



**PragueONCO 2020**

**January 29, 2020**



# **Circulating Biomarkers in Precision Oncology and Immunoncology**

**Filip Janku, MD, PhD**

**Associate Professor**

**Investigational Cancer Therapeutics (Phase I Clinical Trials Program)**

**Center Medical Director**

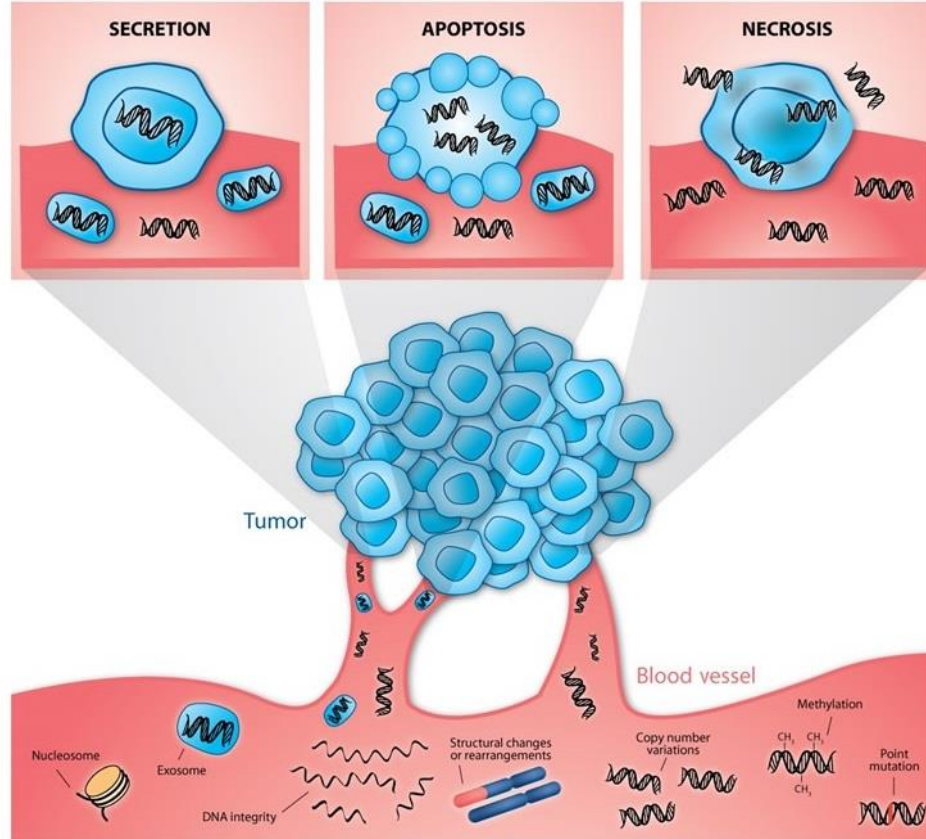
**Clinical & Translational Research Center**



# Disclosures

- **Research Funding (through institution):** Agios, Asana, Astellas, Astex, Bayer, BioMed Valley Discoveries, Bristol-Myers Squibb, Cotinga, Ideaya, Deciphera, FujiFilm Pharma, Genentech, Novartis, Piquor, Plexxikon, Proximagen, Symphogen, Sotio, Sanofi, SynthoRx, SpringBank Pharma, Synlogic
- **Consulting:** Baush, Bicara, Deciphera, Guardant Health, Grail, Ideaya, IFM Therapeutics, Immunomet, Illumina, Jazz Pharmaceuticals, Novartis, Primmune Therapeutics, PureTech Health, Sotio, Synlogic, SpringBank Pharma, Tessa Therapeutics, Trovogene
- **Ownership Interests:** Trovogene
- **Other:** Bio-Rad, Biocartis

# Concept of “liquid” biopsy



# Liquid Biopsies in the Clinic

**1. Treatment indication**

**2. Efficacy monitoring**

**3. Molecular profiling in the real-time**

**4. Indirect assessment of target engagement and inhibition**

**5. Early detection**

# Concordance Between Discordantly Collected Liquid (plasma cell-free DNA) and Tissue Biopsies



## PCR and digital PCR

- Idylla QAS PCR: 88%-90%
- BEAMING: 83%-99%
- ddPCR 85%-95%

*Janku F. Mol Cancer Ther 2016*  
*Janku F. Oncotarget 2015*  
*Janku F. Ann Oncol 2017*

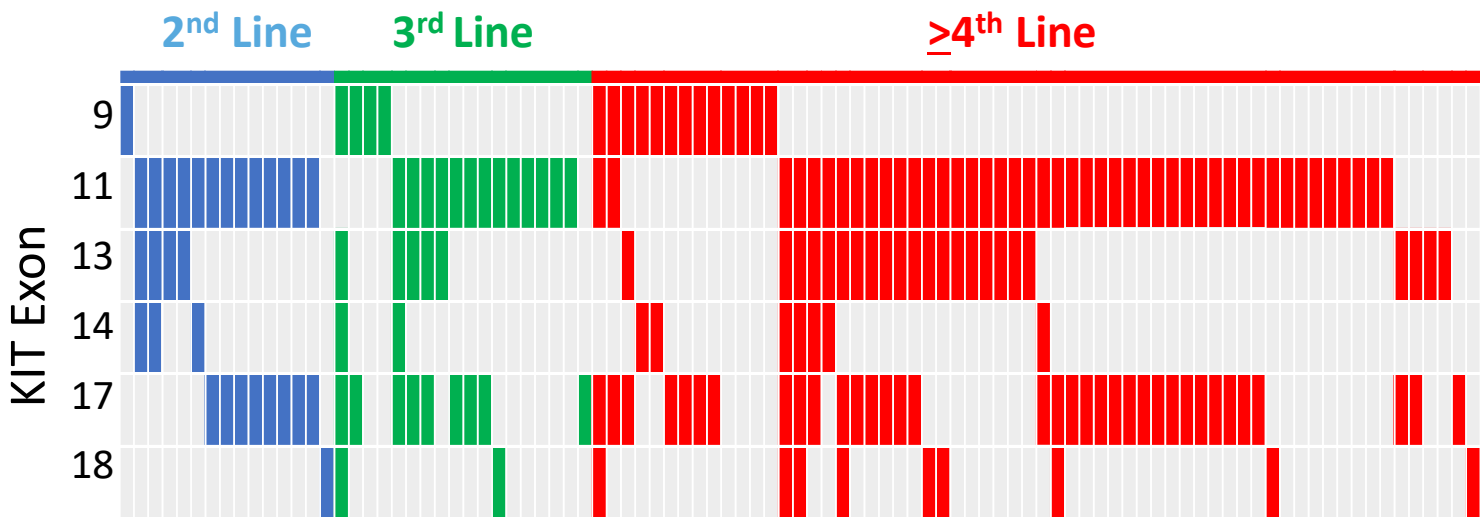
## NGS

*Concordance between ultra-deep NGS of plasma cfDNA and clinical molecular testing of archival tumor tissue for the 55 patients with advanced cancers*

Type of agreement between plasma cfDNA and tumor tissue	Number of patients (%)
Complete detection	45 (82%) 
Partial detection	3 (5%)
Aggregate complete and partial detection	48 (87%) 
Complete disagreement	7 (13%)

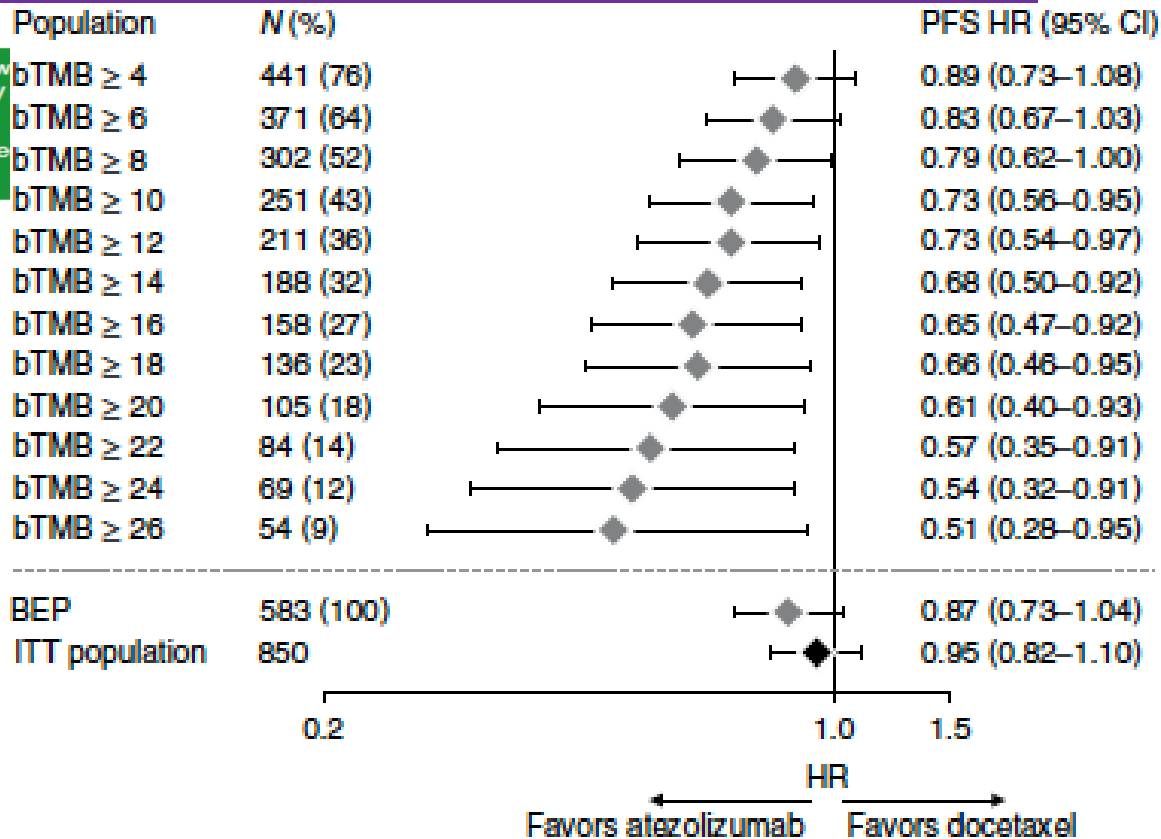
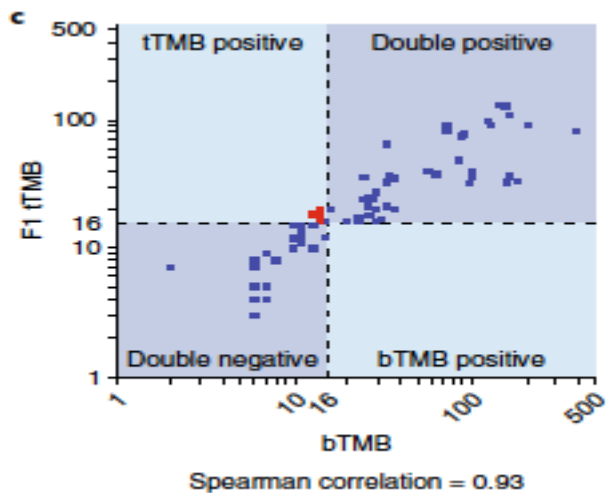
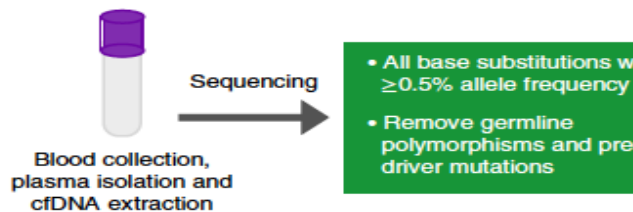
*Janku F. Clin Cancer Res 2017*

# Liquid Biopsies (NGS) Detect Broad Spectrum of KIT Mutations in Previously Treated GIST

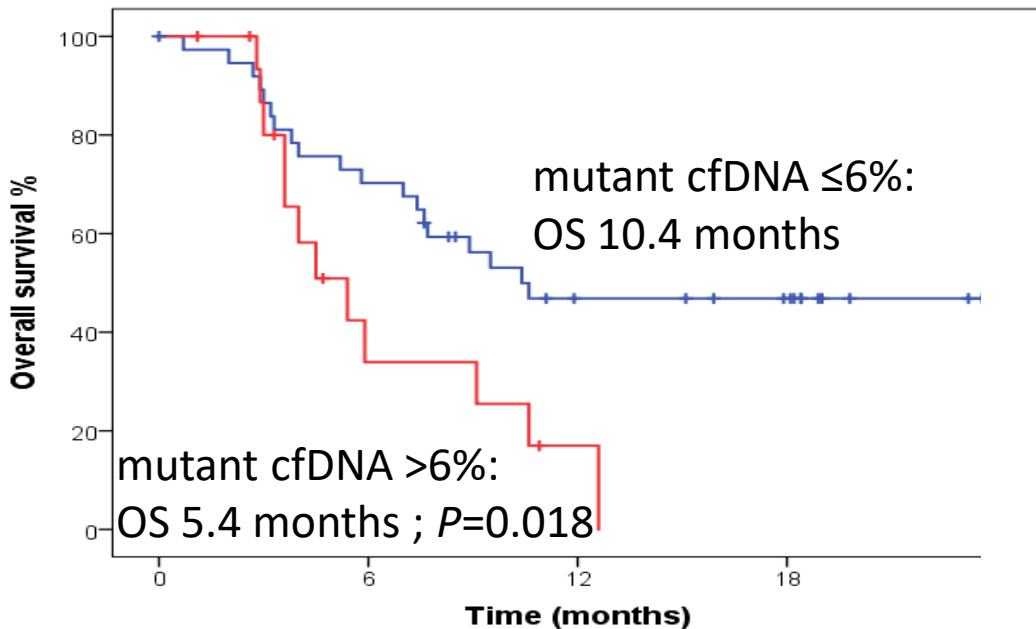


- Each column represents an individual patient
- In pts where a KIT mutation was detected in baseline ctDNA, secondary KIT mutations in exon 13, 14 17 and 18 were found across 2<sup>nd</sup> to ≥4<sup>th</sup>line pts.

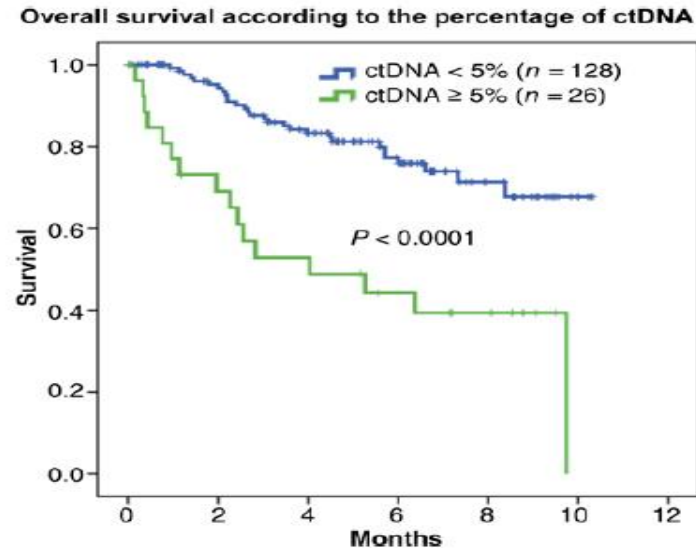
# Blood (cfDNA) TMB and Response to Immune Checkpoint Inhibitors



# The median OS duration in with advanced cancers per variant allele frequency of mutant cfDNA



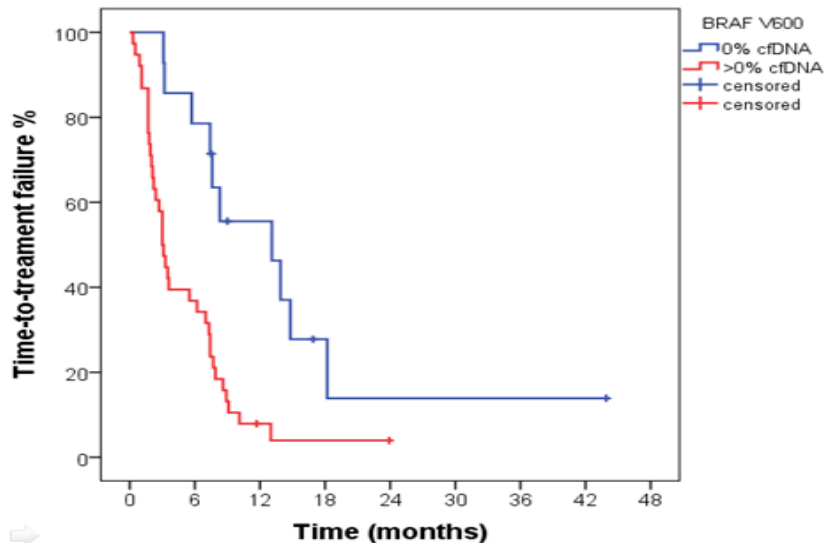
Janku, Salathia. Clin Cancer Res 2017



Schwaederle M, Clin Cancer Res 2016



# Detection of *BRAF* V600 mutant plasma cfDNA is associated with shorter time-to-treatment failure on systemic therapy



## Median TTF in 51 patients per plasma BRAF

**Tumor *BRAF*+ / Plasma *BRAF*-** 13.1 months,  
13 patients  
95% CI 5.0-21.2

**Tumor *BRAF*+ / Plasma *BRAF*+** 3.0 months  
38 patients  
95% CI 2.3-3.7

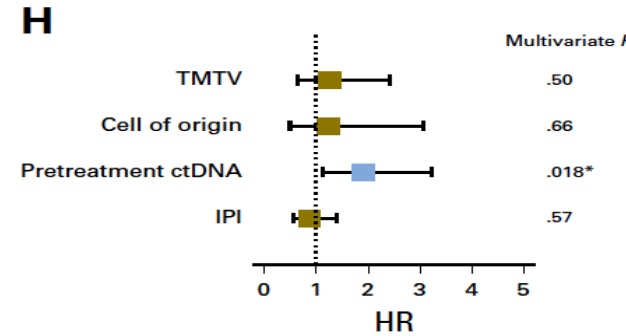
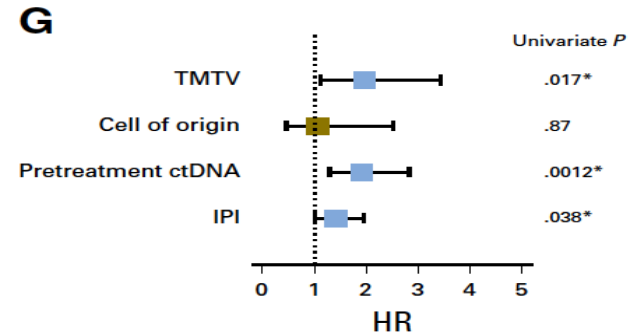
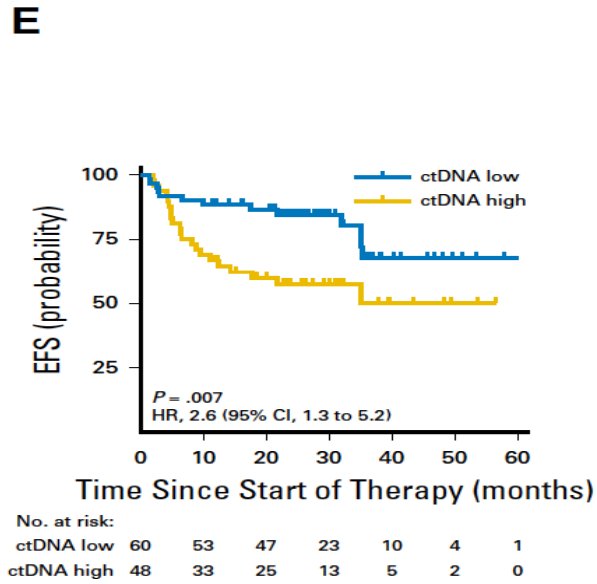
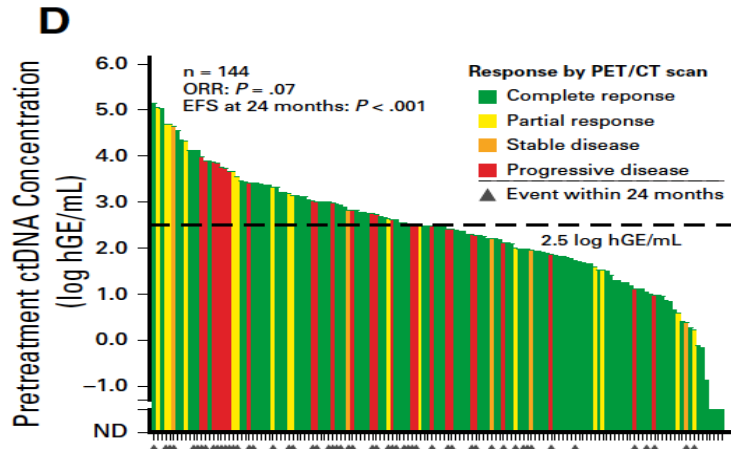
***P*=0.001**

Preliminary data suggest that amount of circulating tumor DNA does correlate with the total tumor volume and liver tumor volume

Ahmed, Colen, Janku. EORTC-NCI-AACR 2018



# Circulating Tumor DNA as Early Outcome Predictor in DLBCL



# Mutation-Enrichment NGS: Association between changes in cfDNA $KRAS^{G12/13}$ copies in URINE and PLASMA and time to treatment failure (TTF)

**TTF and  $KRAS^{G12/G13}$  copy numbers in urine:**

Decrease (4.7 months; blue)

vs.

No change/increase (2.8 months; red;  $P = 0.03$ )

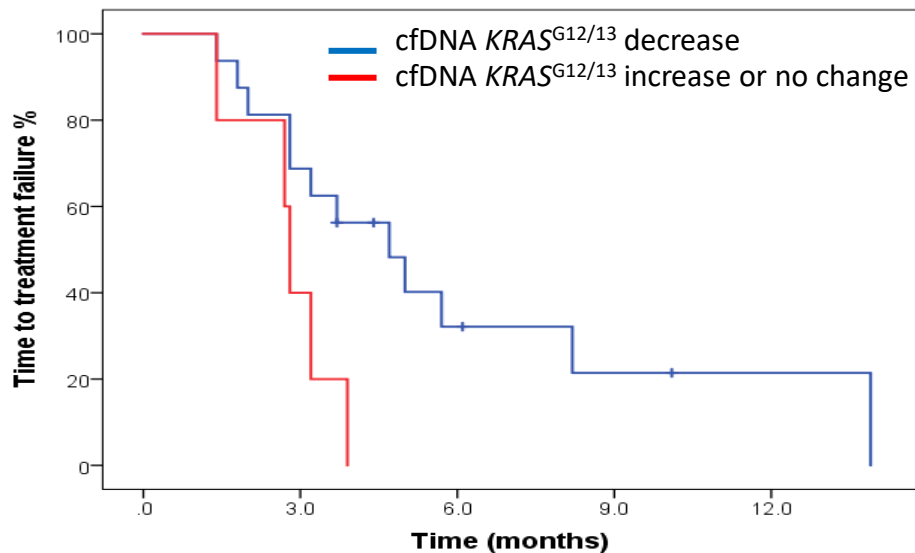
**TTF and  $KRAS^{G12/G13}$  copy numbers in plasma:**

Decrease (5.7 months; blue)

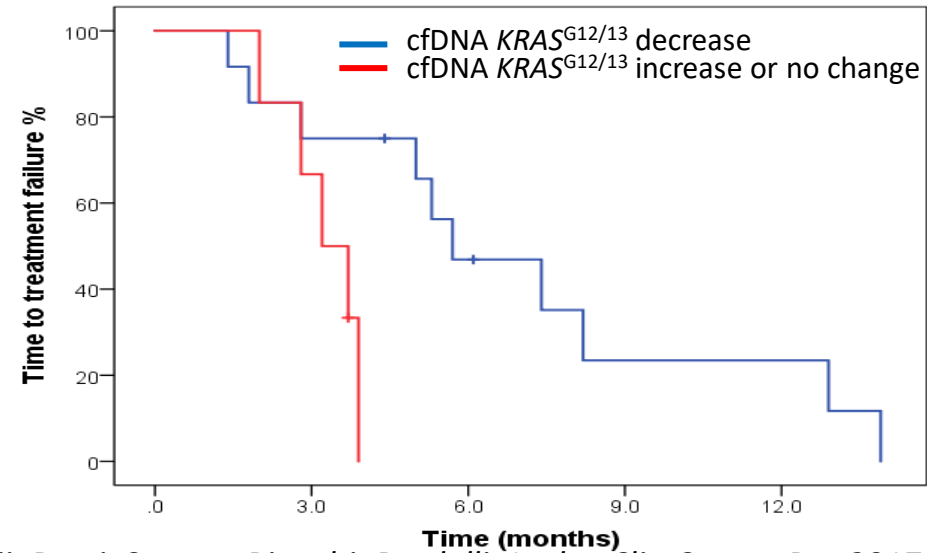
vs.

No change/increase (3.2 months; red;  $P = 0.04$ )

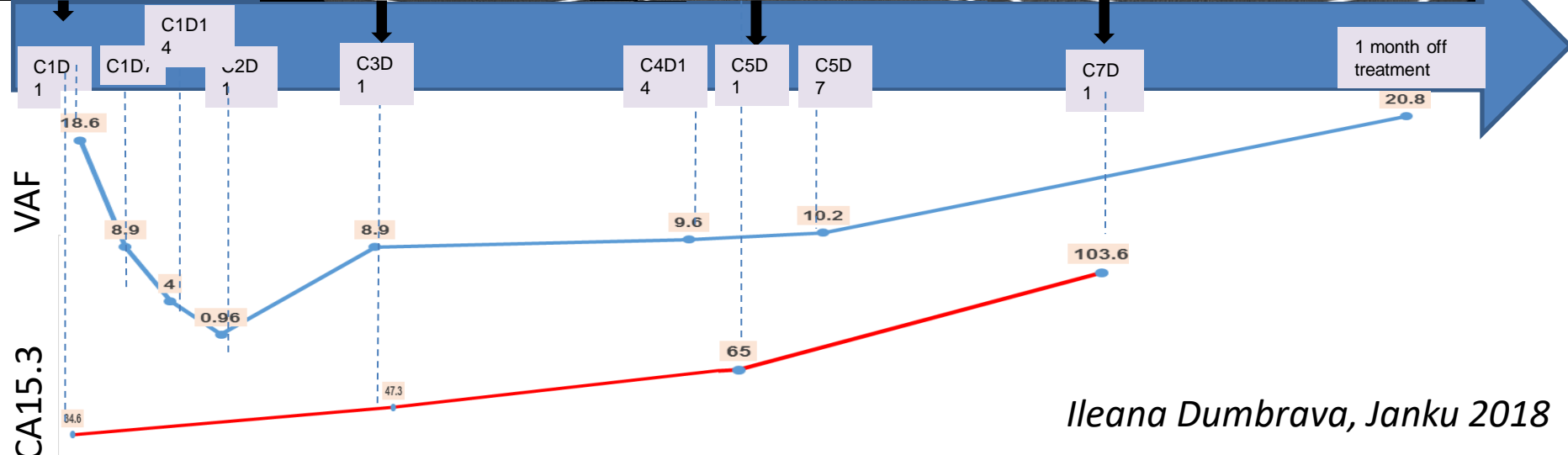
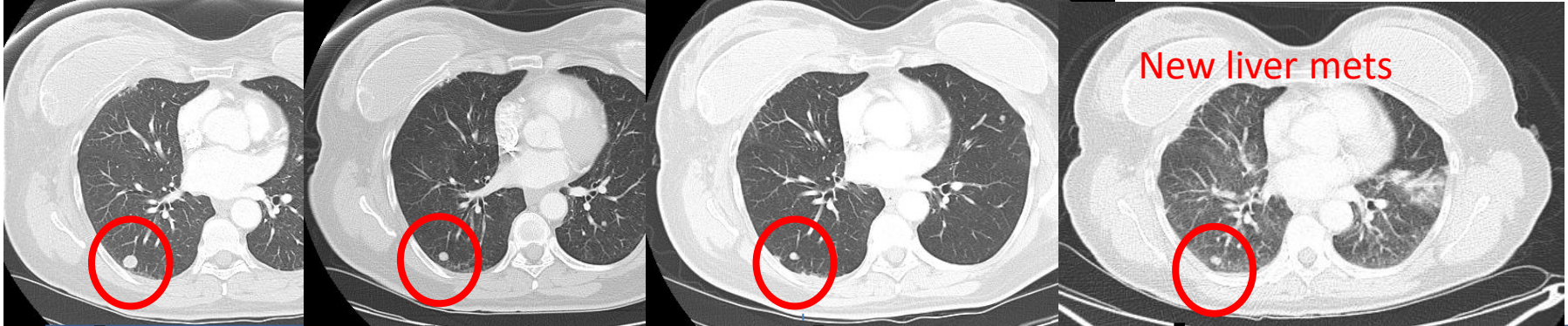
**A. URINE**



**B. PLASMA**

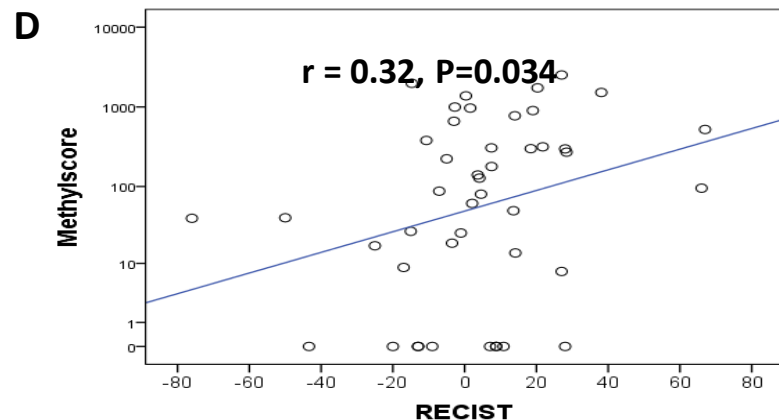
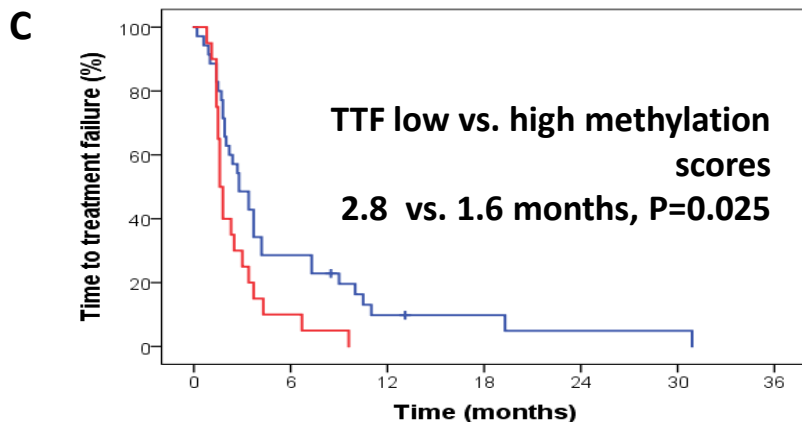
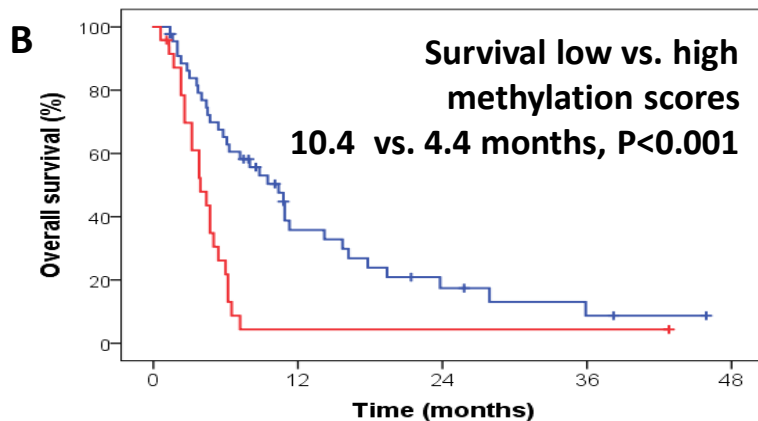
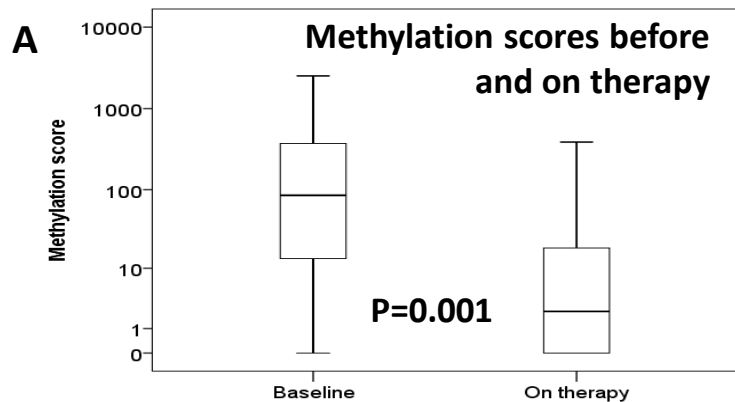


50yo F with metastatic breast cancer *PIK3CA E542K, KRAS G12S*  
 Everolimus-Bevacizumab-Doxorubicin Liposome

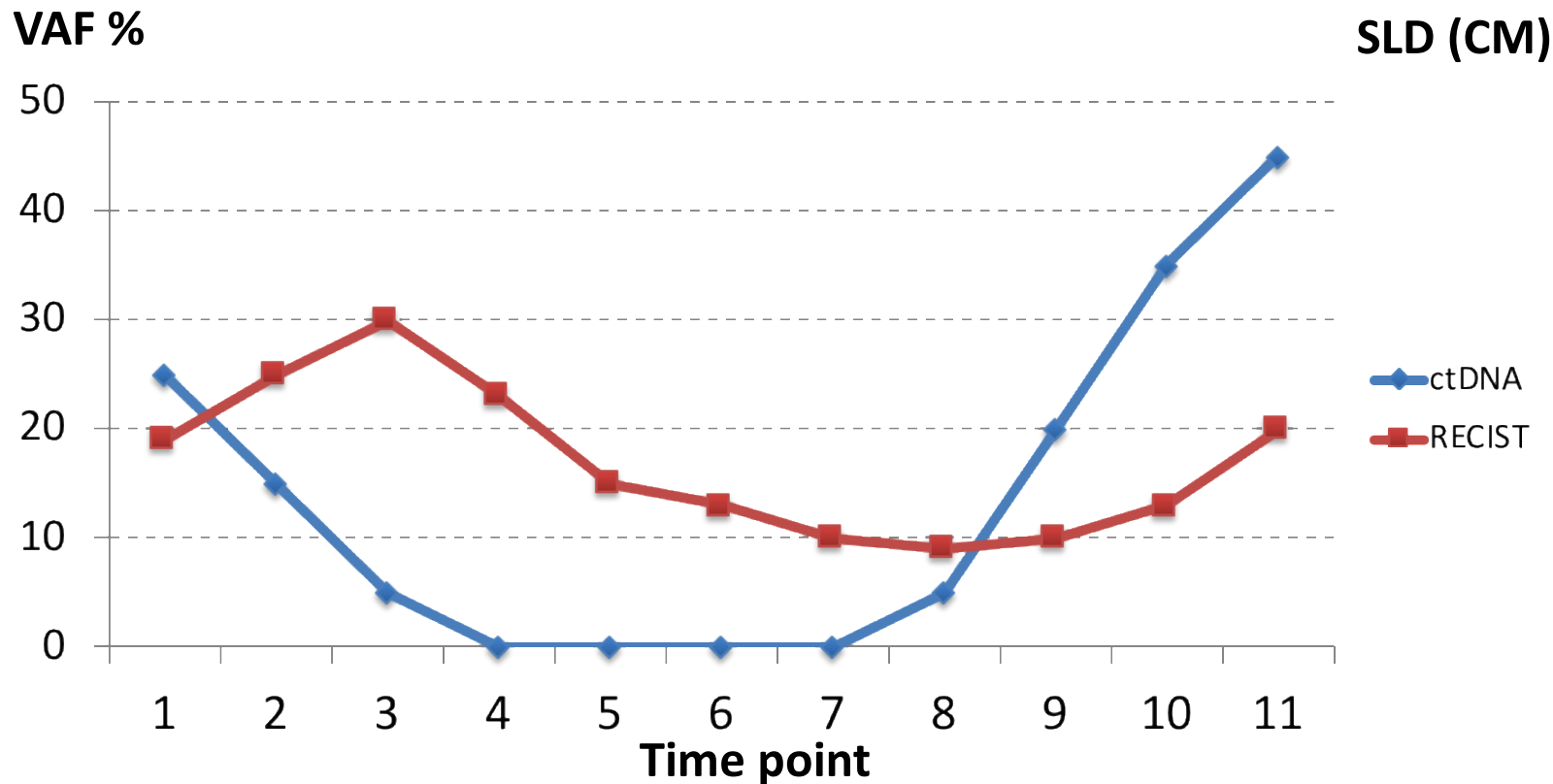


Ileana Dumbrava, Janku 2018

# MUTATION AGNOSTIC APPROACH: Methylation (>9,000 CpG sites) in cfDNA and outcomes in advanced cancers (breast, CRC, NSCLC, melanoma)



# Concept of Dynamic Tracking of Circulating Tumor DNA to Detect Pseudoprogession

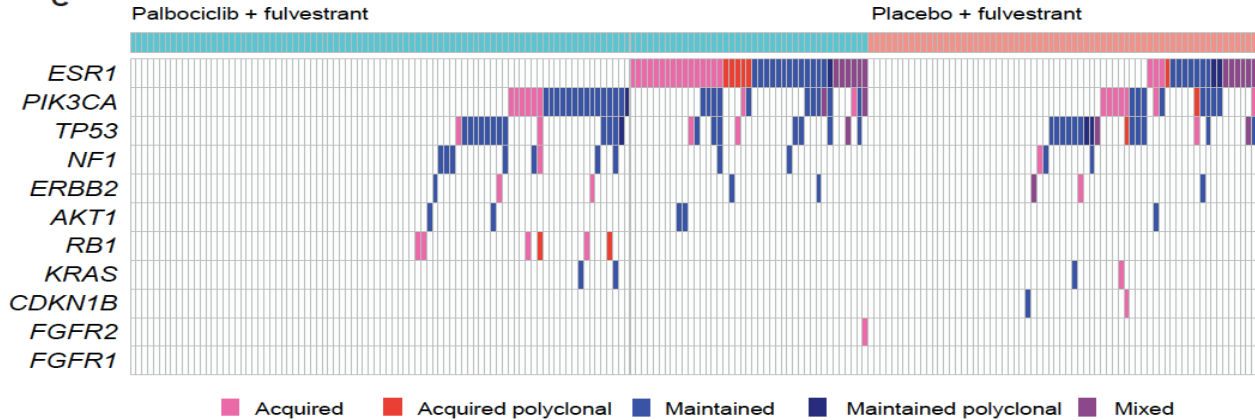


# Association Between Changes in Plasma-Derived Mutated Cell-Free DNA and Pseudoprogression to PD1 Antibodies in Melanoma



# Clonal Evolution in ctDNA and Therapeutic Resistance in HR+ Breast Cancer

C



Phase III Study

R

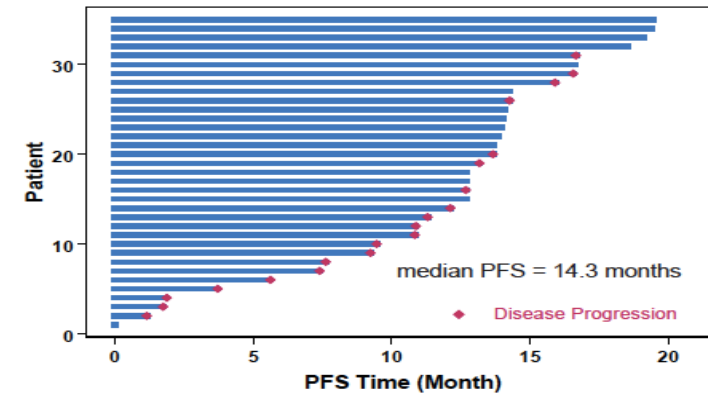
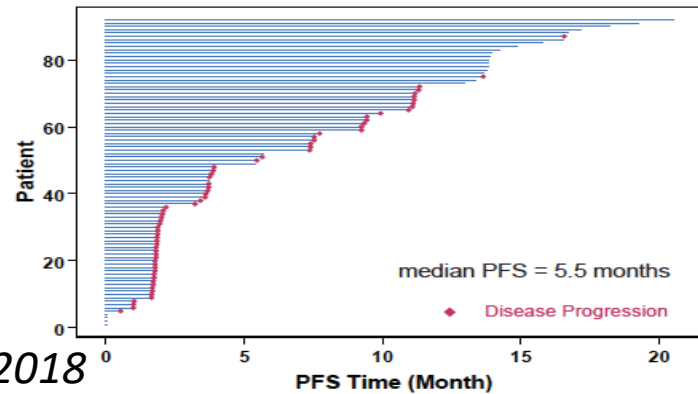
Fulvestrant  
Palbociclib

Fulvestrant  
Placebo

No acquired mutation

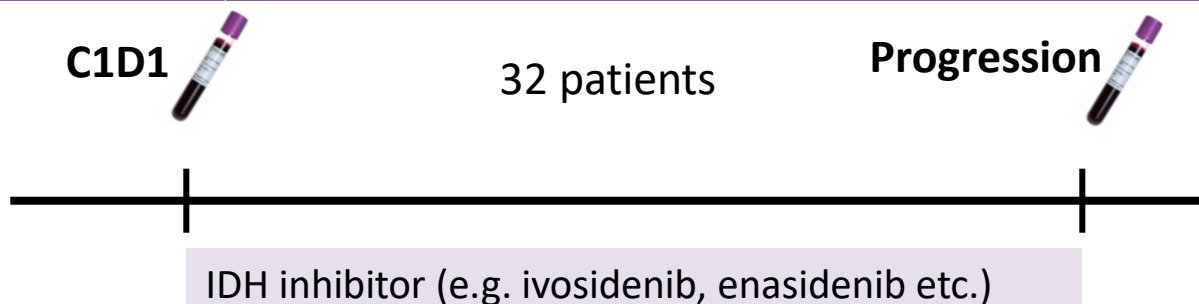
p = 0.0018

Acquired mutation





# Monitoring of dynamic changes and clonal evolution in circulating tumor DNA from patients with *IDH*-mutated cholangiocarcinoma treated with *IDH* inhibitors



## Agreement plasma vs. tissue *IDH* mutations

- Droplet digital PCR:	84%
- NGS:	83%

## Agreement plasma vs. tissue other mutations

- Droplet digital PCR:	60%
- NGS:	100%

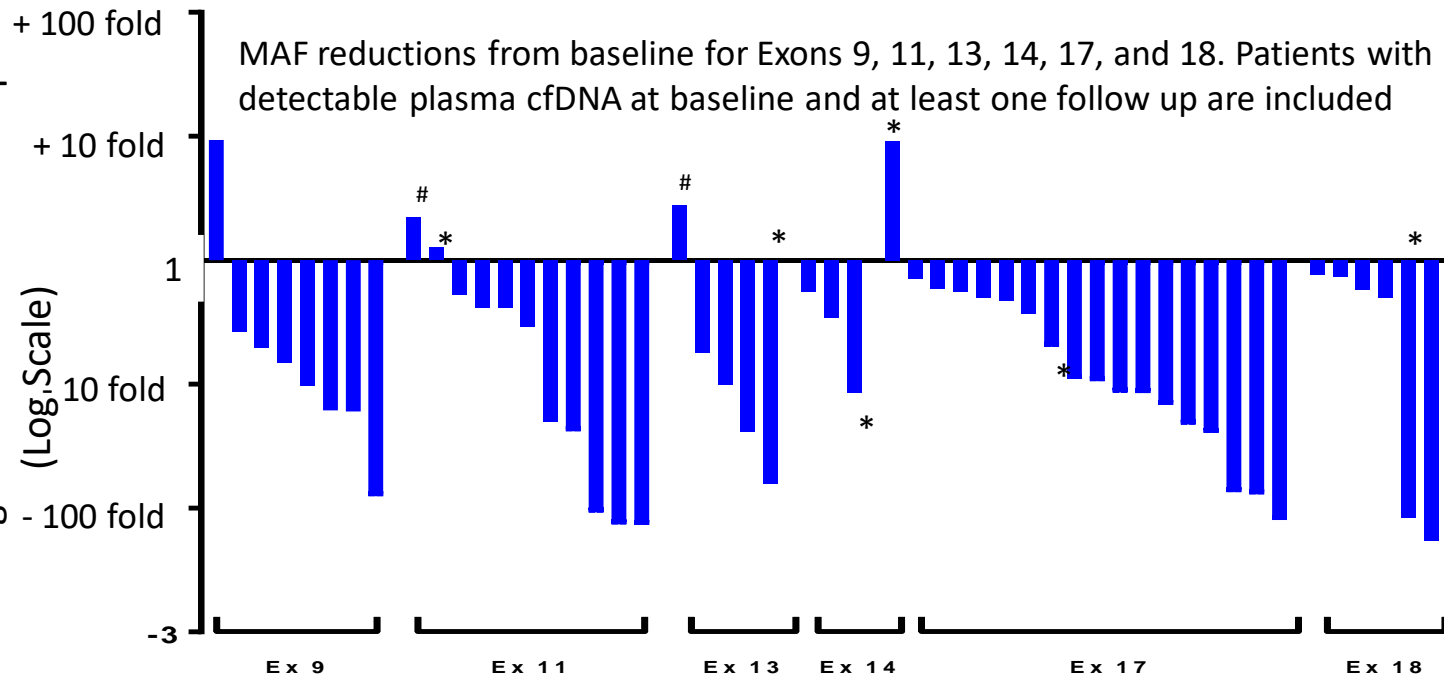
## Time-to –treatment failure: NGS

ctDNA low -	3.6 months
ctDNA high -	1.8 months
	(p=0.01)

Most frequent **emergent** aberrations detected at **progression** were ***ARID1A*** mutations (25%) and ***TP53*** mutations (25%)

# Changes in *KIT*-mutated Plasma cfDNA as a PD Marker in Heavily Pretreated GIST Treated with Allosteric *KIT* inhibitor DCC-2618

Best Fold Change in Mutation Allele Frequency (Log<sub>2</sub>Scale)



- Enrolled patient population reveals broad range of *KIT* mutations
- DCC-2618 leads to reductions in MAF in cfDNA across all exons associated with resistance
- Treatment decisions were made based on disease control and not on changes in MAF

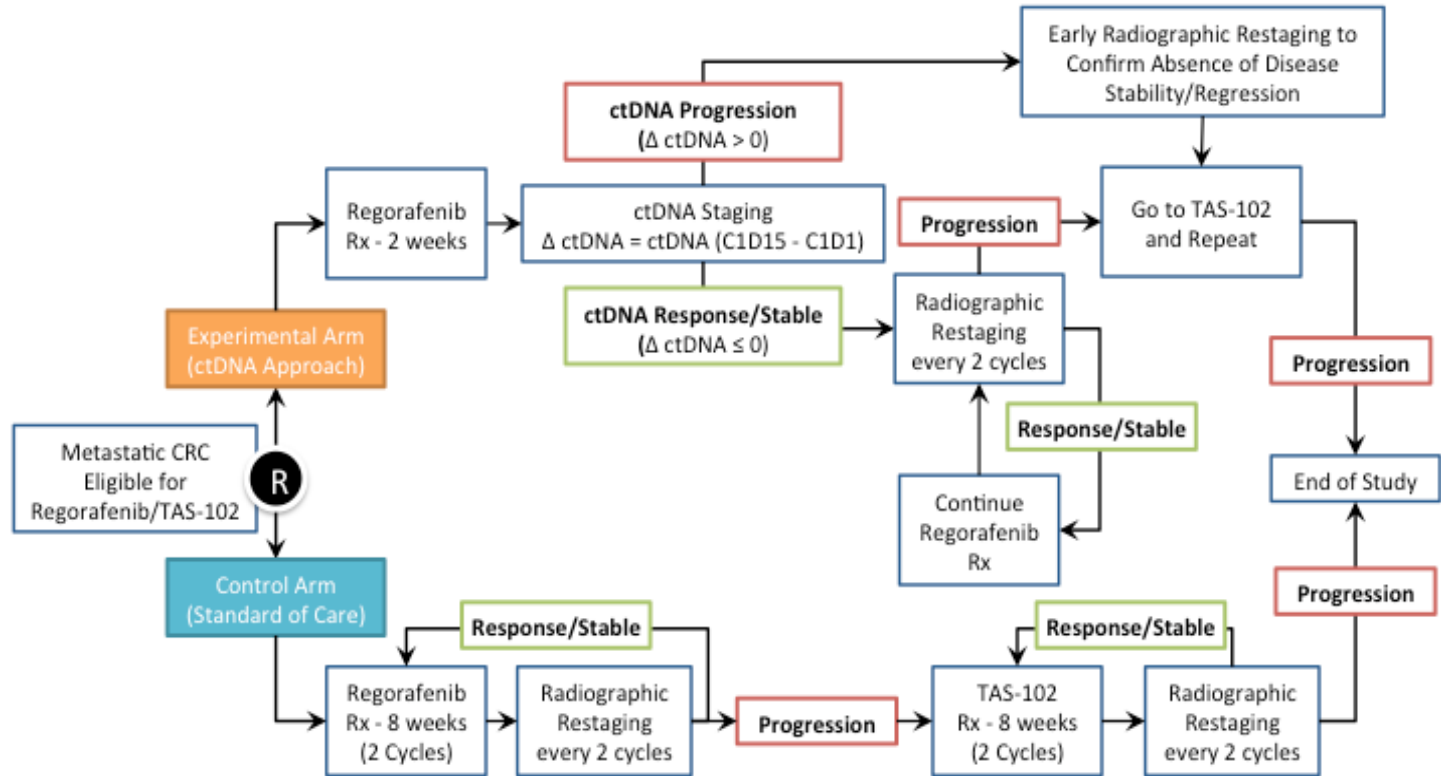
Baseline CT



CT after C2



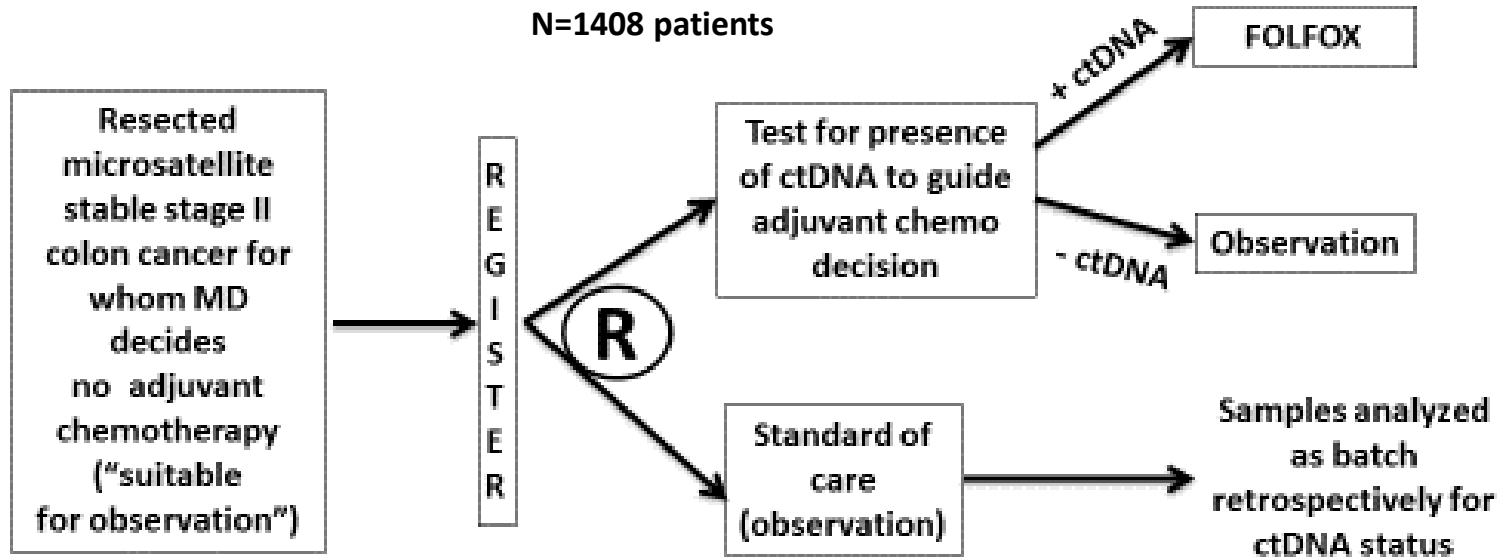
# TACT-D schema



Currently enrolling at MD Anderson as a single-site study

Patients can have treatment at home with ctDNA kits mailed to GuardantHealth

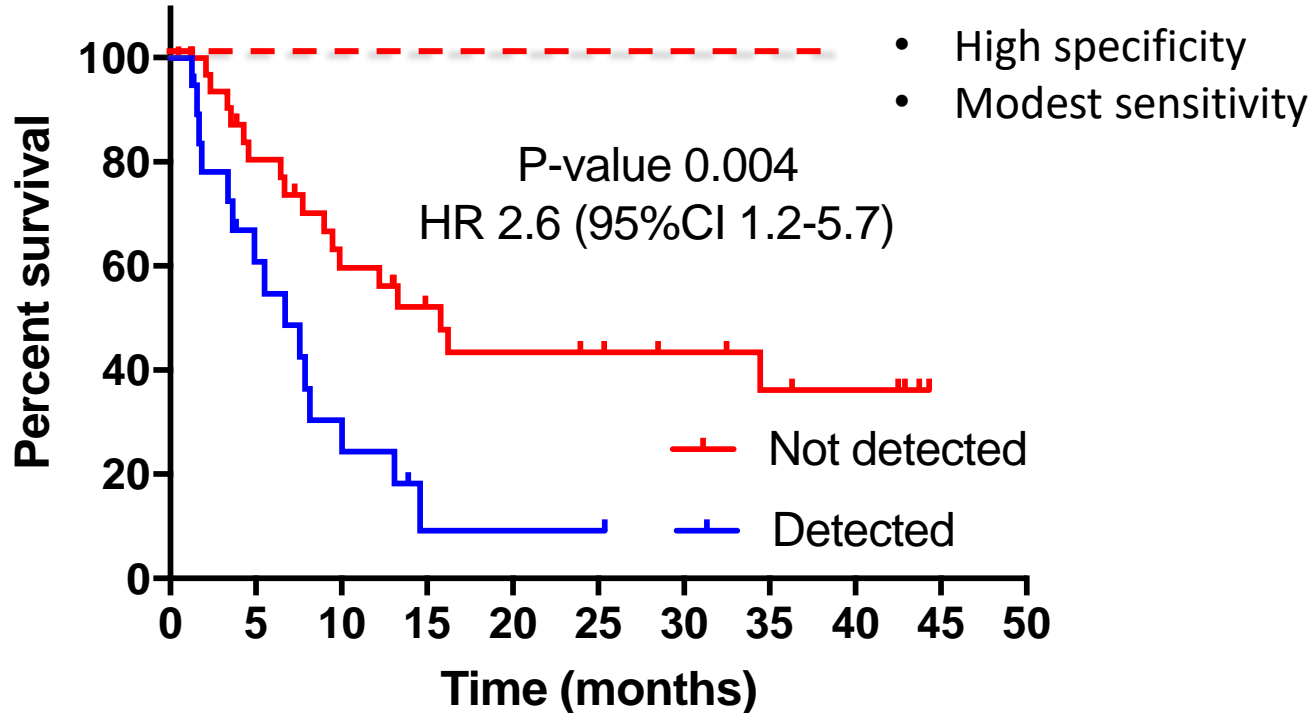
# NRG GI-005 schema



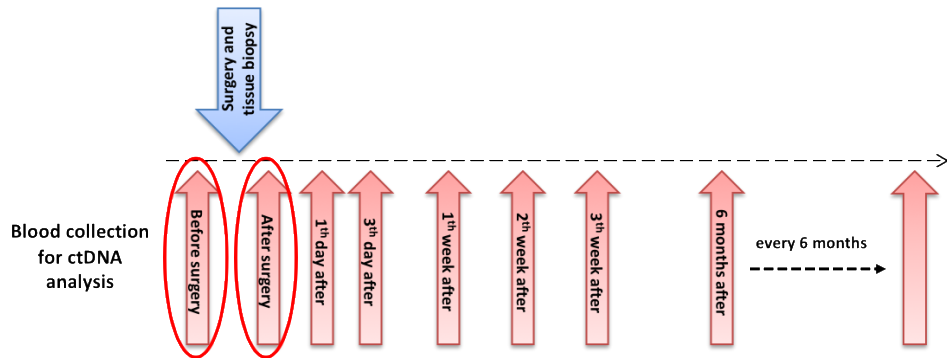
Protocol approved by CTEP/CIRB, with expected activation by 5/2019 across all US and Canadian cooperative groups.

GuardantHealth LUNAR assay – assessing combination of somatic mutations and CRC-specific methylation profiles- will be utilized for study conduct.

# NGS in Post-Operative Recurrence Detection in Stage IV Colorectal Cancer

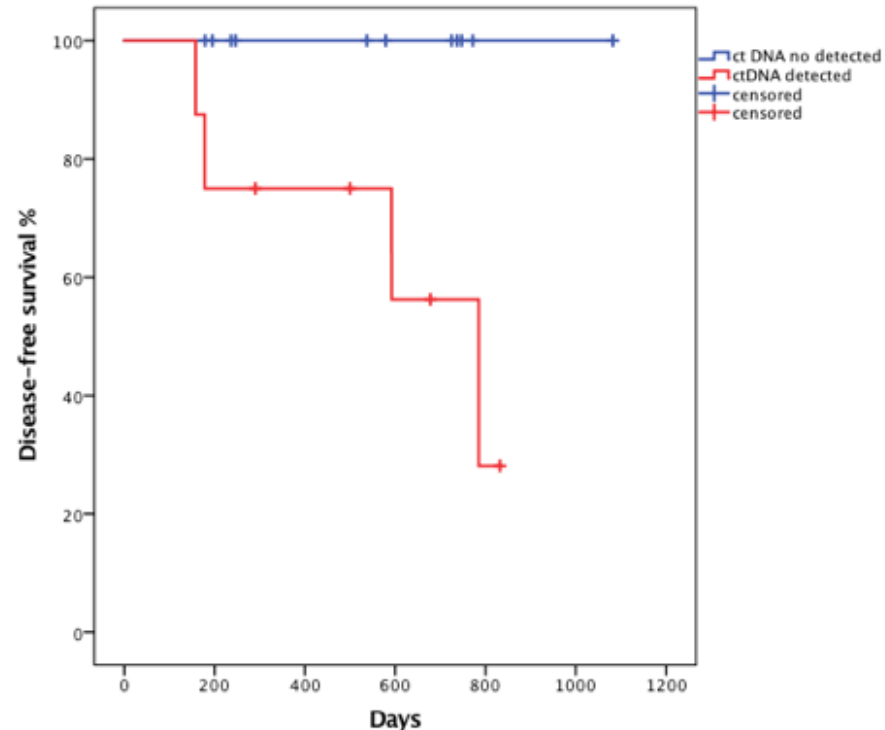


# Ultrasensitive Detection of Circulating Tumor DNA Identifies Patients in High Risk of Recurrence in Early Stages Melanoma (N=23)



***BRAF*<sup>V600E</sup> mutations in ctDNA and melanoma recurrence in 19 patients with available data**

Category	Number	Disease Recurrence (%)	P value
<i>BRAF</i> <sup>V600E</sup> in tissue	23	4 (17)	-
<i>BRAF</i> <sup>V600E</sup> in ctDNA before surgery	11	2 (18)	NS
No <i>BRAF</i> <sup>V600E</sup> in ctDNA before surgery	8	2 (25)	
<i>BRAF</i> <sup>V600E</sup> in ctDNA after surgery	8	4 (50)	<b>0.02</b>
No <i>BRAF</i> <sup>V600E</sup> in ctDNA after surgery	11	0 (0)	



**Patients with ctDNA in samples collected after surgery had shorter Disease-free survival than patients without ctDNA (P=0.03)**

# Methods of ctDNA detection

## Somatic alteration sequencing

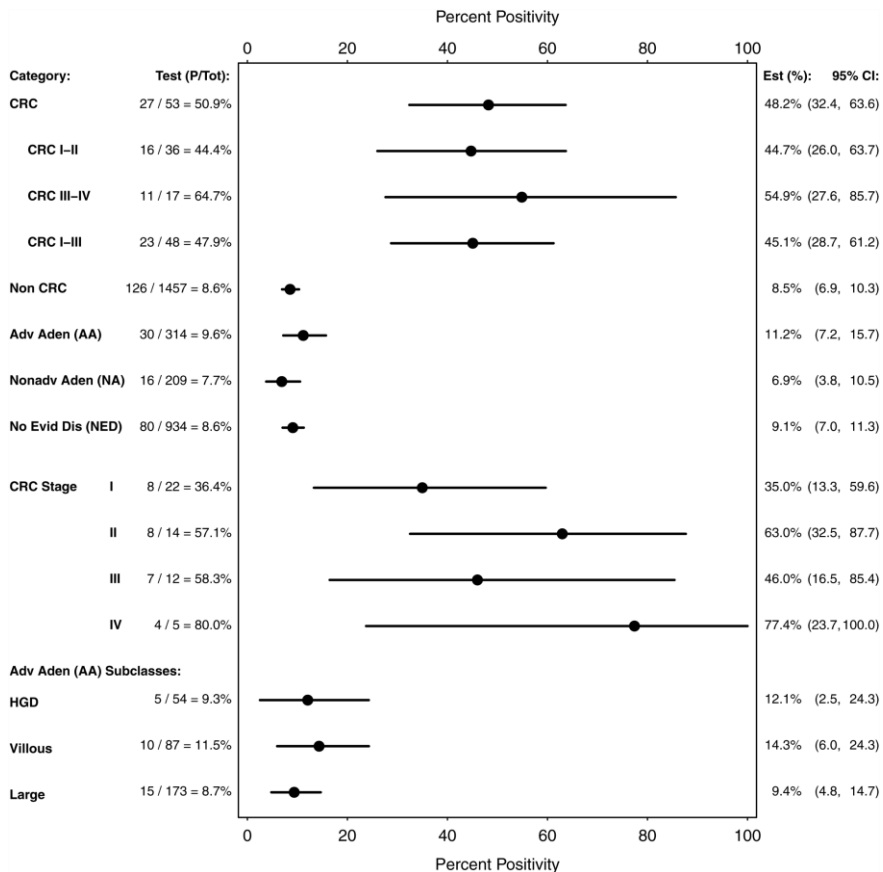
1. Most studied
2. Can detect targets for cancer therapy
3. Lower sensitivity in the absence of recurrent alterations
4. Lower sensitivity in early stages

## Detection methylation changes

1. Tissue and cancer type specific
2. Independent on somatic alterations
3. High DNA degradation during bisulfite conversion

# Testing for mSEPT9 in plasma cfDNA in subjects in colorectal cancer screening

7,941 subjects undergoing screening colonoscopy



	Epi proColon			Total
	Negative	Positive		
Colonoscopy	CRC	14	30	44
	Non-CRC	1182	318	1500
	Total	1196	348	1544

Sensitivity = 68.2% (95% CI, 53.4–80.0)

Specificity = 78.8% (95% CI, 76.7–80.8)

Negative Predictive Value (NPV) = 99.7% (CI, 99.6–99.8)

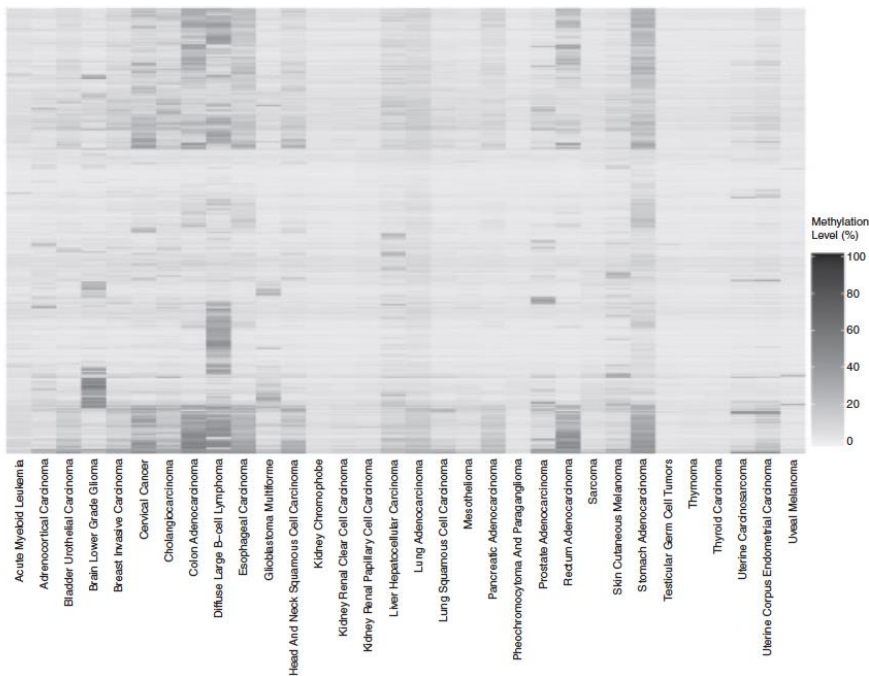
Positive Predictive Value (PPV) = 2.4% (CI, 2.0–3.0)

**Epi proColon test approved by FDA in 2016**

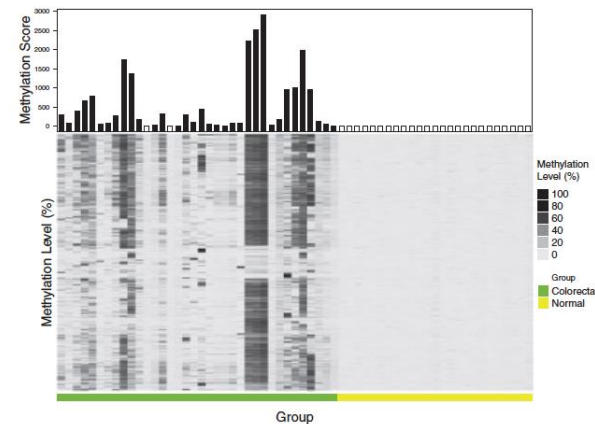


# Targeted Methylation Sequencing (9,223 CpG sites) of Plasma cfDNA in Advanced Cancer

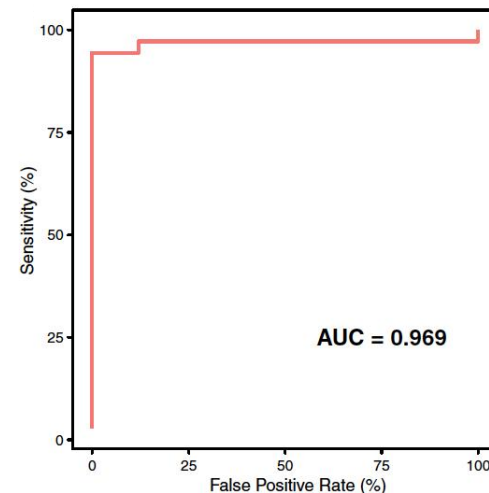
Heat map of methylation profiling in 32 cancers based on TCGA



Assay performance in plasma cfDNA samples from patients with colorectal cancer and healthy controls

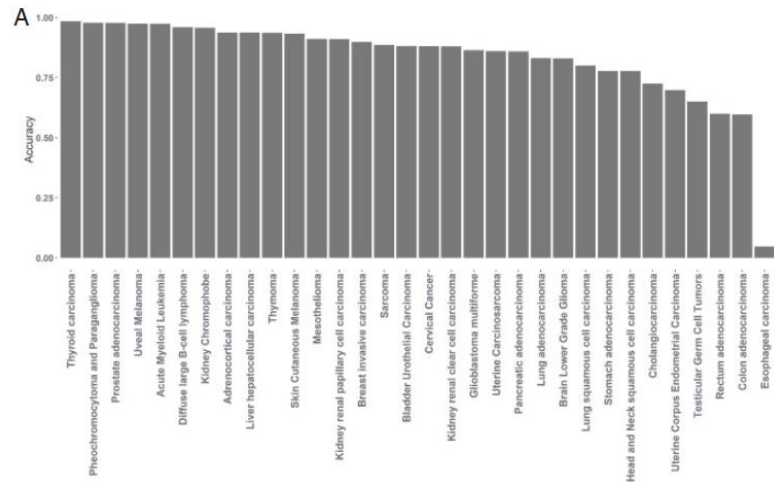


ROC curve for colorectal cancer



# Targeted Methylation Sequencing (9,223 CpG sites) of Plasma cfDNA in Advanced Cancer

Predicting tissue of origin in 32 cancer types in TCGA set (overall accuracy 83.5%)



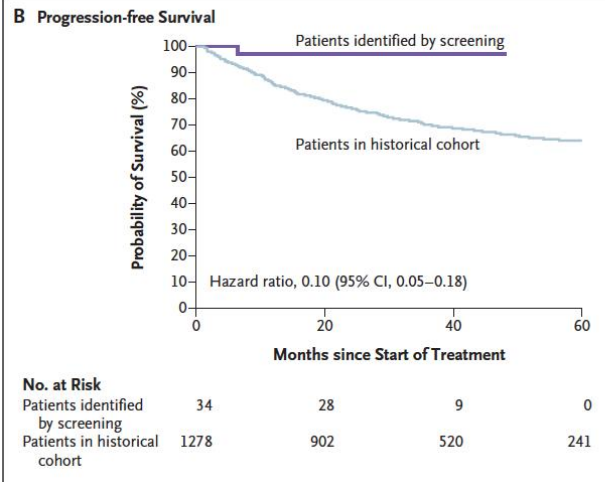
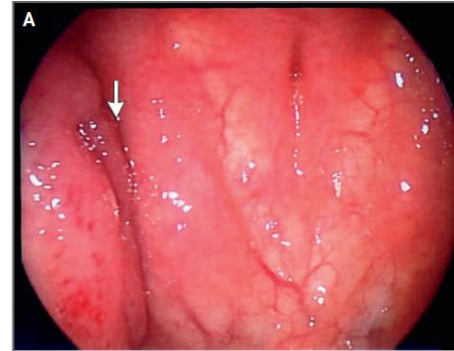
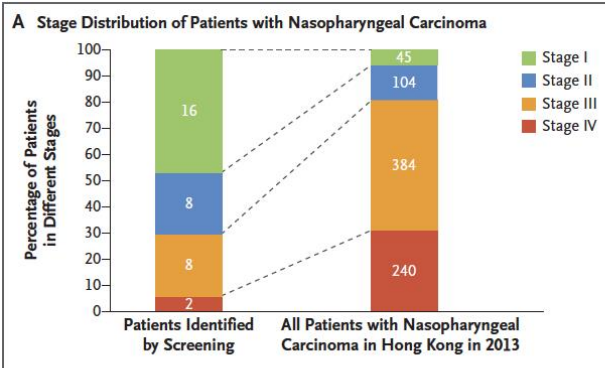
Clinical Validation in Breast Cancer, Colorectal Cancer, Lung Cancer and Melanoma

Plasma samples collected from patients off-therapy					
		Actual class			
		Breast (n=12)	Colorectal cancer (N=27)	NSCLC (N=18)	Melanoma (N=11)
Predicted Class <sup>1</sup>	AML	2	0	0	0
	Breast	8	0	0	0
	Colorectal	1	23	0	0
	Cholangiocarcinoma	0	0	0	1
	Esophageal	0	0	0	1
	Liver	0	1	1	1
	Lung	0	0	9	0
	Lymphoma	0	1	0	0
	Melanoma	0	0	0	5
	Pancreatic	0	1	0	0
	Sarcoma	0	0	1	1
	Stomach	0	0	0	0
	Not cancer	1	1	7	2
	<b>Total</b>	<b>12</b>	<b>27</b>	<b>18</b>	<b>11</b>
Accurate classification of cancer irrespective of cancer type		<b>91.7%</b>	<b>96.3%</b>	<b>86.8%</b>	<b>81.8%</b>
Accurate to classification of cancer type (out of set classified as cancer)		<b>72.7%</b>	<b>88.5%</b>	<b>76.3%</b>	<b>81.8%</b>

<sup>1</sup> Each sample was evaluated against 24 cancer type signatures. Cancer types to which no samples were as signed are not listed in this table.

<sup>2</sup> Non-small cell lung cancer.

# Plasma EBV DNA in Screening of Nasopharyngeal Carcinoma



# CONCLUSIONS

- ❑ Liquid biopsies help to further advance personalized targeted therapy and immunotherapy by offering a source of easily obtainable material for mutation analysis.
- ❑ Liquid biopsies have a potential to be used in efficacy assessment especially if imaging cannot be used or the interpretation is problematic.
- ❑ Liquid biopsies can be used for monitoring of molecular profile and clonal evolution in patients undergoing cancer therapy to detect mechanisms of resistance.
- ❑ Liquid biopsies can be used to address pharmacodynamic endpoints in clinical trials.
- ❑ Liquid biopsies have potential to determine prognosis, early detection , detect early recurrence and disease progression.



[fjanku@mdanderson.org](mailto:fjanku@mdanderson.org)



# Acknowledgements

## ICT faculty (past and current)

- Dr. Funda Meric-Bernstam
- Dr. Razelle Kurzrock
- Dr. David Hong
- Dr. Aung Naing
- Dr. Gerald Falchook
- Dr. Jennifer Wheler
- Dr. Apostolia Tsimberidou
- Dr. Stacy Moulder
- Dr. Siqing Fu
- Dr. Sarina Piha-Paul
- Dr. Vivek Subbiah
- Dr. Ralph Zinner
- Dr. Dan Karp
- Dr. Timothy Yap
- Dr. Jordi Rodon
- Dr. Shubham Pant
- Dr. Shumei Kato

## ICT fellows, trainees, ICT research staff

- Dr. Takeo Fujii
- Dr. Cathy Dumbrava
- Dr. Lino Mohrmann
- Dr. Adam Jassowicz
- Jindrich Polivka Jr.

## ICT Lab and Team Janku (past and current)

- **Dr. Helen Huang**
- Goran Cabrilo and collection team
- Kiran Madwani,
- Anjali Raina
- Guo Chen, Giovanni Nitti
- Veronica Holley, Nishma Ramzanali
- Vanda Stepanek

## Division of Cancer Medicine

- Dr. Patrick Hwu
- Dr. Waun Ki Hong

## GI, Melanoma Oncology

- Dr. Scott Kopetz
- Dr. Van Morris
- Dr. Sapna Patel
- Dr. Isabella Glitza

## Molecular Diagnostic Lab

- Dr. Raja Luthra
- Dr. Stan Hamilton

## Translational Oncology

- Dr. Ignacio Wistuba

## Charles University, Czech Republic

- Jiri Polivka, Jr.
- Dr. Martin Pesta

## IRCCS, NCC

- Dr. Alberto Bardelli
- Dr. Andrea Sartore Bianchi

## USC

- Dr. Afsaneh Barzi
- Dr. Heinz Lenz

## UCLA

- Dr. Andrew Gianoukakis

## BioRad

- Dr. George Karlin-Neumann
- Dr. Dawne Shelton
- Dr. Paula Stonmetz

## Trovagene

- Dr. Cecile Rose Vibat
- Dr. Mark Erlander
- Dr. Vlada Melnikova

## illumina

- Dr. Li Liu
- Dr. Jian-Bing Fan
- Dr. Neeraj Salathia, Dr. Shile Zhang

## Funding

- Sidney Kimmel Foundation
- Khalifa Foundation
- NCI/NIH
- Elsa U Pardee Foundation
- UT Brain
- MD Anderson GBM Moon Shot
- MD Anderson IRG
- ECD Global Alliance
- Norris Foundation
- Sabin Family Foundation
- Rising Tide Foundation

**OUR PATIENTS AND  
THEIR FAMILIES**