



Real world applications for ctDNA in colorectal cancer

THE UNIVERSITY OF TEXAS
MD Anderson
Cancer Center

Making Cancer History®

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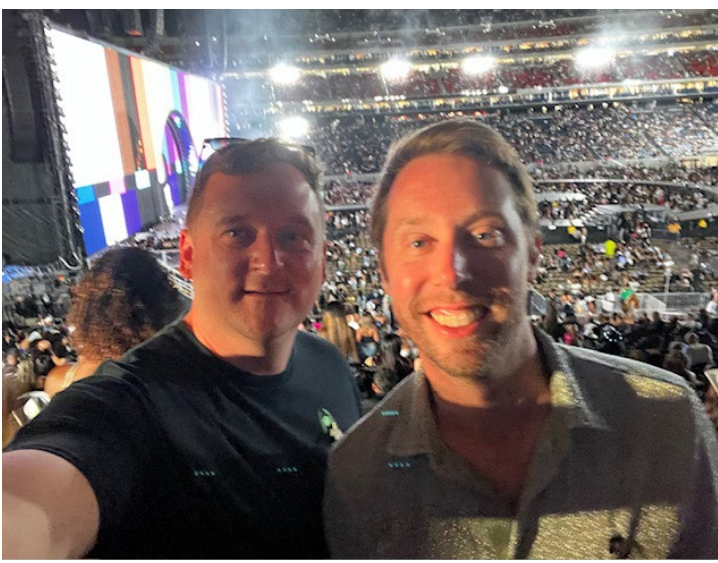
Disclosures

Research Funding (to MD Anderson): Bristol Myers Squibb, Pfizer, EMD Serono, Novartis, BioNTech, Bicara, RedX Pharma

Consulting: Bayer, Regeneron, Novartis

Principal Investigator for ctDNA trials: NRG-GI005 (overall PI), BioNtech (MDACC PI)

Before a Houstonian, forever a Memphian...

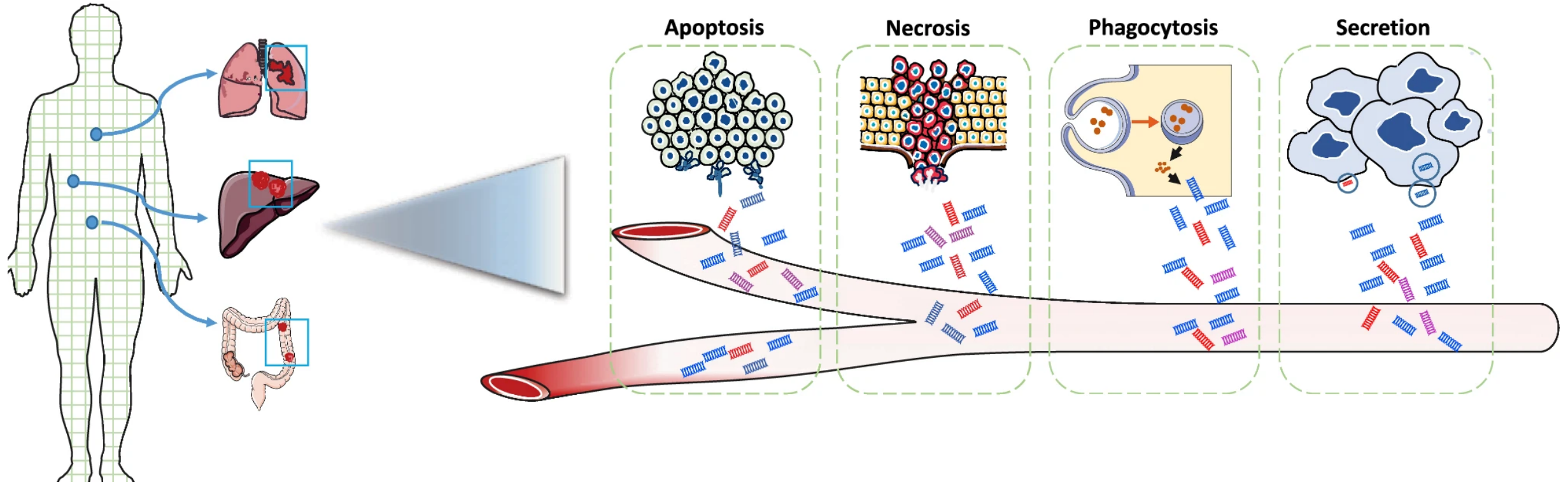


Overview

- Use of ctDNA as a tool to inform cancer biology as a liquid biopsy
- Informing clinical decision making of CRC using ctDNA technologies
- Recognizing micrometastatic CRC as a unique biologic entity with novel therapeutic opportunities to cure more patients

- **Use of ctDNA as a tool to inform cancer biology as a liquid biopsy**
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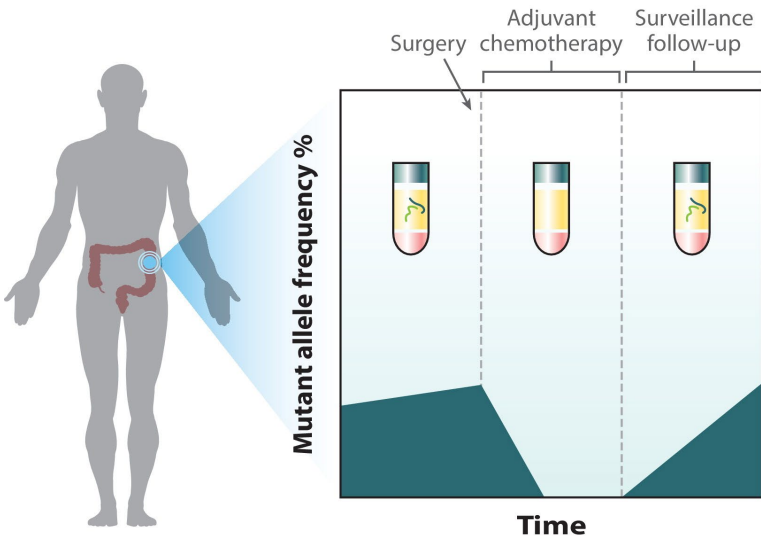
Circulating tumor DNA as a “liquid biopsy”



- Circulating tumor DNA (ctDNA) can be detected in blood following release from tumor cells, predominantly via apoptosis.
- Different fragment size for ctDNA: unlike cfDNA fragments [$\sim(167)_n$ bp in length], ctDNA fragments are ~ 20 - 30 bp shorter
- “Real-time” analysis: half-life of ctDNA in plasma ~ 2 - 3 hours

CURATIVE SETTING

a Detection of MRD



Risk stratifying:

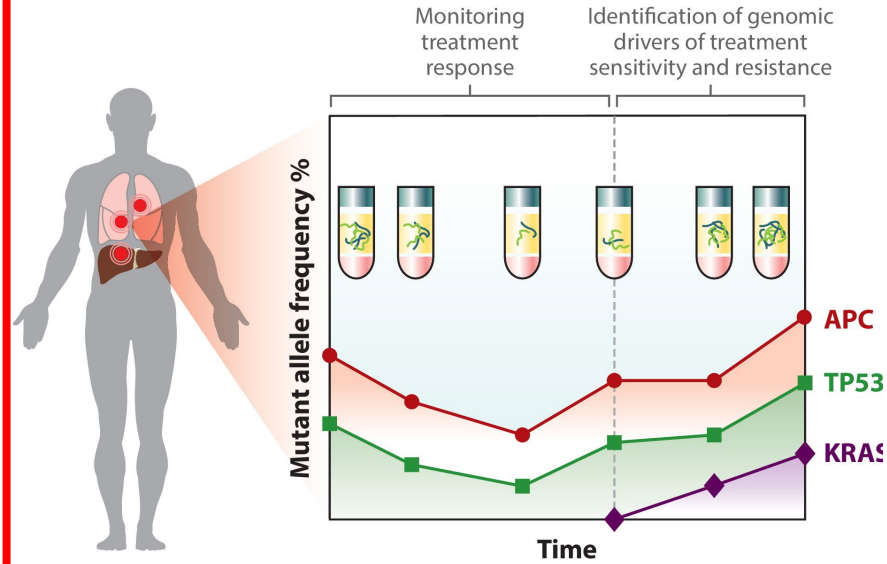
- HIGH RISK patients - in need of (better) curative therapies
- LOW RISK patients needing less toxicity

Better surveillance following curative therapies?

Tumor-agnostic **cancer screening?**

METASTATIC SETTING

b Monitoring dynamic changes in ctDNA



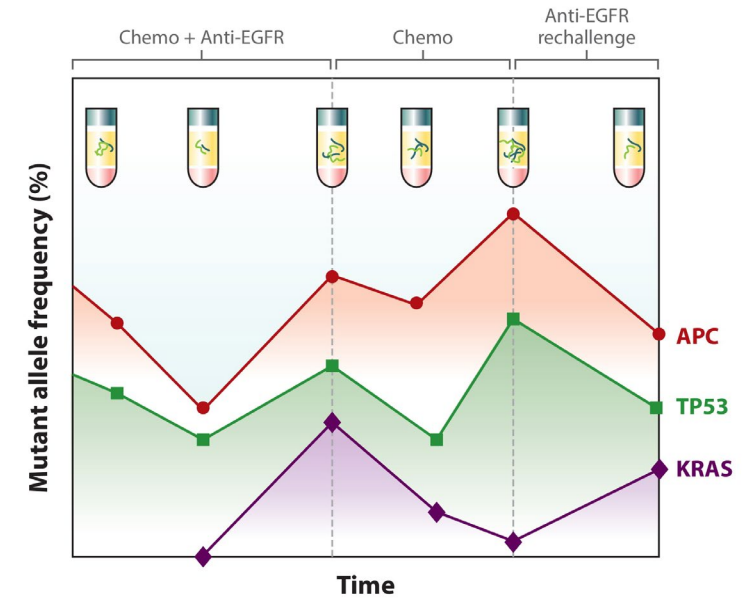
Treatment monitoring:

- EARLY IDENTIFICATION of response to systemic therapies
 - Balance treatment response with associated toxicity
 - Gauging efficacy to neoadjuvant therapies?
- Complement radiographic findings in assessing treatment response
 - Immunotherapy in MSI-H/dMMR GI cancers

Personalizing further targeted therapies:



- Real-time, less-invasive, more comprehensive characterization of clonal evolution driving treatment resistance
 - Informing on pattern/depth of response?
 - Clinical trial eligibility

c Guiding treatment strategies to overcome therapeutic resistance



ctDNA to identify minimal residual disease: practical considerations

- High sensitivity for MRD detection: alterations with VAF < .01% can be detected
- Sensitivity improving with improving cfDNA isolation methods, WES of tumor, and with complementary methylation profiling for cancer-specific aberrations
- High specificity: Detection of ctDNA ~ 100% likelihood for recurrence after resection of CRC

		MRD Present?	
		MRD Present	MRD Absent
Assay Result	ctDNA Detected		False Positive - CHIP
	ctDNA NOT Detected	False Negative - Timing of blood draw - Site of MRD (distant?) - (Assay limit of detection)	

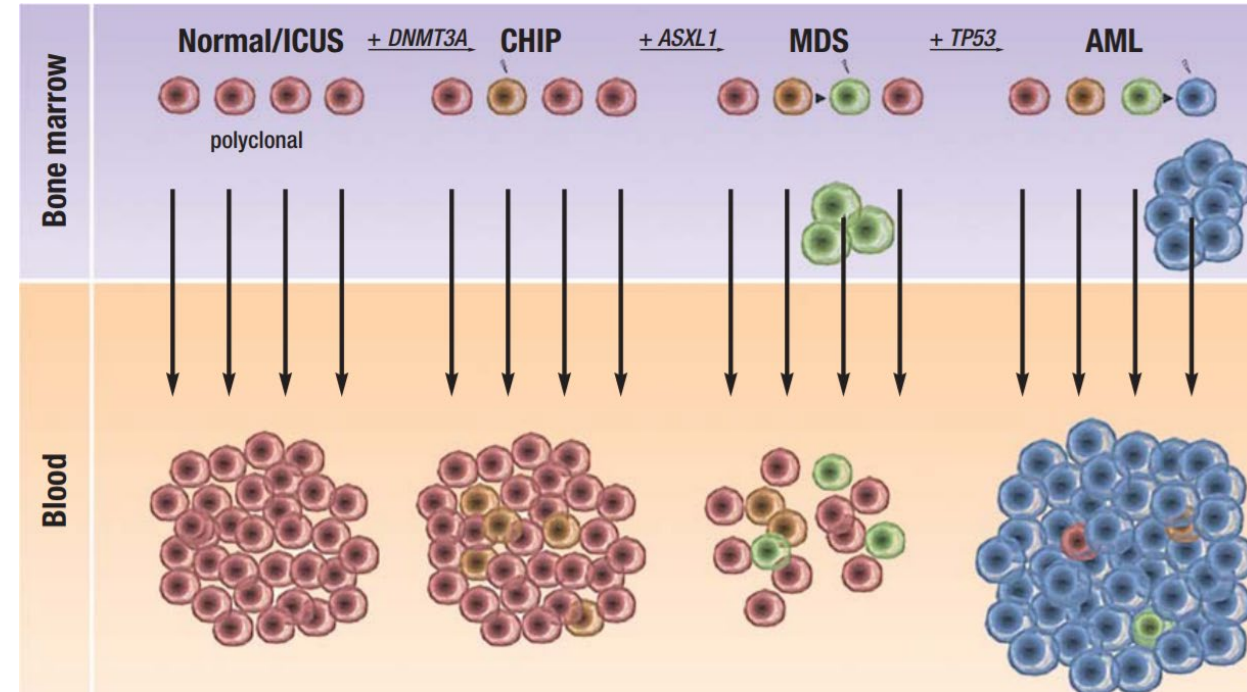
Different methodologies for ctDNA detection: tumor-informed vs tumor-agnostic

	TUMOR-INFORMED	TUMOR AGNOSTIC
Requires matched tumor tissue?	Yes	No
Turn-around time adequate for adjuvant chemotherapy window?	Longer	Shorter
Gene coverage	Personalized according to deep sequencing of tumor	Extensive panel including most commonly mutated genes
Correction for CHIP confounding?	Yes	Maybe

CHIP: blood “contaminant”

Are the ctDNA “positive” results generated reflective of the patient’s underlying tumor biology, and how do we account for this in design of clinical trials (especially MRD studies)?

- Clonal hematopoiesis of indeterminate potential (CHIP) refers to the presence of somatic mutations in HSCs detected in the blood, in the absence of an associated hematologic malignancy.
- CHIP occurs more commonly with advancing age and observed especially as mutations in *DNMT3A*, *TET2*, and *ASXL1*.
- CHIP mutations in ctDNA assay have the potential to generate false positives for ctDNA study when assessing for MRD.

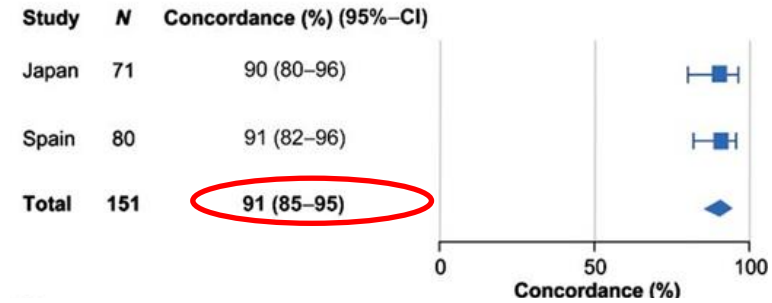


Co-sequencing of tumor tissue or isolated PBMCs isolated can distinguish CHIP and germline aberrations from true ctDNA.

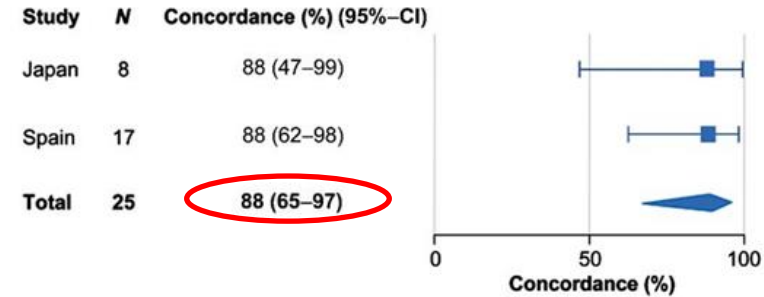
Practical considerations necessary for ctDNA testing

- High concordance of genomic alterations between ctDNA and matched tumor tissue (~80-90%), especially for driver mutations.
- **WHERE** matters!
 - CRC liver mets are more likely to shed ctDNA
- **HOW** matters!
 - Tumor informed vs tumor-agnostic assay selection: high sensitivity/specificity regardless, shorter turn-around time for tumor-agnostic ctDNA
- **WHEN** matters!
 - Increased cfDNA/inflammatory milieu after surgical trauma can increase FN likelihood for MRD detection, up to ~4 weeks after surgery
- **WHAT** matters!
 - Knowing what question you are asking when ordering the test guides your management

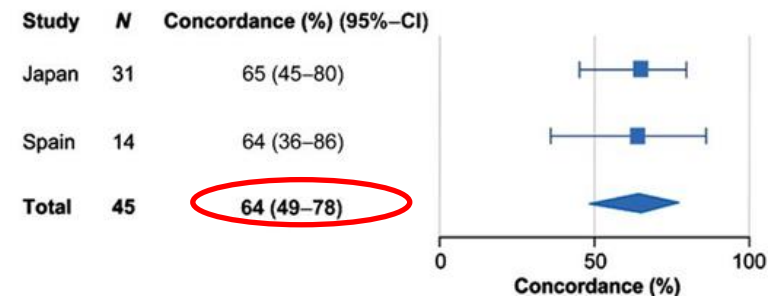
LIVER METASTASES ALONE



PERITONEAL METASTASES ALONE



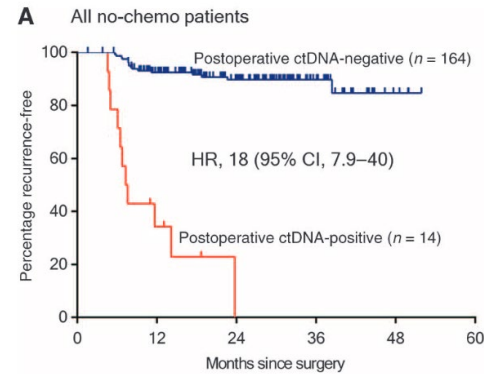
LUNG METASTASES ALONE



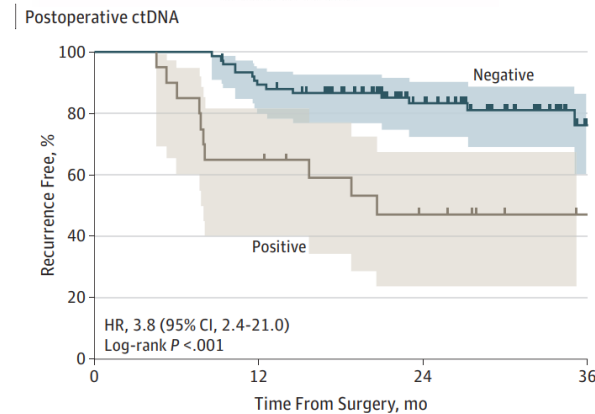
- Use of ctDNA as a tool to inform cancer biology as a liquid biopsy
- **Informing clinical decision making of CRC using ctDNA technologies**
- Recognizing micrometastatic CRC as a unique biologic entity with novel therapeutic opportunities to cure more patients

ctDNA detection as a prognostic biomarker in CRC

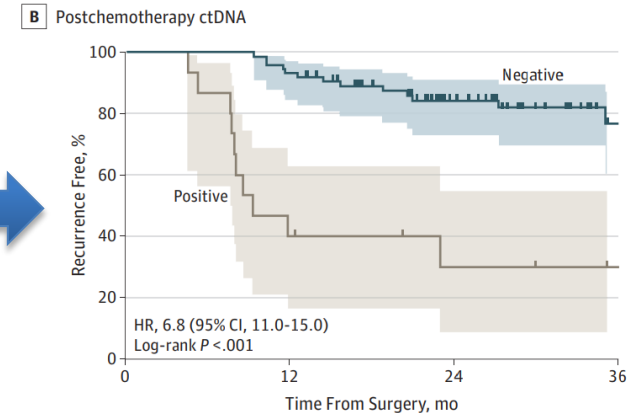
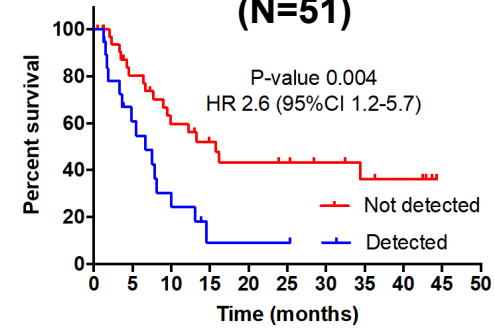
**Stage II CC
(N=178)**



**Stage III CC
(N=96)**



**Stage IV CC
(N=51)**

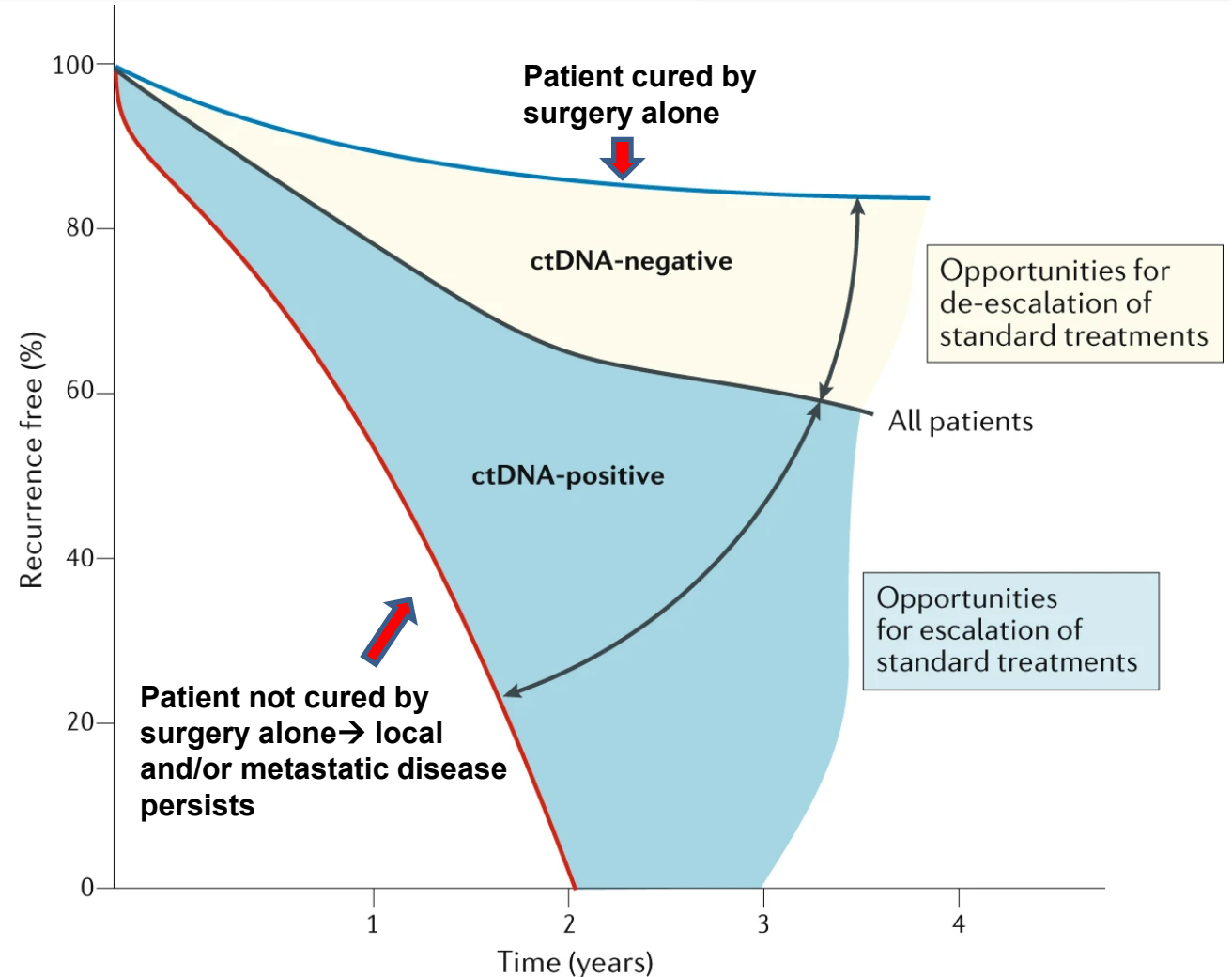


Detection of ctDNA is a biomarker for poor prognosis across all stages of colorectal cancer.

Detection of ctDNA precedes clinical/radiographic recurrence by median ~5-6 months in CRC.

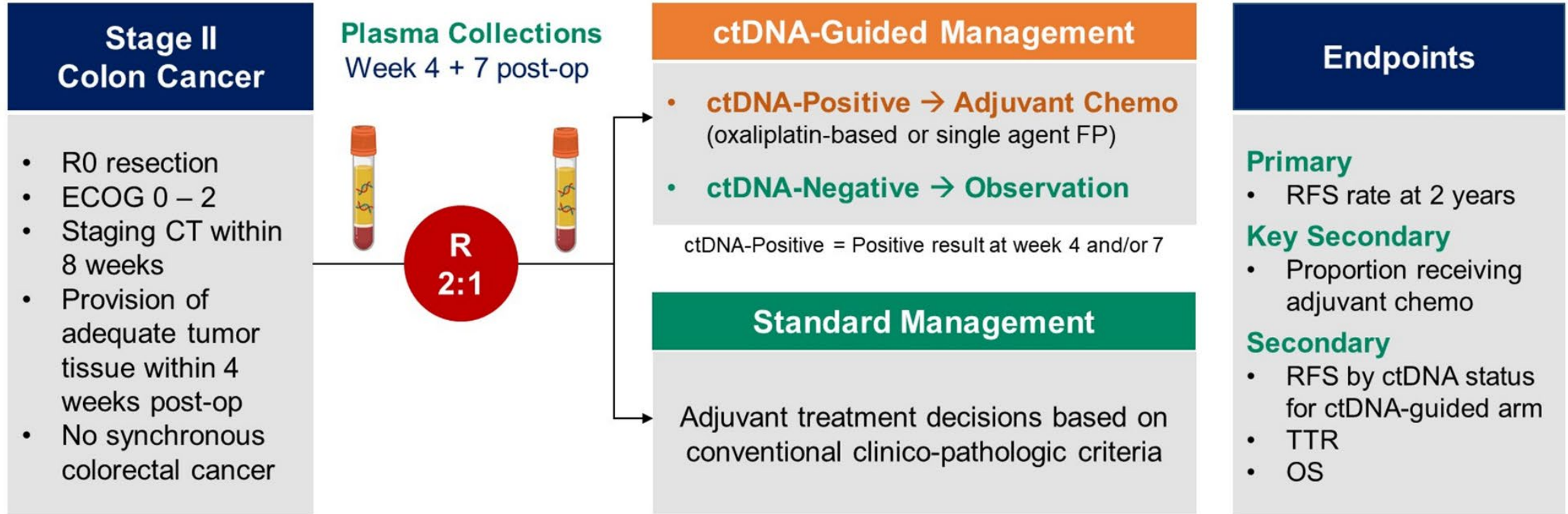
Application of ctDNA towards treatment of MRD in colon cancer

- ctDNA(-) patients: **UNLIKELY** to recur
 - Opportunities for **de-escalation**?
 - Minimizing (unnecessary?) toxicity of treatment without affecting survival outcome?
- ctDNA(+) patients: **LIKELY** to recur
 - Opportunities for **escalation**?
 - Accepting toxicity of (additional?) treatment to improve likelihood of favorable outcome



Is ctDNA ready for routine use in adjuvant treatment decision making following resection of stage II/III colon cancer?

DYNAMIC schema



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

Study was designed to investigate whether a **ctDNA-guided approach vs standard approach** could reduce the use of adjuvant chemotherapy without compromising the recurrence risk for patients with stage II colon cancer.

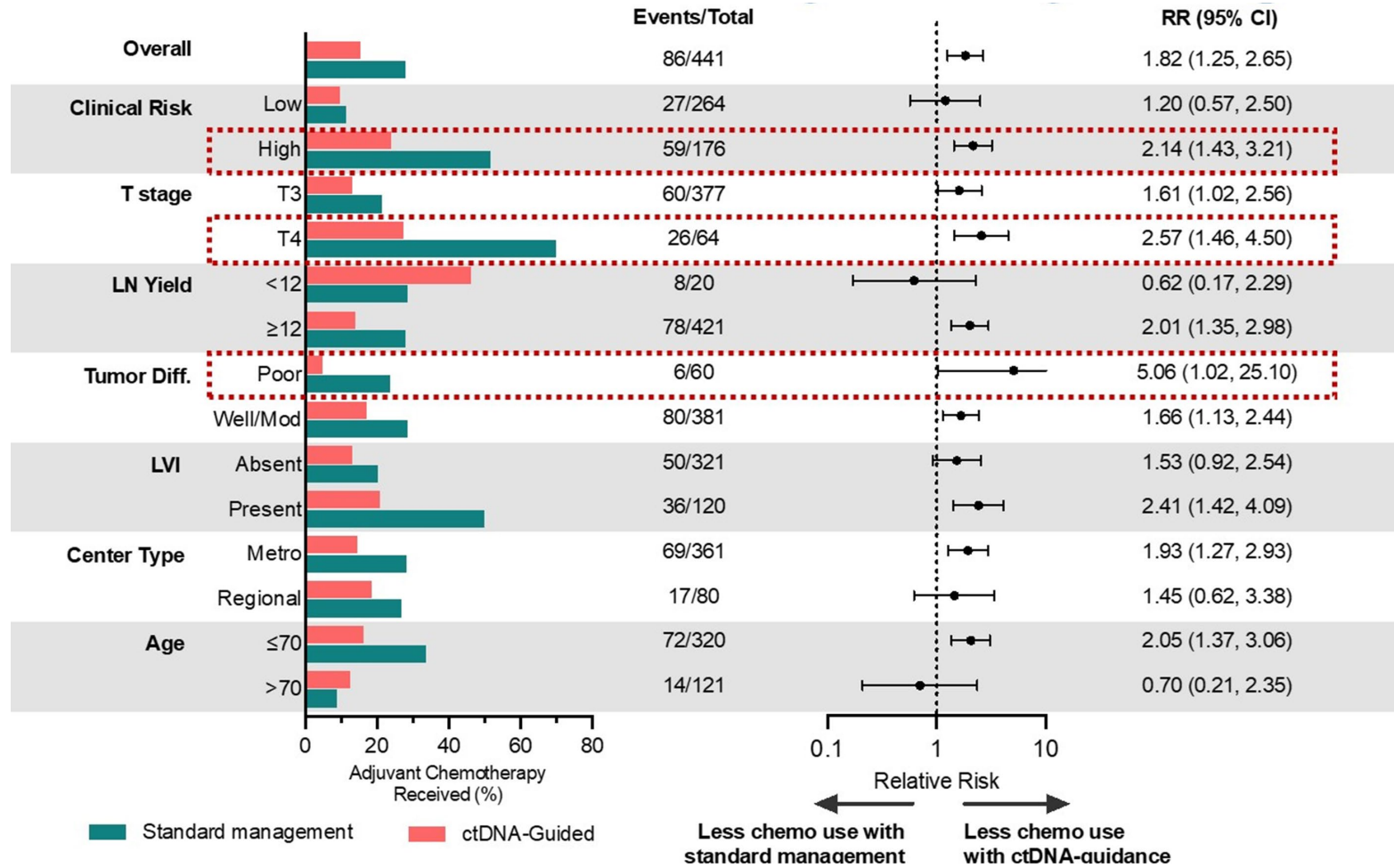
Chemotherapy selection according to treatment approach (DYNAMIC)

Treatment Information	ctDNA-Guided N = 294	Standard Management N = 147	P-value
Adjuvant Chemotherapy received, n	45 (15%)	41 (28%)	0.0017
Chemotherapy regimen received, n			
Oxaliplatin-based doublet	28/45 (62%)	4/41 (10%)	<.0001
Single agent fluoropyrimidine	17/45 (38%)	37/41 (90%)	
Time from surgery to commencing chemotherapy, median (IQR), days	83 (76, 89)	53 (49, 61)	<.0001
Treatment duration, median (IQR), weeks	24 (19, 24)	24 (21, 24)	0.9318
Completed planned treatment, n	38 (85%)	32 (78%)	0.7036
Percentage of full dose delivered, median (IQR)	78 (56, 100)	84 (64, 100)	0.6194

For stage II colon cancer, ctDNA-informed decision making resulted in

- LESS overall use of chemotherapy (more DE-ESCALATION)
- When used, MORE use of (escalated) chemotherapy

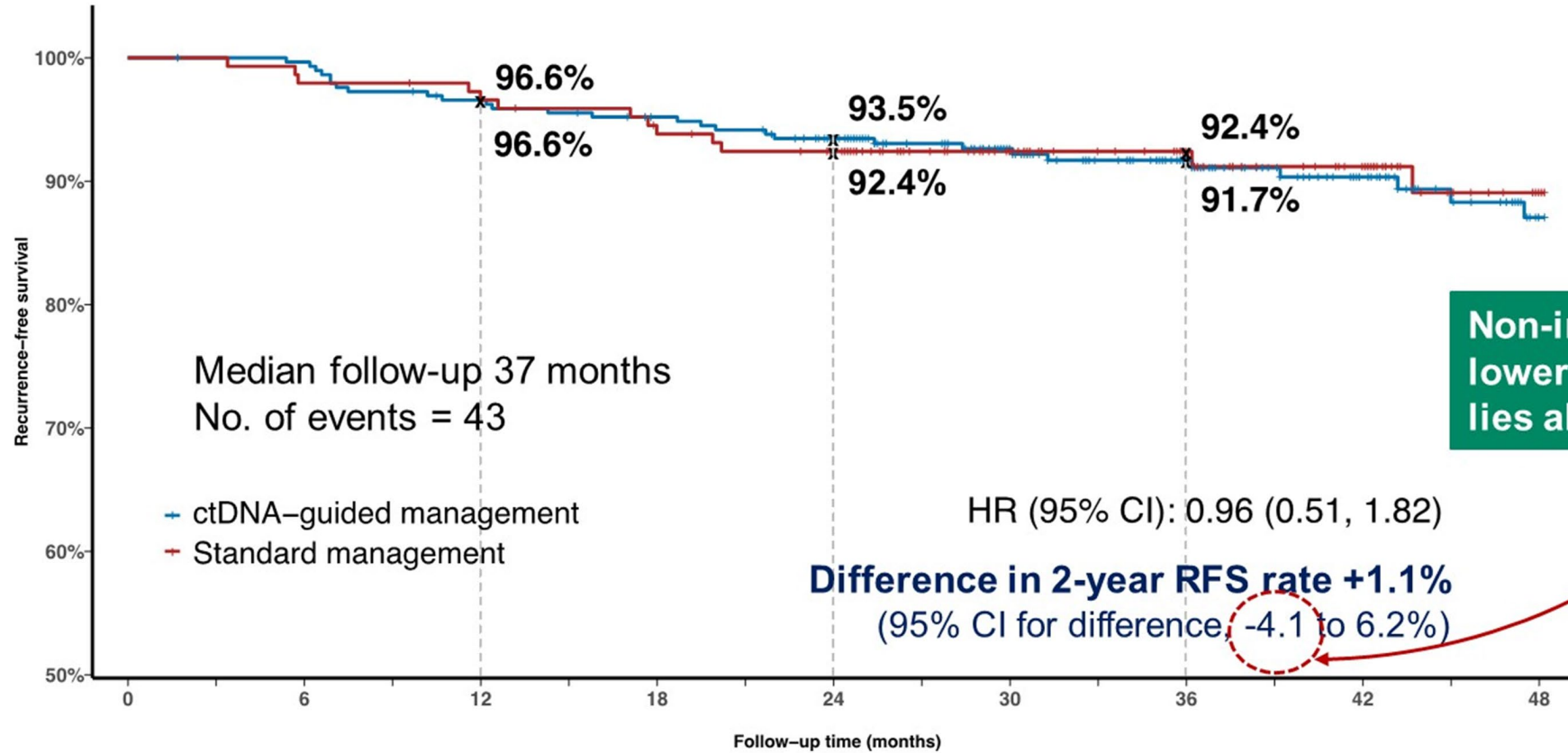
DYNAMIC: association of ctDNA status with chemotherapy use



For stage II colon cancer, ctDNA results directed less chemotherapy for:

- clinically “high risk” stage II colon cancers
- T4 primary tumors
- poorly differentiated tumors

DYNAMIC: recurrence-free survival outcomes

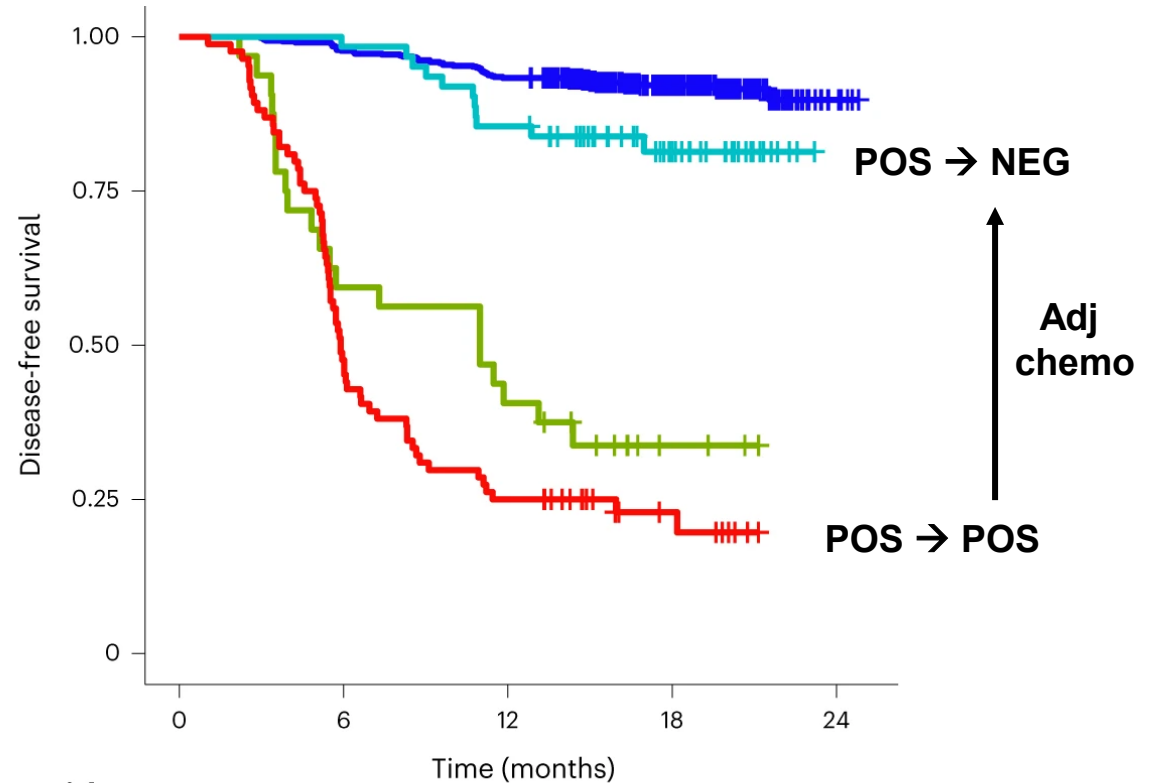


Numbers at risk

ctDNA-guided	294	292	281	273	259	207	155	109	64
Standard	147	144	142	136	128	97	78	57	33

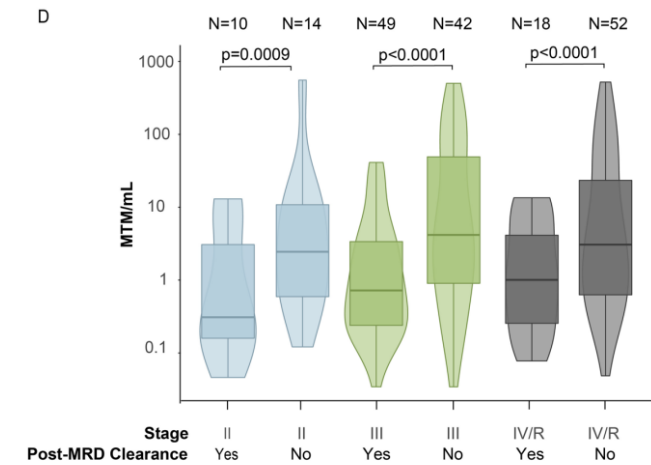
Evaluating ctDNA kinetics qualitatively in treatment of MRD (GALAXY)

- Observational study evaluating changes in ctDNA from weeks 4 → 12 post-op (N=838) in patients with resected colon cancer.
- Clearance of ctDNA with adjuvant chemo was associated with improved 18-month DFS (81% vs 22%).
- Clearance of ctDNA was linked to lower total ctDNA burden at time of MRD detection:



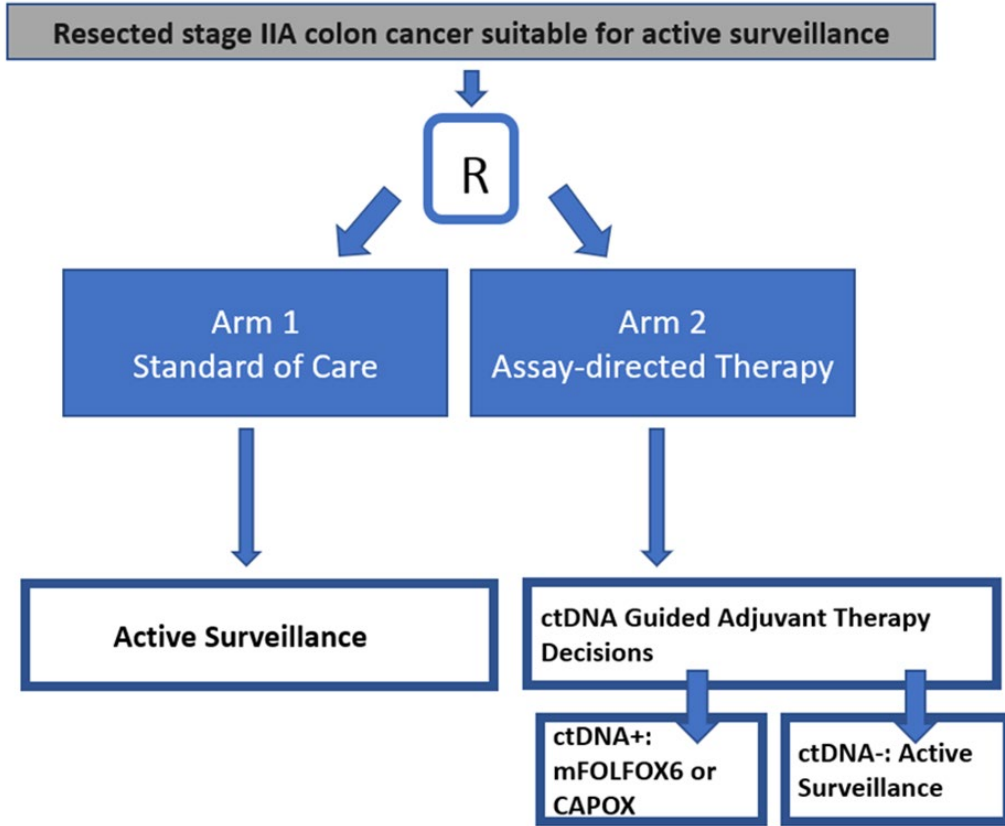
Number at risk

	0	6	12	18	24
Persistently negative	660	645	616	271	5
Converted positive	32	19	13	3	0
Converted negative	62	61	53	28	0
Persistently positive	84	40	21	7	0



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Does chemotherapy clear ctDNA in stage II colon cancer?



Primary Endpoints:
 ctDNA clearance (phase II)
 Recurrence-free survival (phase III)
 ctDNA assay: LUNAR-1 (blood-only)

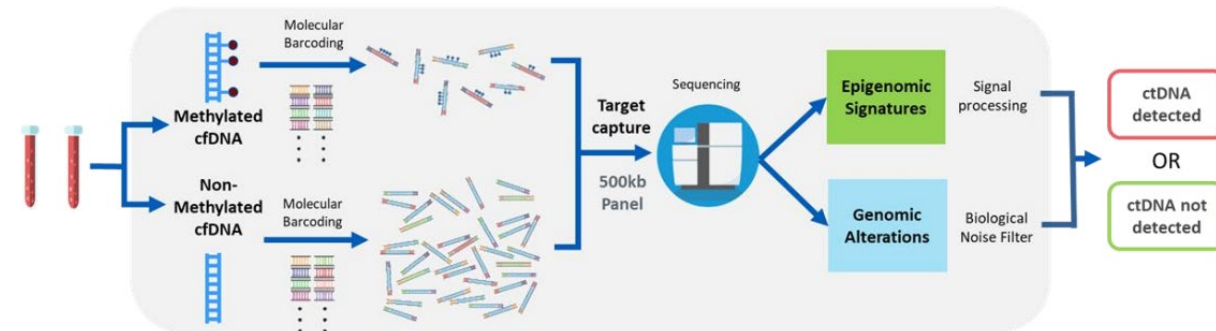
PI: Van Morris (MD Anderson)

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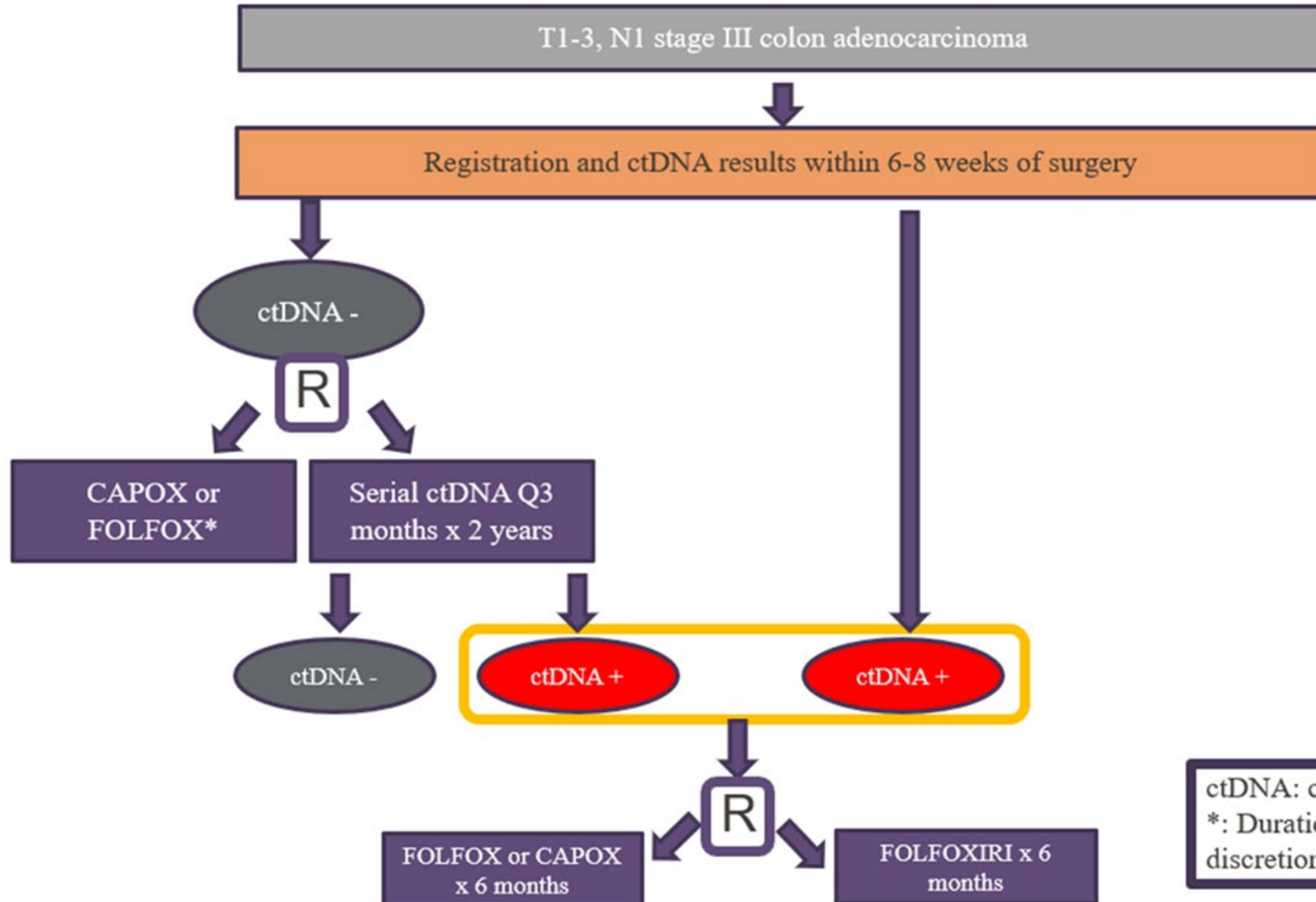
First NCI-supported trial for any solid tumor type to incorporate ctDNA as an intergal biomarker :
 Developed here at MD Anderson!!

NRG GI005
COBRA
 (Low-risk stage IIA)

CLOSED TO
ENROLLMENT
7/2023



ctDNA for escalation/de-escalation of chemotherapy in stage III colon cancer



CIRCULATE-US (High-risk stage II/stage III)

ctDNA assay: Signatera (tumor-informed)

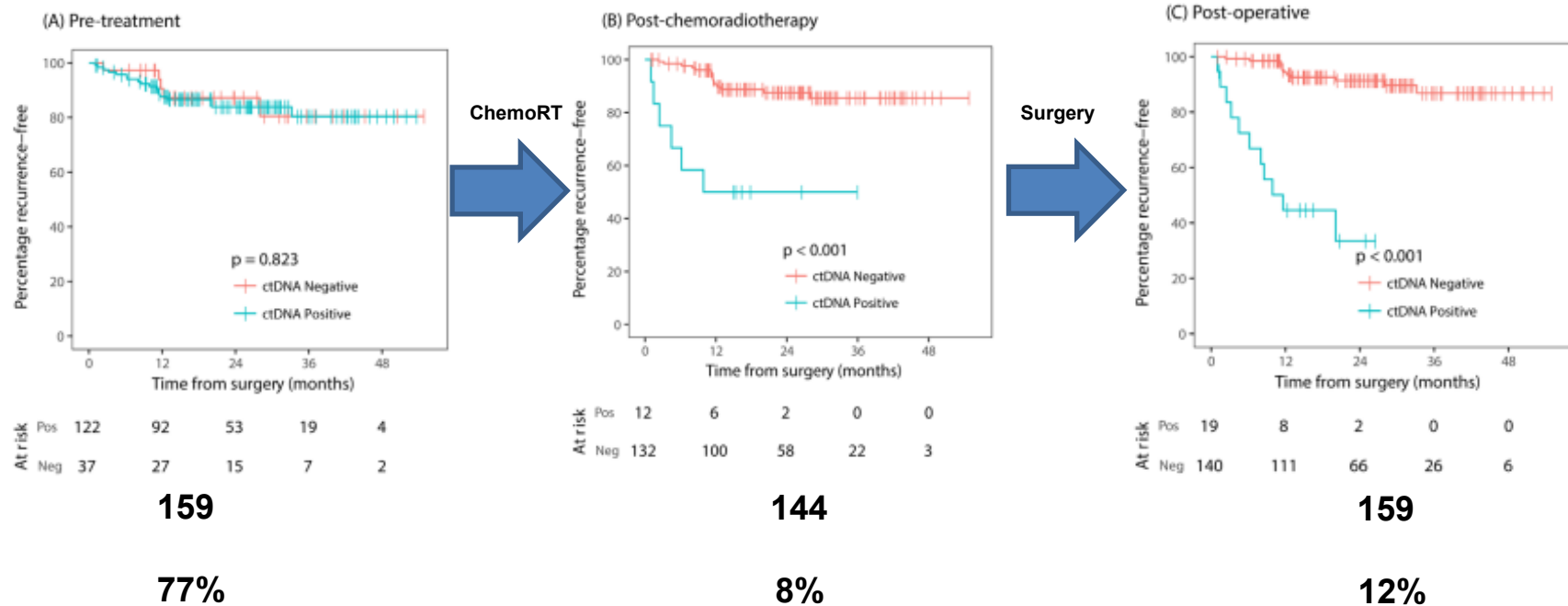
Principal Investigators:
Arvind Dasari (MD Anderson)
Christopher Lieu (Colorado)

NCT04089631

ctDNA: cir
*: Duration
discretion

ctDNA for evaluating treatment response for rectal cancer

- Management of localized rectal cancer has shifted to total neoadjuvant therapy (scRT → FP/oxaliplatin), with a goal of non-operative, “watch and wait” approach for patients with complete endoscopic and radiographic response...
- Can we identify patients cured by TNT approach?



Does this identify patients experiencing pCR?

Association between post chemoRT ctDNA status and pCR

Table 1 Clinicopathological characteristics and recurrence, according to ctDNA status

Variable	Pretreatment ctDNA (n=159)			Postchemoradiotherapy ctDNA (n=144)			Postoperative ctDNA (n=159)		
	Positive (n=122)	Negative (n=37)	P	Positive (n=12)	Negative (n=132)	P	Positive (n=19)	Negative (n=140)	P
Age, years									
Median	63	59	0.69	61	62	0.97	59	63	0.97
Range	28–85	31–86		41–86	28–86		41–86	28–86	
Sex, n (%)									
Female	40 (33)	12 (32)	1.00	4 (33)	43 (33)	1.00	6 (32)	46 (33)	1.00
Male	82 (67)	25 (68)		8 (67)	89 (67)		13 (68)	94 (67)	
Distance from anal verge (cm), n (%)									
0–5	44 (36)	13 (35)	0.77	4 (33)	48 (36)	0.79	6 (32)	51 (37)	0.01
> 5–10	55 (45)	19 (51)		5 (42)	62 (47)		5 (26)	69 (49)	
> 10	23 (19)	5 (14)		3 (25)	22 (17)		8 (42)	20 (14)	
Clinical disease stage, n (%)									
Stage II	23 (19)	12 (32)	0.11	2 (17)	29 (22)	1.00	2 (11)	33 (24)	0.25
Stage III	99 (81)	25 (68)		10 (83)	103 (78)		17 (89)	107 (76)	
Pathological T stage, n (%)									
ypT0-2	65 (53)	23 (62)	0.36	5 (42)	73 (55)	0.38	5 (26)	83 (59)	0.01
ypT3-4	57 (47)	14 (38)		7 (58)	59 (45)		14 (74)	57 (41)	
Pathological N stage, n (%)									
ypN0	91 (75)	25 (68)	0.40	6 (50)	97 (73)	0.10	10 (53)	106 (76)	0.05
ypN1-2	31 (25)	12 (32)		6 (50)	35 (27)		9 (47)	34 (24)	
Pathological complete response, n (%)									
Yes	24 (20)	10 (27)	0.36	1 (9)	28 (21)	0.46	2 (11)	32 (23)	0.37
No	98 (80)	27 (73)		11 (89)	104 (79)		17 (89)	108 (77)	
Adjuvant chemotherapy, n (%)									
Yes	40 (33)	17 (46)	0.17	4 (33)	43 (33)	1.00	11 (58)	91 (65)	0.61
No	82 (67)	20 (54)		8 (67)	89 (67)		8 (42)	49 (35)	
Recurrence at any site, n (%)									
Yes	18 (15)	5 (14)	1.00	6 (50)	15 (11)	0.003	11 (58)	12 (9)	< 0.001
No	104 (85)	32 (86)		6 (50)	117 (89)		8 (42)	128 (91)	
Site of recurrence, n (%)									
Locoregional only	3/18 (17)	0/5 (0)	1.00	0/6 (0)	3/15 (20)	0.53	1/11 (9)	2/12 (17)	1.00
Distant±locoregional	15/18 (83)	5/5 (100)		6/6 (100)	12/15 (80)		10/11 (91)	10/12 (83)	

ctDNA, circulating tumour DNA.

Adding context for assessing response to immunotherapy?

- Anti-PD(L)1 based combinations are very effective (and curative) in patients with advanced MSI-H solid tumors like CRC.
- However, radiographic findings may “overcall” true pathologic response:

14 patients with MSI-H CRC treated with anti-PD1 +/- anti-CLTA-4 antibodies
 13/14 with radiographically persistent disease
13/14 with pathologic CR at resection; 1/14 with near-pCR

Patient number	Location of primary tumor in the colon	Stage of colon cancer	Age at diagnosis, y	Sex	Deficient mismatch repair protein (by IHC)	Etiology (Lynch or sporadic)	Immunotherapy	No. of cycles before surgery	Surgery	Intent of surgery	Pathology postresection	Best overall radiographic response
1	Transverse	IV	33	M	MSH2	Lynch	Pembro	3	Right hemicolectomy	Curative	Near pCR	SD
2	Right	IV	48	F	MLH1/PMS2	Lynch	Pembro	4	Right hemicolectomy	Palliative	pCR	SD
3	Right	III	70	F	MLH1/PMS2	Sporadic	Nivo	8	Right hemicolectomy	Curative	pCR	SD
4	Left	IV	45	M	MSH2/MSH6	Lynch-like	Nivo	14	Rectal stump resection and hepatic metastasectomy	Curative and palliative	pCR	PR
5	Right	IV	30	M	MSH2/MSH6	Lynch	Nivo	56	Peritoneal metastasectomy	Curative	pCR	PR
6	Left	IV	55	M	MSH6	Lynch	Nivo + Ipi	27	Pelvic mass metastasectomy	Palliative	pCR	PR
7	Right	IV	67	F	MLH1	Sporadic	Pembro	35	Peritoneal metastasectomy	Curative	pCR	PR
8	Left	IV	45	F	MLH1	Lynch	Pembro	16	Hepatic metastasectomy	Curative	pCR	PR
9	Right	IV	38	M	MSH2	Lynch	Nivo + Ipi	54	Right hemicolectomy	Curative	pCR	CR
10	Right	IV	37	M	MSH2/MSH6	Lynch	Nivo + Ipi	24	Ileocelectomy and peritoneal metastasectomy	Curative	pCR	SD
11	Left	IV	37	M	MLH1/PMS2	Lynch	Nivo+ Ipi	12	Laparoscopic jejunostomy	Palliative	pCR	SD
12	Left	IV	39	M	MLH1	Lynch-like	Nivo + Ipi	24	Liver metastasectomy	Curative	pCR	PR
13	Right	IV	31	M	MLH1	Lynch-like	Pembro	15	Liver metastasectomy	Curative	pCR	PR
14	Left	IV	59	M	MSH2/MSH6	Sporadic	Nivo + Ipi	24	Sigmoidectomy	Curative	pCR	PR




Adding context for assessing response to immunotherapy?

- Patient with newly diagnosed stage IV rectal cancer with oligometastatic disease to the liver presented to MDACC for further treatment.
- Molecular profiling notable for *POLE* mutation/ hypermutated status.

Molecular Diagnostics									
AKT1	BTK	CREBBP	FGF19	HRAS	MAPK1	NBN	PIK3CB	RAF1	SPOP
AKT2	CBL	CSF1R	FGF3	IDH1	MAX	NF1	PIK3R1	RB1	SRC
AKT3	CCND1	CTNNB1	FGFR1	IDH2	MDM2	NF2	PMS2	RET	STAT3
ALK	CCND2	DDR2	FGFR2	IGF1R	MDM4	NFE2L2	POLE	RHEB	STK11
AR	CCND3	EGFR	FGFR3	JAK1	MED12	NOTCH1	PPARG	RHOA	TERT
ARAF	CCNE1	ERBB2	FGFR4	JAK2	MET	NOTCH2	PPP2R1A	RICTOR	TOP1
ARID1A	CDK12	ERBB3	FLT3	JAK3	MLH1	NOTCH3	PTCH1	RNF43	TP53
ATM	CDK2	ERBB4	FOXO2	KDR	MRE11A	NRAS	PTEN	ROS1	TSC1
ATR	CDK4	ERCC2	GATA2	KIT	MSH2	NTRK1	PTPN11	SETD2	TSC2
ATRX	CDK6	ESR1	GNA11	KNSTRN	MSH6	NTRK2	RAC1	SF3B1	U2AF1
AXL	CDKN1B	EZH2	GNAQ	KRAS	MTOR	NTRK3	RAD50	SLX4	XPO1
BAP1	CDKN2A	FANCA	GNAS	MAGOH	MYC	PALB2	RAD51	SMAD4	
BRAF	CDKN2B	FANCD2	H3F3A	MAP2K1	MYCL	PDGFRA	RAD51B	SMARCA4	
BRCA1	CHEK1	FANCI	HIST1H3B	MAP2K2	MYCN	PDGFRB	RAD51C	SMARCB1	
BRCA2	CHEK2	FBXW7	HNF1A	MAP2K4	MYD88	PIK3CA	RAD51D	SMO	

FINDINGS:

Copy Number Variations
None identified

4 doses of ICB

 complete molecular response!

Molecular Diagnostics						
AKT1	CCND1	ESR1	HRAS	MAPK3	NPM1	RB1
ALK	CCND2	EZH2	IDH1	MET	NRAS	RET
APC	CCNE1	FBXW7	IDH2	MLH1	NTRK1	ROS1
AR	CDK4	FGFR1	JAK2	MPL	NTRK3	SMAD4
ARAF	CDK6	FGFR2	JAK3	MTOR	PDGFRA	SMO
ARID1A	CDKN2A	FGFR3	KIT	MYC	PIK3CA	STK11
ATM	CTNNB1	GNA11	KRAS	NF1	PTEN	TERT
BRAF	DDR2	GNAQ	MAP2K1	NFE2L2	PTPN11	TP53
BRCA1	EGFR	GNAS	MAP2K2	NOTCH1	RAD51	TSC1
BRCA2	ERBB2	HNF1A	MAPK1	NOTCH2	RAF1	VHL

FINDINGS:

Copy Number Variations
None identified
 Somatic Mutations
None identified
 Gene Fusions
None identified

- Liver “metastasis” remains “stable” though patient remains without evidence of clinical, biochemical, or radiographic recurrence off treatment for > 2 years.

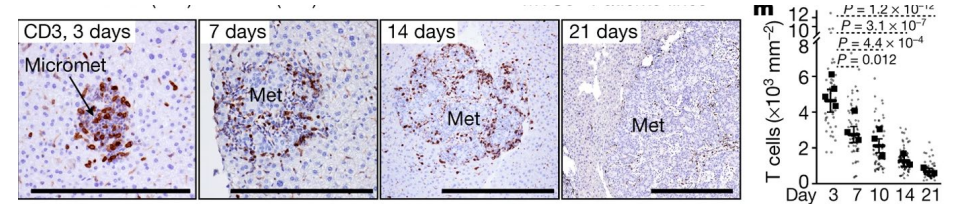
Are we ready to replace standard imaging for use of ctDNA to gauge curative response?

- Use of ctDNA as a tool to inform cancer biology as a liquid biopsy
- Informing clinical decision making of CRC using ctDNA technologies
- **Recognizing micrometastatic CRC as a unique biologic entity with novel therapeutic opportunities to cure more patients**

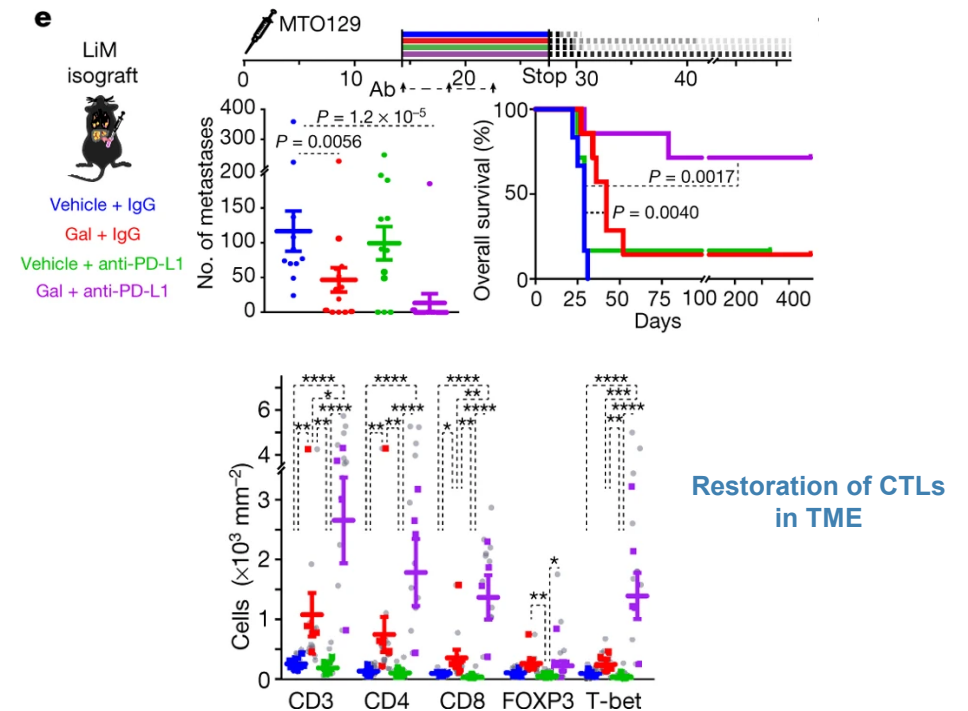
Immune cell inclusion: specific to CRC micromets?

- CRC is characterized transcriptomically by ↓ CD8 T cell signature and low immune activation (desert/exclusion) phenotype.
- *In vivo*, CRC micrometastases may harbor ↑ T cells than macrometastases.
- Increased TGF-β signature has been linked with immune exclusion and worse survival following atezolizumab⁷.
- As tumors grow, TGF-β drives exclusion of immune cells from tumor microenvironment in CRC preclinical models.
- Concomitant targeting of TGF-β overcomes de novo anti-PD-1 resistance.

Exclusion of T cells in TME with time



Anti-tumor activity in LiM CRC model with dual TGFβ/PD1 targeting

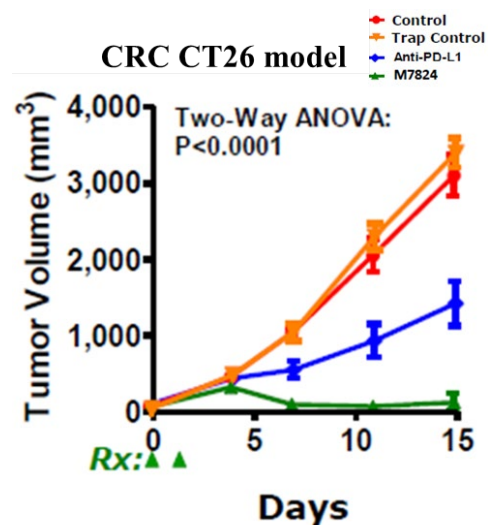
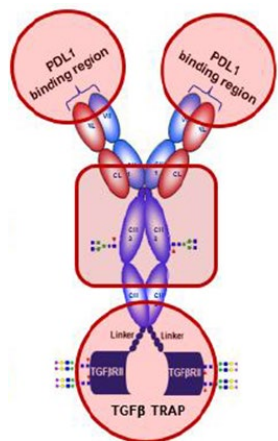


Can clearance of TGF-β systemically prime CRC micrometastases for response to immune checkpoint blockade?

Can we utilize ctDNA technologies to identify such patients?

Targeting TGF- β and PD-L1 in patients w/ ctDNA(+) liver-limited resected met CRC

- Bintrafusp alfa is a dual TGF- β trap: anti-PD-L1 molecule safe and well tolerated in patients with advanced cancers.
- Addition of a TGF- β trap has been shown to augment sensitivity to anti-PD-1 therapies in preclinical models of CRC and melanoma².



Patients with liver-limited metastatic colorectal cancer with detectable ctDNA following resection and completion of all standard therapy

Bintrafusp alfa (1200 mg IV) x 6 doses every 2 weeks

Test for ctDNA clearance

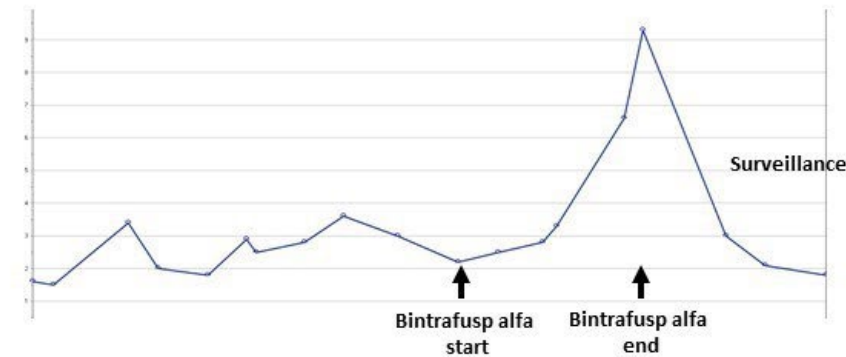
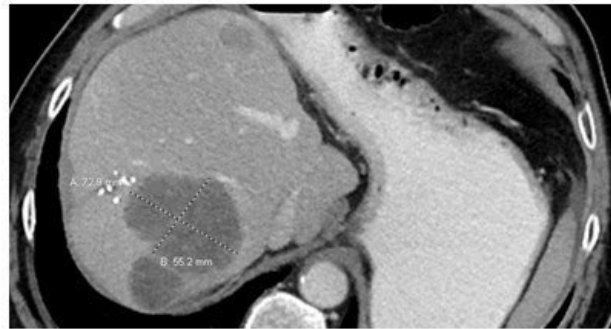
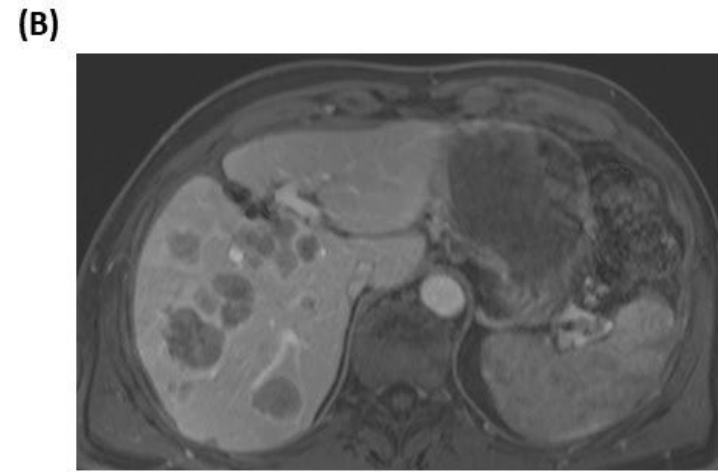
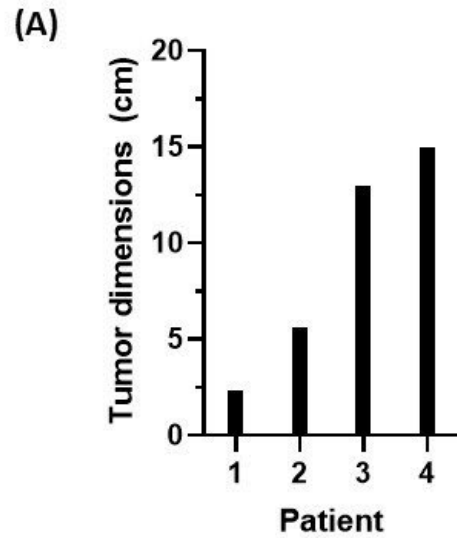
N=15

- Eligibility criteria:
 - MSS/pMMR CRC s/p complete resection of primary tumor and all liver mets
 - Completion of all standard of care adjuvant therapy
 - **No radiographic evidence of disease**
 - ctDNA+ using CLIA-compliant Guardant assay collected > 14 days after treatment completion
- Primary endpoint
 - Clearance of ctDNA in >30% of patients at 12 weeks

To our knowledge, the first trial (for CRC) to use (1) ctDNA as an integral biomarker and (2) use ctDNA clearance for response evaluation.

Bintrafusp alfa for ctDNA(+) liver-limited resected met CRC: clinical outcomes

4 participants treated with bintrafusp alfa:

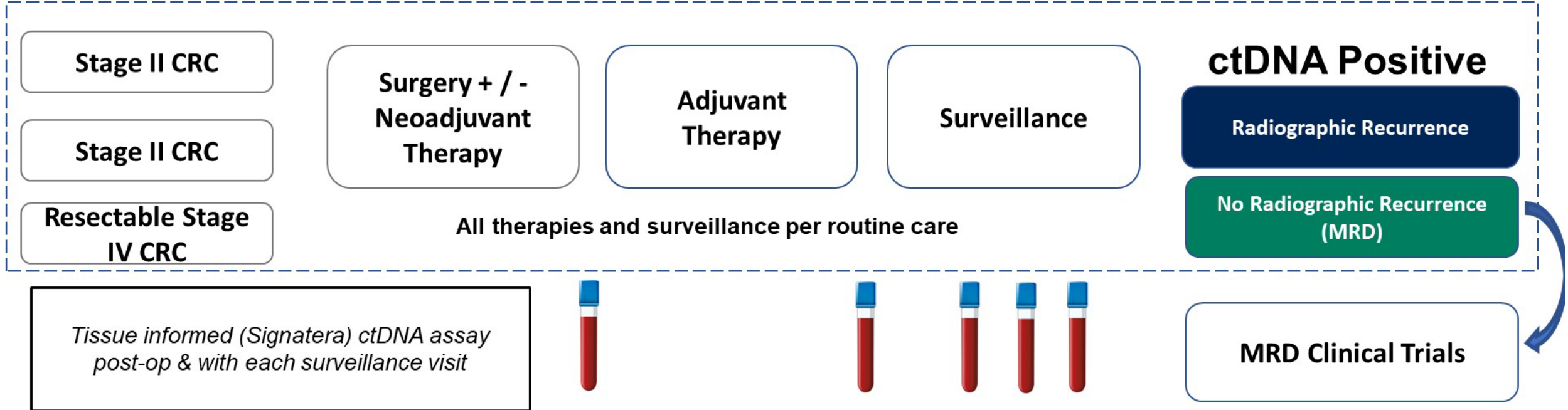


Trial stopped early due to concern for loss of equipoise.

Biochemical progression following bintrafusp alfa: a ctDNA analysis

Patient	Mutation	Pretreatment VAF (%)	Post-recurrence VAF (%)
1	<i>APC</i> ^{A703fs}	0.5	0.4
	<i>TP53</i> ^{P278fs}	< 0.3	0.3
	<i>TP53</i> ^{C277G}	0.4	---
2	<i>TP53</i> ^{R196*}	0.5	65.7
	<i>APC</i> ^{R876*}	< 0.3	64.7
	<i>KRAS</i> ^{G12D}	< 0.3	60.8
	<i>MET</i> ^{N786fs}	0.3	< 0.3
	<i>MTOR</i> ^{R206H}	< 0.3	---
	<i>BRCA2</i> ^{D1360Y}	---	0.3
3	<i>TP53</i> ^{C238Y}	0.3	< 0.2
	<i>SMAD4</i> ^{D335G}	---	31.5
	<i>APC</i> ^{R1450*}	---	23.3
	<i>APC</i> ^{R216*}	---	23.0
	<i>KRAS</i> ^{G12D}	---	21.0
	<i>MAPK1</i> ^{Q97K}	---	1.2
	<i>STK11</i> ^{D330E}	---	0.4
	<i>KIT</i> ^{R804W}	---	< 0.2
4	<i>ERBB2</i> ^{R288W}	< 0.2	(not tested)

Integrating post-surgical surveillance, MRD monitoring and intervention (INTERCEPT)

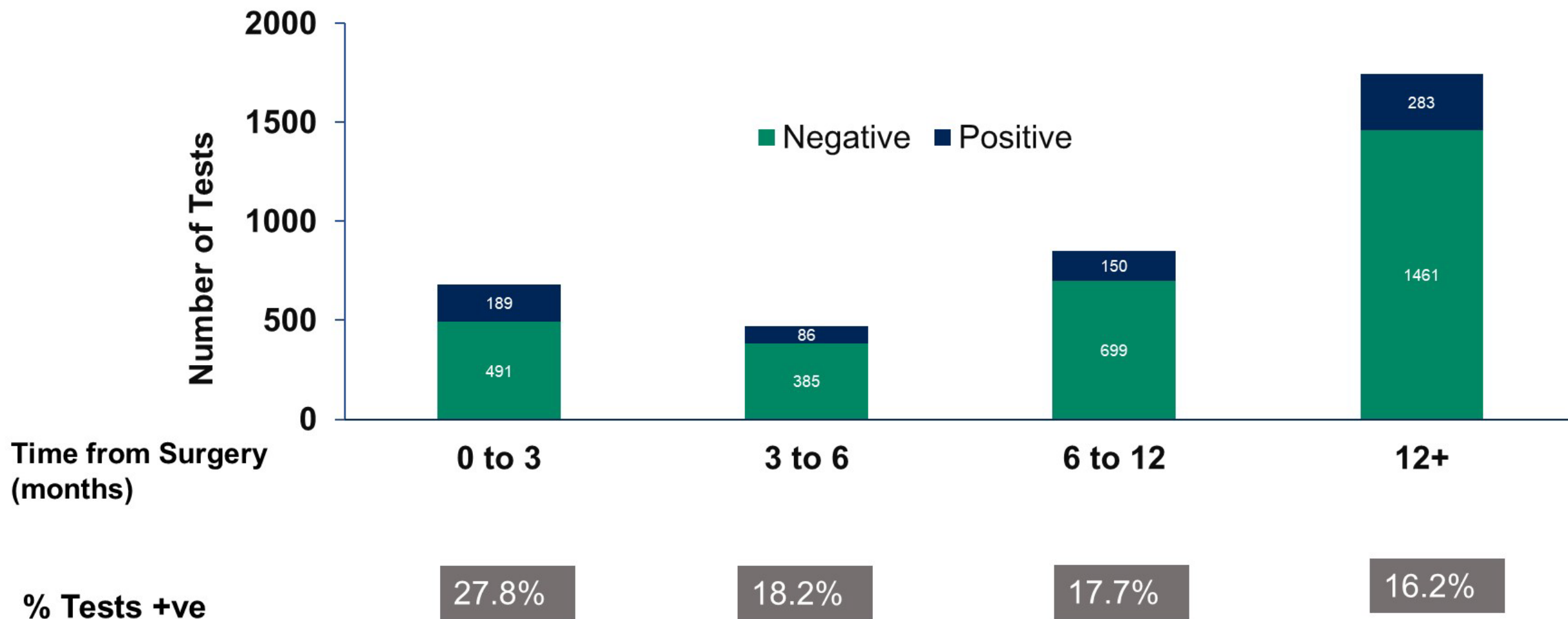


Characteristic	Category	N (%)
Age (years)	Median	58
	Range	21-93
Gender	Male	611 (55)
	Female	504 (45)
Primary Location	Colon	680 (61)
	Rectum	389 (35)
	Not Specified	46 (4)
Pathologic Stage	0-II	260 (24)
	III	294 (26)
	IV/Recurrent	561 (50)
# of ctDNA Assays	Median	3
	Range	1-11

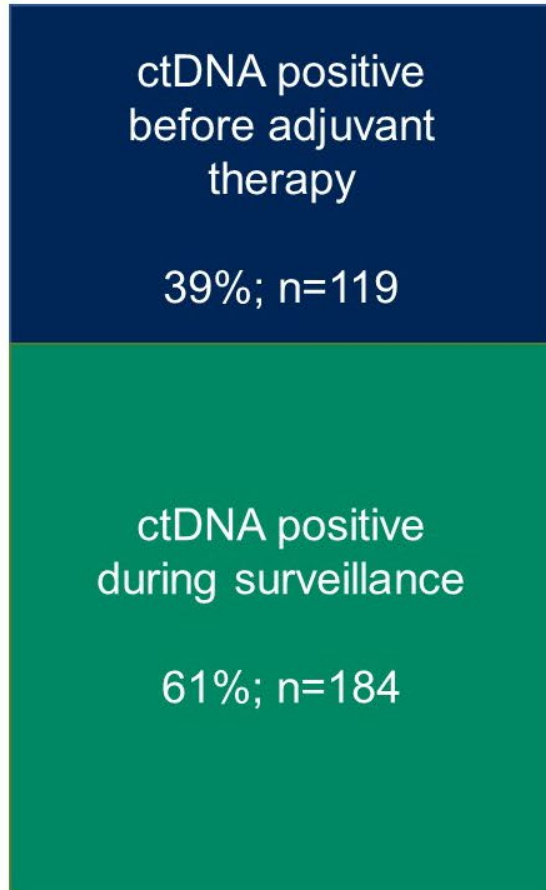
1115 patients with CRC evaluated at MD Anderson between 12/2021 - 3/2023.



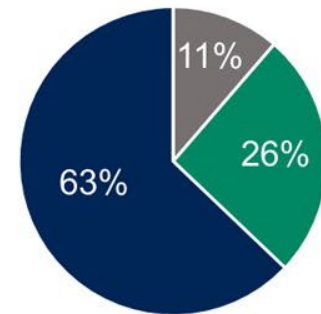
ctDNA results according to time from surgery for CRC (INTERCEPT)



Distribution of ctDNA(+) status by stage and location of CRC (INTERCEPT)

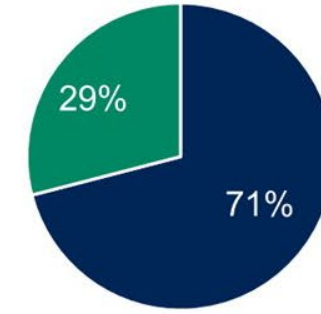


Stage of disease

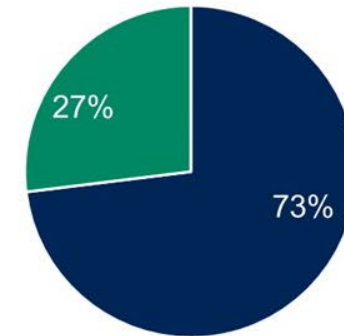
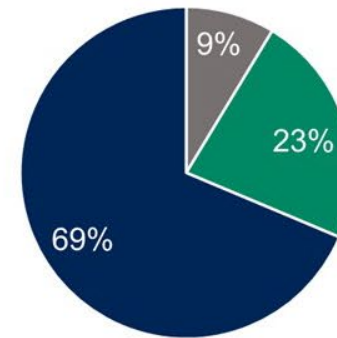


■ I-II ■ III ■ IV

Location of disease



■ Colon ■ Rectum



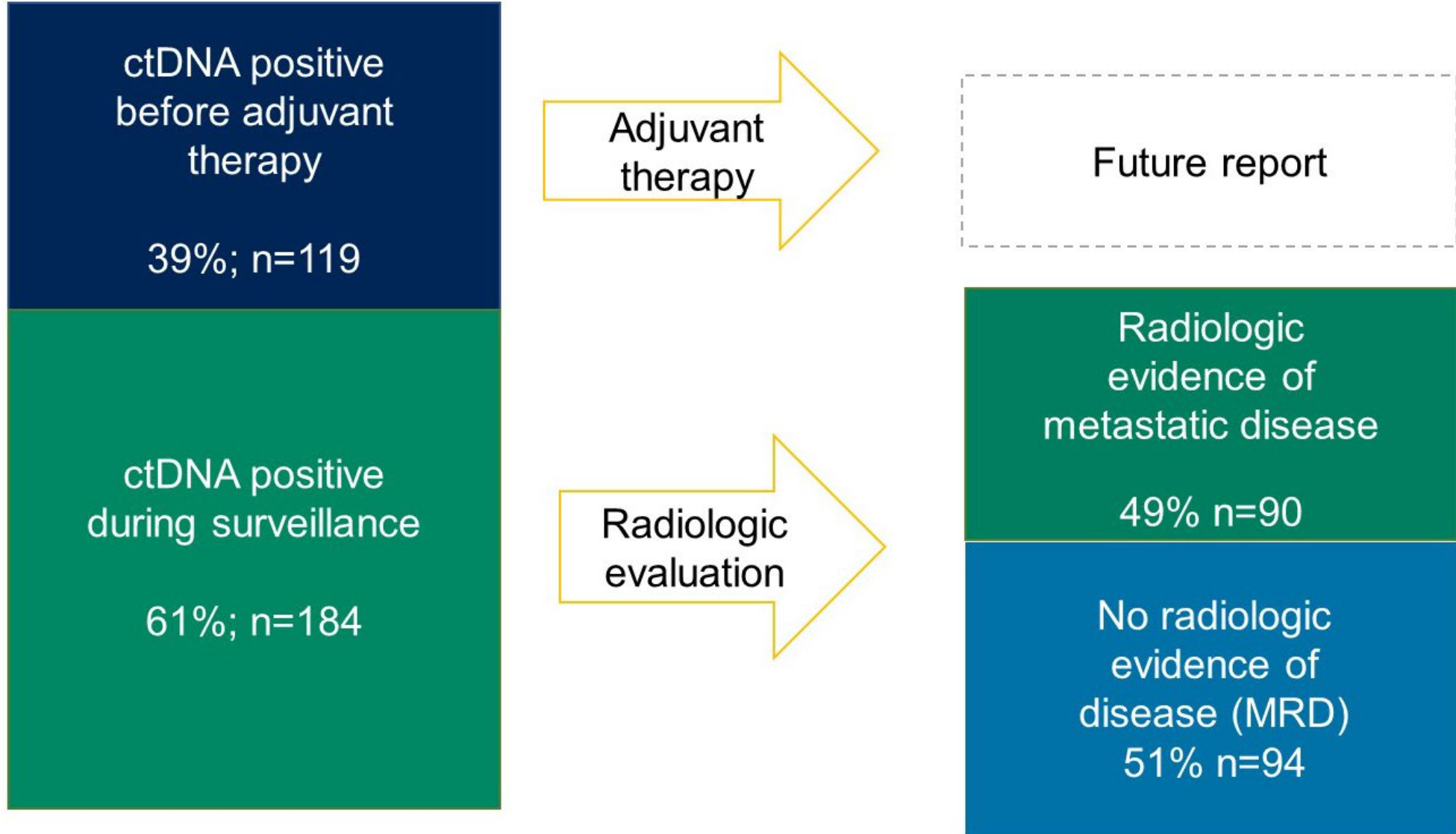
Evaluations driven by ctDNA(+) status during surveillance for CRC (INTERCEPT)



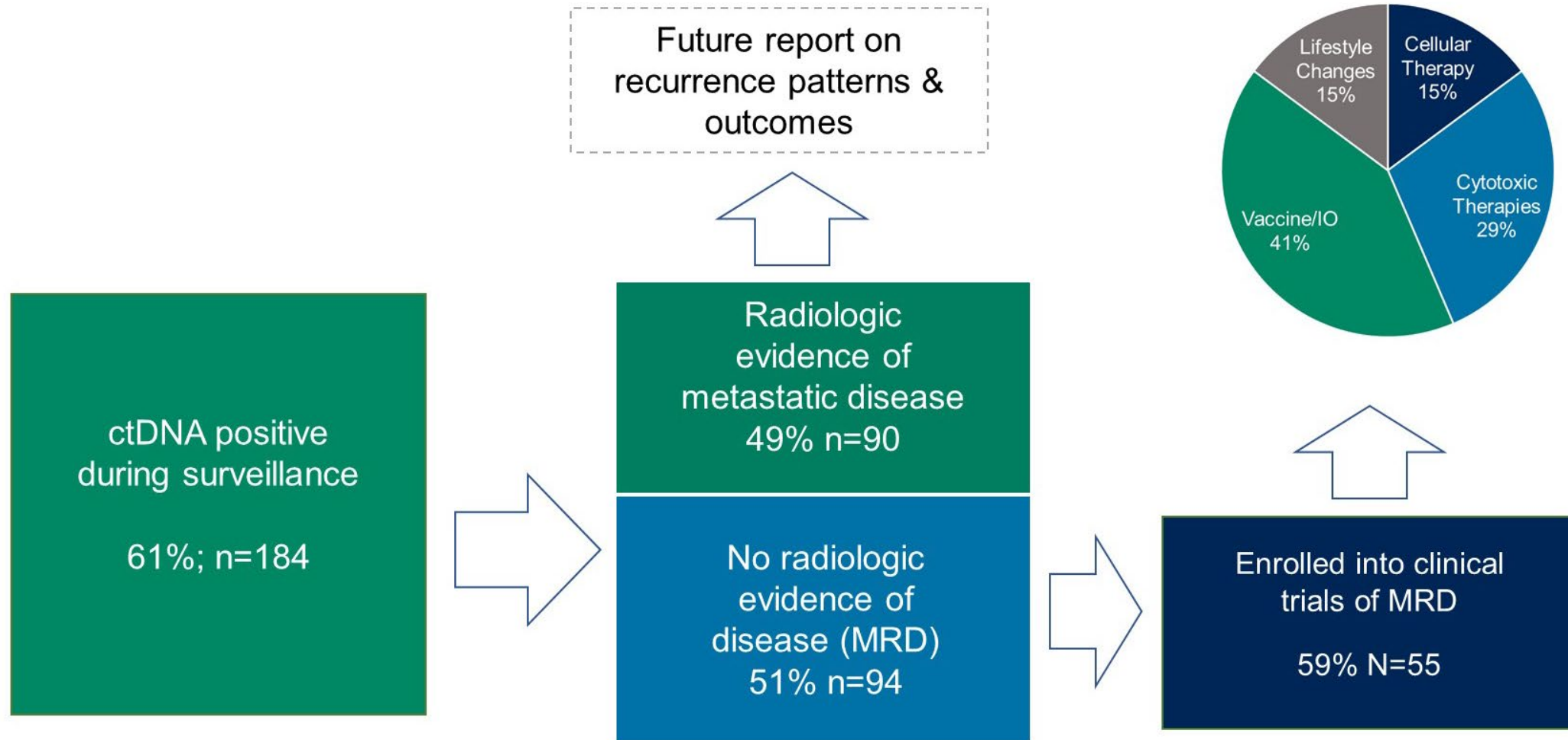
# of Reflex Investigations	# of Patients
1	48
2	18
> 2	7

Type of Reflex Investigation	# of Patients
Additional CT	25
MRI	21
PET, PET/CT	37
Biopsy	13
Ultrasound	1

Radiographic findings of CRC patients with ctDNA(+) status during surveillance (INTERCEPT)



ctDNA treatment trials for intervention on MRD at MDACC (INTERCEPT)



More than a somatic mutation test....

Tumor mutation burden

- higher TMB reported for ctDNA > tissue
- clinical context matters: can targeted therapy resistance signature overcall true TMB?

MSI status

- correlates w/ "gold-standard" tissue specimens - improved sensitivity at higher total ctDNA level

Fusion detection

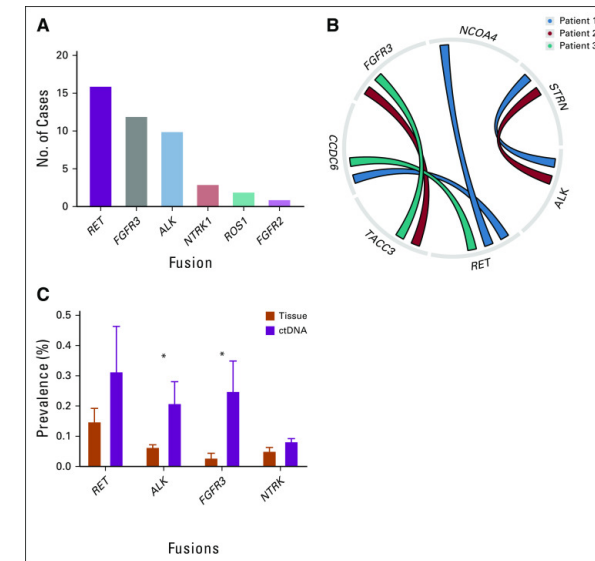
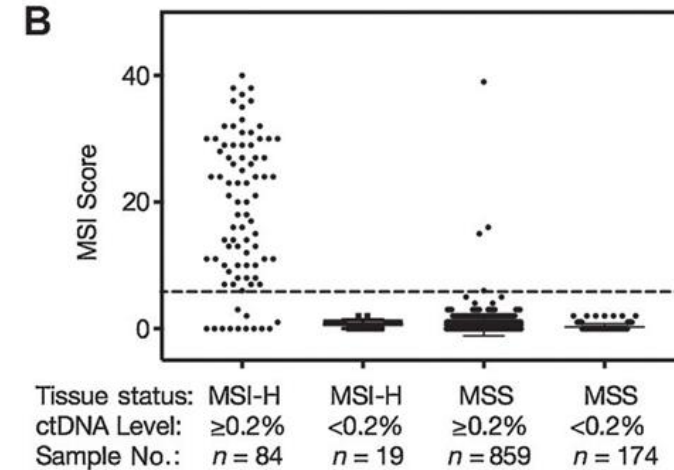
- Rare in patients with colorectal cancer
- Low VAF fusion detection possible

Methylation

- Unique CRC methylation markers identifiable and distinguish from other cancers
- Improved sensitivity for MRD detection in CRC

Viral (HPV) integration

- The power of great collaboration at MD Anderson!!



Summary

- Use of ctDNA as a tool to inform cancer biology as a liquid biopsy
 - High-performance test for detection of somatic mutations, TMB, MSI status, fusions,
- Complementing current management of CRC using ctDNA
 - Very sensitive method for reliably identifying MRD and prognosticating recurrence risk
 - Informative tool to complement standard approaches to assessing response
- Defining ctDNA as the gold standard for guiding adjuvant therapy decisions
 - De-escalation:
 - Escalation: ongoing clinical trials will inform on predictive utility
- Recognizing micrometastatic CRC as a unique biologic entity
 - Bench discoveries may translate to novel treatment approaches to cure more patients
 - INTERCEPT program for CRC: proof-of-concept for intervening on ctDNA(+) identification of MRD with novel therapeutic approaches

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