



Memorial Sloan Kettering
Cancer Center

Opportunities and Limitations of ctDNA as a Clinical Biomarker in Cancer Management: New Insights in the Clinical Application of ctDNA

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Memorial Sloan Kettering Cancer Center
October 4, 2018

Disclosures of potential COI

Company

Jounce Therapeutics

Personal Genome Diagnostics, Inc.

PapGene, Inc.

Merck

Phoremest

Lyndra

Caris

Genocea

Cell Design Labs

15 Patents – multiple managed by Johns
Hopkins and MSK conflict of interest office

Relationship

Board of Directors

Board of Directors, Consultant and Stock
Stock

Consultant

SAB, Consultant

Consultant (not active)

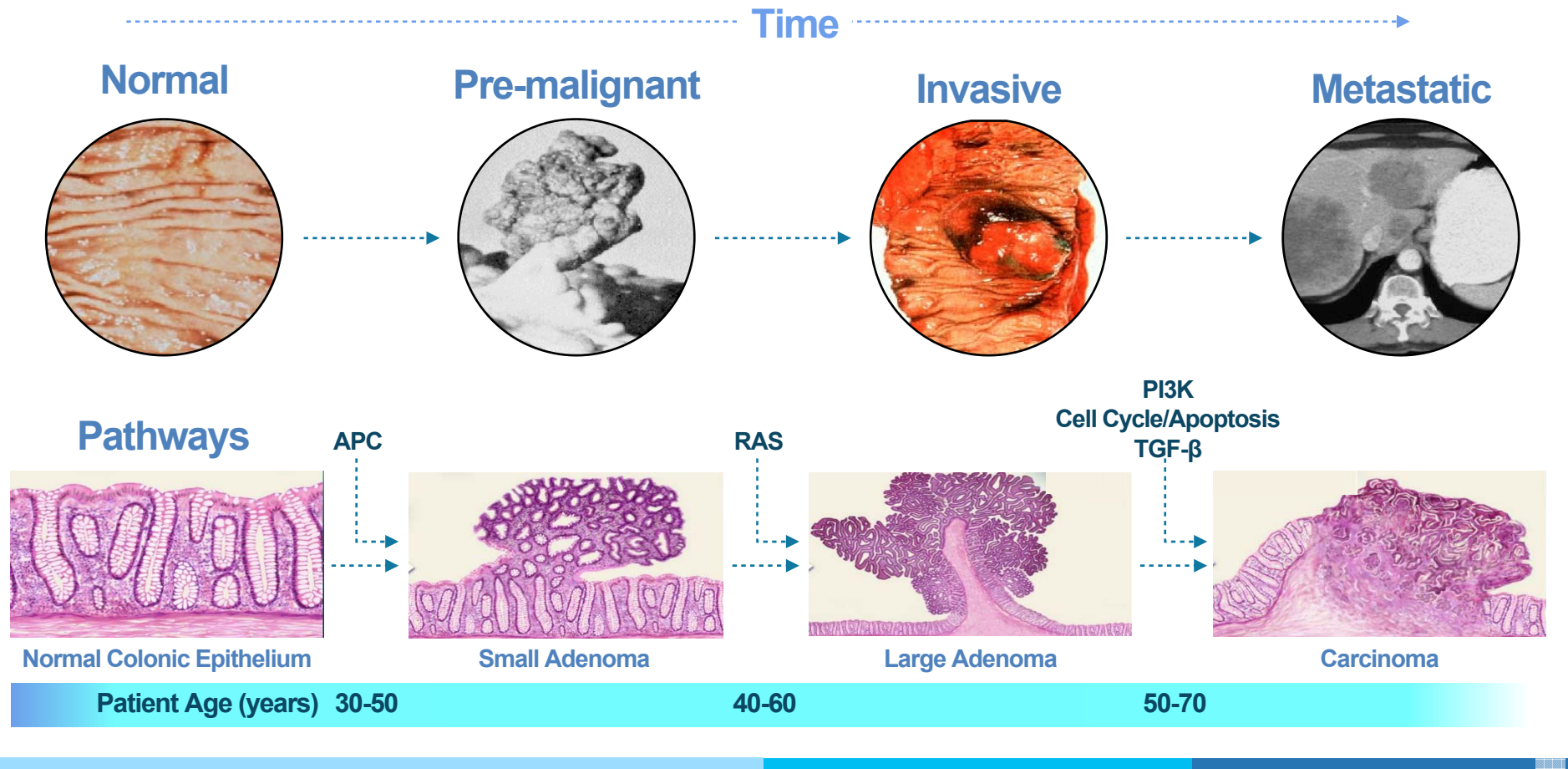
Consultant (not active)

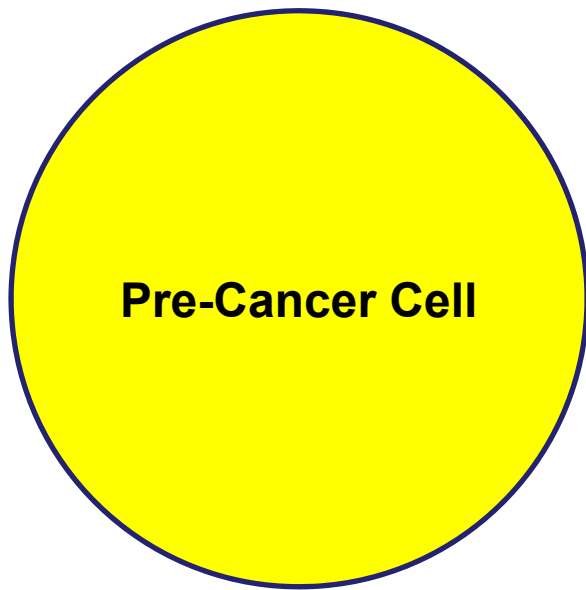
Consultant (not active)

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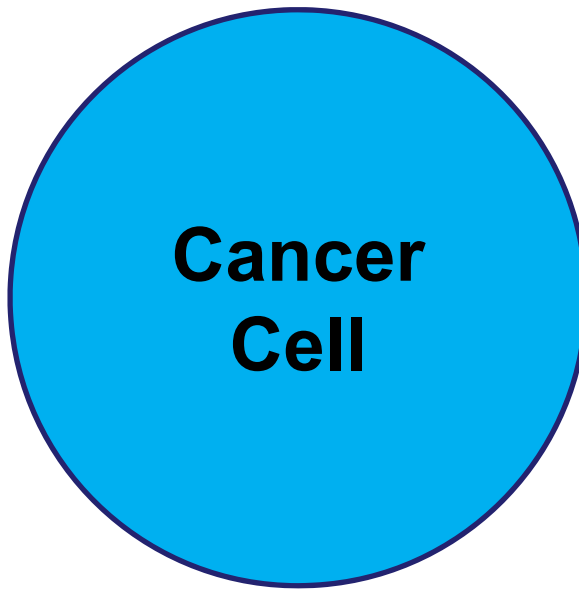
Royalties related to applications of ctDNA
analysis and mismatch repair deficiency for
diagnosis and therapy

How Does Cancer Evolve?

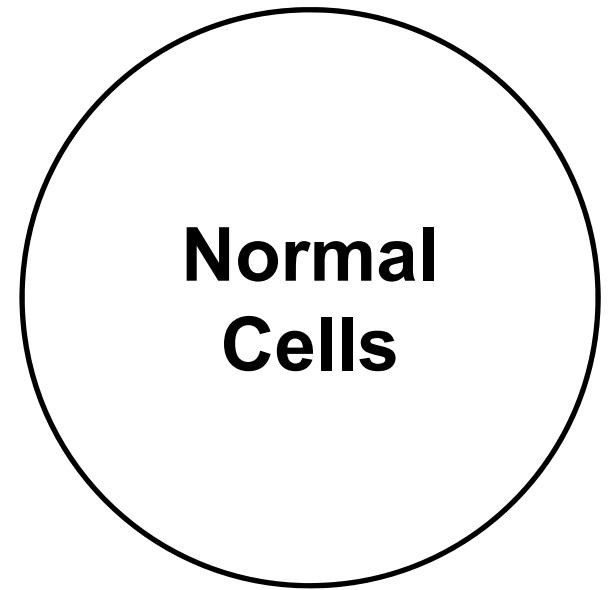




Pre-Cancer Cell



**Cancer
Cell**

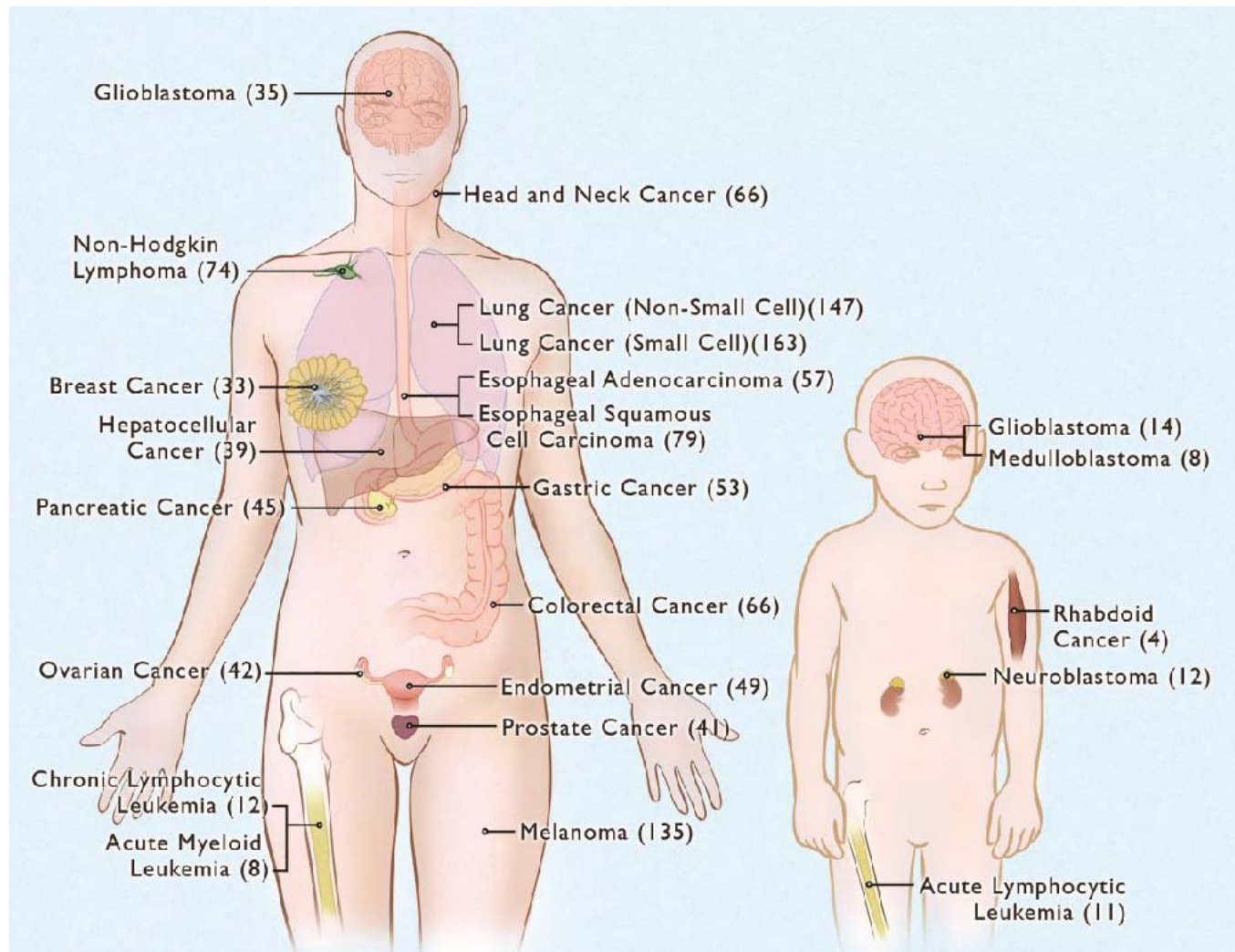


**Normal
Cells**

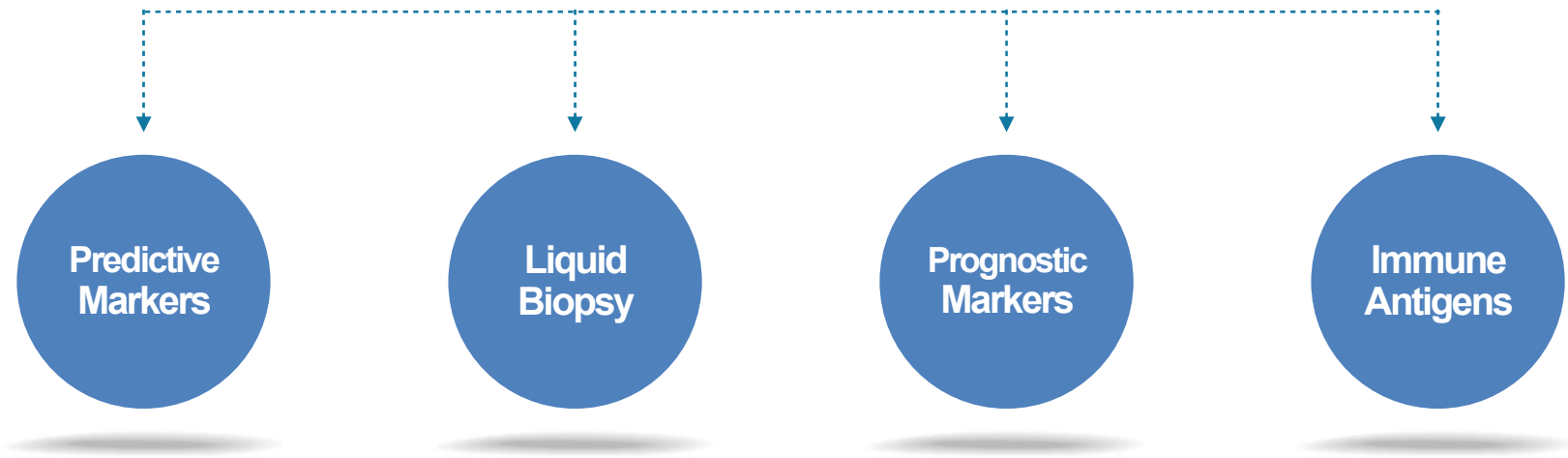
Mutations

No Mutations

Human Cancer Exomes Sequenced

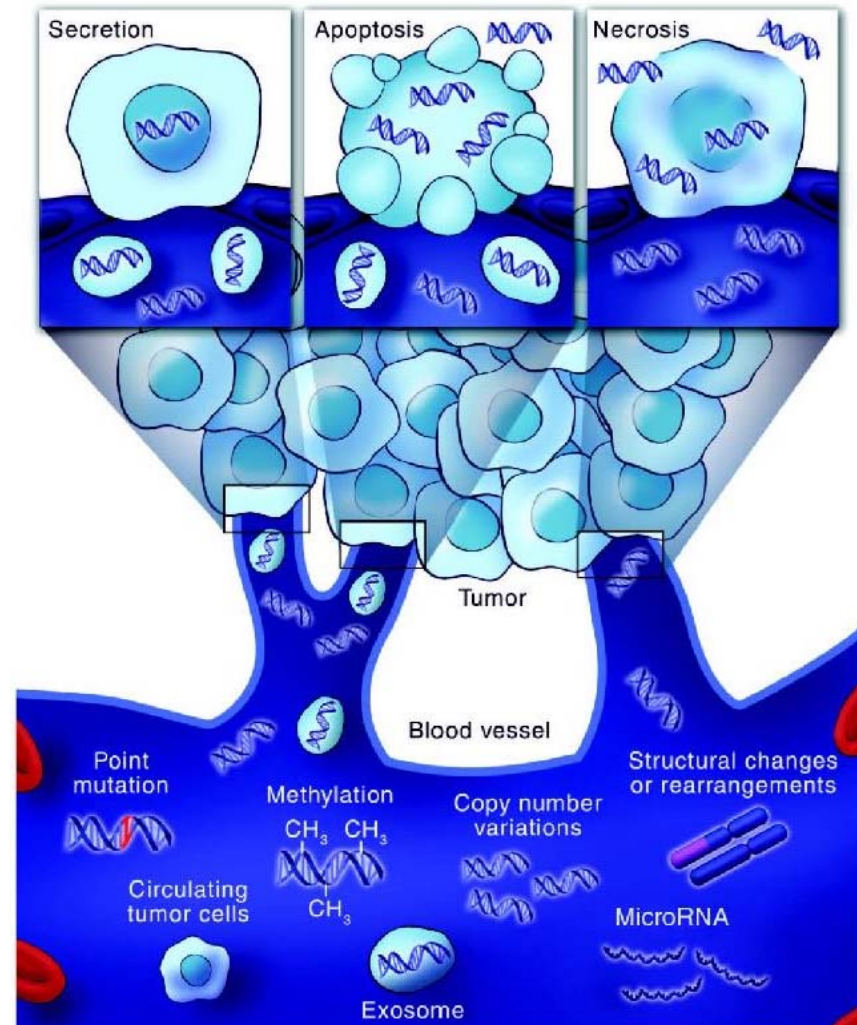


Somatic Cancer Genome Data



Liquid Biopsies

- DNA fragments of 120-200 bp 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



Access to Somatic Mutations

Tumor Tissue

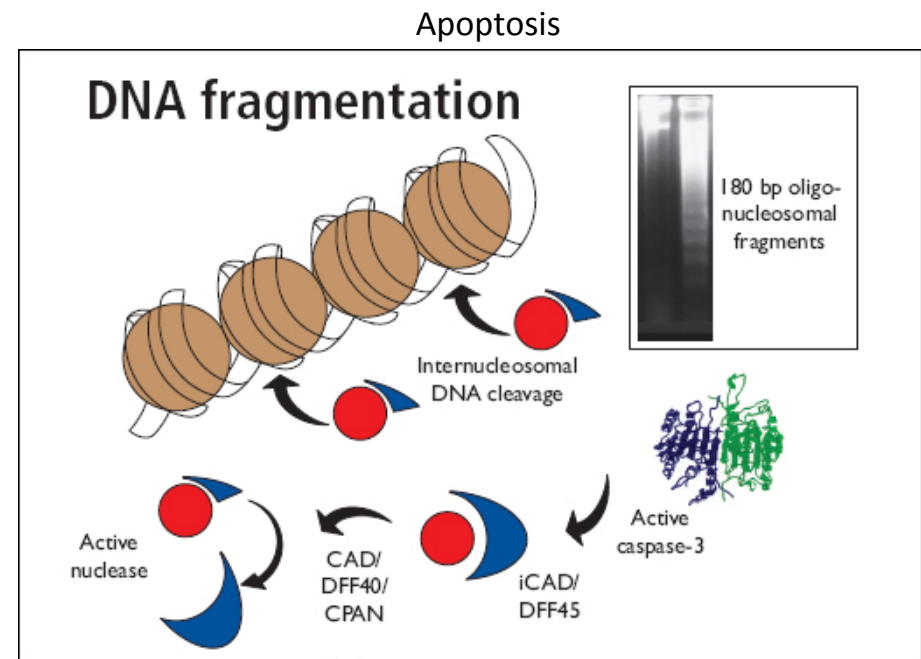
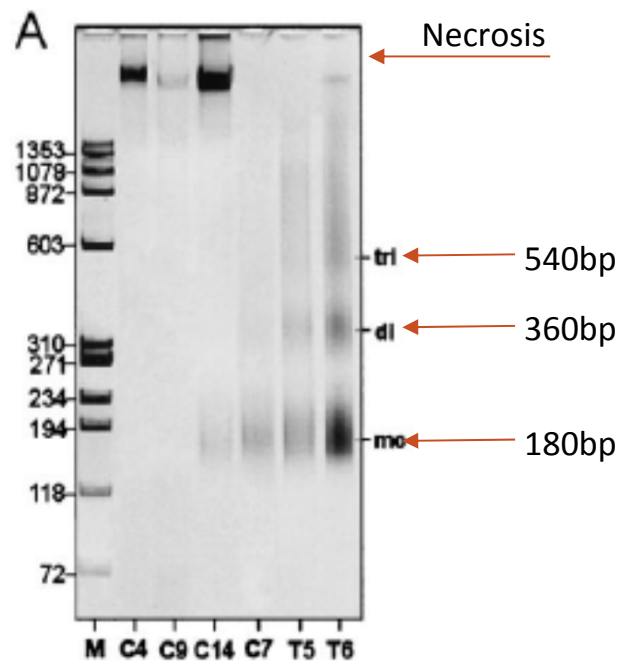
- Formalin Fixed
Parrafin-Embedded
(FFPE)
- Frozen tissue

Blood & Other Bodily Fluids

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

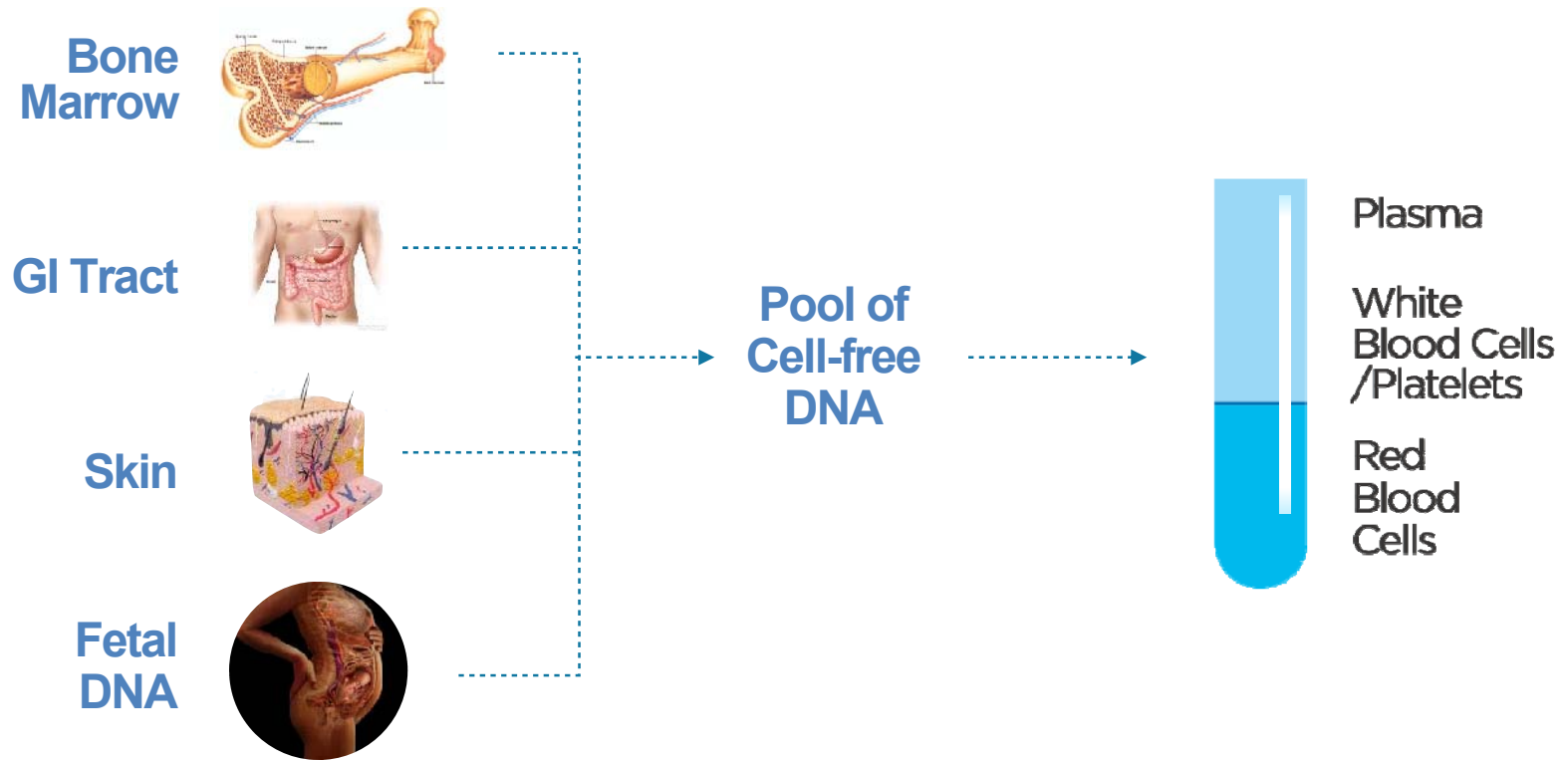


Cell-free DNA – origin

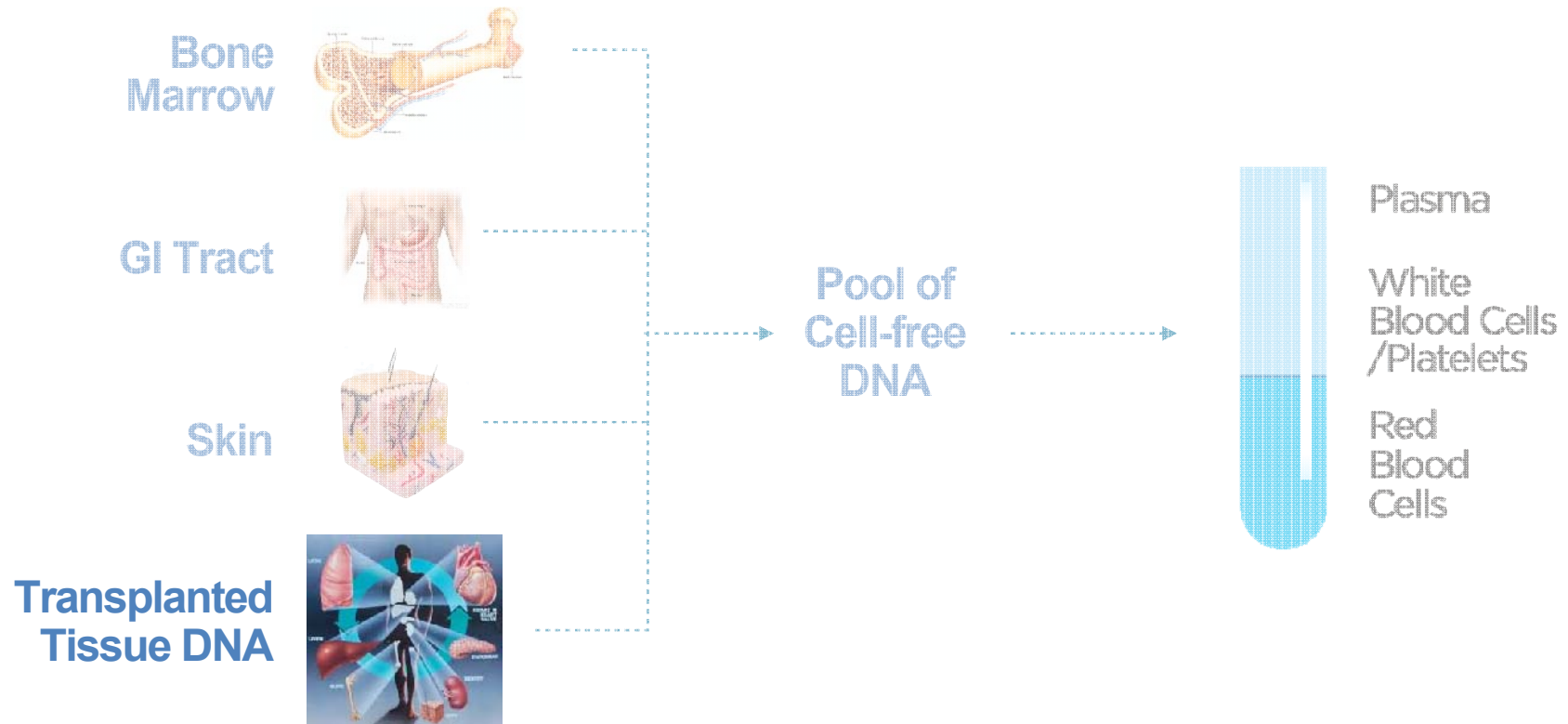


Jahr, S. Cancer Res, 2001

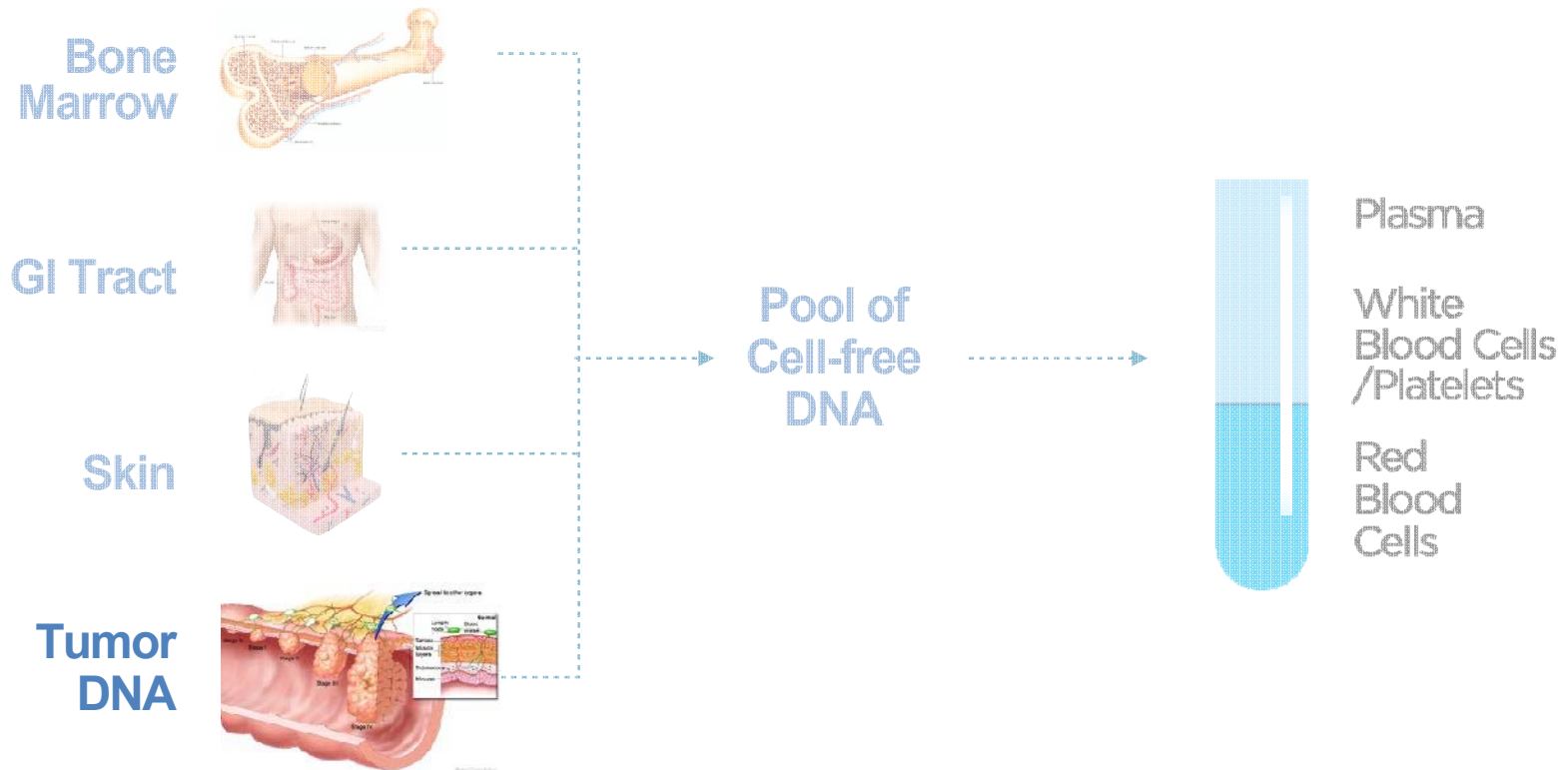
Source Circulating Cell-Free DNA



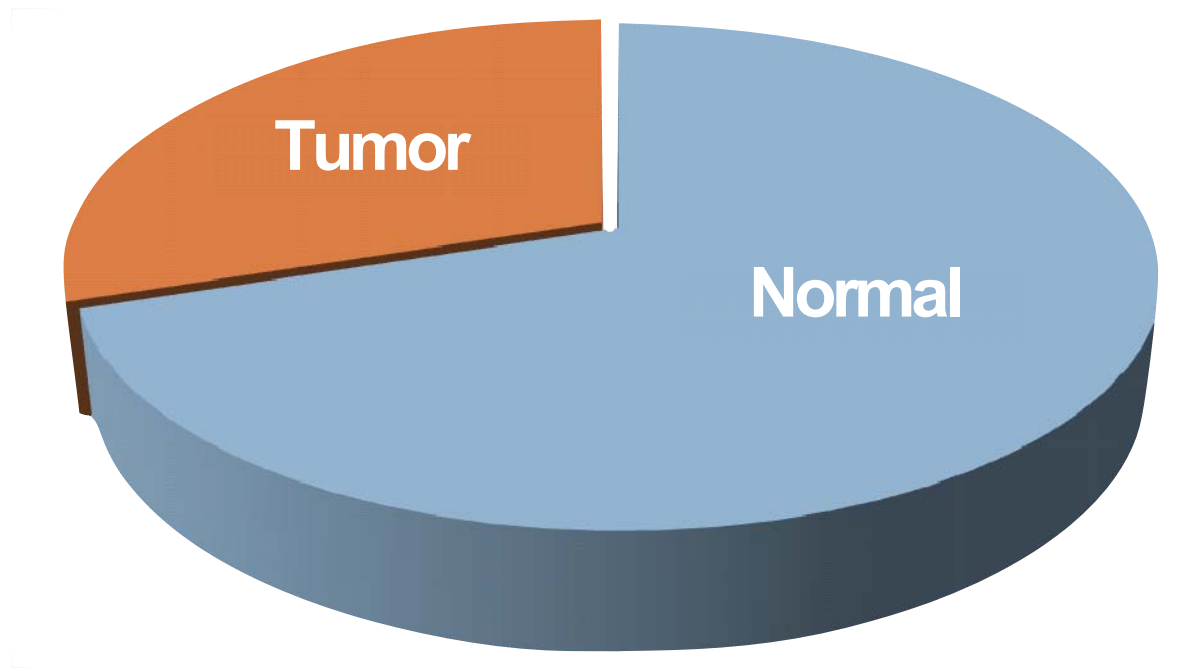
Source Circulating Cell-Free DNA



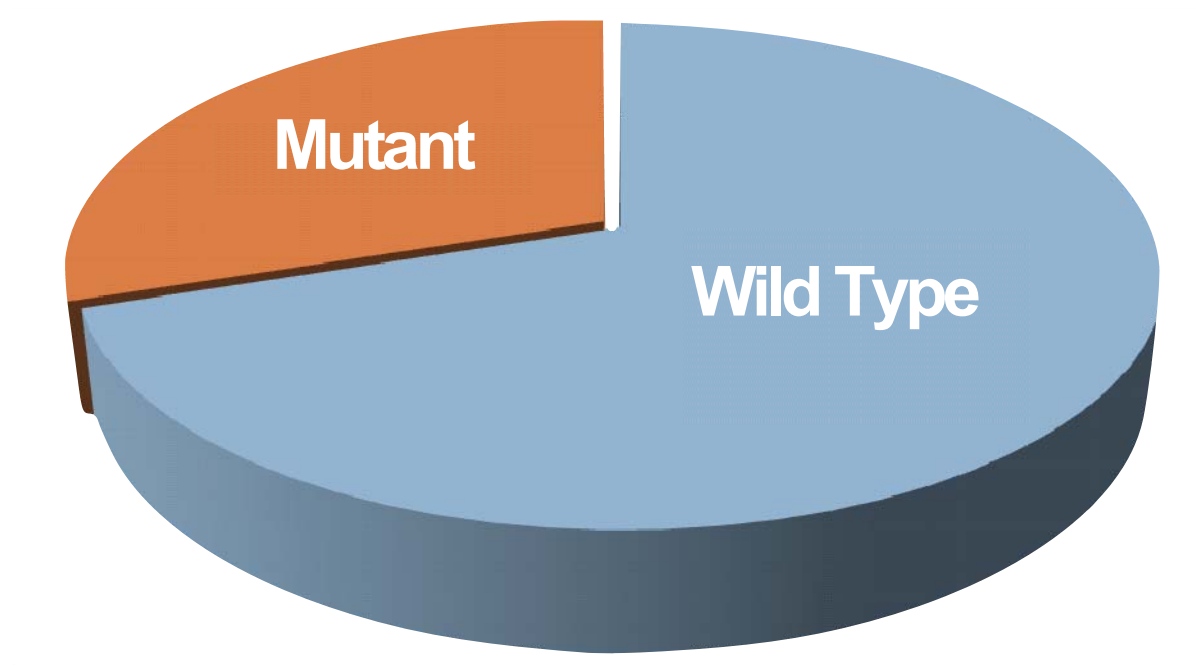
Source Circulating Cell-Free DNA



Circulating Cell-Free DNA in a Cancer Patient



Circulating Cell-Free DNA in a Cancer Patient



Technology To Assess Circulating Tumor DNA

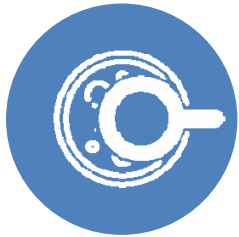
Digital PCR

- 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

Potential of Liquid Biopsies in Precision Medicine



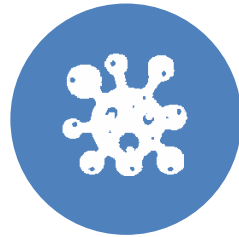
**Mutations
as
Biomarkers**



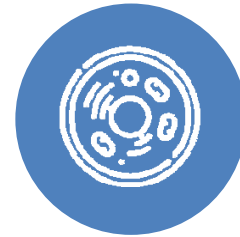
**Monitoring
Tumors**



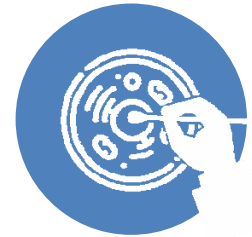
**Tracking
Resistance**



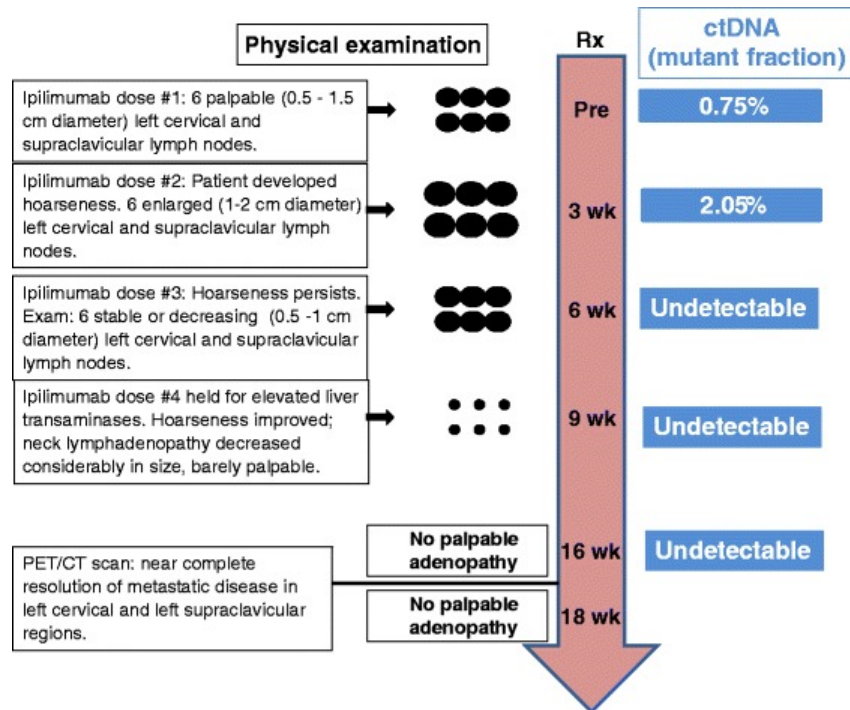
**Minimal
Residual
Disease**



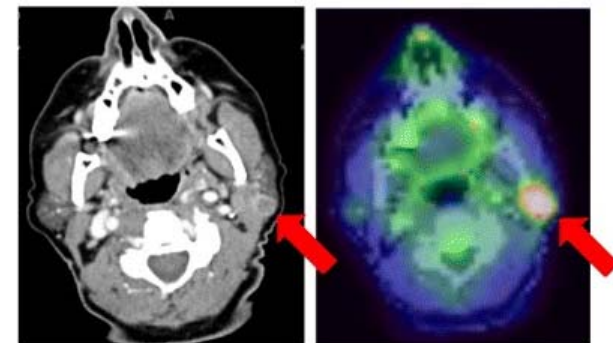
**Molecular
Remission**



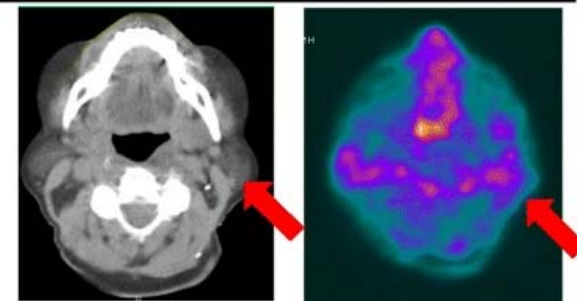
**Early
Detection**



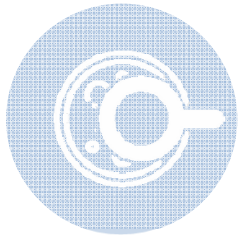
2 months pretreatment



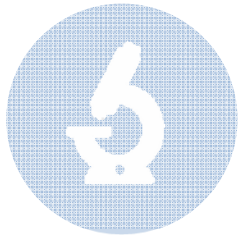
4 months post-treatment



Potential of Liquid Biopsies in Precision Medicine



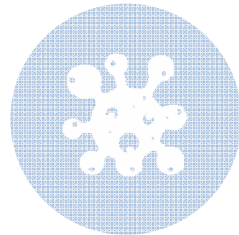
Mutations
as
Biomarkers



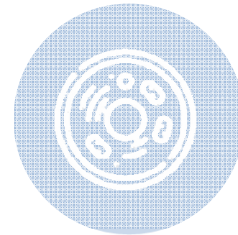
Monitoring
Tumors



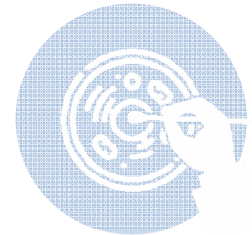
Tracking
Resistance



Minimal
Residual
Disease

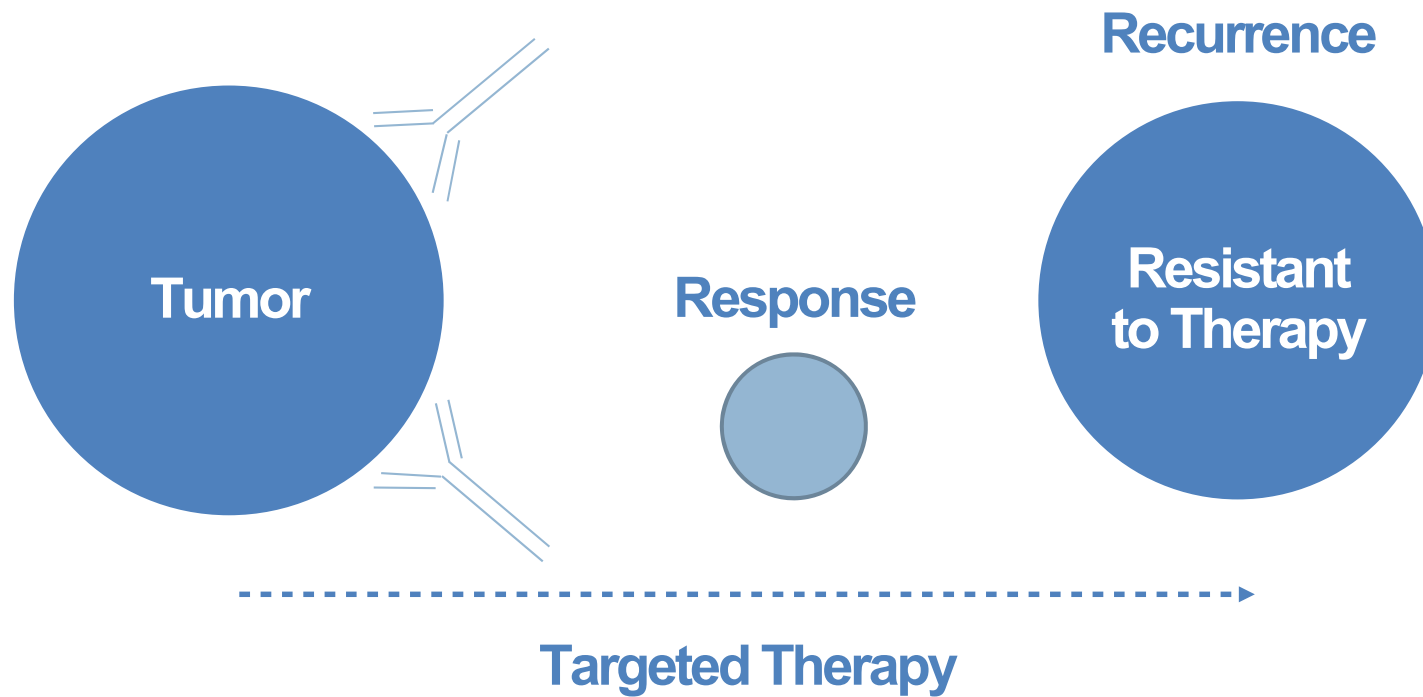


Molecular
Remission



Early
Detection

Tracking Resistance



Genetic Heterogeneity

EGFR blockade in Colorectal Cancer

Primary resistant

Exon 12 or 13 KRAS mutation

Response Rate

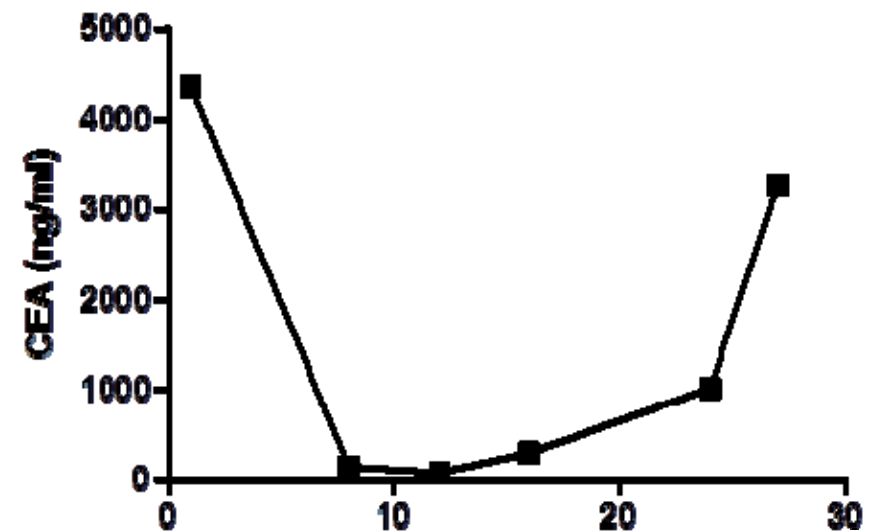
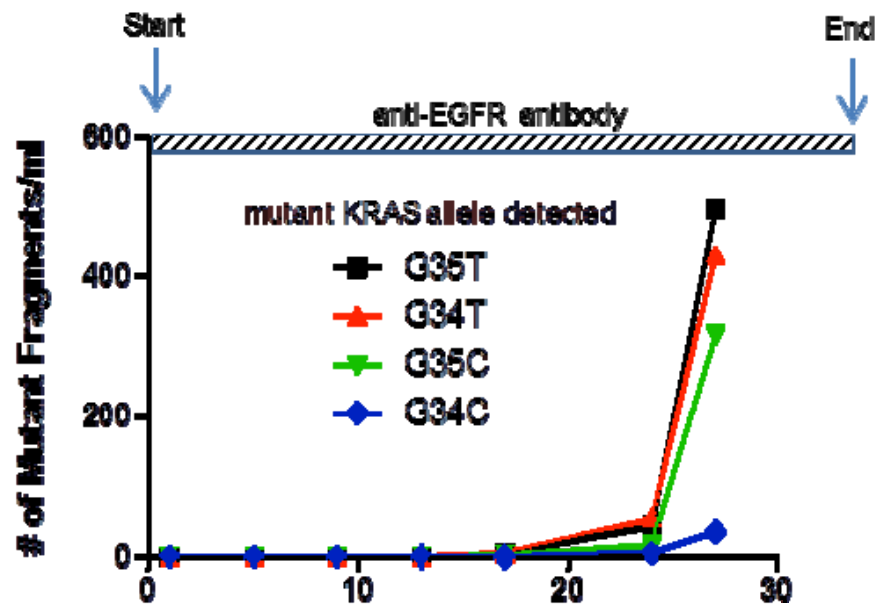
17%

**Secondary
resistance**

Mutations in KRAS, NRAS, EGFR
and Amplification in MET

Tracking Resistance

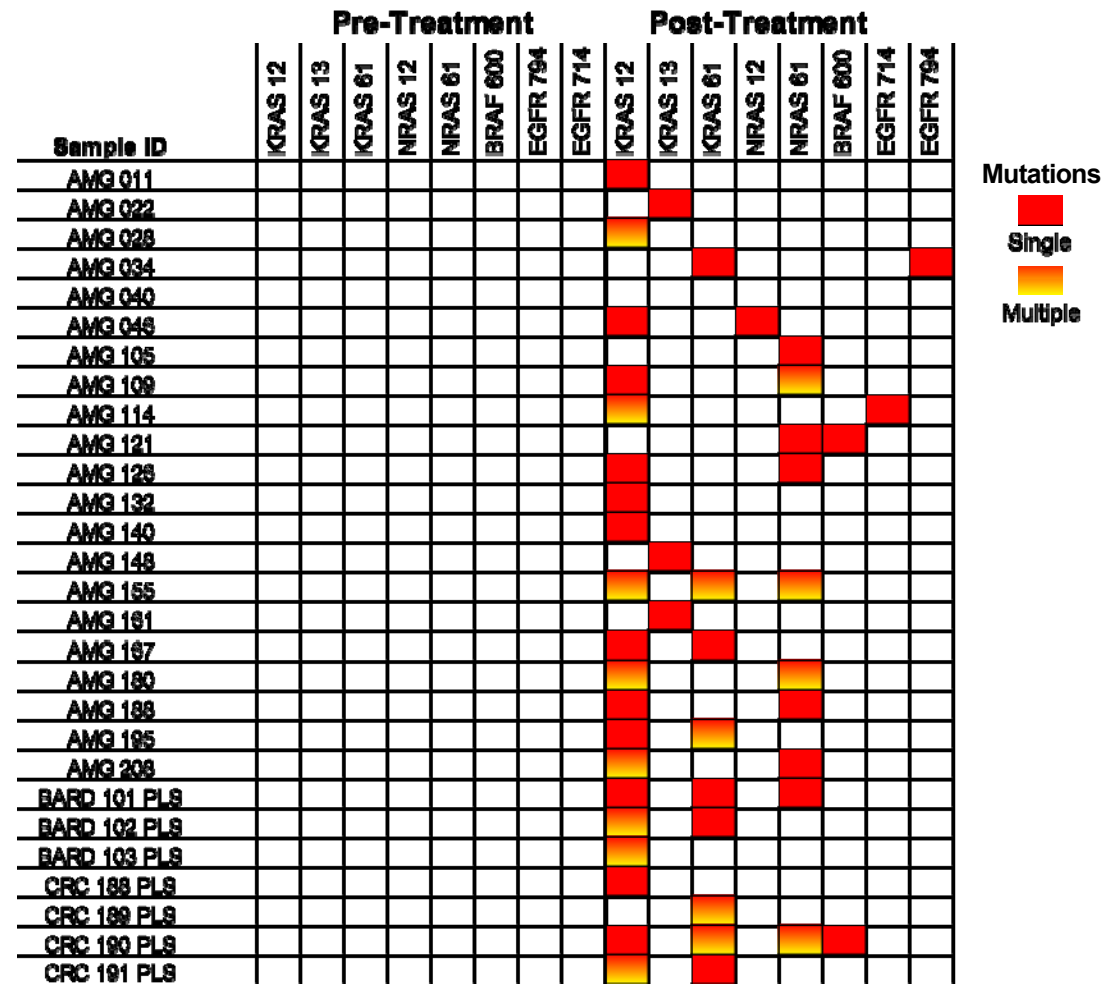
Monitoring the emergence of resistant mutations in KRAS WT patients treated with EGFR blockade

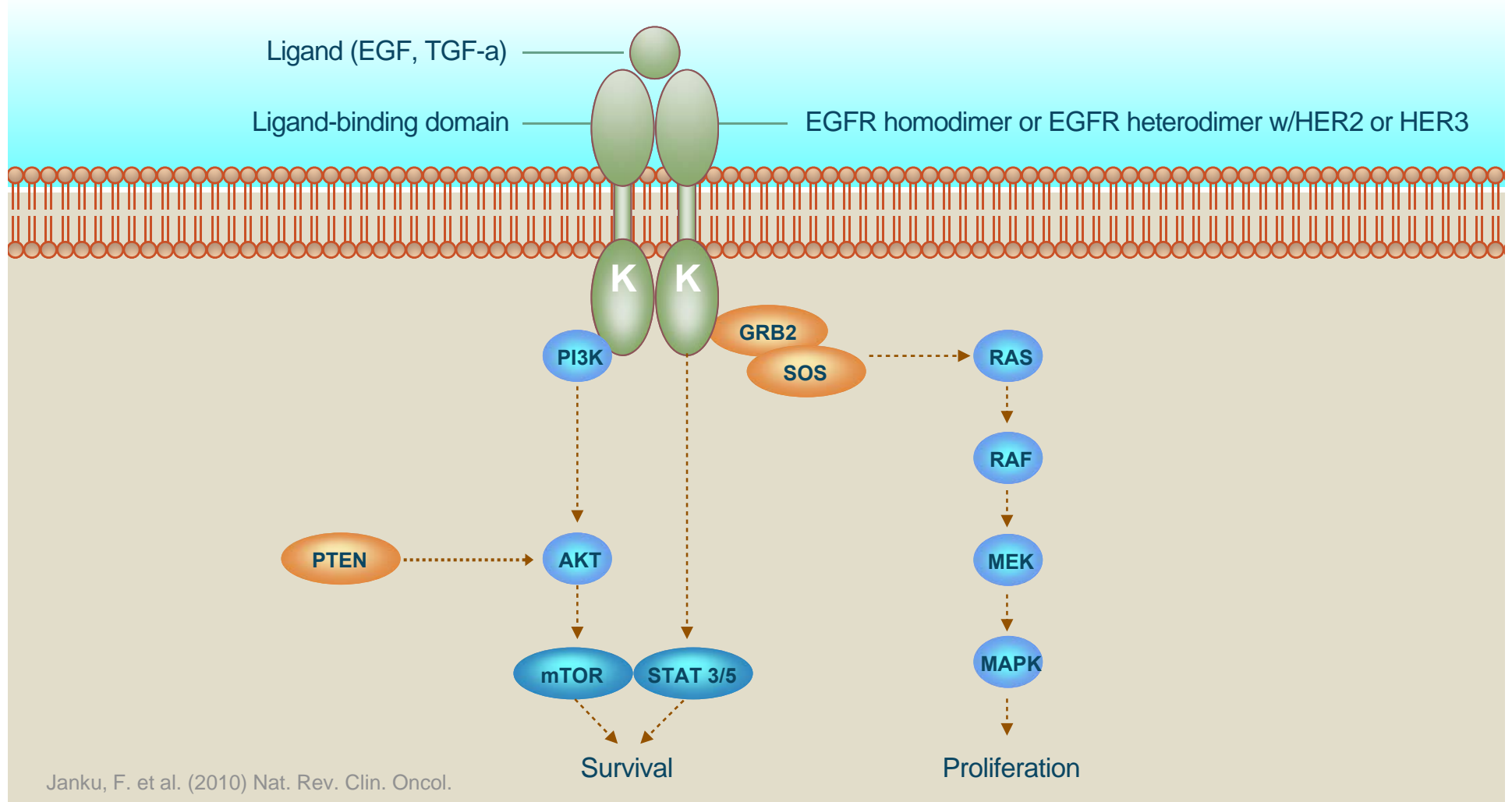


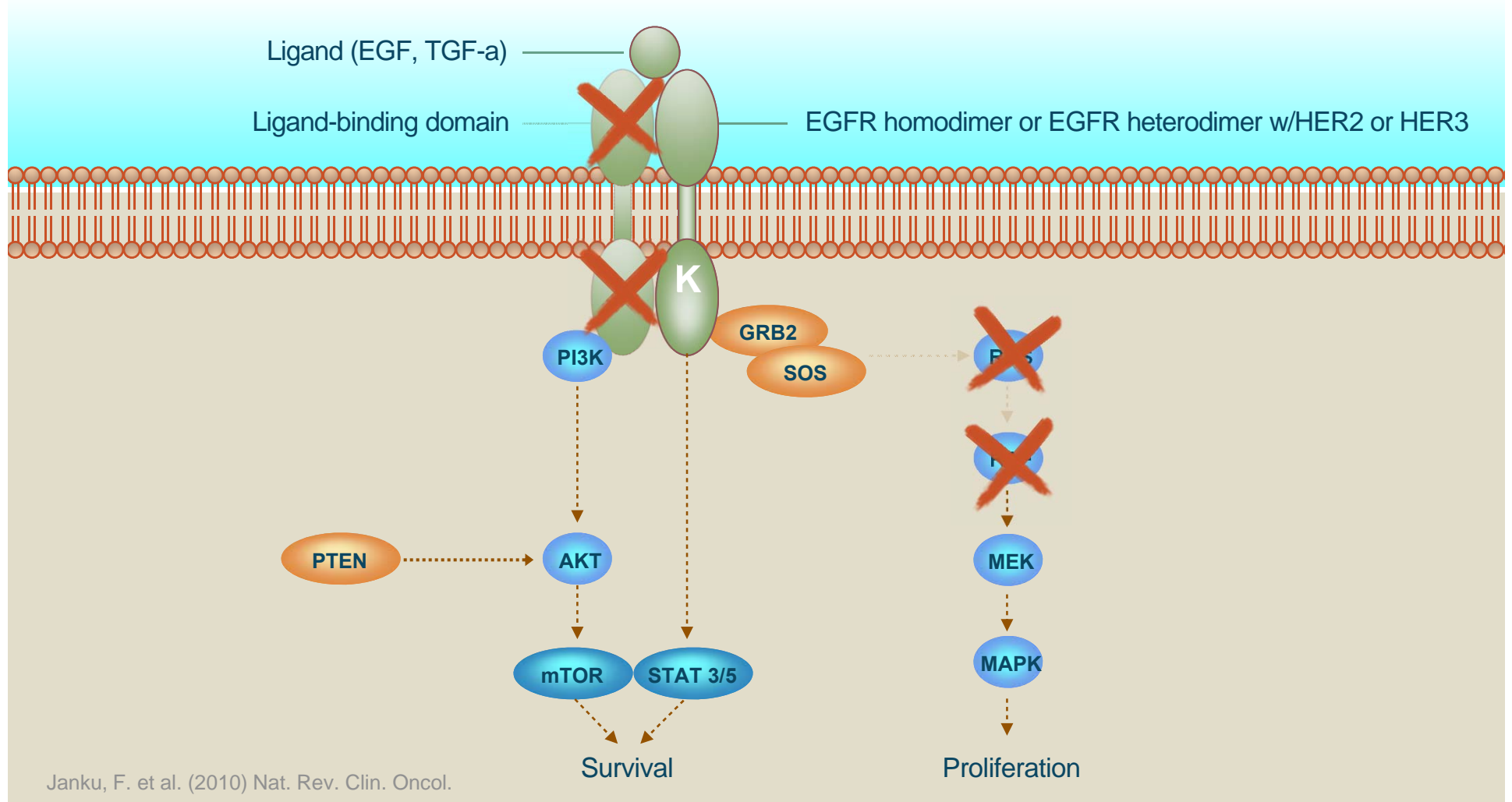
Tracking Resistance

Interrogated all exons of
KRAS, NRAS, BRAF,
PIK3CA and EGFR

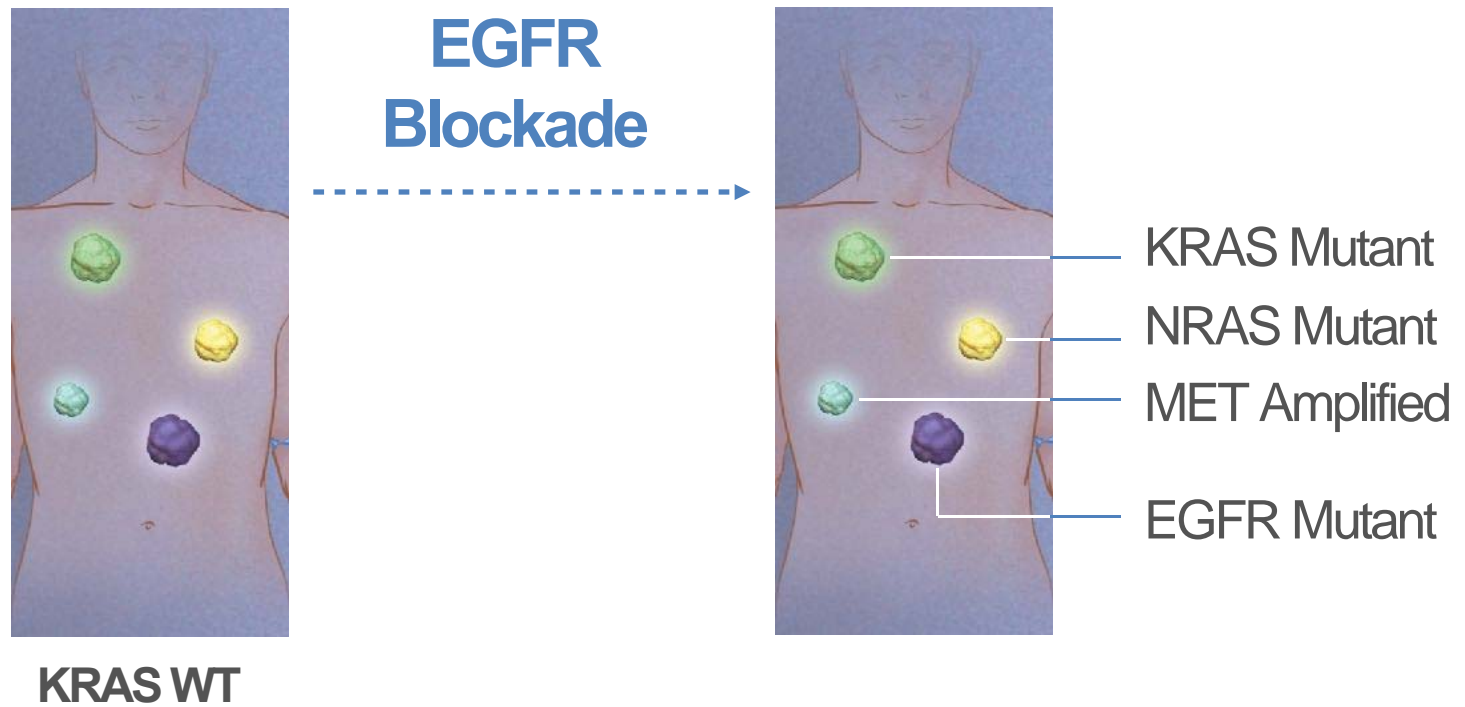
96% of cases had
at least 1 mutation
KRAS or NRAS



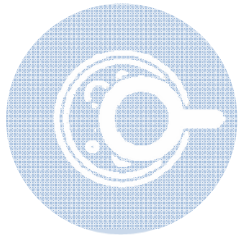




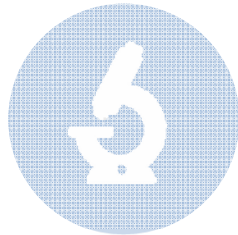
Tracking Resistance



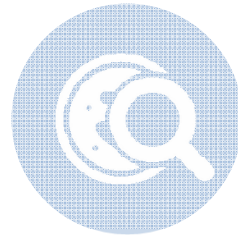
Potential of Liquid Biopsies in Precision Medicine



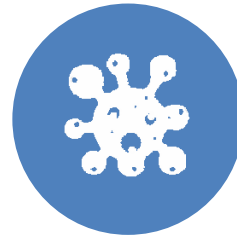
Mutations
as
Biomarkers



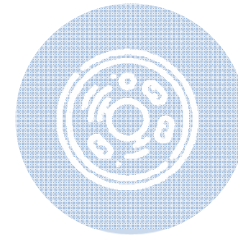
Monitoring
Tumors



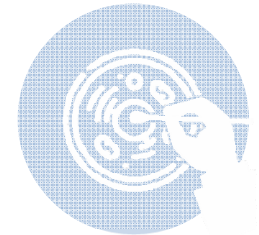
Tracking
Resistance



Minimal
Residual
Disease

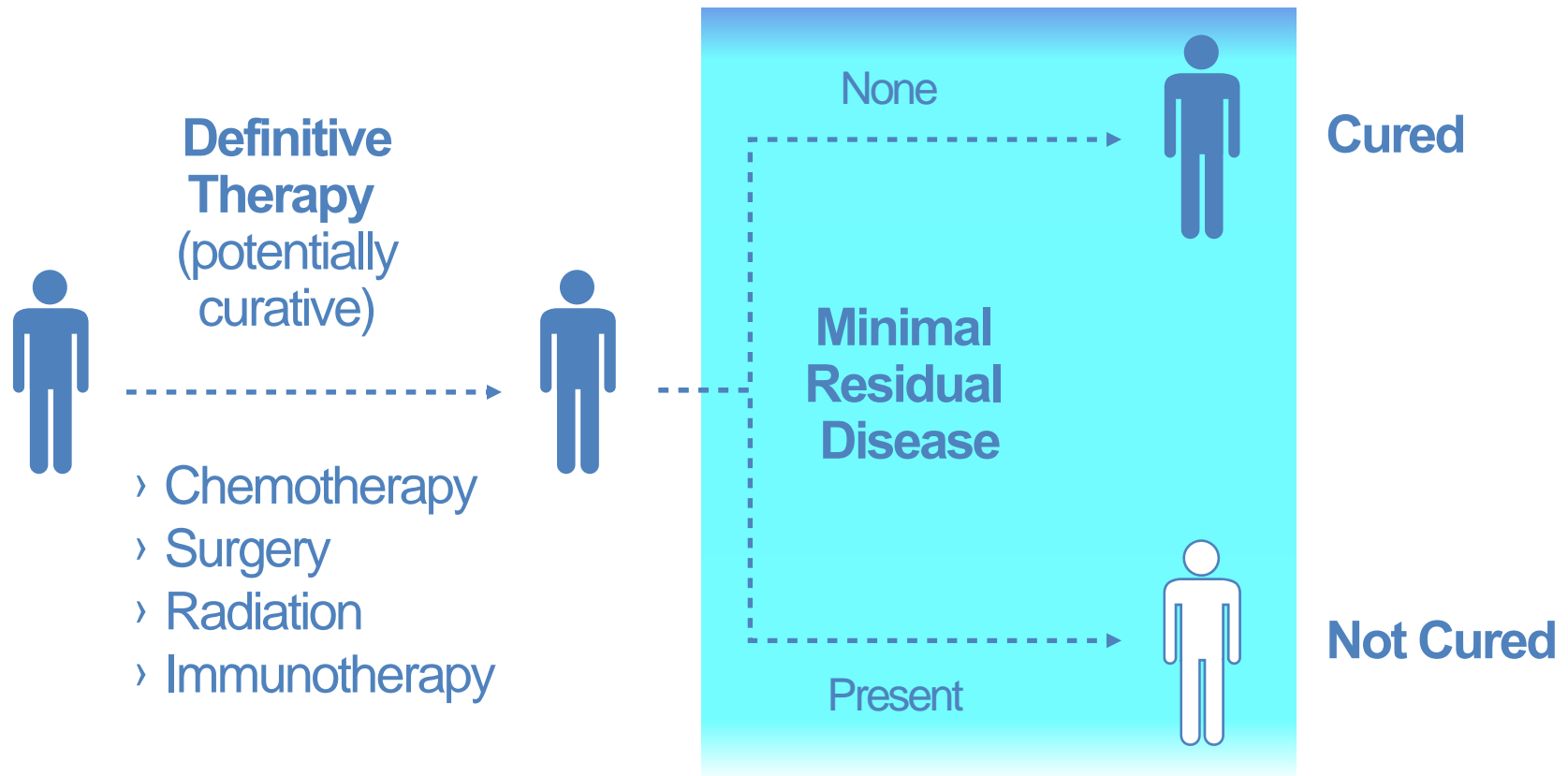


Molecular
Remission



Early
Detection

Minimal Residual Disease (MRD) Defined



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

Surgery

Pre

Post

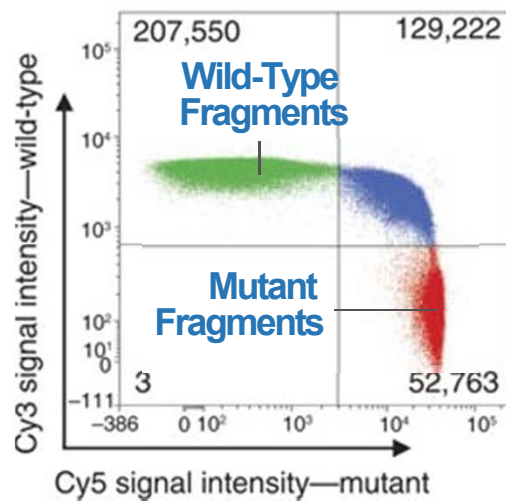
Day

0

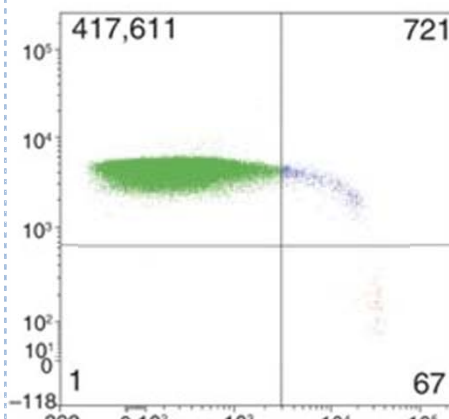
1

42

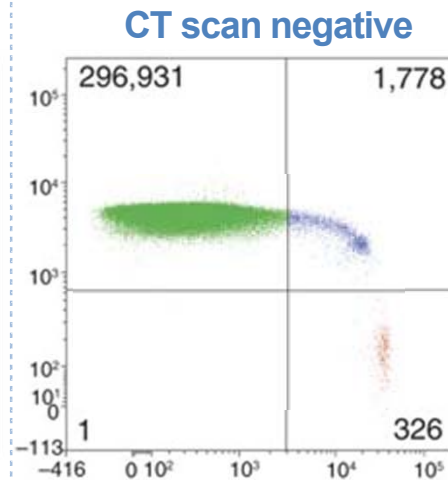
244



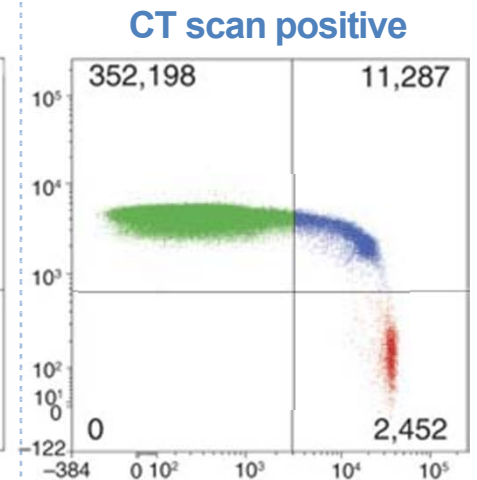
13.4 %



0.015 %



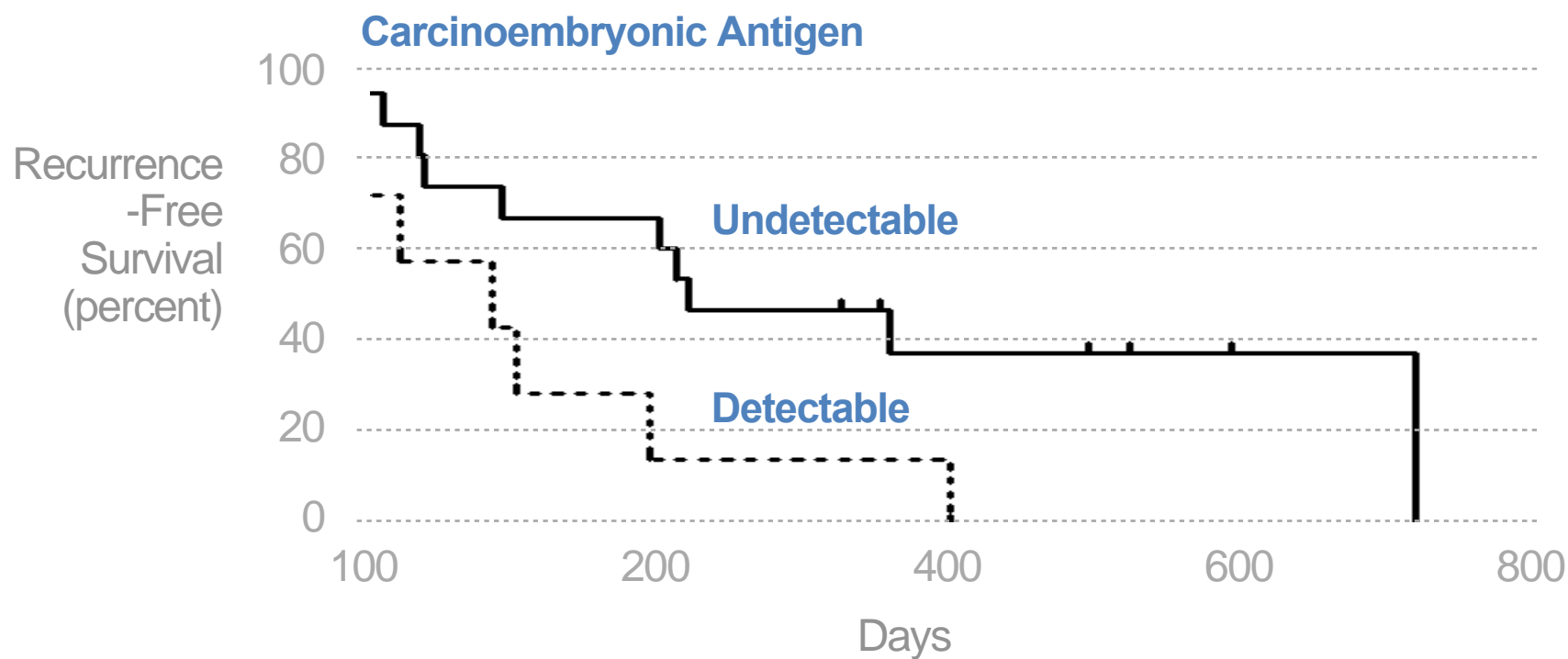
0.11 %



0.66 %

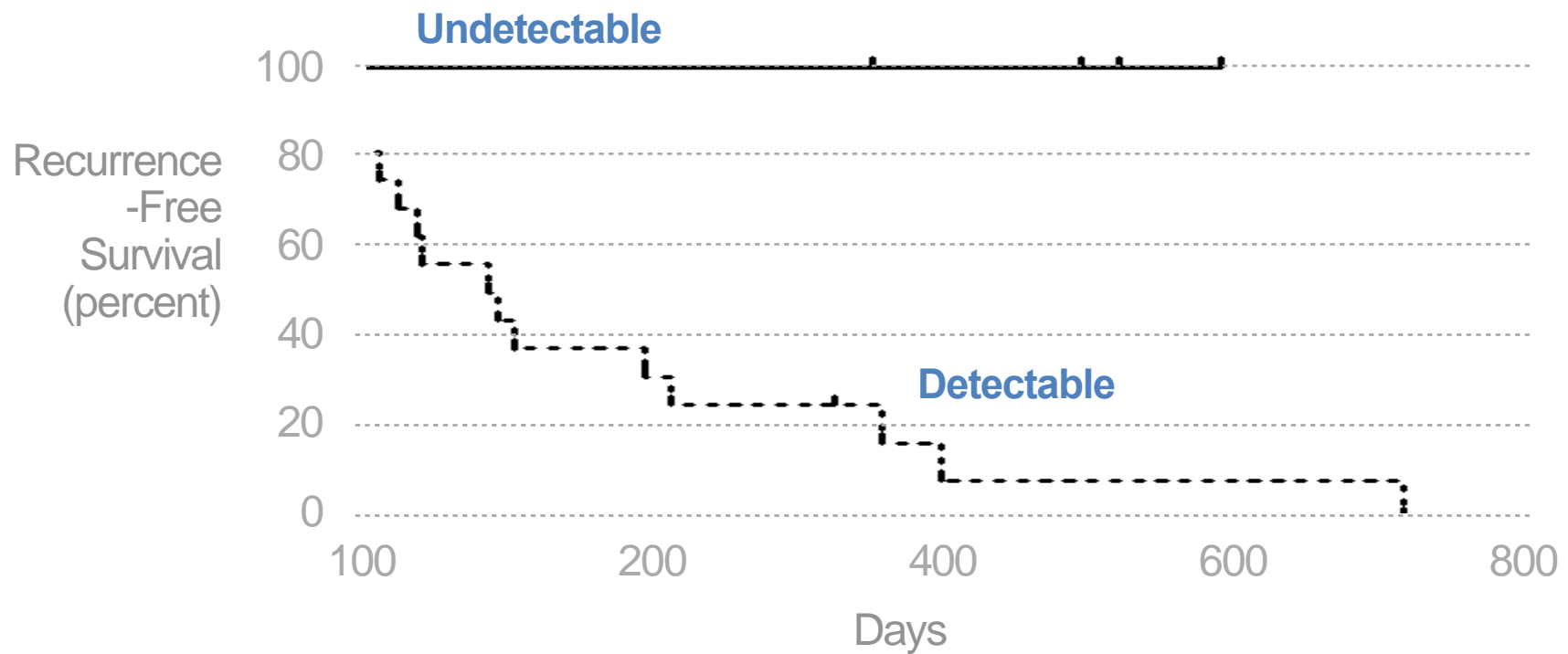
Percent Mutant

Carcinoembryonic Antigen (CEA) measured 6-8 weeks following curative resection of metastatic Colorectal Cancer (mCRC)



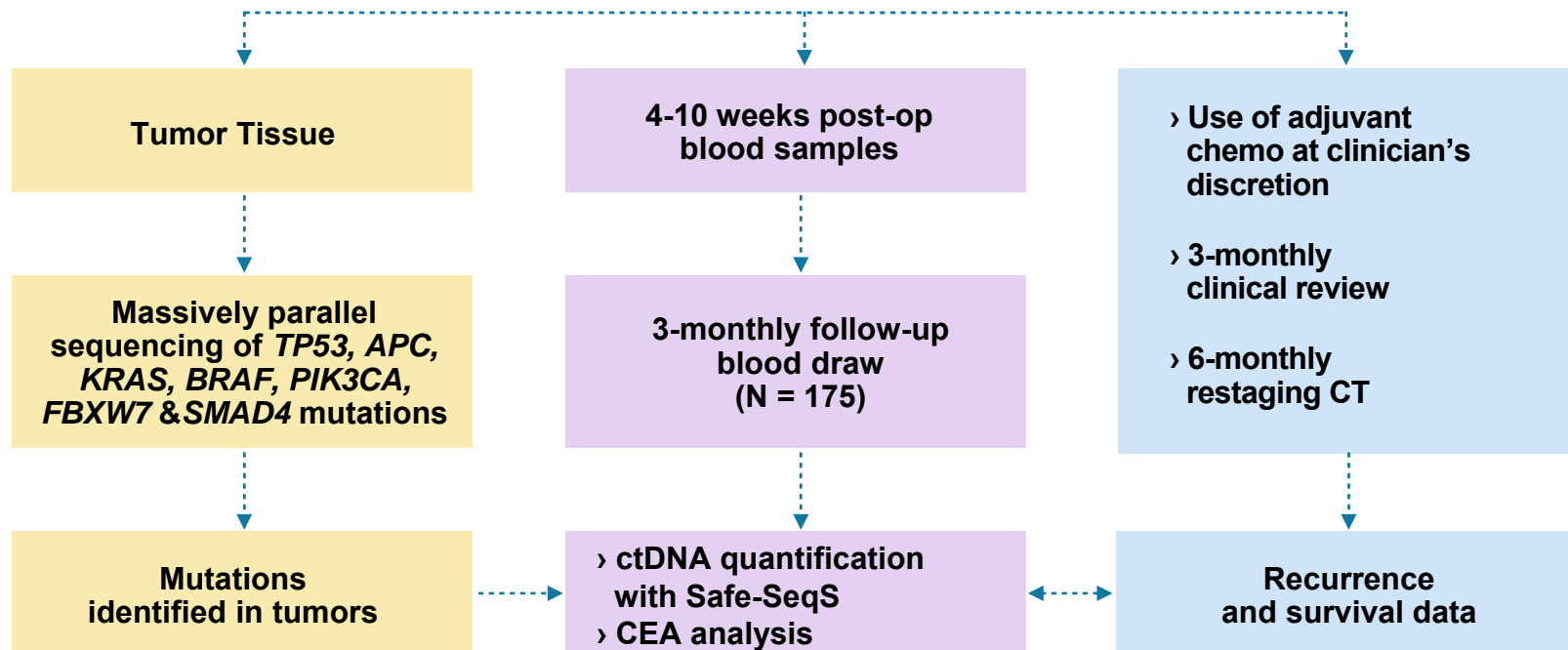
Diehl et al Nature Medicine, 2008

ctDNA measured 6-8 weeks following curative resection of mCRC

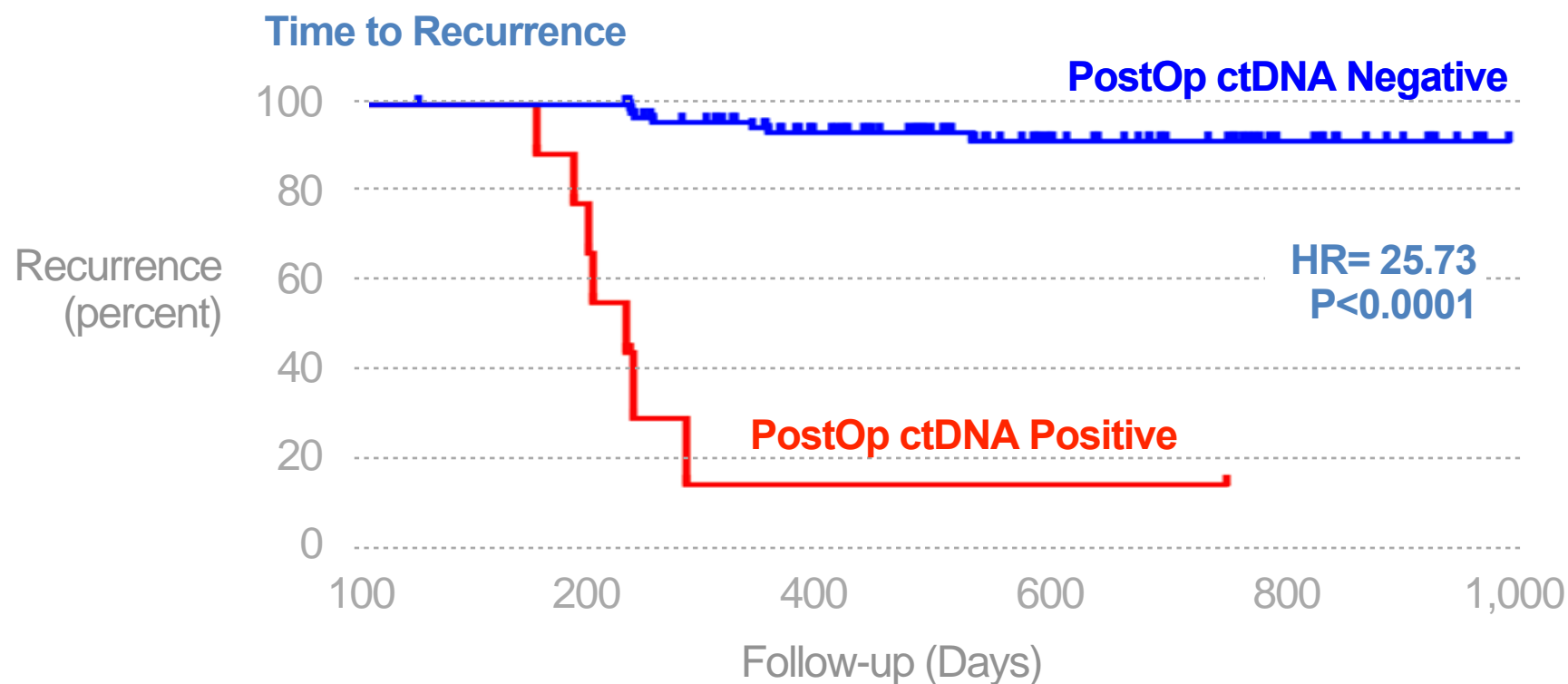


Diehl et al Nature Medicine, 2008

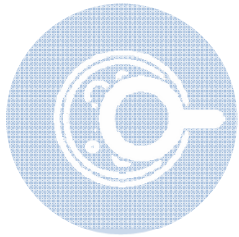
250* patients with Stage II Colon Cancer



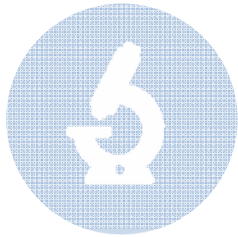
ctDNA Measured 6-8 weeks following curative resection of Stage II CRC



Potential of Liquid Biopsies in Precision Medicine



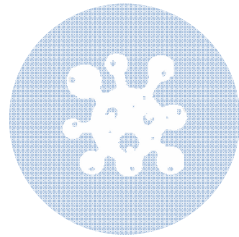
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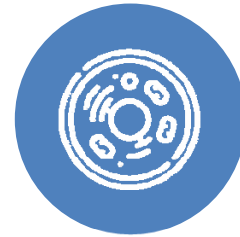
Monitoring
Tumors



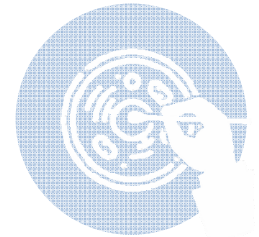
Tracking
Resistance



Minimal
Residual
Disease



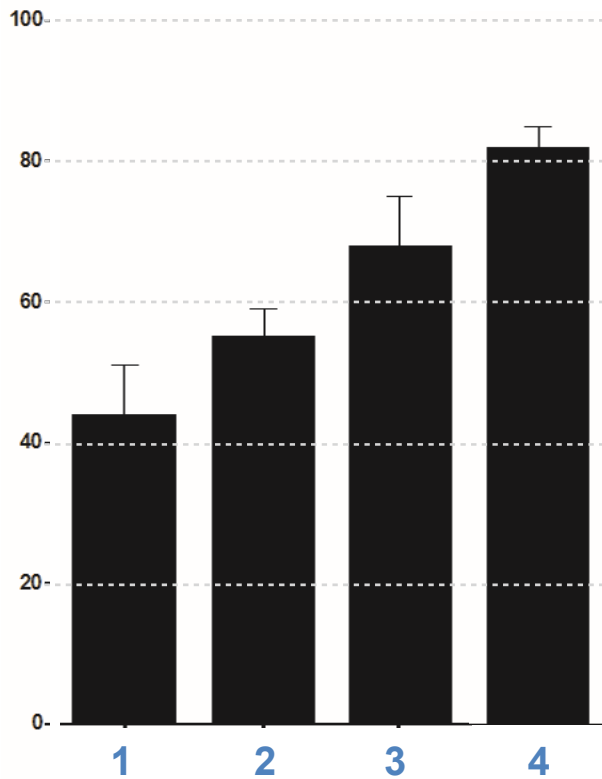
Molecular
Remission



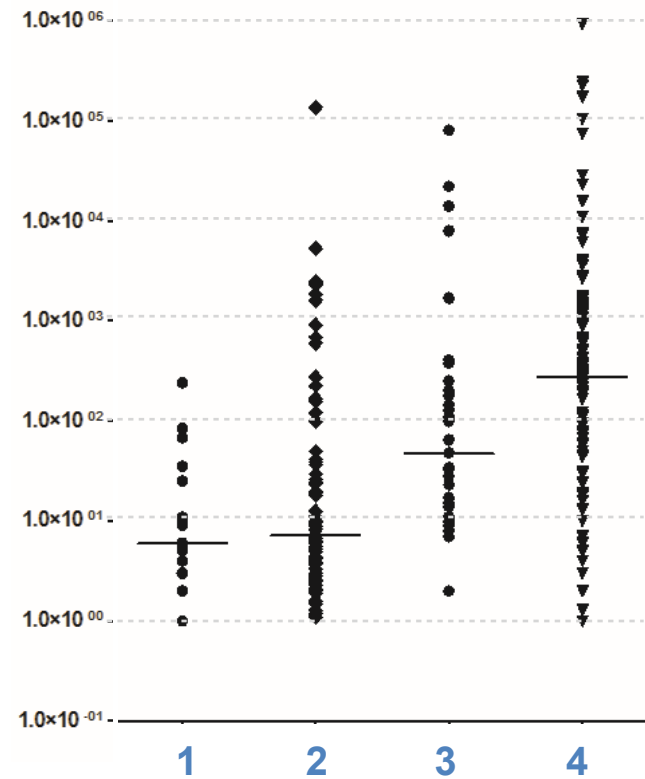
Early
Detection

Early Detection using ctDNA Analyses

Frequency
of cases
with
detectable
ctDNA
analyses



Mutant
fragments
per 5mL



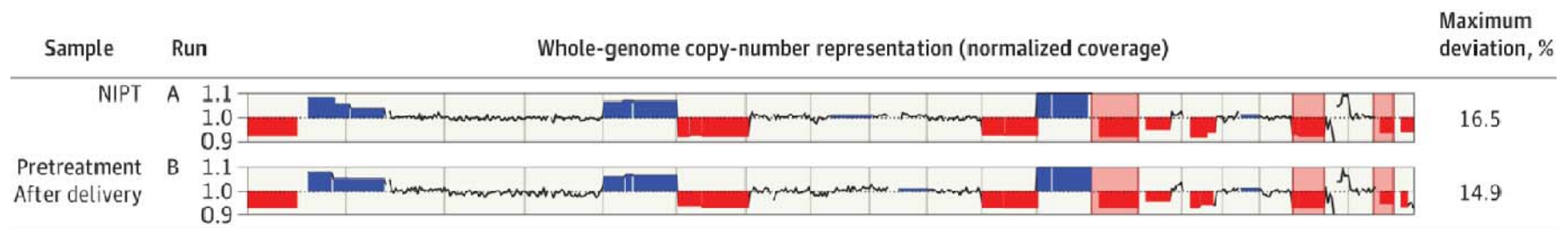
14 Tumor types (n = 684)

Detection of Occult Malignancy from Analyses of cell free Fetal DNA

Non-Invasive Prenatal (NIPT) Tests 125,426

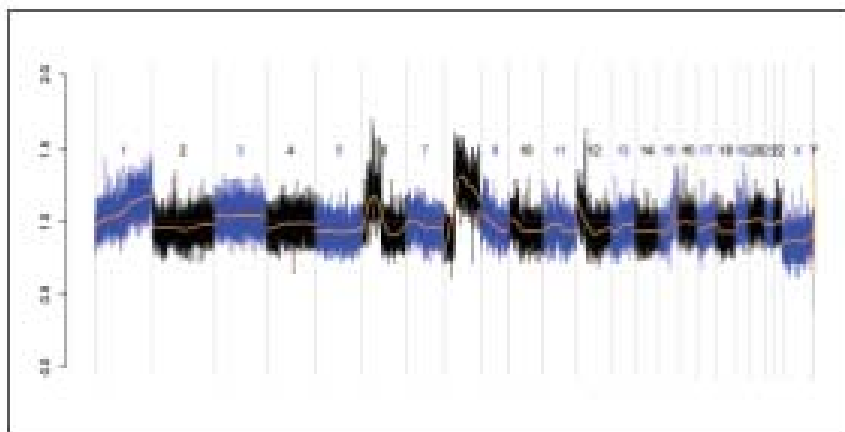
Positive for 1 or More Aneuploidies 3757 (3%)

Cases of Maternal Cancer Identified 10



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

Potential of Liquid Biopsies in Precision Medicine



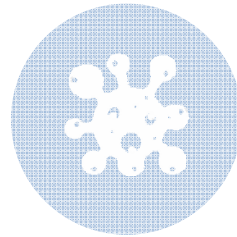
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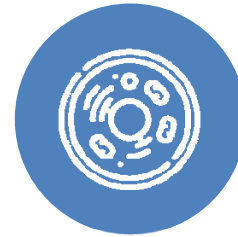
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Tumors



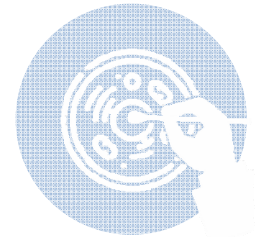
Tracking
Resistance



Minimal
Residual
Disease

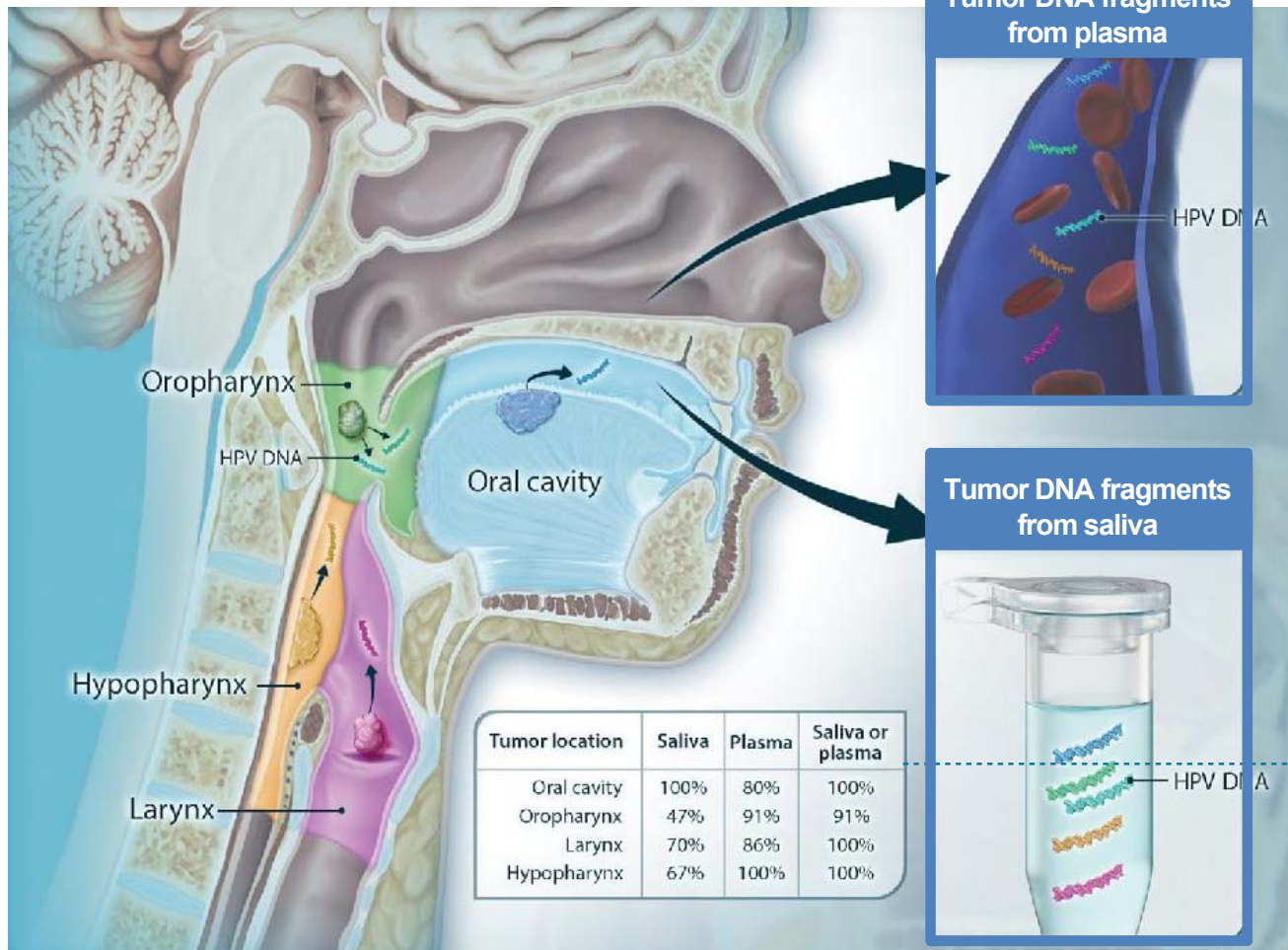


Molecular
Remission



Early
Detection

Tumor DNA in Saliva / Plasma

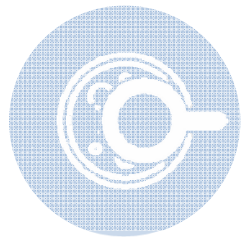


Sensitivity

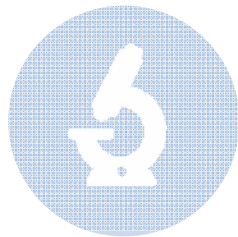
Tumor location	Saliva	Plasma	Saliva or plasma
Oral cavity	100%	80%	100%
Oropharynx	47%	91%	91%
Larynx	70%	86%	100%
Hypopharynx	67%	100%	100%

Wang et al., Sci Transl Med 2015

Potential of Liquid Biopsies in Precision Medicine



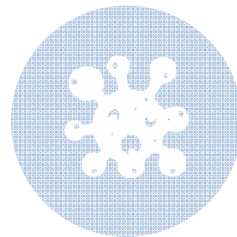
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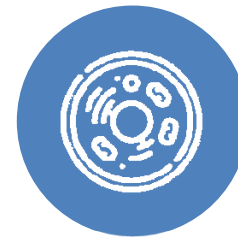
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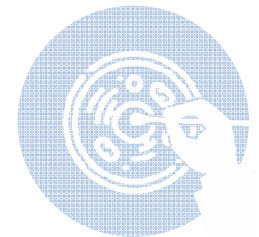
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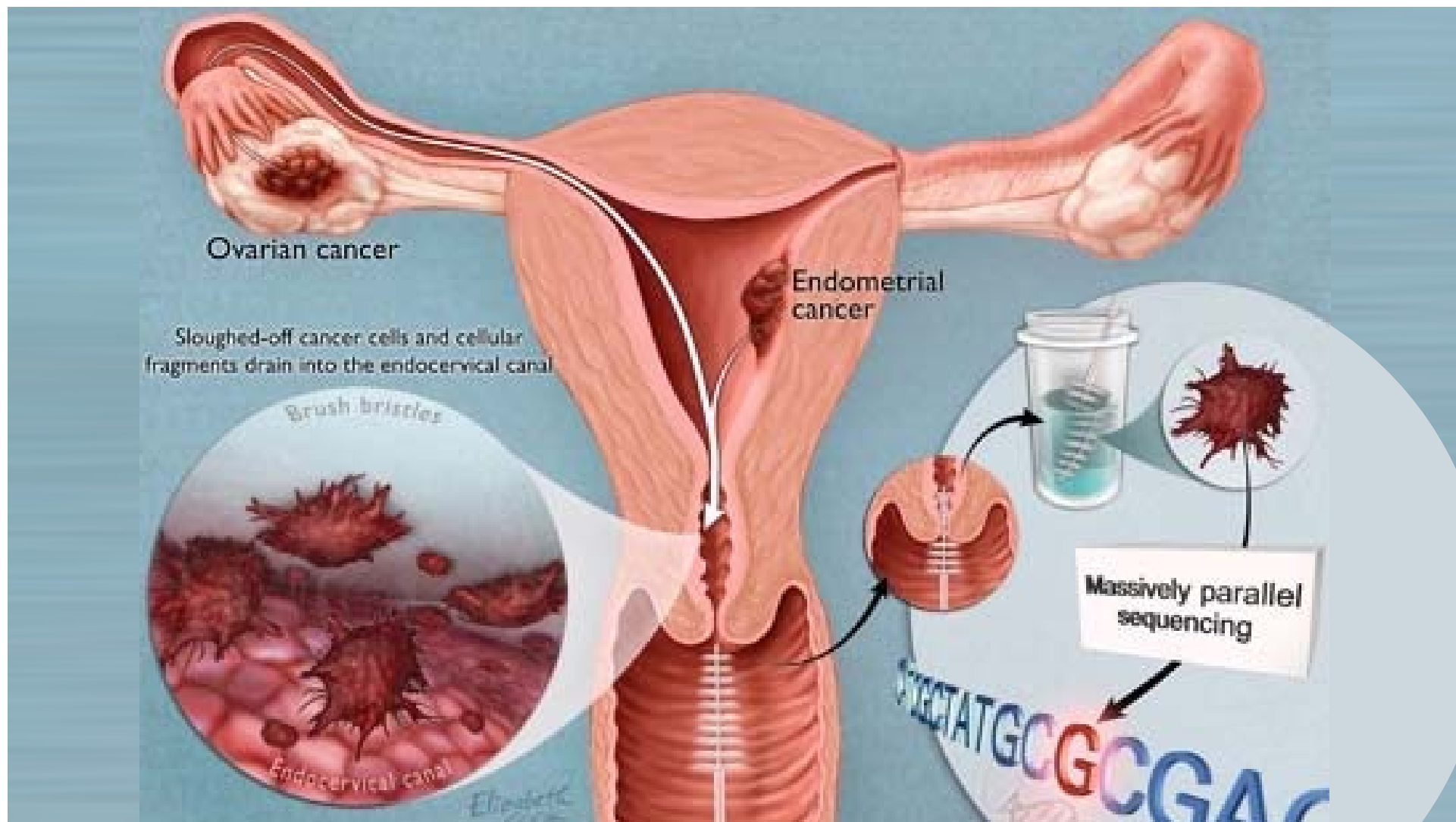
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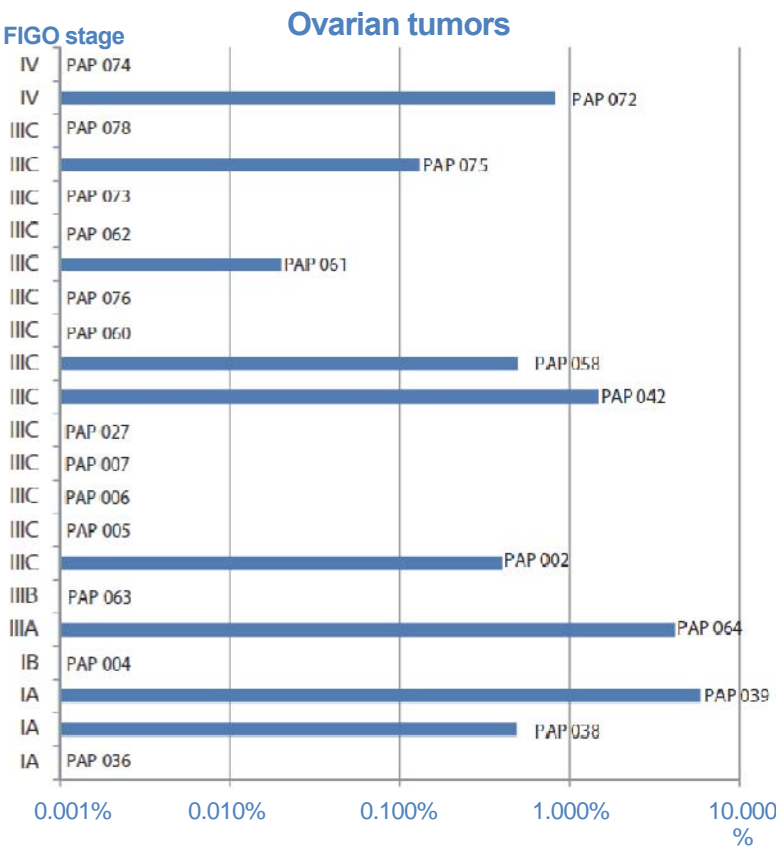
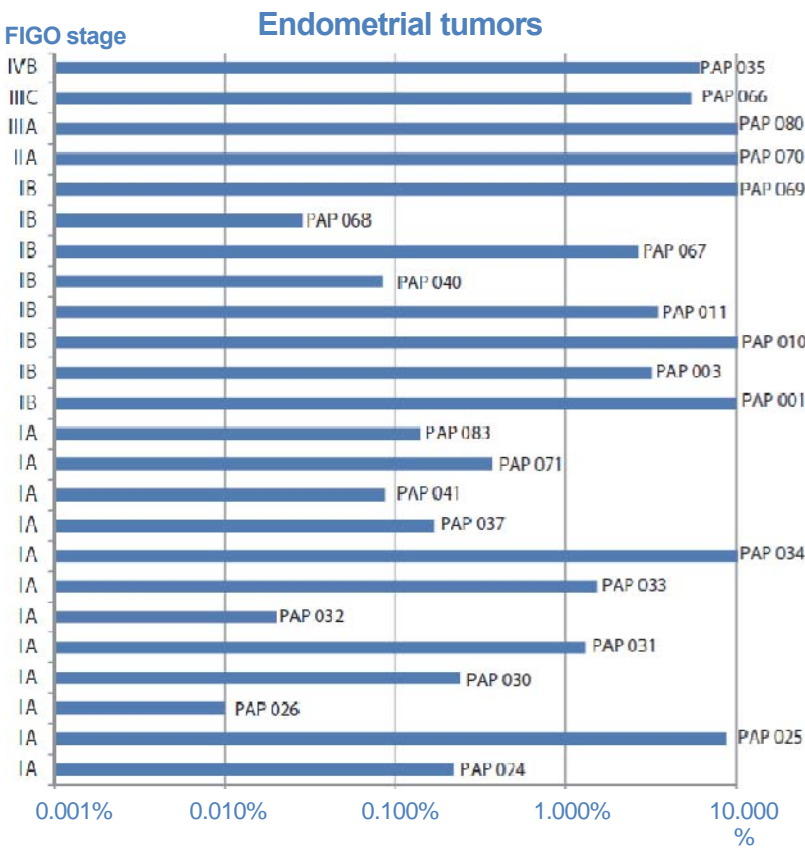
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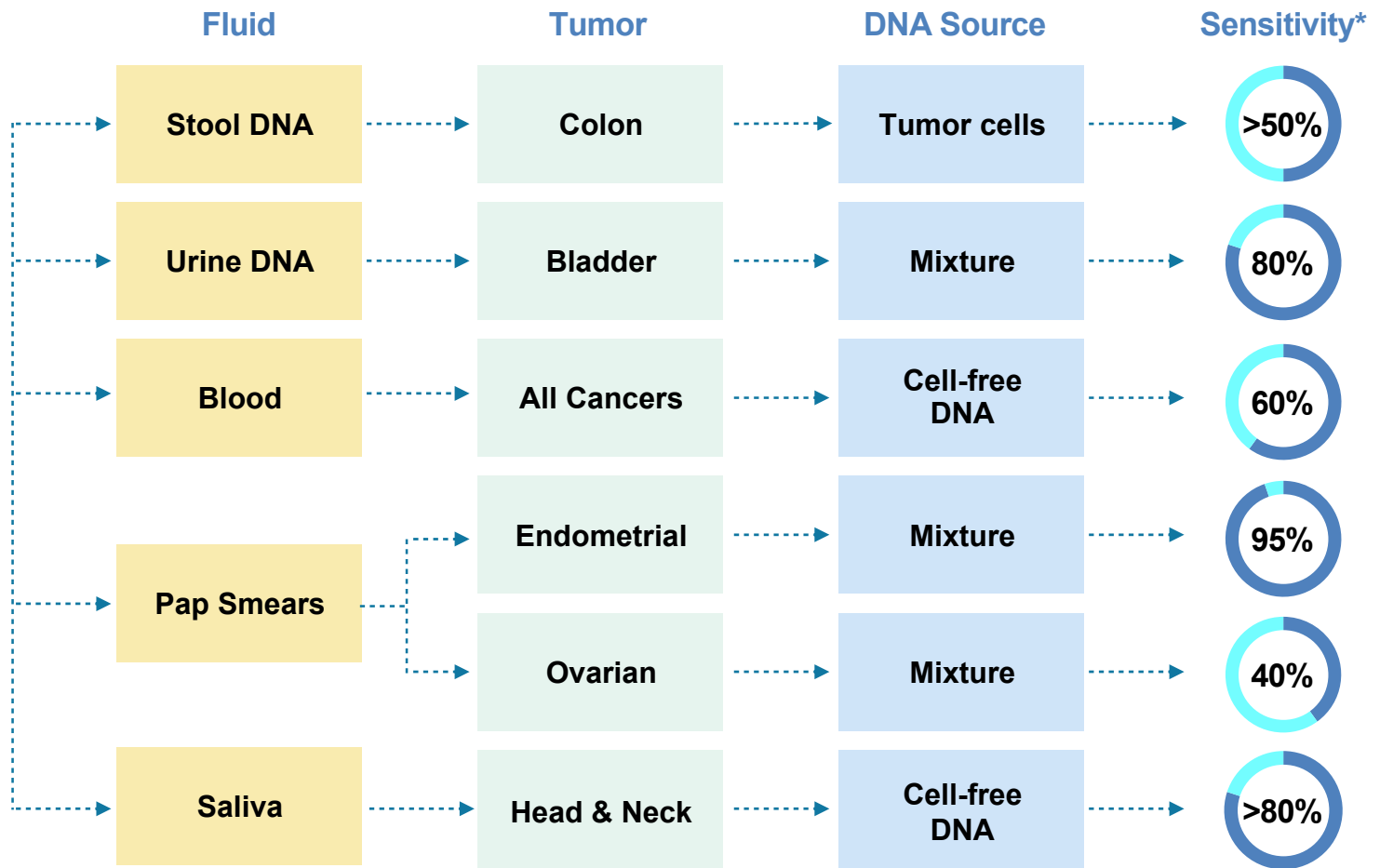


Early Detection - PapGene



Percent mutant alleles in liquid Pap smear specimen

Somatic Mutation as Biomarkers



*Stage I and II Disease

Challenges

Not all clonal events are cancer

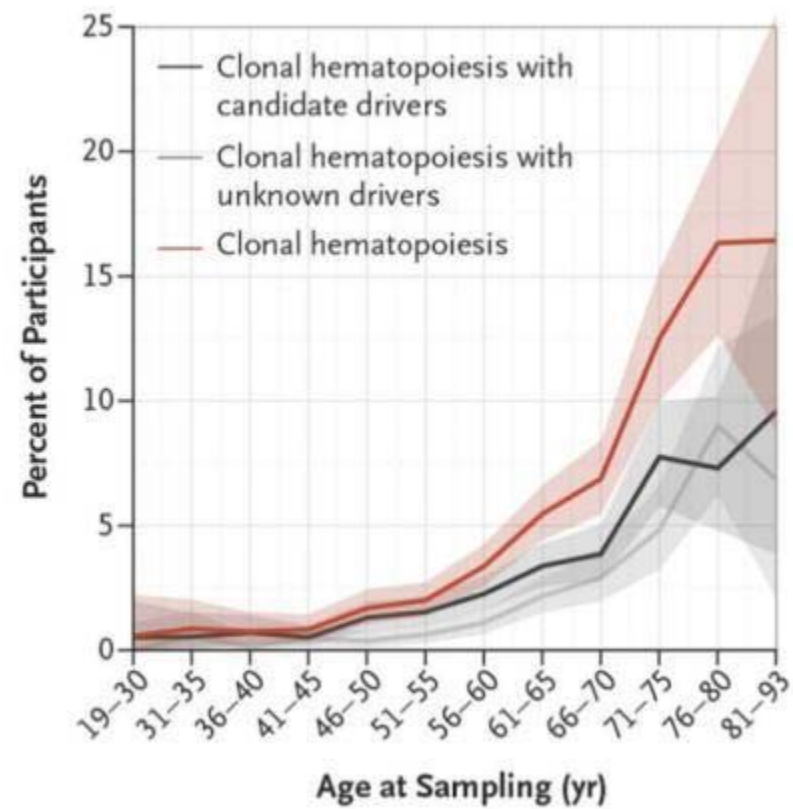
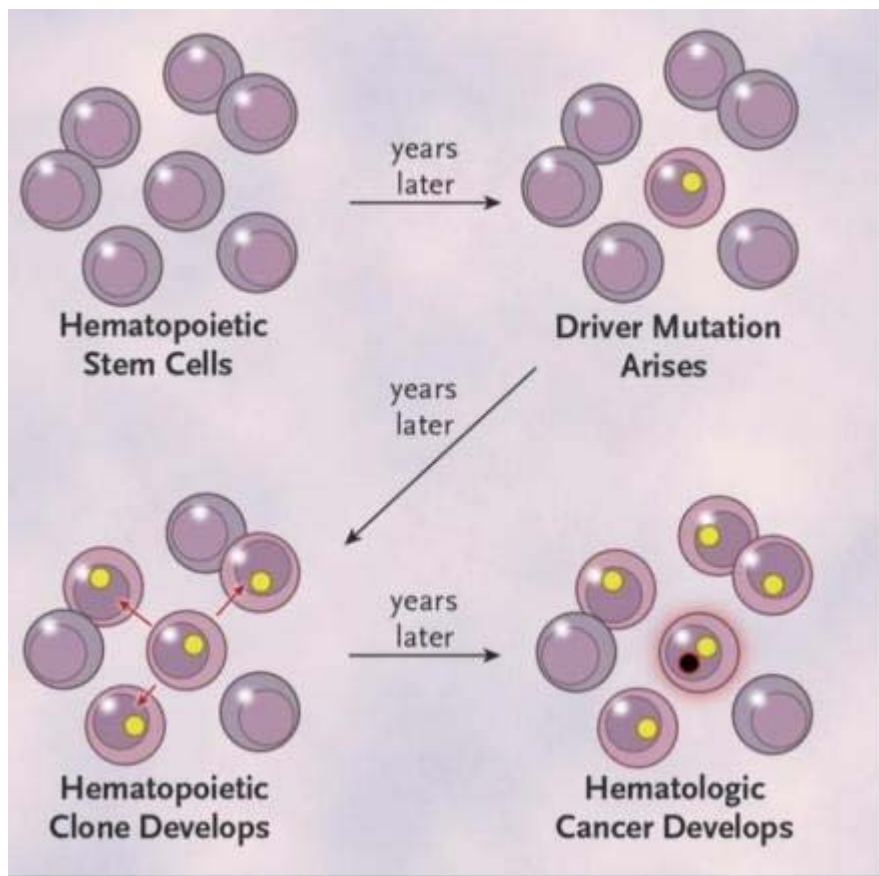
The NEW ENGLAND JOURNAL of MEDICINE

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



NOT ALL SOMATIC MUTATIONS ARE CANCER

The NEW ENGLAND JOURNAL of MEDICINE

ORIGINAL ARTICLE

Cancer-Associated Mutations in Endometriosis without Cancer

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H. Ogawa, B. Tessier-Cloutier, R. Alhassan, A. Wang, Y. Wang, J.D. Cohen,
F. Wong, A. Hasanovic, N. Orr, M. Zhang, M. Popoli, W. McMahon, L.D. Wood,
A. Mattox, C. Allaire, J. Segars, C. Williams, C. Tomasetti, N. Boyd, K.W. Kinzler,
C.B. Gilks, L. Diaz, T.-L. Wang, B. Vogelstein, P.J. Yong, D.G. Huntsman,
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The NEW ENGLAND JOURNAL of MEDICINE

ORIGINAL ARTICLE

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

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ORIGINAL ARTICLE

Aneurysm Syndromes Caused by Mutations in the TGF- β Receptor

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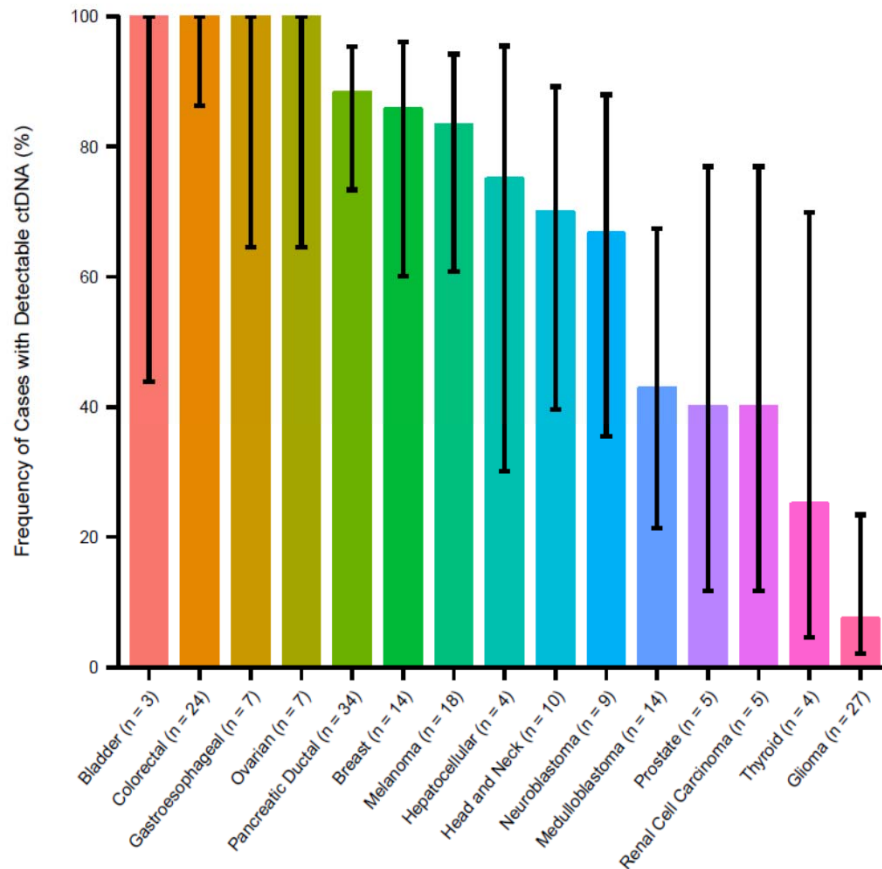
Localization

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? Cancer of the Lung, Colon Pancreas?
Precursor?

Heterogeneity



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

Biological Limitations

- Not many mutant molecules in blood
- On average 1,000-3,000 genome equivalents per mL
- Need at least 3 molecules to call a positive result
- Sensitivities are limited by insufficient mutant molecules

Challenges for ctDNA in the future

Biology

- Not all clonal events are cancer
- Heterogeneity
- Localization
- Very few molecules in blood

Lack of focus on feasible unmet clinical need

- Few targeted therapeutics
- Cost does not match clinical benefit or need

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 SURVIVAL will require prospective clinical trials and partnership with FDA.

Ludwig Center for Cancer Genetic and Therapeutics



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Kelly Oliner



Memorial Sloan Kettering
Cancer Center

Opportunities and Limitations of ctDNA as a Clinical Biomarker in Cancer Management: New Insights in the Clinical Application of ctDNA

QUESTIONS

