



# Novel Advances in Colorectal Cancer Other Than Immunotherapy



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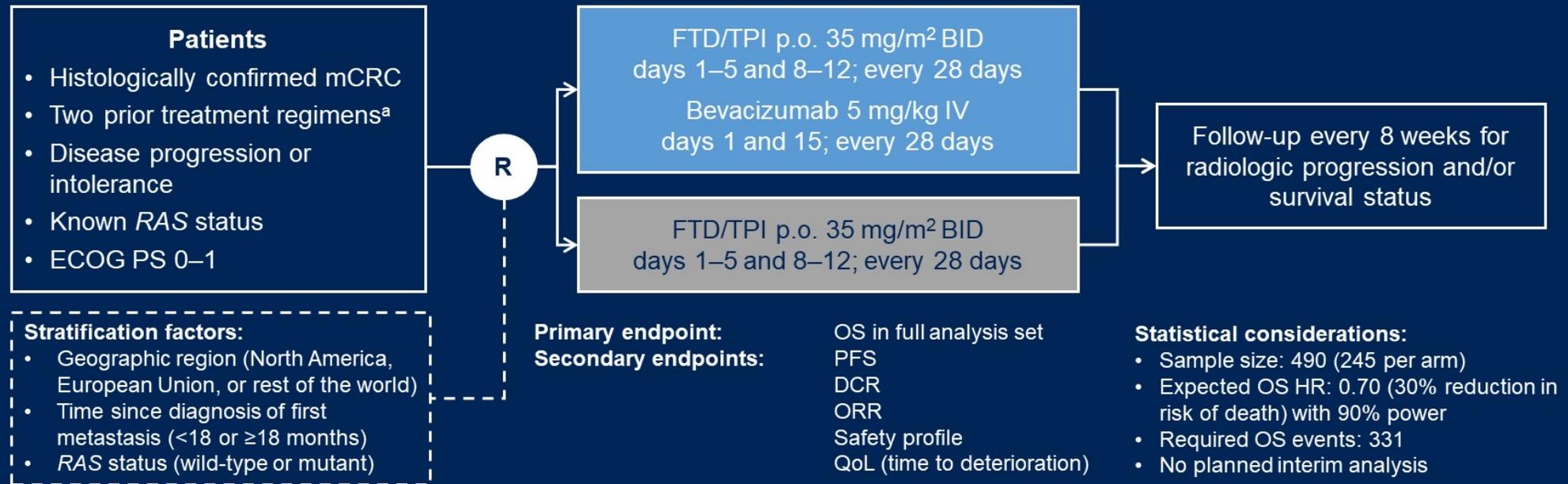


# Discussion Points

- Historic pivotal trials in 2023
- Molecular subsets
- The role of ctDNA

# SUNLIGHT study design

- An open-label, randomized, phase 3 study in patients with refractory mCRC (NCT04737187)



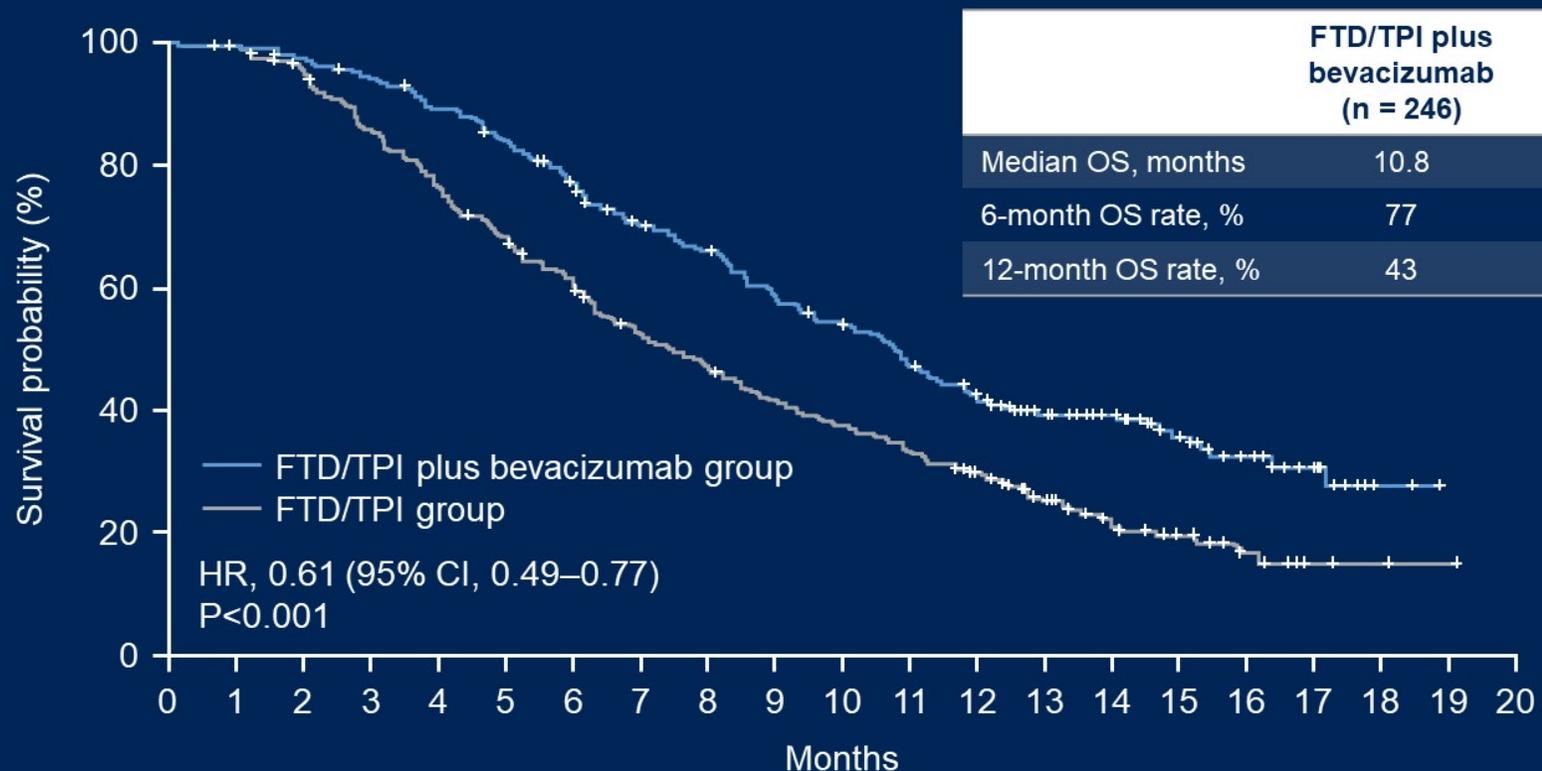
<sup>a</sup> Prior treatment must have included a fluoropyrimidine, irinotecan, oxaliplatin, an anti-VEGF monoclonal antibody (not necessarily bevacizumab), and/or an anti-EGFR monoclonal antibody for patients with *RAS* wild-type and could have included (neo)adjuvant chemotherapy if disease had recurred during treatment or within 6 months of the last administration of (neo)adjuvant therapy. BID, twice daily; DCR, disease control rate; ECOG PS, Eastern Cooperative Oncology Group performance status; EGFR, epidermal growth factor receptor; FTD/TPI, trifluridine/tipiracil; HR, hazard ratio; IV, intravenous; mCRC, metastatic colorectal cancer; ORR, objective response rate; OS, overall survival; PFS, progression-free survival; p.o., orally; QoL, quality of life; R, randomization; VEGF, vascular endothelial growth factor.

# Key baseline characteristics

Characteristic		FTD/TPI plus bevacizumab (n = 246)	FTD/TPI (n = 246)
<b>Age</b>	Median (range), years	62 (20–84)	64 (24–90)
	<65 years, n (%)	146 (59)	129 (52)
	≥65 years, n (%)	100 (41)	117 (48)
<b>Sex, n (%)</b>	Male	122 (50)	134 (55)
<b>Region</b>	European Union	158 (64)	157 (64)
	North America	8 (3)	8 (3)
	Rest of the world	80 (33)	81 (33)
<b>Primary tumor localization, n (%)</b>	Right	62 (25)	77 (31)
	Left	184 (75)	169 (69)
<b>Time from diagnosis of first metastasis to randomization,<sup>a</sup> n (%)</b>	<18 months	104 (42)	105 (43)
	≥18 months	142 (58)	141 (57)
<b>RAS status,<sup>a</sup> n (%)</b>	Mutant	171 (70)	170 (69)
	Wild-type	75 (31)	76 (31)
<b>Prior treatment with bevacizumab, n (%)</b>	No	68 (28)	70 (29)
	Yes	178 (72)	177 (72)
<b>ECOG PS, n (%)</b>	0	119 (48)	106 (43)
	1	127 (52)	139 (57)
	2	0	1 (0.4) <sup>b</sup>

<sup>a</sup> As documented in the Interactive Web Response System set for randomization. <sup>b</sup> Patient had an ECOG PS of 1 at randomization but was assessed as having an ECOG PS of 2 on day 1, cycle 1.  
ECOG PS, Eastern Cooperative Oncology Group performance status; FTD/TPI, trifluridine/tipiracil.

# OS in full analysis set (primary endpoint)



## No. at risk

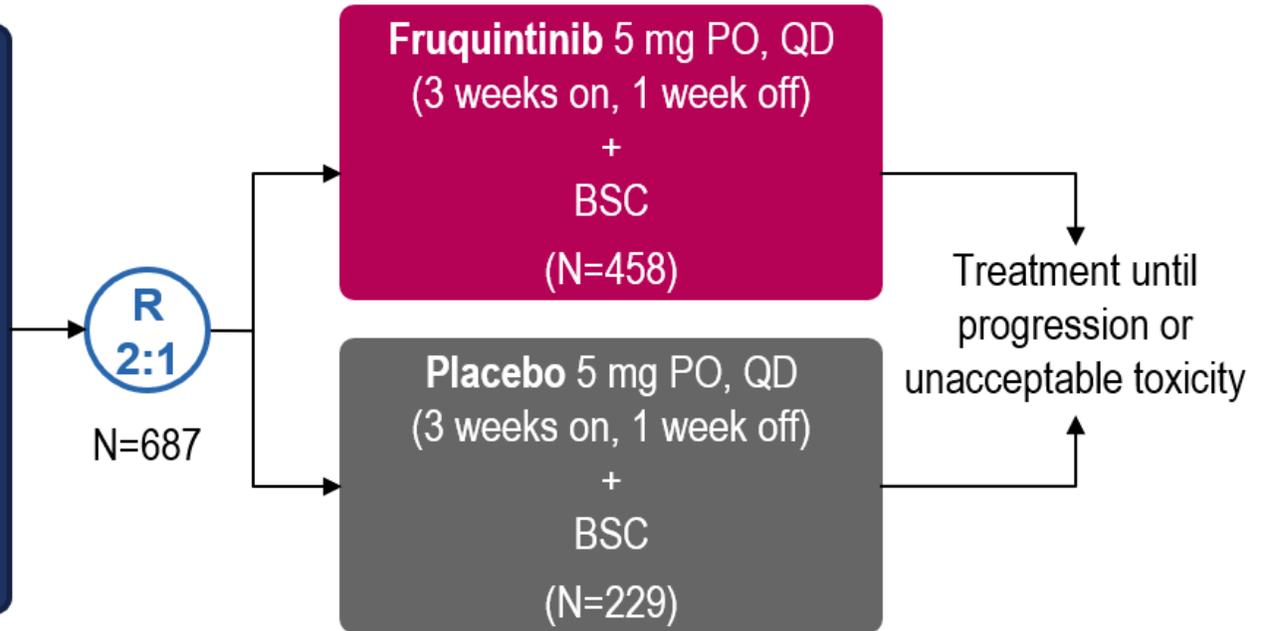
FTD/TPI plus bevacizumab group	246	244	239	230	217	203	183	160	149	131	119	104	88	69	52	37	24	13	2	0	0
FTD/TPI group	246	242	230	205	184	163	143	120	108	95	85	76	63	44	24	16	10	5	2	1	0

CI, confidence interval; FTD/TPI, trifluridine/tipiracil; HR, hazard ratio; OS, overall survival.

# FRESCO-2 Study Design

## Patient Eligibility

- Prior treatment with fluoropyrimidine-, oxaliplatin- and irinotecan-based chemotherapy, an anti-VEGF biological therapy, and, if *RAS* wild type, an anti-EGFR therapy
- Progression on, or intolerance to, TAS-102 and/or regorafenib
- Prior treatment with an immune checkpoint inhibitor or BRAF inhibitor if indicated



## Stratification Factors

- Prior therapy (TAS-102 vs regorafenib vs TAS-102 and regorafenib)
- *RAS* mutational status (wild-type vs mutant)
- Duration of metastatic disease ( $\leq 18$  months vs  $> 18$  months)

**Mechanism of action: Highly selective oral tyrosine kinase inhibitor of VEGFRs-1, -2, and -3**

Note: To ensure the patient population is reflective of clinical practice, the number of patients treated with prior regorafenib was limited to 344 patients (50%)

# Patient and Disease Characteristics

ITT Population

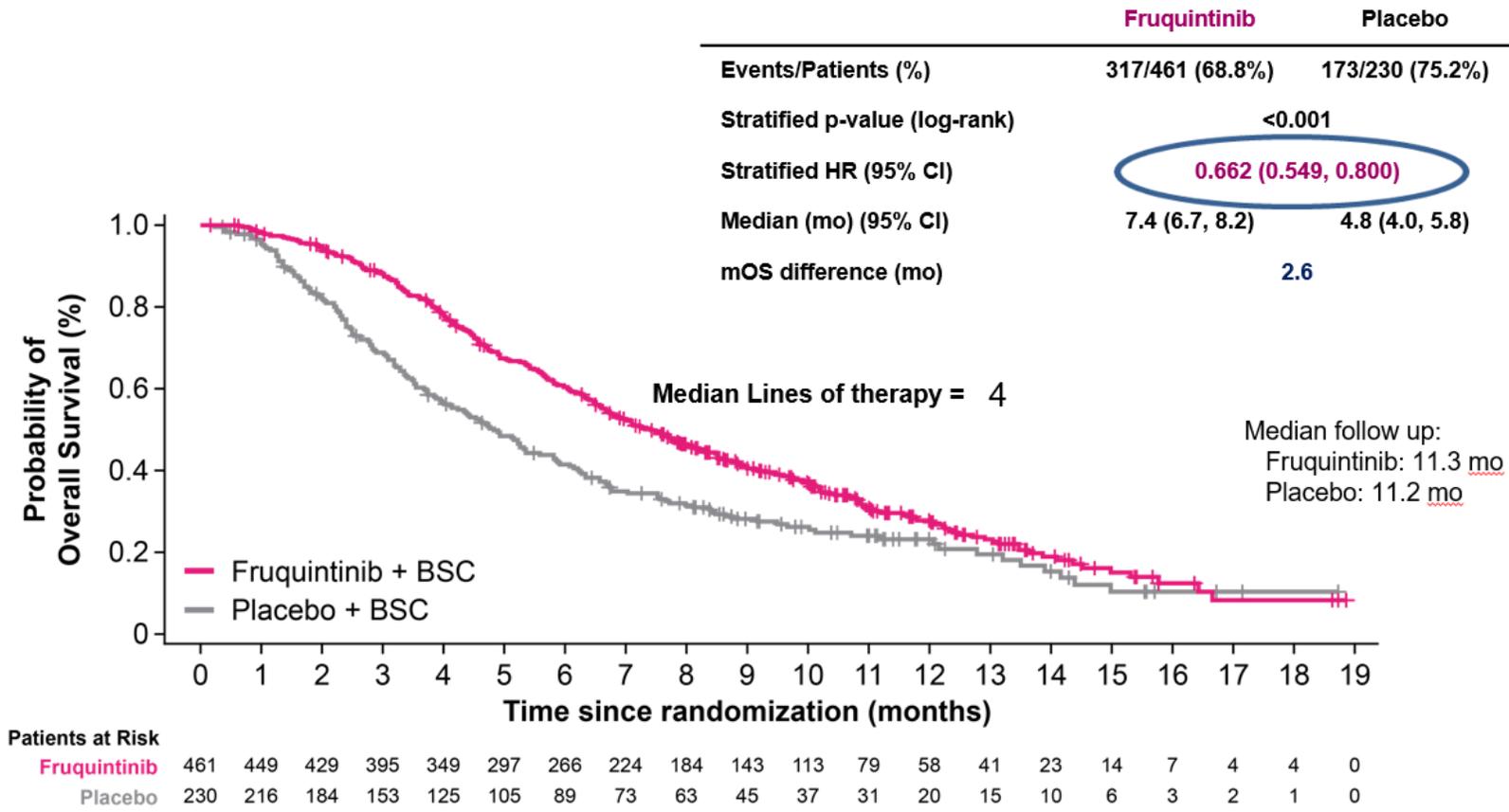
Enrollment: Sep 2020 to Dec 2021

Data Cutoff: 24 June 2022

Characteristic, n (%)		Fruquintinib (N=461)	Placebo (N=230)	Characteristic, n (%)		Fruquintinib (N=461)	Placebo (N=230)
Age, y	Median (range)	64 (25, 82)	64 (30, 86)	Duration of metastatic disease	≤ 18 mo	37 (8.0)	13 (5.7)
	≥ 65	214 (46.4)	111 (48.3)		> 18 mo	424 (92.0)	217 (94.3)
Sex	Female	216 (46.9)	90 (39.1)	RAS status	WT	170 (36.9)	85 (37.0)
	Male	245 (53.1)	140 (60.9)		Mutant	291 (63.1)	145 (63.0)
Region	North America	82 (17.8)	42 (18.3)	BRAF V600E mutation	No	401 (87.0)	198 (86.1)
	Europe	329 (71.4)	166 (72.2)		Yes	7 (1.5)	10 (4.3)
	Asia Pacific	50 (10.8)	22 (9.6)		Other/Unknown	5 (11.5)	22 (9.6)
ECOG PS	0	196 (42.5)	102 (44.3)	<b>Number of previous treatment lines in metastatic disease</b>			
	1	265 (57.5)	128 (55.7)	Median	4 (3–6)	4 (3–6)	
Primary site at 1st diagnosis	Colon left	192 (41.6)	92 (40.0)	≤3	125 (27%)	64 (28%)	
	Colon right	97 (21.0)	53 (23.0)	>3	336 (73%)	166 (72%)	
	Colon left and right	4 (0.9)	2 (0.9)	<b>Previous therapies</b>			
	Colon unknown	25 (5.4)	13 (5.7)	VEGF inhibitor	145 (97%)	221 (96%)	
	Rectum only	143 (31.0)	70 (30.4)	EGFR inhibitor	180 (39%)	88 (38%)	
Liver metastases	Yes	339 (73.5)	156 (67.8)	Immune checkpoint inhibitor	21 (5%)	11 (5%)	
	No	122 (26.5)	74 (32.2)	BRAF inhibitor	9 (2%)	7 (3%)	
				<b>Previous trifluridine–tipiracil or regorafenib</b>			
				Trifluridine–tipiracil	240 (52%)	121 (53%)	
				Regorafenib	40 (9%)	18 (8%)	
				Both	181 (39%)	91 (40%)	

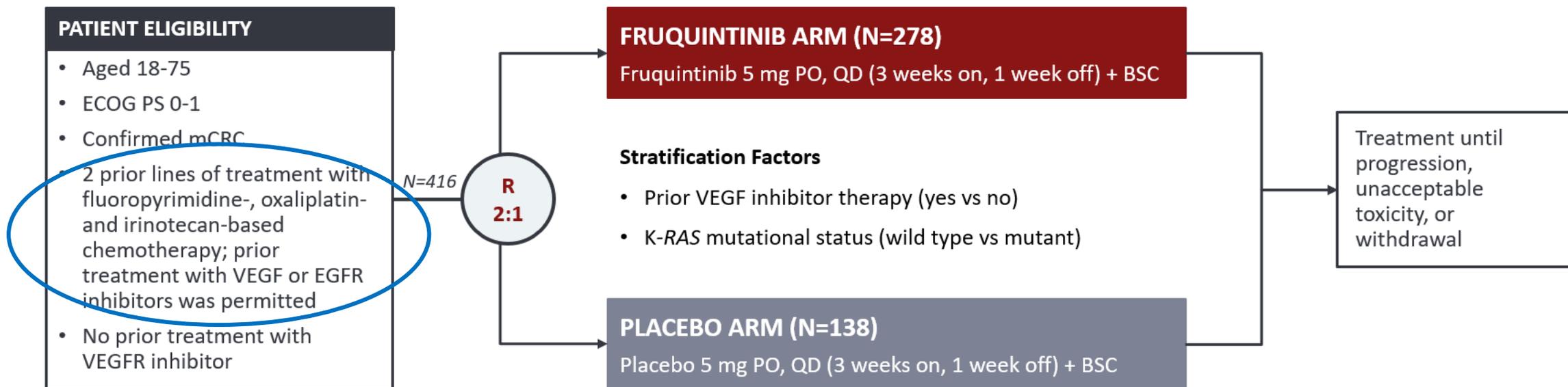
# FRESCO-2: A global phase 3 multiregional clinical trial evaluating the efficacy and safety of fruquintinib in patients with refractory mCRC

(FDA Approved 11/2023: 3<sup>rd</sup> line setting based on FRESCO and FRESCO2 trials)



# FRESCO (NCT02314819): Study Design

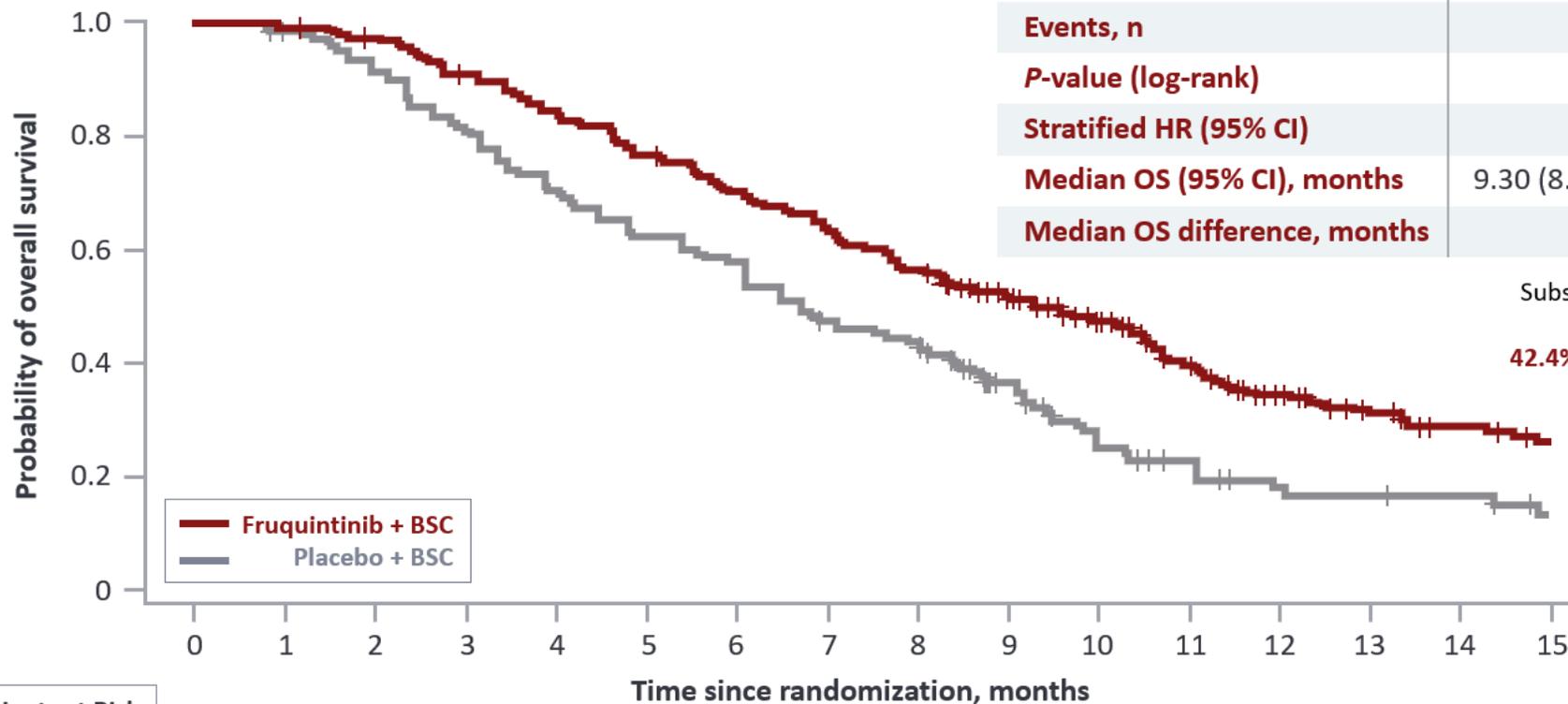
Phase 3, Conducted in China



Primary endpoint	Secondary endpoints		Statistical assumptions
<ul style="list-style-type: none"> <li>• Overall survival</li> </ul>	<p><b>Key</b></p> <ul style="list-style-type: none"> <li>• Progression-free survival</li> <li>• ORR</li> <li>• DCR</li> </ul>	<p><b>Other</b></p> <ul style="list-style-type: none"> <li>• DOR</li> <li>• Safety</li> </ul>	<p><b>Sample size</b></p> <ul style="list-style-type: none"> <li>• ~400 patients (280 OS events) would provide 80% power to detect a difference in OS with a HR of 0.70 at a 2-sided <i>P</i> value of 0.05</li> <li>• Median OS assumption in the placebo arm is 6.3 months and median OS in fruquintinib arm is 9.0 months</li> </ul>

# FRESCO: Primary Endpoint – Overall Survival (ITT Population)

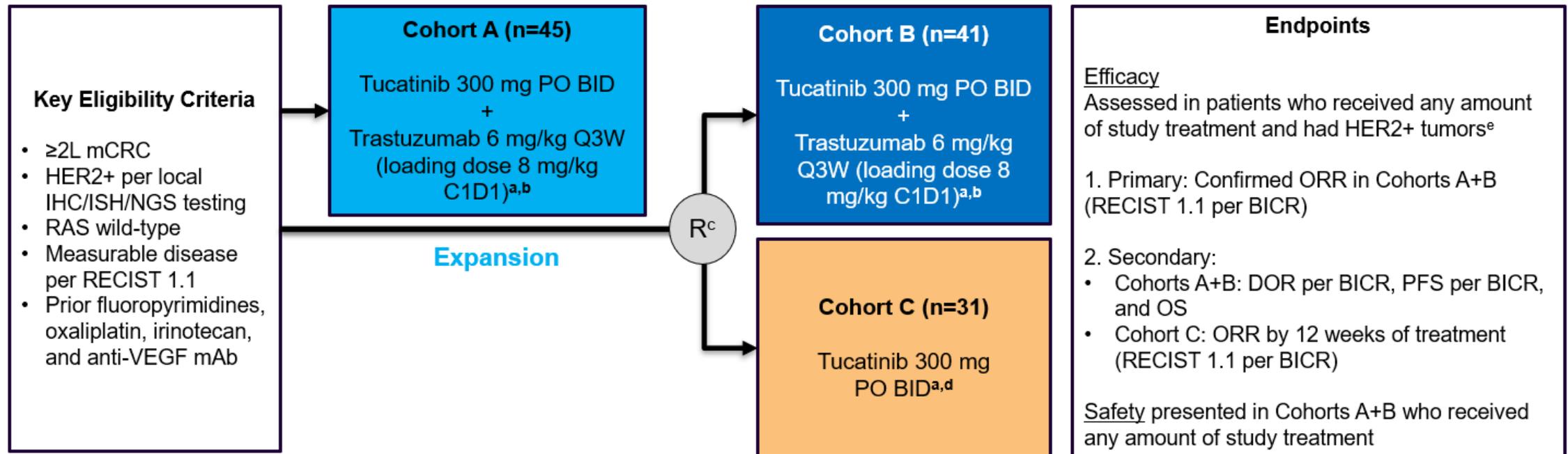
	FRUQUINTINIB + BSC (N=278)	PLACEBO + BSC (N=138)
Median follow-up, months	13.3	13.2
Events, n	297	
P-value (log-rank)	<0.001	
Stratified HR (95% CI)	0.65 (0.51–0.83)	
Median OS (95% CI), months	9.30 (8.18–10.45)	6.57 (5.88–8.11)
Median OS difference, months	2.73	



Patients at Risk		0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Fruquintinib	278	276	269	249	229	210	191	174	154	127	105	77	56	44	34	28	
Placebo	138	133	122	109	95	83	74	63	57	39	25	19	13	12	11	7	

# Molecular Subsets in mCRC

# Moutaineer-02



MOUNTAINEER began as a US Investigator-Sponsored Trial and initially consisted of a single cohort (Cohort A) and was expanded globally to include patients randomised to receive tucatinib + trastuzumab (Cohort B) or tucatinib monotherapy (Cohort C)

# Tucatinib + Trastuzumab: Efficacy Outcomes

	Tucatinib + Trastuzumab Cohorts A+B n=84
<b>Responses</b>	
Best overall response per BICR <sup>a</sup> , n (%)	
CR	3 (3.6)
PR	29 (34.5)
SD <sup>b</sup>	28 (33.3)
PD	22 (26.2)
Not available <sup>c</sup>	2 (2.4)
<b>cORR per BICR, % (95% CI)<sup>d</sup></b>	<b>38.1 (27.7, 49.3)</b>
cORR per Investigator, % (95% CI) <sup>d</sup>	42.9 (32.1, 54.1)
Median time to objective response per BICR <sup>e</sup> , months (range)	2.1 (1.2, 9.8)
DCR <sup>f</sup> per BICR, n (%)	60 (71.4)
<b>Median DOR per BICR, months (95% CI)</b>	<b>12.4 (8.5, 20.5)</b>

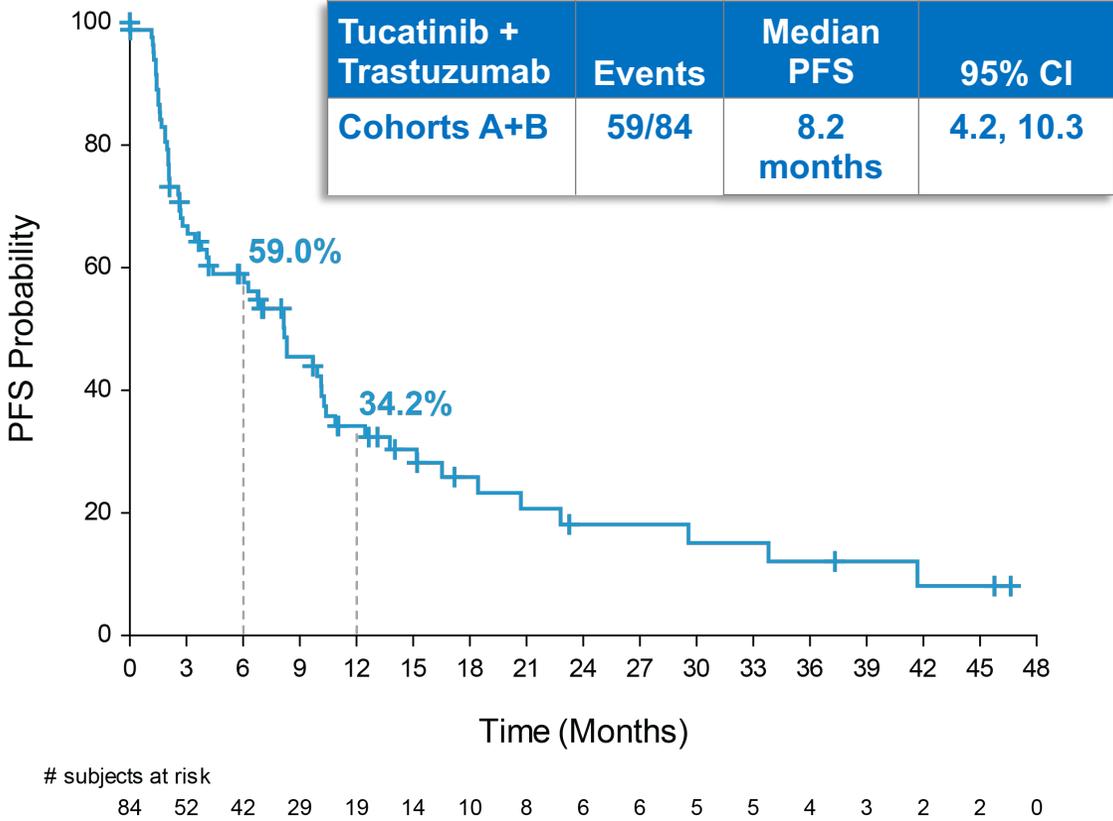
<sup>a</sup> Confirmed best overall response assessed per RECIST 1.1; <sup>b</sup> Includes SD and non-CR/non-PD; <sup>c</sup> Includes patients with no post-baseline response assessment and patients whose disease assessments are not evaluable; <sup>d</sup> Two-sided 95% exact confidence interval, computed using the Clopper-Pearson method (1934); <sup>e</sup> Time from the start of study treatment (Cohort A) or date of randomisation (Cohort B) to the first documentation of objective response (CR or PR that is subsequently confirmed); <sup>f</sup> Defined as sum of CR, PR, and SD

BICR, blinded independent central review; cORR, confirmed objective response rate; CR, complete response; DCR, disease control rate; PD, progressive disease; PR, partial response; RECIST, Response Evaluation Criteria in Solid Tumors; SD, stable disease.

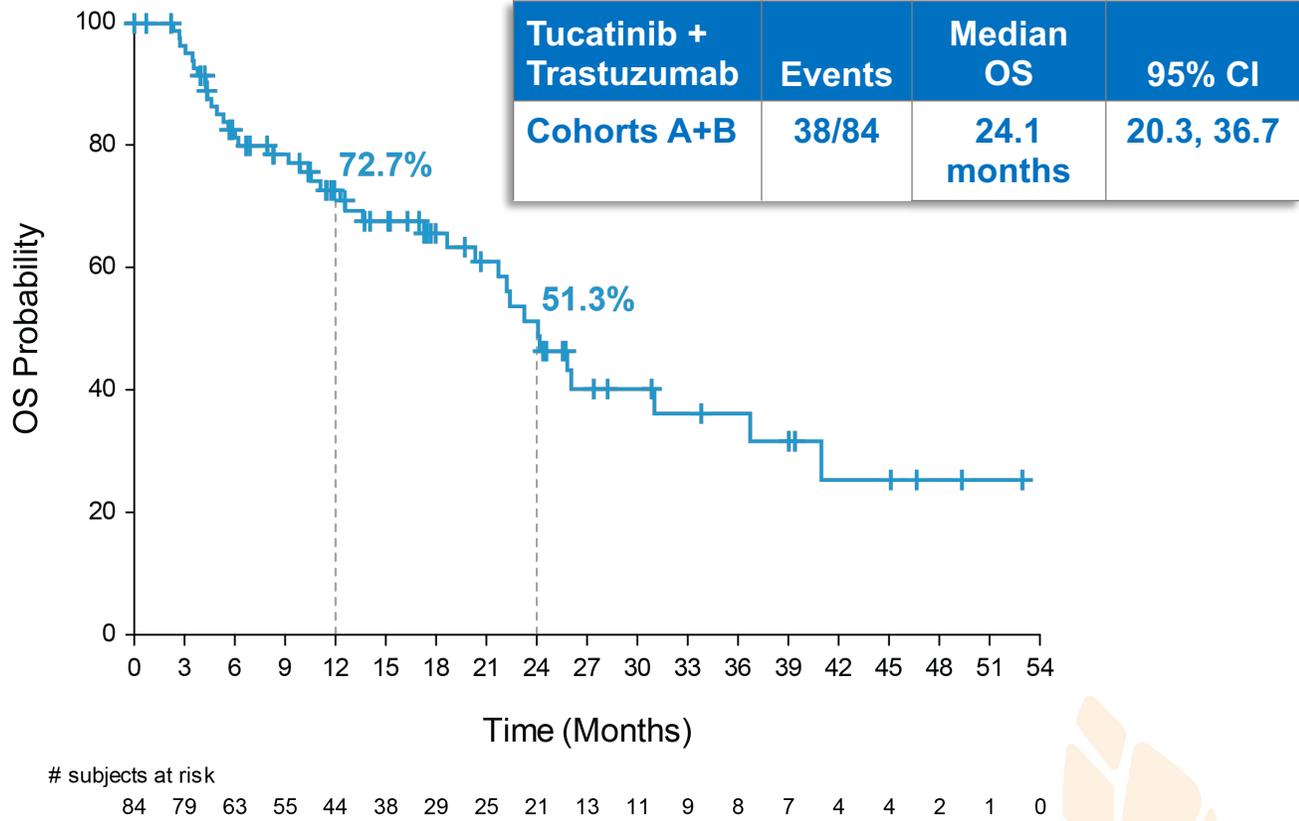
Data cutoff: 28 Mar 2022

# Tucatinib + Trastuzumab: PFS and OS

Progression-free Survival per BICR



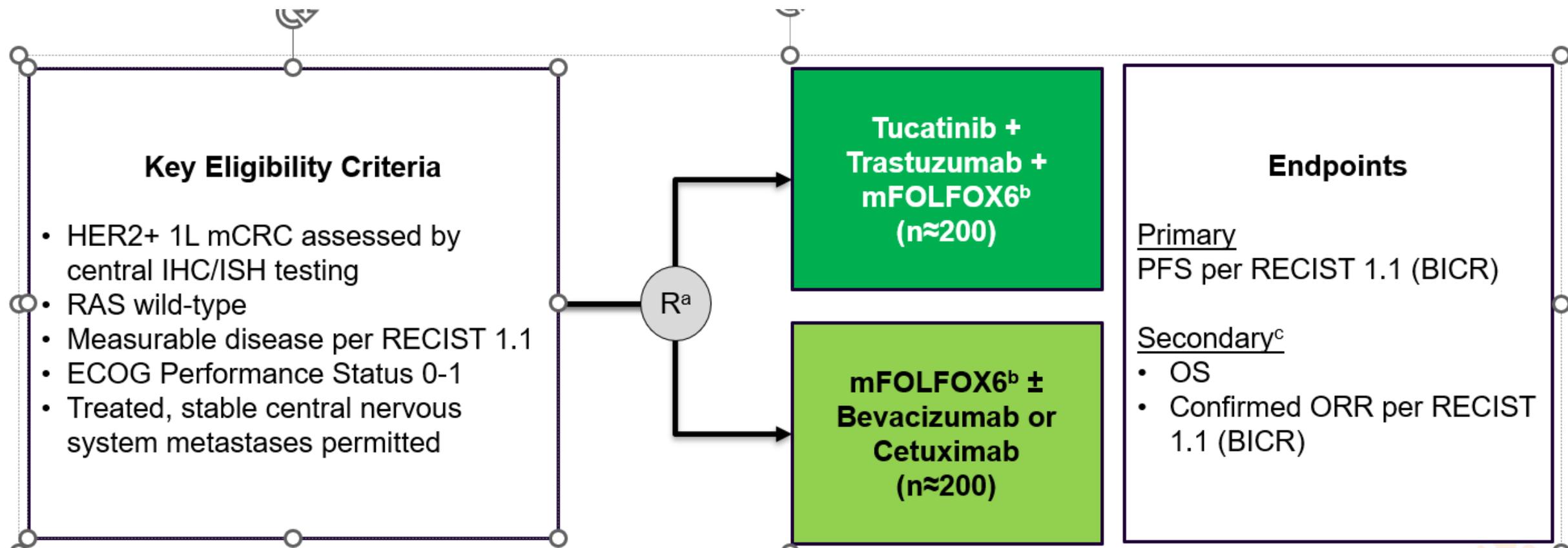
Overall Survival



Median follow-up for Cohorts A+B was 20.7 months (IQR, 11.7, 39.0)

BICR, blinded independent central review; IQR, interquartile range; OS, overall survival; PFS, progressive-free survival.  
Data cutoff: 28 Mar 2022

# Mountaineer - 03



# CodeBreakK 300 Phase 3 Study Design

Global, randomized, open-label, active-controlled study of sotorasib + panitumumab in mCRC (NCT05198934)

## Key eligibility criteria

- $\geq 18$  years of age
- KRAS G12C–mutated mCRC, identified through central molecular testing
- $\geq 1$  prior line of therapy for mCRC; progressed on or after fluoropyrimidine, irinotecan, and oxaliplatin\*
- ECOG  $\leq 2$
- Measurable disease per RECIST 1.1
- No prior KRAS<sup>G12C</sup> inhibitor†

Randomization  
1:1:1 (N = 160)

Sotorasib 960 mg daily +  
panitumumab 6 mg/kg 2QW  
(n = 53)

Sotorasib 240 mg daily +  
panitumumab 6 mg/kg 2QW  
(n = 53)

Investigator's choice:  
trifluridine/tipiracil or regorafenib  
(n = 54)

**Stratified by:** prior anti-angiogenic therapy (yes / no), time from diagnosis of mCRC ( $\geq 18$  mo /  $< 18$  mo), ECOG status (0 or 1 / 2)

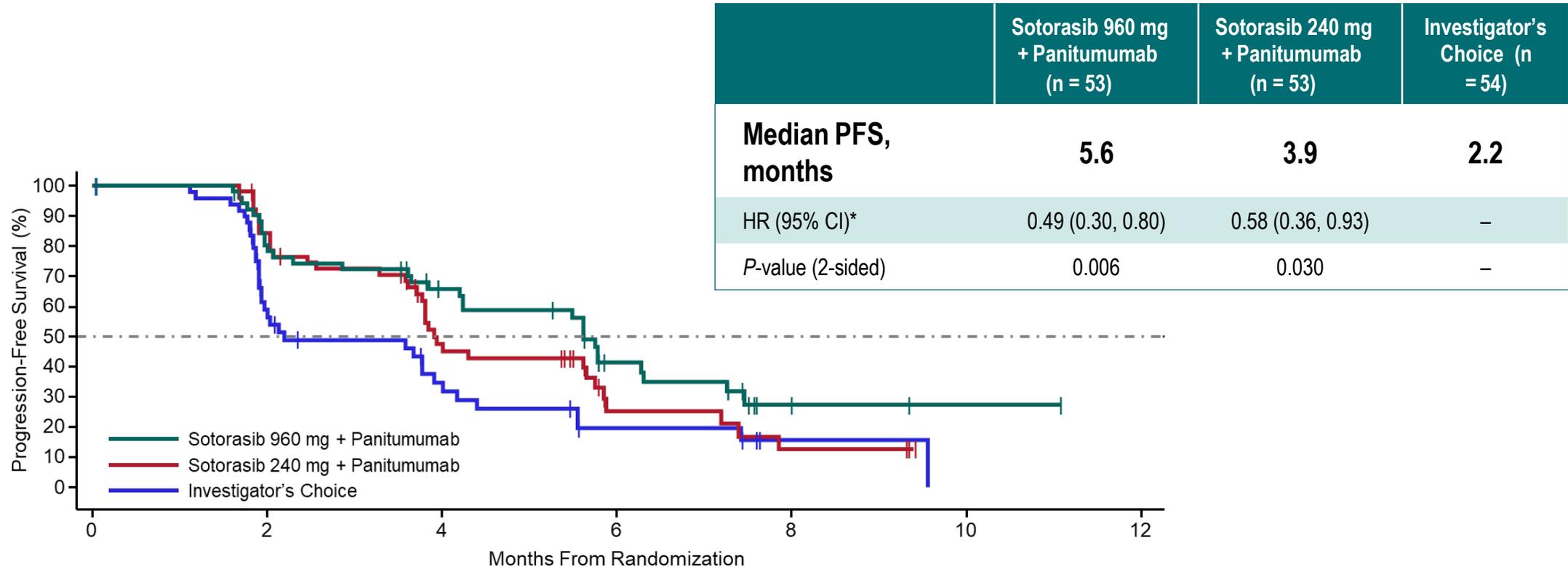
Treat until disease progression, start of another anti-cancer treatment, withdrawal of consent, or intolerance of treatment

**Primary endpoint: PFS by BICR** (measured by CT / MRI and assessed by RECIST v1.1)

**Key secondary endpoints:** OS, ORR

\*Patients deemed by the investigator not to be candidates for fluoropyrimidine, irinotecan, or oxaliplatin may still be eligible if  $\geq 1$  prior line of therapy was received for metastatic disease and trifluridine and tipiracil and/or regorafenib were deemed MADRID-eligible. †Patients with prior treatment with trifluridine and tipiracil and with regorafenib were excluded, where the investigator's choice would be these agents. 2QW, every 2 weeks; BICR, blinded independent central review; CT, computed tomography; ECOG, Eastern Cooperative Oncology Group; KRAS, Kirsten rat sarcoma; mCRC, metastatic colorectal cancer; MRI, magnetic resonance imaging; OS, overall survival; ORR, objective response rate; PFS, progression-free survival; RECIST, Response Evaluation Criteria in Solid Tumors.

# Primary Endpoint: PFS in Intent-to-Treat Population



Number of Patients at Risk:

	0	2	4	6	8	10	12
Sotorasib 960 mg + Panitumumab	53	40	28	13	2	1	0
Sotorasib 240 mg + Panitumumab	53	43	20	6	3	0	
Investigator's Choice	54	24	12	5	1	0	

**After a median follow-up of 7.8 months, sotorasib (960 mg and 240 mg) in combination with panitumumab significantly improved PFS by BICR versus investigator's choice**

PFS was tested using stratified log-rank test. \*HR is sotorasib 960 mg + panitumumab / investigator's choice therapy, or sotorasib 240 mg + panitumumab / investigator's choice therapy. BICR, blinded independent central review; HR, hazard ratio; PFS, progression-free survival.

# Activity Outcomes

Response by BICR	Sotorasib 960 mg + Panitumumab (n = 53)	Sotorasib 240 mg + Panitumumab (n = 53)	Investigator's Choice (n = 54)
<b>ORR, % (95% CI)*†</b>	26 (15.3–40.3)	6 (1.2–15.7)	0 (0–6.6)
Complete response, n (%)	1 (2)	0	0
Partial response, n (%)	13 (25)	3 (6)	0
Stable disease, n (%)	24 (45)	33 (62)	25 (46)
Progressive disease, n (%)	12 (23)	13 (25)	17 (31)
Not evaluable / not done, n (%)	3 (6)	2 (4)	11 (20)
<b>DCR, % (95% CI)*</b>	72 (57.7–83.2)	68 (53.7–80.1)	46 (32.6–60.4)

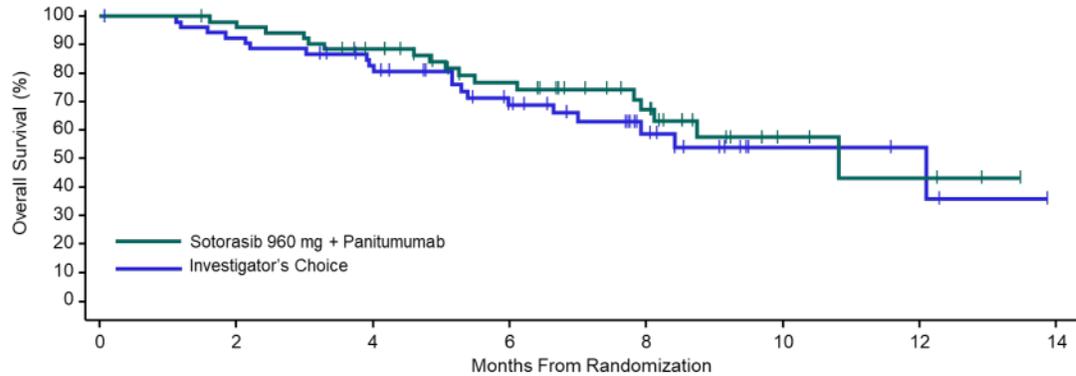
**ORR and DCR by BICR were higher with sotorasib (960 mg and 240 mg) + panitumumab versus investigator's choice**

The intention-to-treat analysis set included all patients who underwent randomization.

\*95% CIs were estimated using the Clopper-Pearson method. BICR, blinded independent central review; DCR, disease control rate; ORR, objective response rate

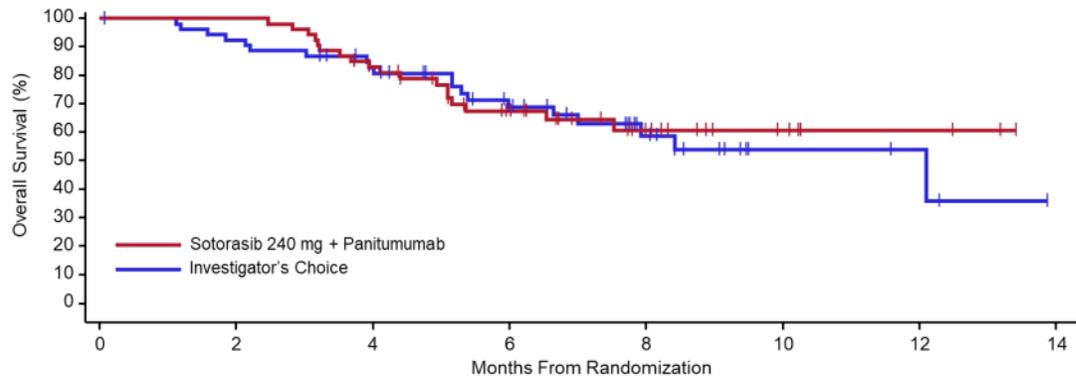
†Two patients (4%) in the 240 mg arm and 1 patient (2%) in the investigator's choice arm had non-complete response/non-progressive disease; these patients had BICR assessed non-target disease only

# Overall Survival



Number of Patients at Risk:

Months From Randomization	0	2	4	6	8	10	12	14
Sotorasib 960 mg + Panitumumab	53	51	43	31	19	5	3	0
Investigator's Choice	54	49	40	27	14	4	3	0



Number of Patients at Risk:

Months From Randomization	0	2	4	6	8	10	12	14
Sotorasib 240 mg + Panitumumab	53	53	40	26	13	6	3	0
Investigator's Choice	54	49	40	27	14	4	3	0

	Sotorasib 960 mg + Panitumumab (n = 53)	Sotorasib 240 mg + Panitumumab (n = 53)	Investigator's Choice (n = 54)
HR (95% CI)*	0.77 (0.41, 1.45)	0.91 (0.48, 1.71)	–
Deaths, n (%)	17 (32)	18 (34)	20 (37)
Median follow-up, months (95% CI)	8.1 (6.7, 8.7)	7.7 (6.2, 8.3)	7.8 (6.5, 8.5)

Overall survival data were not mature at data cutoff, with 55 (34%) deaths observed

# The role of ctDNA in CRC

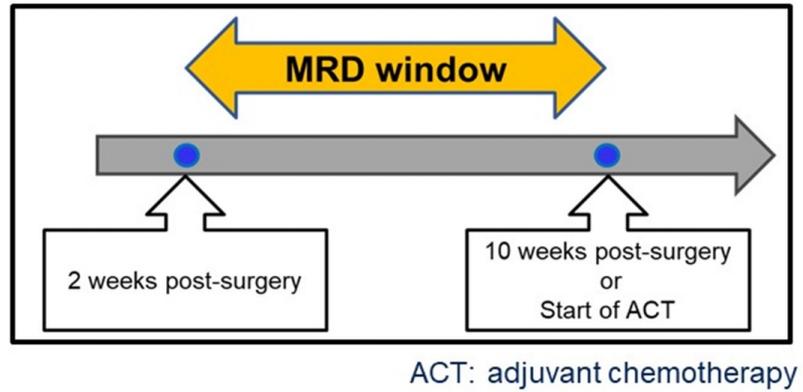
# Circulating tumor DNA (ctDNA) dynamics in colorectal cancer (CRC) patients with molecular residual disease: Updated analysis from GALAXY study in the CIRCULATE-JAPAN

Presenting Author: Hiroki Yukami, MD, PhD

Co-authors: Yoshiaki Nakamura, Saori Mishima, Koji Ando, Hideaki Bando, Jun Watanabe, Keiji Hirata, Naoya Akazawa, Masataka Ikeda, Mitsuru Yokota, Kentaro Kato, George Laliotis, Vasily N. Aushev, Adham A. Jurdi, Minetta C. Liu, Daisuke Kotani, Eiji Oki, Ichiro Takemasa, Takeshi Kato, Takayuki Yoshino

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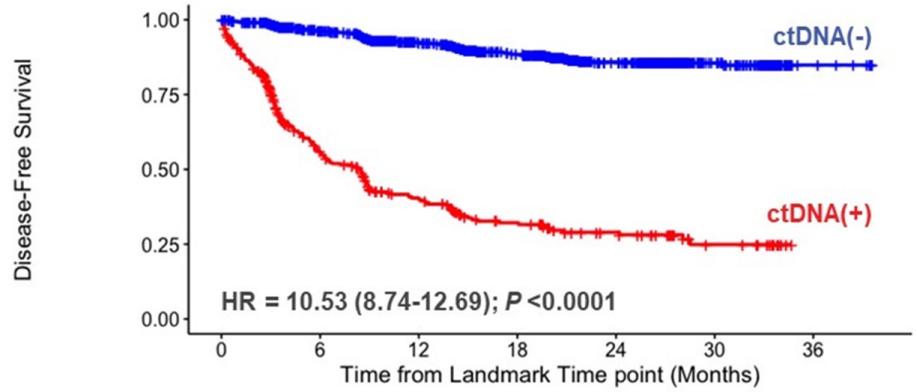
# DFS according to status in the MRD window in all stage



2,998 stage I-IV patients included in the outcome cohort

**Excluded (N=138)**  
 •DFS event prior to the 10 weeks landmark timepoint (n=138)

MRD Window analysis cohort (n=2,860)



	Number at risk						
	0	6	12	18	24	30	36
ctDNA Negative	2491	2031	1441	1041	495	135	8
ctDNA Positive	369	165	98	59	35	13	0

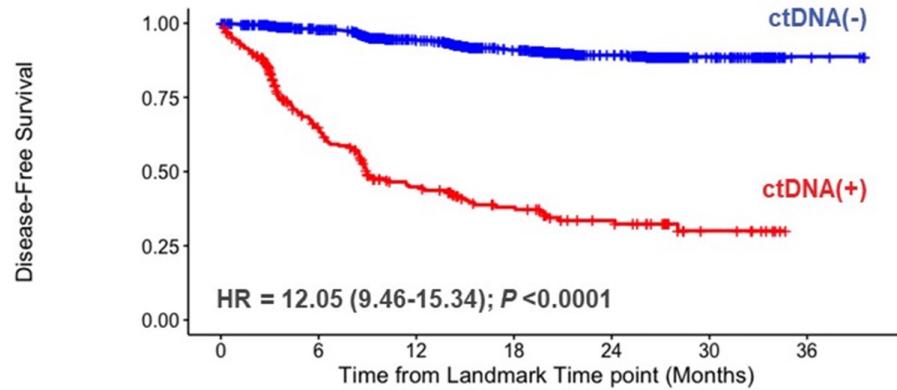
ctDNA status	Negative	Positive
Events %	9.4 (235/2491)	58.8 (217/369)
24M-DFS % (95% CI)*	85.9 (83.9–87.7)	28.9 (23.4–34.8)

\*DFS % from landmark time point

MRD window: 2-10 weeks post surgery, prior to start of any adjuvant therapy - Landmark 10 weeks post-surgery

**ctDNA-positive in the MRD window is predictive inferior DFS**

# DFS according to status in the MRD window in pStage II/III

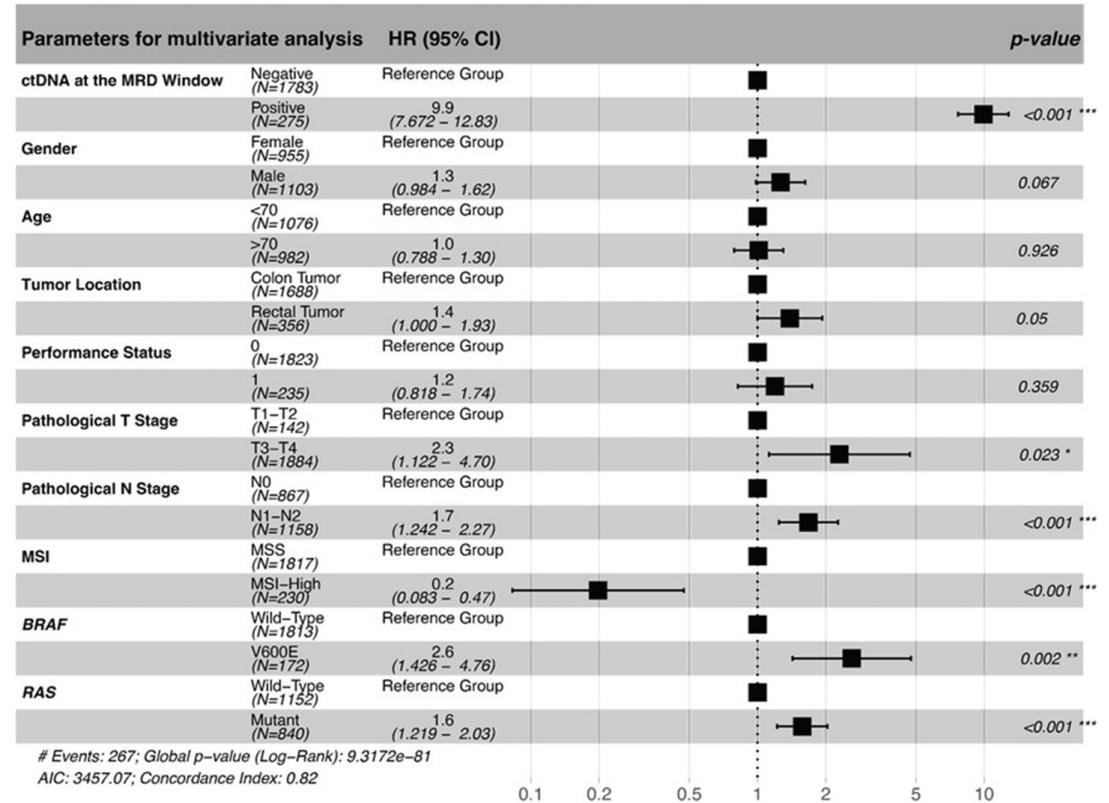


Dynamics	ctDNA Negative	ctDNA Positive
Events %	7.8 (126/1783)	56.5 (143/275)
24M-DFS % (95% CI)*	89.3 (87.2-91.1)	33.5 (26.5-40.7)

\*DFS % from landmark time point

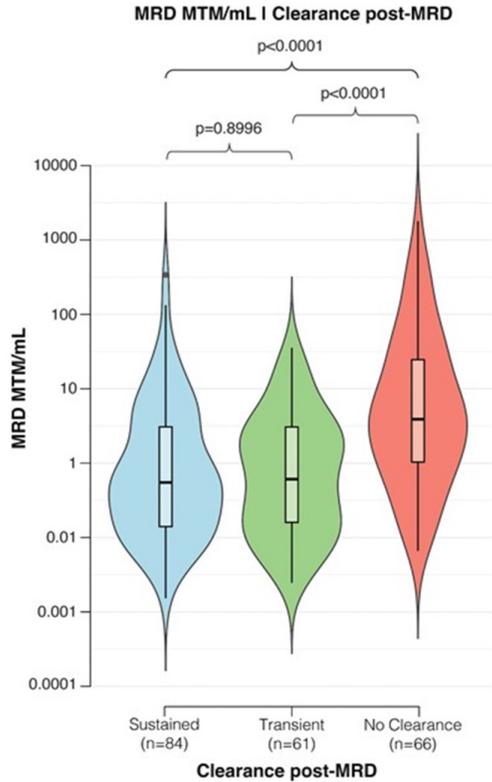
MRD window: 2-10 weeks post surgery, prior to start of any adjuvant therapy - Landmark 10 weeks post-surgery

## Multivariate Regression Model for DFS



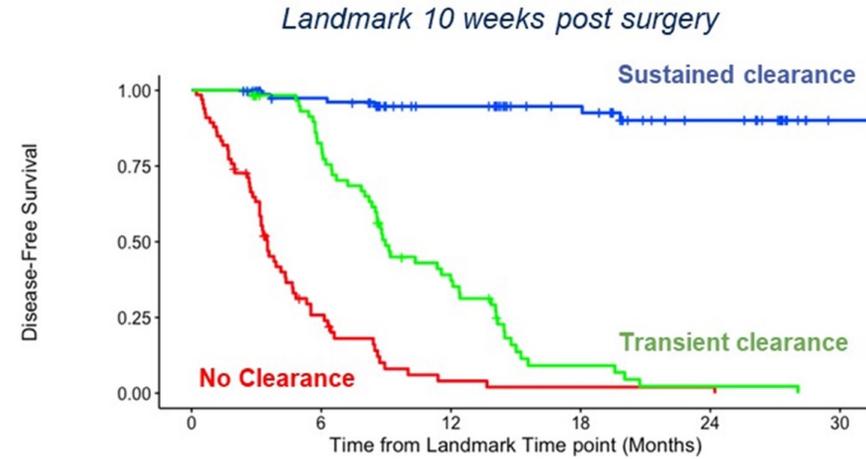
**ctDNA-positive in the MRD window is predictive of inferior DFS (pStage II/III)**

# DFS according to ctDNA clearance in Patients with ctDNA positive in the MRD window



Group	Median MRD MTM/mL
Sustained	0.61
Transient	0.53
No Clearance	3.89

\*P values from Wilcoxon rank-sum test



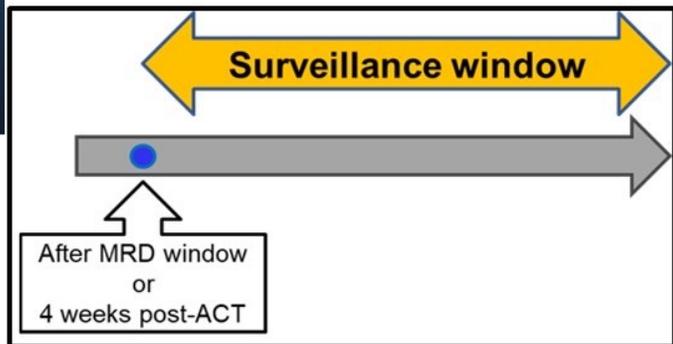
	0	6	12	18	24	30
No Clearance	66	14	2	1	1	0
Sustained	84	74	58	44	27	12
Transient	61	47	19	4	1	0

ctDNA Clearance	Sustained Clearance	Transient Clearance	No Clearance
Events %	7.1 (6/84)	85.2 (52/61)	89.4 (59/66)
Median DFS months (95% CI)	NR	9 (8.5–12.4)	3.5 (3.2–4.7)
24M-DFS % (95% CI)*	90.1 (78.6–95.6)	2.3 (0.02–10.3)	2 (0.02–9.2)
HR	Reference	25.13	87.08
95% CI	Not applicable	10.57–59.73	36.14–209.84
P	Not applicable	<0.0001	<0.0001

\*DFS % from landmark time point

**Sustained clearance indicates superior DFS compared to Transient or No clearance**

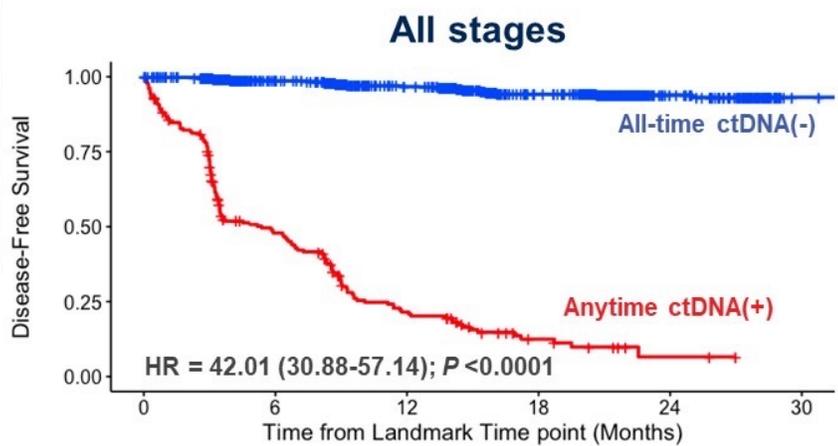
# DFS according to ctDNA status in the Surveillance window



2,998 stage I-IV patients included in the outcome cohort

- Excluded (N=1,212)**
- No subsequent timepoints available (n=858)
  - DFS event prior to the 8 months landmark timepoint (n=354)

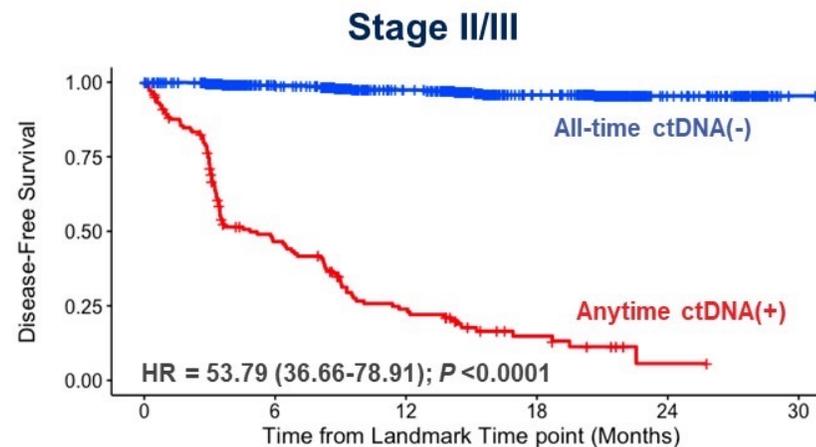
Surveillance Window analysis cohort (n=1,786)



ctDNA status	Number at risk					
ctDNA Negative	1582	1211	885	432	125	8
ctDNA Positive	204	84	33	10	2	0

ctDNA status	All-time Negative	Anytime Positive
Events %	3.7 (58/1582)	77.5 (158/204)
24M-DFS % (95% CI)*	93.9 (92-95.4)	6.6 (2-14.9)



ctDNA status	Number at risk					
ctDNA Negative	1326	1022	737	355	97	5
ctDNA Positive	146	57	26	9	1	0

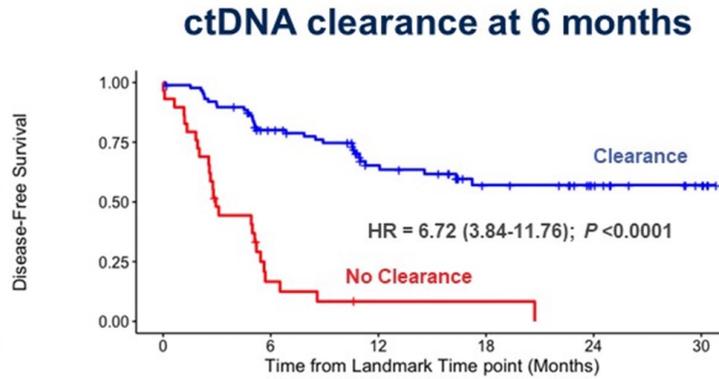
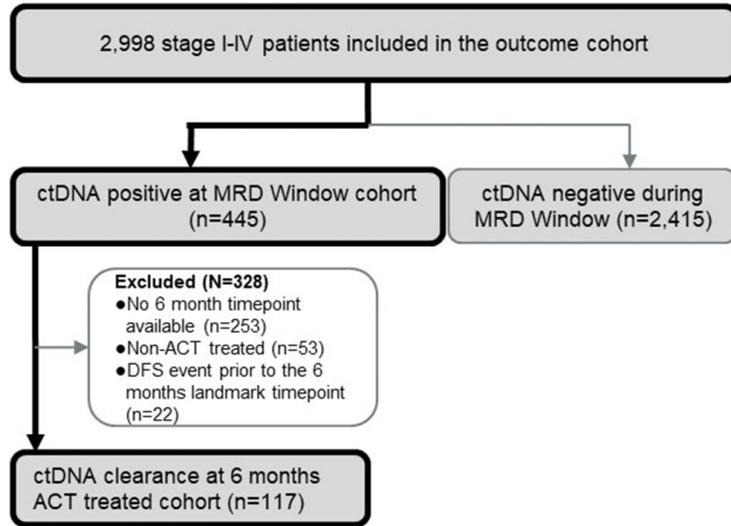
ctDNA status	All-time Negative	Anytime Positive
Events %	2.7 (36/1326)	75.3 (110/146)
24M-DFS % (95% CI)*	95.4 (93.5-96.8)	5.6 (0.8-18.3)

\*DFS % from landmark time point

- Surveillance window starts from 4 weeks post-ACT or at the end of MRD window if patient had no ACT, until the last follow up or relapse.
- Landmark 8 months post-surgery (2 months for ACT initiation + 6 months of ACT duration)

**ctDNA-positive in the surveillance window is predictive of inferior DFS**

# Clearance and reduction in MTM/mL at 6 months in ACT treated patients

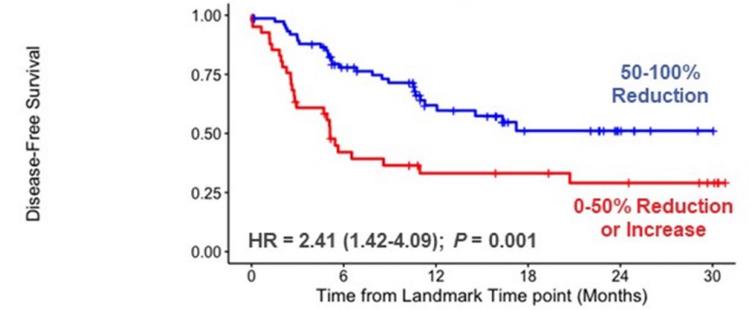


Number at risk

Clearance	88	62	37	21	13	5
No Clearance	29	4	1	1	0	0

ctDNA Clearance	Clearance	No Clearance
Events %	35.2 (31/88)	89.7 (26/29)
24M-DFS % (95% CI)	57.1 (44-68.2)	NR

## Positive at the MRD window to 6 months MTM/mL Reduction | ACT-treated



Number at risk

50-100%	75	51	28	13	6	1
0-50% or Increased MTM	41	15	10	9	7	4

ctDNA Clearance	50-100% Reduction	0-50% Reduction or Increase
Events %	38.7 (29/75)	65.9 (27/41)
24M-DFS % (95% CI)	51.1 (36.4-64.1)	29 (15-44.6)

\*DFS % from landmark time point

Landmark 6 months post-surgery

**ctDNA clearance and MTM/mL reduction on ACT is an indicator of treatment efficacy and results in better outcomes**



*Advancing Research. Improving Lives.™*

# Phase II results of circulating tumor DNA as a predictive biomarker in adjuvant chemotherapy in patients with stage II colon cancer: NRG-GI005 (COBRA) phase II/III study

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# NRG-GI005 (COBRA) Study Schema

Resected stage IIA colon cancer for which the physician decides no adjuvant chemotherapy (i.e., “suitable for active surveillance”)

R  
1:1

**Arm 1**

Standard of care  
(active surveillance)

**Arm 2**

Assay-directed therapy

All patients were followed with radiographic restaging assessments every 6 months.

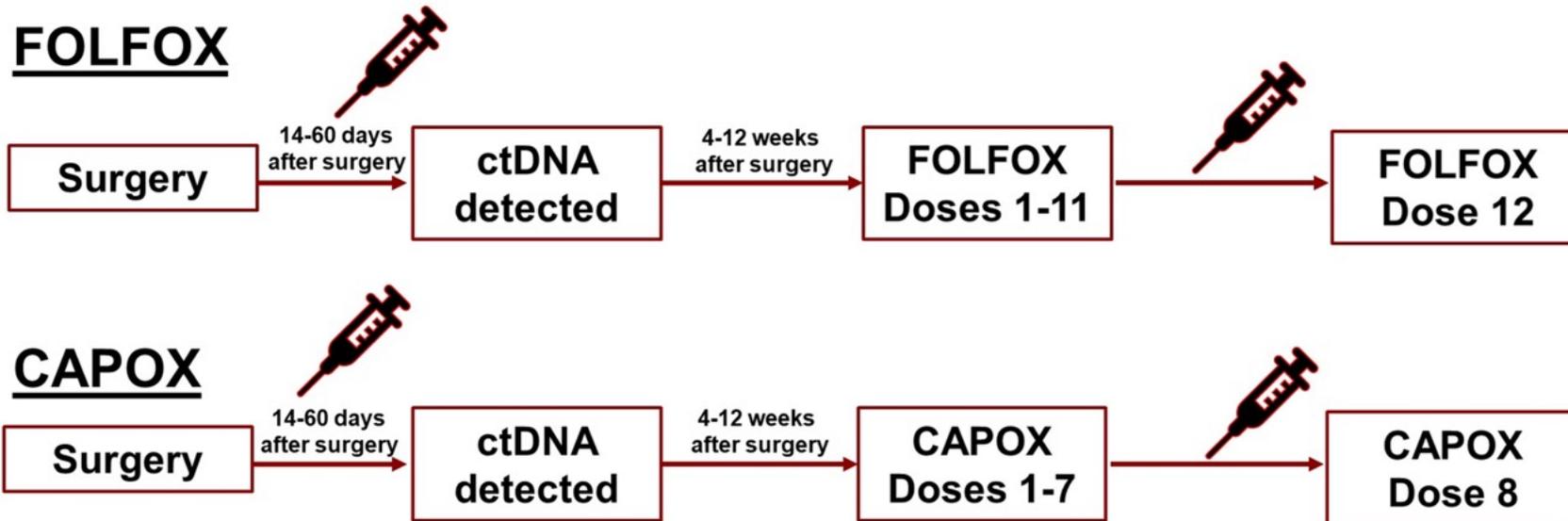
**ctDNA detected**

Chemotherapy (mFOLFOX6  
or CAPOX) x 6 months

**ctDNA NOT detected**

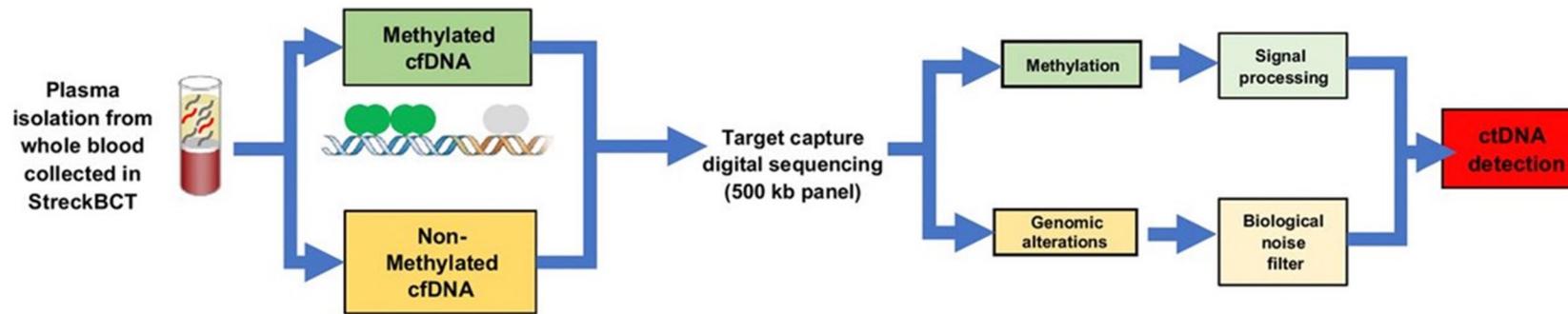
Active surveillance

## Treatment schema: Arm 2 “ctDNA detected”



The 6-month timepoint was collected two weeks after prior dose of chemotherapy/ immediately prior to the administration of the last dose of chemotherapy.

# ctDNA assay

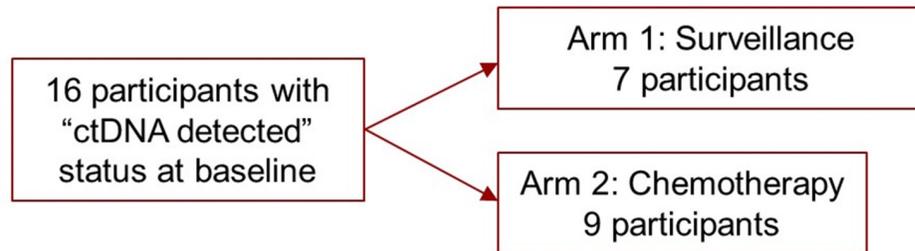


- Guardant LUNAR assay was selected for NRG GI005 through an open RFA and peer-reviewed process as a tissue-agnostic assay that incorporates mutation/genomic and methylation/epigenomic markers alike for detection of ctDNA.
- Guardant LUNAR had undergone previous clinical and analytic validation:
  - In a previously reported cohort of 70 patients with stage I-IV colorectal cancer, sensitivity and specificity for were 56% and 95% (100% for those with one year of follow-up), respectively, when drawn one month after completion of definitive therapy.
  - Adding epigenomic profiling improved sensitivity relative to mutation calling alone by 25%.

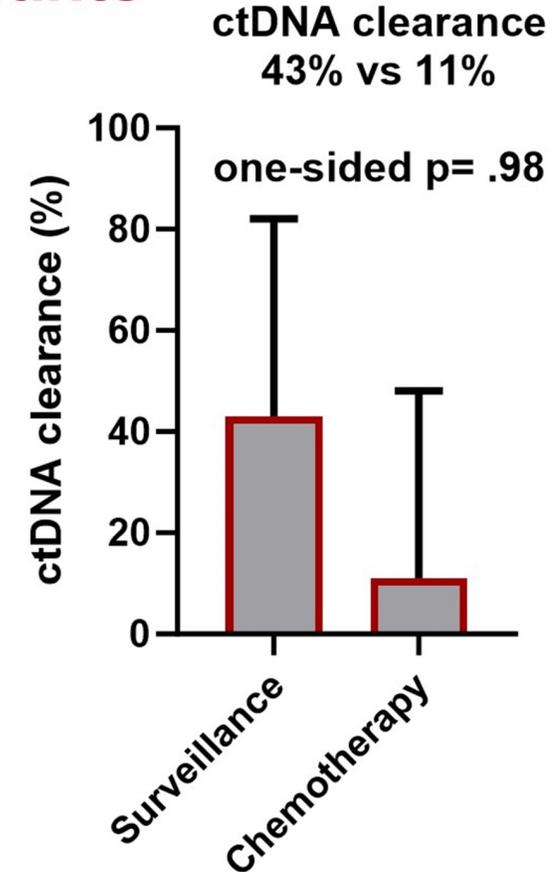
Parikh A et al, Clin Cancer Res 2021

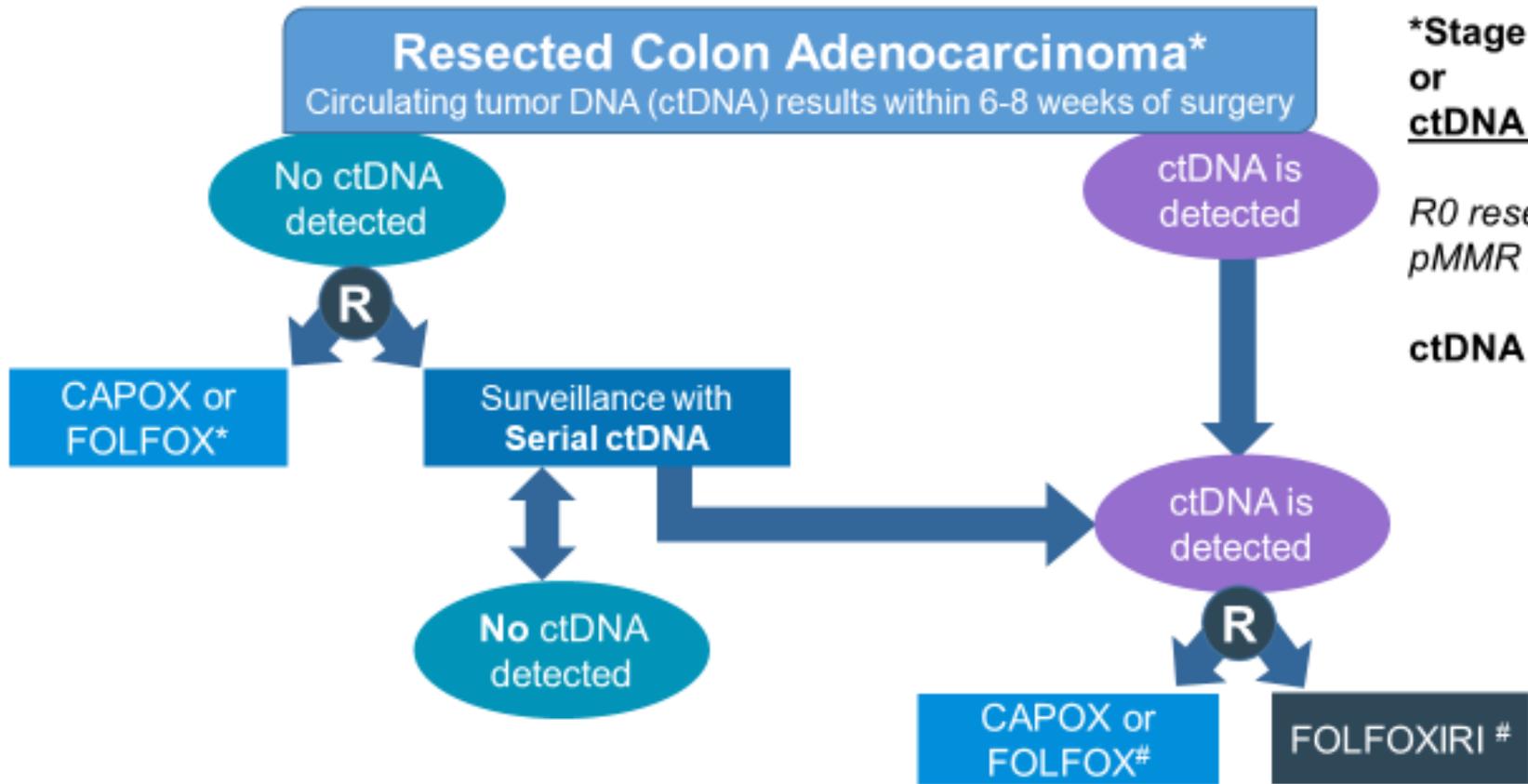
# Phase II Endpoint Analysis: ctDNA(+) baseline participants

- Among 596 participants with baseline ctDNA status available, ctDNA(+) detection was observed in 33 (5.54%).



- Clearance of ctDNA at 6 months among ctDNA(+) participants at baseline was observed in:
  - **Arm 1 (surveillance):** 3 of 7 (43%, 95% CI 10 - 82%) participants
  - **Arm 2 (chemotherapy):** 1 of 9 patients (11%, 95% CI 0.3 - 48%) participants
- **Because the 1-sided Fisher's Exact Test yields  $p = 0.98$  exceeded 0.35,  $H_0$  was not rejected, and the decision rule calls for early stopping due to futility.**





**\*Stage III (T1-3, N1/N1c)**  
**or**  
**ctDNA +ve Stage II or Stage IIIC**

*R0 resection*  
*pMMR / MSS*

**ctDNA Assay: Signatera**

**PIs:**  
Arvind Dasari (MDACC – NRG)  
Christopher Lieu (UCCC – SWOG)

\*: Duration and regimen per physician discretion  
#: 6 months duration

**NRG-GI008**

## Conclusions:

- Molecular testing should be conducted in all patients
- COBRA demonstrates the challenges in an evolving field.
  - ctDNA remains exploratory but demonstrates the impact on prognosis