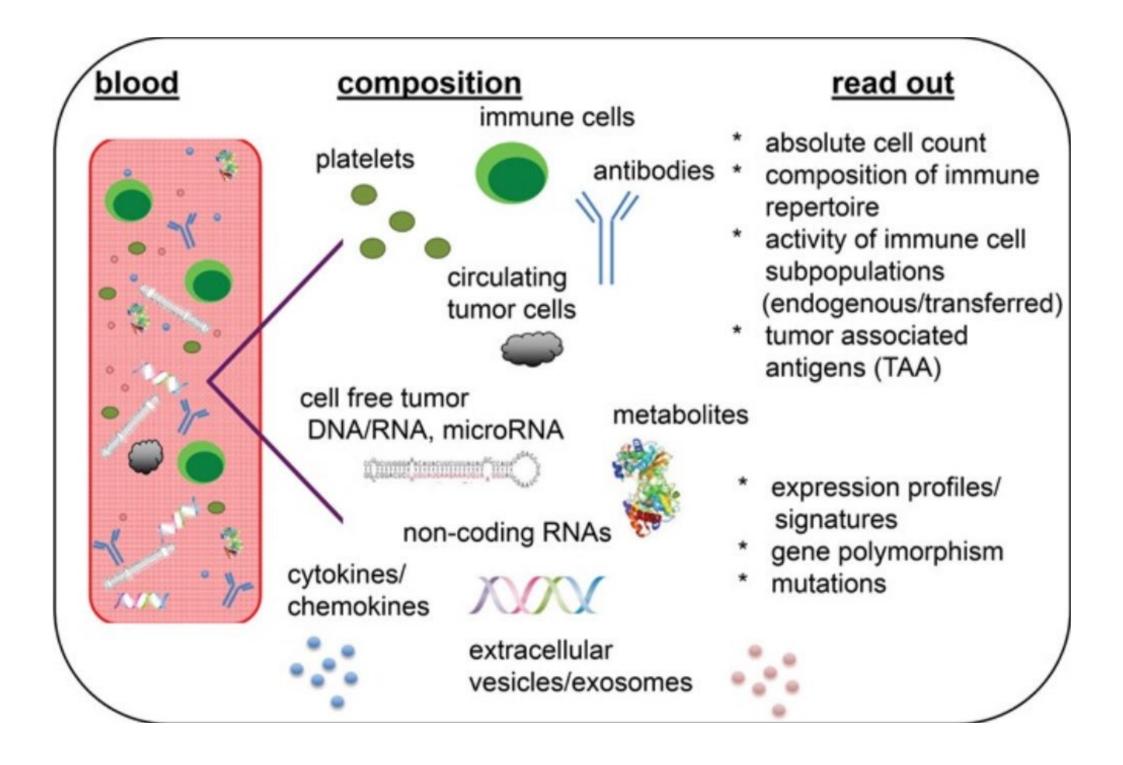


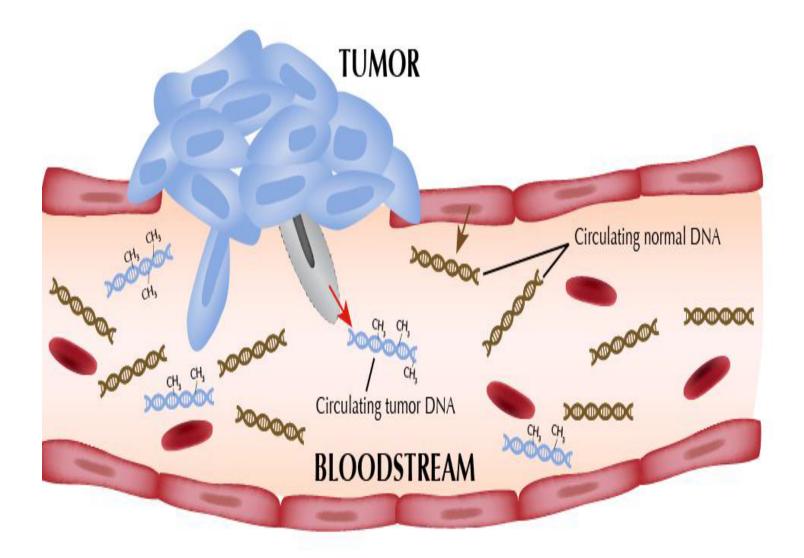
Tumor DNA (FFPE - biopsy)

Circulating tumor cells (CTC in liquid biopsy)

Circulating tumor DNA (ctDNA in liquid biopsy)

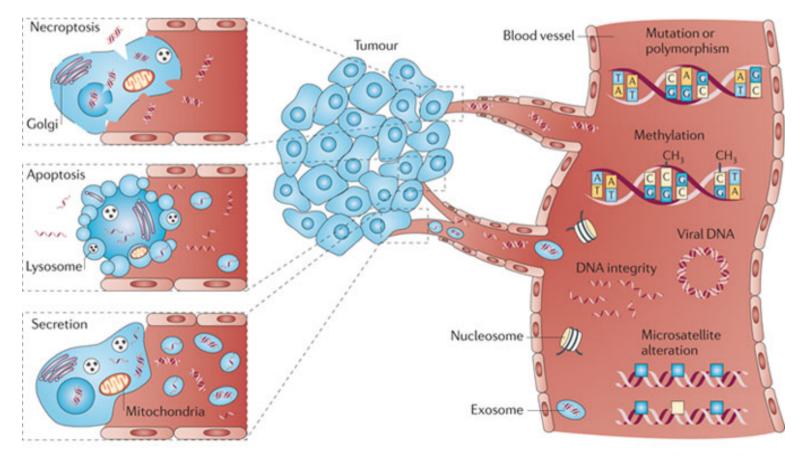


## **Circulating tumor DNA (ctDNA)**



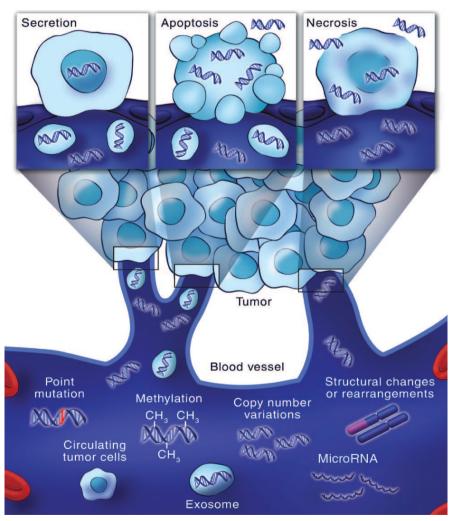
# ctDNA

ctDNA from tumor tissue is released through secretion, necrosis and apoptosis, but mainly through apoptosis.



Nature Reviews | Cancer

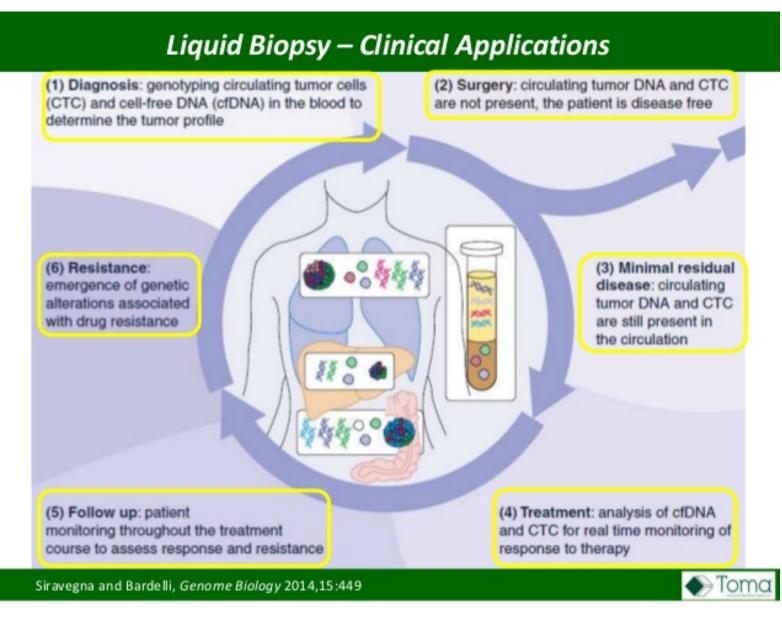
## **Circulating Tumour DNA (ctDNA)**



Diaz and Bardelli, 2014 Journal of Clincial Oncology 32



- ctDNA is tumour DNA that has been shed into the bloodstream
- ctDNA can be present in 0.01% - >90% of the total Cell Free DNA (cfDNA)
- The amount of ctDNA is related to the tumour burden and varies between patients with different clinical presentations



Cell-free DNA (cfDNA) is found in blood plasma at concentrations of 10-100 ng/ml, in fragments of 150 base pairs. When cfDNA comes from tumor cells, it is called ctDNA, and can be identified by point mutations and chromosome rearrangements typically found in cancer genomes.

## **FFPE versus ctDNA**

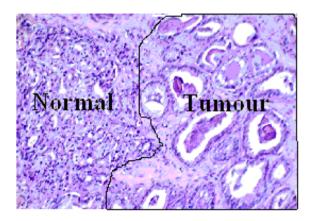


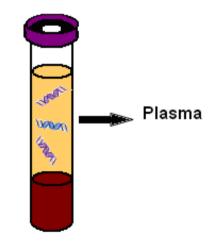
#### • FFPE Samples

- Tumour DNA extracted from fixed biopsy samples or tumour resections
- Problems with quality of DNA due to fixation
- Mixture of normal and tumour DNA
- Long time to process by histopathologists.
- Macrodissected to enrich tumour content
- Some patients have no tumour sample available
- The sample represents the tumour at one fixed time point

#### ctDNA Samples

- ctDNA shed directly from tumour
- Extracted from the plasma component of whole blood
- Large fragment sizes possible
- Small quantities extracted ~ 30ng/ 5ml plasma
- Separate out plasma within a few hours of receipt of blood sample.
- Serial samples can be taken at various time points during the patient's treatment





## cell-free DNA (cfDNA) testing

- Cell-free DNA (cfDNA) in plasma of healthy individuals : Mandel and Métais (1948)
- A proportion of cfDNA in pregnant women is fetus-derived (cffDNA) : Lo et al. (1997)
- Non-Invasive Prenatal testing (NIPT) : 2012 : start

2015 : > 1 million tests Market : 4 billion USD

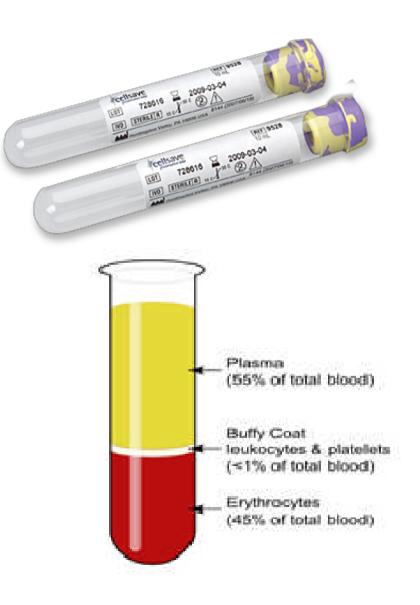
- Increased concentrations of cfDNA in the circulation of cancer patients : Leon et al. (1977)
- A proportion of cfDNA is tumor-derived : Stroun et al. (1987)
- Circulating tumor DNA (ctDNA) testing (liquid biopsy) : 2015 : start

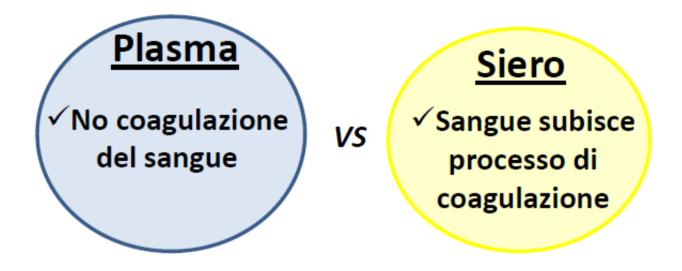
Market: 40 billion USD

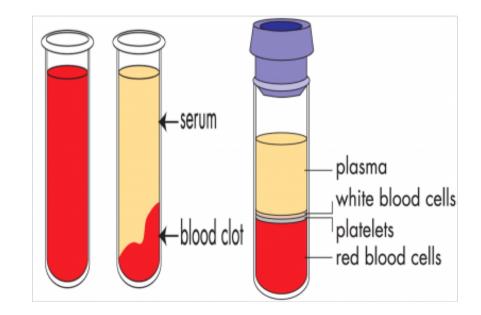
## **ctDNA Collection**



- ctDNA has a very short half life ranging from 15 minutes to several hours
- It is stable in plasma at -80°c
- Blood can be sampled in ETDA tubes but the plasma has to isolated and stored at -80°c within one hour of collection
- Preservative tubes can be used to stabilise the cfDNA in blood for up to 4 days at room temperature.

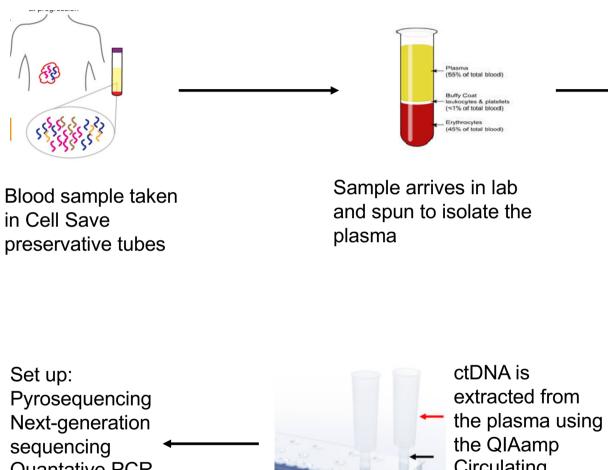






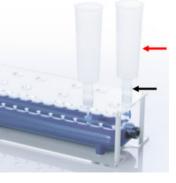
## ctDNA Workflow





Plasma is stored at -80°c

Pyrosequencing Next-generation sequencing Quantative PCR BEAMing **Digital PCR** 



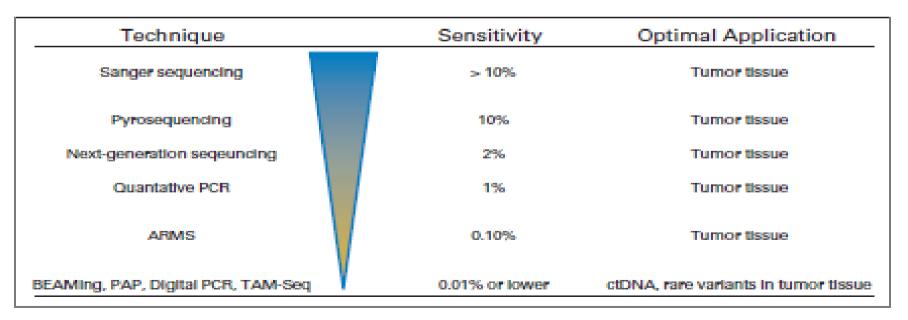
Circulating Nucleic Acid on the QIAVac system

Sample is extracted on the same day as the downstream process set up due to ctDNA instability

# **Problems with ctDNA**

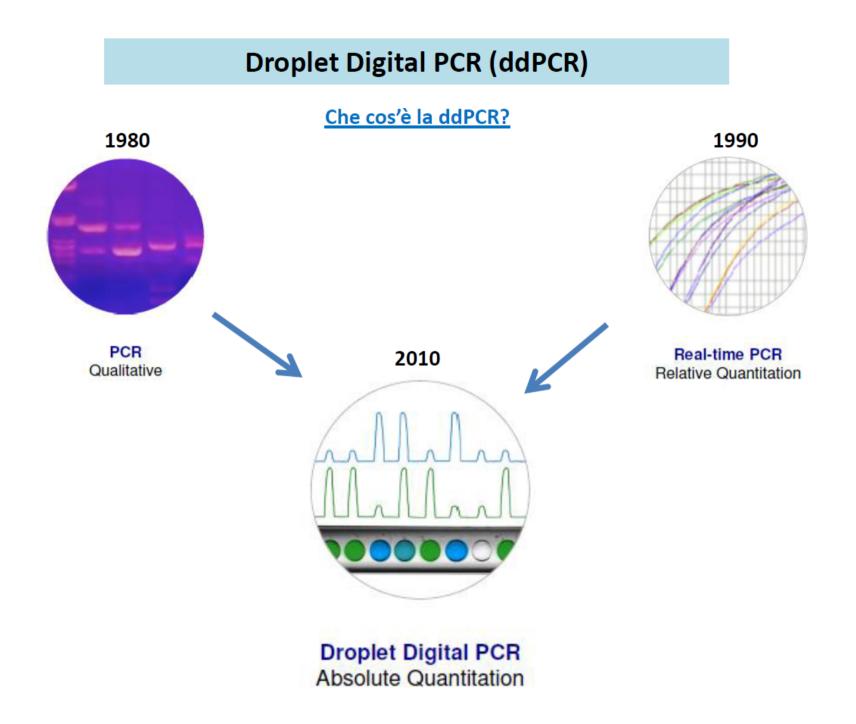


- Due to the unstable nature of ctDNA the sample is has to be collected and processed correctly
- Only get **30ng** of **cfDNA** per **5ml** plasma extraction
- The amount of ctDNA is related to the tumour burden and varies between patients
- Difficult to discriminate ctDNA from normal cfDNA
- The technique used must be sensitive enough to pick up the low level variants



# Summary of sensitivity and specificity methods used for cfDNA analysis (Rolfo et al., 2014)

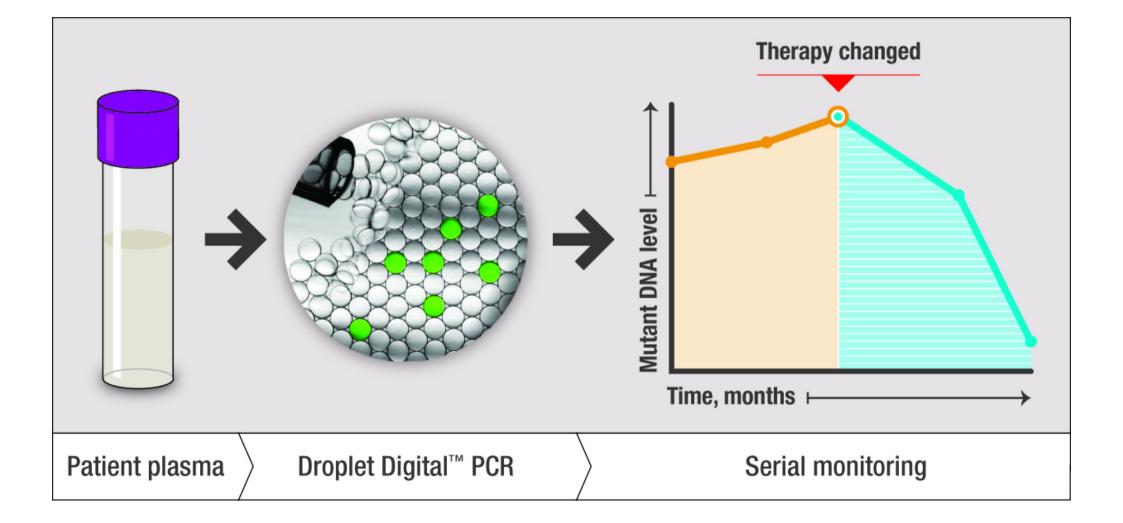
Method	Sensitivity	Specificity
qPCR	high	low
Methylation specific polymerase chain reaction (MS-PCR)	high	high
Sanger sequencing	very low	high
Pyrosequencing	low	low
NGS	low	high
ARMS	low	high
BAEMing (beads, emulsion, amplification, magnetics)	high	high
Digital PCR	high	high
TAM-sequencing	high	high



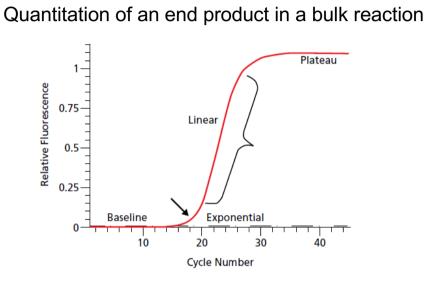
## **Droplet digital PCR**

Accurate absolute quantification of template molecules by separation of target molecules and counting statistics.

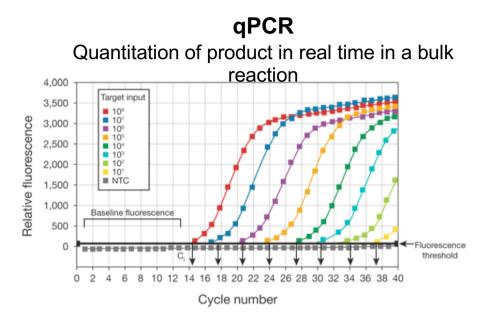
A sample is fractionated into 20,000 droplets, and PCR amplification of the template molecules occurs in each individual droplet.



## ddPCR Principle



Standard PCR

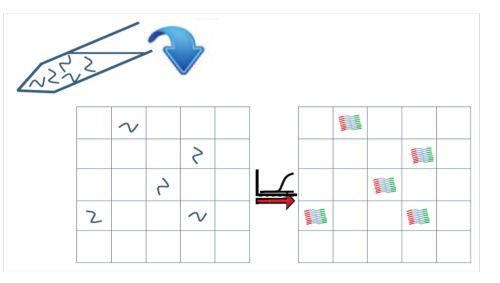


#### ddPCR

•Bulk reaction separated into smaller partitions.

•Each partition intended to contain zero or one copy of DNA.

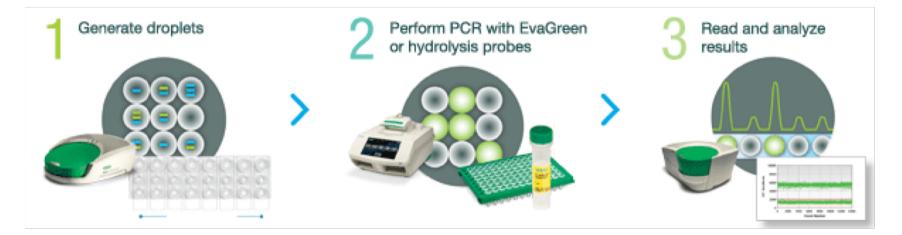
•The fraction of positive partitions is fitted to a Poisson distribution to determine the absolute starting copy number of DNA.

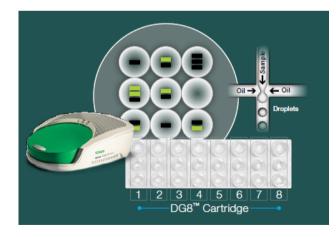




## ddPCR Principle: Process

#### Bio-Rad QX200 System







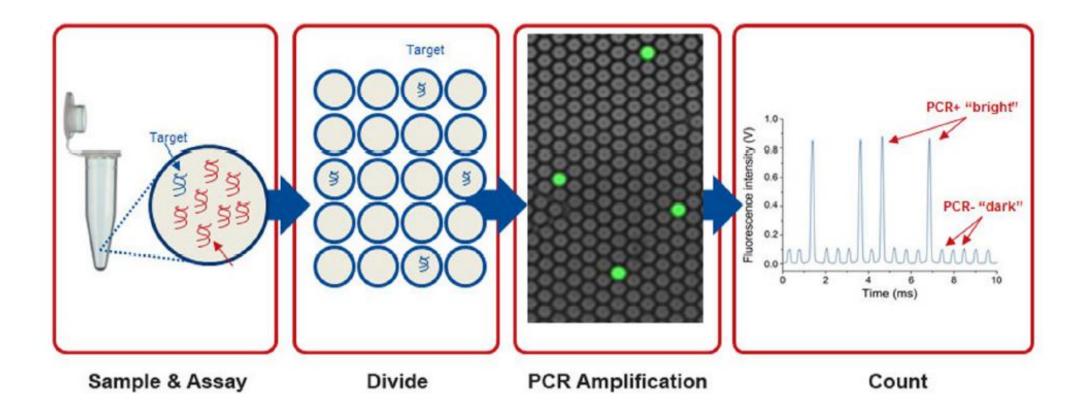
**Absolute Quantification:** No need for a standard curve because number of targets in a given volume (i.e. concentration) is counted directly (and adjusted for multiple targets/droplet by **Poisson statistics**)

- **Precision**: The ability to consistently make the same measurement on replicates of a sample
- Reproducibility: The ability of a researcher to obtain the same measurement on the same sample from experiment to experiment in the same lab OR in another lab across the globe.
- **Sensitivity**: The ability to measure very few copies of a target with precision mostly limited by the technology independent statistics of sampling
- Accuracy: The ability to make the correct measurement this requires validation before this can be claimed, but is then an intrinsic property of the ddPCR assay used.

## Bio-Rad QX200<sup>™</sup> Droplet Digital PCR System

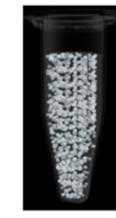








One measurement



Nanodroplet PCR reactions are independent, single

amplification events

Many thousands of discrete measurements •Removal of PCR bias — error rates are reduced by removing the amplification efficiency reliance of qPCR, enabling the detection of small (1.2-fold) differences Prepare ddPCR reaction mix

- Combine DNA/RNA sample, primers, and/or probes with one of Bio-Rad's ddPCR supermixes
- Fully validated PrimePCR<sup>™</sup> ddPCR assays can be used

### Generate droplets

- Load the ddPCR reaction mix into the wells of a droplet generator cartridge
- 8 x 20,000 droplets are generated from each run in the QX100<sup>™</sup> or QX200 droplet generator
- Target DNA (-) and background DNA
  (-) are randomly distributed in droplets

## Perform PCR

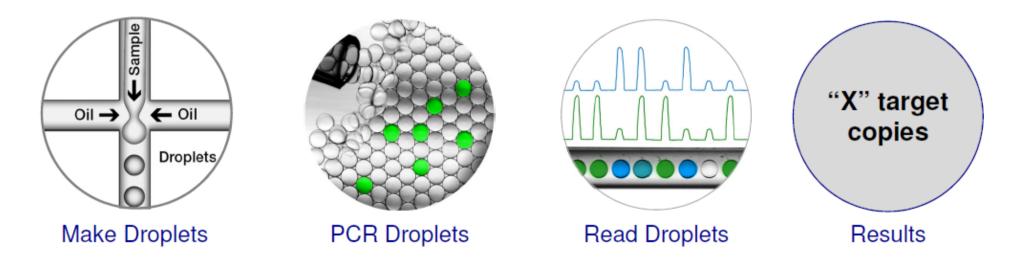
- Transfer the droplets to a 96-well PCR plate and seal the plate
- Run the PCR protocol

### Read and analyze results

- After PCR, load the 96-well PCR plate into the QX100 or QX200 droplet reader
- Positive and negative droplets in each sample are read
- Analyze concentrations with QuantaSoft<sup>™</sup> software

## **Droplet Digital PCR Workflow**

- Partition reagents and sample into thousands of droplets
- Perform PCR on thermal cycler
- Count droplets with a positive PCR product (fluorescent) and a negative PCR product
- Digital readout provides concentration of target DNA

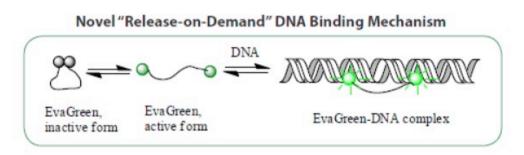




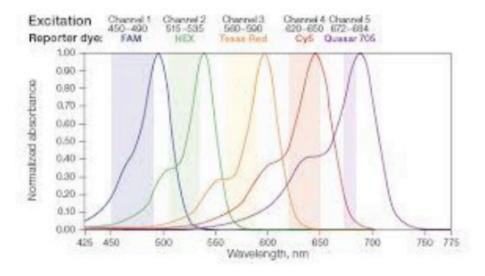
### Che molecole può leggere?

#### **EvaGreen**<sup>™</sup>

#### Sonde TaqMan<sup>™</sup>







✓ FAM

✓ HEX/VIC

Principali vantaggi ddPCR

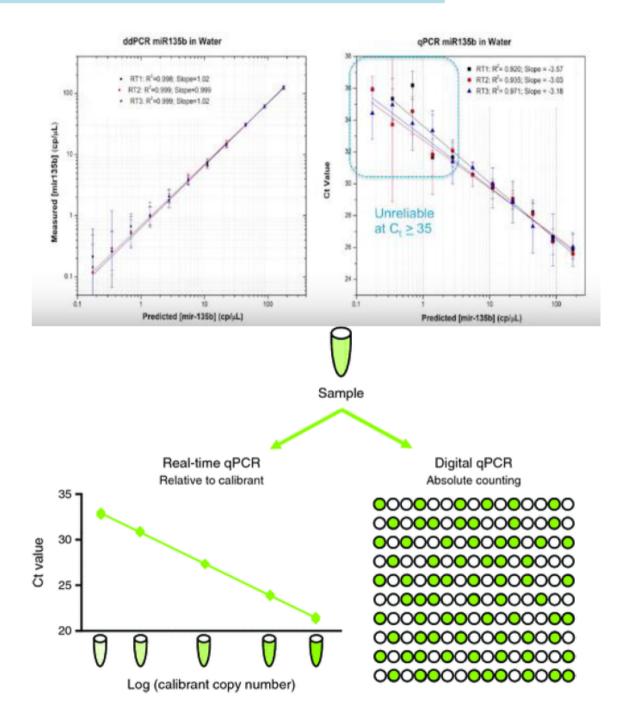
✓Non sono necessari replicati

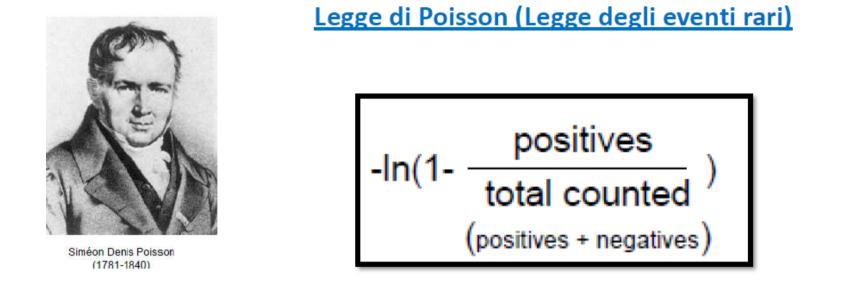
✓ Maggiore riproducibilità alle basse concentrazioni

✓ Quantificazione assoluta (copie/ul per pozzetto)

 ✓ Meno sensibili agli inibitori della reazione di amplificazione

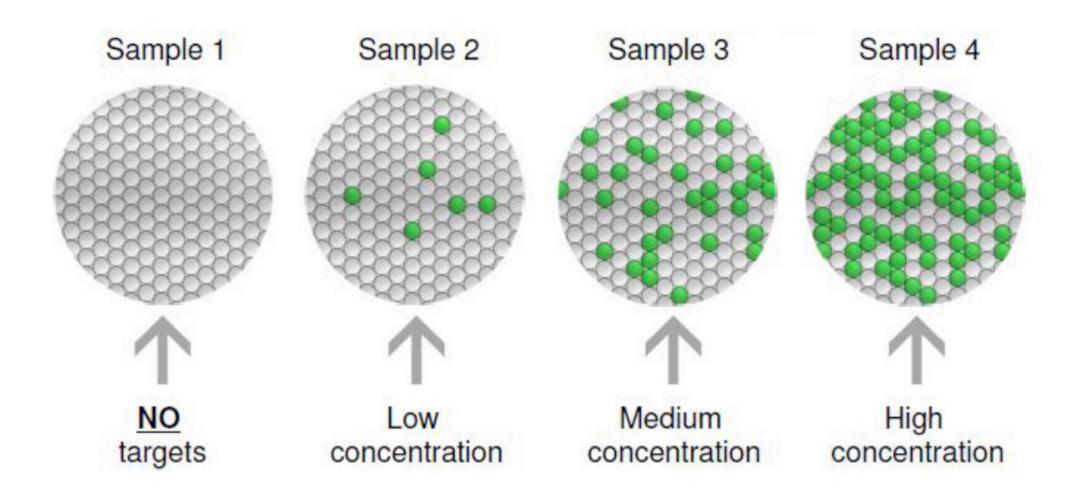
 ✓ Possibilità di confrontare campioni analizzati in momenti diversi e/o in laboratori diversi





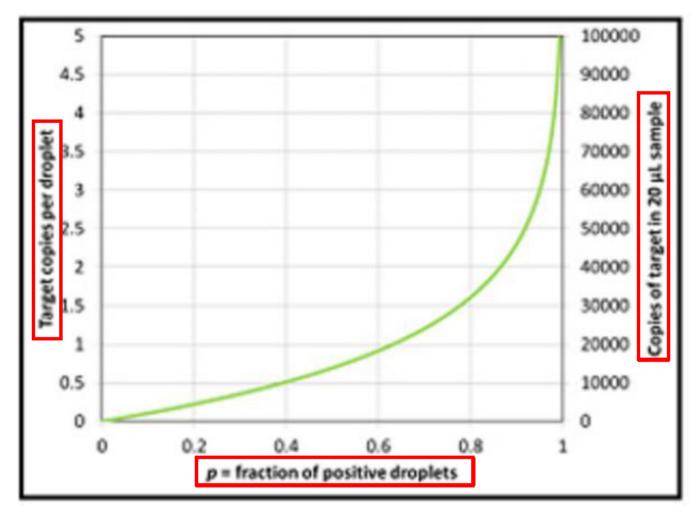
Vi è una distribuzione casuale (di eventi indipendenti) delle molecole di DNA da analizzare nelle gocce: queste molecole vengono ripartite casualmente durante la formazione dell'emulsione del campione. Alcune non conterranno templato, altre 1 sola molecola, altre ancora più di una. Producendo un numero sufficientemente elevato (20.000) di gocce avremo più probabilità che queste conterranno una sola molecola di DNA.

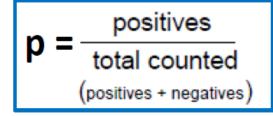
## Il numero di gocce contenenti una molecola di DNA/cDNA dipenderà dalla concentrazione di DNA/cDNA del campione di partenza



L'equazione di Poisson può essere utilizzata per determinare il numero di molecole di templato che andranno a finire in ogni goccia.

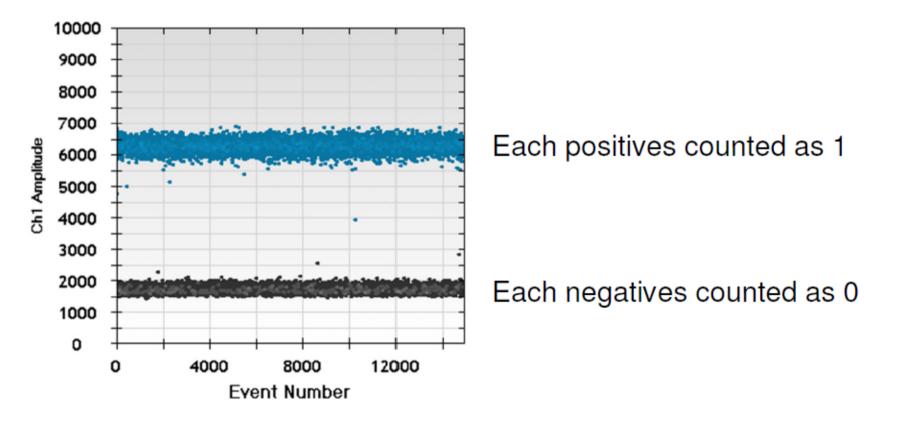
### Legge di Poisson (Legge degli eventi rari)



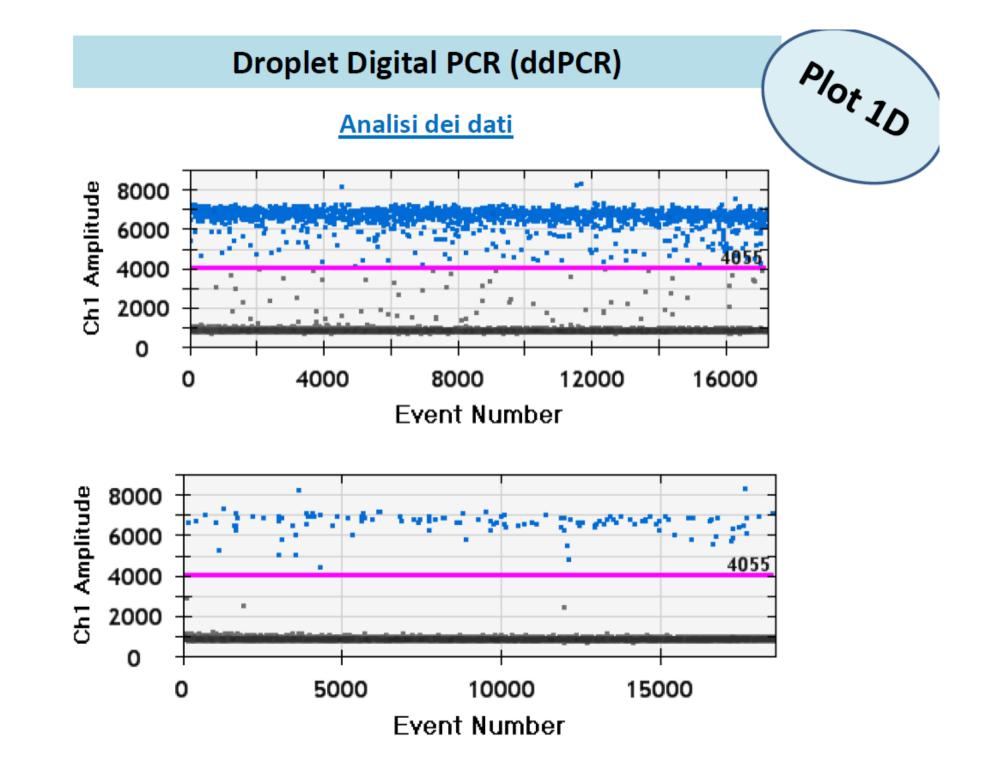


## Droplet Fluorescence Converted to a Digital Signal

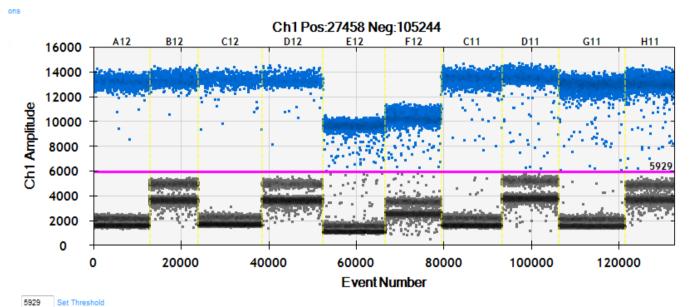
- Positive droplets contain at least one copy of target DNA (cDNA)
- Positive droplets have increased fluorescence vs. negatives
- Quantasoft software measures the number of positive and negative droplets per fluorophore per sample





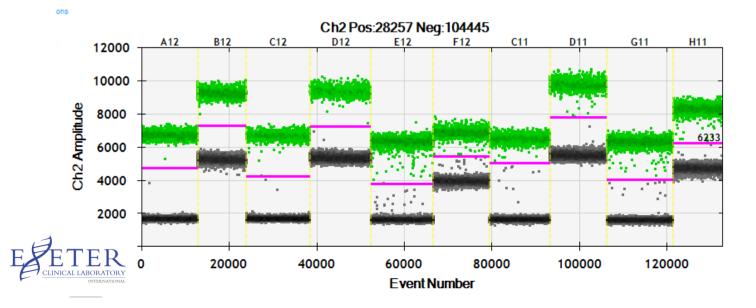


## **Bio-Rad Quantasoft 1D Amplification**



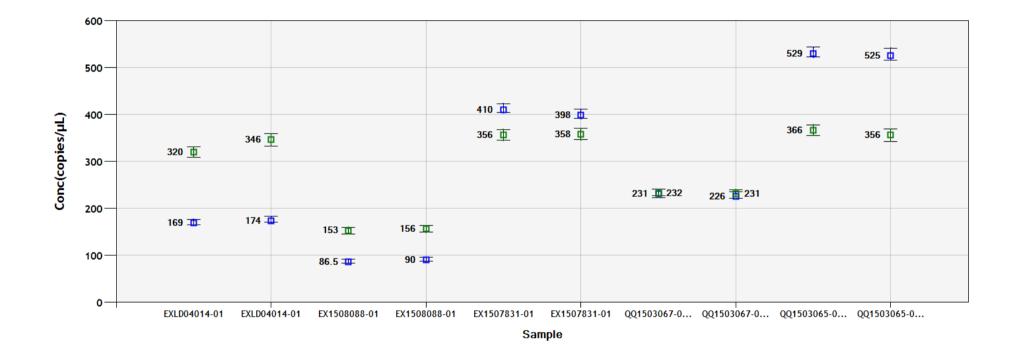
#### **Channel One**

5929



#### **Channel Two**

## Bio-Rad Quantasoft Concentration



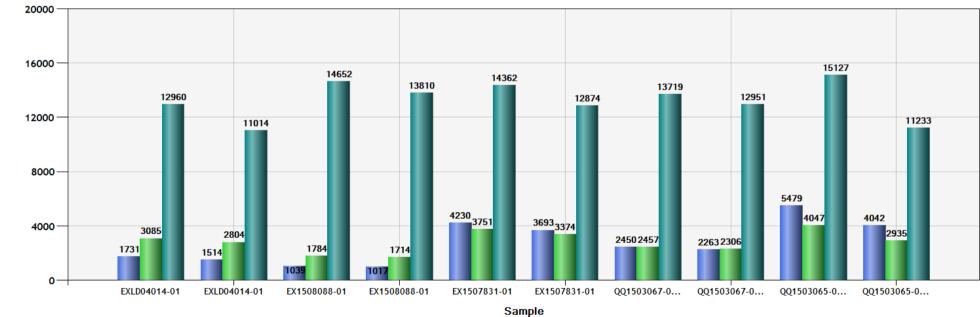
**Channel 1 concentration** 



## **Bio-Rad Quantasoft Events**

Ch1 Pos:27458 Ch2 Pos:28257 Accepted:132702

V P



Total droplets



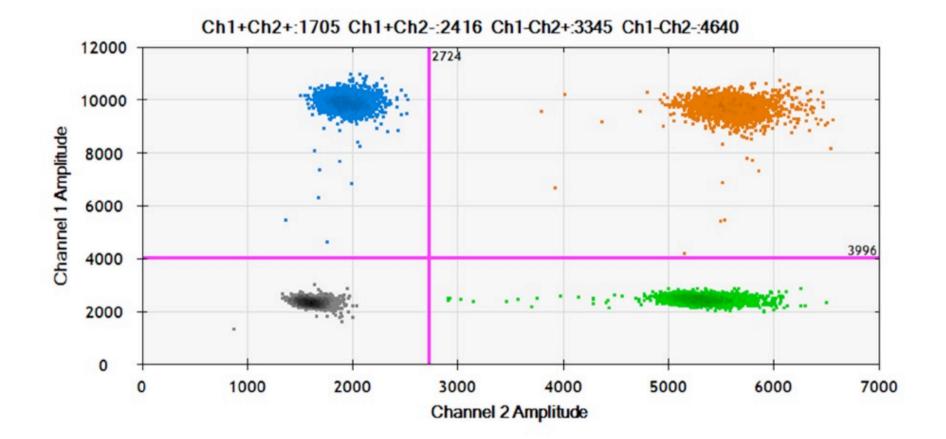
Events



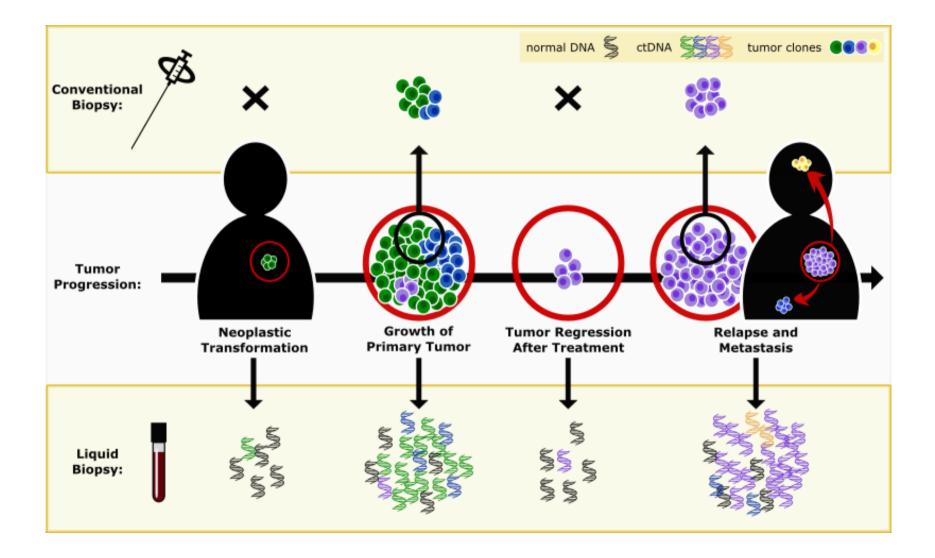
Channel 2 droplets

Channel 1 droplets

## Simultaneous Detection of Two Targets

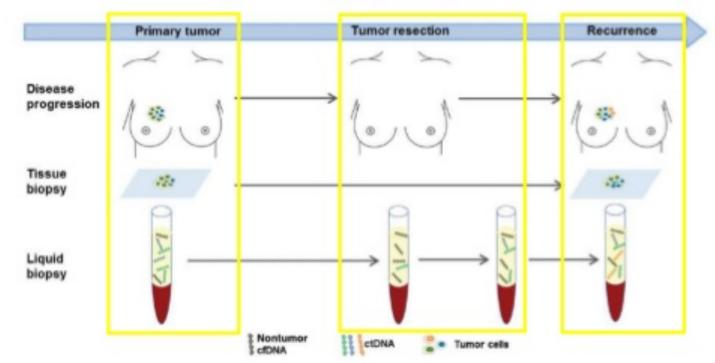


BIO RAD



## Liquid Biopsy – Clinical Applications

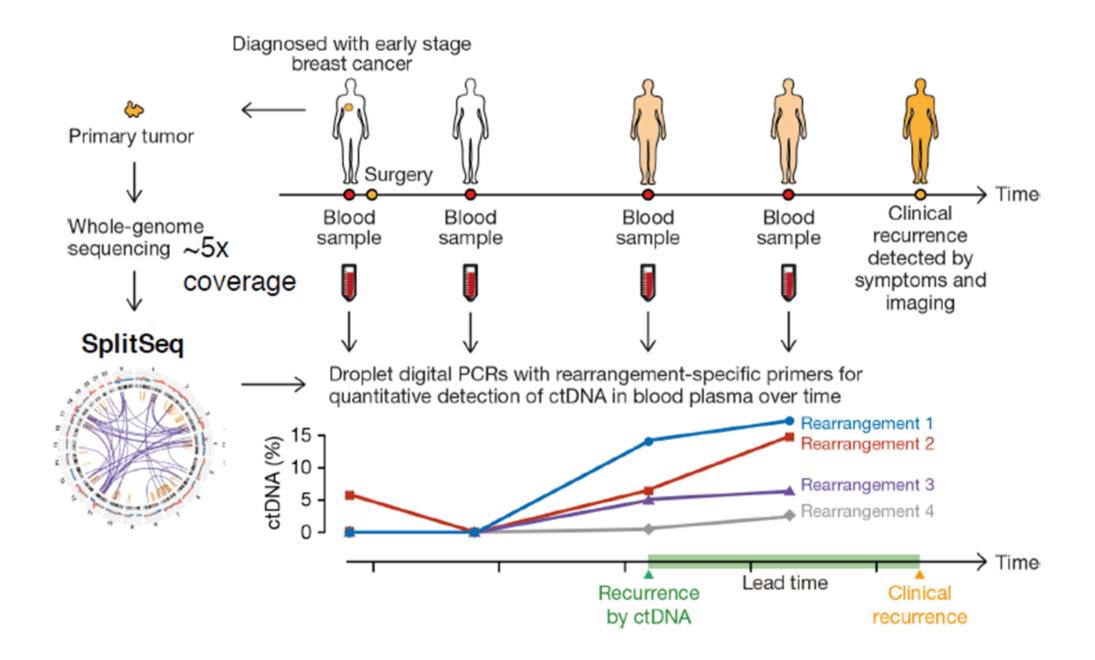
### The improved sensitivity and specificity of ddPCR present the opportunity of using blood:



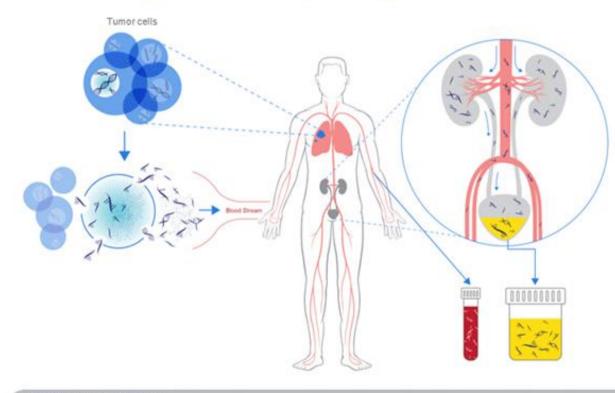
- 1. For mutations detection in patients with early-stage breast cancer
- For minimal residual disease may help guide individualized decisions about adjuvant systemic therapies
- 3. For surveillance of patients with a high risk for cancer recurrence

Beaver et al, Clin Cancer Res; 20(10) May 15, 2014; Heitzer et al, Clinical Chemistry 61:1 (2015)





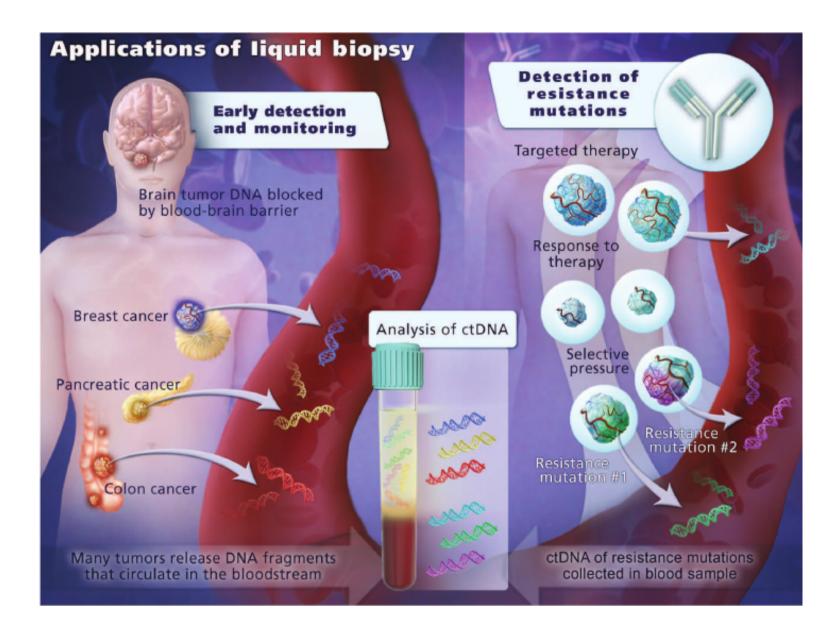
### Circulating Tumor DNA (ctDNA)



#### Main Advantages of ctDNA

- Captures intratumor heterogeneity
- Systemic overview of cancer
- Frequent sampling options for monitoring applications
- Different analyte options depending on clinical context

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#### New UltraSEEK<sup>™</sup> Lung Panel

Gene	Coverage (Missense mutations)
BRAF	Codon 469 (exon 11) and codons 594, 600 (exon 15)
EGFR	E709A, E709G, E709K, E709V, G719A, G719D, G719S, G719C, S768I, T790M, L858R, L861Q, L861R, C797S, Exon 19 indels, Exon 20 insertions
KRAS	G12A, G12C, G12D, G12R, G12S, G12V, G13C, G13D, Q61H, Q61K, Q61E, Q61P, Q61R, Q61L
ERBB2	A775_G776insYVMA, G776>VC
PIK3CA	Codons 542, 545 (exon 9), codon 1047 of (exon 20)
TOTAL	5 Genes

