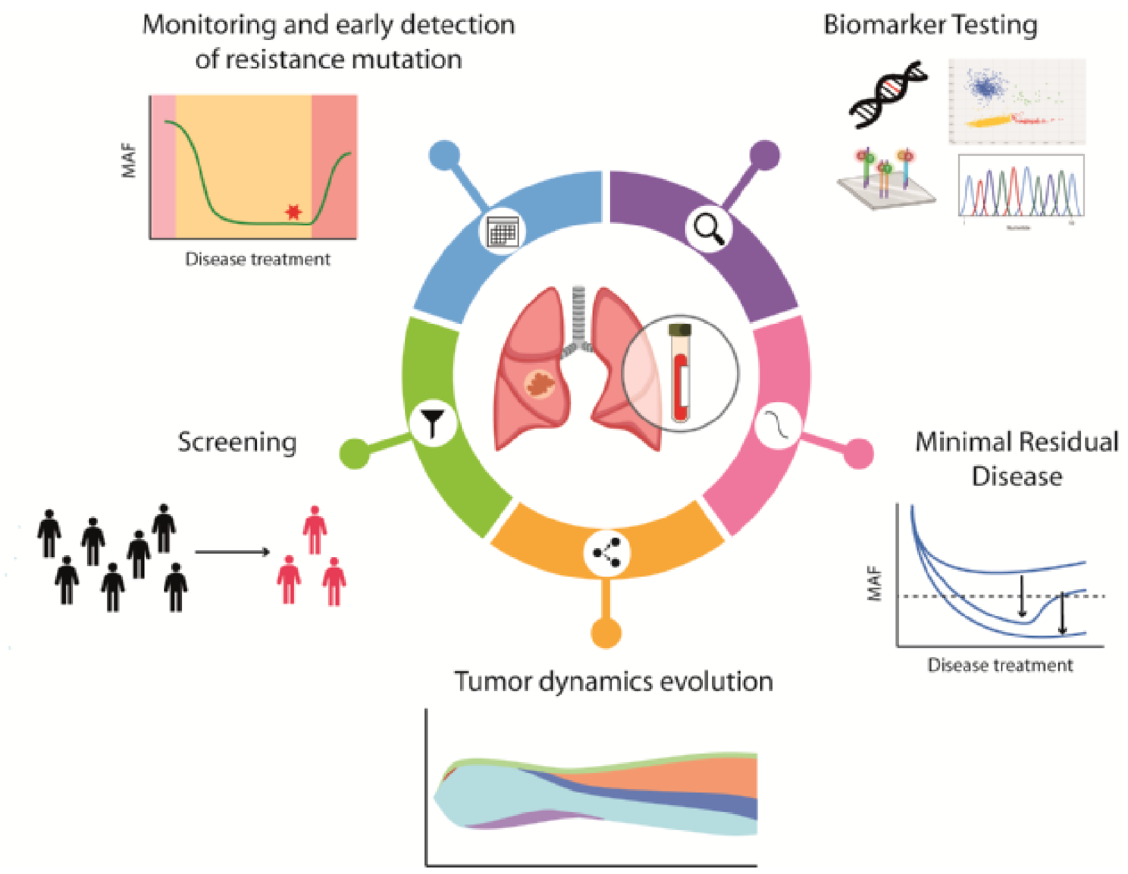
Atocha Romero
Hospital Universitario Puerta de Hierro

Organizador por:
HENDERE HEALTHCARE

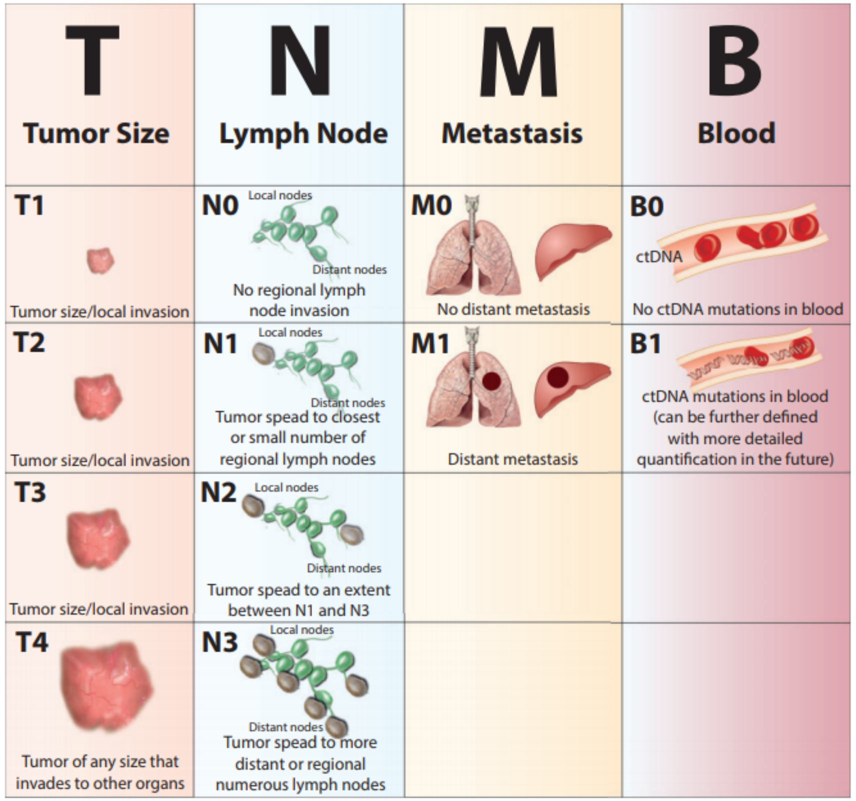


TEST NO INVASIVO EN SANGRE PARA BIOPSIA LÍQUIDA

CLINICAL UTILITY OF LIQUID BIOPSY



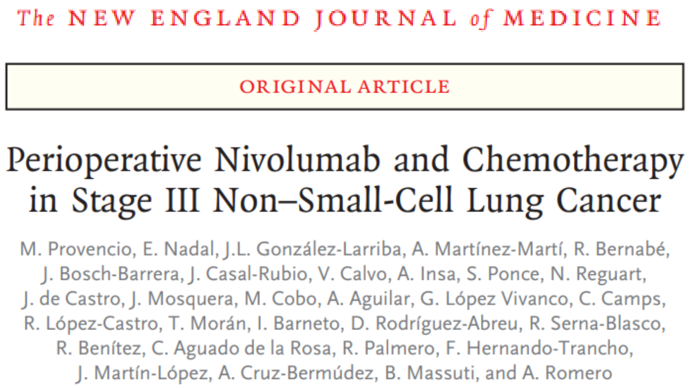
Romero, A et al. Curr Treat Options Oncol. 2021 Aug 23;22(10):86.



T Tumor Size	N Lymph Node	M Metastasis	B Blood
T1 Tumor size/local invasion	N0 Local nodes Distant nodes No regional lymph node invasion	M0 No distant metastasis	B0 ctDNA No ctDNA mutations in blood
T2 Tumor size/local invasion	N1 Local nodes Distant nodes Tumor spead to closest or small number of regional lymph nodes	M1 Distant metastasis	B1 ctDNA mutations in blood (can be further defined with more detailed quantification in the future)
T3 Tumor size/local invasion	N2 Local nodes Distant nodes Tumor spead to an extent between N1 and N3		
T4 Tumor of any size that invades to other organs	N3 Local nodes Distant nodes Tumor spead to more distant or regional numerous lymph nodes		

Yang, M et al. Ann Oncol. 2018;29:311-323.

NEOADJUVANT SETTING: BASELINE CTDNA IS OF PROGNOSTIC SIGNIFICANCE



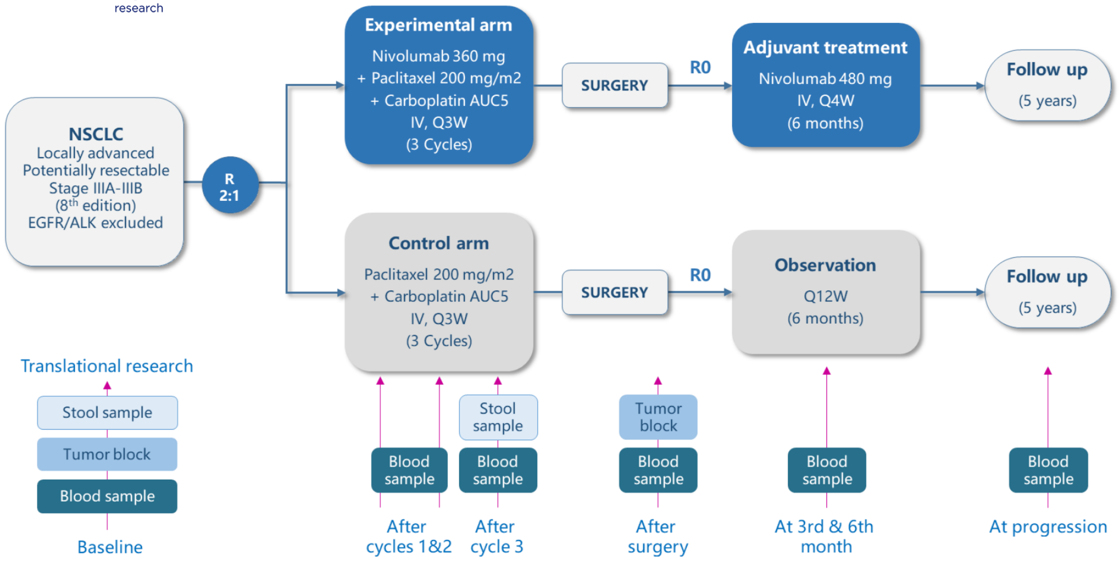
The NEW ENGLAND JOURNAL of MEDICINE

ORIGINAL ARTICLE

Perioperative Nivolumab and Chemotherapy in Stage III Non–Small-Cell Lung Cancer

M. Provencio, E. Nadal, J.L. González-Larriba, A. Martínez-Martí, R. Bernabé, J. Bosch-Barrera, J. Casal-Rubio, V. Calvo, A. Insa, S. Ponce, N. Reguart, J. de Castro, J. Mosquera, M. Cobo, A. Aguilar, G. López Vivanco, C. Camps, R. López-Castro, T. Morán, I. Barneto, D. Rodríguez-Abreu, R. Serna-Blasco, R. Benítez, C. Aguado de la Rosa, R. Palmero, F. Hernando-Trancho, J. Martín-López, A. Cruz-Bermúdez, B. Massuti, and A. Romero

GECP lung cancer research



NSCLC
Locally advanced
Potentially resectable
Stage IIIA-IIIB
(8th edition)
EGFR/ALK excluded

R
2:1

Experimental arm
Nivolumab 360 mg
+ Paclitaxel 200 mg/m2
+ Carboplatin AUC5
IV, Q3W
(3 Cycles)

SURGERY

R0

Adjuvant treatment
Nivolumab 480 mg
IV, Q4W
(6 months)

Follow up
(5 years)

Control arm
Paclitaxel 200 mg/m2
+ Carboplatin AUC5
IV, Q3W
(3 Cycles)

SURGERY

R0

Observation
Q12W
(6 months)

Follow up
(5 years)

Translational research

Stool sample
Tumor block
Blood sample
Baseline

Blood sample
After cycles 1&2

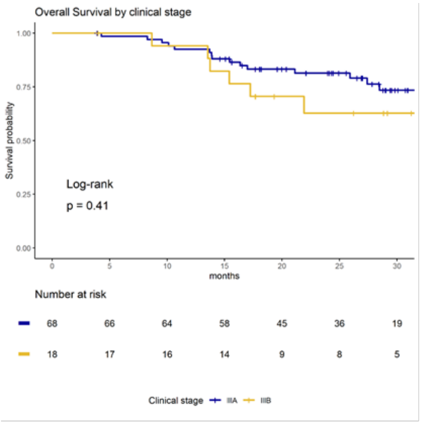
Stool sample
Blood sample
After cycle 3

Tumor block
Blood sample
After surgery

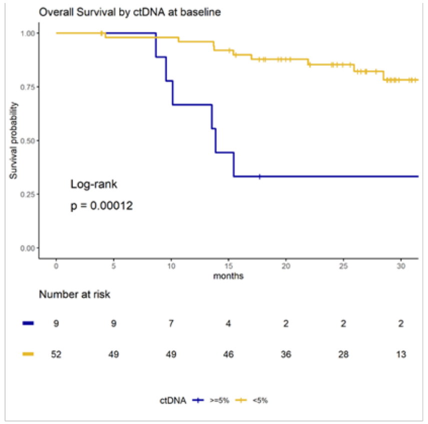
Blood sample
At 3rd & 6th month

Blood sample
At progression

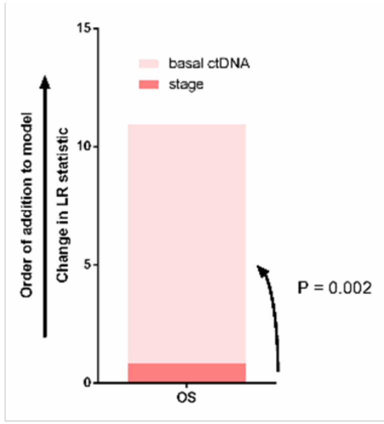
NADIM II (NCT03838159)

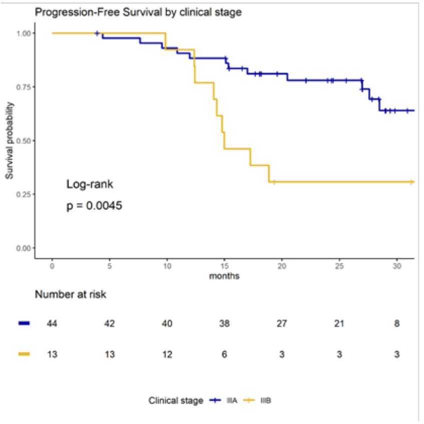


Overall Survival by clinical stage

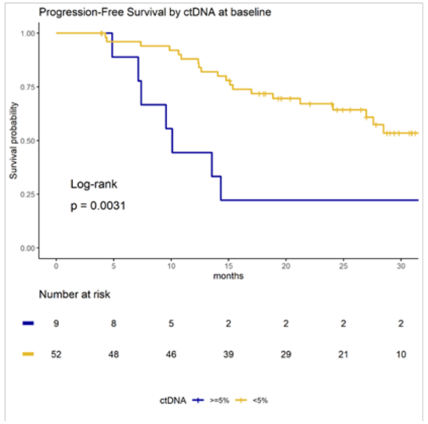


Overall Survival by ctDNA at baseline

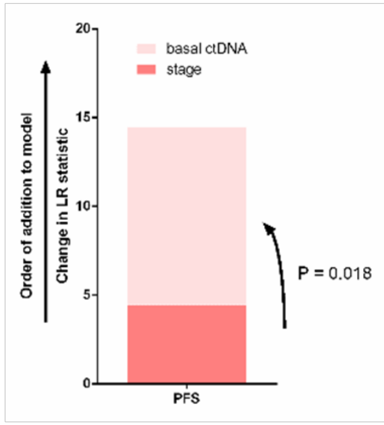




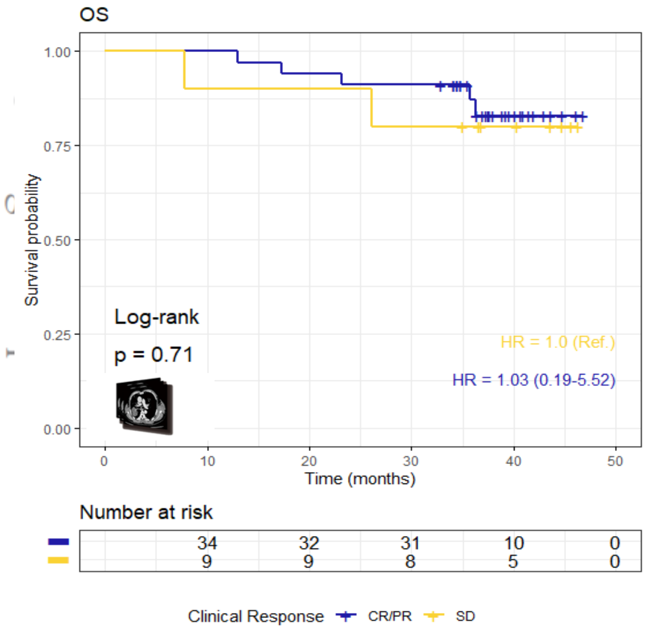
Progression-Free Survival by clinical stage

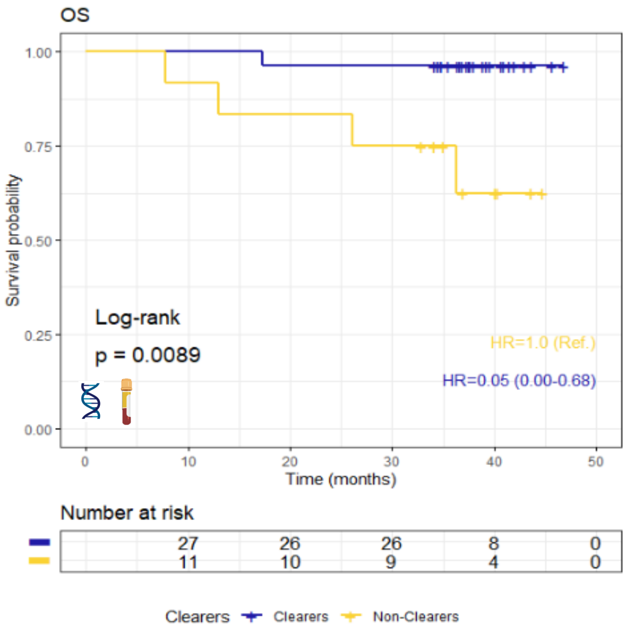


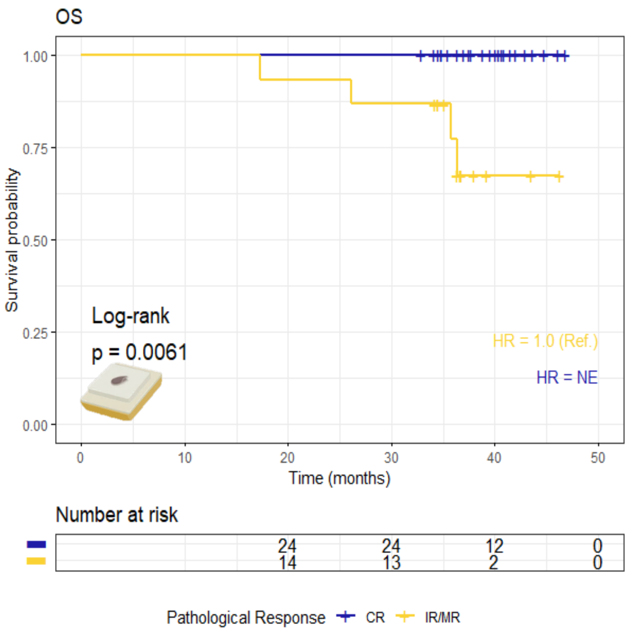
Progression-Free Survival by ctDNA at baseline



CTDNA CLEARANCE AFTER NEOADJUVANT TREATMENT IS OF PROGNOSTIC SIGNIFICANCE

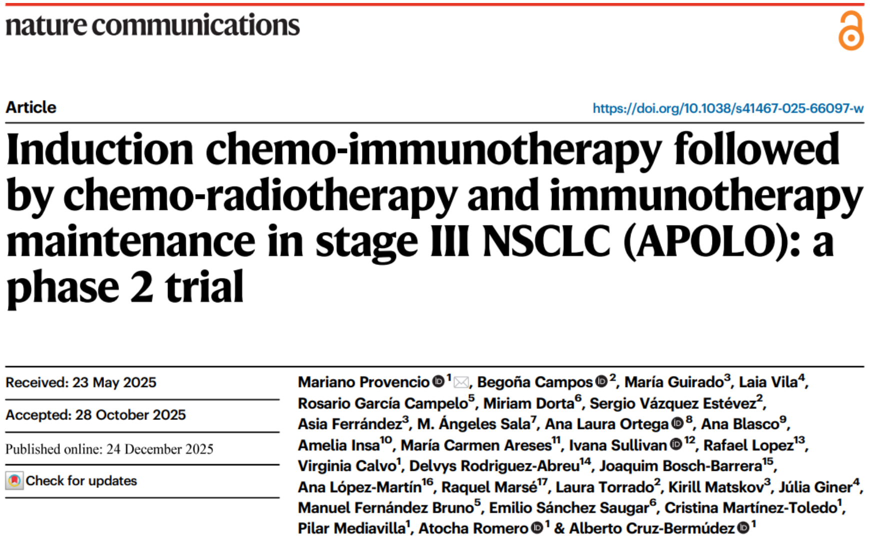






Survival surrogate	No.	HR (PFS)[a]	95% CI[a]	*P*[a]	C-index (PFS)	95% CI	HR (OS)[a]	95% CI[a]	*P*[a]	C-index (OS)	95% CI
Clinical response (CR plus PR *v* SD)	46	0.79	0.24 to 2.59	.698	0.62	0.47 to 0.77	0.87	0.20 to 3.75	.848	0.72	0.51 to 0.90
Pathologic response (pCR *v* major plus incomplete)	41	0.38	0.12 to 1.25	.111	0.63	0.47 to 0.78	0.24	0.04 to 1.33	.102	0.65	0.43 to 0.86
Undetectable ctDNA after treatment	40	0.26	0.07 to 0.93	.038	0.63	0.45 to 0.81	0.04	0.00 to 0.55	.015	0.82	0.61 to 1.00

CTDNA CLEARANCE AFTER NEOADJUVANT TREATMENT IS OF PROGNOSTIC SIGNIFICANCE



nature communications

Article https://doi.org/10.1038/s41467-025-66097-w

Induction chemo-immunotherapy followed by chemo-radiotherapy and immunotherapy maintenance in stage III NSCLC (APOLO): a phase 2 trial

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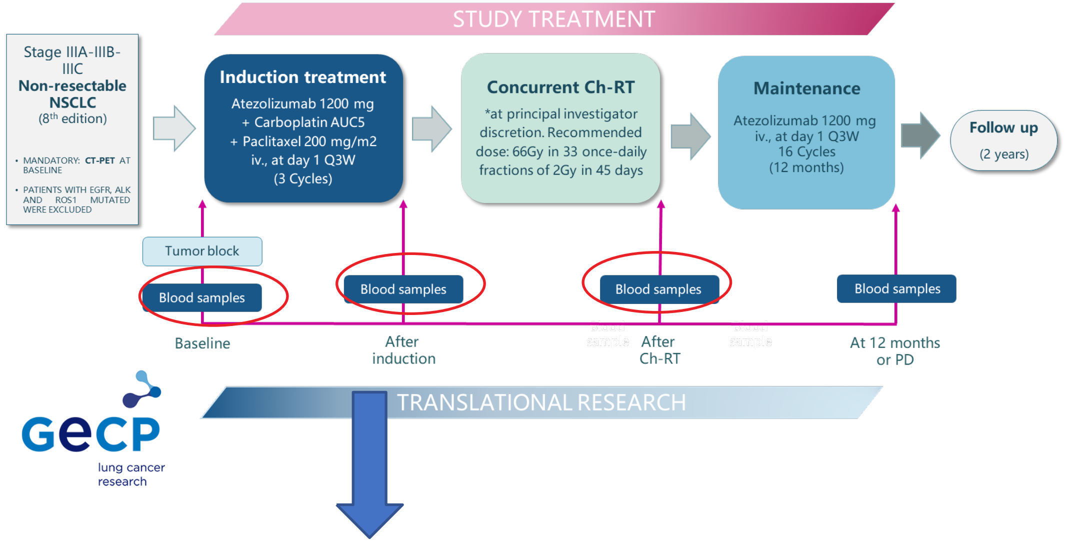
Check for updates

Mariano Provencio[1], Begoña Campos[2], María Guirado[3], Laia Vila[4], Rosario García Campelo[5], Miriam Dorta[6], Sergio Vázquez Estévez[2], Asia Ferrández[3], M. Ángeles Sala[7], Ana Laura Ortega[8], Ana Blasco[9], Amelia Insa[10], María Carmen Areses[11], Ivana Sullivan[12], Rafael Lopez[13], Virginia Calvo[1], Delvys Rodriguez-Abreu[14], Joaquim Bosch-Barrera[15], Ana López-Martín[16], Raquel Marsé[17], Laura Torrado[2], Kirill Matskov[3], Júlia Giner[4], Manuel Fernández Bruno[5], Emilio Sánchez Saugar[6], Cristina Martínez-Toledo[1], Pilar Mediavilla[1], Atocha Romero[1] & Alberto Cruz-Bermúdez[1]



STUDY TREATMENT

Stage IIIA-IIIB-IIIC
Non-resectable NSCLC
(8th edition)

- MANDATORY: **CT-PET** AT BASELINE
- PATIENTS WITH EGFR, ALK AND ROS1 MUTATED WERE EXCLUDED

Induction treatment
Atezolizumab 1200 mg
+ Carboplatin AUC5
+ Paclitaxel 200 mg/m2
iv., at day 1 Q3W
(3 Cycles)

Concurrent Ch-RT
*at principal investigator discretion. Recommended dose: 66Gy in 33 once-daily fractions of 2Gy in 45 days

Maintenance
Atezolizumab 1200 mg
iv., at day 1 Q3W
16 Cycles
(12 months)

Follow up
(2 years)

Tumor block

Blood samples — Baseline

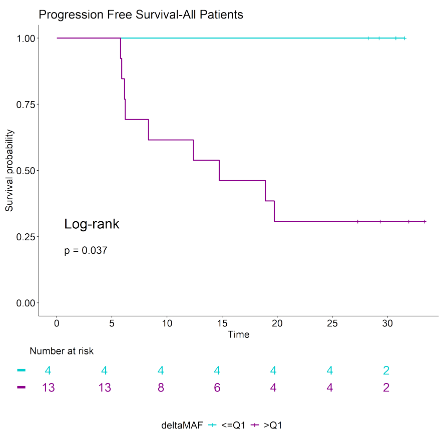
Blood samples — After induction

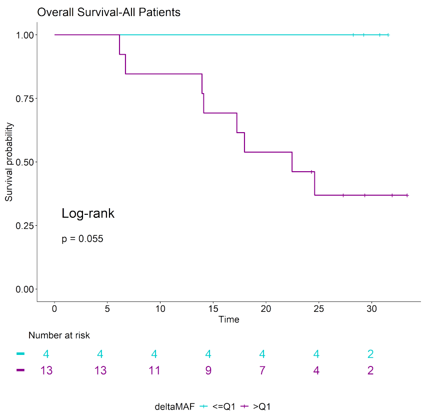
Blood samples — After Ch-RT

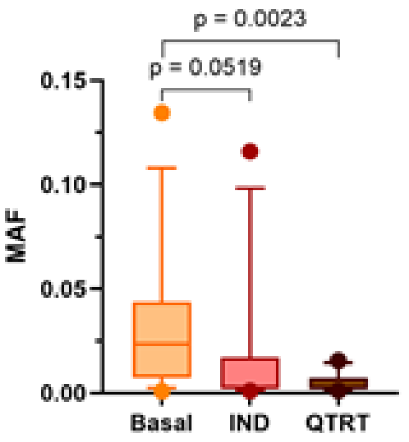
Blood samples — At 12 months or PD

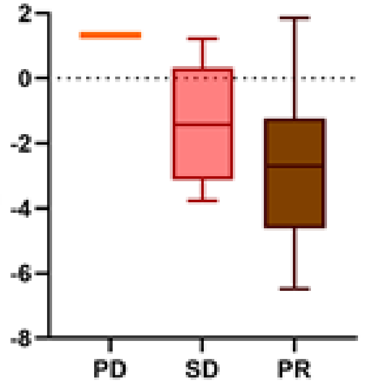
TRANSLATIONAL RESEARCH

GECP lung cancer research

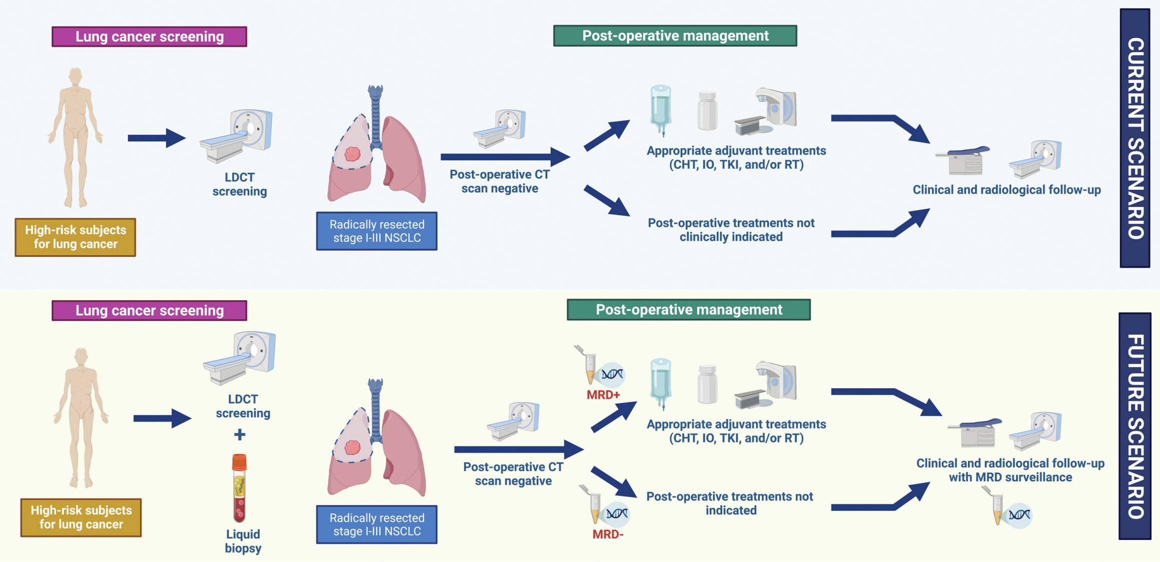




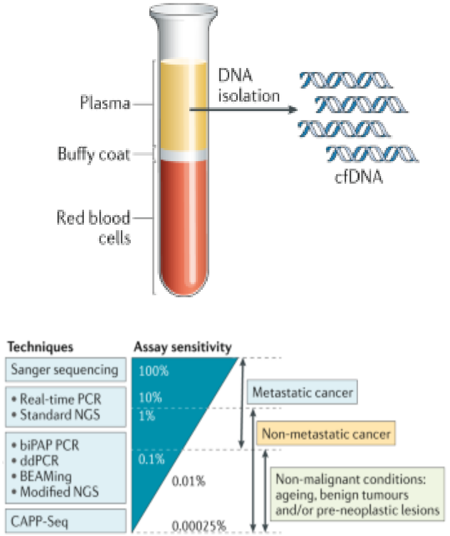


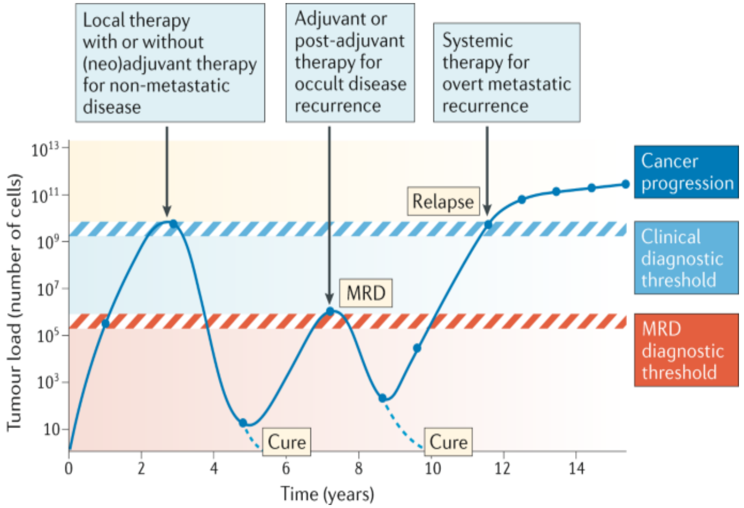


ADJUVANT SETTING: ROLE OF MRD IN NSCLC



https://www.thelancet.com/journals/ebiom/article/PIIS2352-3964%2823%2900170-6/fulltext





Pantel, K et al. Nat Rev Clin Oncol. 2019;16:409-424.

TUMOR-INFORMED VS. TUMOR-NAÏVE ASSAYS

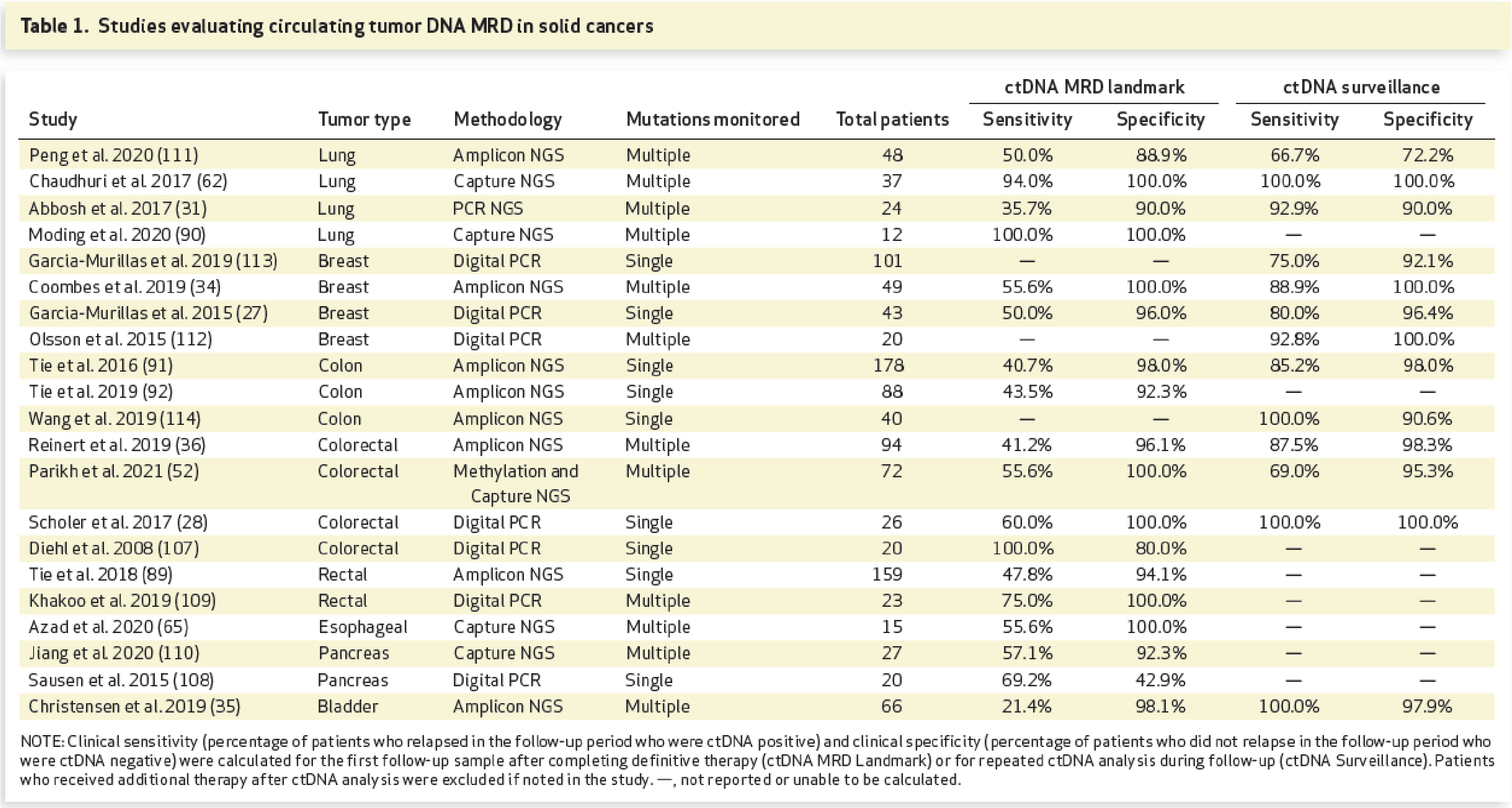


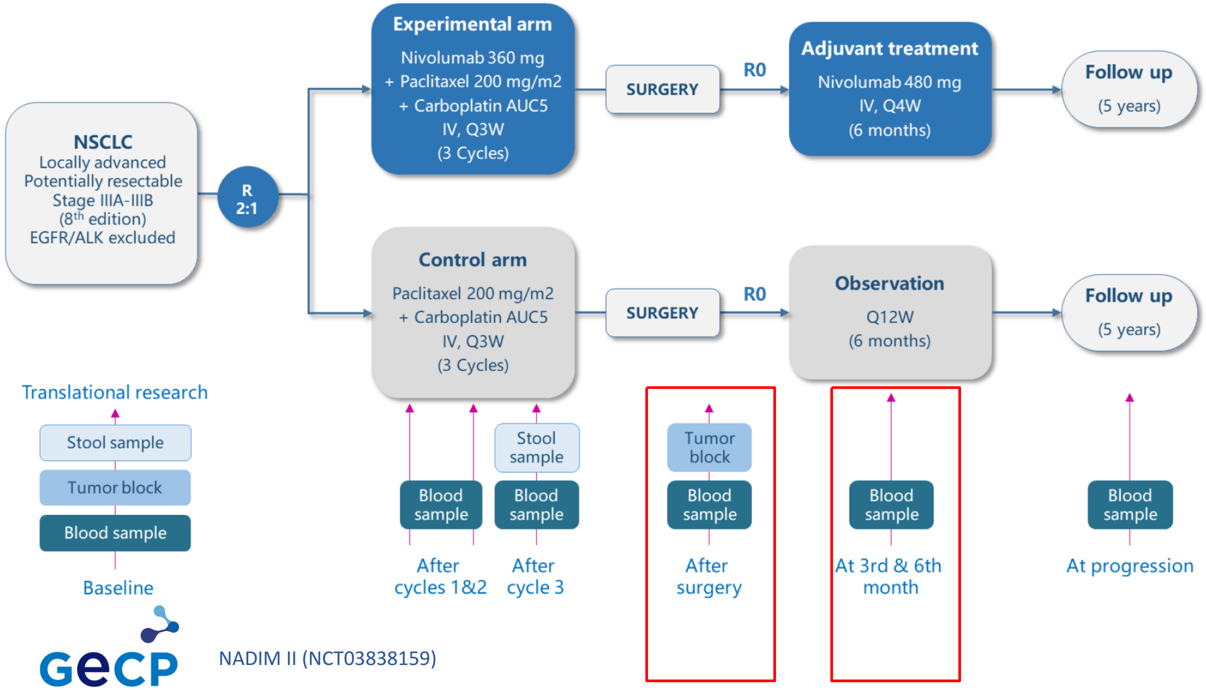
Table 1. Studies evaluating circulating tumor DNA MRD in solid cancers

Study	Tumor type	Methodology	Mutations monitored	Total patients	ctDNA MRD landmark		ctDNA surveillance	
					Sensitivity	Specificity	Sensitivity	Specificity
Peng et al. 2020 (111)	Lung	Amplicon NGS	Multiple	48	50.0%	88.9%	66.7%	72.2%
Chaudhuri et al. 2017 (62)	Lung	Capture NGS	Multiple	37	94.0%	100.0%	100.0%	100.0%
Abbosh et al. 2017 (31)	Lung	PCR NGS	Multiple	24	35.7%	90.0%	92.9%	90.0%
Moding et al. 2020 (90)	Lung	Capture NGS	Multiple	12	100.0%	100.0%	—	—
Garcia-Murillas et al. 2019 (113)	Breast	Digital PCR	Single	101	—	—	75.0%	92.1%
Coombes et al. 2019 (34)	Breast	Amplicon NGS	Multiple	49	55.6%	100.0%	88.9%	100.0%
Garcia-Murillas et al. 2015 (27)	Breast	Digital PCR	Single	43	50.0%	96.0%	80.0%	96.4%
Olsson et al. 2015 (112)	Breast	Digital PCR	Multiple	20	—	—	92.8%	100.0%
Tie et al. 2016 (91)	Colon	Amplicon NGS	Single	178	40.7%	98.0%	85.2%	98.0%
Tie et al. 2019 (92)	Colon	Amplicon NGS	Single	88	43.5%	92.3%	—	—
Wang et al. 2019 (114)	Colon	Amplicon NGS	Single	40	—	—	100.0%	90.6%
Reinert et al. 2019 (36)	Colorectal	Amplicon NGS	Multiple	94	41.2%	96.1%	87.5%	98.3%
Parikh et al. 2021 (52)	Colorectal	Methylation and Capture NGS	Multiple	72	55.6%	100.0%	69.0%	95.3%
Scholer et al. 2017 (28)	Colorectal	Digital PCR	Single	26	60.0%	100.0%	100.0%	100.0%
Diehl et al. 2008 (107)	Colorectal	Digital PCR	Single	20	100.0%	80.0%	—	—
Tie et al. 2018 (89)	Rectal	Amplicon NGS	Single	159	47.8%	94.1%	—	—
Khakoo et al. 2019 (109)	Rectal	Digital PCR	Multiple	23	75.0%	100.0%	—	—
Azad et al. 2020 (65)	Esophageal	Capture NGS	Multiple	15	55.6%	100.0%	—	—
Jiang et al. 2020 (110)	Pancreas	Capture NGS	Multiple	27	57.1%	92.3%	—	—
Sausen et al. 2015 (108)	Pancreas	Digital PCR	Single	20	69.2%	42.9%	—	—
Christensen et al. 2019 (35)	Bladder	Amplicon NGS	Multiple	66	21.4%	98.1%	100.0%	97.9%

NOTE: Clinical sensitivity (percentage of patients who relapsed in the follow-up period who were ctDNA positive) and clinical specificity (percentage of patients who did not relapse in the follow-up period who were ctDNA negative) were calculated for the first follow-up sample after completing definitive therapy (ctDNA MRD Landmark) or for repeated ctDNA analysis during follow-up (ctDNA Surveillance). Patients who received additional therapy after ctDNA analysis were excluded if noted in the study. —, not reported or unable to be calculated.

Cancer Discov. 2021;11(12):2968-2986. doi:10.1158/2159-8290.CD-21-0634

ADJUVANT SETTING: ROLE OF MRD IN NSCLC



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(3 Cycles)

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Follow up
(5 years)

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Follow up
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Tumor block
Blood sample
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Blood sample
After cycles 1&2

Stool sample
Blood sample
After cycle 3

Tumor block
Blood sample
After surgery

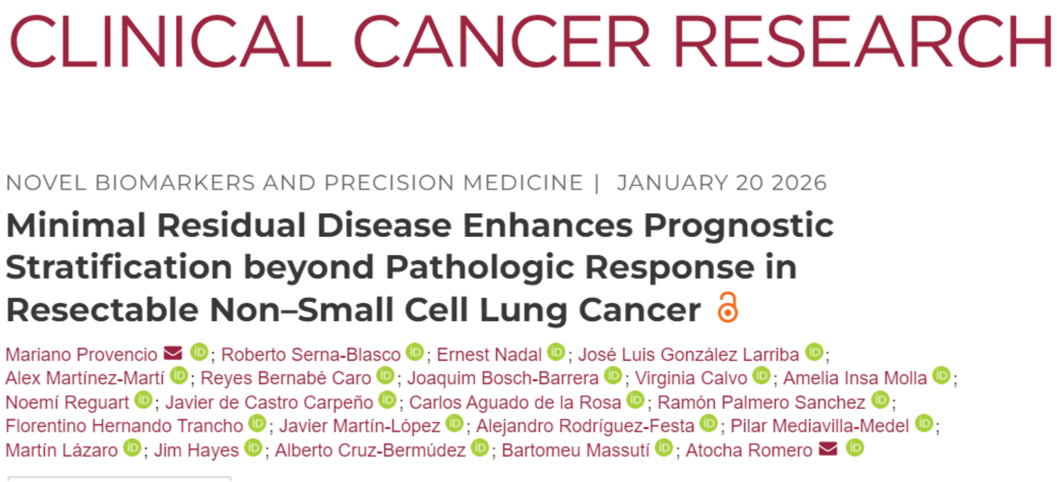
Blood sample
At 3rd & 6th month

Blood sample
At progression

GECP lung cancer research

NADIM II (NCT03838159)

GUARDANTREVEAL



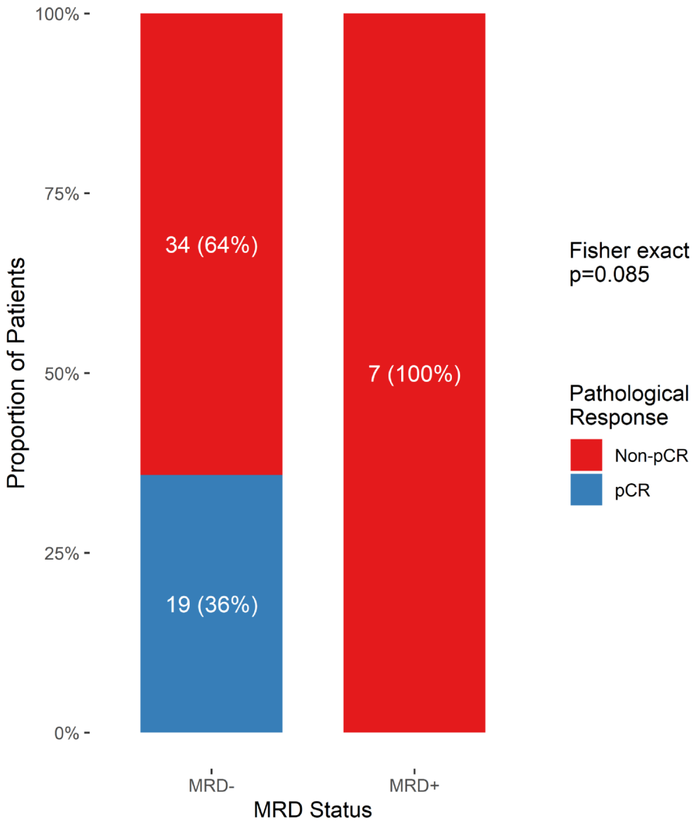
CLINICAL CANCER RESEARCH

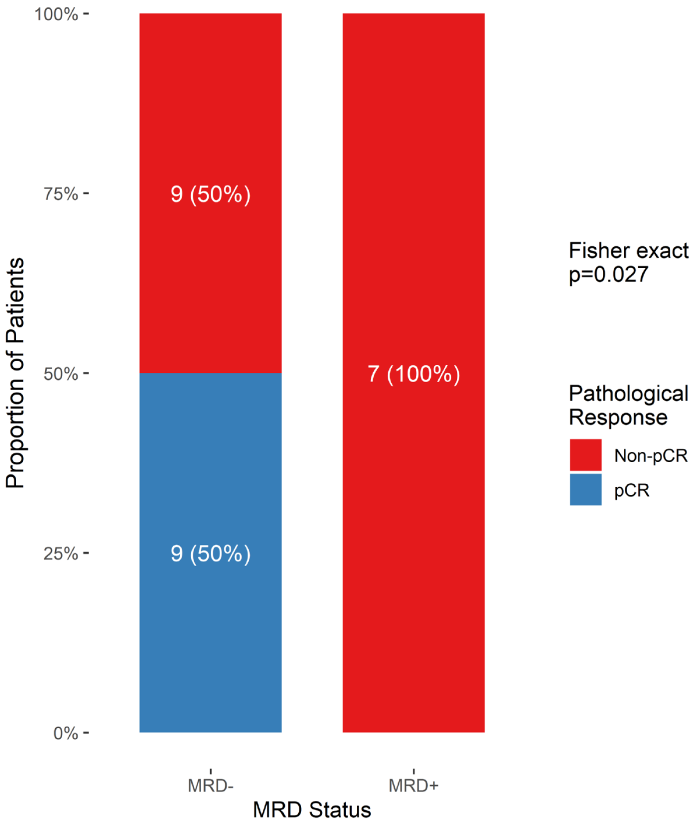
NOVEL BIOMARKERS AND PRECISION MEDICINE | JANUARY 20 2026

Minimal Residual Disease Enhances Prognostic Stratification beyond Pathologic Response in Resectable Non–Small Cell Lung Cancer

Mariano Provencio; Roberto Serna-Blasco; Ernest Nadal; José Luis González Larriba; Alex Martínez-Martí; Reyes Bernabé Caro; Joaquim Bosch-Barrera; Virginia Calvo; Amelia Insa Molla; Noemí Reguart; Javier de Castro Carpeño; Carlos Aguado de la Rosa; Ramón Palmero Sanchez; Florentino Hernando Trancho; Javier Martín-López; Alejandro Rodríguez-Festa; Pilar Mediavilla-Medel; Martín Lázaro; Jim Hayes; Alberto Cruz-Bermúdez; Bartomeu Massutí; Atocha Romero

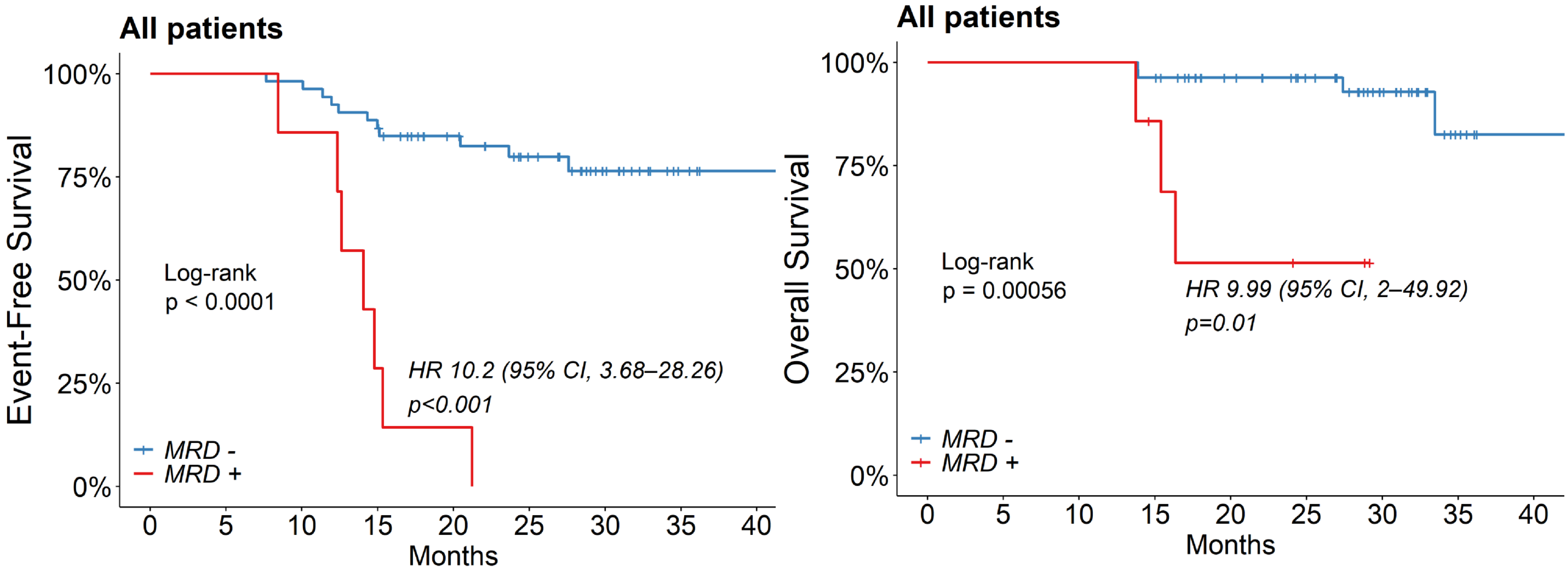
ASSOCIATION OF PCR WITH MRD DETECTION





Provencio M et al Clin Can res 2026. Manuscript DOI: 10.1158/1078-0432.CCR-25-2958

EFS AND OS ACCORDING TO MRD STATUS



Patients at risk

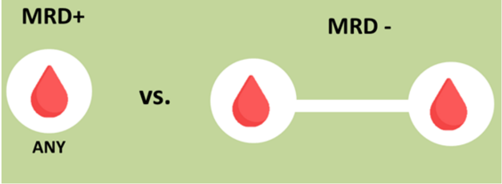
MRD -	53	53	52	46	36	27	15	4	1
MRD +	7	7	6	2	1	0	0	0	0

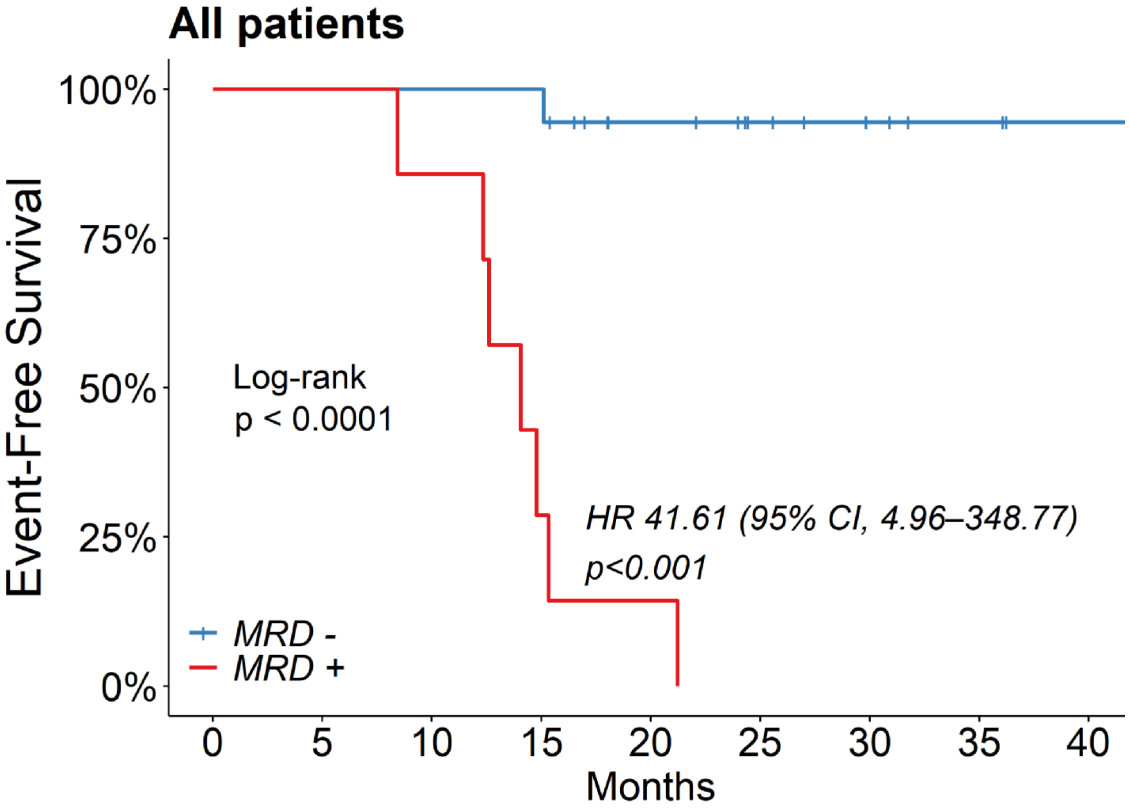
Patients at risk

MRD -	53	53	53	51	40	33	20	5	1
MRD +	7	7	7	5	3	2	0	0	0

Provencio M et al Clin Can res 2026. Manuscript DOI: 10.1158/1078-0432.CCR-25-2958c

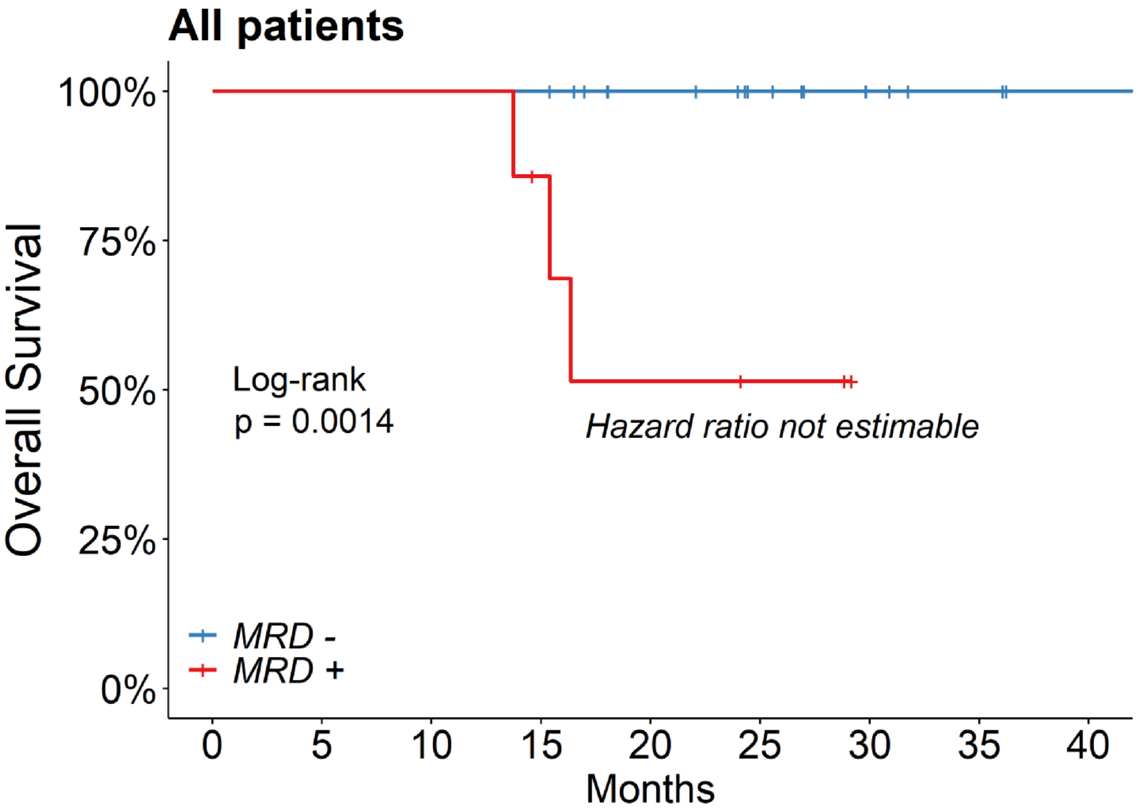
EFS AND OS ACCORDING TO MRD STATUS





Patients at risk

	0	5	10	15	20	25	30	35	40
MRD -	18	18	18	18	12	8	5	3	1
MRD +	7	7	6	2	1	0	0	0	0

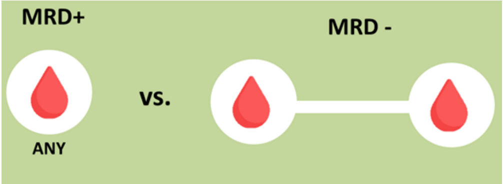


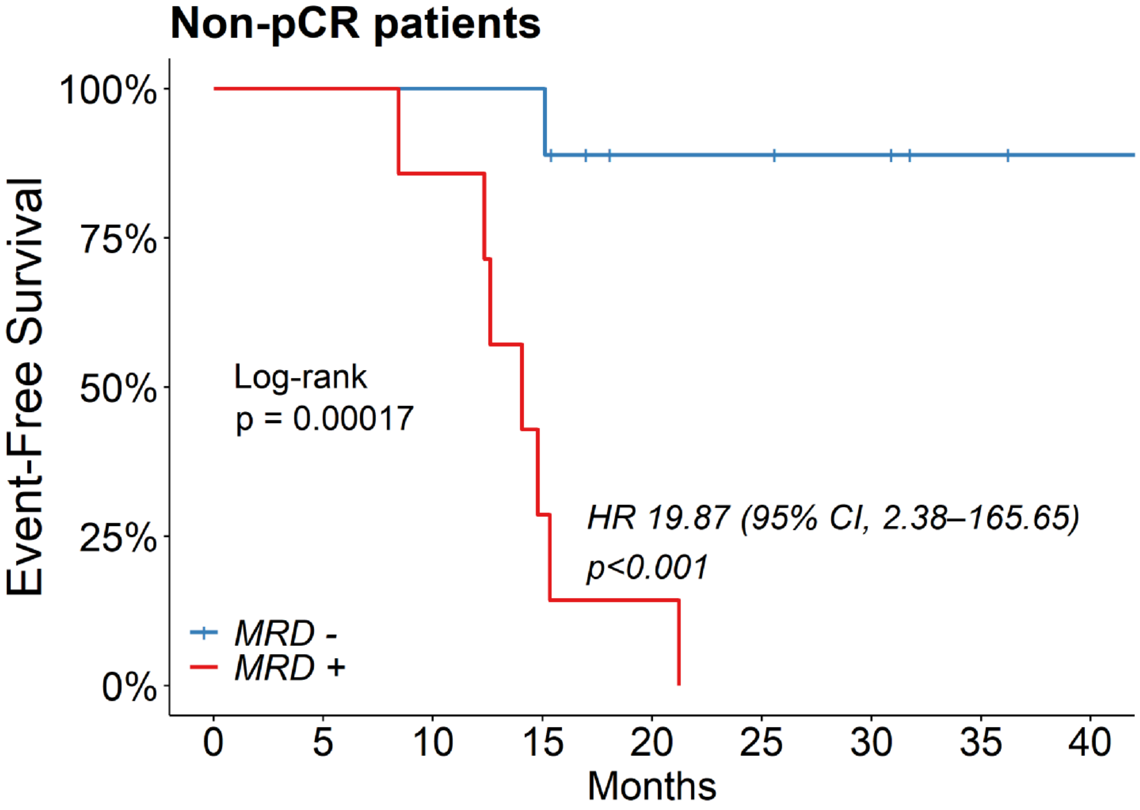
Patients at risk

	0	5	10	15	20	25	30	35	40
MRD -	18	18	18	18	13	9	5	3	1
MRD +	7	7	7	5	3	2	0	0	0

Provencio M et al Clin Can res 2026. Manuscript DOI: 10.1158/1078-0432.CCR-25-2958

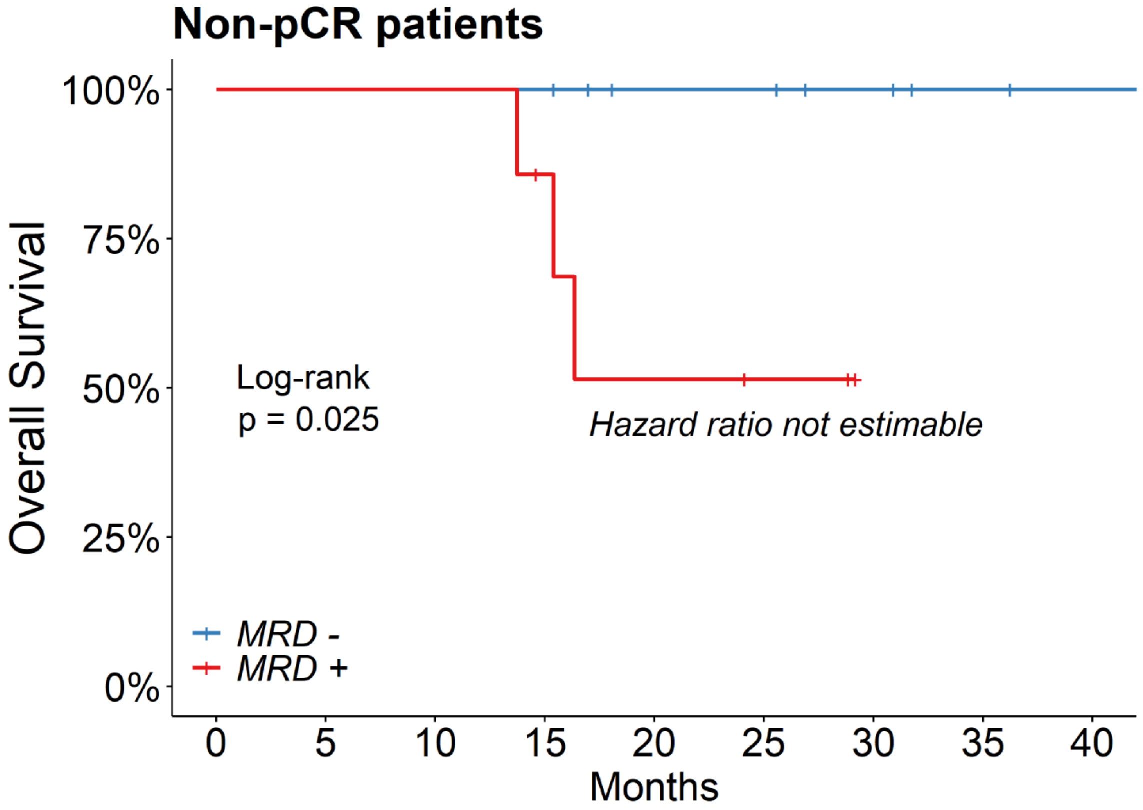
EFS AND OS ACCORDING TO MRD STATUS IN NON PCR POPULATION





Patients at risk

MRD -	9	9	9	9	5	5	4	2	1
MRD +	7	7	6	2	1	0	0	0	0



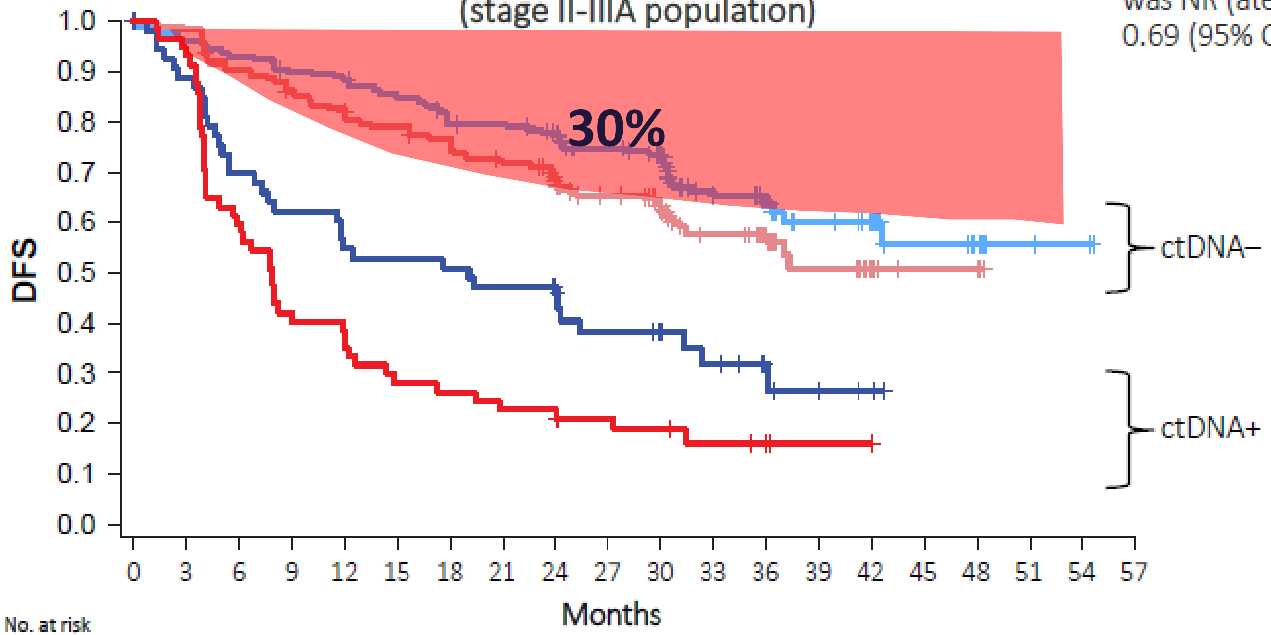
Patients at risk

MRD -	9	9	9	9	6	6	4	2	1
MRD +	7	7	7	5	3	2	0	0	0

Provencio M et al Clin Can res 2026. Manuscript DOI: 10.1158/1078-0432.CCR-25-2958

MRD IN IMPOWER010

DFS in ctDNA-defined subgroups
(stage II-IIIA population)



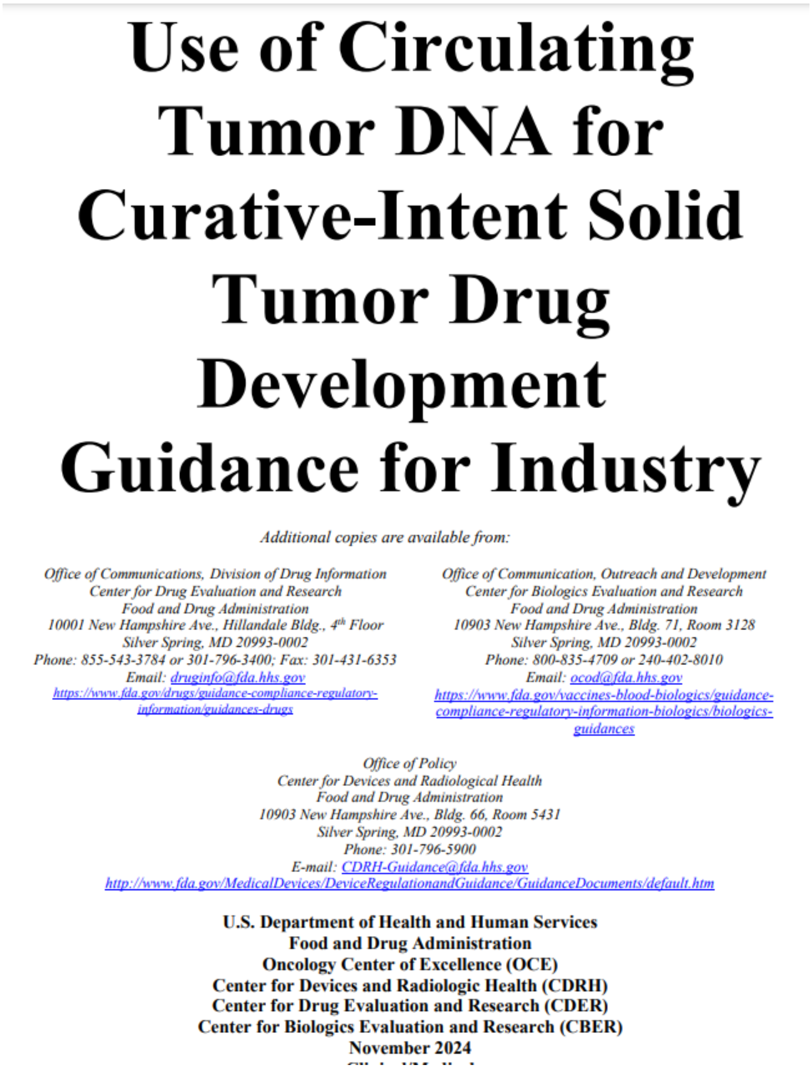
No. at risk	0	3	6	9	12	15	18	21	24	27	30	33	36	39	42	45	48	51	54	57
Atezo, ctDNA–	218	206	199	192	189	180	170	166	151	131	112	73	58	33	24	12	8	3	2	0
Atezo, ctDNA+	53	47	37	33	29	28	27	25	23	17	14	10	6	3	2	0	0	0	0	0
BSC, ctDNA–	204	193	176	167	158	152	143	137	124	106	88	62	44	19	9	3	3	0	0	0
BSC, ctDNA+	59	53	34	24	21	16	15	13	13	9	8	6	4	1	1	0	0	0	0	0

- In all ctDNA-evaluable stage II-IIIA patients, mDFS was NR (atezo) vs 31.4 months (BSC), with an HR of 0.69 (95% CI: 0.53, 0.89)

ctDNA–	**Atezo (n=218)**	**BSC (n=204)**
mDFS, mo	NR	NR
HR (95% CI)	0.72 (0.52, 1.00)	

ctDNA+	**Atezo (n=53)**	**BSC (n=59)**
mDFS, mo	19.1	7.9
HR (95% CI)	0.61 (0.39, 0.94)	

MRD post-surgery is prognostic but neither predictive nor sufficiently sensitive for de-escalation decisions



Use of Circulating Tumor DNA for Curative-Intent Solid Tumor Drug Development Guidance for Industry

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Food and Drug Administration
Oncology Center of Excellence (OCE)
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Center for Drug Evaluation and Research (CDER)
Center for Biologics Evaluation and Research (CBER)
November 2024

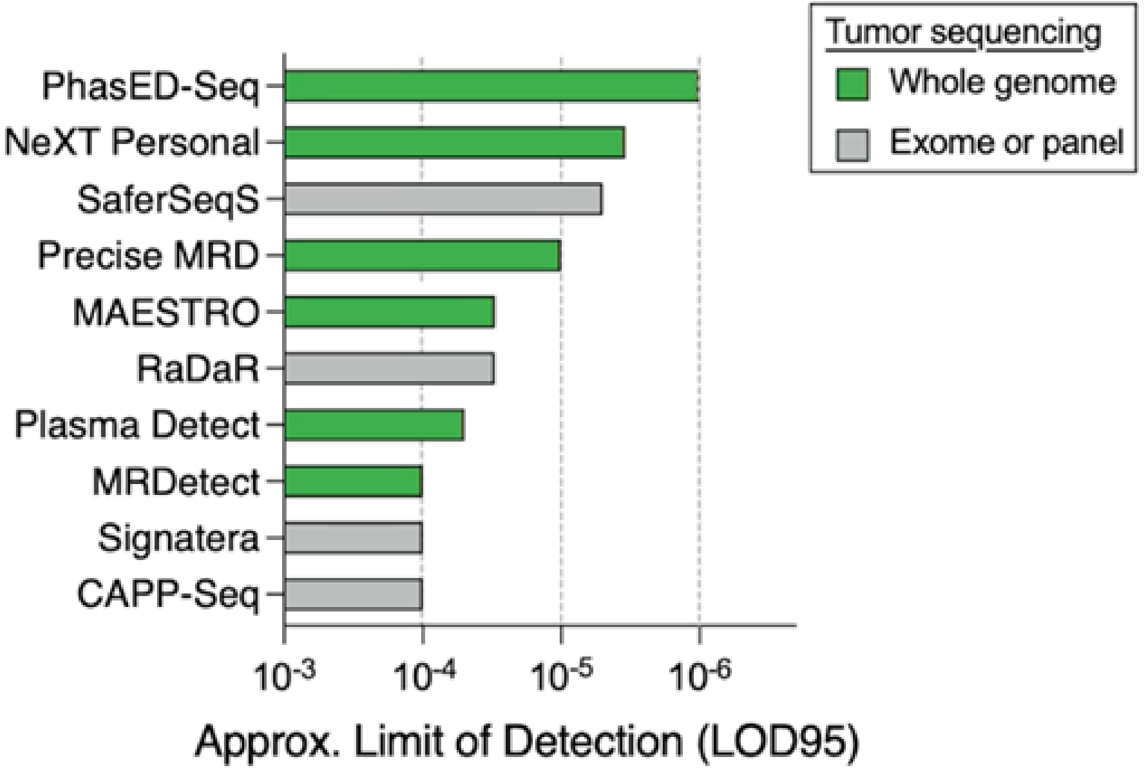
ctDNA MRD could be used for treatment optimization, to add on therapy for patients who are at higher risk of disease recurrence (i.e., ctDNA MRD positive) or to de-escalate therapy for patients with lower risk of disease recurrence (i.e., ctDNA MRD negative)

The MRD assay should have high sensitivity and negative predictive value (NPV) for supporting de-escalation of treatment and high specificity and positive predictive value (PPV) for supporting escalation of treatment.

- MRD detection with 1st generation assays has a high positive predictive value.
- Sensitivity remains a challenge

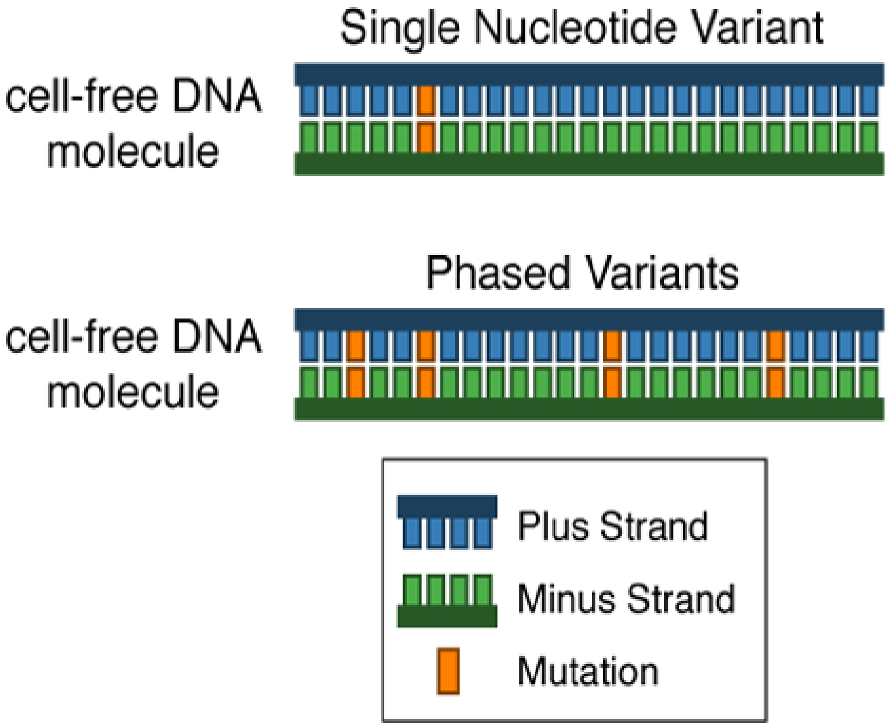
APPROACHES TO IMPROVE LOD

- ✓ **Sequence more genome**
- ✓ **Track more samples**
- ✓ **Decrease error rate**



https://foresight-dx.com/wp-content/uploads/2024/08/ASCO_2024-Isbell_MSKCC-Poster.pdf

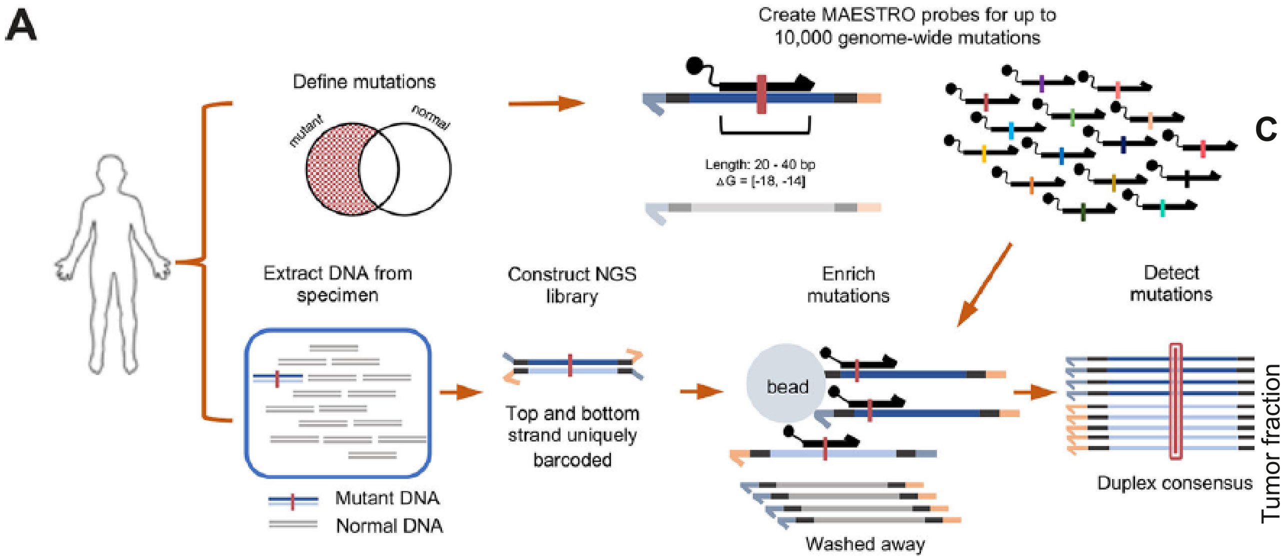
Phased variants in ctDNA

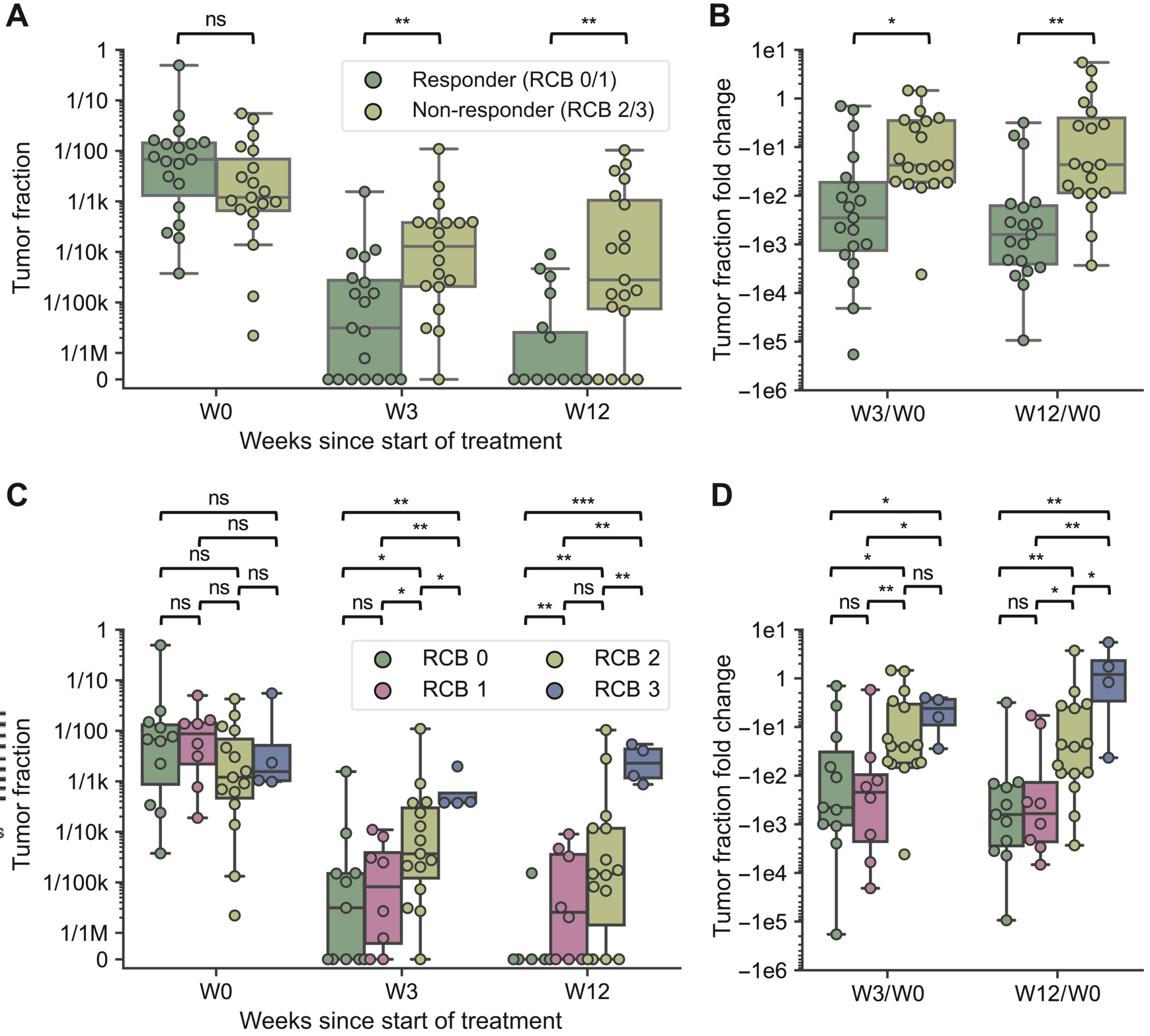


Nat Biotechnol. 2021 Dec;39(12):1537-1547

APPROACHES TO IMPROVE LOD

- ✓ Sequence more genome
- ✓ Track more samples
- ✓ Decrease error rate
- ✓ Enrichment of minor alleles

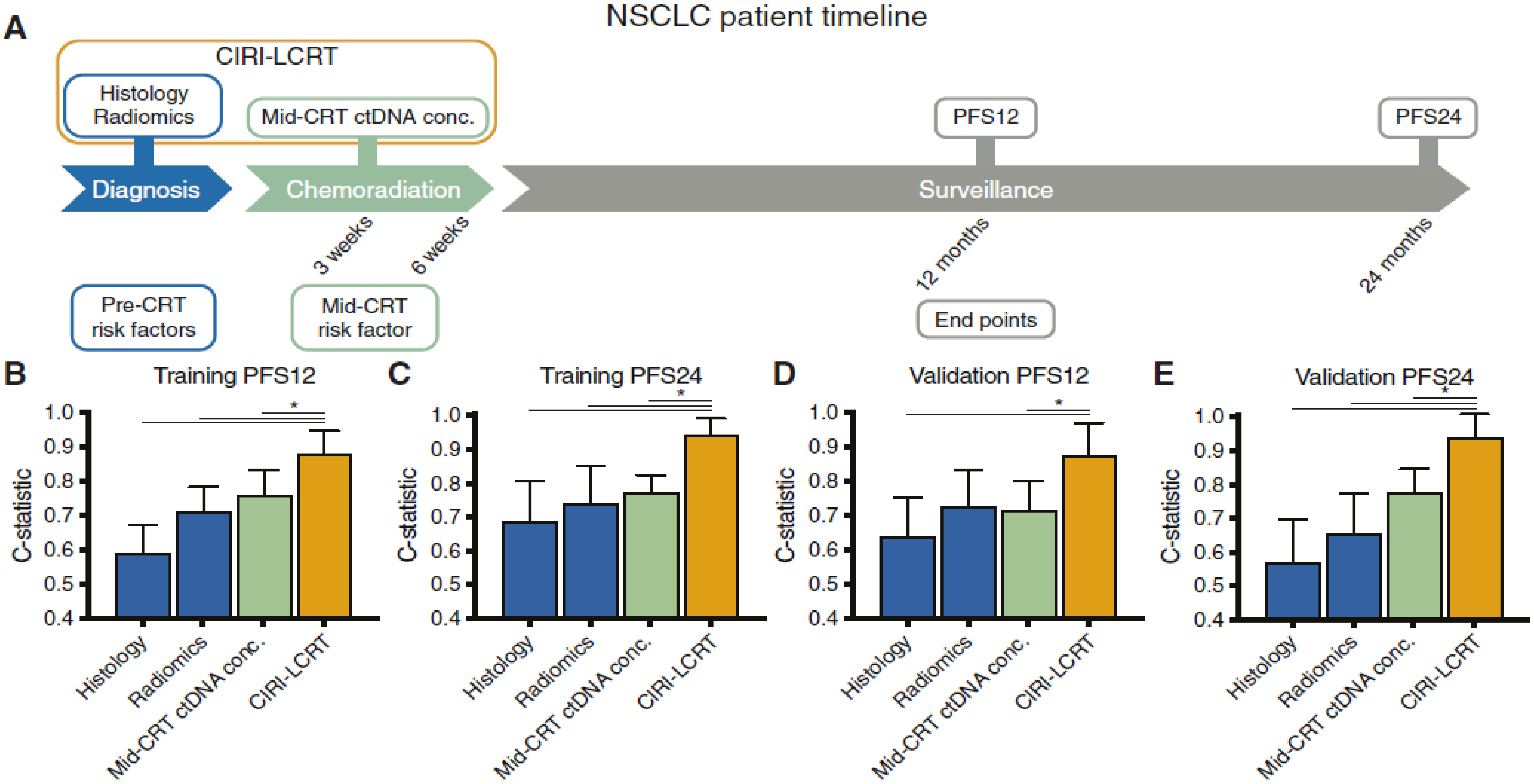




Nat Biomed Eng. 2022 Mar;6(3):257-266. doi: 10.1038/s41551-022-00855-9.

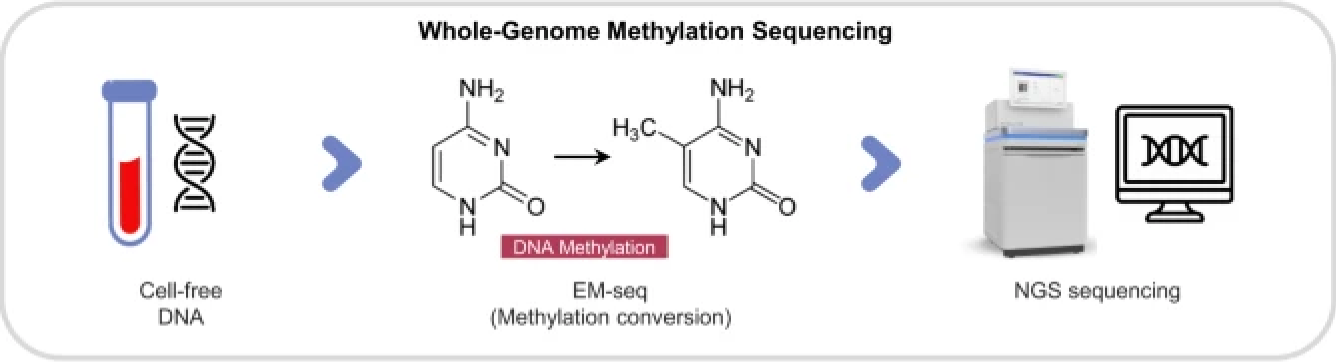
https://doi.org/10.1016/j.annonc.2023.08.004

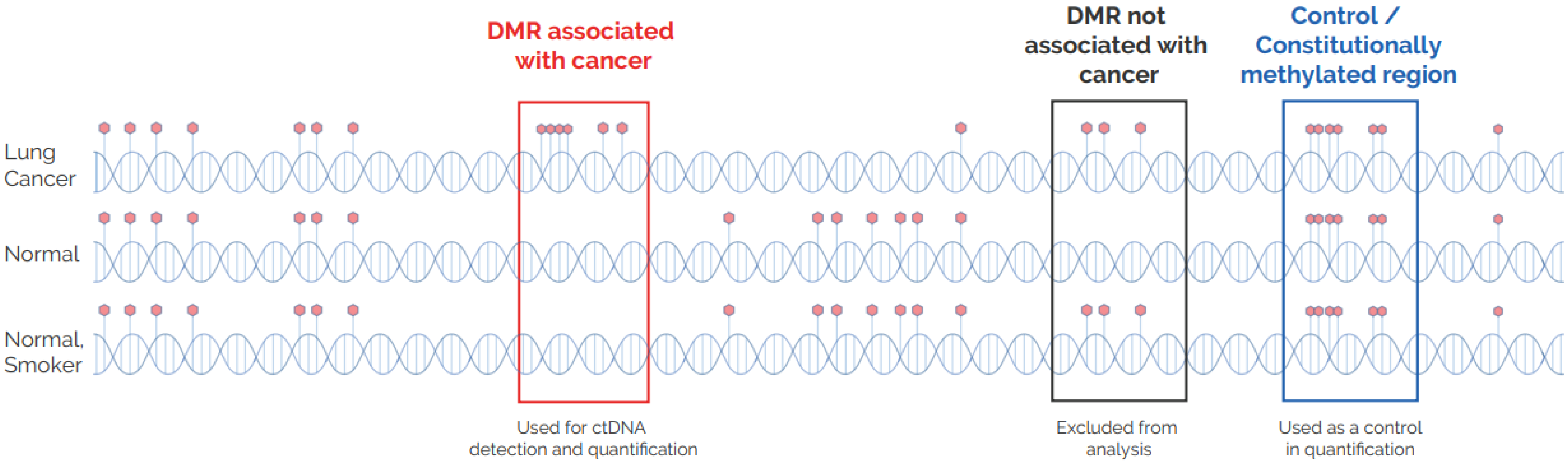
APPROACHES TO IMPROVE LOD



APPROACHES TO IMPROVE LOD: TUMOR FRACTION. METILATION

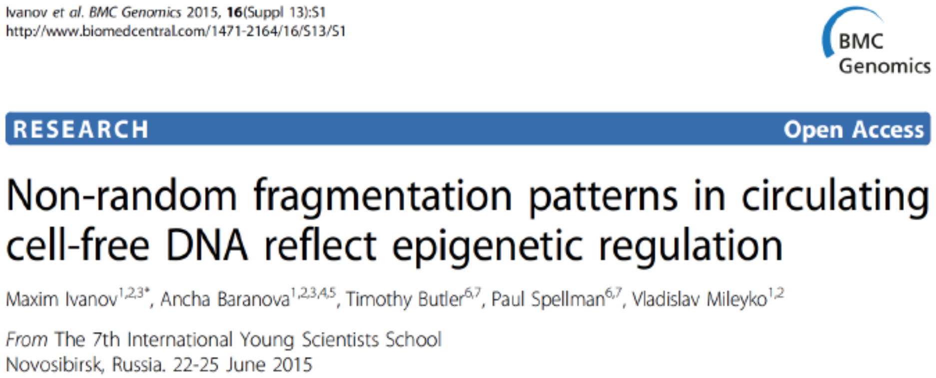
- ✓ Sequence more genome
- ✓ Track more samples
- ✓ Decrease error rate
- ✓ Enrichment of minor alleles
- ✓ Integrate radiomics and other biomarkers
- ✓ Combine variant detection with non-genetic features





Quantifying ctDNA Using a Tissue-Free Test for Minimal Residual Disease (MRD) Detection. Guardant Health

APPROACHES TO IMPROVE LOD: FRAGMENTOMICS



Ivanov *et al. BMC Genomics* 2015, **16**(Suppl 13):S1
http://www.biomedcentral.com/1471-2164/16/S13/S1

BMC Genomics

RESEARCH **Open Access**

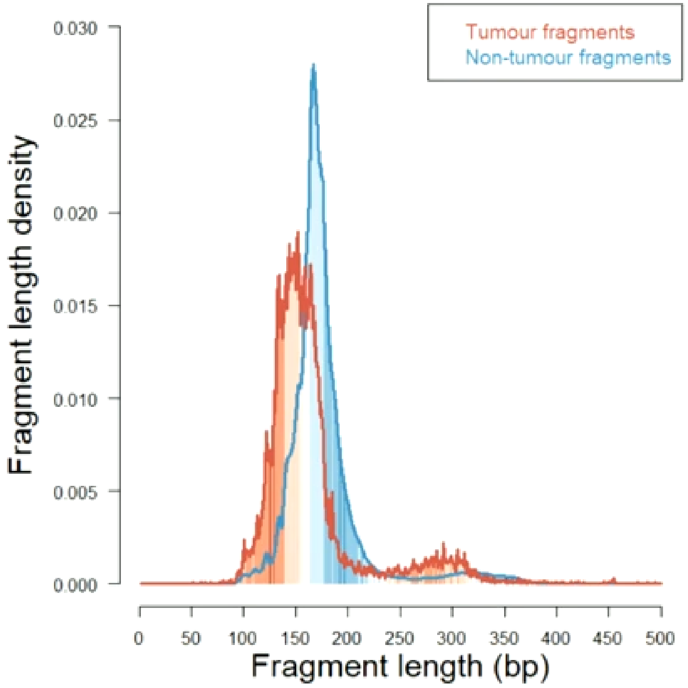
Non-random fragmentation patterns in circulating cell-free DNA reflect epigenetic regulation

Maxim Ivanov[1,2,3*], Ancha Baranova[1,2,3,4,5], Timothy Butler[6,7], Paul Spellman[6,7], Vladislav Mileyko[1,2]

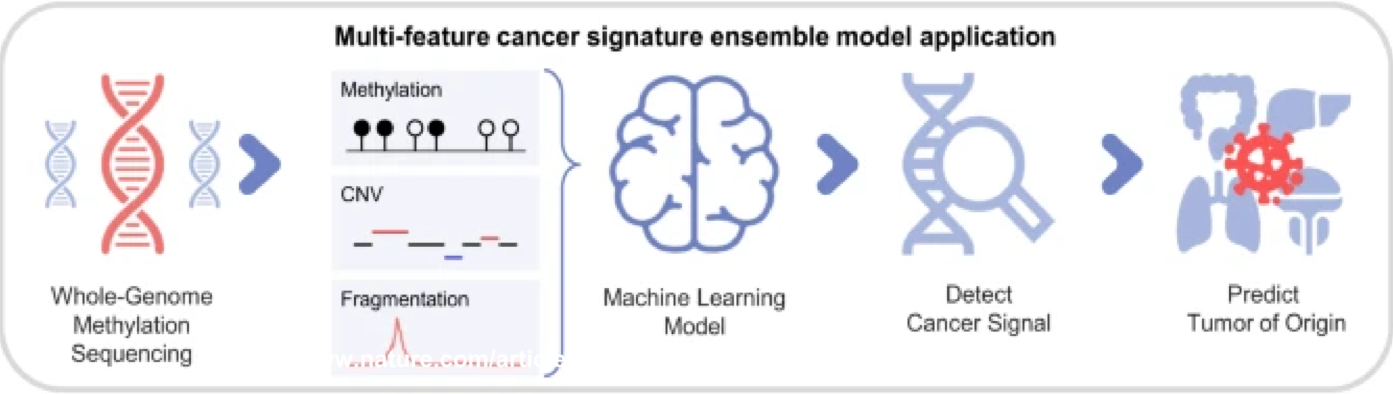
From The 7th International Young Scientists School
Novosibirsk, Russia. 22-25 June 2015

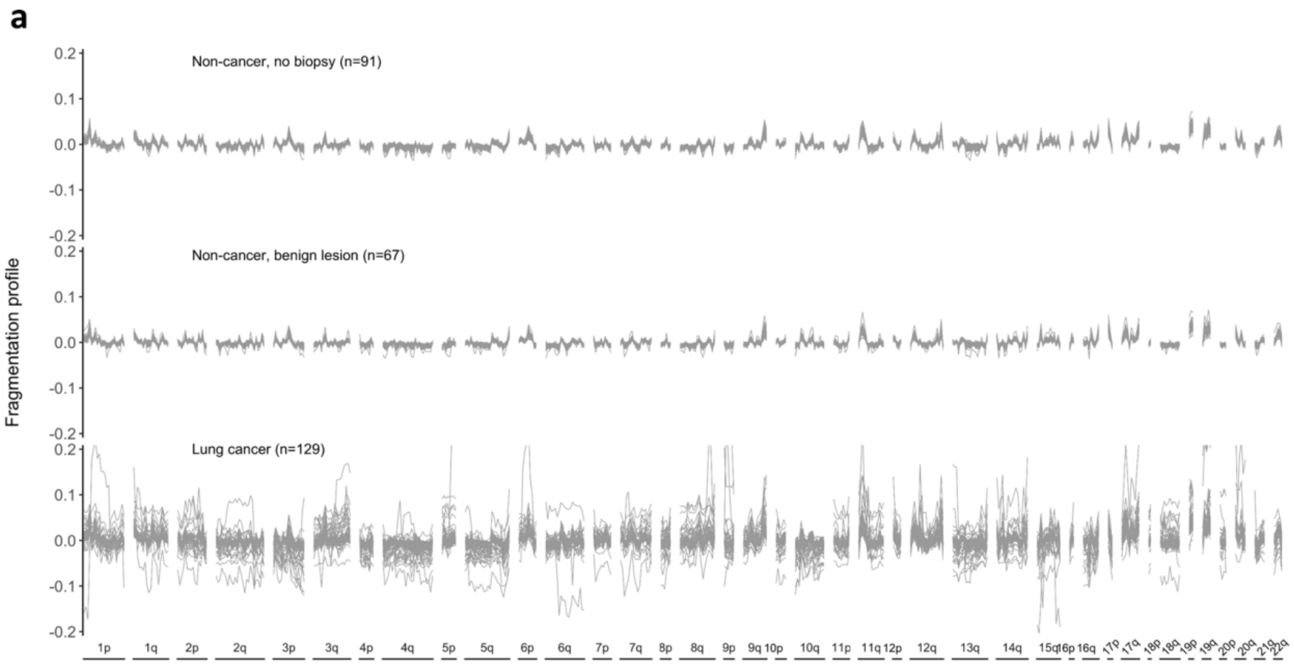
*"…Thus, opening a novel filed in biomarker research that we may tentatively call "**fragmentomics**"….In this paper, we employ high throughtput sequencing of human cfDNA to analyze the properties of cfDNA fragmentation patterns."*

Ivanov M et al. BMC Genomics 2015

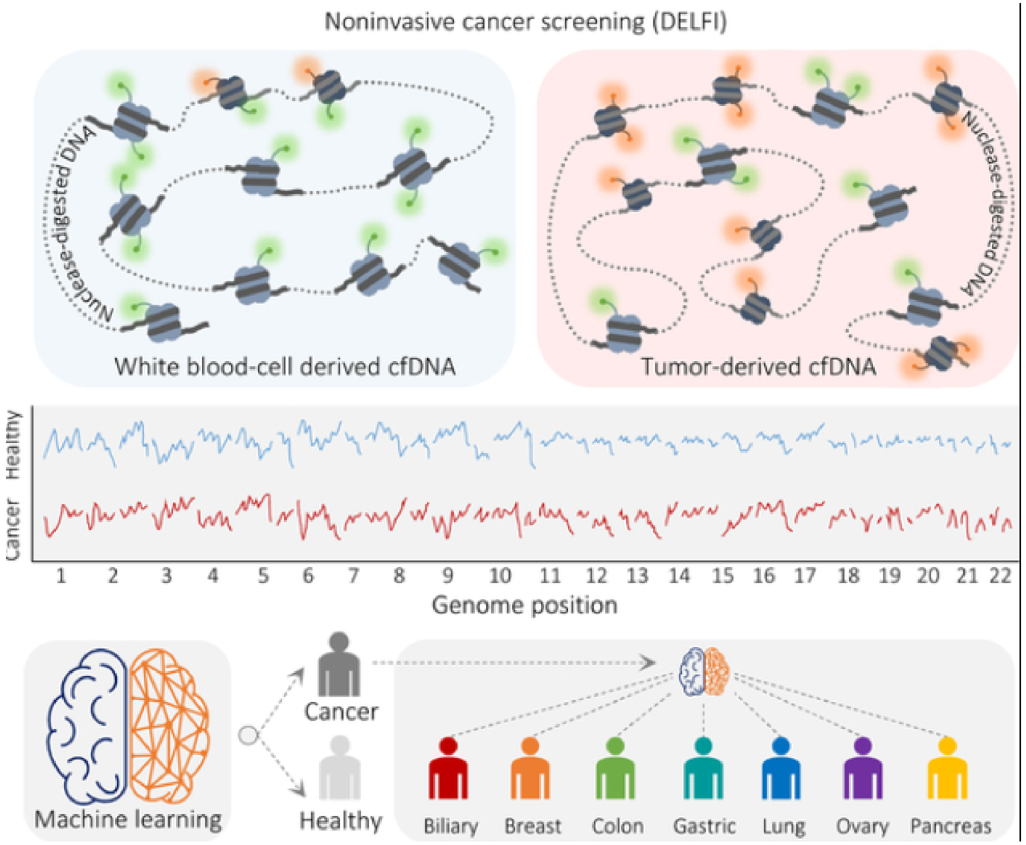


Vessies et al., Molecular Oncology 16:2719–2732 (2022)

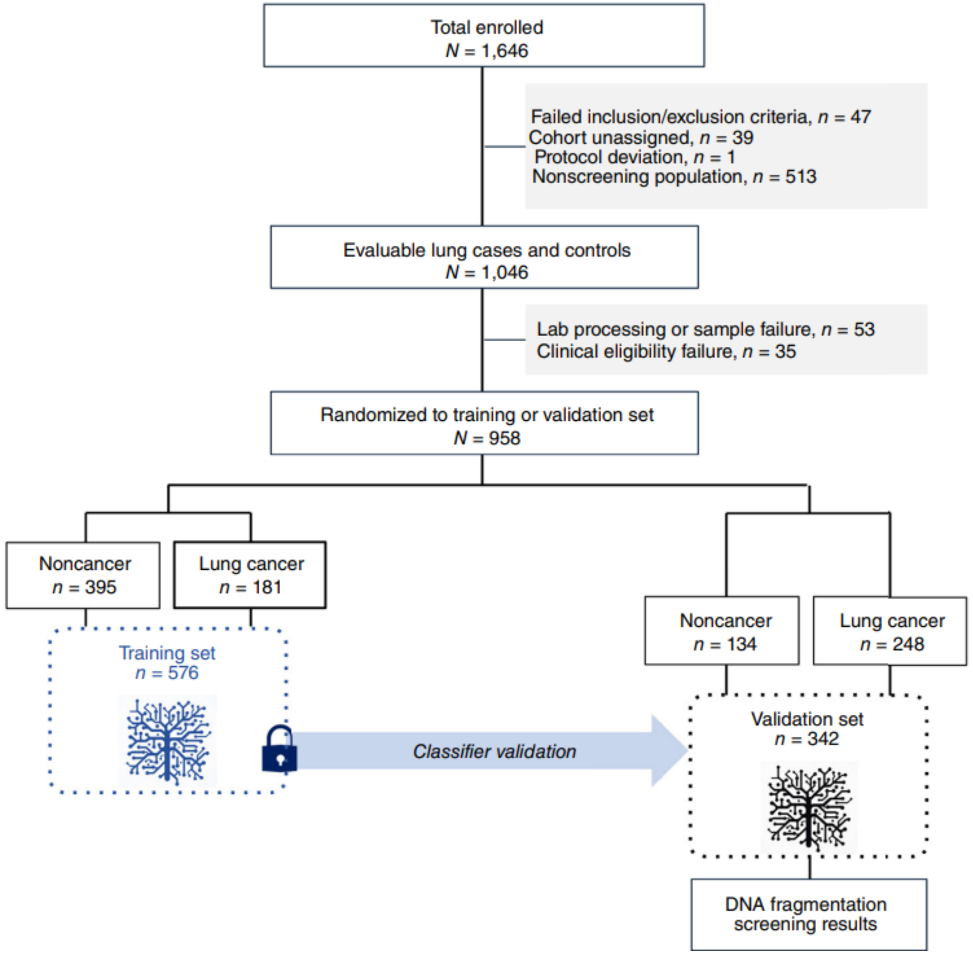




Mathios D, et al. Nature Communications, 2021;12(1):5060.



Nature. 2019 Jun;570(7761):385-389.



Total enrolled
N = 1,646

Failed inclusion/exclusion criteria, *n* = 47
Cohort unassigned, *n* = 39
Protocol deviation, *n* = 1
Nonscreening population, *n* = 513

Evaluable lung cases and controls
N = 1,046

Lab processing or sample failure, *n* = 53
Clinical eligibility failure, *n* = 35

Randomized to training or validation set
N = 958

Noncancer
n = 395

Lung cancer
n = 181

Training set
n = 576

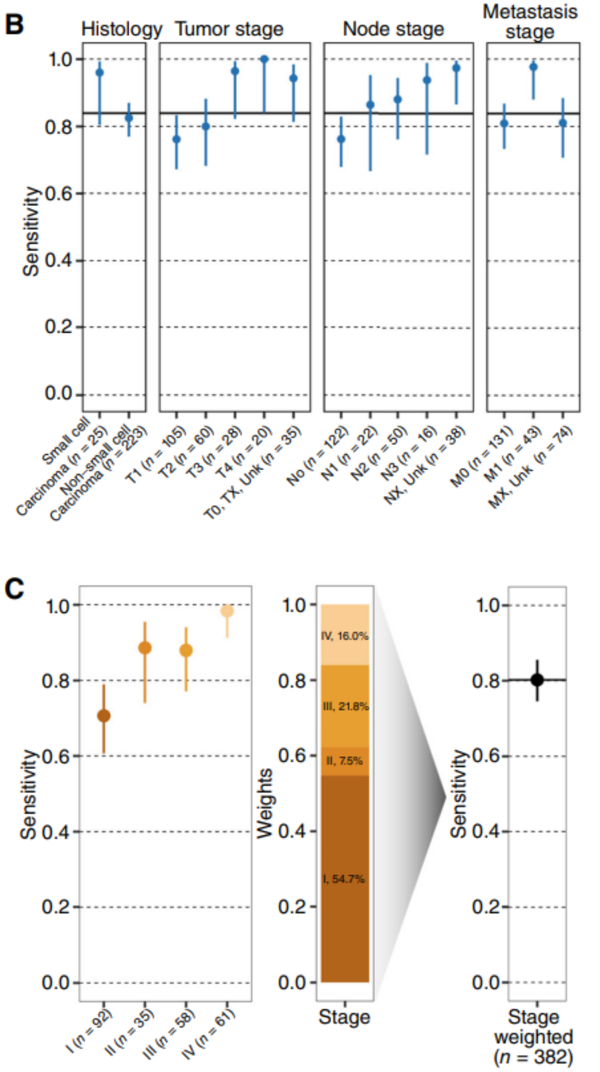
Classifier validation

Noncancer
n = 134

Lung cancer
n = 248

Validation set
n = 342

DNA fragmentation screening results



https://aacrjournals.org/cancerdiscovery/article/14/11/2224/749197/Clinical-Validation-of-a-Cell-Free-DNA-Fragmentome

APPROACHES TO IMPROVE LOD: FRAGMENTOMICS

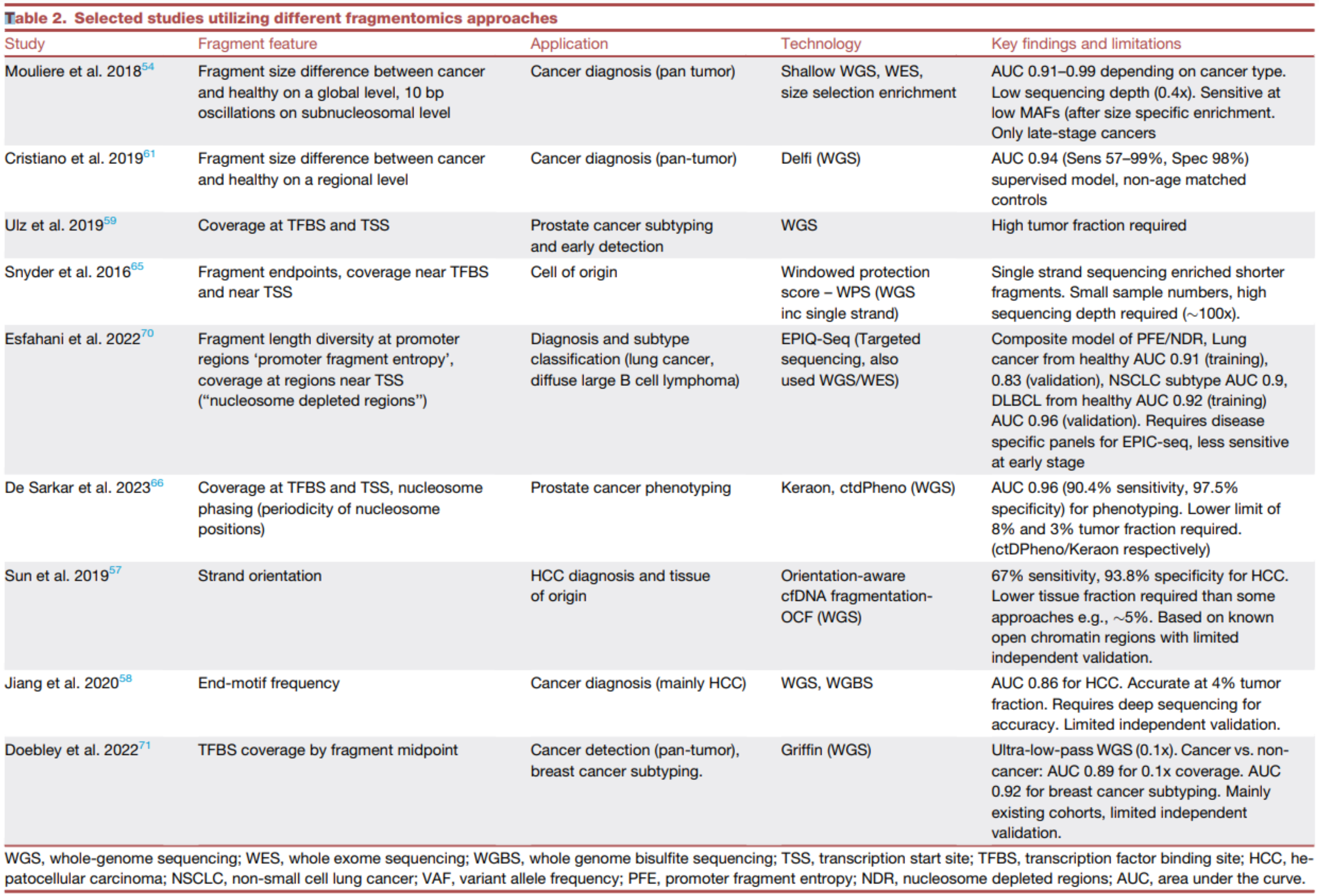


Table 2. Selected studies utilizing different fragmentomics approaches

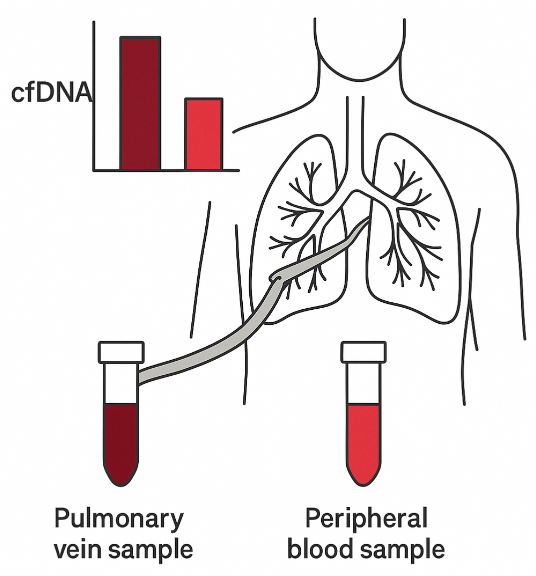
Study	Fragment feature	Application	Technology	Key findings and limitations
Mouliere et al. 2018[54]	Fragment size difference between cancer and healthy on a global level, 10 bp oscillations on subnucleosomal level	Cancer diagnosis (pan tumor)	Shallow WGS, WES, size selection enrichment	AUC 0.91–0.99 depending on cancer type. Low sequencing depth (0.4x). Sensitive at low MAFs (after size specific enrichment. Only late-stage cancers
Cristiano et al. 2019[61]	Fragment size difference between cancer and healthy on a regional level	Cancer diagnosis (pan-tumor)	Delfi (WGS)	AUC 0.94 (Sens 57–99%, Spec 98%) supervised model, non-age matched controls
Ulz et al. 2019[59]	Coverage at TFBS and TSS	Prostate cancer subtyping and early detection	WGS	High tumor fraction required
Snyder et al. 2016[65]	Fragment endpoints, coverage near TFBS and near TSS	Cell of origin	Windowed protection score – WPS (WGS inc single strand)	Single strand sequencing enriched shorter fragments. Small sample numbers, high sequencing depth required (∼100x).
Esfahani et al. 2022[70]	Fragment length diversity at promoter regions 'promoter fragment entropy', coverage at regions near TSS ("nucleosome depleted regions")	Diagnosis and subtype classification (lung cancer, diffuse large B cell lymphoma)	EPIQ-Seq (Targeted sequencing, also used WGS/WES)	Composite model of PFE/NDR, Lung cancer from healthy AUC 0.91 (training), 0.83 (validation), NSCLC subtype AUC 0.9, DLBCL from healthy AUC 0.92 (training) AUC 0.96 (validation). Requires disease specific panels for EPIC-seq, less sensitive at early stage
De Sarkar et al. 2023[66]	Coverage at TFBS and TSS, nucleosome phasing (periodicity of nucleosome positions)	Prostate cancer phenotyping	Keraon, ctdPheno (WGS)	AUC 0.96 (90.4% sensitivity, 97.5% specificity) for phenotyping. Lower limit of 8% and 3% tumor fraction required. (ctDPheno/Keraon respectively)
Sun et al. 2019[57]	Strand orientation	HCC diagnosis and tissue of origin	Orientation-aware cfDNA fragmentation-OCF (WGS)	67% sensitivity, 93.8% specificity for HCC. Lower tissue fraction required than some approaches e.g., ∼5%. Based on known open chromatin regions with limited independent validation.
Jiang et al. 2020[58]	End-motif frequency	Cancer diagnosis (mainly HCC)	WGS, WGBS	AUC 0.86 for HCC. Accurate at 4% tumor fraction. Requires deep sequencing for accuracy. Limited independent validation.
Doebley et al. 2022[71]	TFBS coverage by fragment midpoint	Cancer detection (pan-tumor), breast cancer subtyping.	Griffin (WGS)	Ultra-low-pass WGS (0.1x). Cancer vs. non-cancer: AUC 0.89 for 0.1x coverage. AUC 0.92 for breast cancer subtyping. Mainly existing cohorts, limited independent validation.

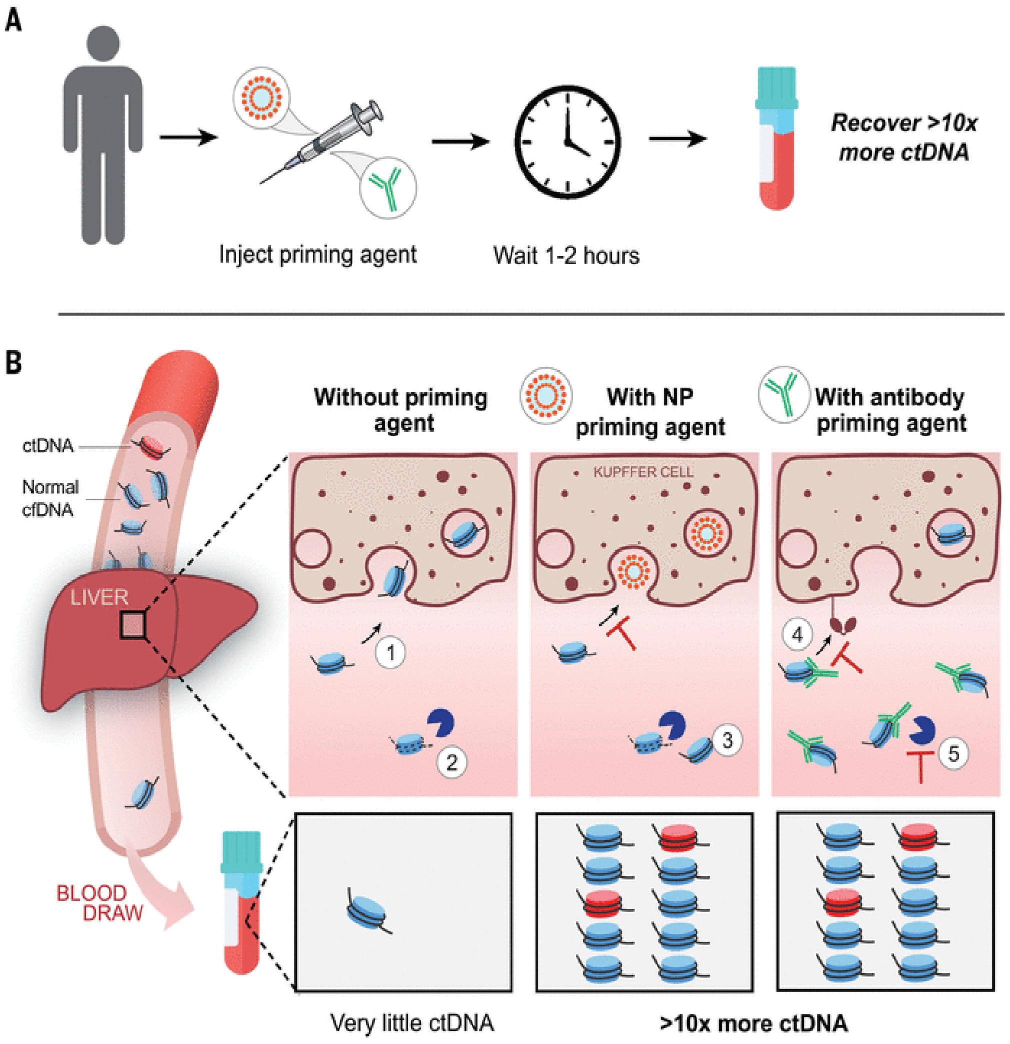
WGS, whole-genome sequencing; WES, whole exome sequencing; WGBS, whole genome bisulfite sequencing; TSS, transcription start site; TFBS, transcription factor binding site; HCC, hepatocellular carcinoma; NSCLC, non-small cell lung cancer; VAF, variant allele frequency; PFE, promoter fragment entropy; NDR, nucleosome depleted regions; AUC, area under the curve.

https://doi.org/10.1016/j.xcrm.2024.101736

APPROACHES TO IMPROVE LOD: FRAGMENTOMICS

- ✓ Sequence more genome
- ✓ Track more samples
- ✓ Decrease error rate
- ✓ Enrichment of minor alleles
- ✓ Integrate radiomics and other biomarkers
- ✓ Combine variant detection with non-genetic features
- ✓ Increase the amount of cfDNA





DOI:10.1126/science.adf2341

TAKE HOME MESSAGE

- ctDNA levels at baseline as well as ctDNA clearance are of prognostic significance in the neoadjuvant setting
- MRD monitoring can help identify cancer patients with excellent prognosis who may be candidates for treatment de-escalation.
- MRD assays used for de-escalation should demonstrate high sensitivity and high negative predictive value (NPV).
- 1st generation MRD assays provide high positive predictive value but may be less suitable for guiding treatment de-escalation.
- Novel methods such as Phased-Seq and Minor Allele Enriched Sequencing show promise for improving MRD measurement.
- While cfDNA profiling has traditionally relied on mutation detection, moving beyond mutations—through fragmentation-based profiling—offers the potential for greater sensitivity.
- Approaches to improve DNA yield are under investigation and may improve LOD; EVs also show promise as an alternative source
- Multimodal approaches (e.g., combining radiomics and ctDNA MRD) may enhance the prediction of survival outcomes.

GRACIAS!

II JORNADA TRASLACIONAL
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