



**NCCN 2021 Virtual Congress:
Biomarkers in Solid Tumors**

**Friday, November 12, 2021
4:40 PM – 5:25 PM EST**

What's on the Horizon?

Jennifer J.D. Morrisette, PhD

*Abramson Cancer Center
at the University of Pennsylvania*

Aparna R. Parikh, MD, MS

Massachusetts General Hospital Cancer Center

David T. Ting, MD

Massachusetts General Hospital Cancer Center



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What's on the Horizon?

Biomarkers in Solid Tumors

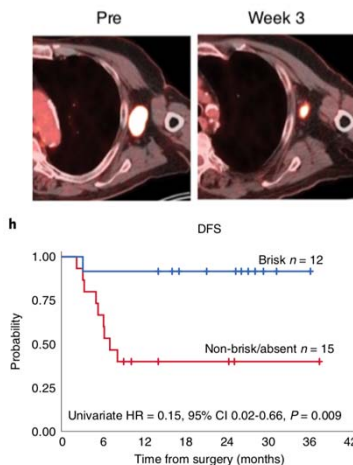
Jennifer J.D. Morrisette, PhD

Abramson Cancer Center at the University of Pennsylvania

New applications of known technologies

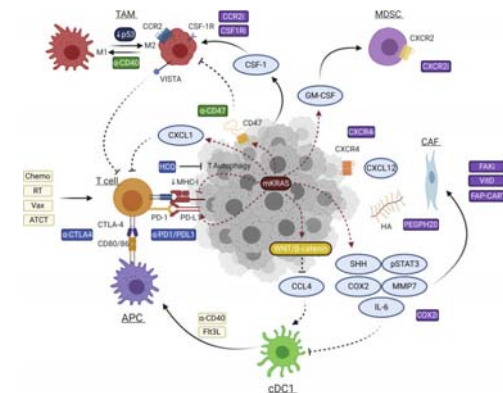
► Immunotherapy

- Currently using markers like microsatellite instability (MSI) and tumor mutational burden (TMB) with PDL1 IHC to assist in identifying patients likely to respond to IO
- Future: capturing data from the TME
 - Immune system as a “sensory organ”: immune profiling to capture “brisk” responders to IO
 - Cellular therapy to target driver mutations in solid tumors



Melanoma patients:

- Immune responses in blood to predict tumor responses
- Single dose of immunotherapy
- Key immune correlates



Bear et al Cancer Cell. 2020. 38:788-802.. PMID: 32946773

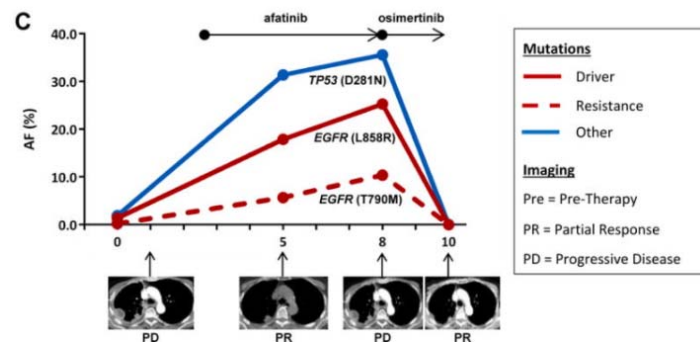
Bear et al Nat Commun. 2021 12:4365. PMID: 34272369;

Byrne et al Clin Cancer Res. 2021. 27:4574-4586. PMID: 34112709.

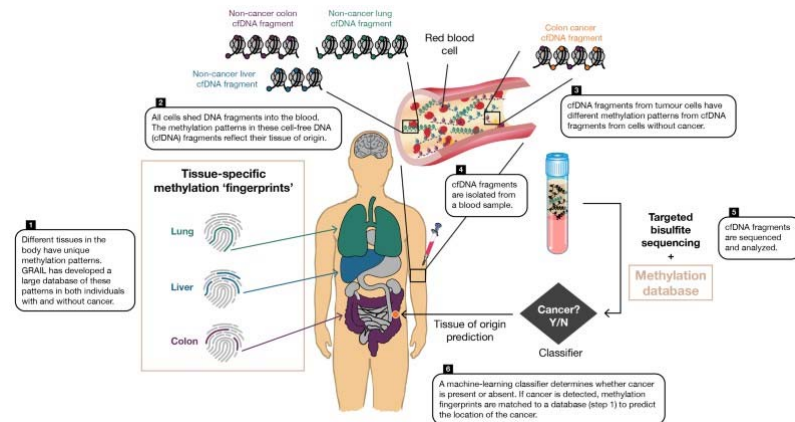
New applications of known technologies

► Circulating tumor DNA (ctDNA)

- Currently using to detect disease associated variants at diagnosis and through monitoring
- Future:
 - Early detection of cancers (presymptomatic)
 - Definitive surgical resection [discussed next by Dr. Aparna Parikh]



Thompson et al Clin Cancer Res. 2016. 22:5772-5782. PMID: 27601595

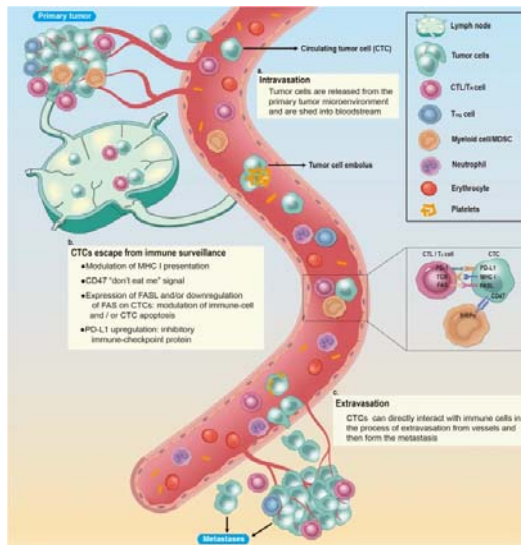


Ofman J et al. Nature Portfolio. Sponsor Feature. 25 Mar 2020.
<https://www.nature.com/articles/d42473-020-00079-y>.

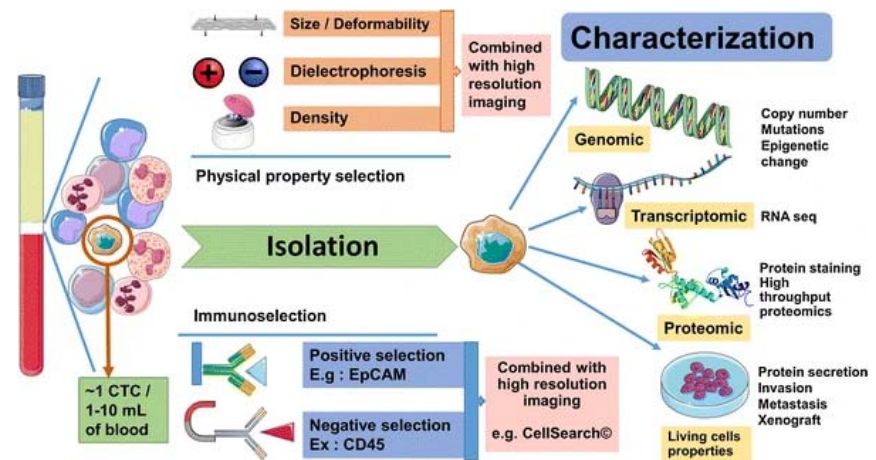
New applications of known technologies

► Circulating tumor cells (CTCs)

- Current: FDA-approved: CTCs counts associated with PFS and OS in metastatic prostate, colorectal and breast cancer
- Future: identifying EMT transition associated with chemoresistance [discussed by Dr. David Ting]



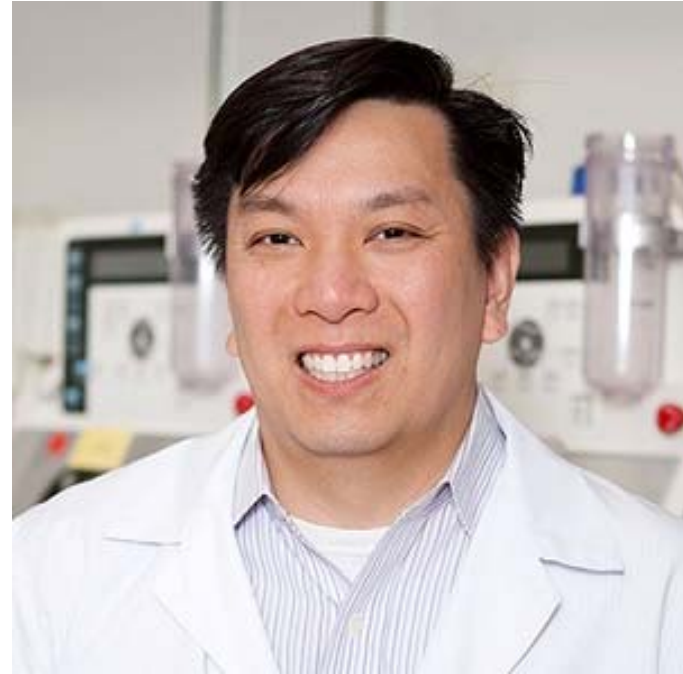
Zhong et al. *Mol Cancer* **19**, 15 (2020).



Cabel et al. *Int J Clin Oncol* **22**, 421-430 (2017).



Aparna R. Parikh, MD, MS



David T. Ting, MD





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Biomarkers in Solid Tumors**

What's on the Horizon?

Liquid Biopsies in Colorectal Cancer

Aparna R. Parikh, MD, MS

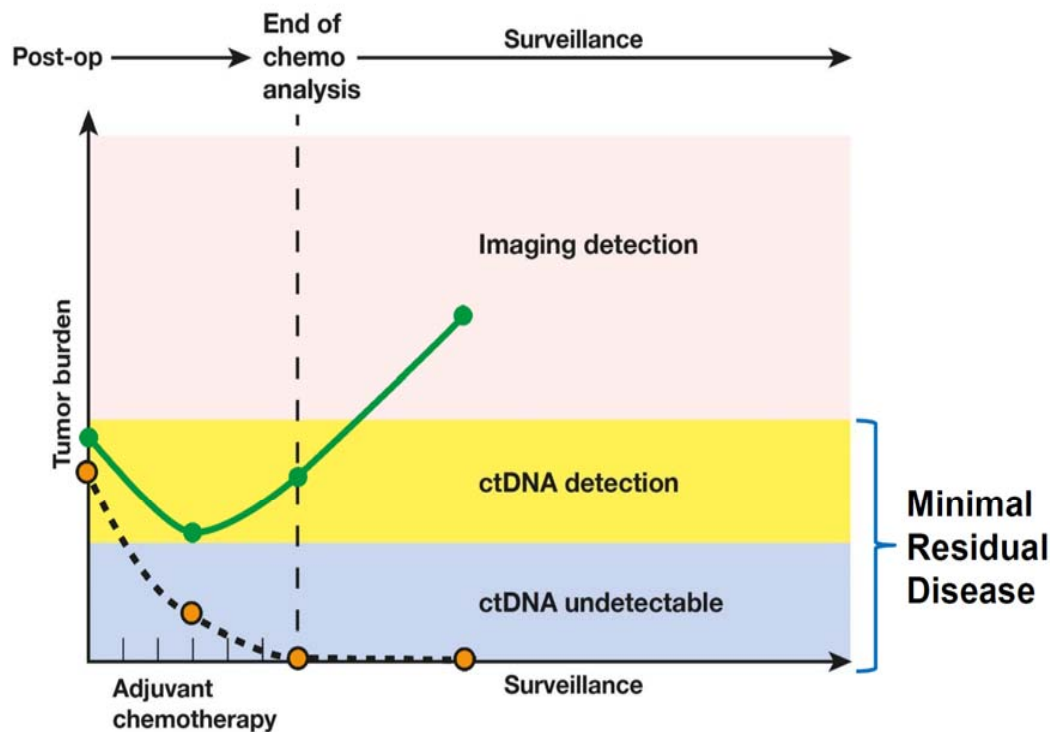
Massachusetts General Hospital Cancer Center



Minimal Residual Disease in Colorectal Cancer

S

ctDNA Marker of Minimal Residual Disease:

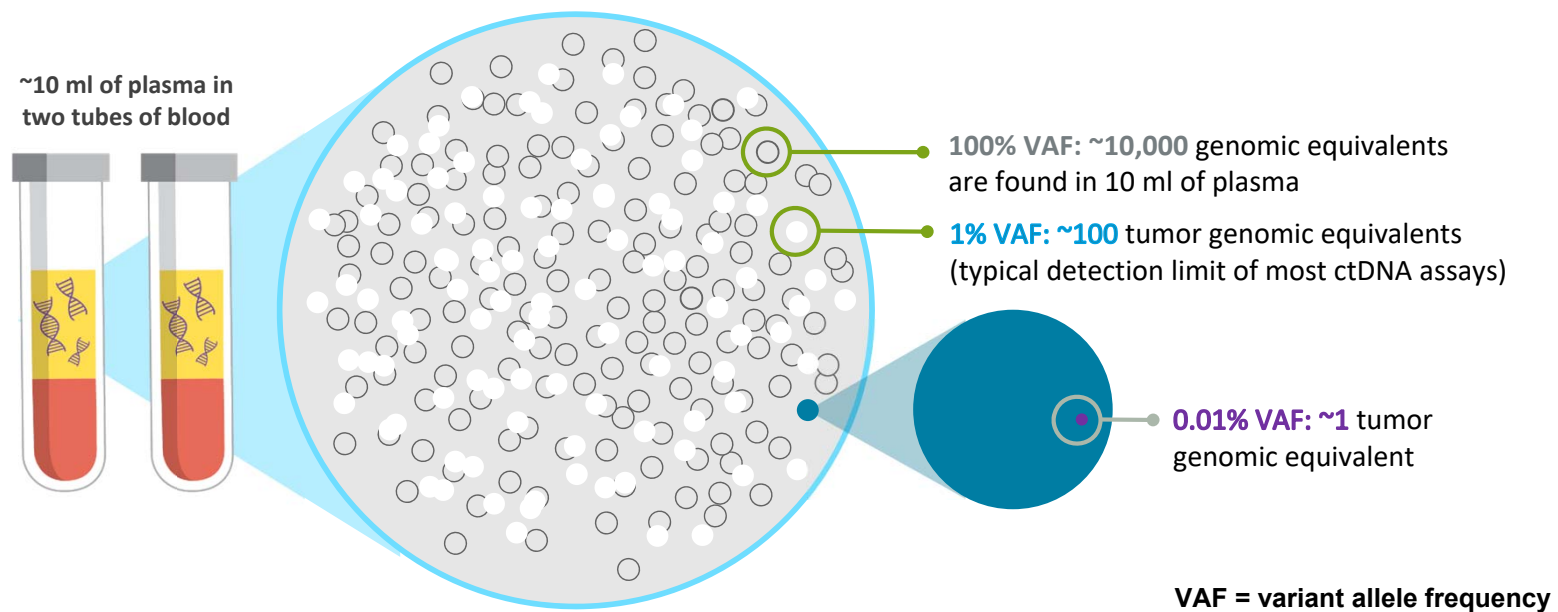


- MRD applications high **positive predictive value (low false positives)** for recurrent disease in patients with ctDNA detected in the “adjuvant” setting
- **Defines molecular persistence of disease**
 - Stage I-III patients with ctDNA+ after definitive interventions should be considered as a Stage IV minimal residual disease, or Stage IV MRD

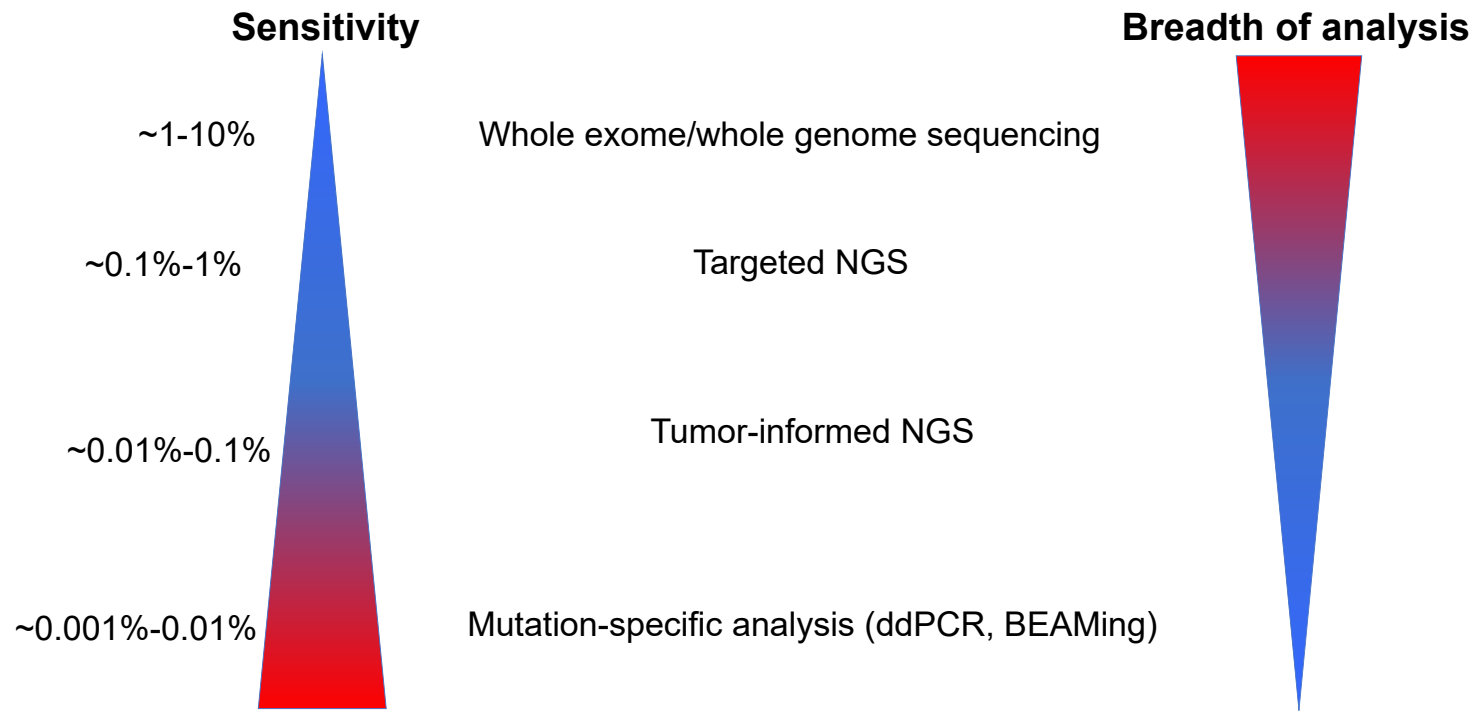
Dasari A, Grothey A, Kopetz S. J Clin Oncol. 2018.; Kasi P, The 2019 Gastrointestinal Oncology Conference. October 10-11, 2019. Arlington, VA.

Detection Down to as Few as One Genomic Equivalent in 10 ml of Plasma (VAF = 0.01%) Critical

Higher blood volumes may improve performance but requires prospective studies



Methods for ctDNA Analysis





Case 1

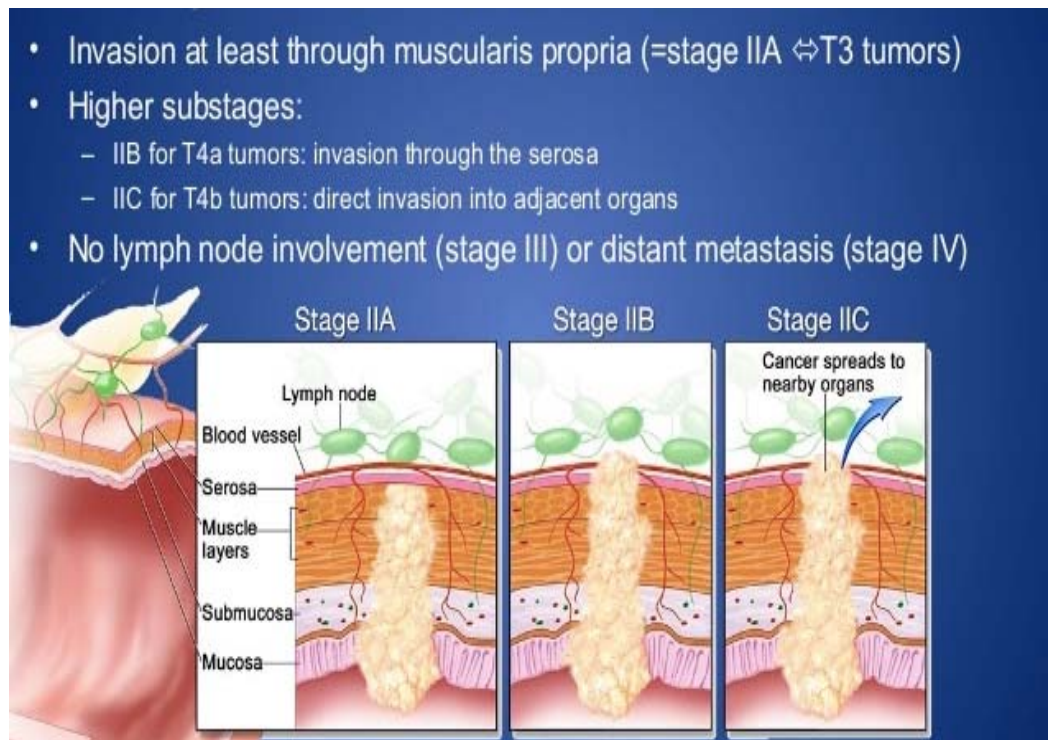
29-year-old male musician no family history presents with rectal bleeding

- **Colonoscopy**
Sigmoid Mass
MSS adenoCA
- **LAR**
Stage II CRC
Path T3N0
0/26 nodes
Tumor Budding Score of 12
Poorly Differentiated



Stage II CRC

- Nearly 100K cases of CRC annually
- 25% of diagnosed cases are Stage II
- 20-30% of patients with Stage II CRC receive adjuvant chemotherapy
- Most cured by surgery alone
- Overall benefit of adjuvant chemotherapy in stage II colon cancer is marginal (~5%) in an unselected population
- Reduces risk of death 5FU 3-3.5 %
- Many patients “overtreated” with associated risk/toxicity of chemotherapy



PDQ Adult Treatment Editorial Board. Colon Cancer Treatment (PDQ®): Health Professional Version. 2021 Aug 13. In: PDQ Cancer Information Summaries [Internet]. Bethesda (MD): National Cancer Institute (US); 2002-. [Table], Table 4. Definitions of TNM Stages IIIA, IIB, and IIICa. Available from: https://www.ncbi.nlm.nih.gov/books/NBK65858/table/CDR0000062687__580/

Decisions in Stage II are Dizzying

6m of oxaliplatin-based treatment is option in high-risk Stage II

NCCN
recommends
consideration of
adjuvant
chemotherapy
(5-FU or
FOLFOX)
for patients with
“high-risk” colon
cancer

T4, inadequate nodal harvest, poorly differentiated, obstruction, perforation, vascular/perineural invasion, tumor budding, margins

FOLFOX ok for Stage II w/ high-risk factors (not for good- or average-risk Stage II)

No survival benefit for addition of oxaliplatin to 5-FU/leucovorin in Stage II

Pooled analysis of high-risk Stage II patients in IDEA collaboration did not show non-inferiority of 3 months compared to 6 months of adjuvant treatment

Duration associated with small (not statistically significant) difference in DFS between 3 and 6 months of CAPEOX

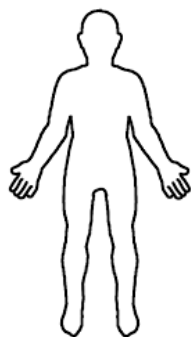
Less grade 3–5 toxicities with 3 months versus 6 months

The NCCN Clinical Practice Guidelines in Oncology (NCCN Guidelines®) Colon Cancer (Version 3.2021). © 2021 National Comprehensive Cancer Network, Inc. Available at: [NCCN.org](https://www.nccn.org).

Minimal Residual Disease: The Problem

Stage III CRC:

All patients get adjuvant chemo
>50% cured by surgery alone



**Curative
Intent
Surgery**

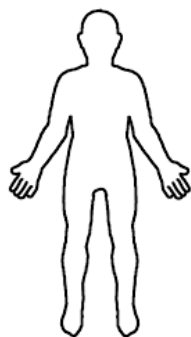
Stage II CRC:

SOC is NO adjuvant chemo
10-15% of patients recur

Minimal Residual Disease: The Problem

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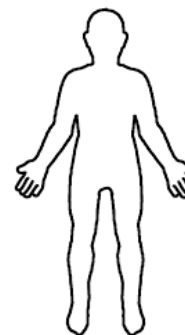
SOC is NO adjuvant chemo
10-15% of patients recur

Negative



None

Cured

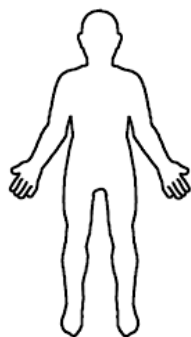


Minimal Residual Disease

Minimal Residual Disease: The Problem

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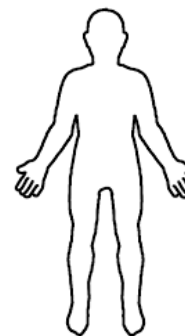


Positive

None



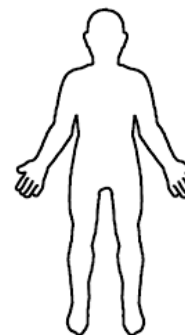
Cured



Present



Not
Cured



Minimal Residual Disease

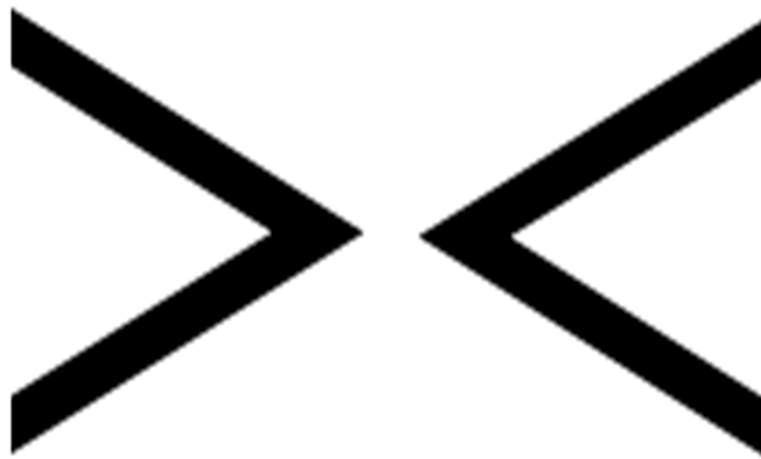
We have no way
to determine
who is cured and
who will recur

Biomarker

There is a need for a **PREDICTIVE BIOMARKER to identify:**

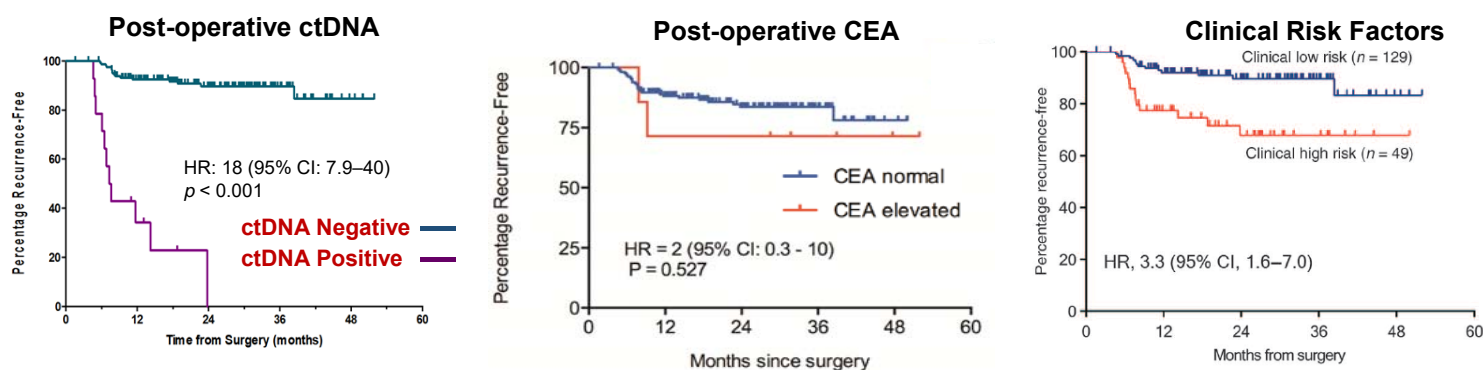
Stage II/III colon cancer patients at **highest risk** for recurrence who may benefit from adjuvant chemotherapy

Those at **lowest risk** who may be exposed to unnecessary chemotherapy



ctDNA is a Prognostic Biomarker in Resected CRC

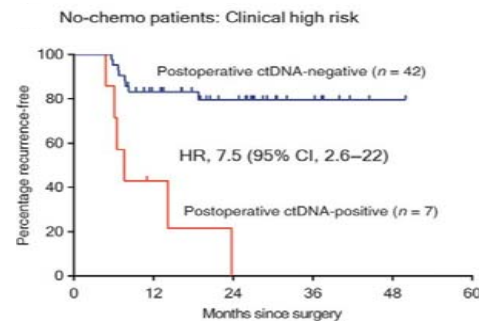
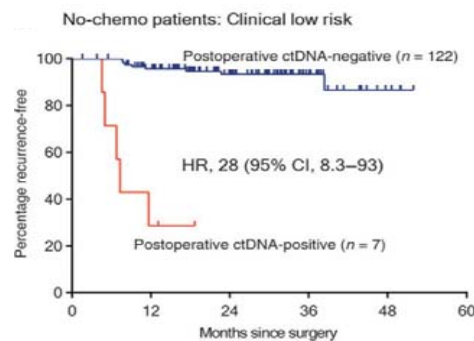
Recurrence-free Survival (Stage II CRC post-resection)



- No consensus for adjuvant chemotherapy for patients with resected stage II colon cancer based on a lack of a predictive biomarker
- Presence of (+) ctDNA postoperatively is associated recurrence
- Despite the prognostic relevance for (+) ctDNA in patients with resected colon cancer, use of ctDNA as a predictive biomarker is not employed currently, **due to the lack of validated prospective data**

Tie J et al, Sci Transl Med. 2016 Jul 6; 8(346): 346ra92

ctDNA is More Prognostic than Standard Risk Factors for Determining Likelihood for Recurrence in Resected Stage II Colon Cancer

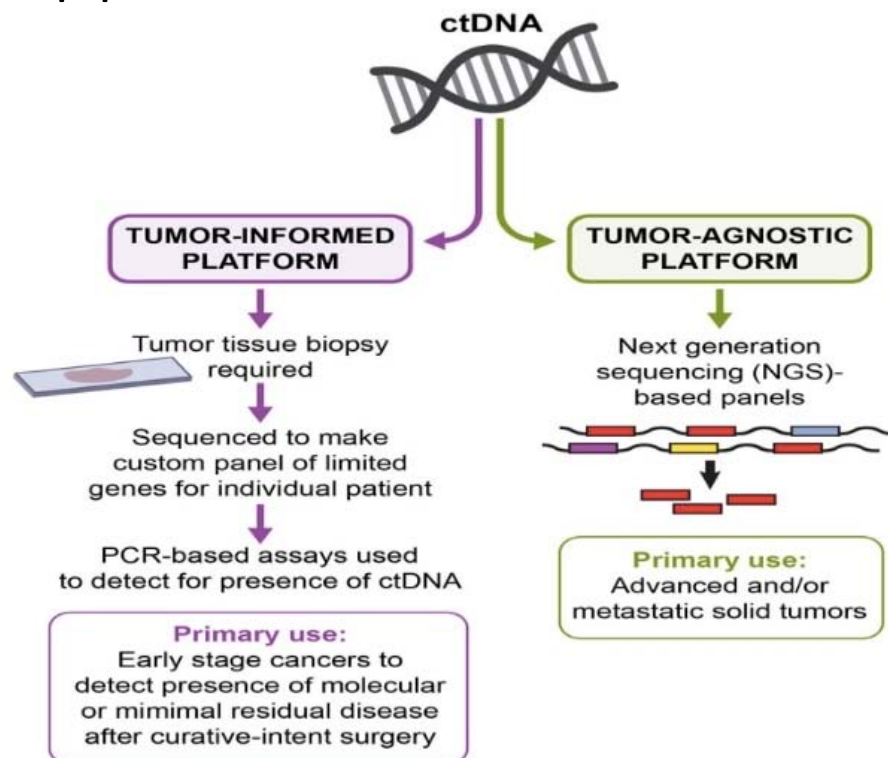
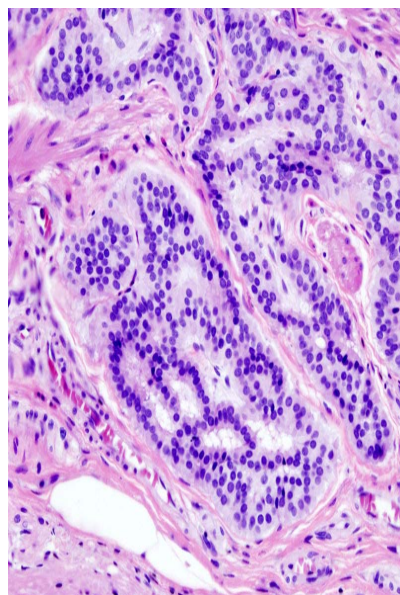


ctDNA(+) status may redefine a patient with stage II colon cancer at “high risk” for recurrence to justify further evaluation with a fluoropyrimidine/oxaliplatin combination

- In 230 patients with resected stage II colon cancer, the detection of postoperative ctDNA outperformed all traditional risk factors traditionally considered for adjuvant chemotherapy selection in identifying patients at high risk for recurrence
- The detection of ctDNA, a surrogate for persistent (microscopic) disease, associates with clinical recurrence within 24 months
- The prognostic implications of ctDNA status link to clinical outcomes, regardless of the traditional “low risk” or “high risk” stratifications

Tie J et al, Sci Transl Med. 2016 Jul 6; 8(346): 346ra92

Generalized Approaches



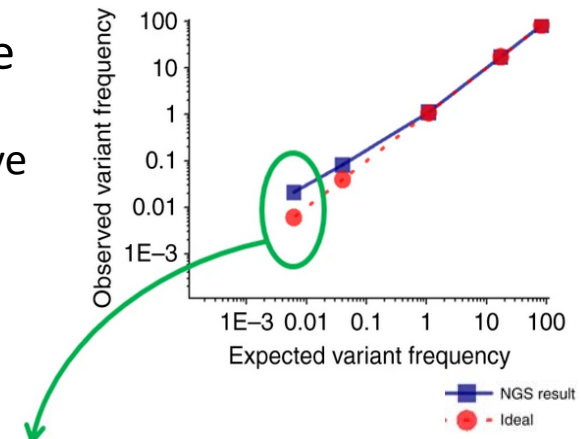
ctDNA: different assays for different purposes

	"Tumor naïve"	"Tumor informed"
Gene coverage	<u>Large panel</u> of commonly altered genes	<u>Limited panel</u> of genes personalized to the patient's tumor
Tissue sequencing required?	No	Yes
Key applications	<ul style="list-style-type: none"> • MRD • Assess heterogeneity • Detect actionable alterations • Identify drivers of resistance • Serial monitoring 	<ul style="list-style-type: none"> • Detect MRD • Assess treatment response • Serial recurrence monitoring
Screens out germline, CHIP alterations?	No*	Yes
Turnaround time	1-2 wks	First test: 2-3 wks (includes tissue WES profiling) Subsequent tests: 1 wk

Tumor Informed Analyses Can Reduce Impact of Assay Error

- Reagents and sequencing error can result in false positive calls

- A small panel can have a million possible false positive nucleotide variants
- When panels are utilized, then bioinformatic efforts are utilized to reduce this error
- As a result, lower limits of detection are impacted to ensure that this noise of the assay can be excluded



- Tumor informed pipelines substantially reduce the spectrum of alterations (i.e. 16 potential variants) allowing theoretically greater sensitivity and reduced risk of false positives

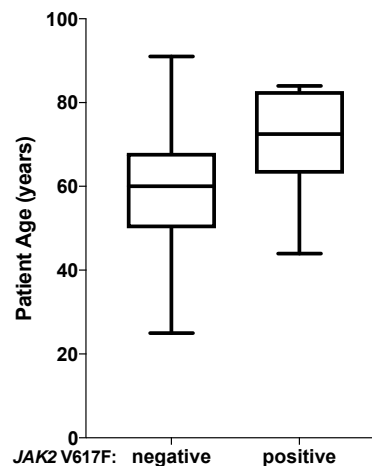
Slide courtesy of Scott Kopetz, MD, PhD

Clonal Hematopoiesis of Indeterminate Potential

JAK2 Mutations as a clear example

Frequency of *JAK2* V617F mutations

cfDNA	16/1397 (1.14%)
TCGA	0/228 (0%)
NHS/HPFS	0/619 (0%)
GENIE	0/1149 (0%)
All tissue cohorts	0/1996 (0%)



... but also TP53

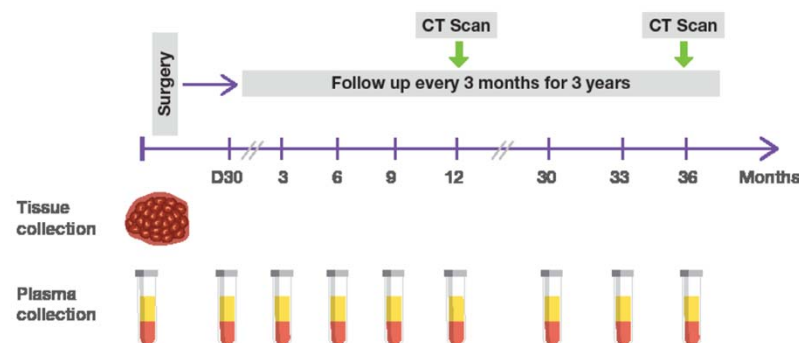


Strickler JH, et al. Cancer Discov. 2018 Feb;8(2):164-173. Kunimoto H, Nakajima H. Int J Hematol. 2017 Jul;106(1):34-44.

Serial ctDNA monitoring: CRC study

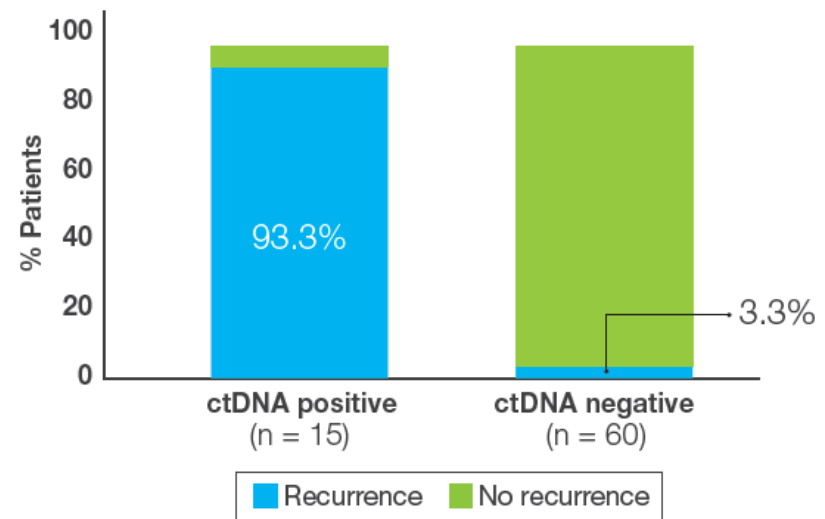
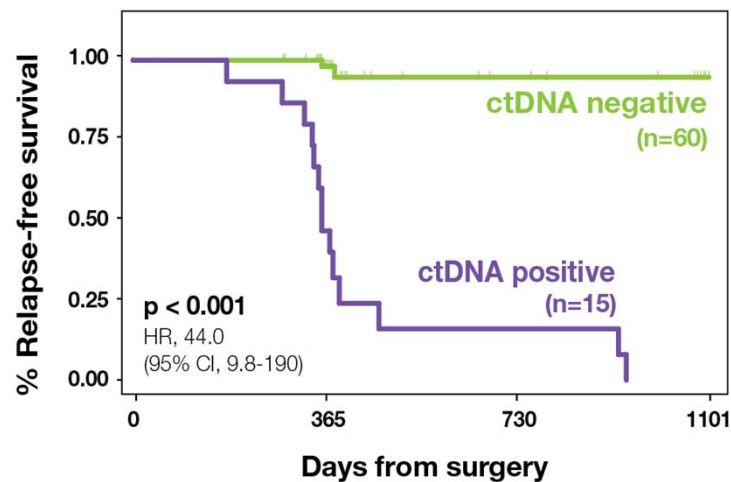
Denmark, May 1, 2014 to January 31, 2017

- 130 patients (**125 eligible**) with stages I-III colorectal cancer
- Treated with curative surgery and optional adjuvant chemotherapy
- **795 plasma samples** were longitudinally collected:
 - at baseline, up to 14 days prior to surgery
 - on post-operative day 30
 - and every third month until death, study withdrawal, or month 36



Reinert et al JAMA Oncology, 2019 May 9;5(8):1124–31

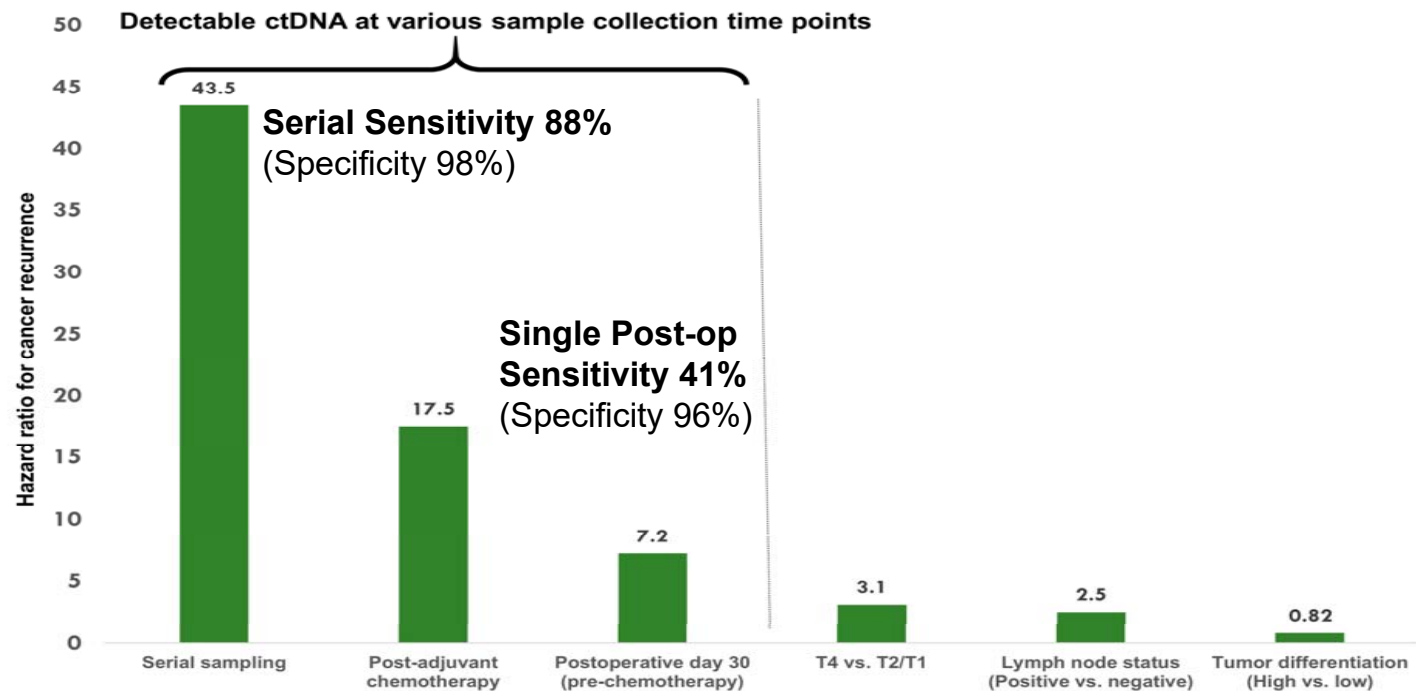
Positive ctDNA Status after Adjuvant Therapy is Highly Predictive of Relapse on Serial Testing



Reinert et al JAMA Oncology, 2019 May 9;5(8):1124-31

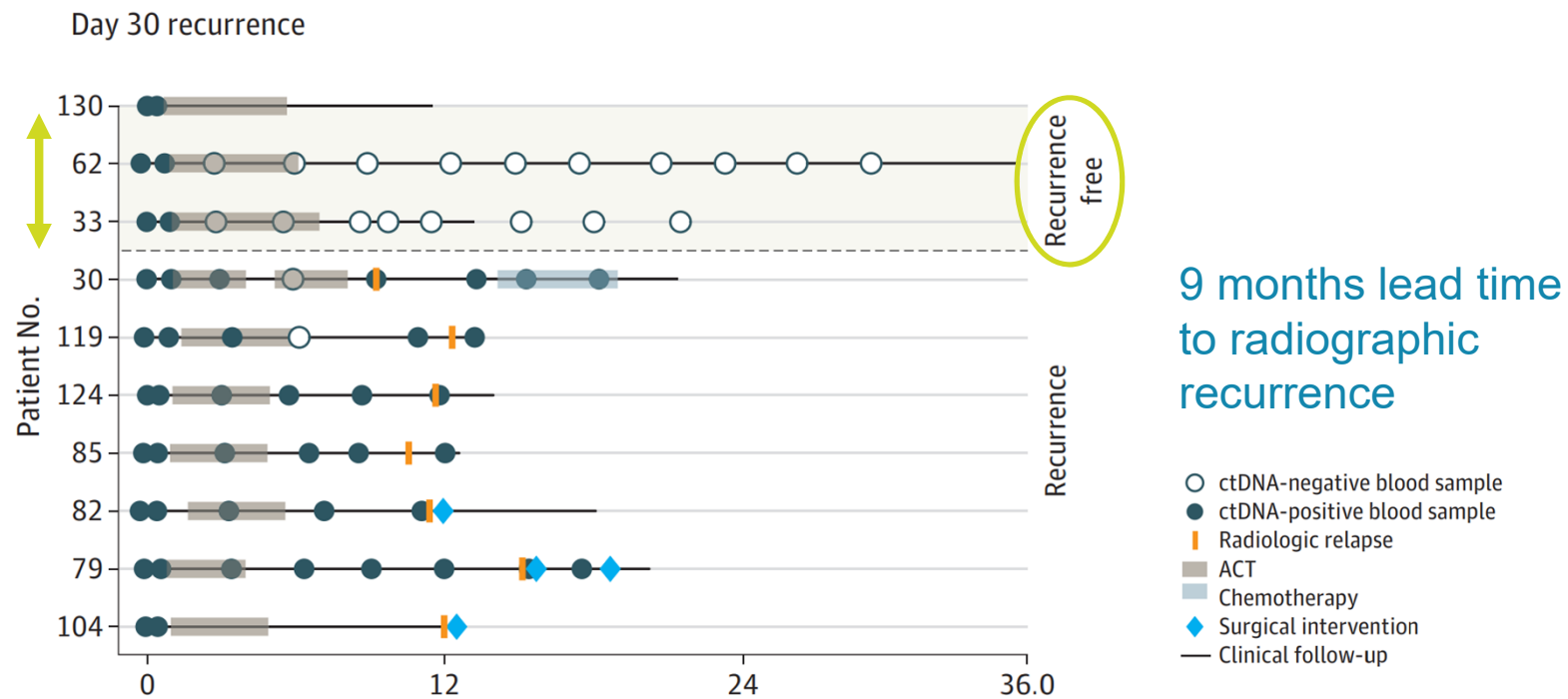
Detectable ctDNA across Various Time Points

ctDNA Outperforms Existing Clinicopathologic Risk Factors as a Prognostic Biomarker



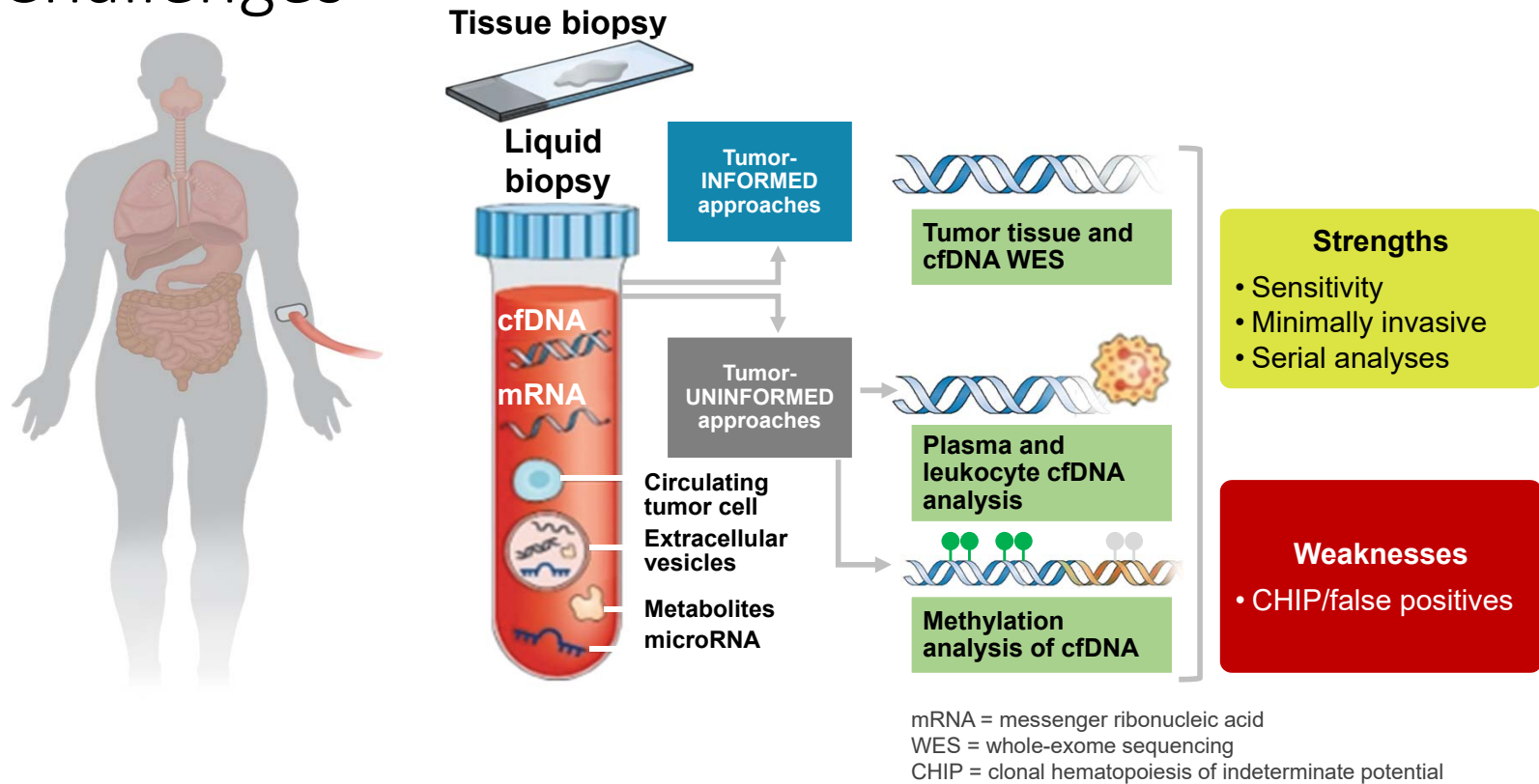
Chakrabarti et al, Cancers (Basel). 2020 Sep 29;12(10):2808

Prognostic and possible predictive of therapeutic response?



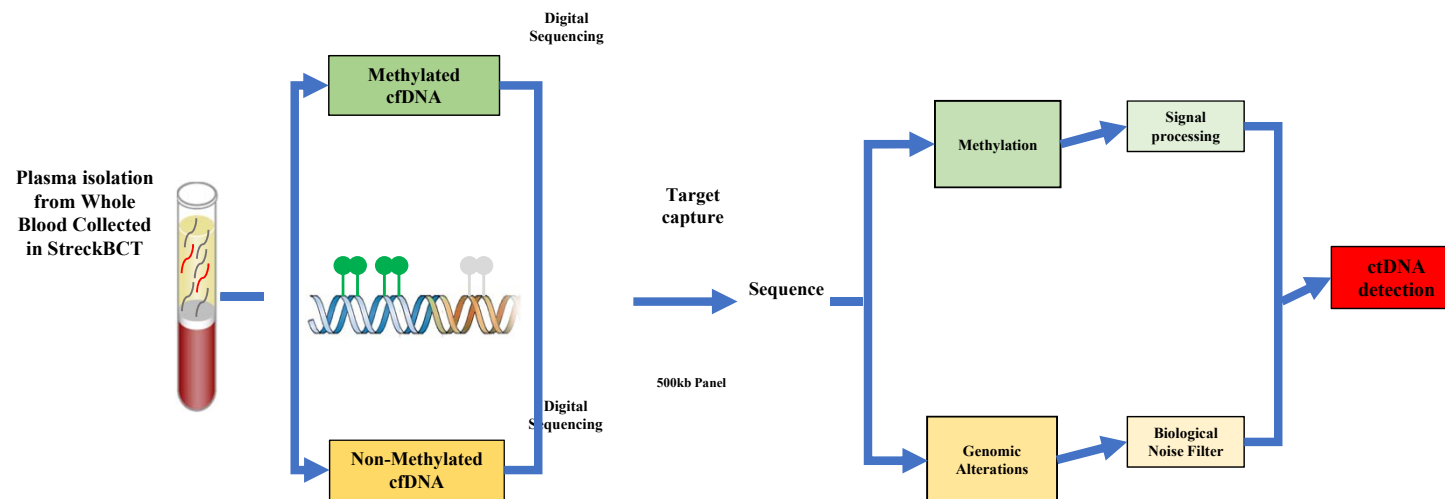
Reinert et al JAMA Oncology, 2019 May 9;5(8):1124–31

Challenges

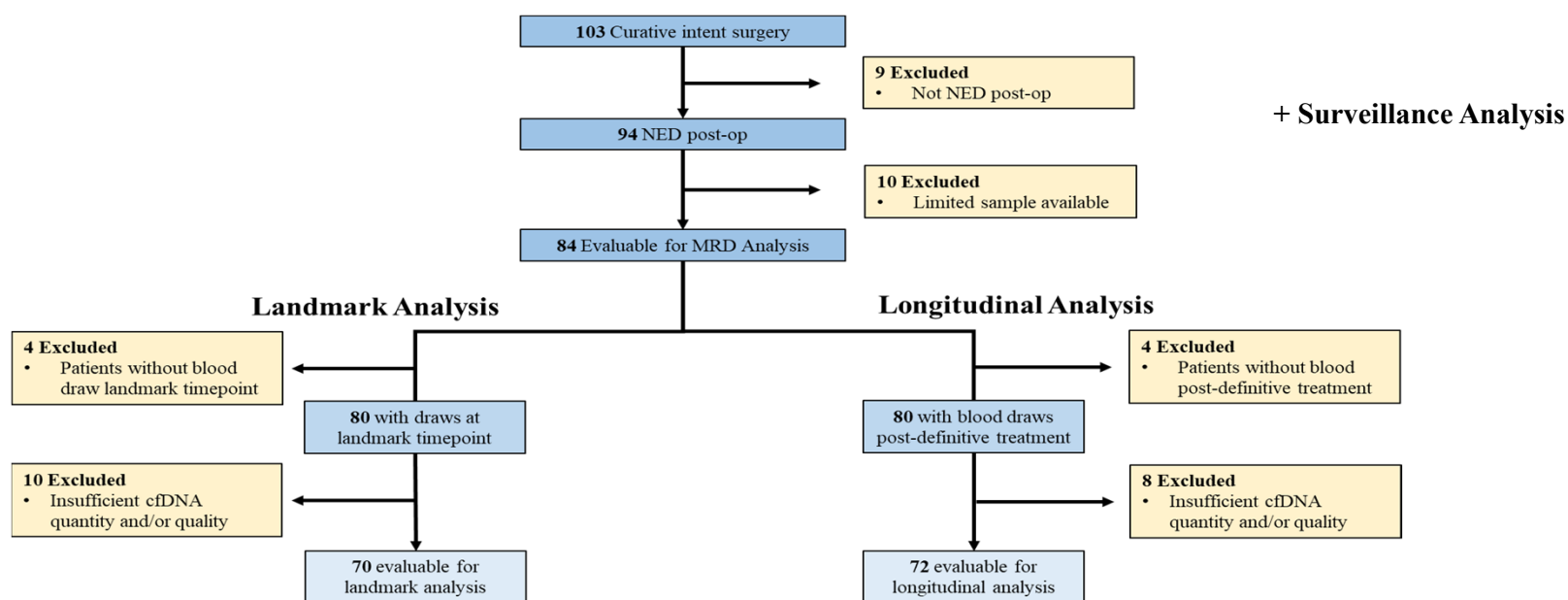


Slide from Dr Charu Aggarwal .

Tumor Uninformed (REVEAL)

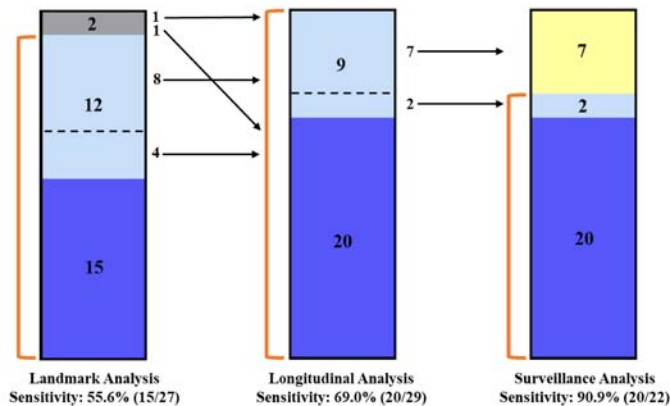
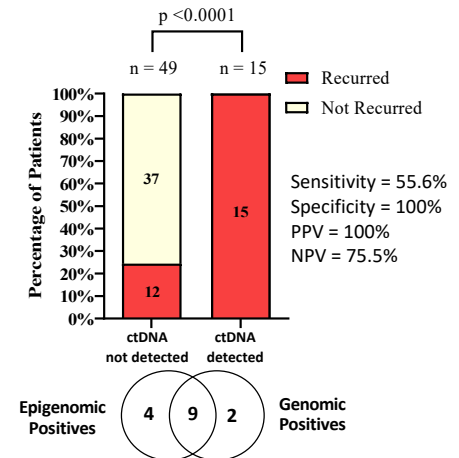
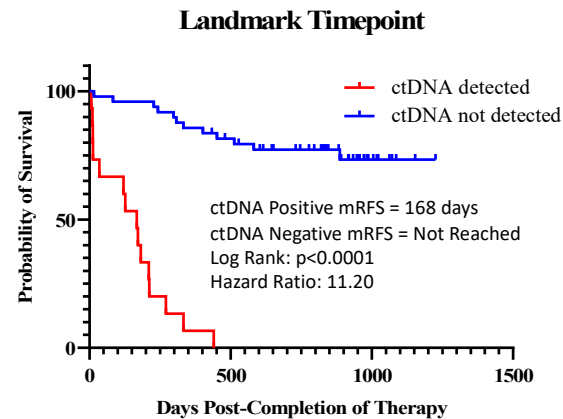


Schema



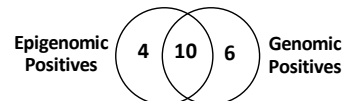
Parikh AR, et al. Clin Cancer Res. 2021 Apr 29;clincanres.0410.2021. doi: 10.1158/1078-0432.CCR-21-0410.

A plasma-only Assay to Detect MRD After Surgery: Results



■ ctDNA detected
■ ctDNA not detected
■ No surveillance draw
■ Failed landmark draw
■ Included in analysis

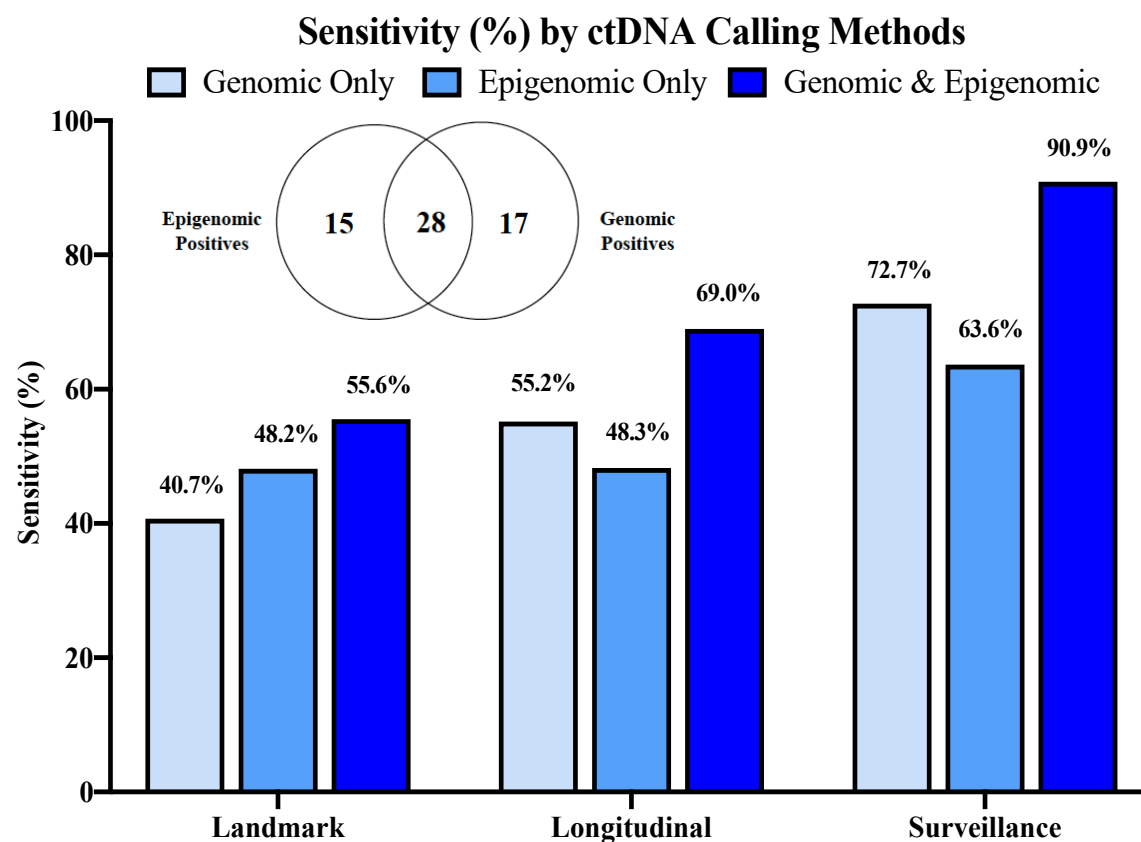
CEA at landmark timepoint failed to predict recurrence



Parikh AR, et al. Clin Cancer Res. 2021 Apr 29;clinres.0410.2021. doi: 10.1158/1078-0432.CCR-21-0410.

MASSACHUSETTS
GENERAL HOSPITAL
CANCER CENTER

The Combination of Genomic and Epigenomic Calls is Key to Improve ctDNA Detection



Parikh AR, et al. Clin Cancer Res. 2021 Apr 29;clinres.0410.2021. doi: 10.1158/1078-0432.CCR-21-0410.





Case 1

29-year-old male musician no family history presents with rectal bleeding

- **Colonoscopy**
Sigmoid Mass
MSS adenoCA
- **LAR**
Stage II CRC
Path T3N0
0/26 nodes
Tumor Budding Score of 12
Poorly Differentiated



What do you do?

Signatera Positive



Date: 10/07/2020
MTM/mL: 0.28

*Mean tumor molecules per mL is
calculated based on the mean of ctDNA
molecules detected per mL of the
patient's plasma.*

COBRA Study NCT04068103

Primary Objective Phase II

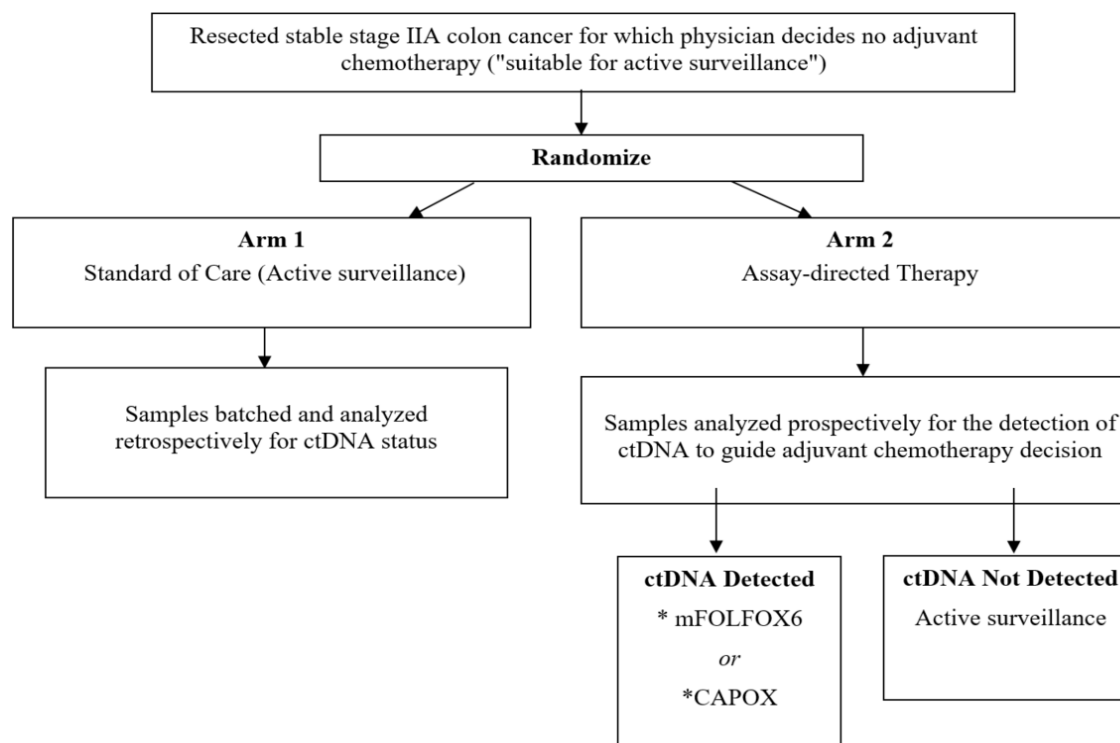
To compare the rate of ctDNA clearance in "ctDNA detected" patients treated with or without adjuvant chemotherapy following resection of stage IIA colon cancer

Phase III

To compare recurrence-free survival (RFS) in "ctDNA detected" patients treated with or without adjuvant chemotherapy following resection of stage IIA colon cancer

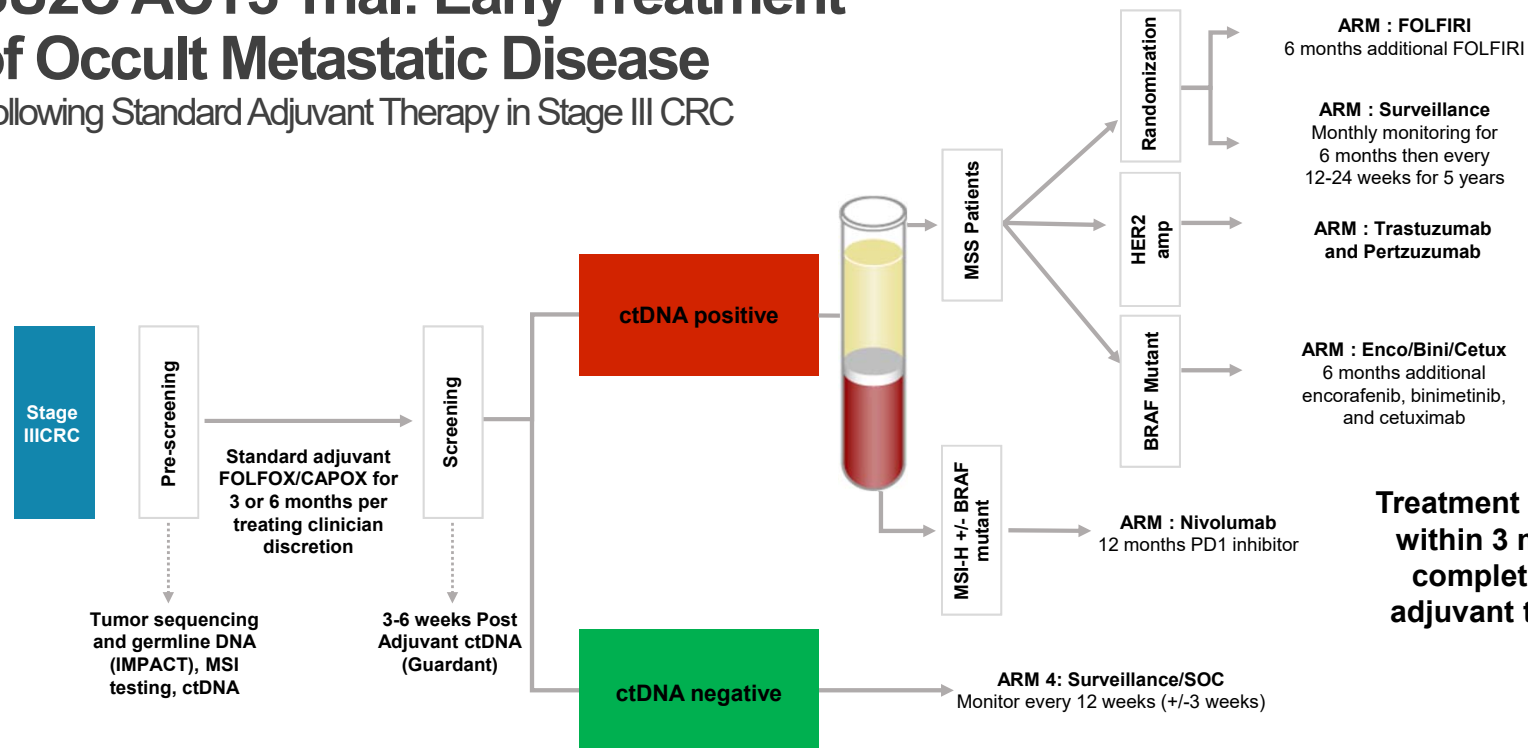
Van K. Morris, MD, Principal Investigator
Greg Yothers, PhD
Scott Kopetz, PhD
Thom George, MD

<https://clinicaltrials.gov/ct2/show/NCT04068103>



SU2C ACT3 Trial: Early Treatment of Occult Metastatic Disease

Following Standard Adjuvant Therapy in Stage III CRC



Treatment to begin within 3 months completion of adjuvant therapy



Assay Characteristics for Routine Testing for MRD



- For escalation applications
 - High specificity/PPV, even at the expense of lower sensitivity
 - PPV should be >90-95%; no more than 1 in 10 false positives
- Turnaround time will be critical to make real-time decisions and may require non-personalized approaches
- Having matched tumor available to minimize false positives (OR PBMCs)
- Multi-gene would be preferred to allow broad capturing of potential patients and high sensitivity

High sensitivity is needed for de-escalation.
What are the limitations to sensitivity?

- Assay technology
- Tumor location
- Number of mutations
- Fragment size
- Methylation
- Amount of blood available for testing
- Number of times sampled: one time point or serial sampling
- Multi-Unique Molecular Identifiers to mitigate PCR errors

High Level Differences

	Tumor Informed	Plasma Only
Volume	2 tubes of blood	4 tubes of blood
Cost	\$850	\$5000
Tube Collection	same	Same
TAT	1 st time 3-4 weeks	7-10 days
Tissue Needed	Yes	No
Technology	16 clonal, need 2	Fixed CRC panel (epigenomic/genomic)
Results	Molecules/ml	Qualitative + or – *
Tumor Type	Any	CRC

Minimal Residual Disease in 2021: Conclusions

ctDNA is prognostic and may be predictive of response to therapy

- Clearance is possible

Minimal residual disease applications have tremendous opportunity

- Requires larger, prospective cohorts
- Trials underway
- Great opportunities for novel drug development following **biology** of MRD

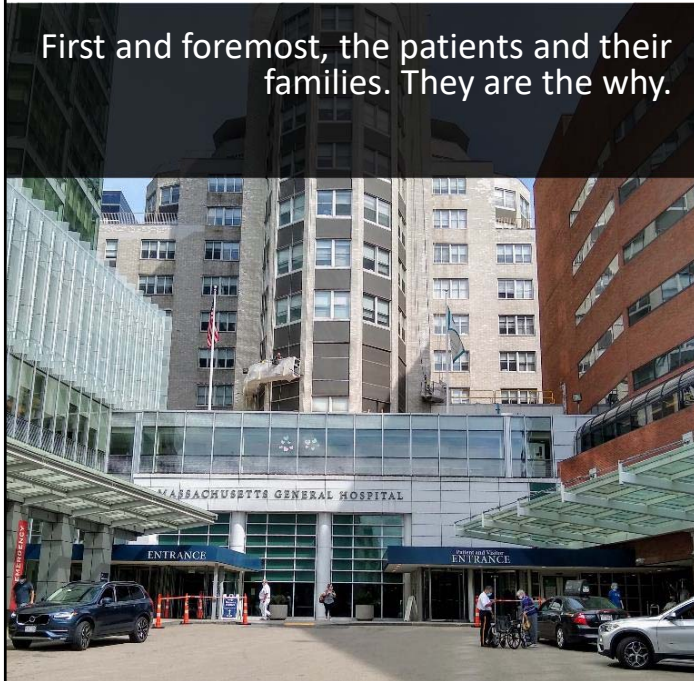
Attention to false positives and improving sensitivities will be critical to ensure success of this effort

- Bioinformatically informed pipelines can address sources of false positives
- More data on Tumor Informed vs Uninformed approach to minimize false positives and ensure clinical relevance of the findings



Acknowledgements

First and foremost, the patients and their families. They are the why.



MGH Center for GI Cancers

Ryan Corcoran, MD, PhD

Director, Gastrointestinal Cancer Center Program

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Lipika Goyal, MD

Jill Allen, MD

Ryan Nipp, MD

Bruce Giantonio, MD

Jennifer Wo, MD

Sam Klempner, MD, PhD

Colin Weekes, MD, PhD

Rocco Ricciardi, MD

Motaz Qadan, MD, PhD

David Berger, MD

James Cusack, MD

MGH Center for Melanoma

Genevieve Boland, MD, PhD

MGH Pathology

John Iafrate, MD, PhD

Dora Dias-Santagata, PhD, FACMG

Joe Lennerz, MD, PhD

Hetal Desai, MD

Nicholas Jessop

MGH Rapid Autopsy Program

Dejan Juric, MD

MGH GI Research Asst Team

Islam Baiev

Emily VanSeventer

Joy Jaqnian

Yojan Shah

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Bruce Chabner, MD

Keith Flaherty, MD

Alan Venook, MD, UCSF

**FUNDING: NIH/NCI
DF/HCC GI SPORE**



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What's on the Horizon?

Pancreatic Cancer Heterogeneity: A Therapeutic Challenge and Opportunity

David T. Ting, MD

Associate Professor of Medicine, *Harvard Medical School*

Associate Clinical Director for Innovation, *Massachusetts General Hospital Cancer Center*



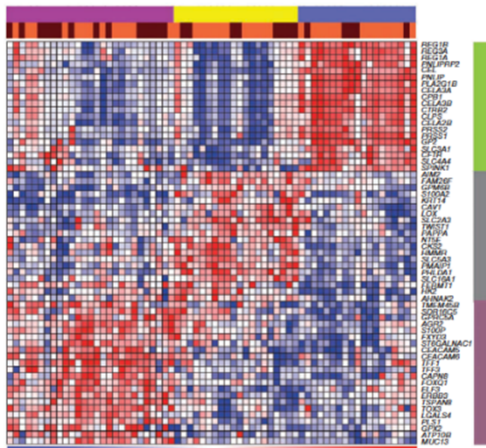
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NCCN.org – For Clinicians | **NCCN.org/patients** – For Patients

Pancreatic Ductal Adenocarcinoma (PDAC) Not a Single Cancer

Subtypes of pancreatic ductal adenocarcinoma and their differing responses to therapy

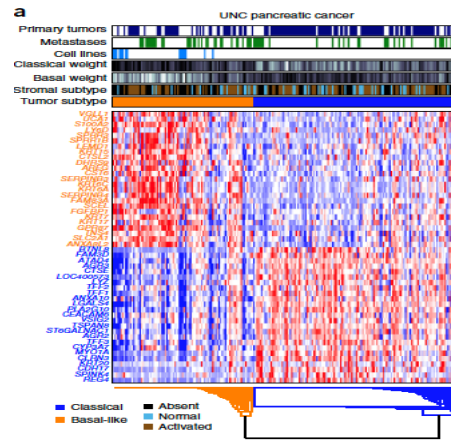
Eric A Collisson^{1,2,10}, Anguraj Sadanandam^{1,3,10}, Peter Olson^{1,9}, William J Gibb^{1,9}, Morgan Truitt⁴, Shenda Gu¹, Janine Cooc⁵, Jennifer Weinkle⁶, Grace F Kim⁶, Lakshmi Jakkula¹, Heidi S Feiler¹, Andrew H Ko², Adam B Olshen⁷, Kathleen L Danenberg¹, Margaret A Tempero², Paul T Spellman¹, Douglas Hanahan^{1,4} & Joe W Gray^{1,8}



Collisson EA et al. *Nature Medicine* 3 2011

Virtual microdissection identifies distinct tumor- and stroma-specific subtypes of pancreatic ductal adenocarcinoma

Richard A Moffitt¹, Raoud Maryati¹, Elizabeth L Hite¹, Keith E Volmar², S Gabriela Herrera Loza¹, Katherine A Hoadley^{1,3}, Naim U Rashid¹, Lindsay A Williams^{1,4}, Samuel C Eaton⁵, Alexander H Chung⁶, Jadwiga K Smyla¹, Judy M Anderson⁶, Hong Jin Kim^{1,2}, David J Bentrem^{6,9}, Mark S Talamonti¹⁰, Christine A Iacobuzio-Donahue¹¹, Michael A Hollingsworth⁶ & Jen Jen Yeh^{1,5,7}



Moffitt RA et al. *Nature Genetics* 2015

ARTICLE

Genomic analyses identify molecular subtypes of pancreatic cancer

Peter Bailey^{1,2}, David K Chang^{1,3,4,5}, Katia Nones^{6,7}, Amber L Johns⁸, Ann-Marie Patch^{1,9}, Marie-Claude Gingras^{8,9}, David K Miller^{1,2}, Angelika N. Christ¹, Tim J. C. Braxner¹, Michael C. Quinn^{1,4}, Craig Nourse^{1,2}, J. Charles Murtaugh¹⁰, Iwon Harliwong¹, Sonel Khrisogul¹, Suzanne Manning¹, Ehsan Nourbakhsh¹, Shuang Wang^{1,6}, Lynn Fink¹, Oliver Holmes^{1,6}, Venessa Chir¹, Matthew J. Anderson¹, Stephen Kazakoff^{1,4}, Conrad Leonard^{1,6}, Felicity Newell¹, Nick Waddell¹, Scott Wood^{1,6}, Qinying Xu^{1,6}, Peter J. Wilson¹, Nicole Cloonan^{1,6}, Karin S. Kassahn^{1,12}, Darrin Taylor¹, Kelly Quek¹, Alan Robertson¹, Lorena Pantano¹, Laura Mincarelli¹, Luis N. Sanchez¹, Lisa Evers¹, Jianmin Wu¹, Mark Pinese¹, Mark J. Cowley¹, Marc D. Jones^{1,3}, Emily K. Colvin¹, Adrian M. Nagra¹, Emily S. Humphrey¹, Lorraine A. Chantiriri^{1,14}, Amanda Maxwell¹, Jeremy Humphris¹, Angela Chou^{1,15}, Marina Pajic^{1,15}, Christopher J. Scarlett^{1,16}, Andreia V. Pinho¹, Marc Giry¹, Leticia Leterriere¹, Ise Rooman¹, Jaswinder S. Samra^{1,17}, James G. Kench^{1,18,20}, Jessica A. Luvell¹, Neil D. Merrett^{1,20}, Christopher W. Toon¹, Kristina Eyrar^{1,2}, Nam Q. Nguyen¹, Andrew Barbour¹, Nikolaus Zep¹, Kim Moran-Jones¹, Nigel B. Jamieson^{1,20,21}, Janet S. Graham^{1,22}, Fraser Duthie¹, Karin Olsen^{1,23}, Jane Hsu^{1,24}, Robert Grützmann¹, Amirhan Maitra¹, Christine A. Iacobuzio-Donahue¹, Christopher L. Wolfgang^{1,25}, Richard A. Morton¹, Rita T. Lawlor^{1,26}, Vincenzo Corbo¹, Claudio Bassi^{1,27}, Borislav Rusev^{1,28}, Paola Capelli¹, Roberto Salvia¹, Giampaolo Tortora¹, Debabrata Mukhopadhyay^{1,29}, Gloria M. Petersen¹, Australian Pancreatic Cancer Genome Initiative¹, Donna M. Munz^{1,3}, William E. Fisher^{1,3}, Susilla A. Karim^{1,3}, James R. Eshleman^{1,3}, Ralph H. Hruban^{1,3}, Christian Pilarsky¹, Jennifer P. Morton^{1,3}, Owen J. Sanson^{1,3,30}, Aldo Scarpa^{1,3,31}, Elizabeth A. Musgraves¹, Ulla-Maja Hagbo Bailey¹, Oliver Hofmann^{1,32}, Robert L. Sutherland¹, David A. Wheeler^{1,3}, Anthony J. Gill^{1,33}, Richard A. Gibbs^{1,3}, John V. Pearson^{1,3}, Nicola Waddell^{1,3}, Andrew V. Biankin^{1,3,3,37} & Sean M. Grimmond^{1,2,44}



Bailey P et al. *Nature* 2016

Epithelial-Mesenchymal Plasticity Drives Tumor Cell Heterogeneity

EPITHELIAL



MESENCHYMAL



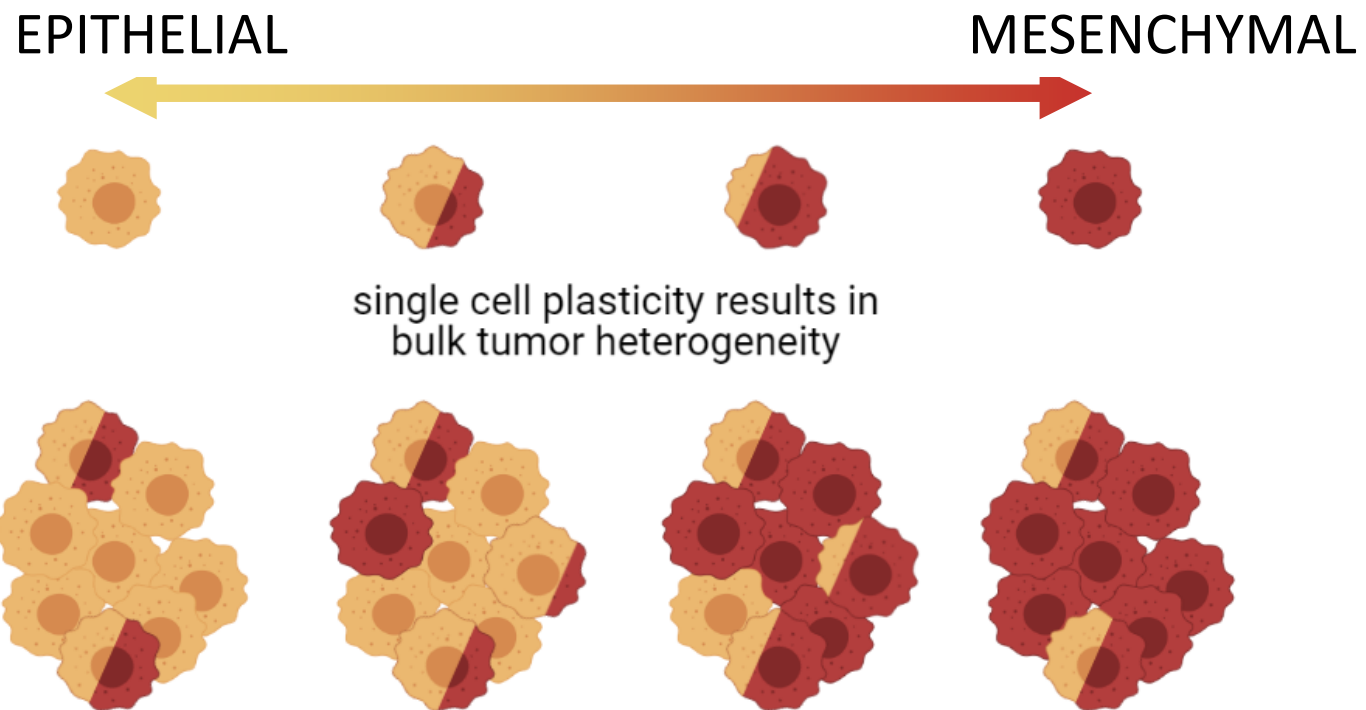
Epithelial-Mesenchymal Plasticity Drives Tumor Cell Heterogeneity

EPITHELIAL

MESENCHYMAL



Epithelial-Mesenchymal Plasticity Drives Tumor Cell Heterogeneity



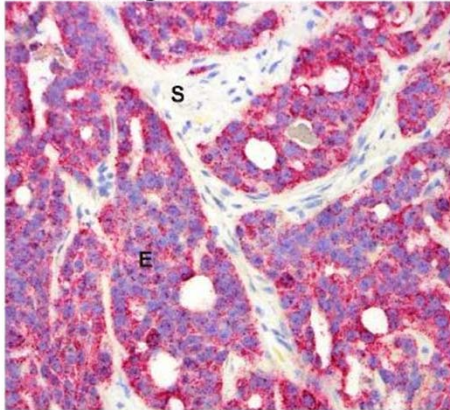
Human Cancers on a Spectrum of Epithelial-Mesenchymal States

Pancreatic cancer (PDAC)

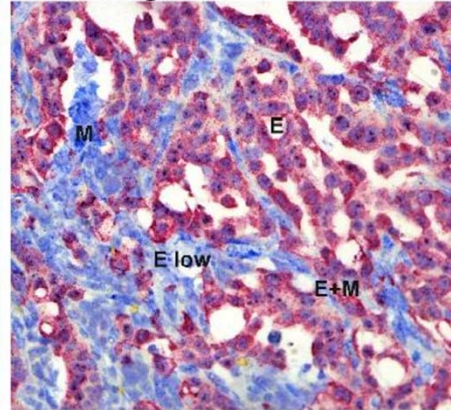
E CELL LINE

M CELL LINE

PDAC6 Xenograft



PDAC3 Xenograft



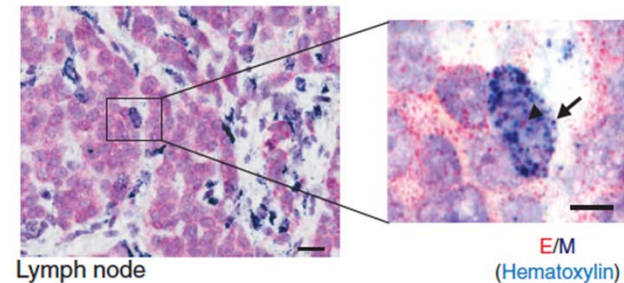
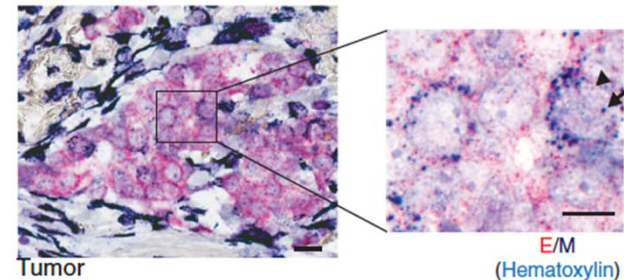
Epithelial Mesenchymal

Epithelial – CDH1, EPCAM, KRT5, KRT7, KRT8, KRT18, KRT19

Mesenchymal – FN1, CDH2, SERPINE1

Porter, *PNAS*, 2019

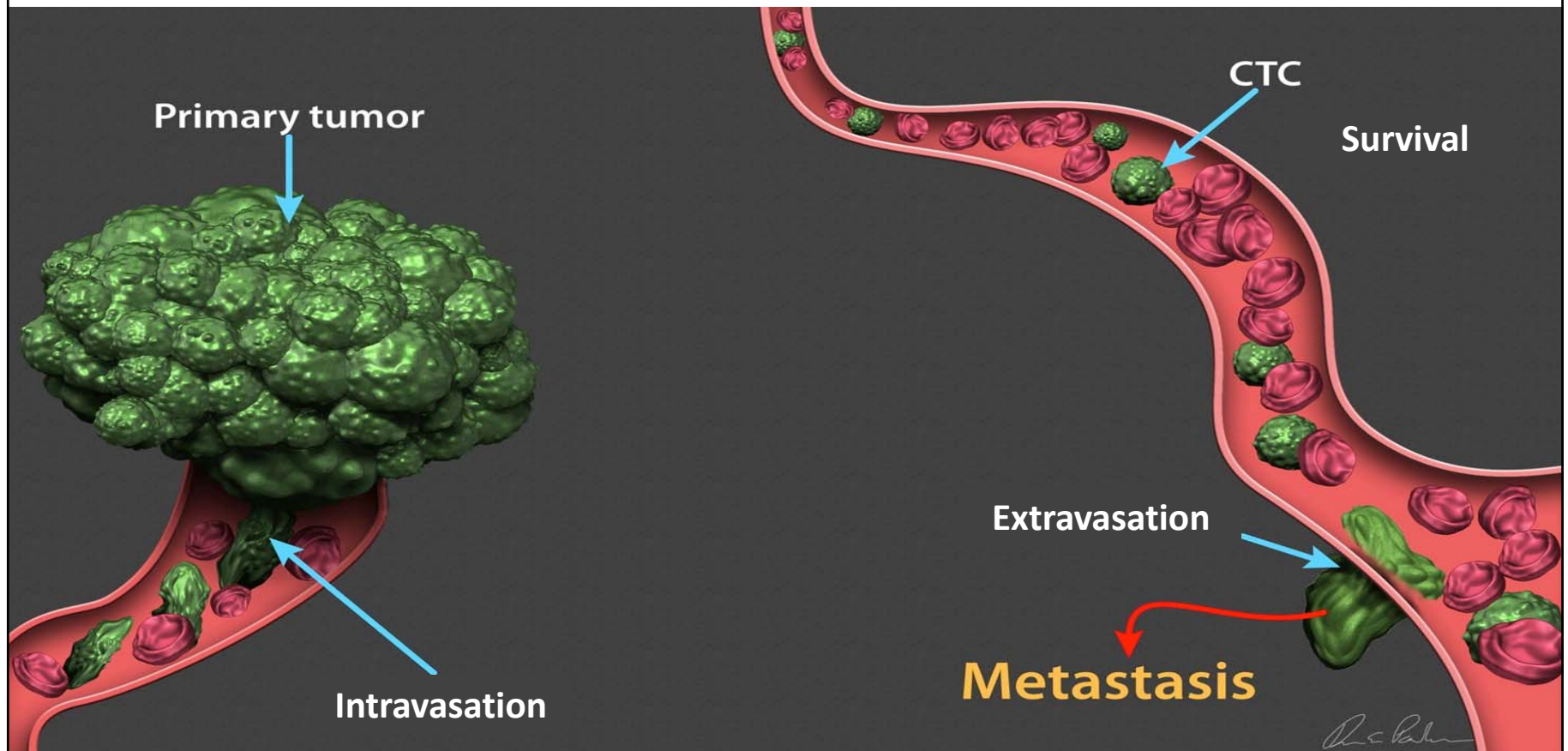
Breast cancer



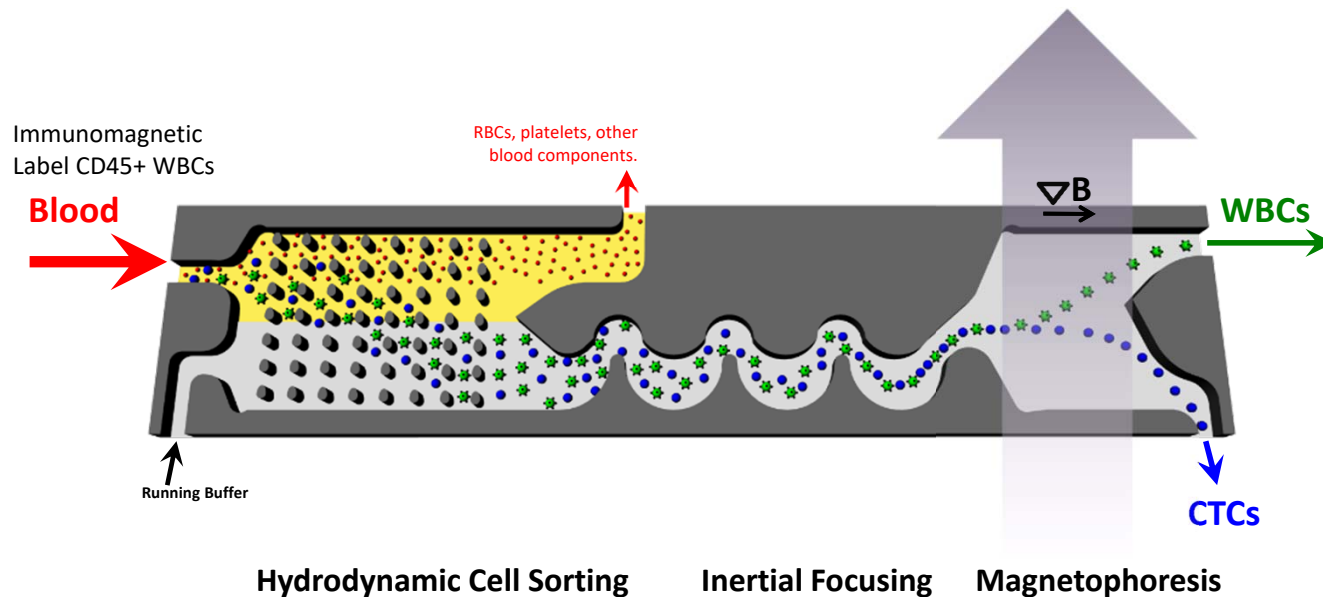
Yu, *Science*, 2013

Cell Autonomous EMT Plasticity

EMT Plasticity Important for Circulating Tumor Cells (CTCs)



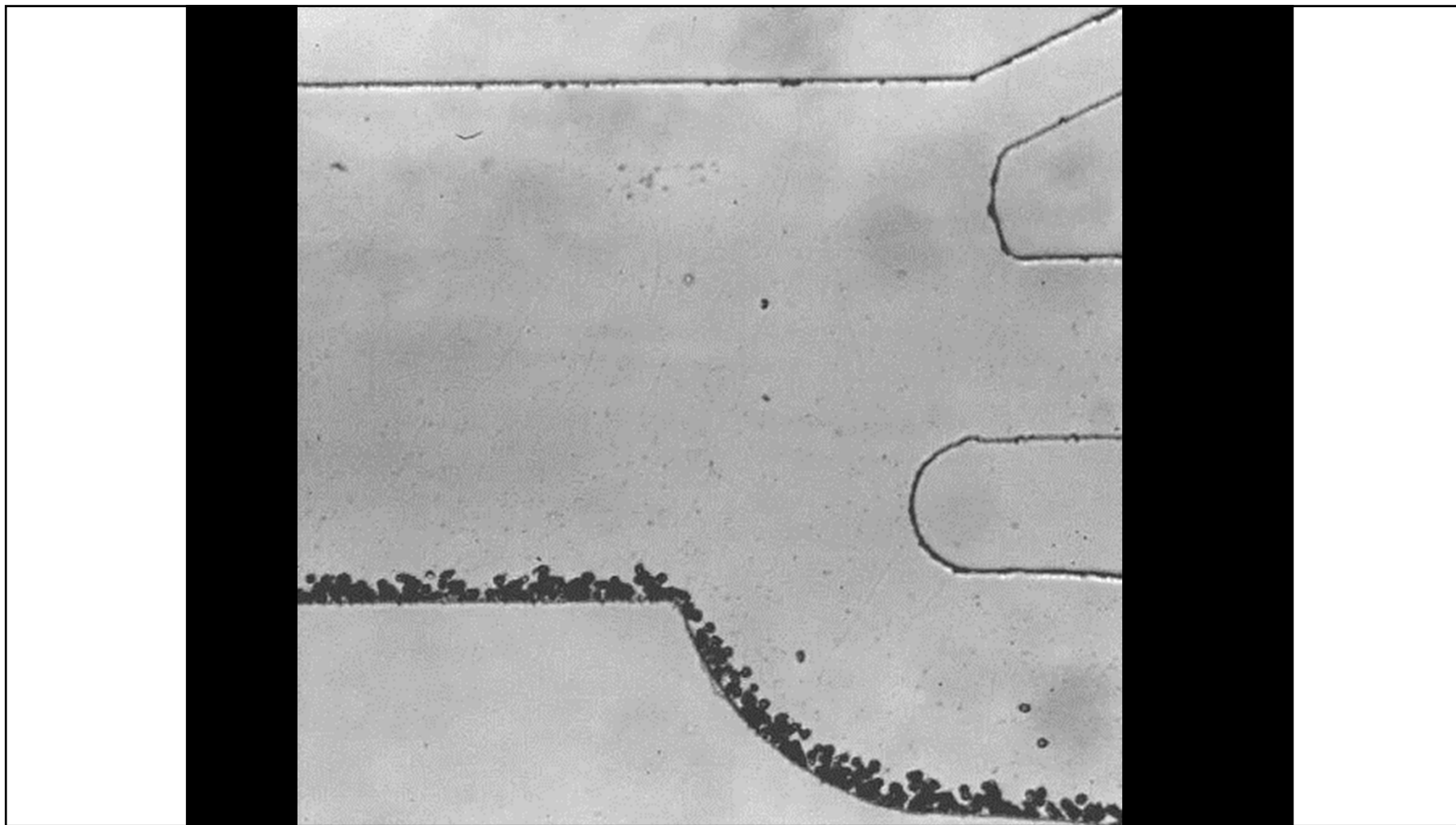
Negative Depletion CTC-iChip



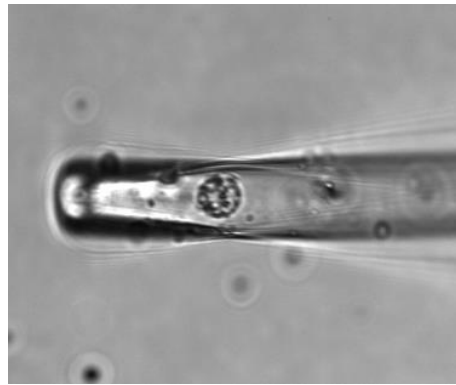
- Red Blood Cell (8 Billion / mL)
- CTCs (1-100 / mL)
- ★ White Blood Cell labeled with anti-CD45 magnetic beads (5 Million / mL)

Ozkumur E*, Shah AM*, et al. *Sci Transl Med*, 2013; 5(179): 179ra47.

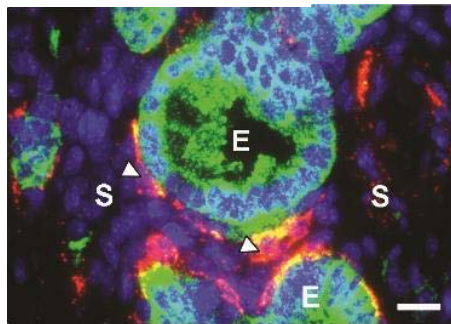
* Equal contribution



Single CTC RNA-seq: Heterogeneous EMT and Stem Cell Gene States

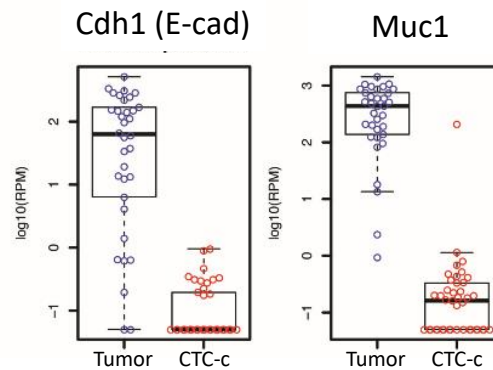


Mouse Primary Tumor

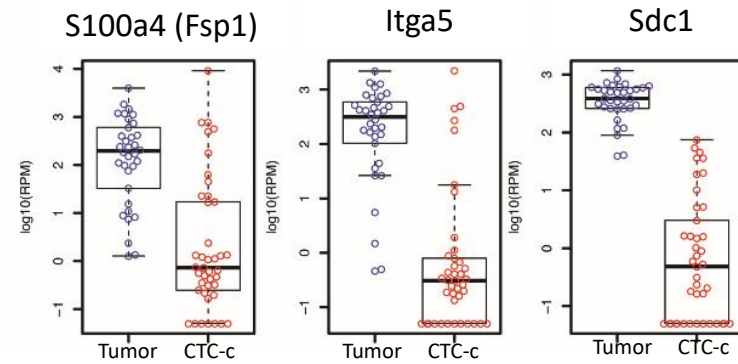


Igfbp5 (CTC gene) / CK / DAPI
Ting DT, et al. *Cell Reports*, 2014; 8:1-14.

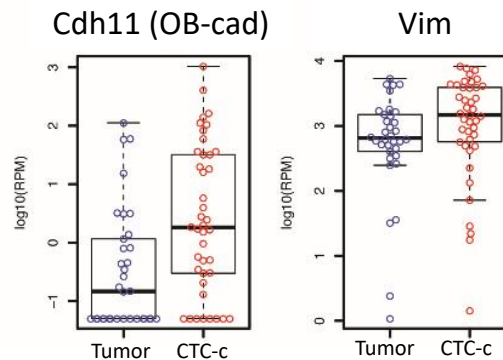
Epithelial Gene Loss



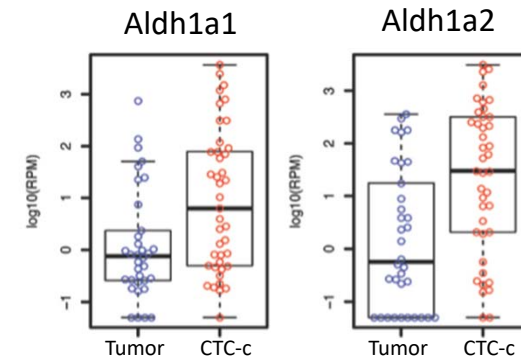
Mesenchymal Gene Loss



Mesenchymal Gene Gain

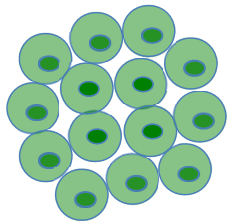


Stem Cell Gene Gain



Microenvironment Driven EMT Plasticity

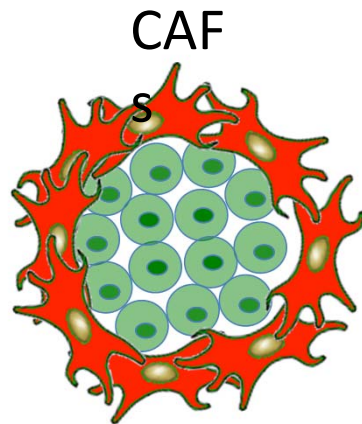
Modeling PDAC:CAF Heterogeneous Interactions



Ligorio M*, Sil S*, et al. *Cell* 2019

* Equal contribution

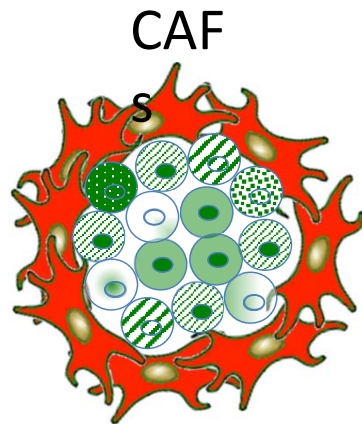
Modeling PDAC:CAF Heterogeneous Interactions



Ligorio M*, Sil S*, et al. *Cell* 2019

* Equal contribution

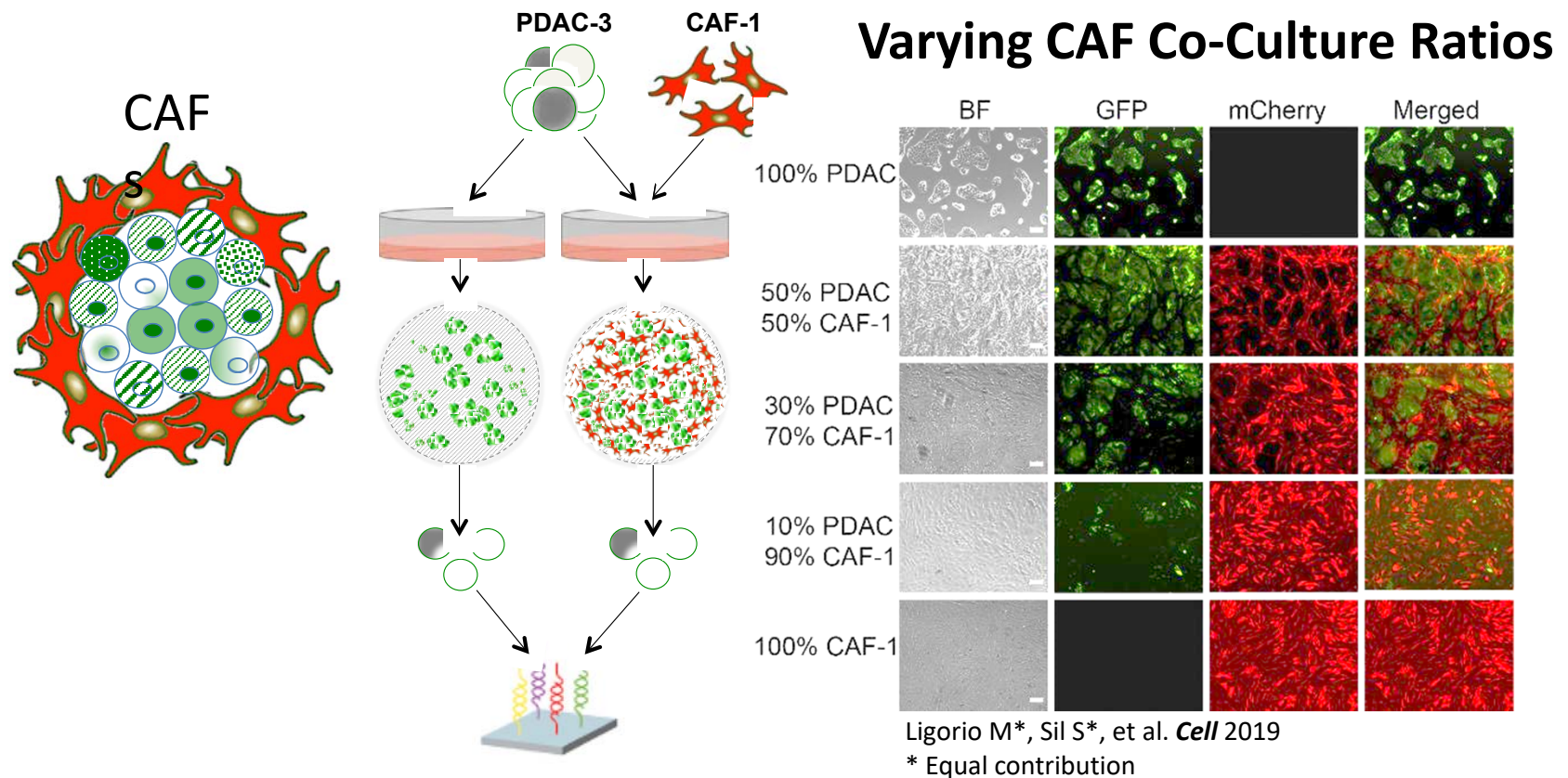
Modeling PDAC:CAF Heterogeneous Interactions



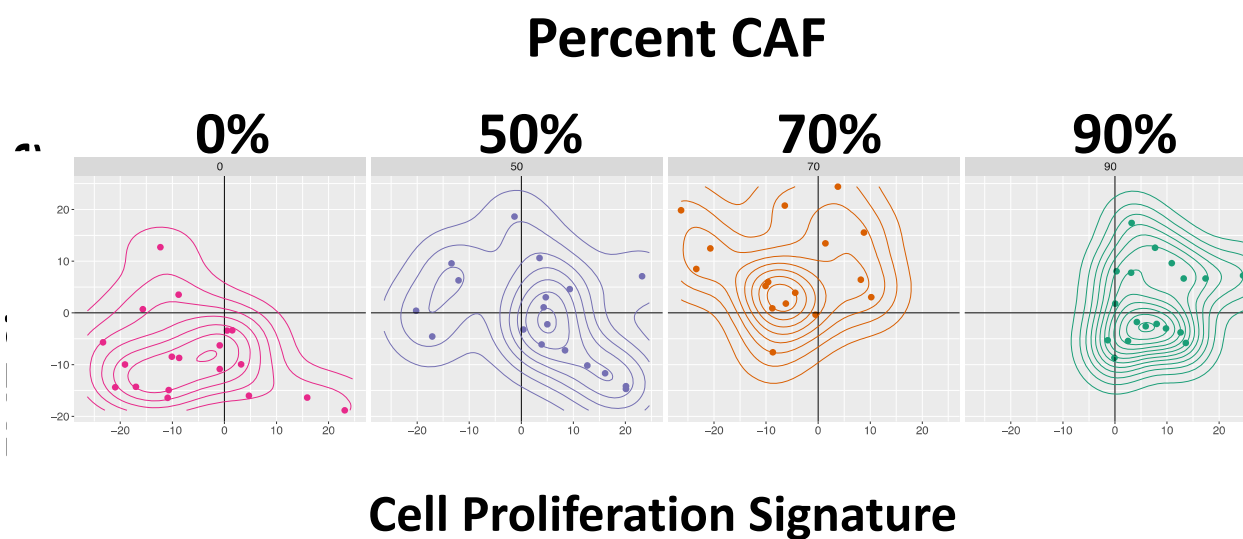
Ligorio M*, Sil S*, et al. *Cell* 2019

* Equal contribution

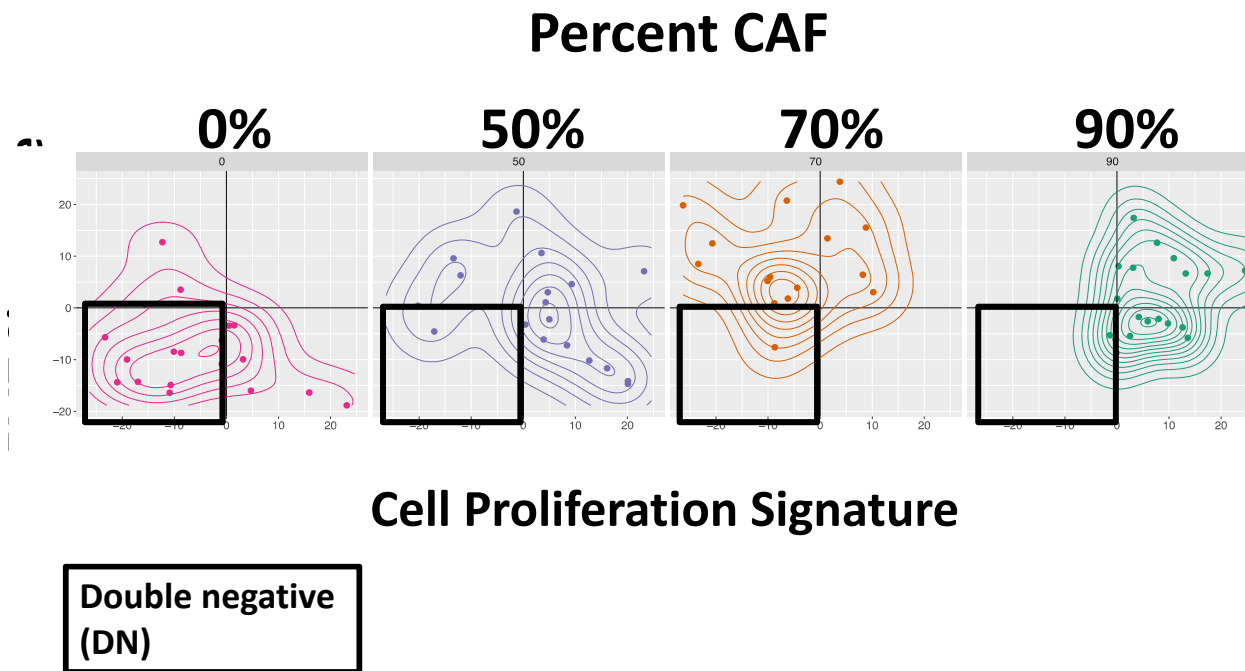
Modeling PDAC:CAF Heterogeneous Interactions



Stromal CAFs Modulate Changes in Single Cell Phenotypes Observed in CTCs



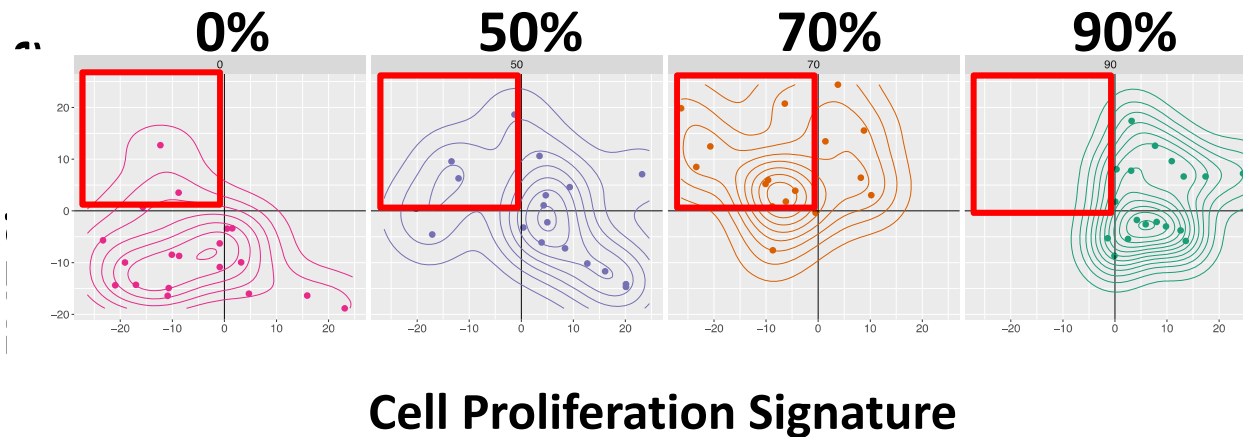
Stromal CAFs Modulate Changes in Single Cell Phenotypes Observed in CTCs



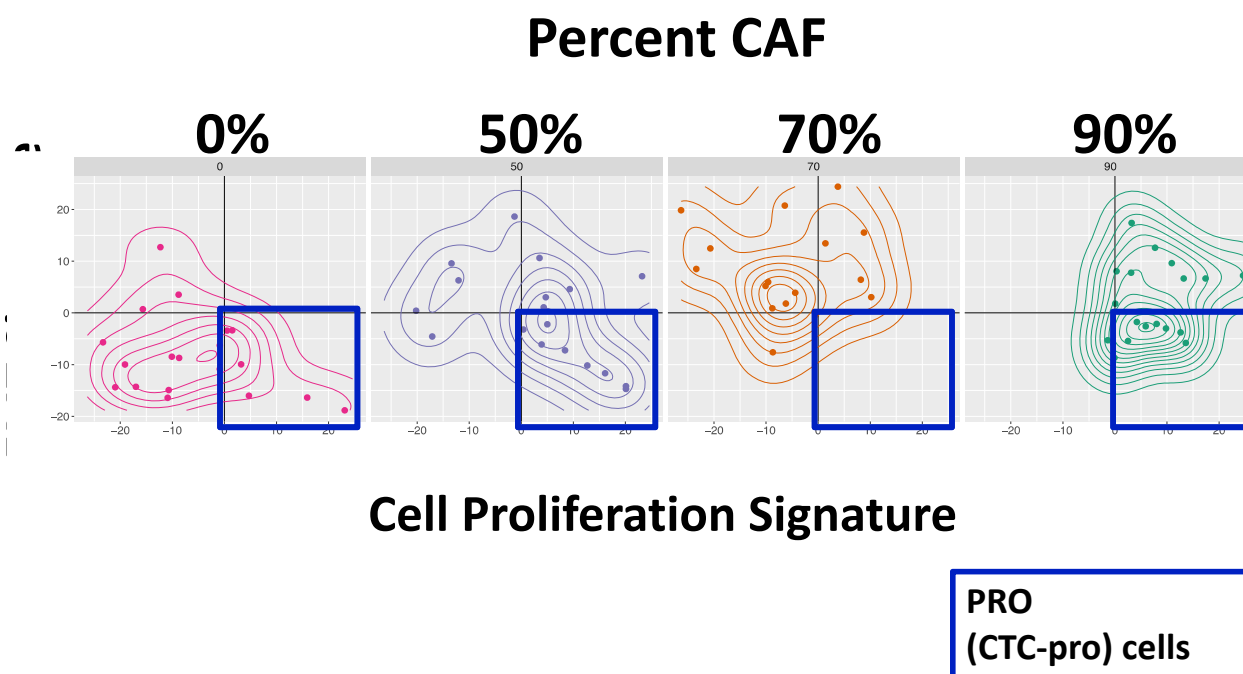
Stromal CAFs Modulate Changes in Single Cell Phenotypes Observed in CTCs

EMT
(CTC-c) cells

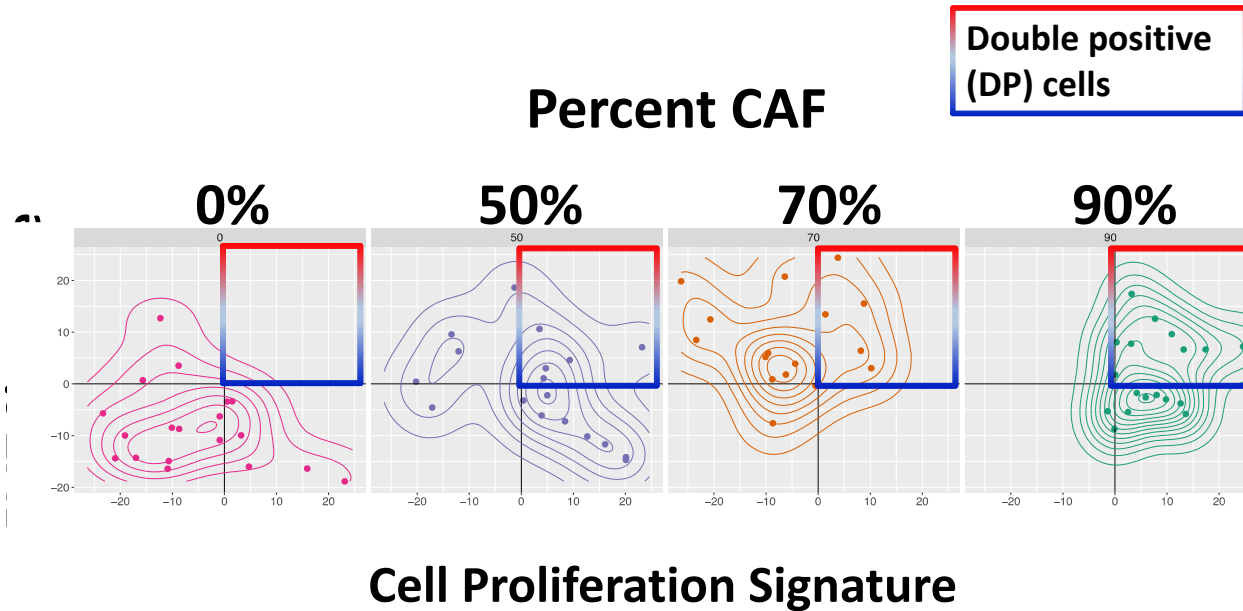
Percent CAF



Stromal CAFs Modulate Changes in Single Cell Phenotypes Observed in CTCs

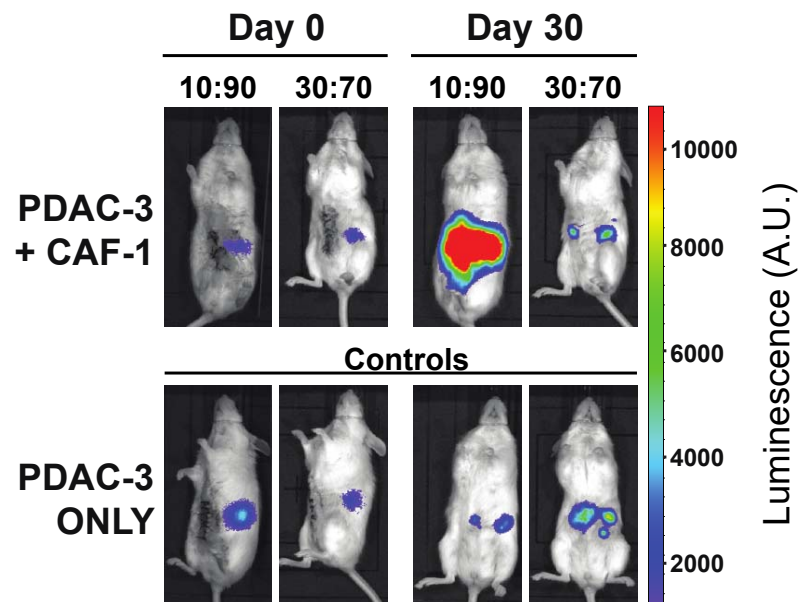


Stromal CAFs Modulate Changes in Single Cell Phenotypes Observed in CTCs

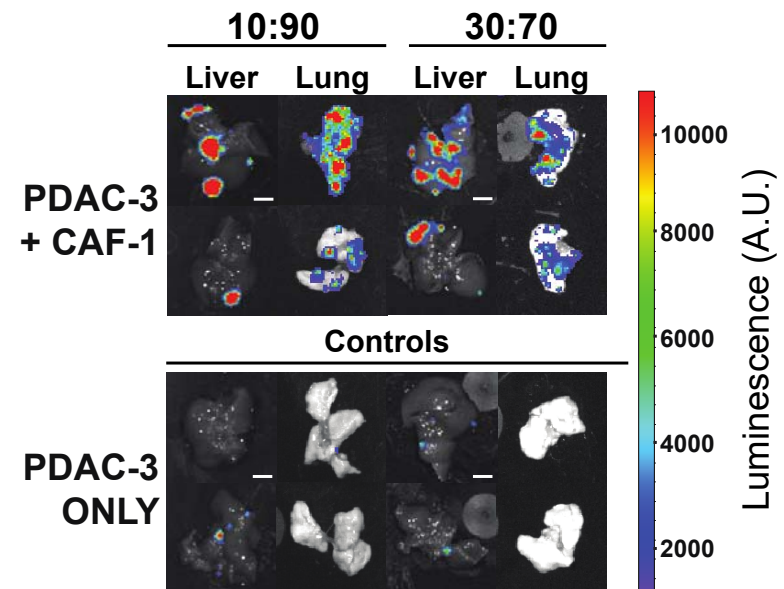


Different proportions of CAFs alters PDAC behavior *in vivo*

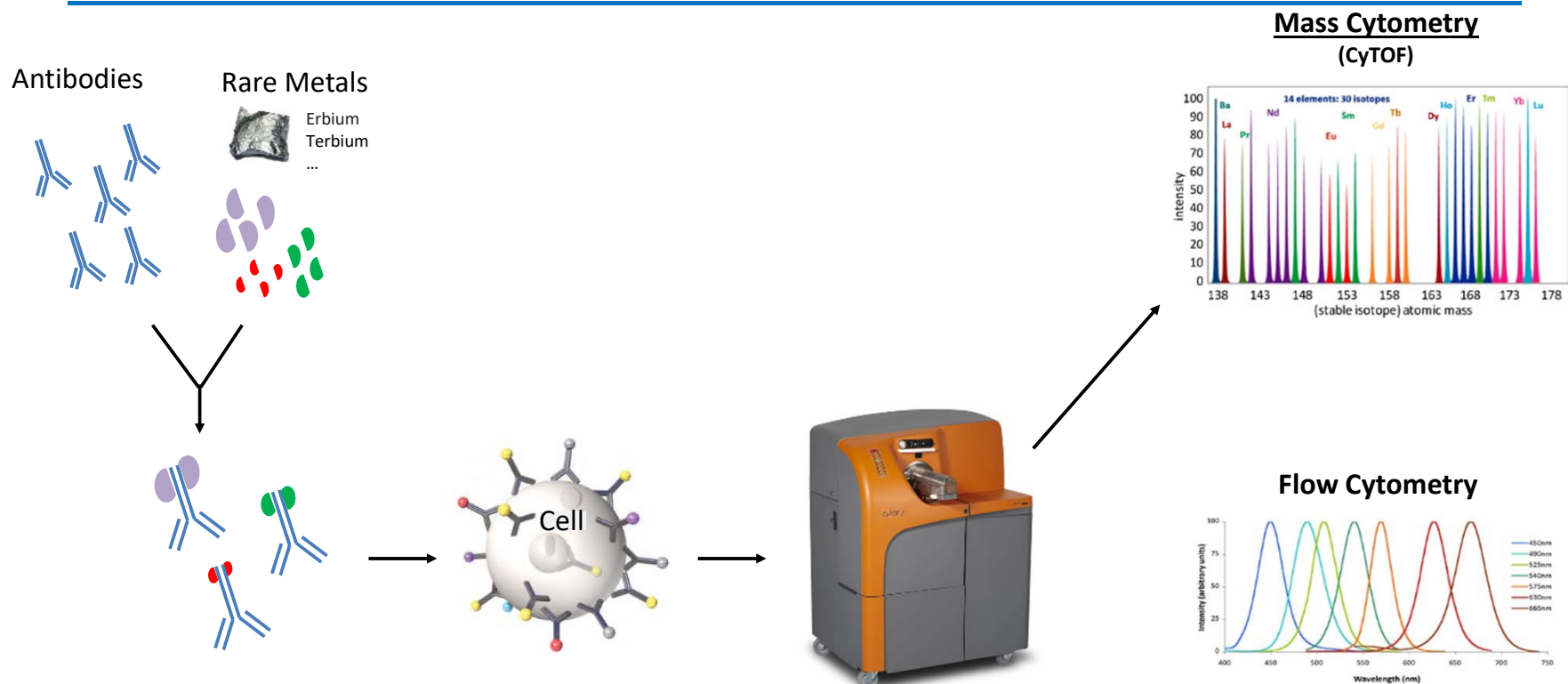
Primary Tumor Growth



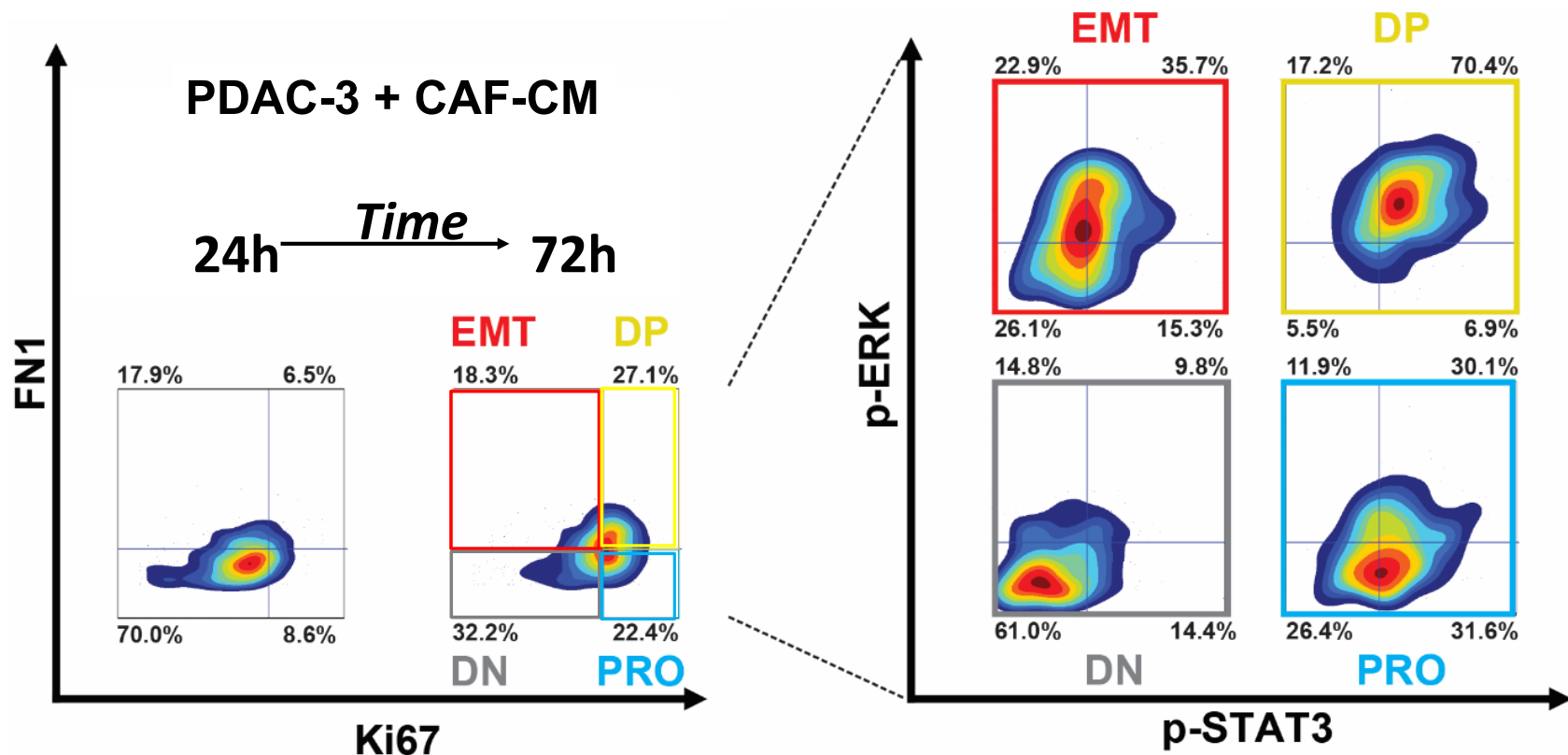
Metastatic Burden



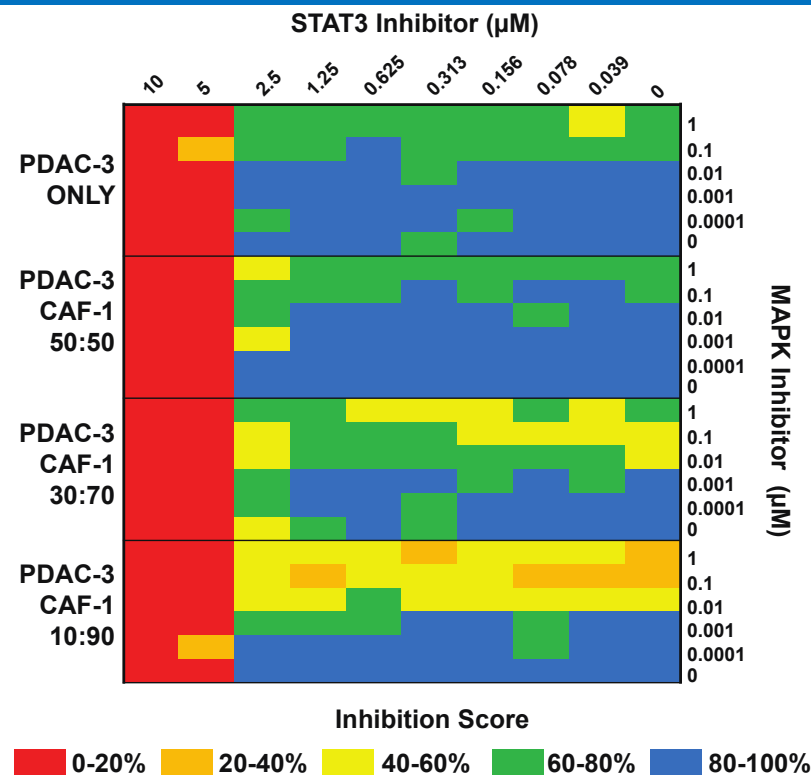
Mass Cytometry (CyTOF) – Single Cell Proteomics



CyTOF Identifies MAPK and STAT3 Single Cell Signaling Enriched in EMT and PRO Phenotypes

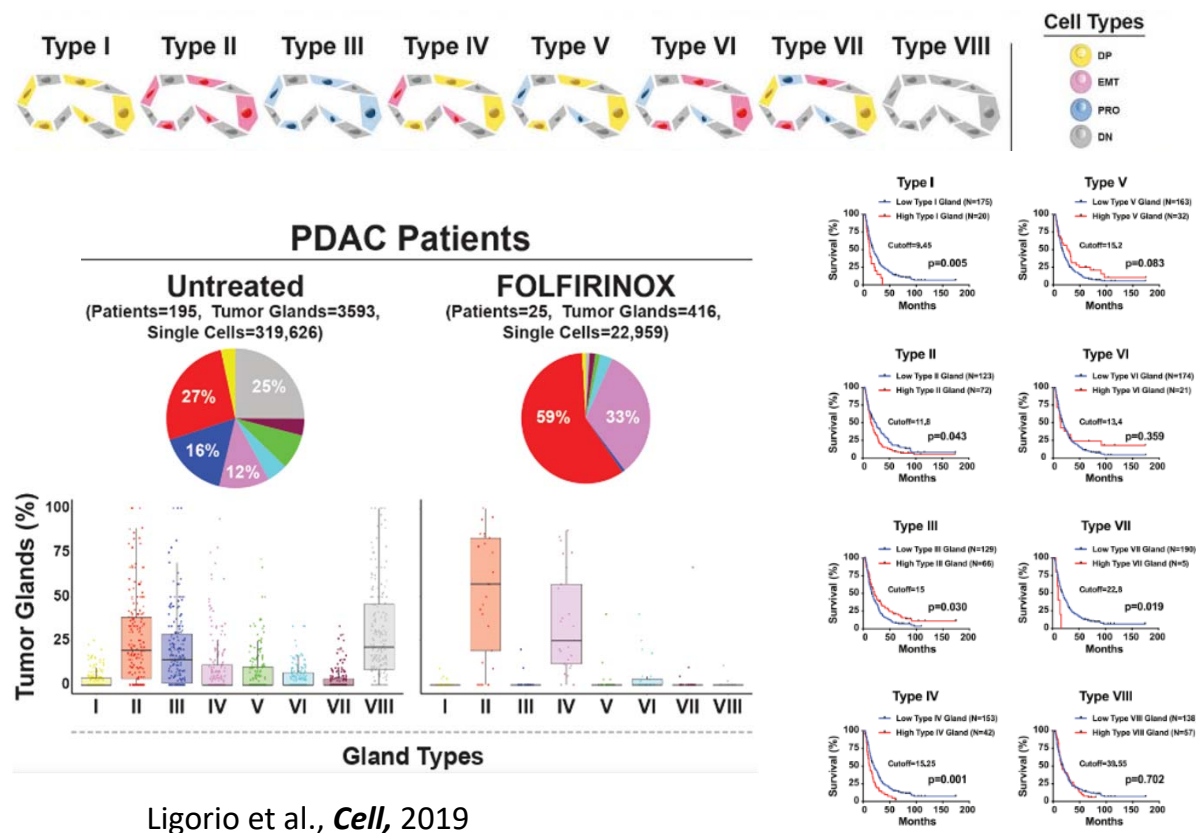


Combination MAPK and STAT3 Inhibitors as a Therapeutic Strategy for High CAF Stromal Tumors

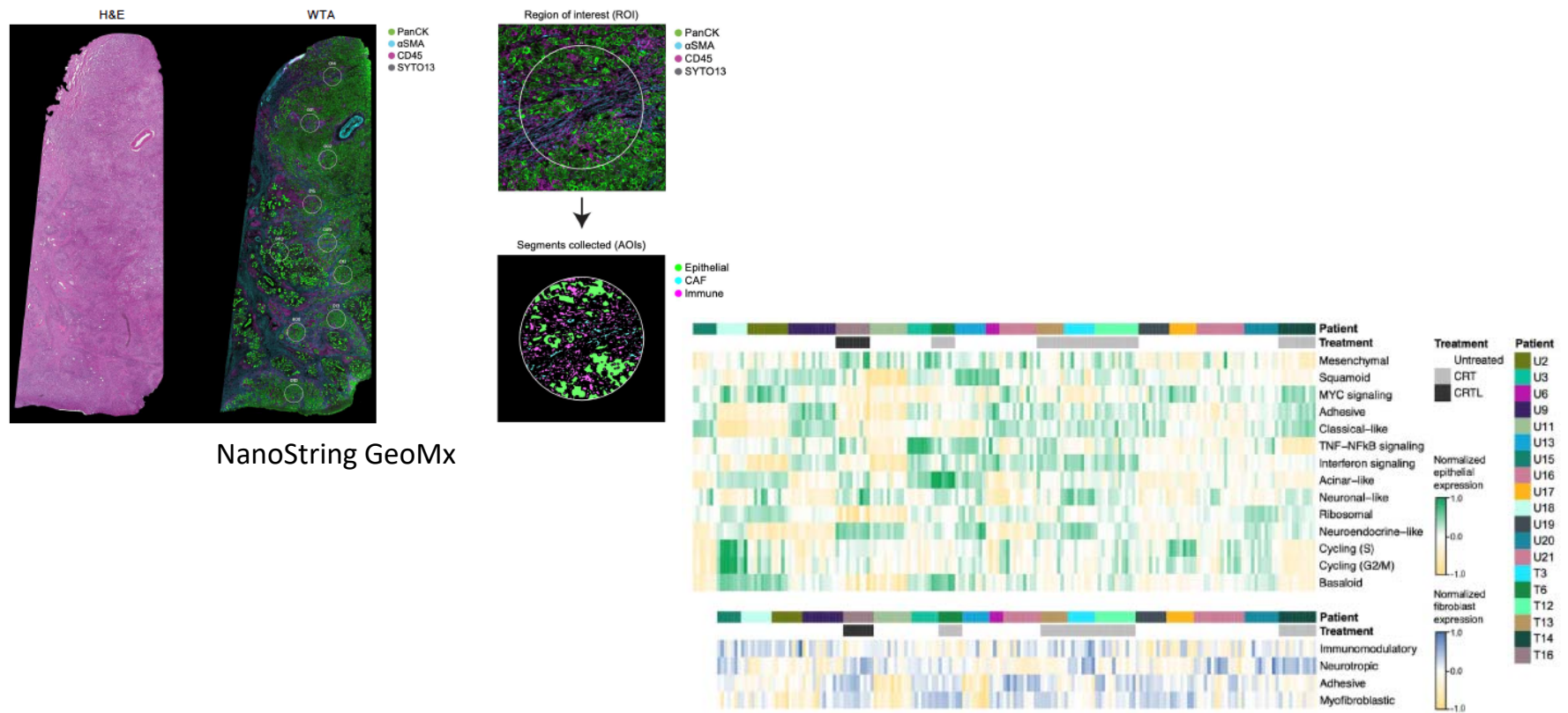


Plasticity leads to chemoresistance in PDAC patients

- Neoadjuvant FOLFIRINOX tumors enriched for mesenchymal tumor glands
- Patients with tumors enriched for mesenchymal glands have worse prognoses



Next Generation Spatial Transcriptomics



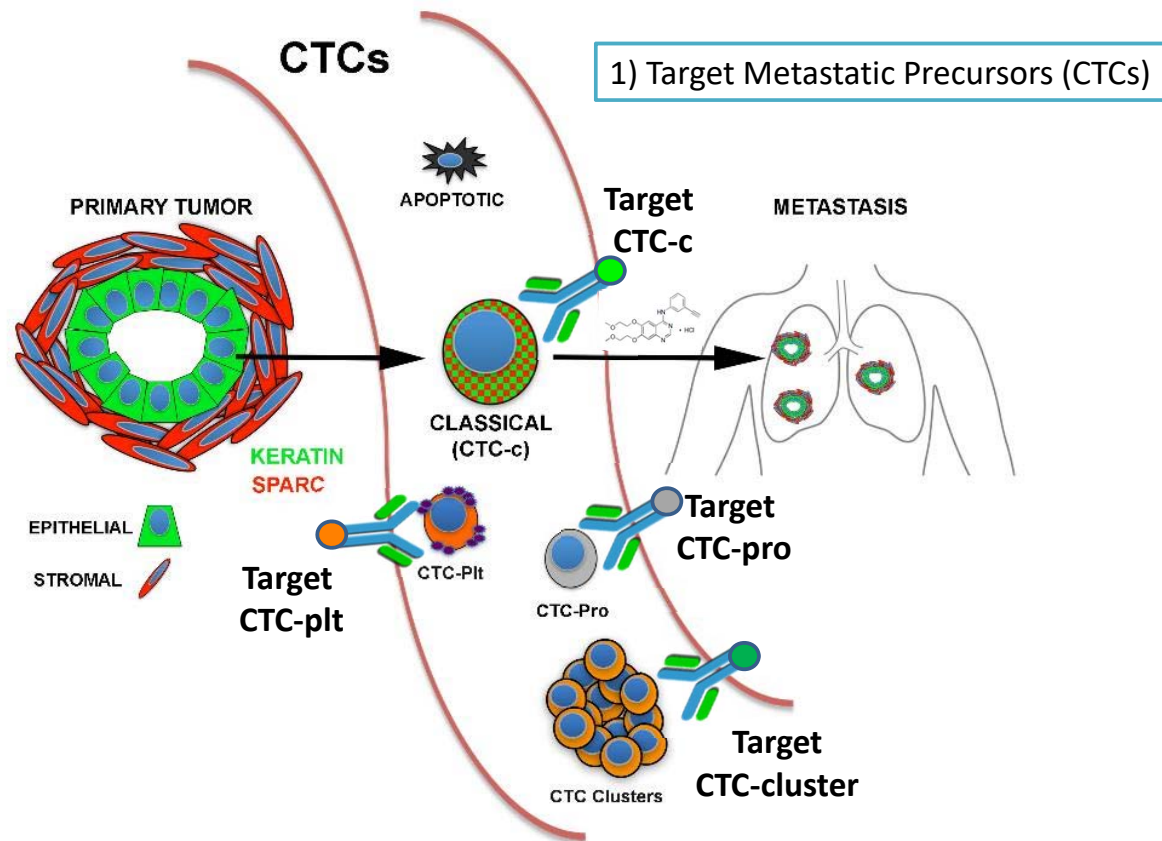
NanoString GeoMx

Hwang et al. (Revision)

Summary: PDAC-CAF Interactions

- Stromal CAFs is a Driver of Single Cell Heterogeneity in PDAC
- PDAC-CAF Interactions result in enhanced EMT and metastasis
- Identification of combination therapies (MEK+STAT3) and PDAC-CAF interacting proteins (TGF- β) as therapeutic candidates
- Spatial Transcriptomics to understand effects of therapies on single cell subpopulations in human tumors

Points of Intervention Targeting EMT Plasticity

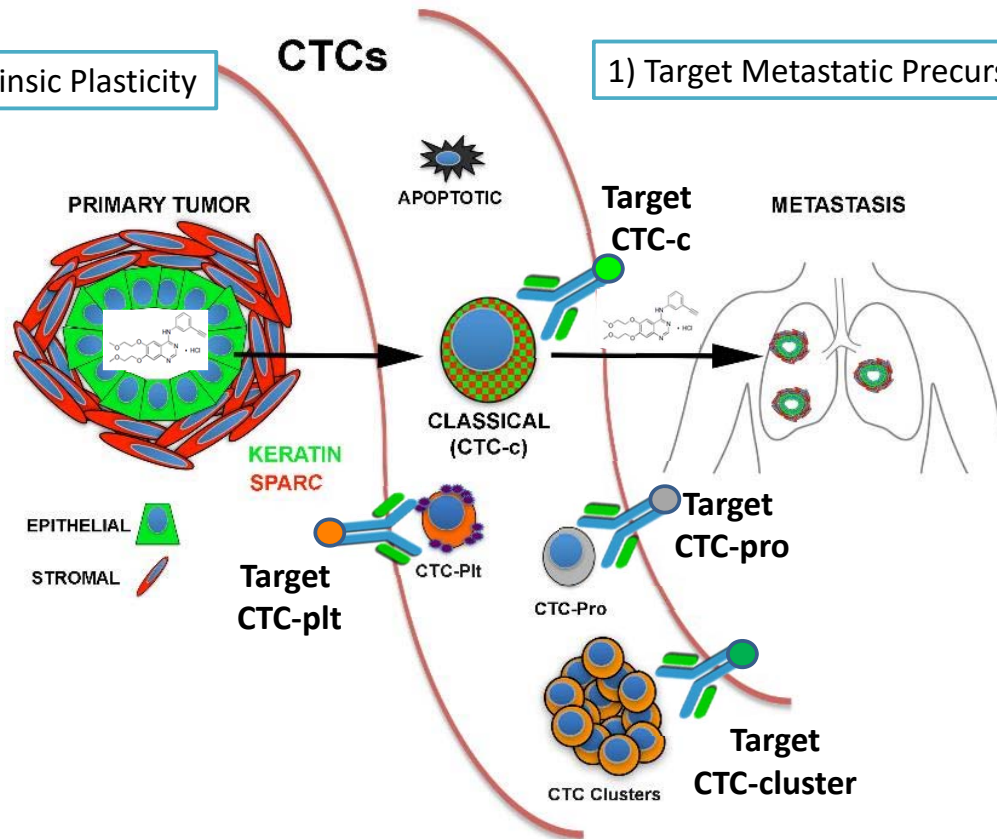


Points of Intervention Targeting EMT Plasticity

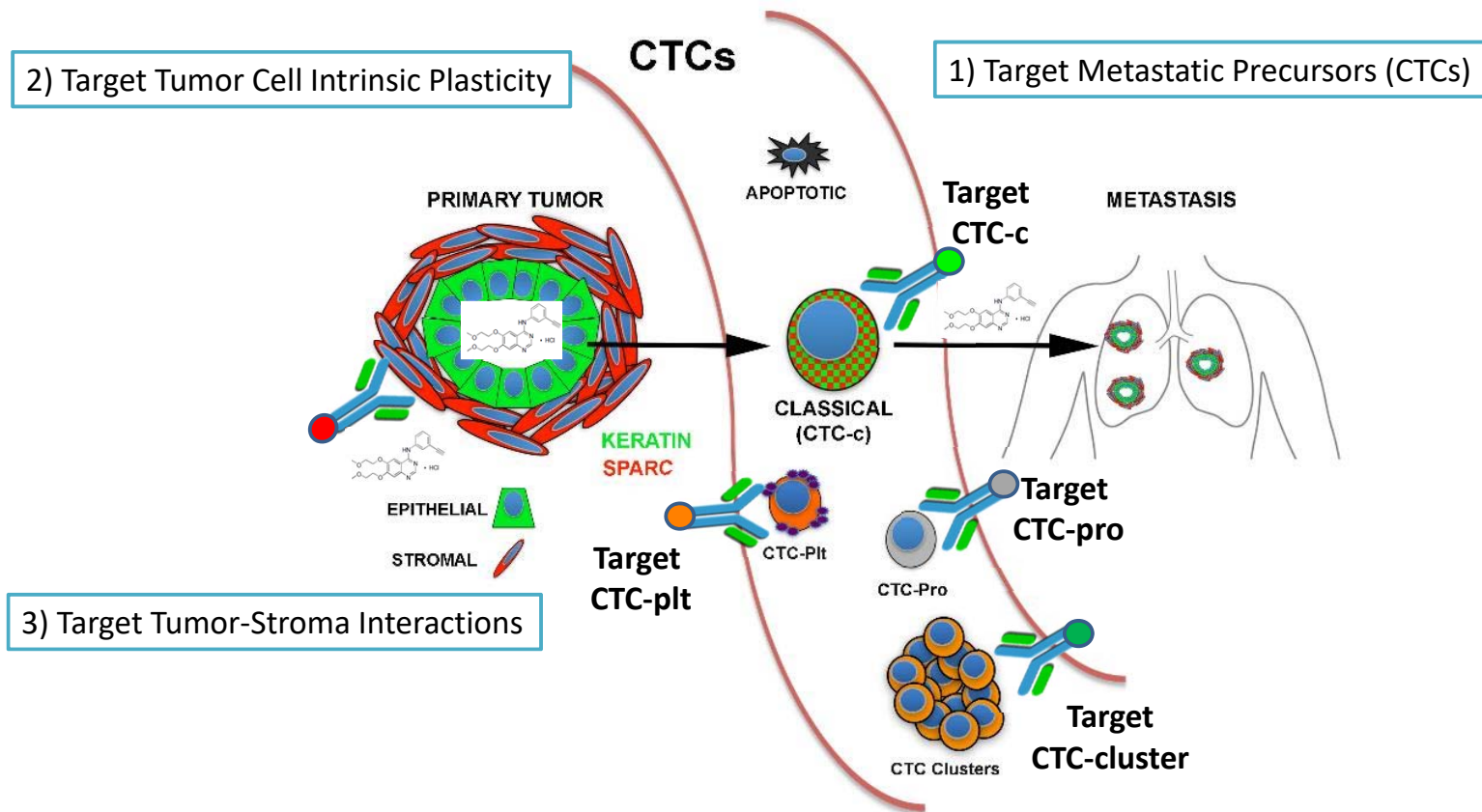
2) Target Tumor Cell Intrinsic Plasticity

CTCs

1) Target Metastatic Precursors (CTCs)



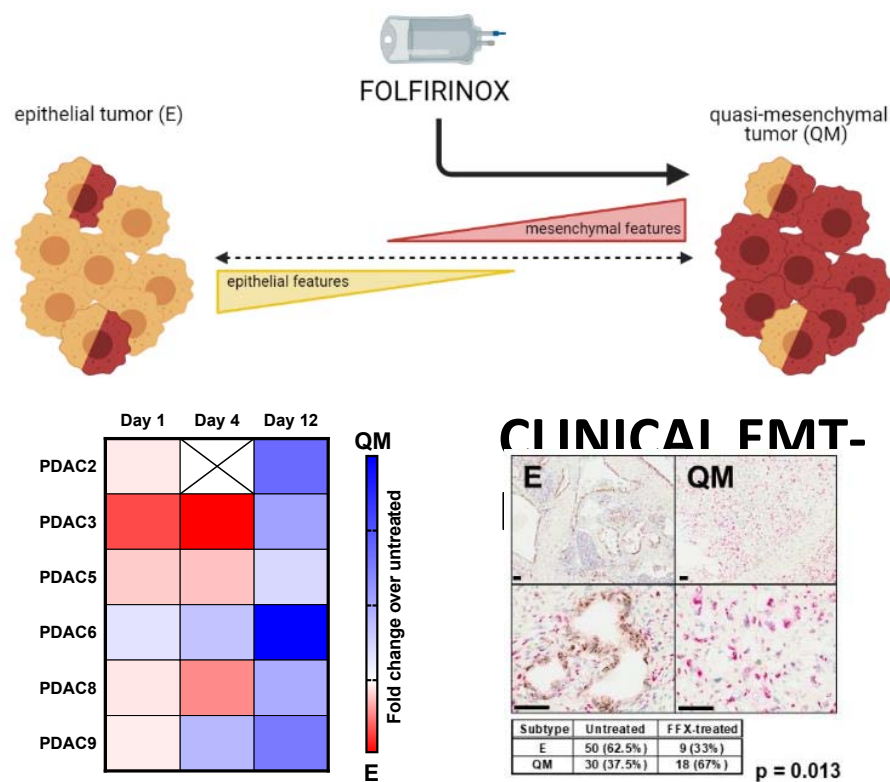
Points of Intervention Targeting EMT Plasticity



Biomarker Translation to the Clinic

EMT Plasticity leads to chemoresistance in PDAC

- Treatment of PDAC cell lines with FOLFIRINOX induces the mesenchymal state
- Neoadjuvant FOLFIRINOX patient PDAC tumors enriched for mesenchymal cells
- **CLIA EMT RNA-ISH assay** operational for patient selection and pharmacodynamic response



Porter, *PNAS*, 2019

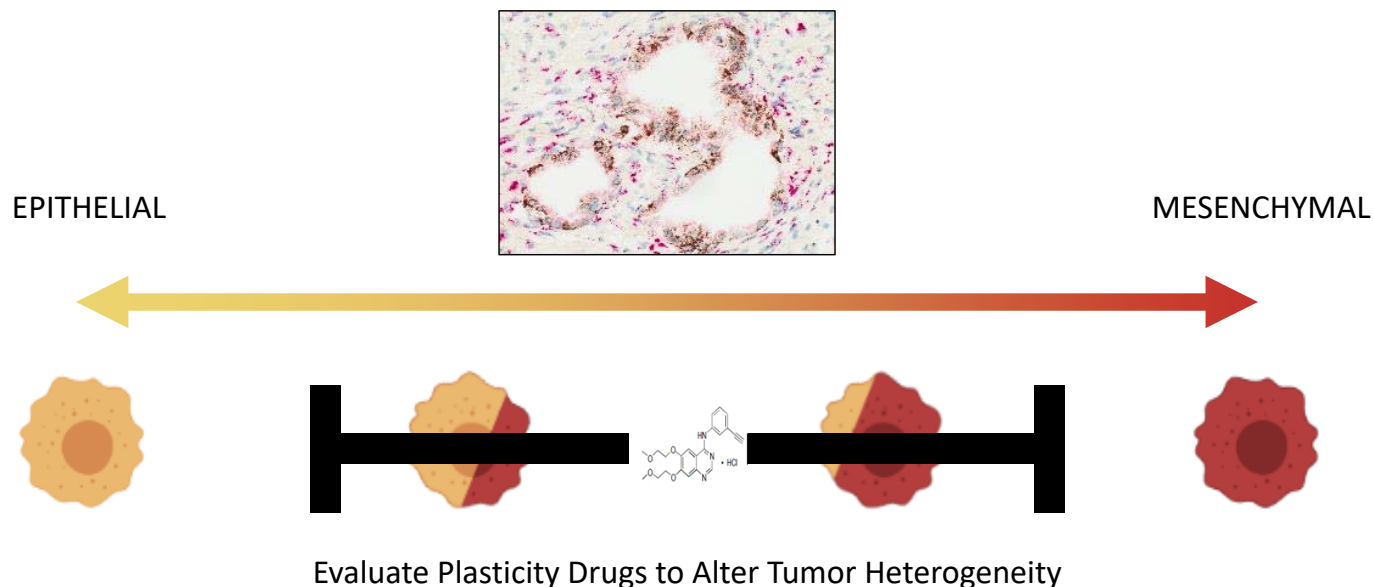
Precision Medicine: EMT RNA-ISH

EMT Status for Patient Selection in Clinical Trials



Precision Medicine: EMT RNA-ISH

EMT Status for Patient Selection in Clinical Trials



CTC Acknowledgments

MGH Cancer Center Team

Ting Lab – Joseph Franes, Matteo Ligorio, Mihir Rajurkur, Kshitij Arora, Niyati Desai, Vishal Thapar, Irun Bhan, Anupriya Kulkarni, Rebecca Porter, Eric Tai, Kevin Vo, Emily Silva, Huili Zhu, Olivia MacKenzie, Srinjoy Sil, Melissa Choz

Daniel Haber & Shyamala Maheswaran

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Daniel Haber & Shyamala Maheswaran

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David Ryan and GI oncology group

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Michael Lawrence

Pathology:

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Imaging Core:

Chen Lu

Linda Nieman

Clinical Collaborators:

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Verville Cancer
Research Foundation



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Cancer Network®

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