

Biology and Background for ctDNA; Advantages and Drawbacks of Assays Currently in Use; Knowledge Gaps

Luis Diaz, M.D.

Workshop on Circulating Tumor DNA assays in Clinical Cancer Research
Cancer Diagnosis Program, NCI
September 29, 2016



Disclosure Information

I have the following financial relationships to disclose:

Founder and shareholder in Pagerbox, Papgene and Personal Genome Diagnostics, Inc.

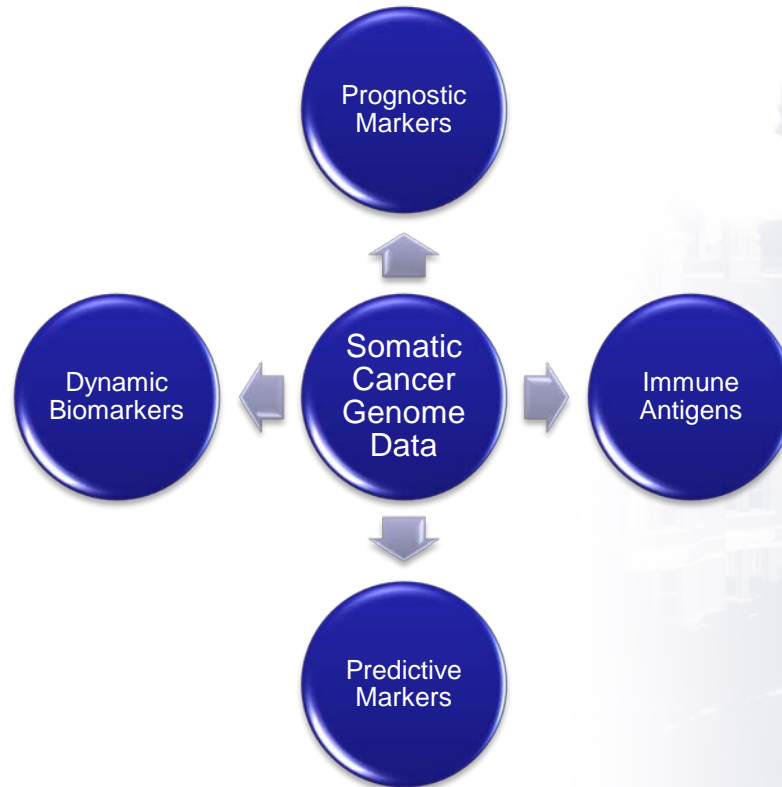
Consultant for Merck, Illumina, PGDx and Cell Design Labs

PapGene and Personal Genome Diagnostics (PGDx) s, as well as other companies, have licensed technologies from Johns Hopkins University, on which LD is an inventor. These licenses and relationships are associated with equity or royalty payments. The terms of these arrangements are being managed by Johns Hopkins University in accordance with its conflict of interest policies.

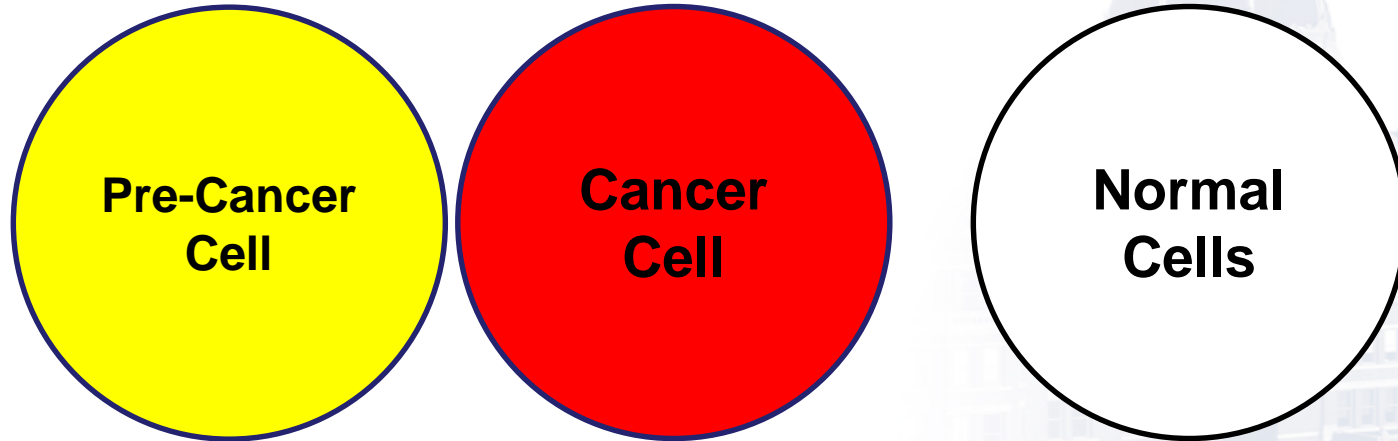
Clinical Application of Cancer Genetics

Mutations as Biomarkers

Clinical Application of Cancer Genetics



Mutations are highly specific



**Pre-Cancer
Cell**

**Cancer
Cell**

**Normal
Cells**

Mutations

No Mutations

Access to Somatic Mutations

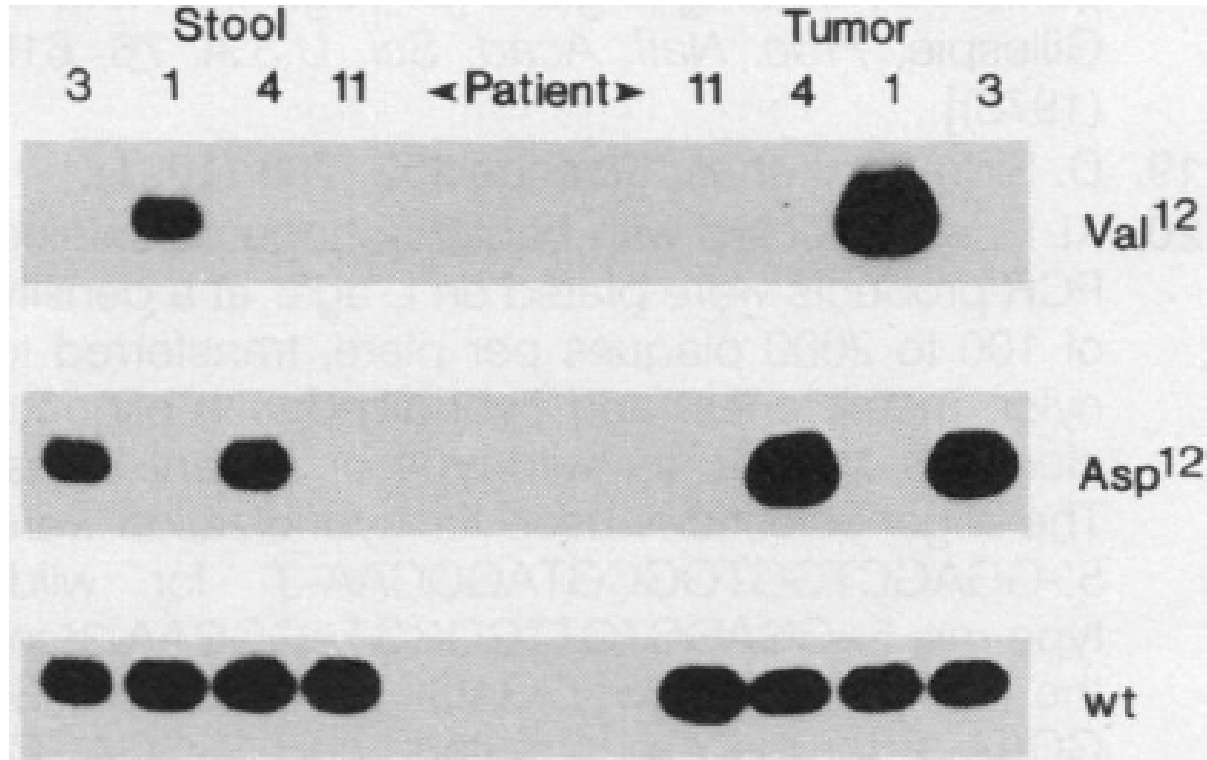
Tumor Tissue

- FFPE
- Frozen tissue

Blood & other bodily fluids

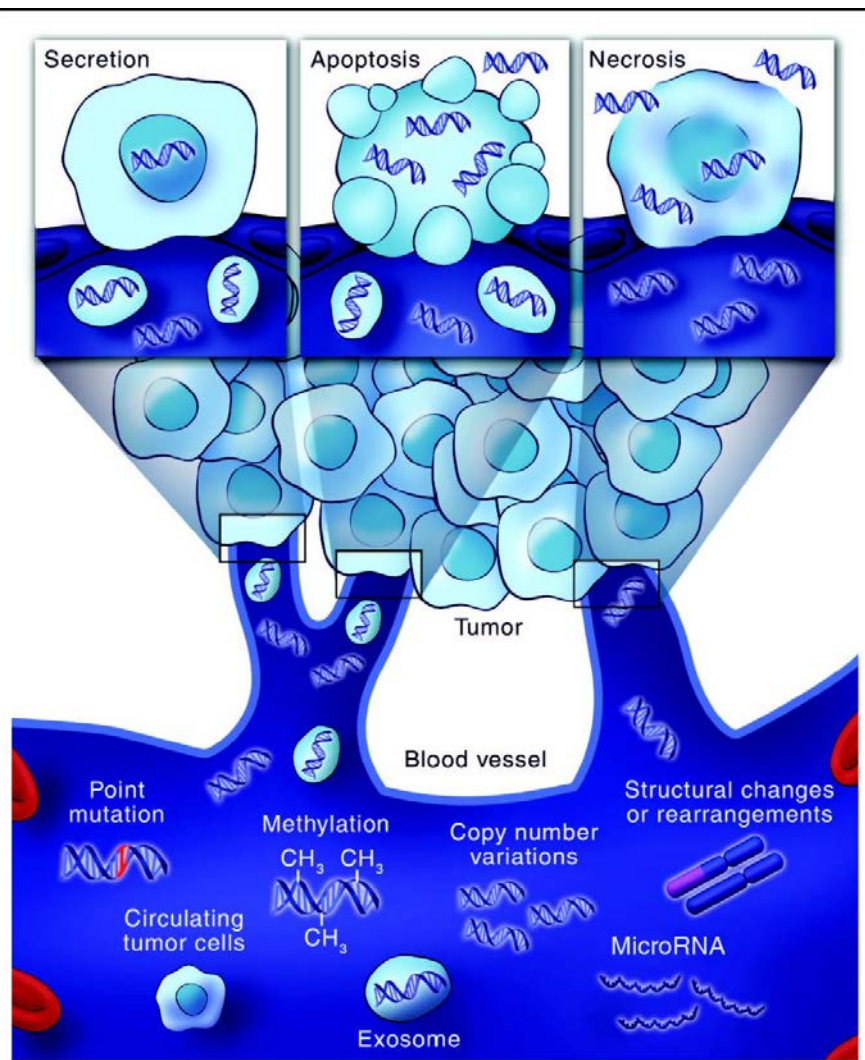
- Cell-free DNA
- Circulating tumor cells (CTCs)

Mutant *RAS* in stool from patients with CRC



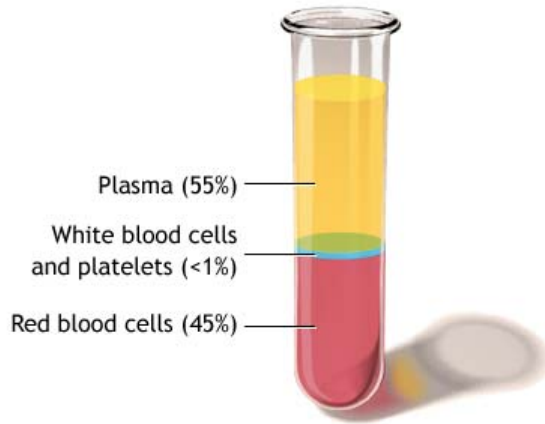
Clinical Application of Cancer Genetics

Liquid Biopsies



- DNA fragments of 120-200bp with half life of ~2 hours
- Real-time, non-invasive, multi-lesions, potentially cheaper (considering cost of biopsies)
- Often very low amount of ctDNA in the sea of wild type DNA - "Needle in a farm"
- Specific to tumor

Liquid Biopsy



Plasma

Water 91%

Proteins 7%

Metabolites (trace)

Cell-free DNA (trace)

Cellular Components

White Blood Cells 2-3%

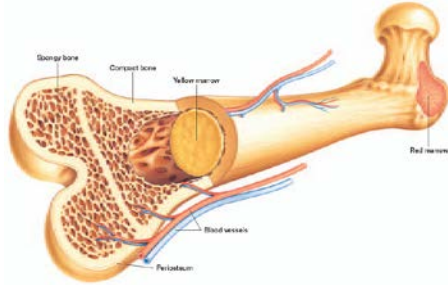
Platelets 2-3%

Red Blood Cells 90%

Circulating tumor cells (trace)

Source circulating cell-free DNA

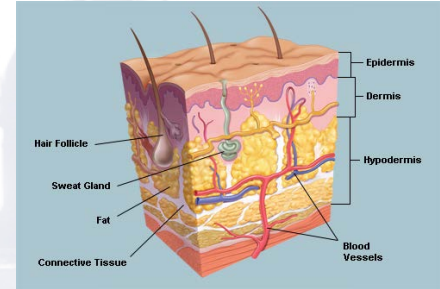
Bone Marrow



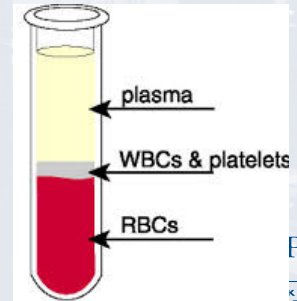
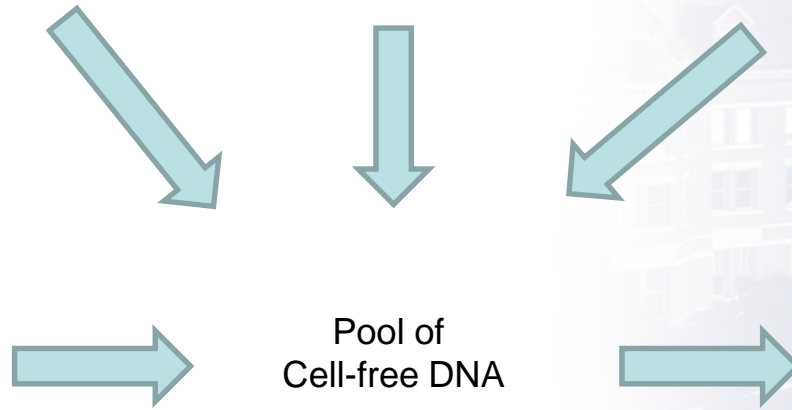
GI Tract



Skin

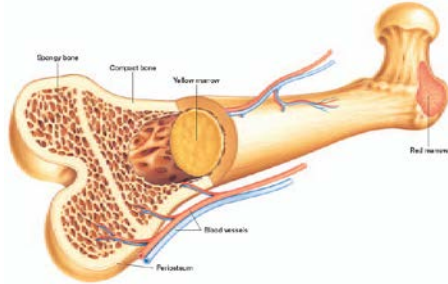


Fetal DNA



Source circulating cell-free DNA

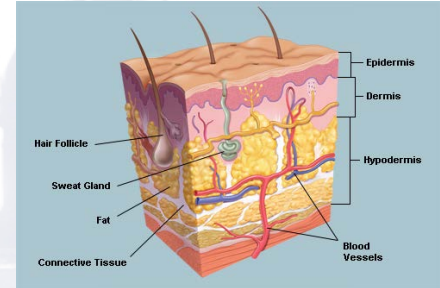
Bone Marrow



GI Tract



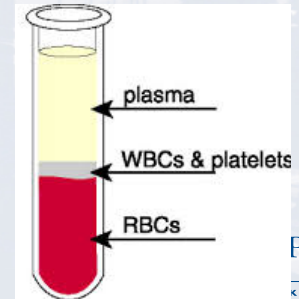
Skin



Transplanted Tissue DNA

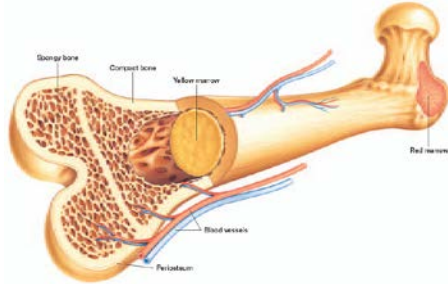


Pool of
Cell-free DNA



Source circulating cell-free DNA

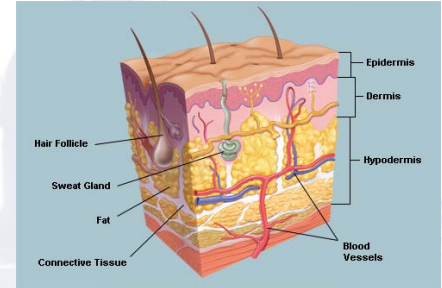
Bone Marrow



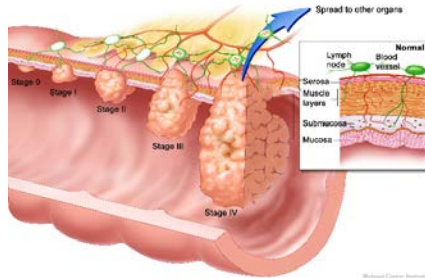
GI Tract



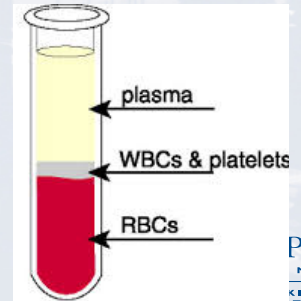
Skin



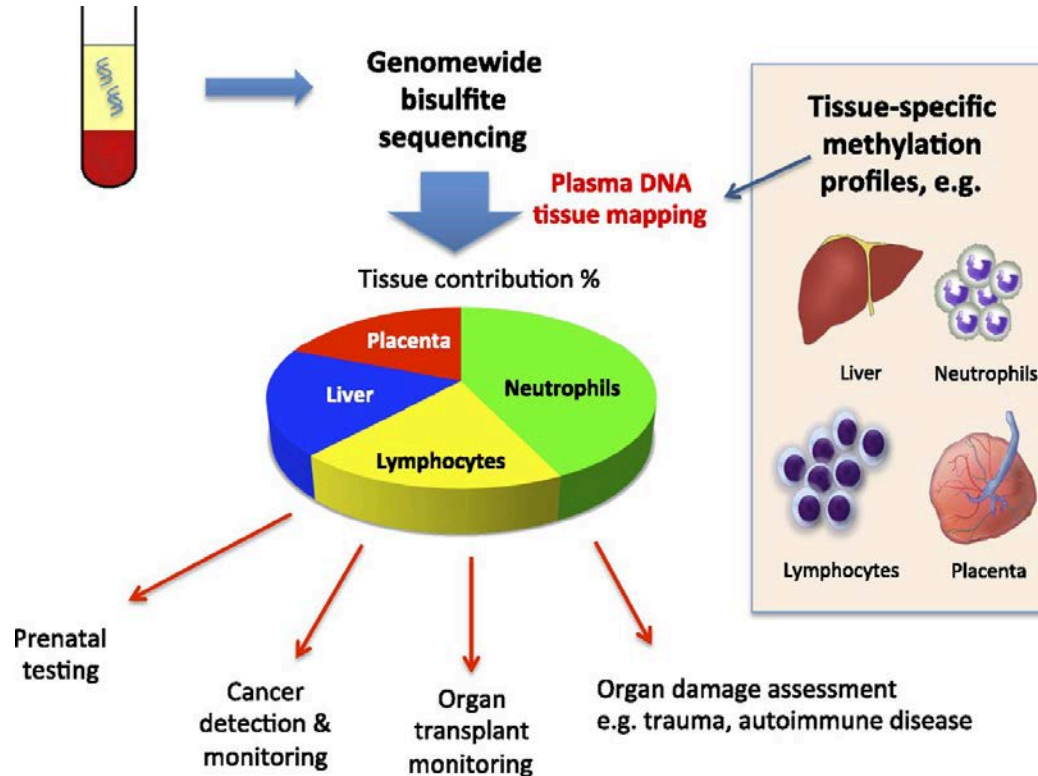
Tumor DNA



Pool of
Cell-free DNA

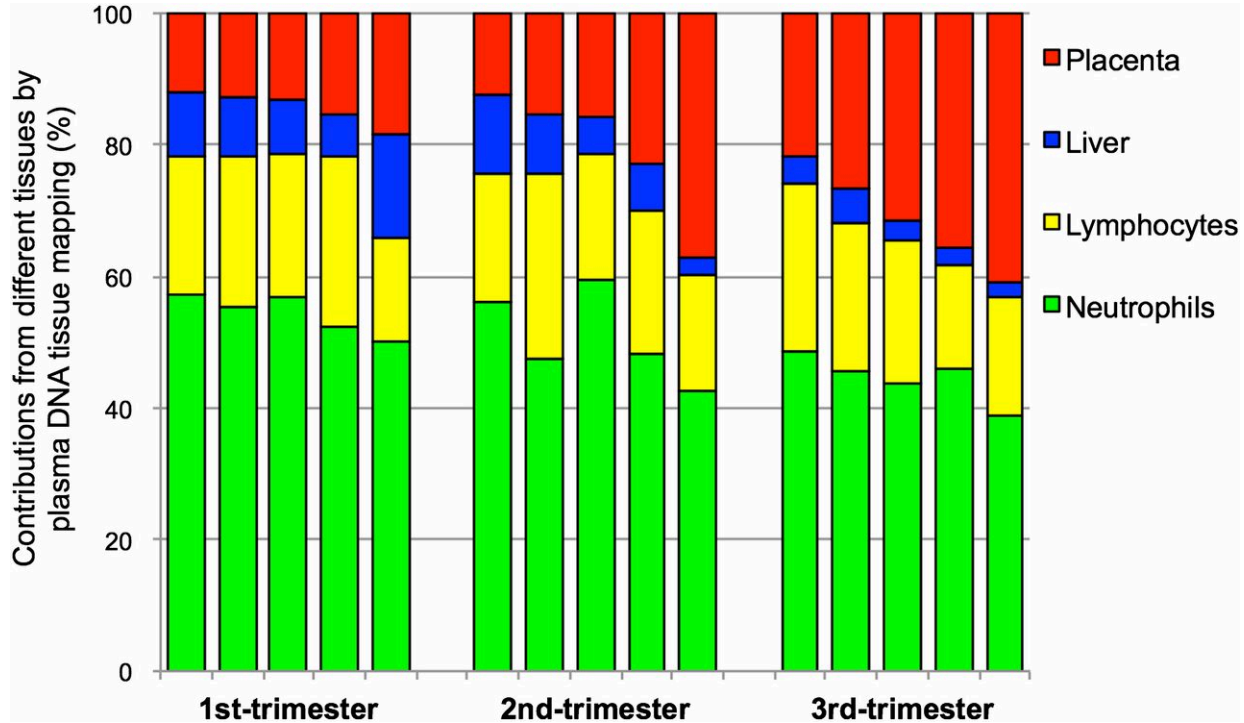


Schematic illustration of the principle of plasma DNA tissue mapping by genome-wide methylation sequencing and its applications.



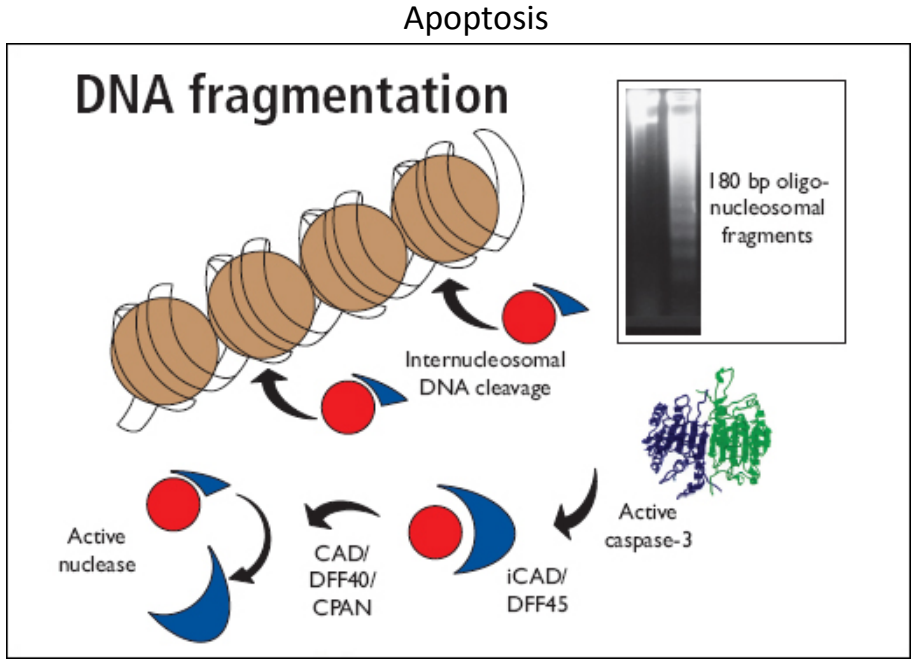
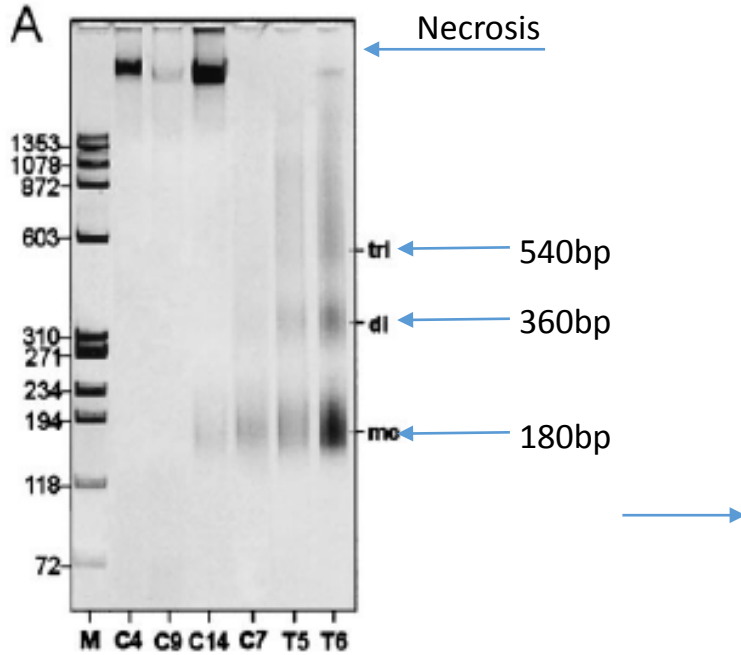
Kun Sun et al. PNAS 2015;112:E5503-E5512

Percentage contributions of different tissues to plasma DNA for 15 pregnant women.

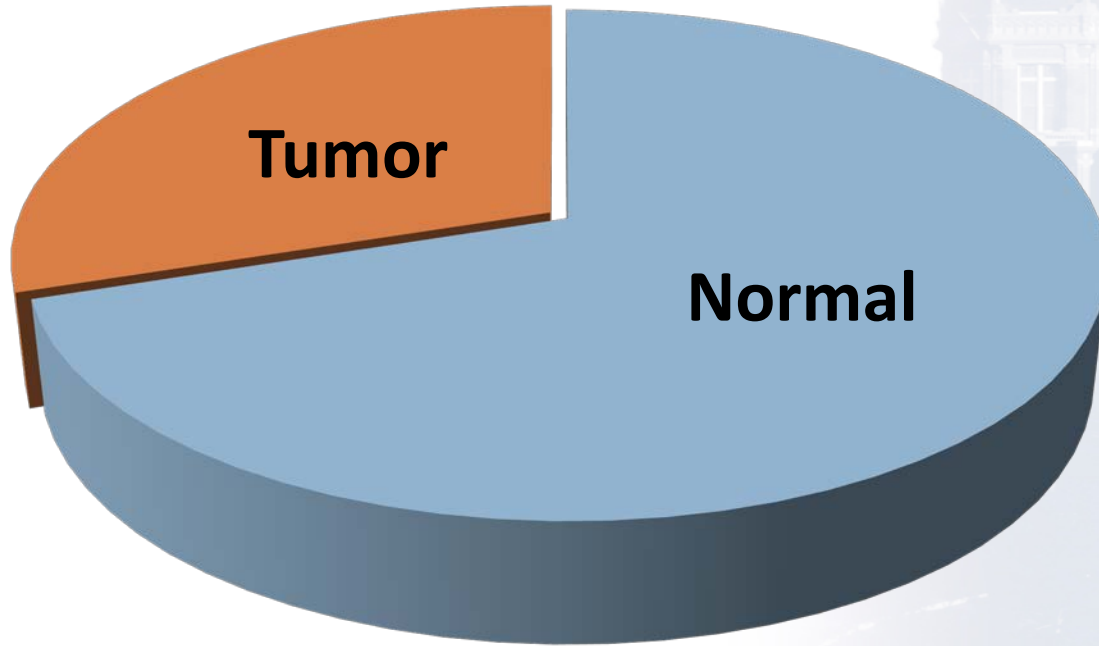


Kun Sun et al. PNAS 2015;112:E5503-E5512

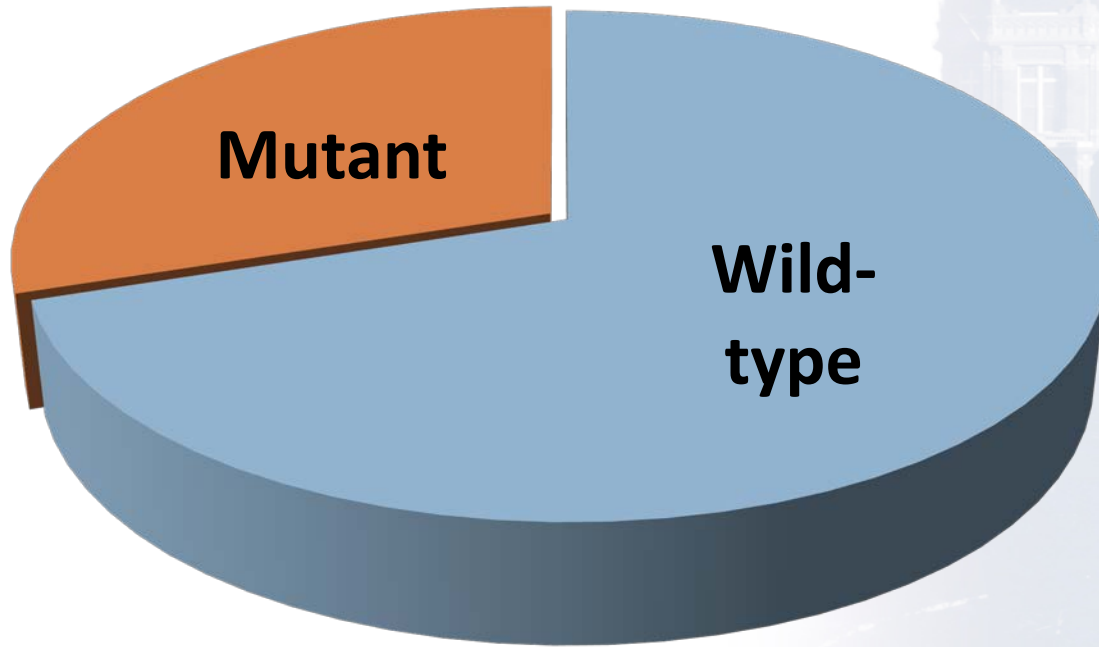
Cell-free DNA – origin



Circulating cell-free DNA in a Cancer Patient



Circulating cell-free DNA in a Cancer Patient



Technology to assess circulating tumor DNA

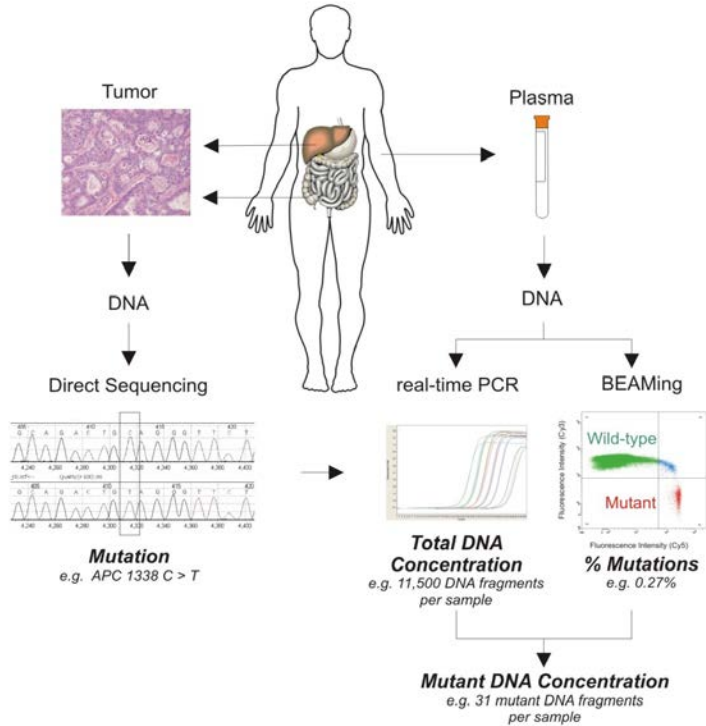
Digital PCR

- Best for individual point mutations but can be used for crude copy number analysis
- Mutation needs to be known ahead of time (ie BRAF v600e)
- Sensitivity is dependent on specific mutation and assay optimization
- Multiplexing assay is possible
- Fast and highly reproducible – results in hours
- Minimal bioinformatics needs
- Inexpensive

Next-generation Sequencing

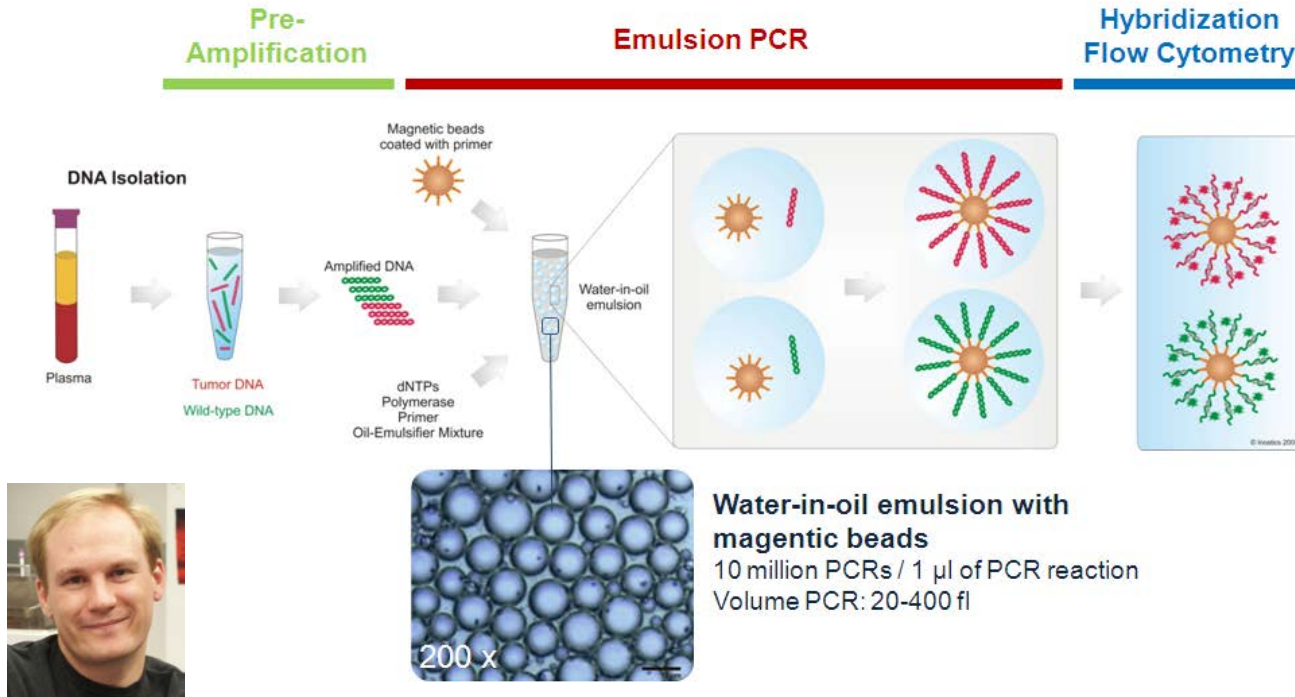
- Evaluates genomic regions of interest using PCR or capture-based methods
- Has been used for point mutations, rearrangements, genomic amplification, aneuploidy, whole exome and whole genome sequencing
- High false discovery rate that requires pre-sequencing barcoding and post-sequencing bioinformatics for error suppression
- Expensive
- Turnaround time 1-2 days at best

Digital PCR



- **BEAMing – emulsion-digital PCR**
- **Sensitivity – 0.01% (depends on mutation)**
- **Mutation to be tested needs to be known ahead of time**

BEAMing



Devin
Dressman

Wild-type fragments

Before Surgery
Day 0

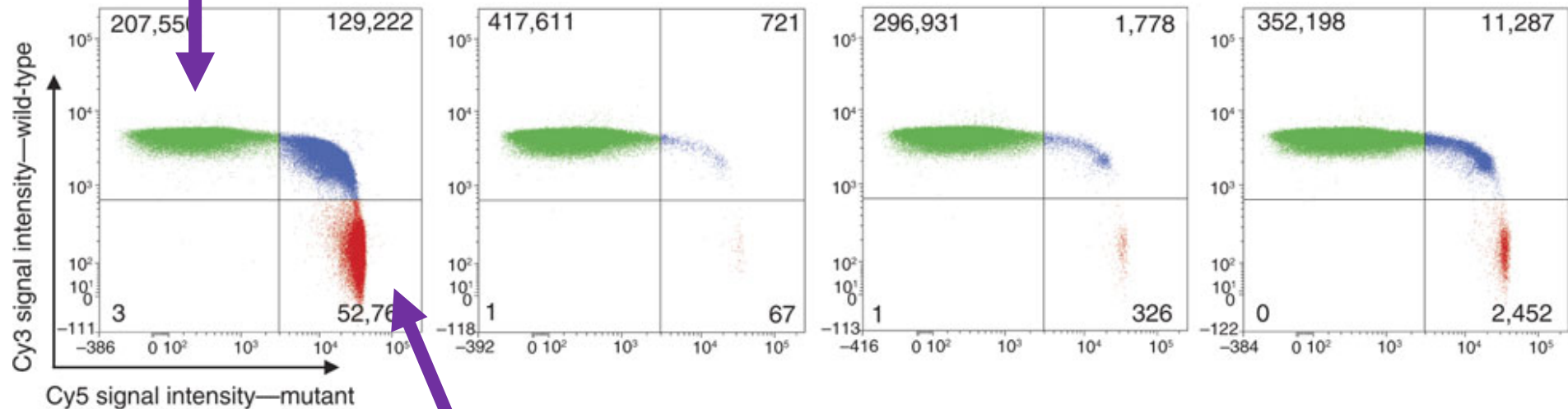
After Surgery
Day 1

CT scan negative

After Surgery
Day 42

CT scan positive

After Surgery
Day 244



13.4 %

0.015 %

0.11 %

0.66 %

Mutant fragments

Percent Mutant APC

Applications of ctDNA

- Genotyping cancer & identify actionable genetic alterations
 - For patients lack tissue for molecular analysis
 - For patients whose tumors have evolved over time and treatment (too risky to perform or after relapse when biopsies are not routine)
 - Discordance between mutations in primary/metastases lesions
 - Acquired resistance (e.g., patients who develop resistance to EGFR blockade)
- Monitoring of tumor burden / response to treatment (vs. CEA or imaging)
- Detection of Occult Disease
 - Minimal Residual Disease
 - Early Detection/Screening

Potential of Liquid Biopsies in Precision Medicine

Monitoring tumor dynamics

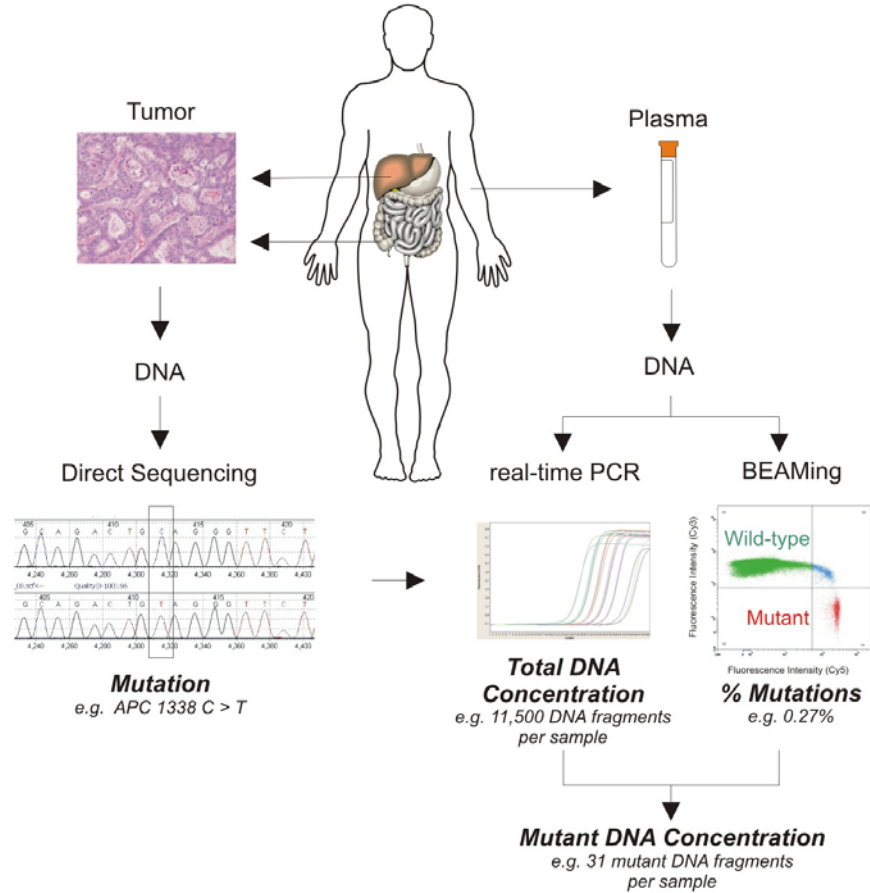
Molecular Analysis



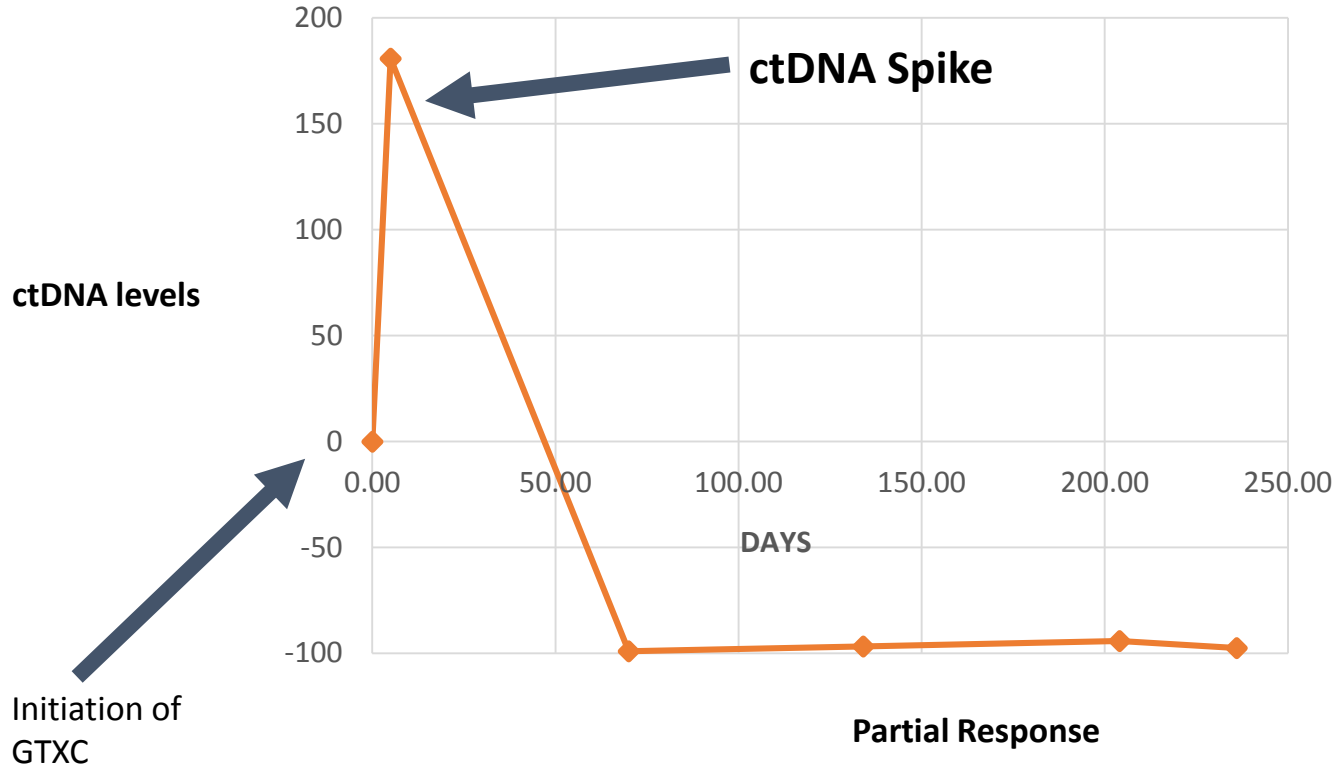
Kerstin Schmidt



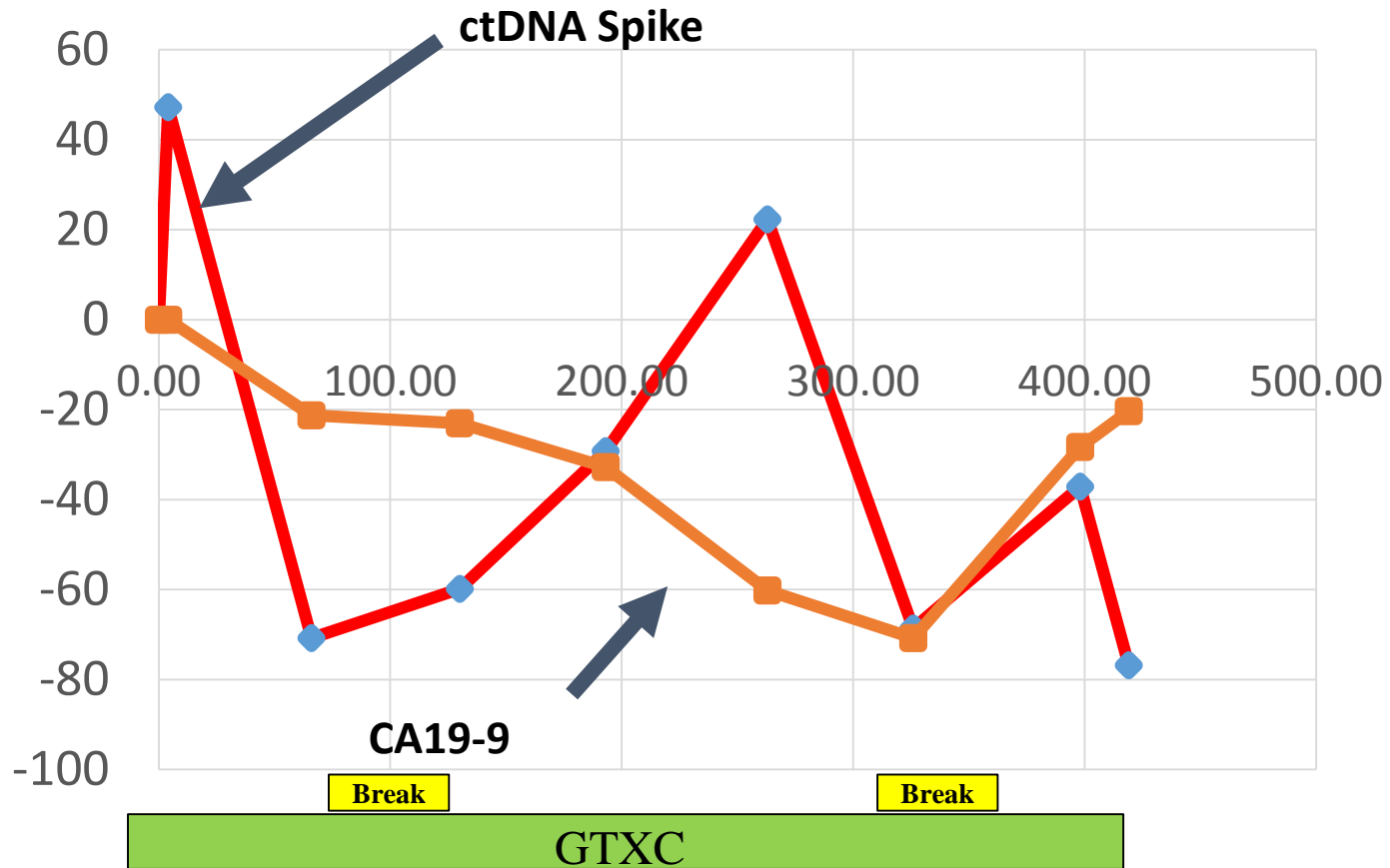
Frank Diehl



Circulating tumor DNA is a rapidly dynamic biomarker

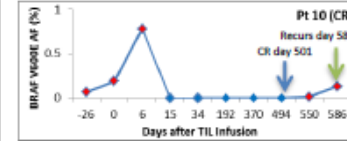
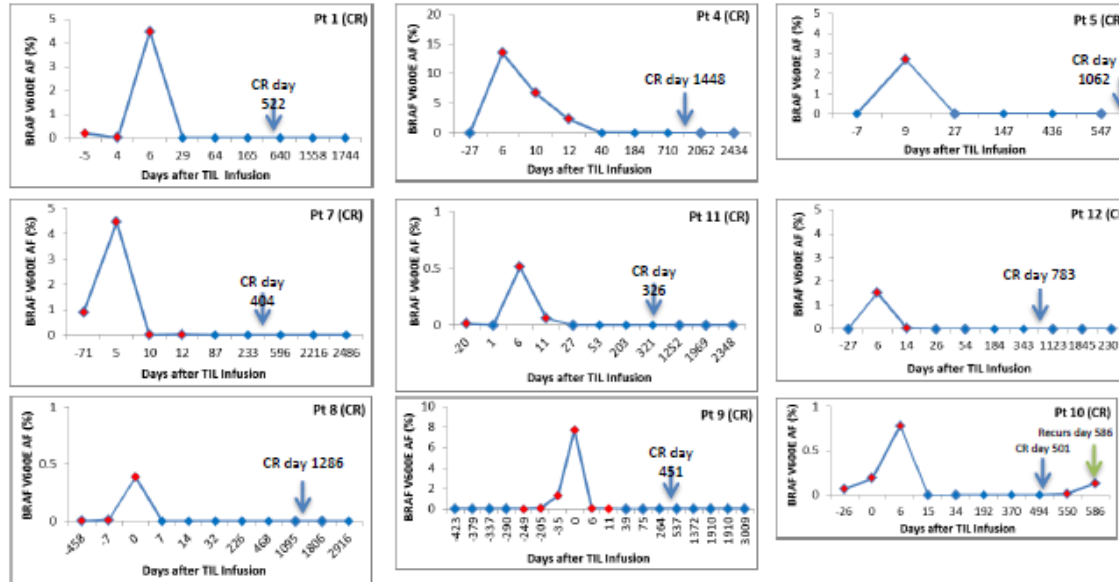


CTDNA VS CA19-9



Circulating Tumor DNA as an Early Indicator of Response to T-Cell Transfer Immunotherapy 2 in Metastatic Melanoma

Patients with CR





Clinical Application of Cancer Genetics

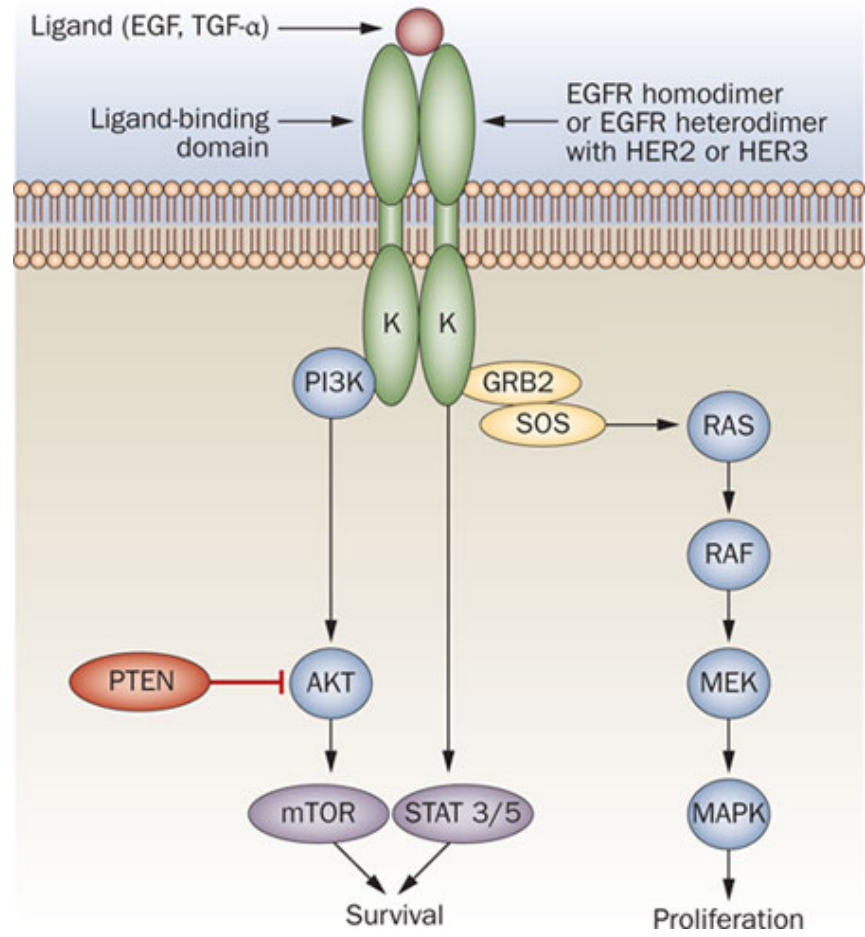
Tracking Resistance

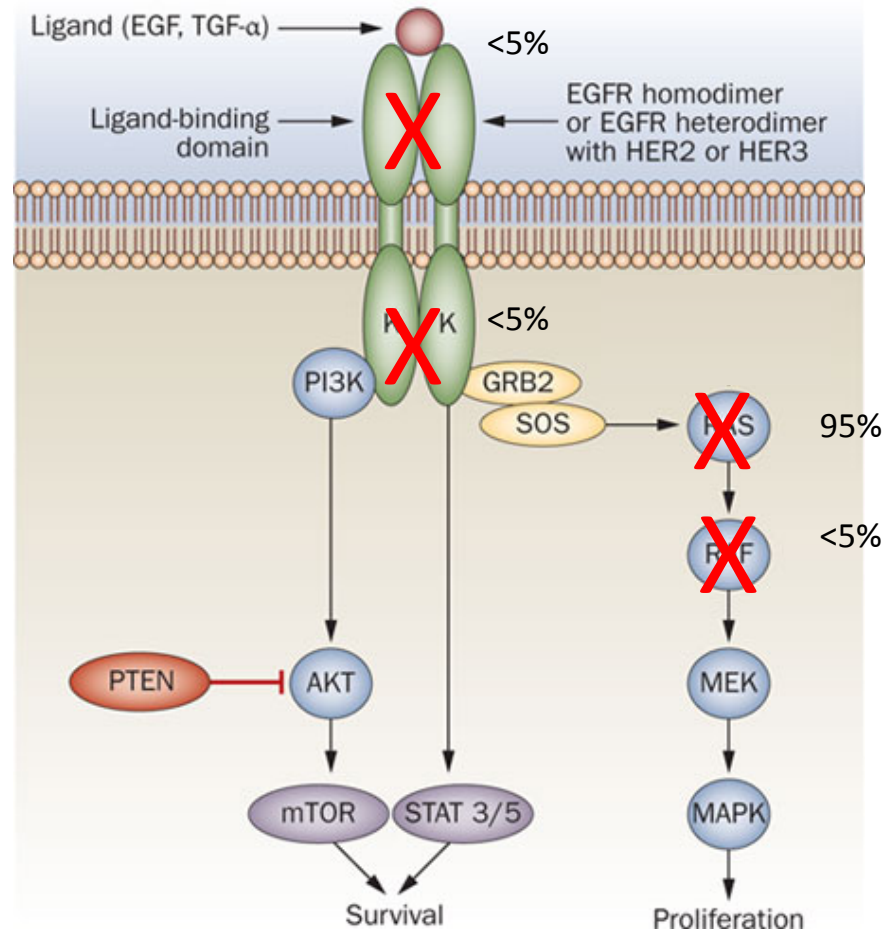
Tracking Resistance

- Interrogated all exons of KRAS, NRAS, BRAF, PIK3CA and EGFR
- 96% of cases had at least 1 mutation KRAS or NRAS

Sample ID	Pre-Treatment							Post-Treatment							
	KRAS 12	KRAS 13	KRAS 61	NRAS 12	NRAS 61	BRAF 600	EGFR 794	EGFR 714	KRAS 12	KRAS 13	KRAS 61	NRAS 12	NRAS 61	BRAF 600	EGFR 714
AMG 011									Single mutation						
AMG 022									Single mutation	Single mutation					
AMG 028									Multiple mutations						
AMG 034										Single mutation					Single mutation
AMG 040															
AMG 046									Single mutation			Single mutation			
AMG 105															
AMG 109									Single mutation				Multiple mutations		
AMG 114									Multiple mutations					Single mutation	
AMG 121													Single mutation	Single mutation	
AMG 126									Single mutation				Single mutation		
AMG 132									Single mutation						
AMG 140									Single mutation						
AMG 148										Single mutation					
AMG 155									Multiple mutations		Multiple mutations		Multiple mutations		
AMG 161										Single mutation					
AMG 167									Single mutation		Single mutation				
AMG 180									Multiple mutations				Multiple mutations		
AMG 188									Single mutation				Multiple mutations		
AMG 195									Single mutation		Multiple mutations				
AMG 208									Multiple mutations				Single mutation		
BARD 101 PLS									Single mutation		Single mutation		Single mutation		
BARD 102 PLS									Multiple mutations		Single mutation				
BARD 103 PLS									Multiple mutations						
CRC 188 PLS									Single mutation						
CRC 189 PLS											Multiple mutations				
CRC 190 PLS									Single mutation		Multiple mutations		Multiple mutations	Single mutation	
CRC 191 PLS									Multiple mutations		Single mutation				

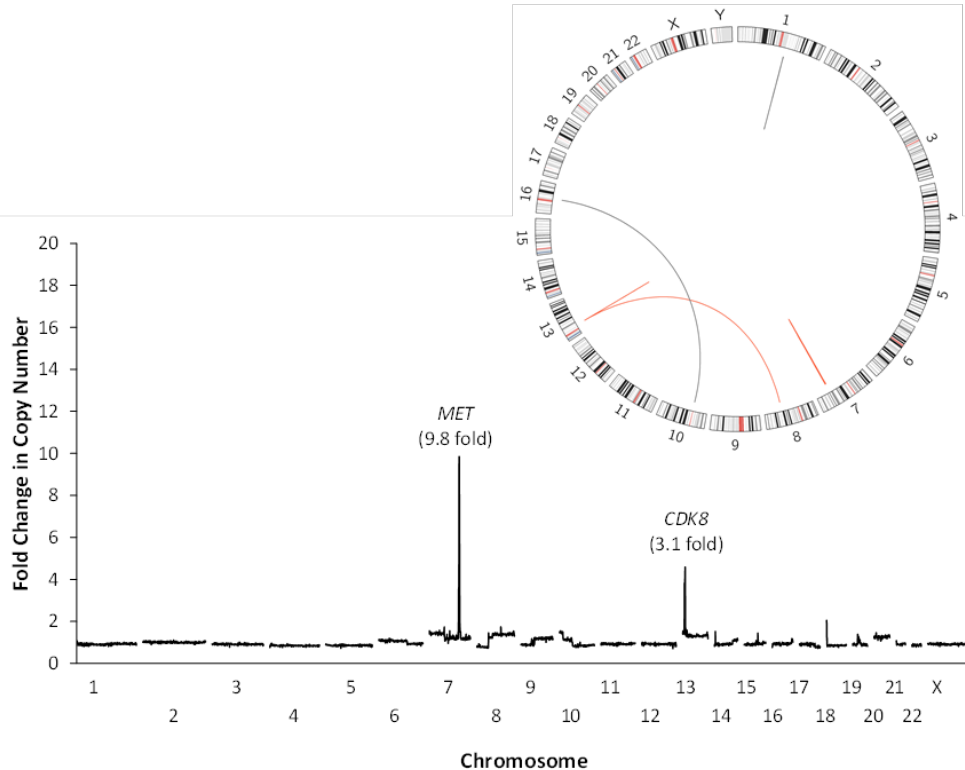
 Single mutation
 Multiple mutations





WGS of plasma DNA in EGFR resistant CRC patient

High-level Focal Amplification of *MET*



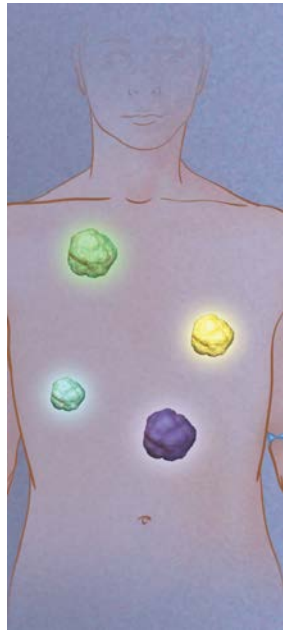
A total of 630 Gb of sequence data were obtained, corresponding to 145x sequence coverage of cell-free plasma genomic DNA.

Identified in plasma sample following clinical resistance:

- Q61H mutation in *KRAS*
- focal high-level (>9 fold) amplification of *MET*
- focal high-level (>3 fold) amplification of *CDK8*

These were not detected in pre-treatment tumor samples

Tracking Resistance



KRAS WT
NRAS WT
EGFR WT
MET WT

EGFR BLOCKADE

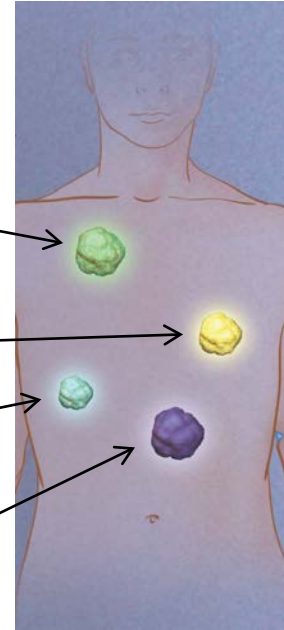


KRAS Mutant

NRAS Mutant

MET Amplified

EGFR Mutant

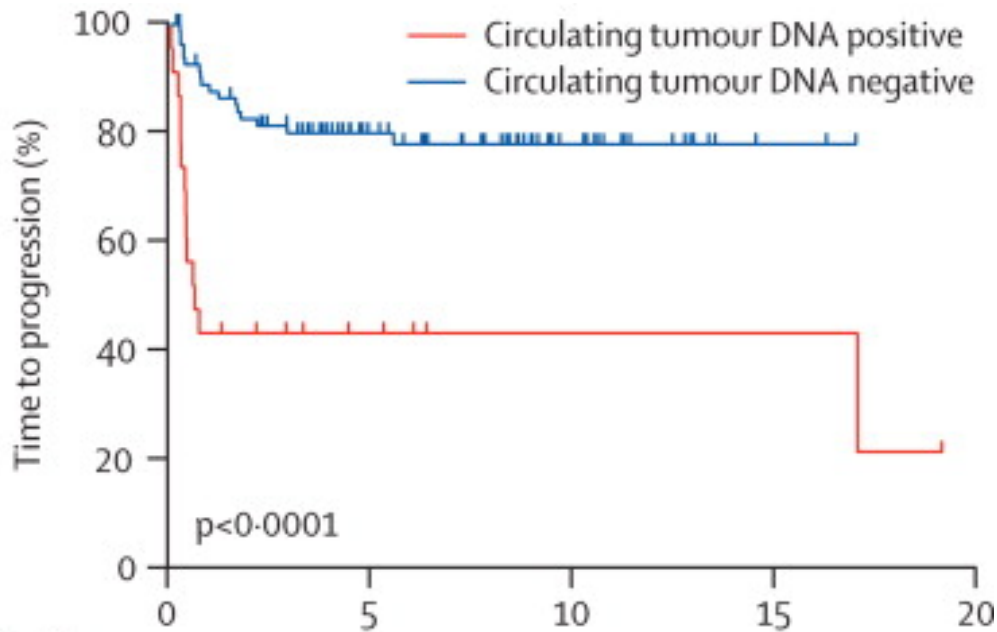


Potential of Liquid Biopsies in Precision Medicine

Molecular Remission

ctDNA monitoring in patients with diffuse large B-cell lymphoma

- 108 patients
- VDJ gene segments of the rearranged immunoglobulin receptor genes
- ctDNA measured after 2 cycles of therapy



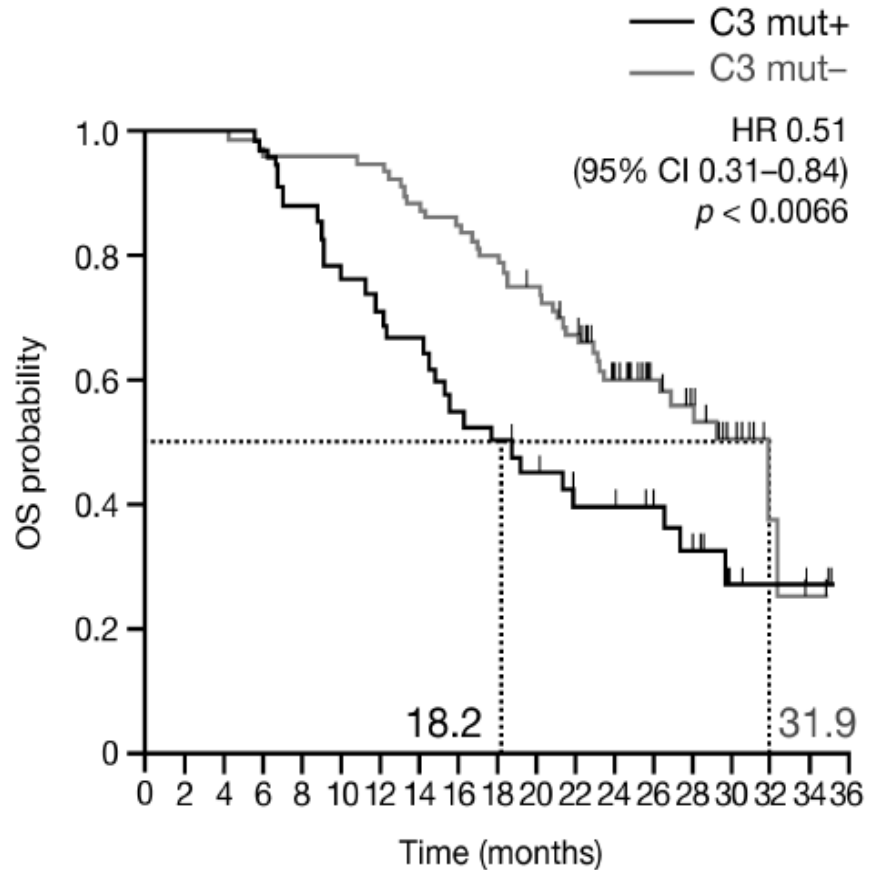
*National Cancer Institute and Adaptive Biotechnologies

	Number at risk							
	0	5	10	15	20	25	30	35
Circulating tumour DNA negative	84	62	42	33	17	8	2	0
Circulating tumour DNA positive	24	8	5	2	2	2	2	1

Clearance of circulating EGFR mutations in metastatic lung cancer

- 122 patients with EGFR mutant NSCLC
- Treated with erlotinib-based regimen
- Determined using allele-specific PCR after 3 cycles of therapy

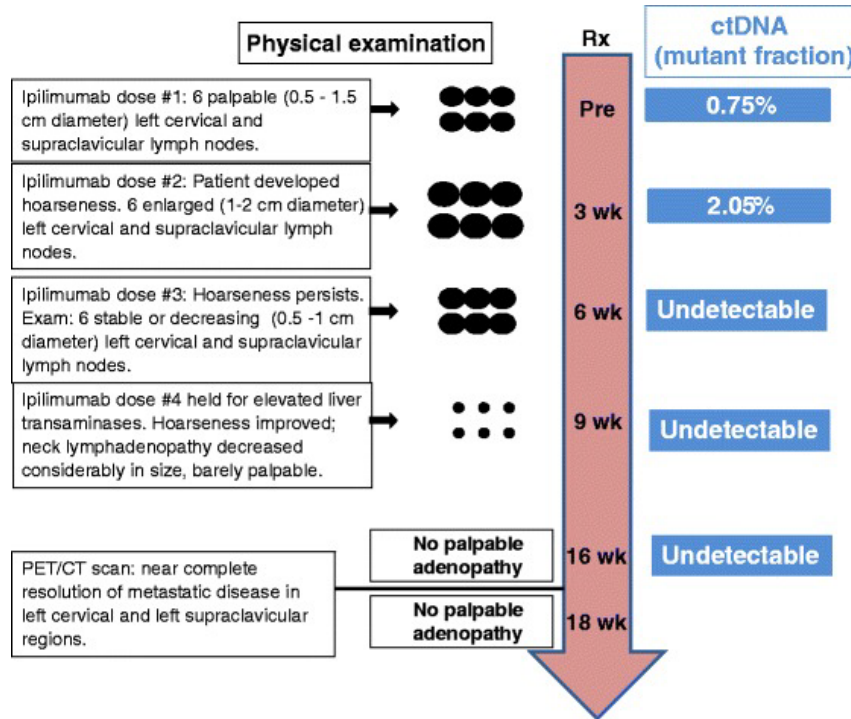
*Hong Kong Cancer Institute,
Roche, Genentech



Patients, n

C3 mut+	42	42	42	41	37	32	30	28	23	21	18	14	14	12	9	4	3	2	0
C3 mut-	80	80	80	77	77	77	76	71	68	64	59	52	38	29	22	12	3	1	0

Monitoring response to checkpoint inhibitors using ctDNA

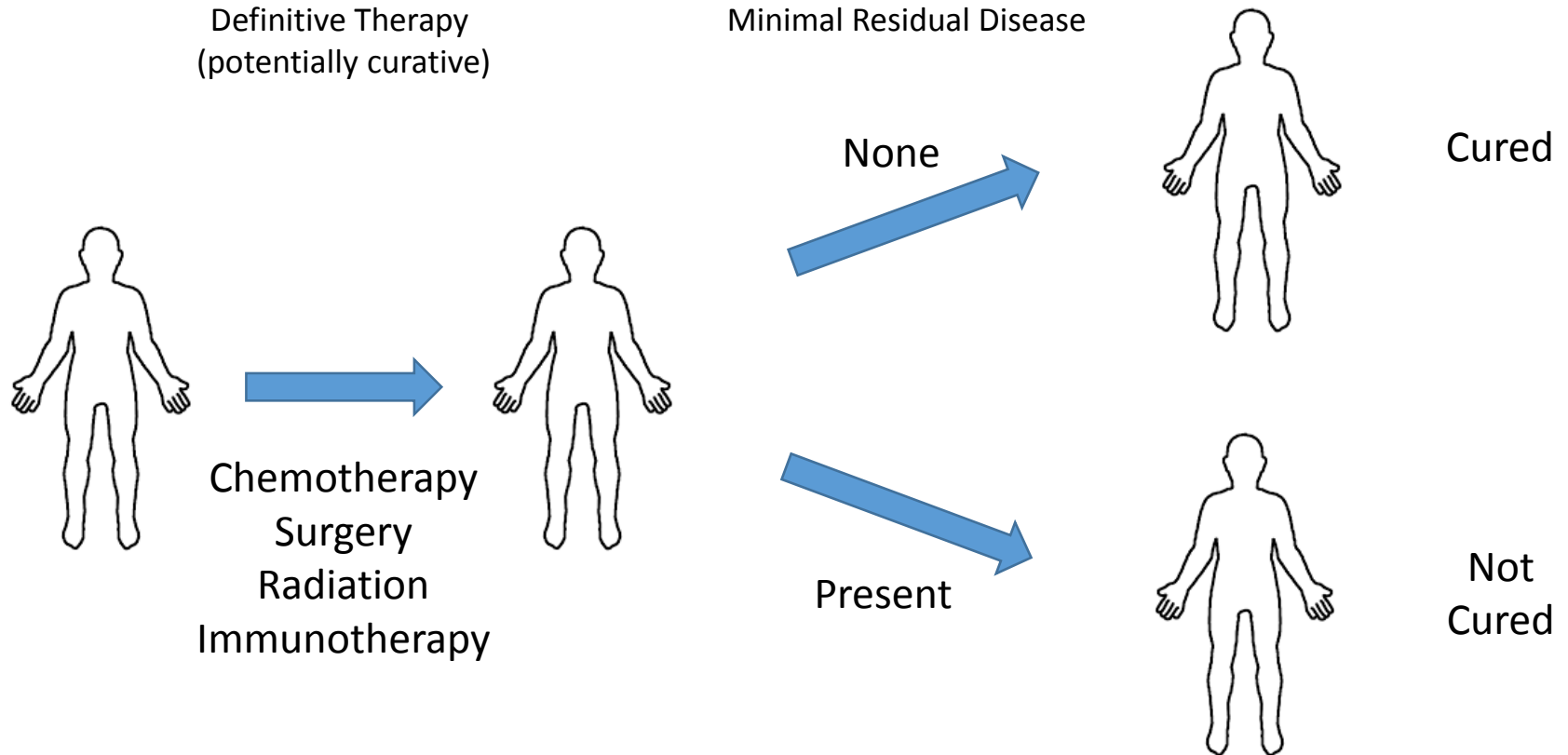


ctDNA levels increased initially as lymphadenopathy progressed by examination, but then became undetectable 3 weeks prior to clinical improvement.

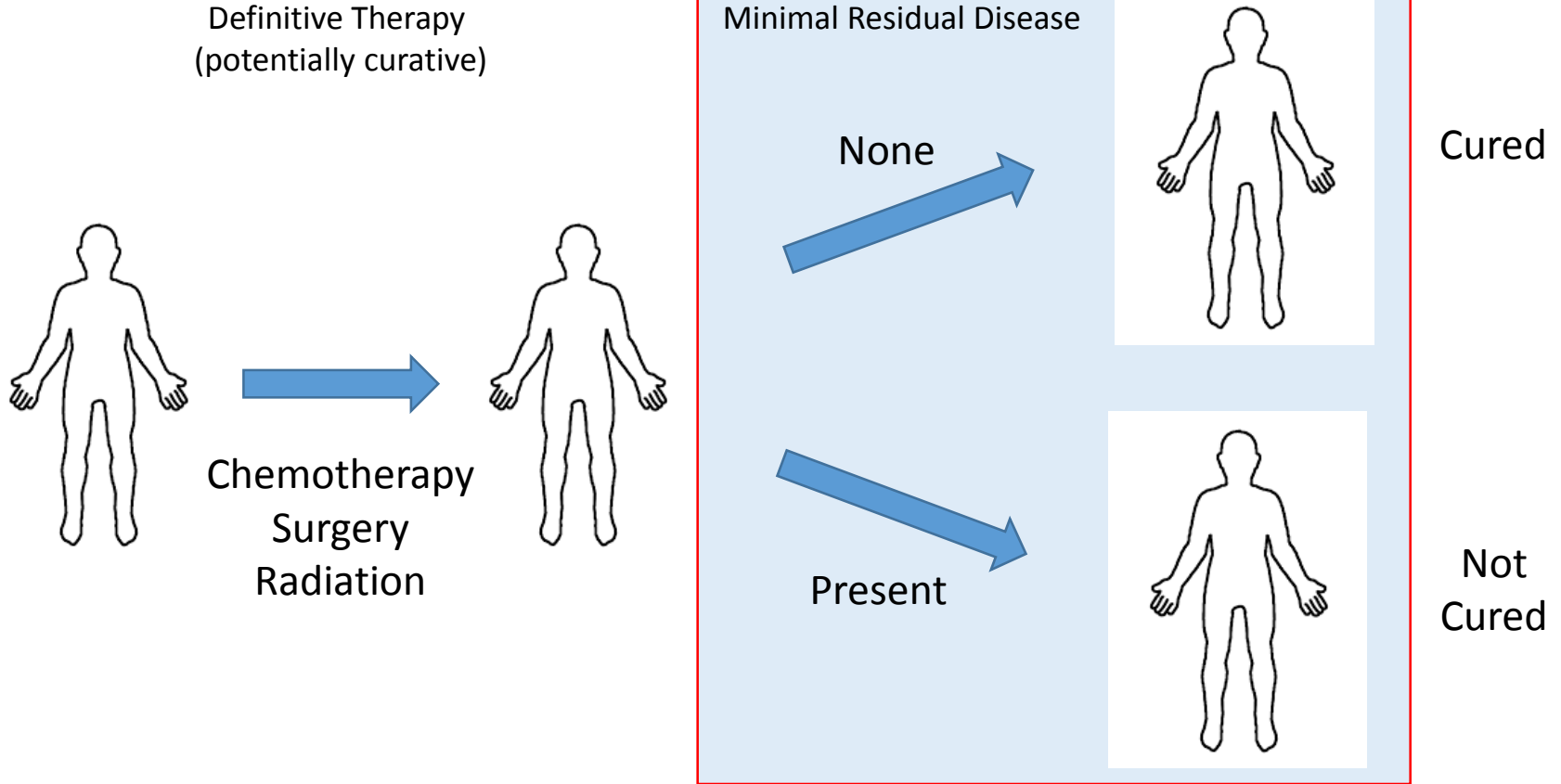
Clinical Application of Cancer Genetics

Minimal Residual Disease

What is Minimal Residual Disease (MRD)?



What is Minimal Residual Disease (MRD)?



Systemic Approaches to Detect MRD

Imaging (FDG-PET or CT Scan)

- Poor sensitivity for microscopic disease
- Variable specificity

Protein Biomarkers(e.g. CA19-9, CEA, CA-125)

- Long half-life
- Often Non-specific

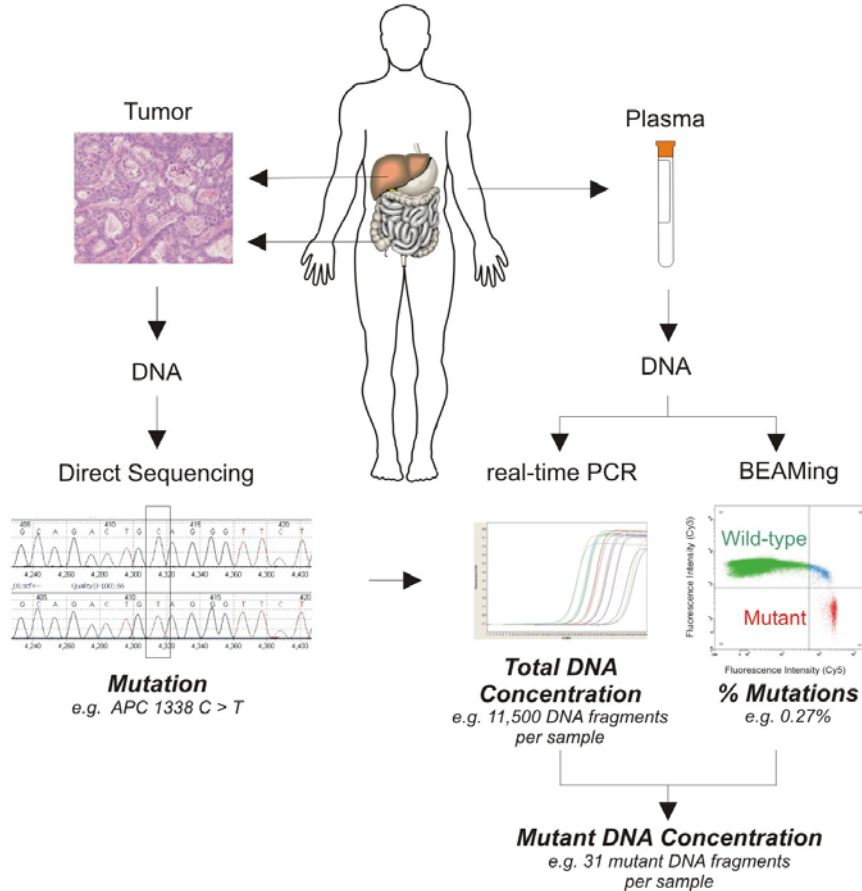
CTCs

- Poor sensitivity for microscopic disease
- Does not localize disease

Circulating Nucleic Acids

- Does not localize disease
- Highly specific

Molecular Analysis



Wild-type fragments

Before Surgery
Day 0

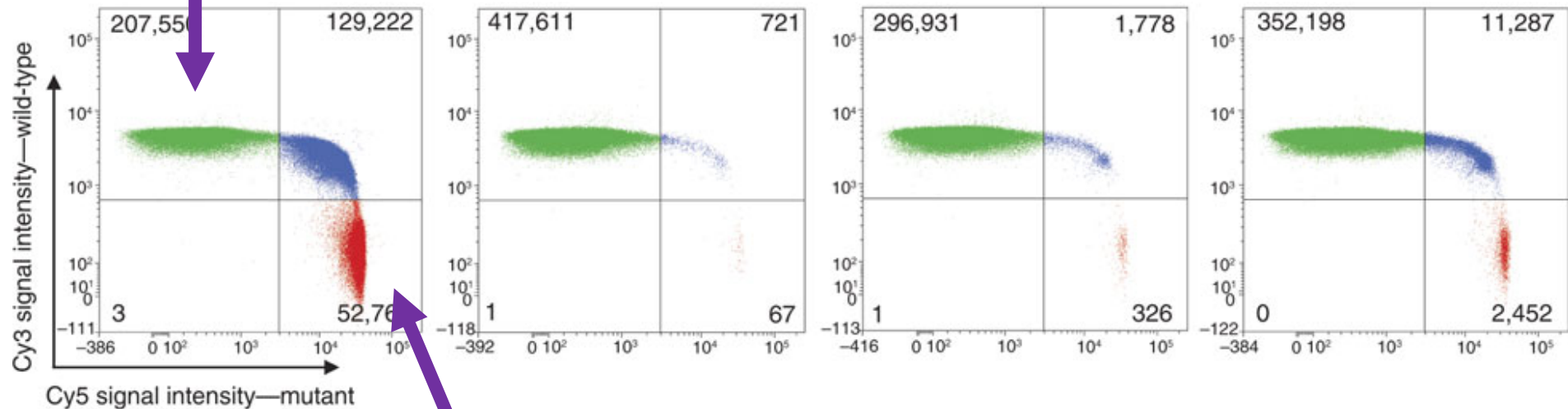
After Surgery
Day 1

CT scan negative

After Surgery
Day 42

CT scan positive

After Surgery
Day 244



13.4 %

0.015 %

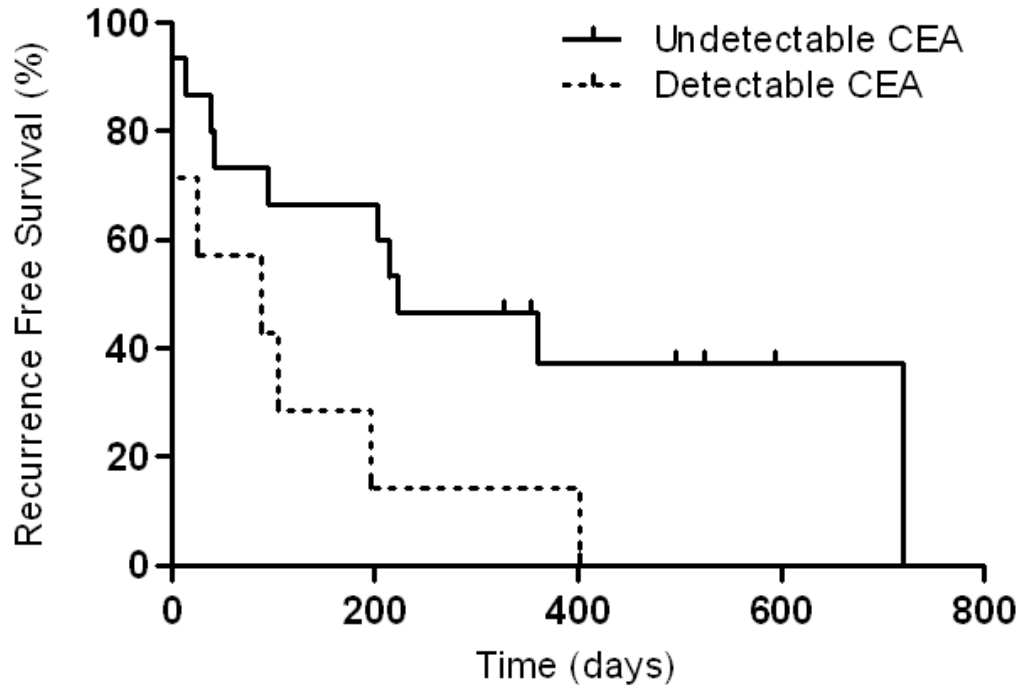
0.11 %

0.66 %

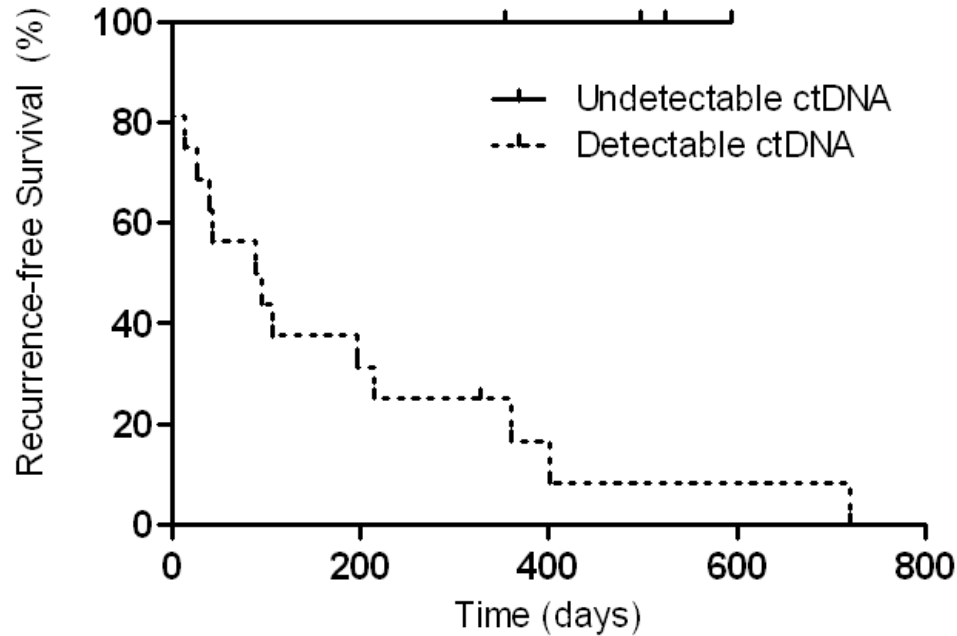
Mutant fragments

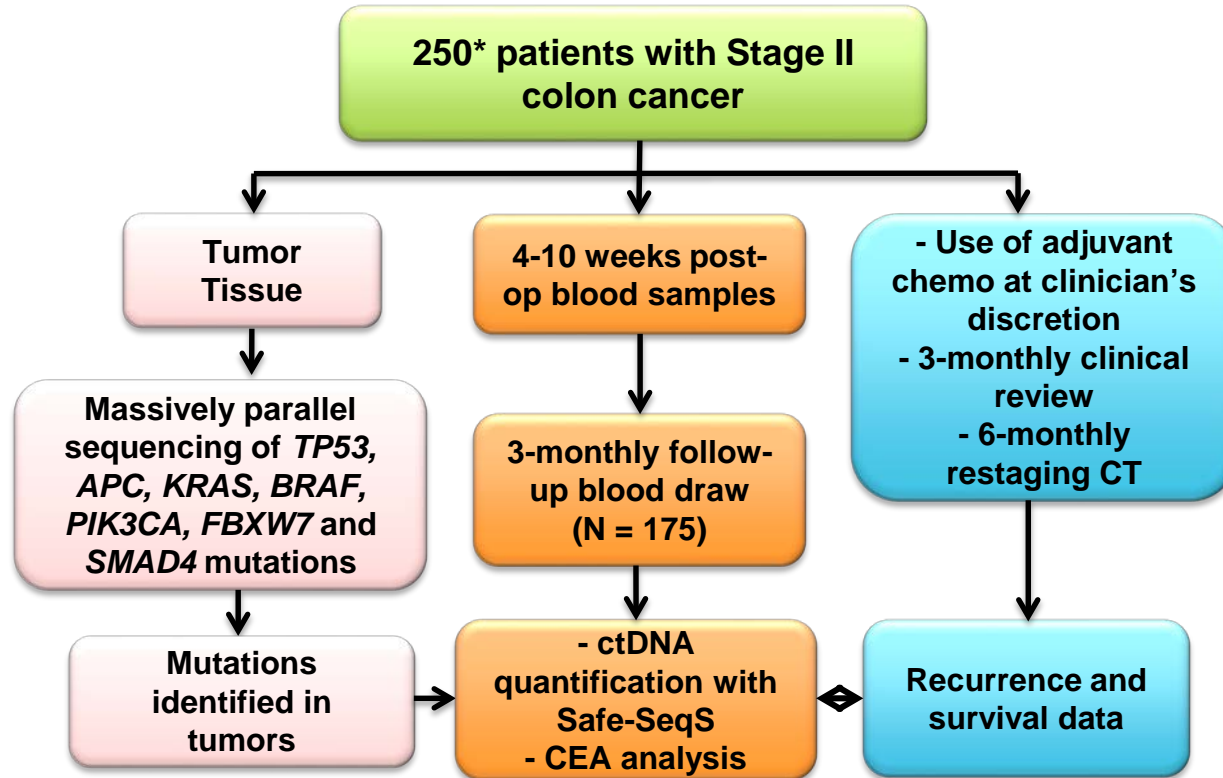
Percent Mutant APC

CEA measured 6-8 weeks following curative resection of mCRC

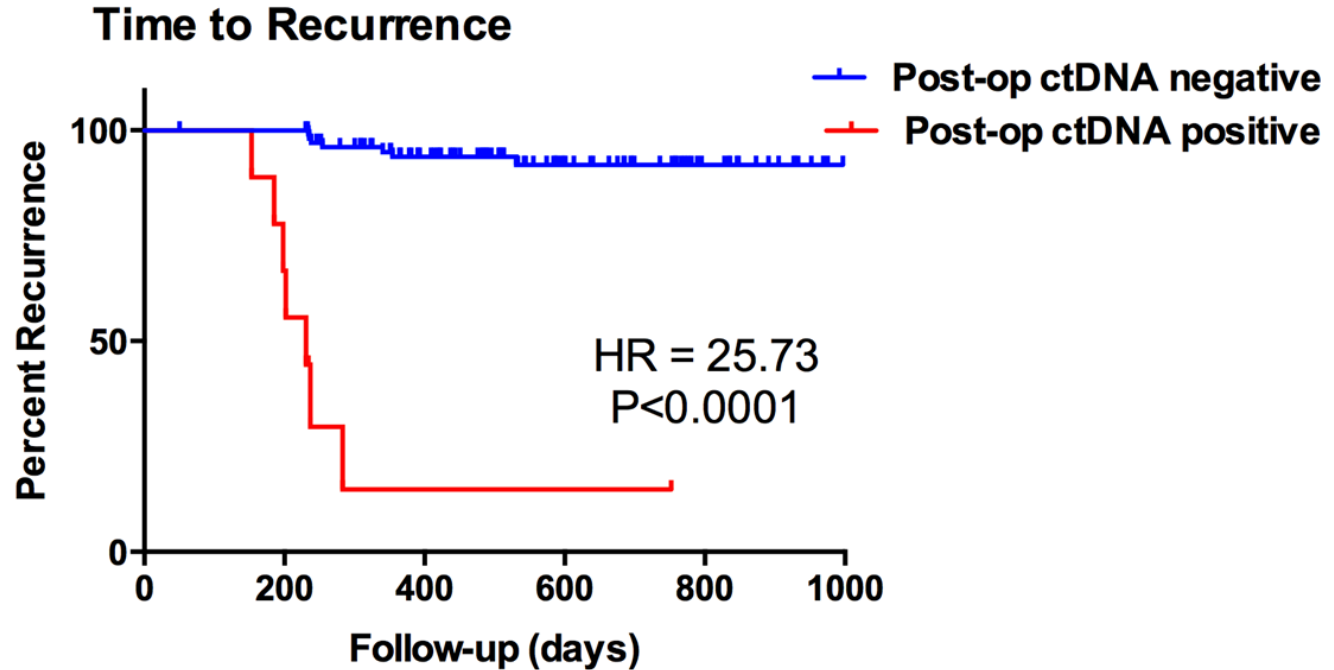


ctDNA measured 6-8 weeks following curative resection of mCRC



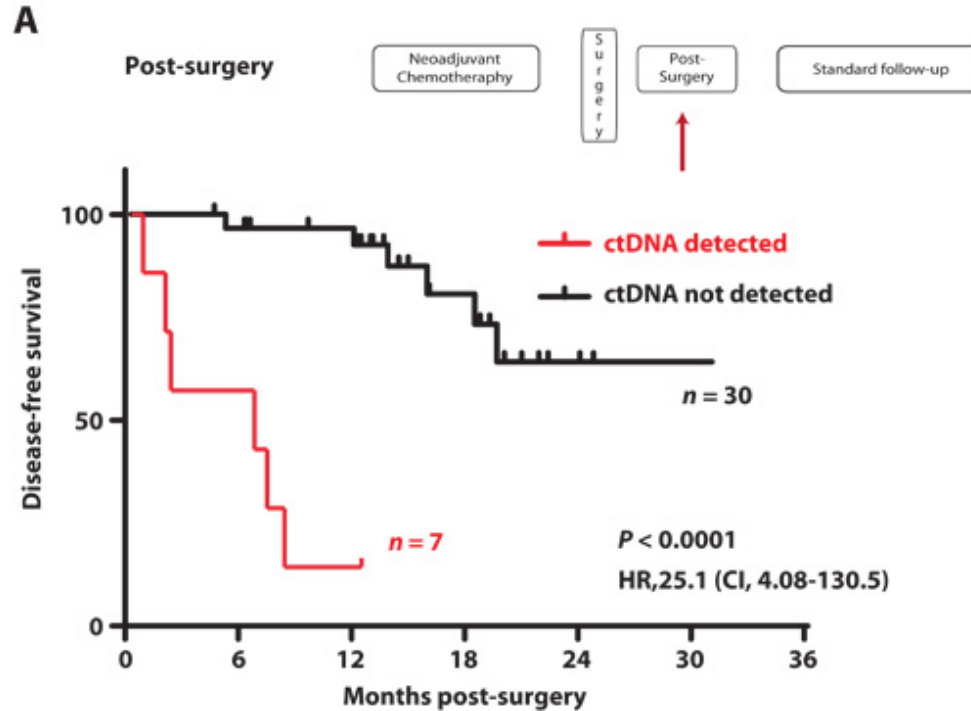


ctDNA measured 6-8 weeks following curative resection of stage II CRC



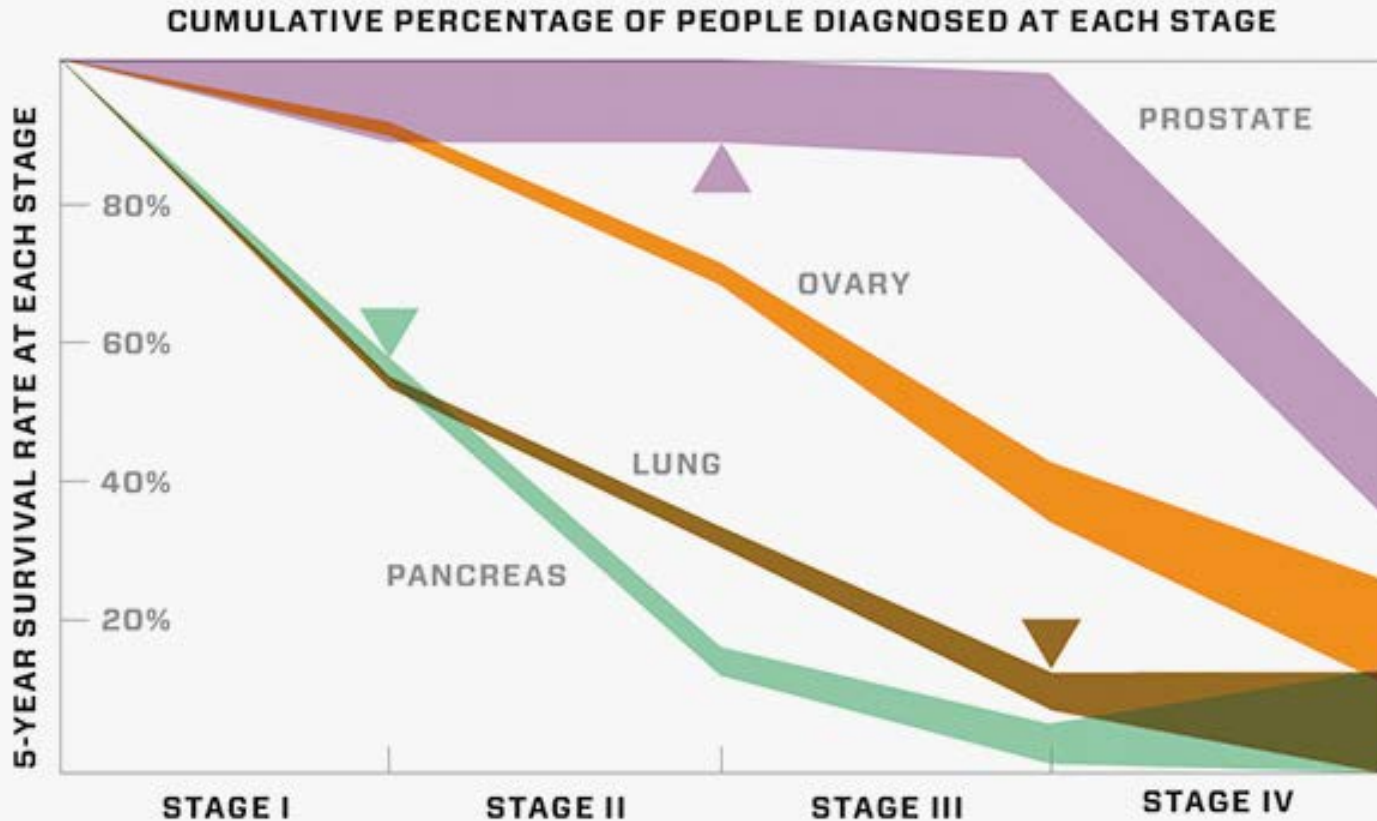
J. Tie and Peter Gibbs, ASCO 2015

MRD detection with ctDNA in breast cancer.



Isaac Garcia-Murillas et al., Sci Transl Med 2015;7:302ra133

Philosophy of Early Detection



Philosophy of Early Detection

Relative 5 Year Cancer Survival Rates

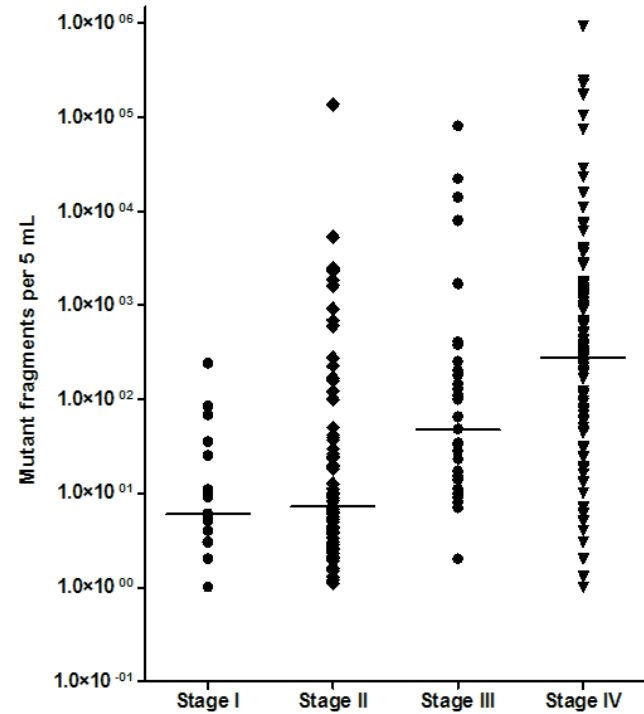
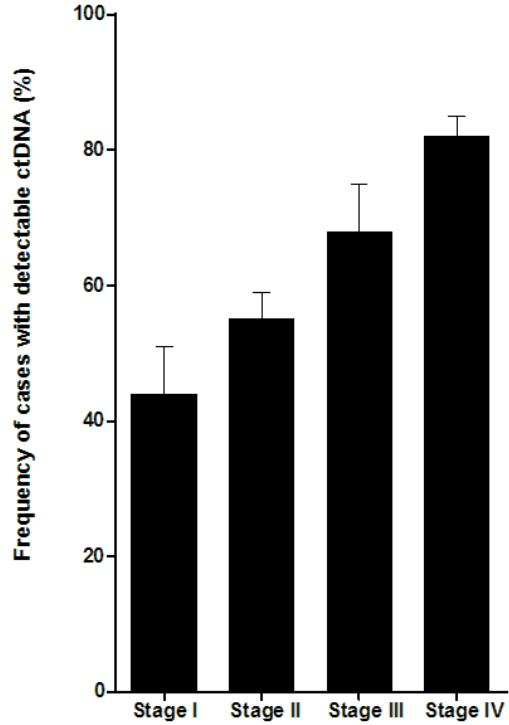
Cancer type	Early detection	Late detection
Colorectal	90%	8%
Breast	97%	21%
Prostate	96%	34%
Melanoma	96%	12%
Cervix	92%	15%

Clinical Application of Cancer Genetics

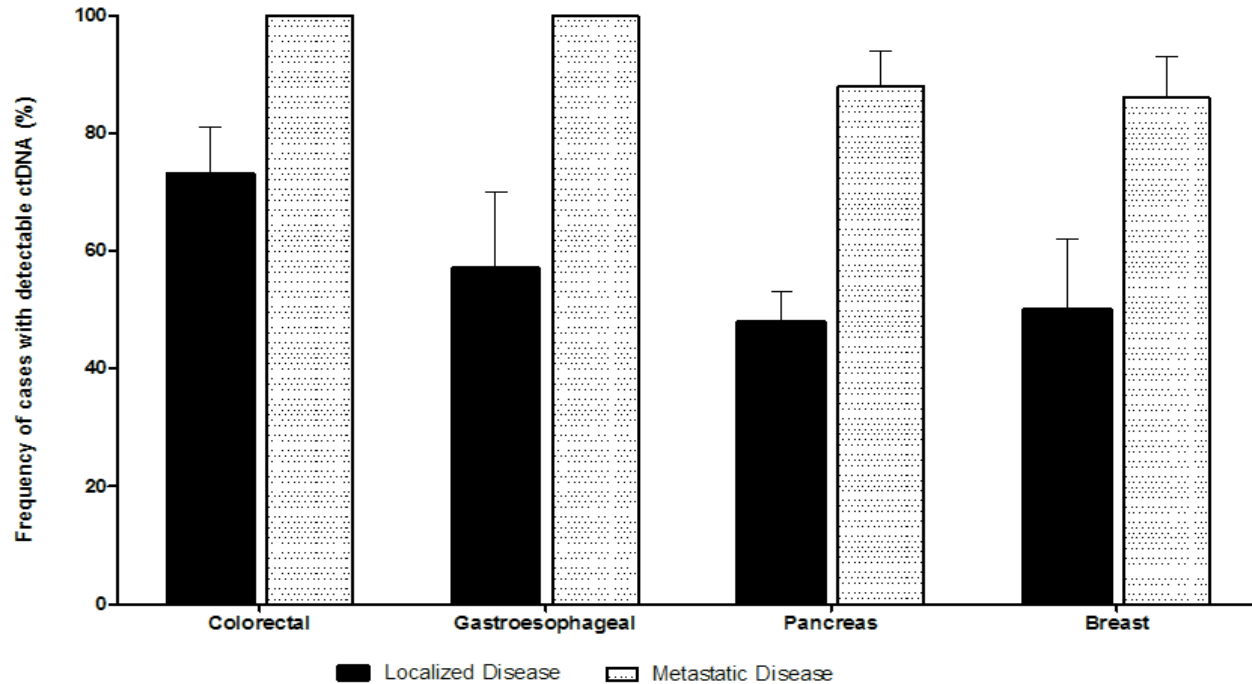
Early Detection – Blood

Early Detection using ctDNA Analyses

14 Tumor types (n = 684)

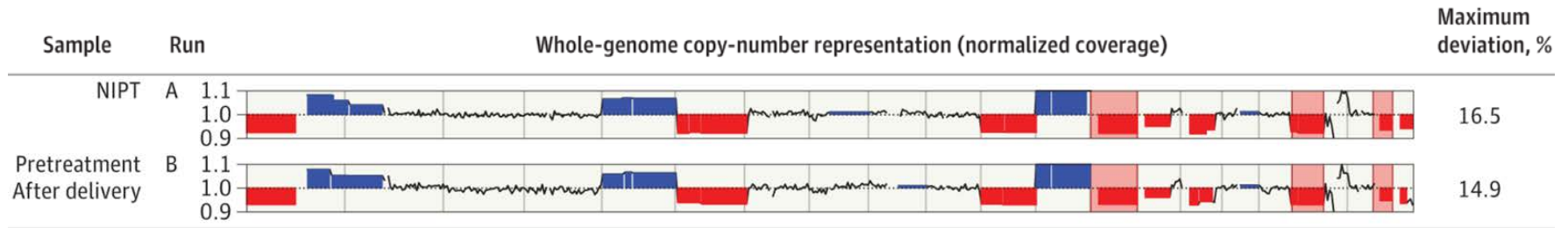


Early Detection using ctDNA Analyses



Detection of Occult Malignancy from analyses of cell free fetal DNA

125,426 NIPT tests
3757 (3%) positive for 1 or more aneuploidies
10 cases of maternal cancer were identified

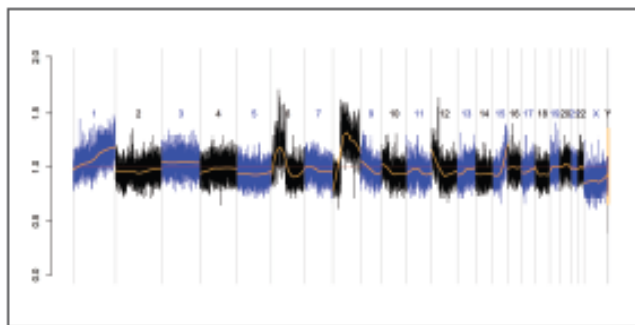


36 year old female at 20 weeks gestation

Monosomy in chromosomes 21, 18 and 13 persisted post-delivery

Diagnosed with stage IIA Hodgkin disease

Detection of Occult Malignancy from analyses of cell free fetal DNA



400,000 NIPT Tests

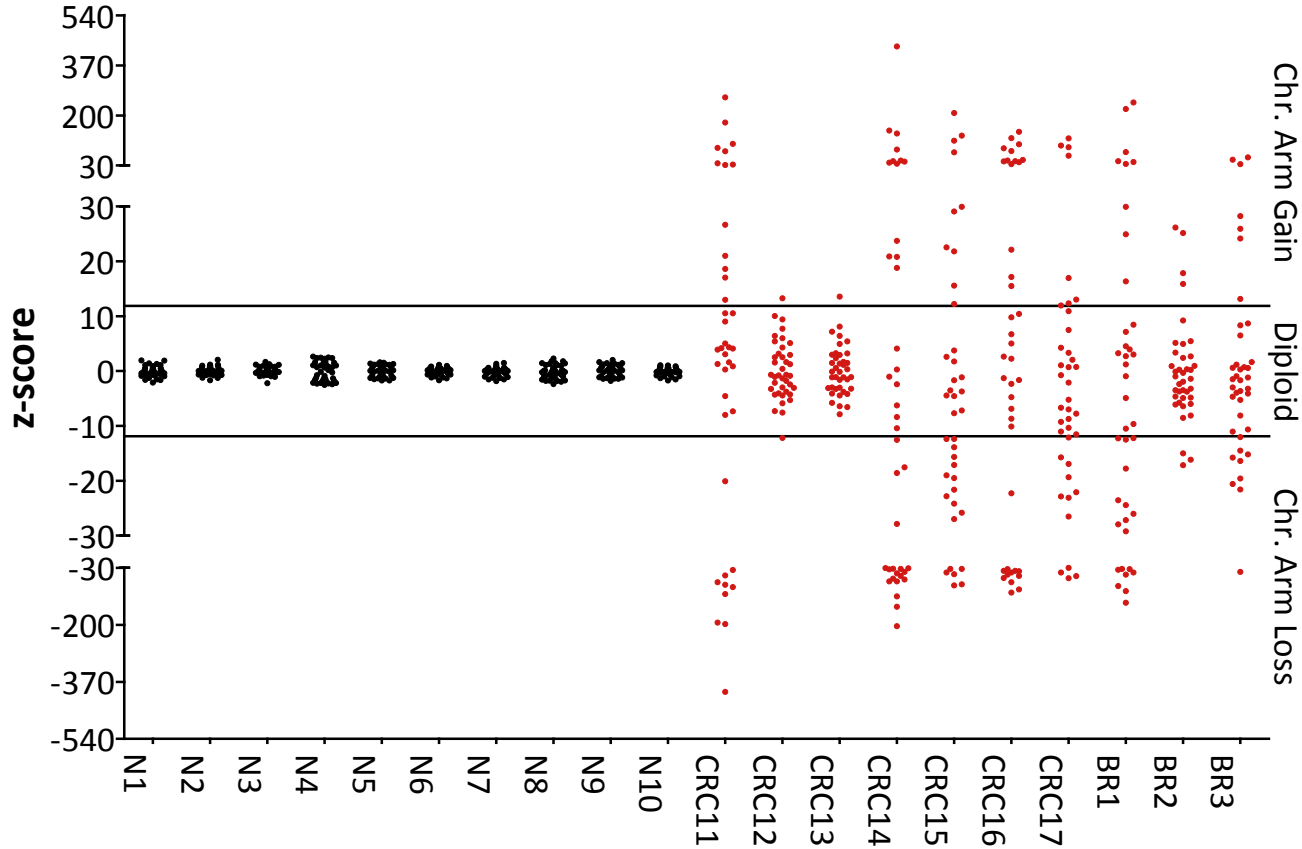
38 confirmed aneuploidies with neoplasm

17 Mutant, 15 benign, 6 Unclassified

Type and frequency of maternal malignancies identified adventitiously by NIPT.

Diagnosis	No. of Cases
Hodgkins Lymphoma	2
Non-Hodgkin's Lymphoma	2
Follicular Lymphoma	1
Multiple Myeloma	1
Breast Carcinoma	3
Angiosarcoma	1
Colon Carcinoma	2
Uterine Leiomyoma	11
Uterine Leiomyosarcoma	1
Teratoma (Dermoid Cyst) of Right Ovary	1
Mass on Right Fallopian Tube	1
Non-Reportable, Clinical Feedback Pending	12
Total	38

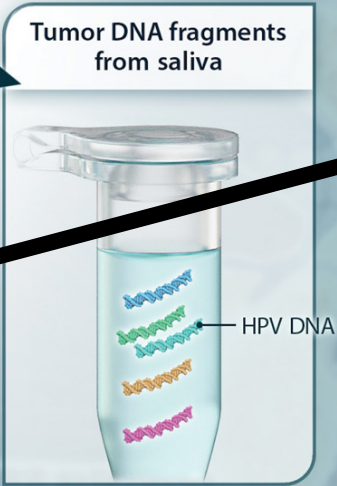
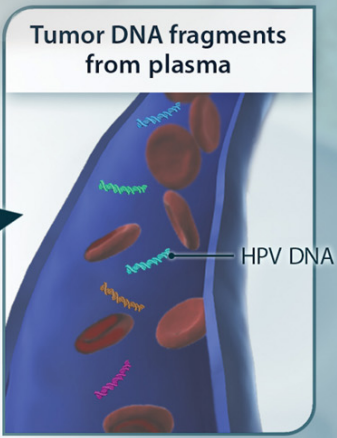
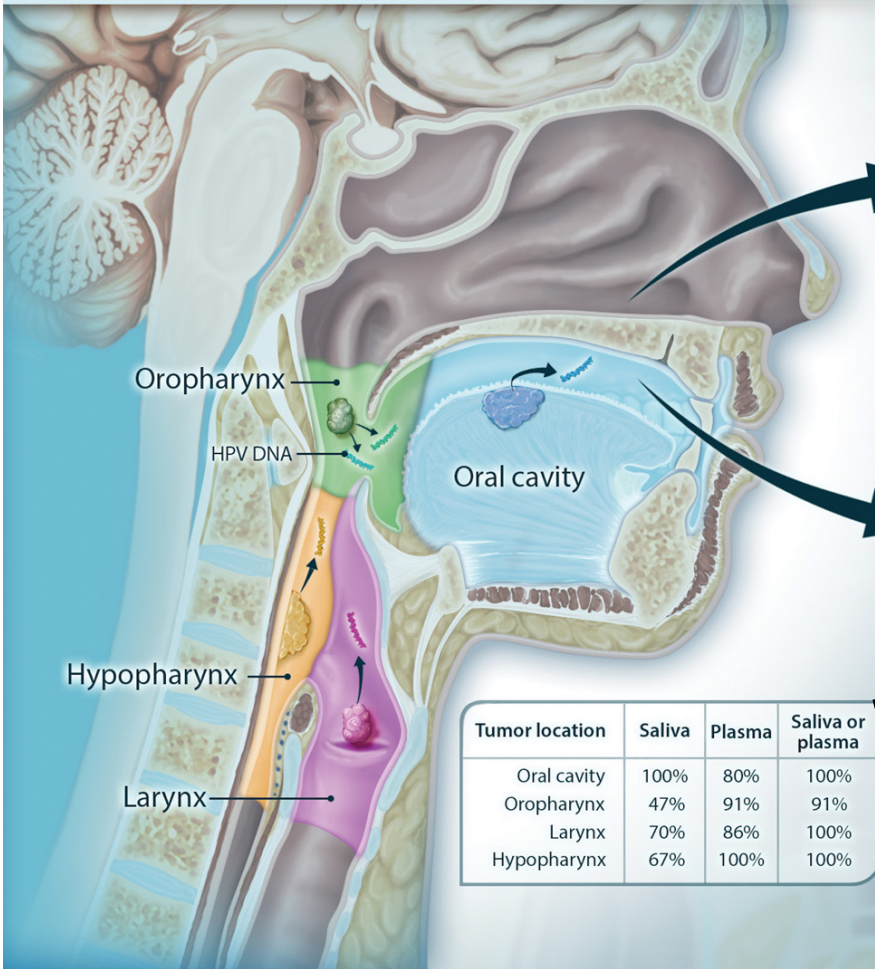
Aneuploidy in normal in cancer patients ctDNA



Clinical Application of Cancer Genetics

Early Detection – Saliva

Tumor DNA in saliva or plasma



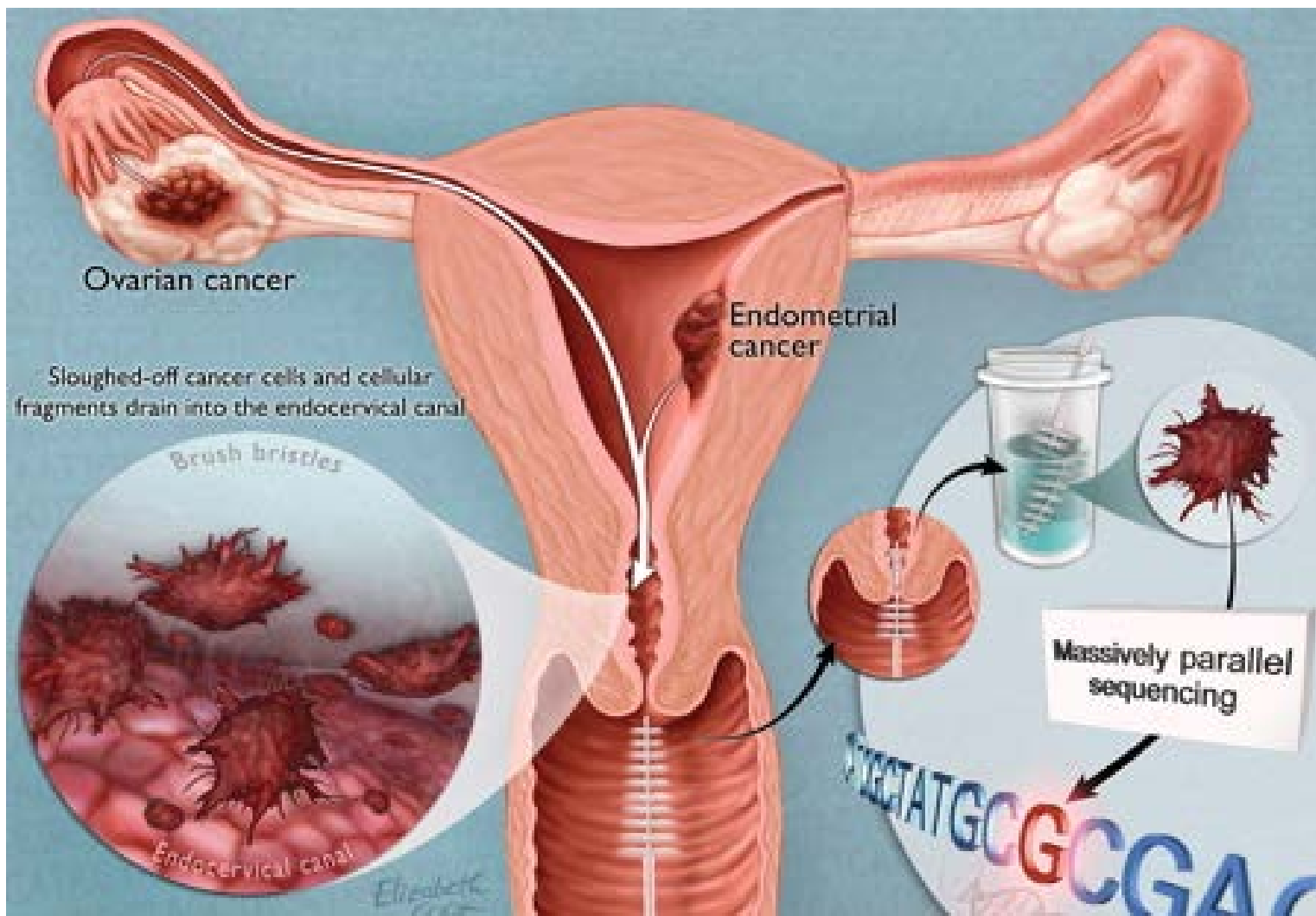
Tumor location	Saliva	Plasma	Saliva or plasma
Oral cavity	100%	80%	100%
Oropharynx	47%	91%	91%
Larynx	70%	86%	100%
Hypopharynx	67%	100%	100%

Sensitivity

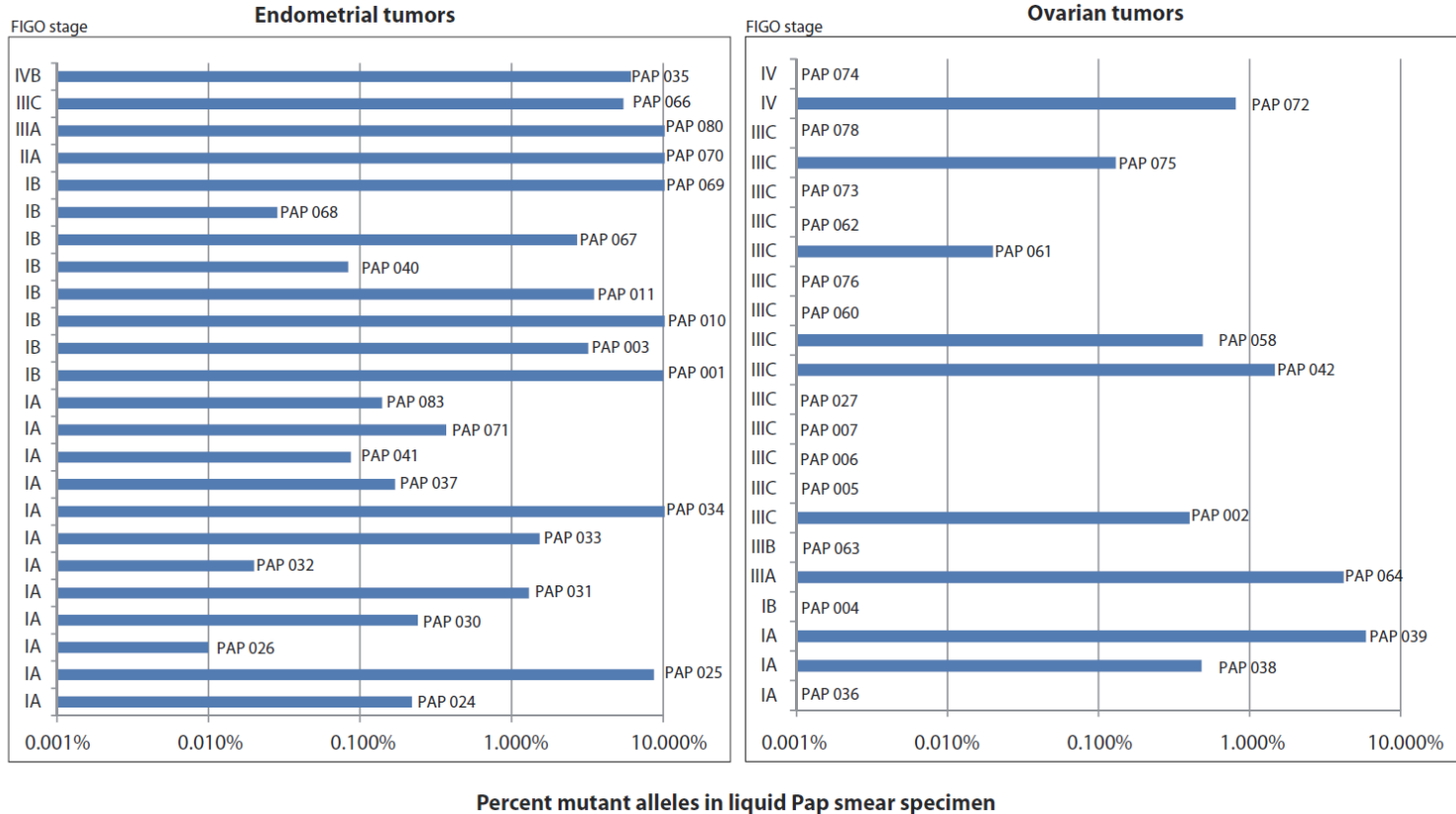
Tumor location	Saliva
Oral cavity	100%
Oropharynx	47%
Larynx	70%
Hypopharynx	67%

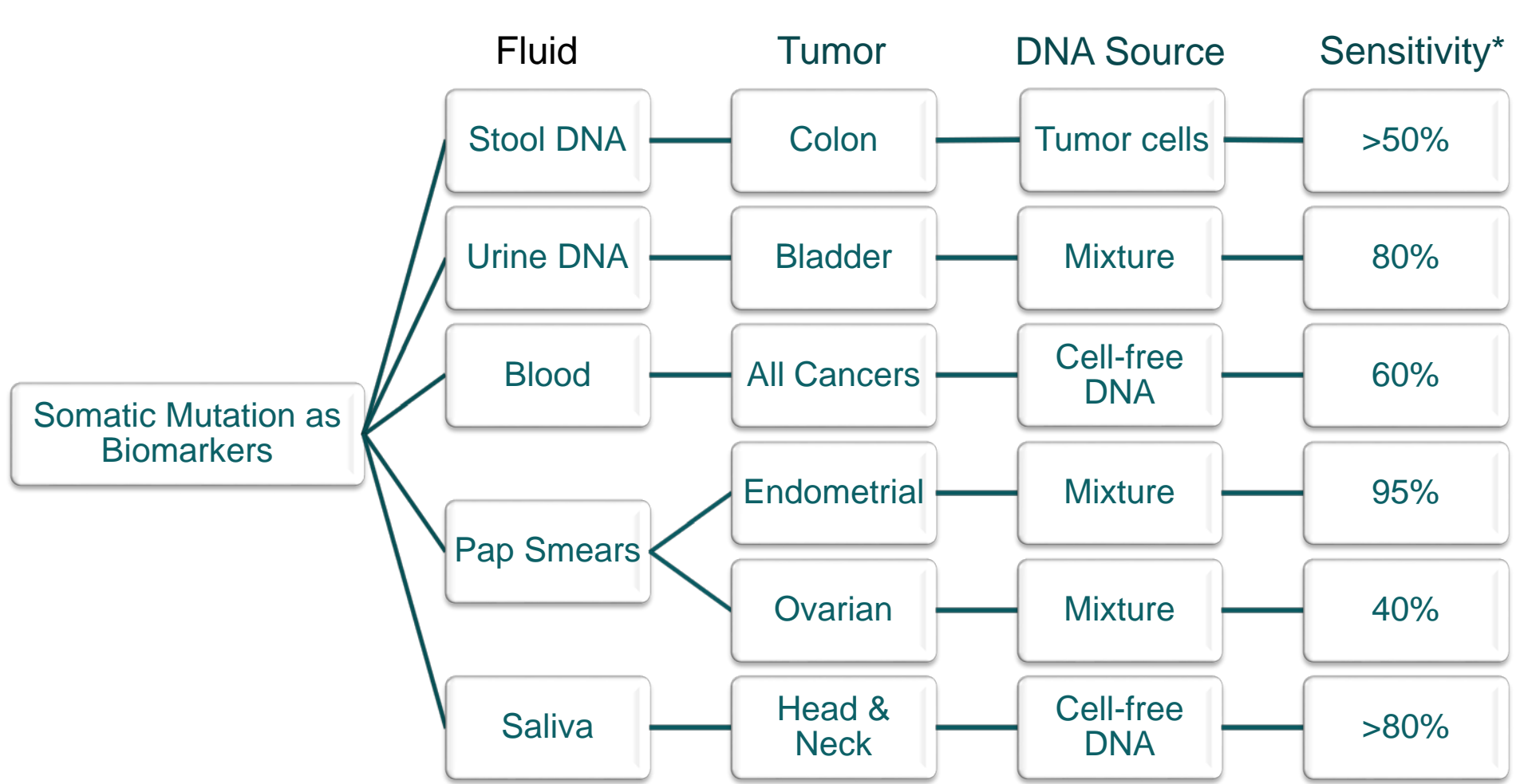
Clinical Application of Cancer Genetics

Early Detection – Pap Smears



Early Detection - GenePap





*Stage I and II Disease

Clinical Application of Cancer Genetics

Challenges

Not all clonal events are cancer

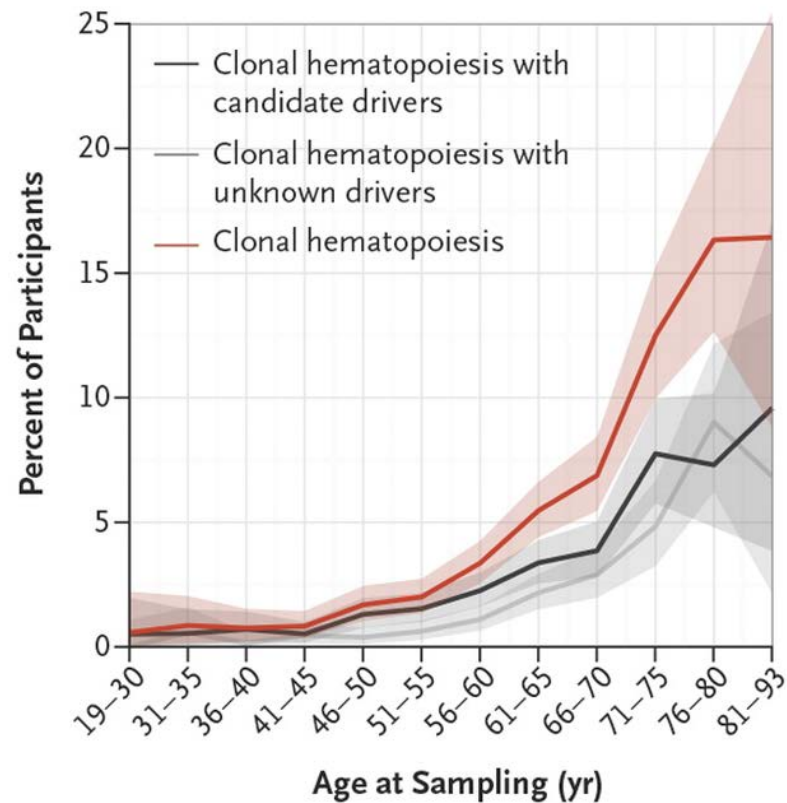
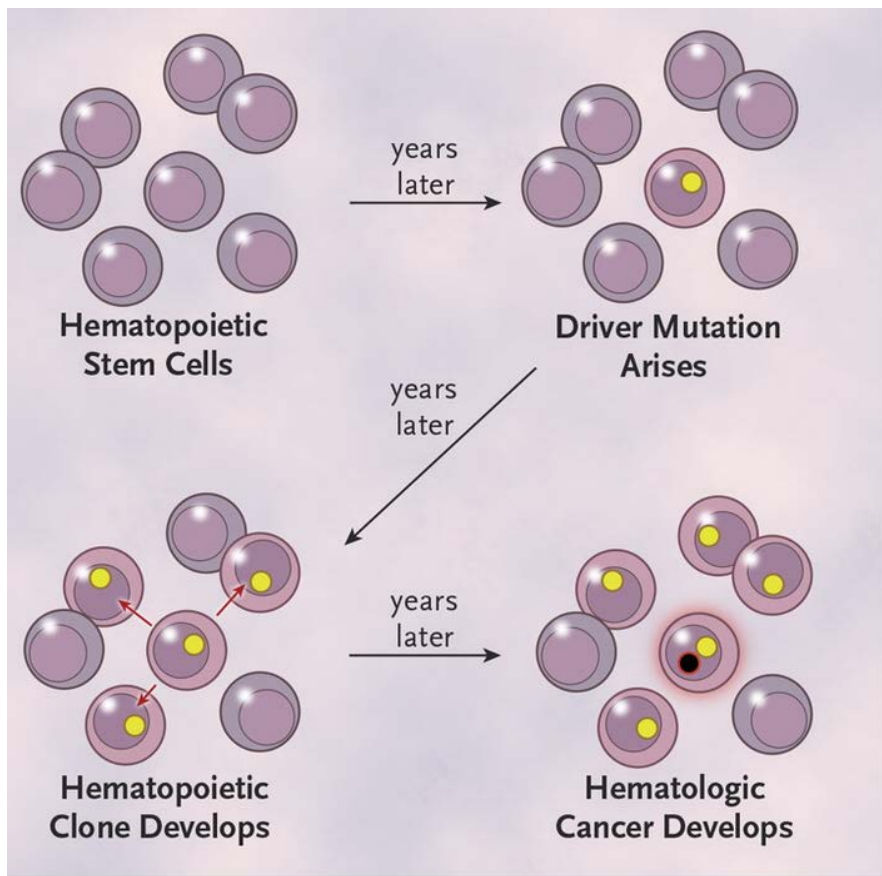
The NEW ENGLAND JOURNAL of MEDICINE

ORIGINAL ARTICLE

Clonal Hematopoiesis and Blood-Cancer Risk Inferred from Blood DNA Sequence

Whole-exome sequencing of DNA in peripheral-blood cells from 12,380 persons → somatic mutations characteristic of hematologic malignancies were observed in 10% of persons older than 65 years of age

Genovese et al., N Engl J Med 2014; 371:2477-2487

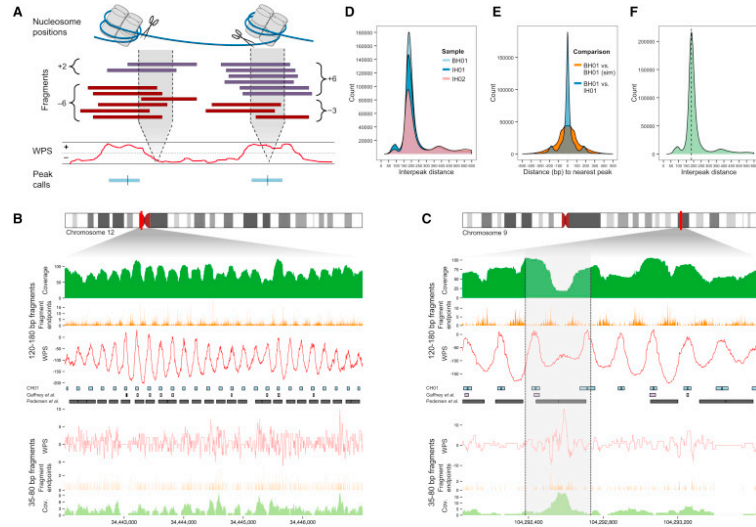
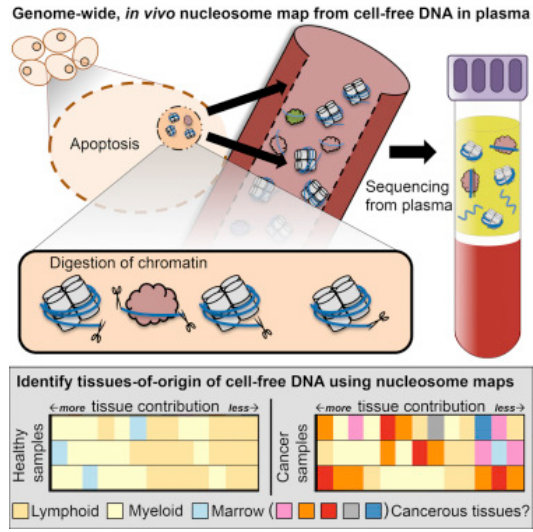


Localization

CASE: A 55 year old male was found to have a persistent KRAS mutation (G12D) in ctDNA at >0.8%

CT Scan, PET Scan, Colonoscopy and PSA are normal.

What is this? Lung, Colon Pancreas?

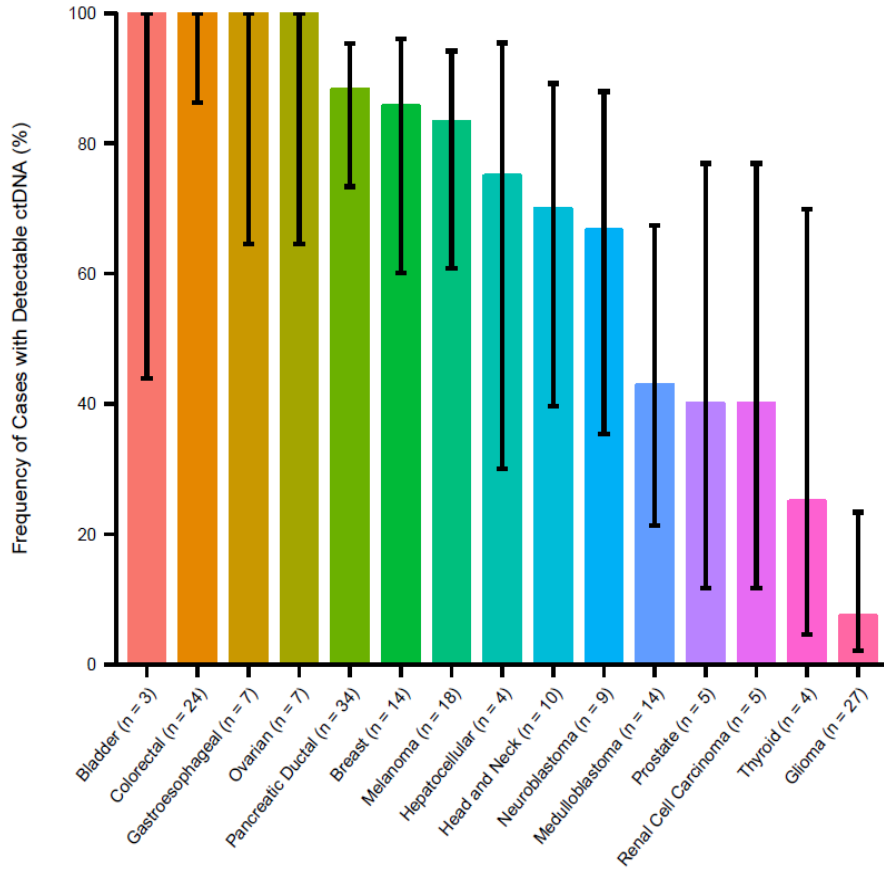


Matthew W. Snyder, Martin Kircher, Andrew J. Hill, Riza M. Daza, Jay Shendure

Cell-free DNA Comprises an In Vivo Nucleosome Footprint that Informs Its Tissues-Of-Origin

Cell, Volume 164, Issues 1–2, 2016, 57–68

Heterogeneity



- ~80% late stage tumors shed ctDNA
- Anatomic barriers to tumor DNA release into circulation
- Heterogeneity in shedding

Future for ctDNA

Incremental improvements in technology

- Increase in comprehensive panels
- Limited by biology more than technology
- Need a biologic based discovery to drive dramatic improvement

Future for ctDNA

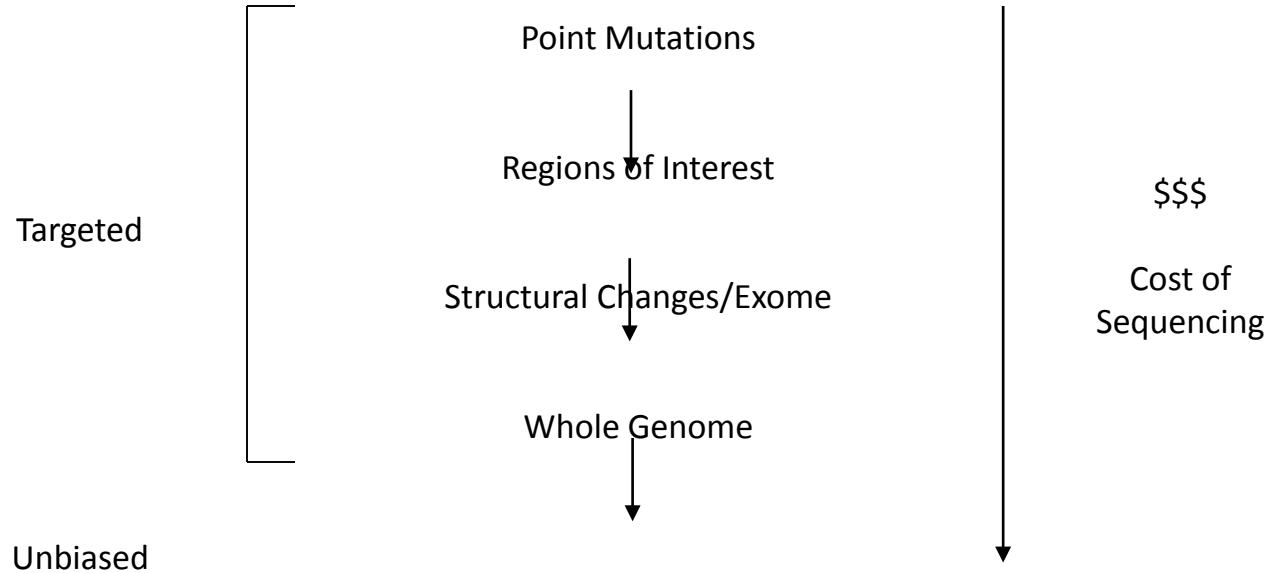
Incremental improvements in technology

- Increase in comprehensive panels
- Limited by biology more than technology
- Need a biologic based discovery to drive dramatic improvement

Clinical Application

- Tumor genotyping in plasma will be integrated into routine practice
– based on concordance studies
- High impact applications that drive improvements in OS will require prospective clinical trials and partnership with FDA.

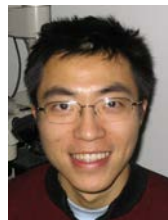
Summary



Summary

- Somatic mutations can be effective biomarkers largely because of specificity
- Digital Genomics has improved sensitivity and throughput sufficient for real clinical application
- Applications for detecting occult disease for minimal residual disease detection and screening for cancer
- Broad commercialization will require overcoming cost, regulatory, payor and definitive clinical studies demonstrating clinical benefit.

Acknowledgments



Acknowledgments



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LUDWIG
CENTER | JOHNS
HOPKINS