

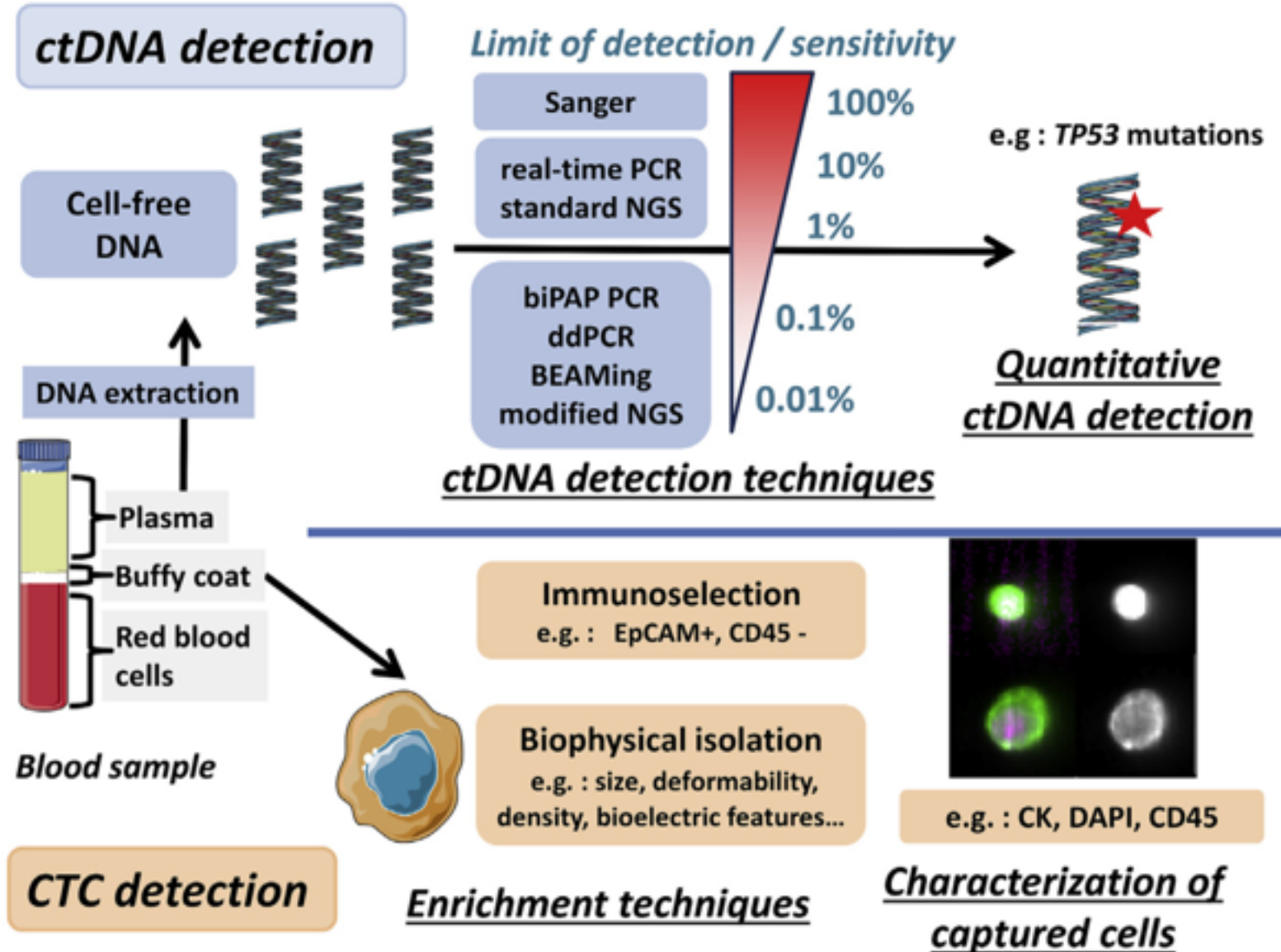
Circulating Tumor Cells in brain metastatic patients

Jean-Yves Pierga

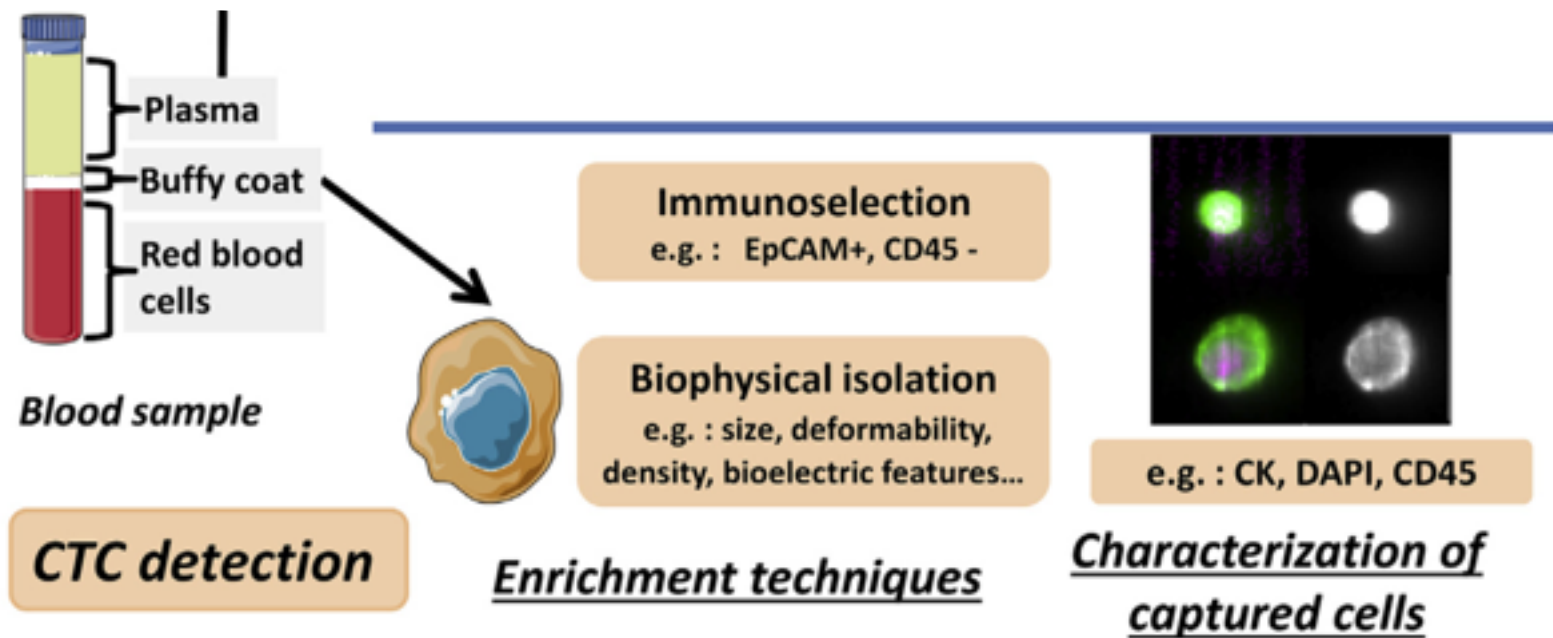
**Medical Oncology Department & Circulating Biomarkers
Lab, SIRIC, Institut Curie, Paris France**



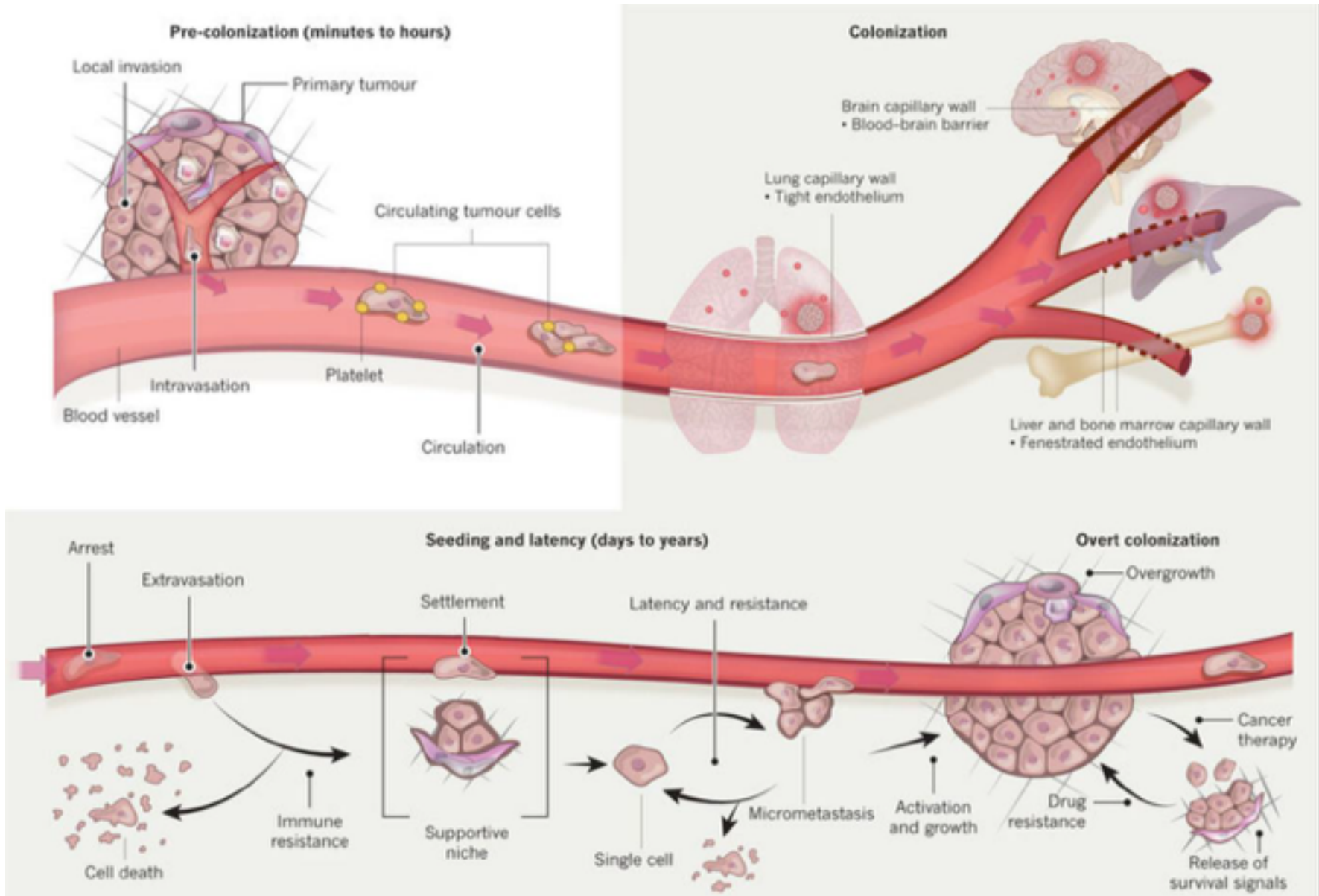
CTC and ctDNA detection



CTC and ctDNA detection

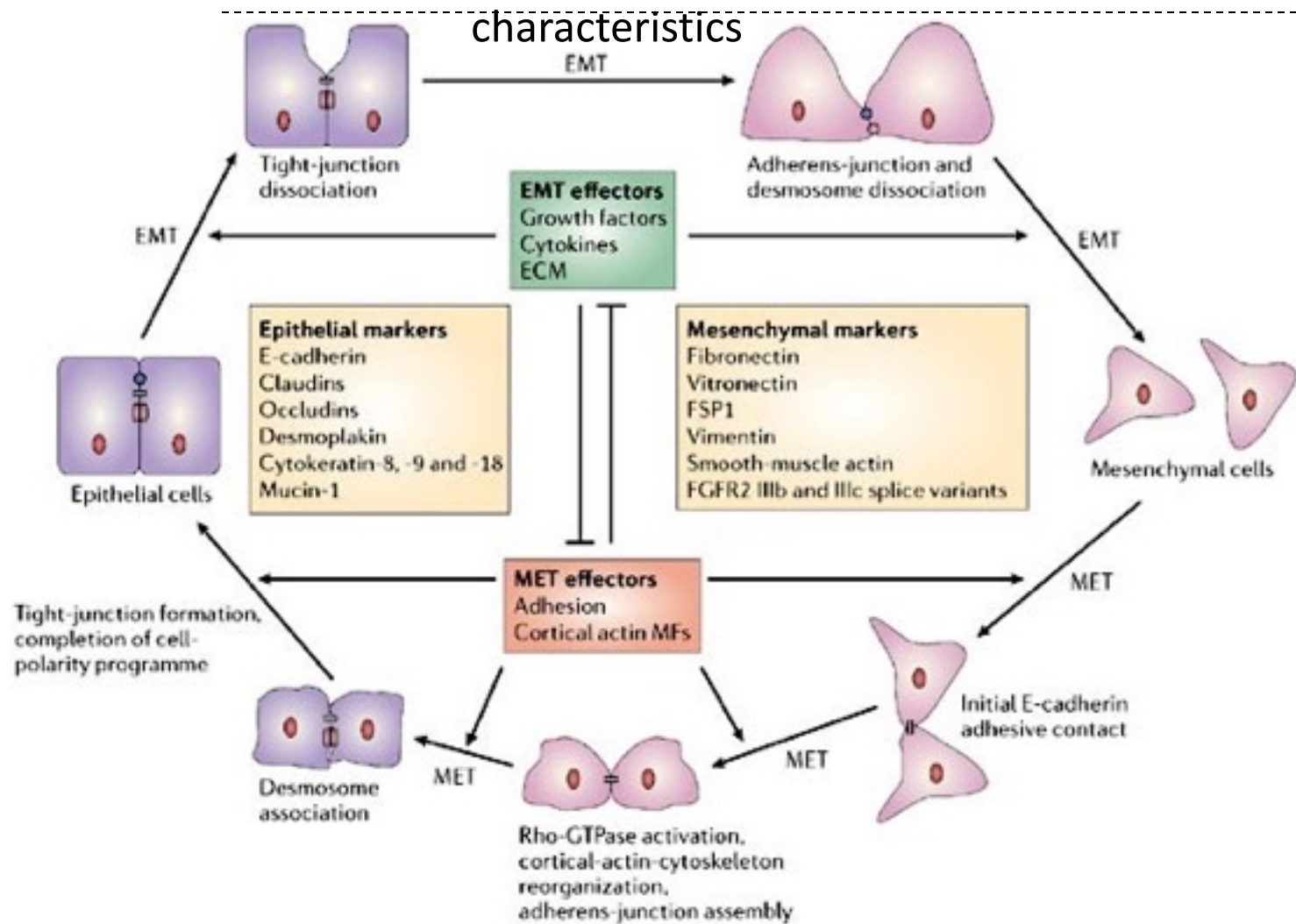


Metastatic process

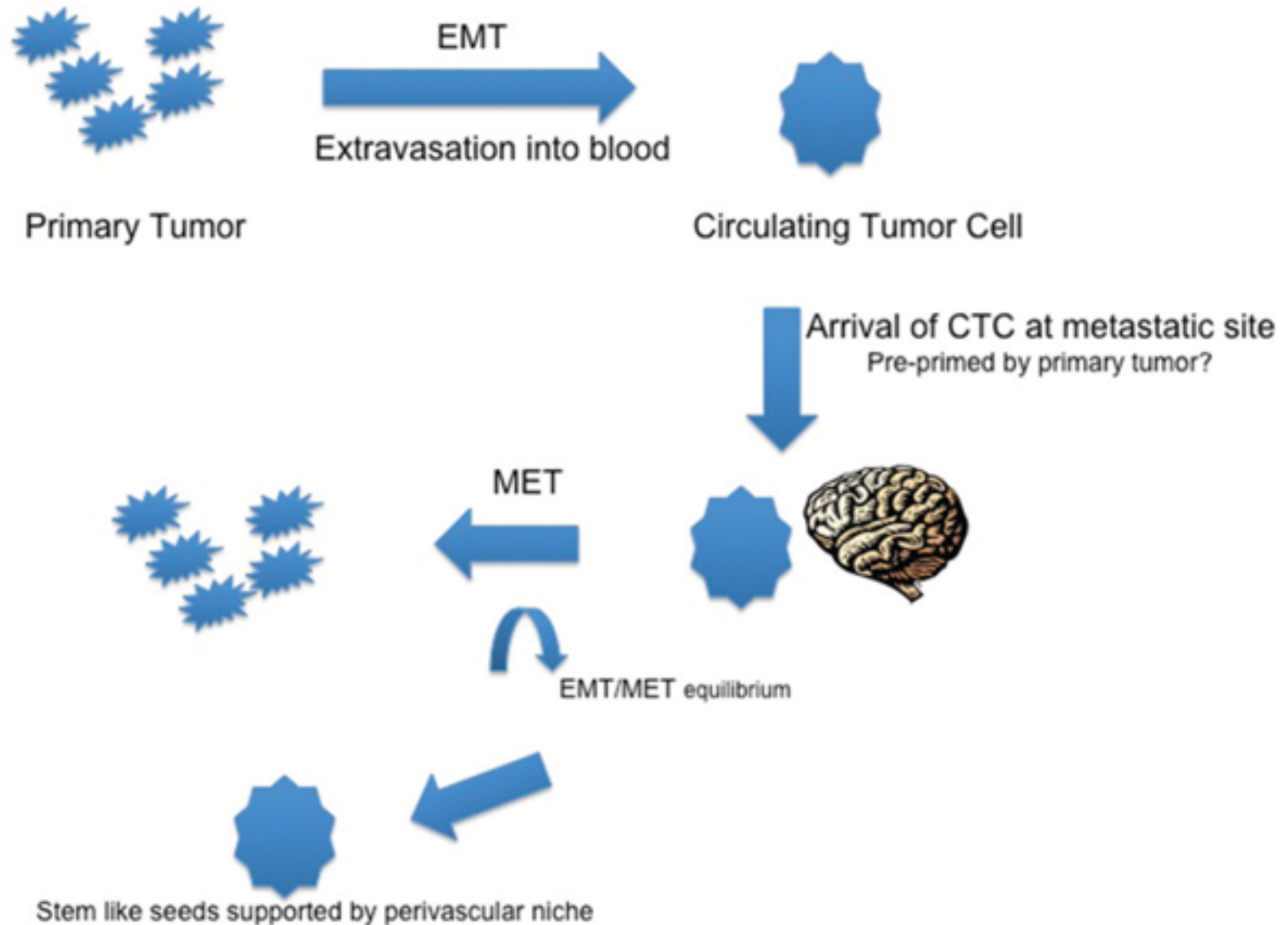


Epithelial-mesenchymal transition (EMT)

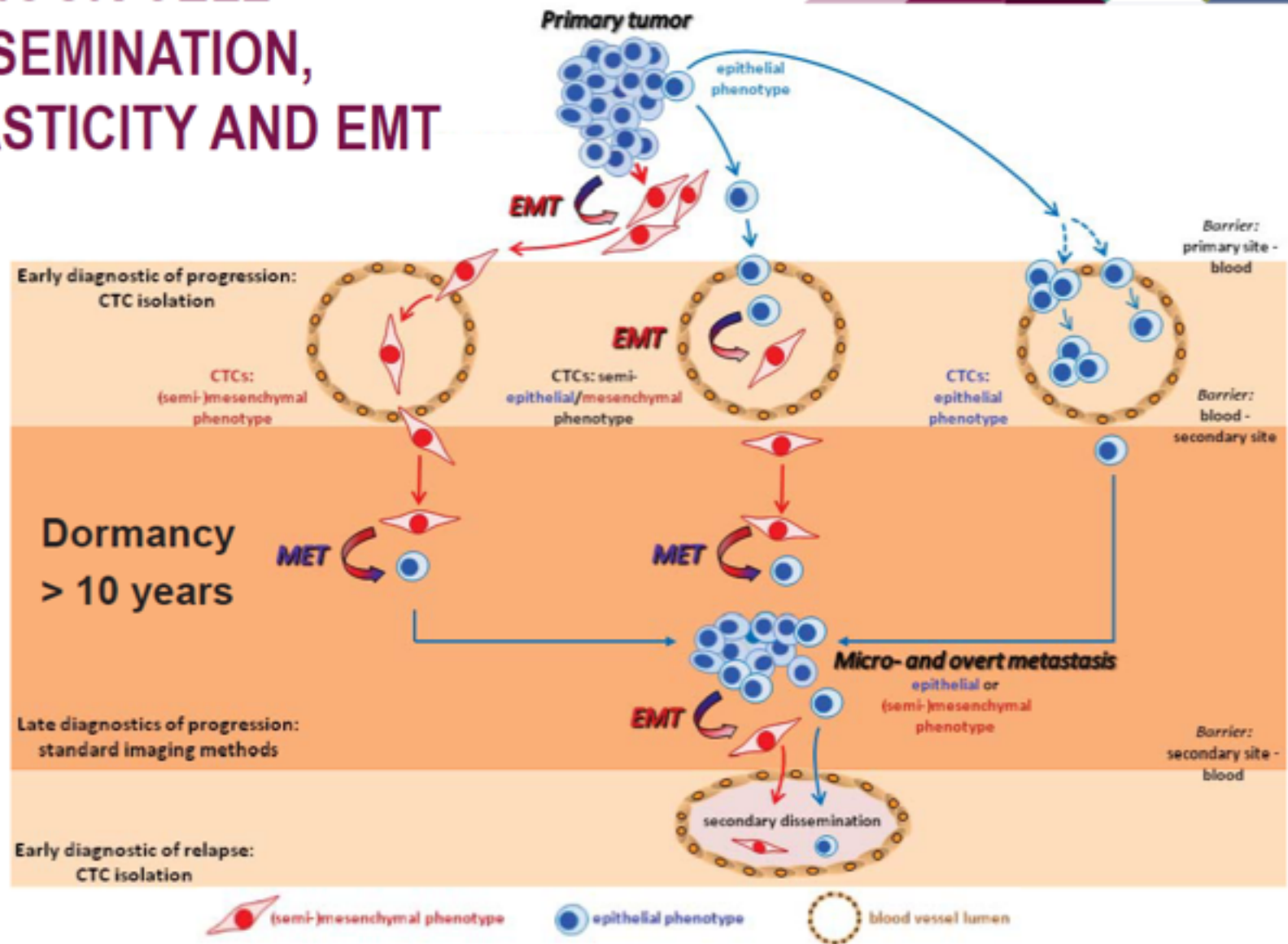
a process by which epithelial breast cancer cells acquire mesenchymal



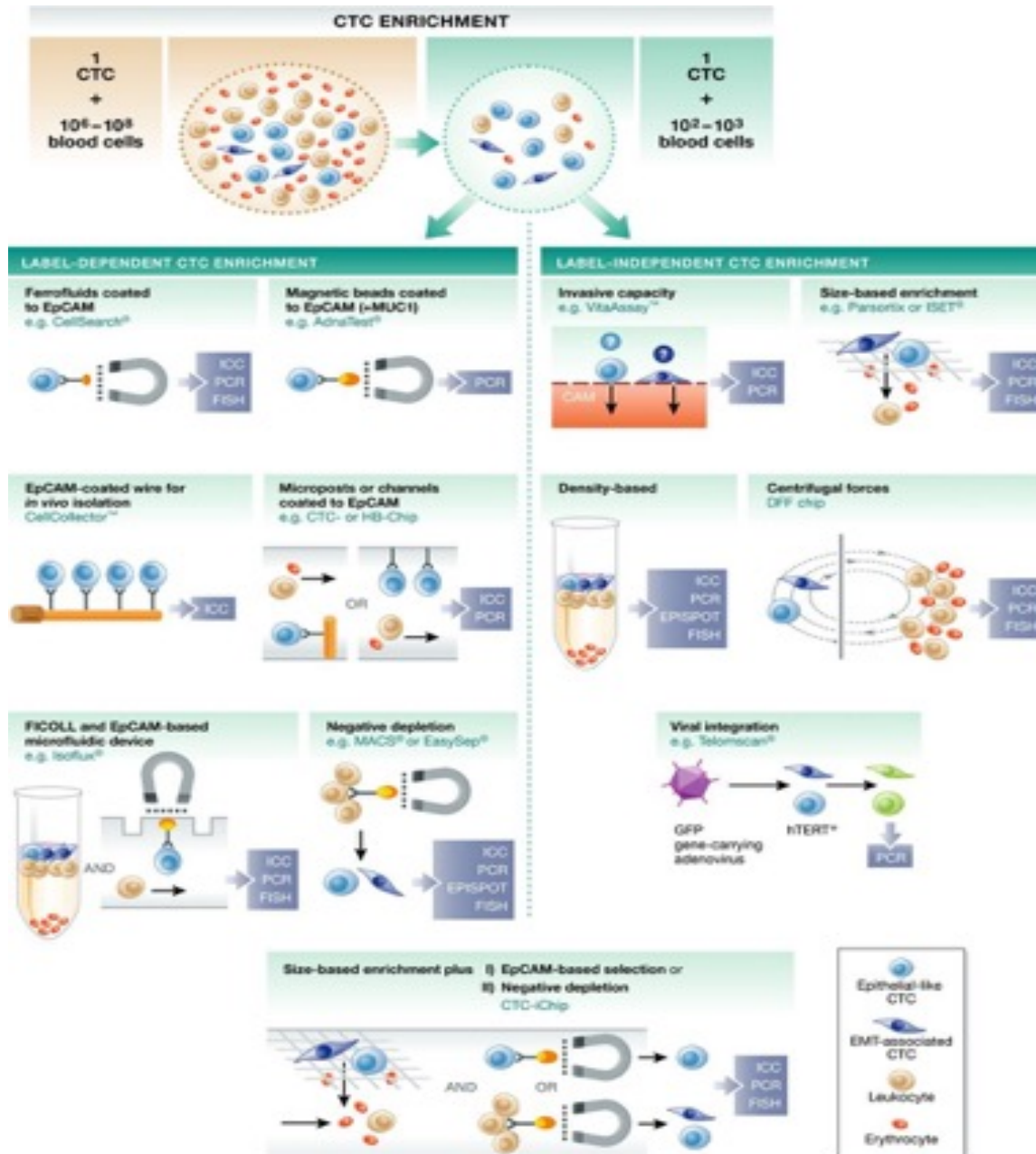
EMT/MET pathobiology of metastasis



TUMOUR CELL DISSEMINATION, PLASTICITY AND EMT



CTC detection techniques

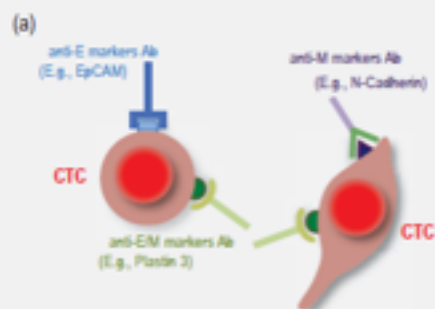


CTC ENRICHMENT STRATEGIES

Biological properties
Protein expression

Physical properties
Label-free strategies

Positive selection



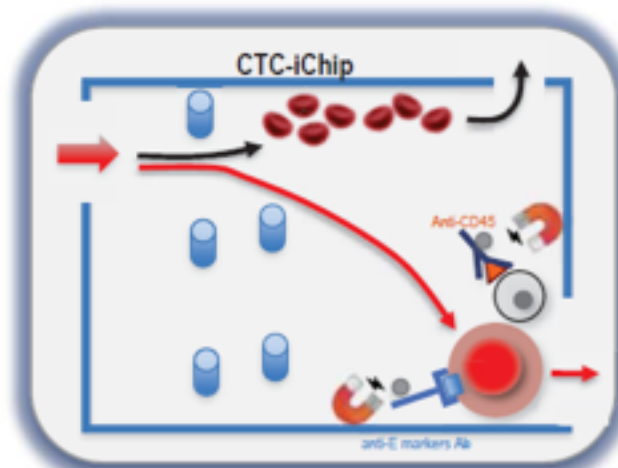
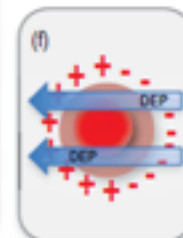
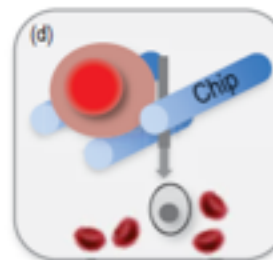
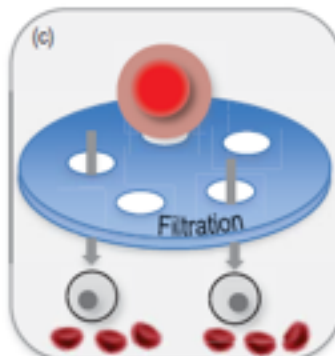
Ex vivo

- CellSearch® system
- MagSweeper™
- EPHESIA CTC-chip
- CTC-chip
- Velcro-like device

In vivo

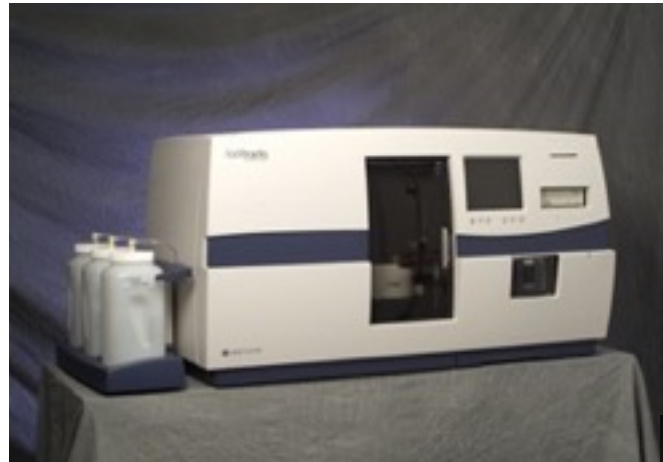
- CellCollector®
- Photoacoustic nanodetector

Negative selection



Circulating Tumor Cells Detection

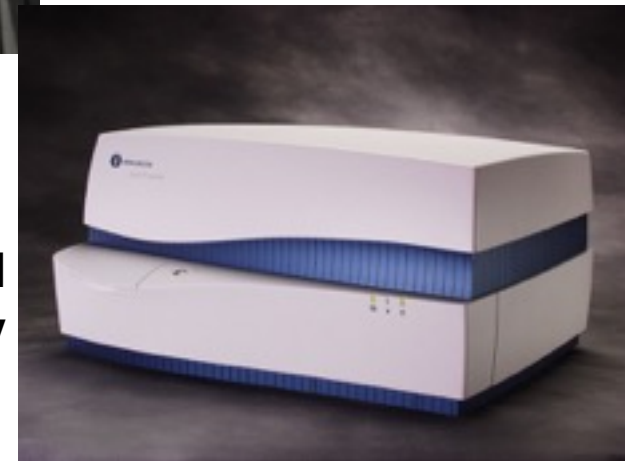
CellSearch™ System



MagNest™



+ 3 channel capability



CellSearch™ System: Images of Tumor Cells

Cytoplasm Nucleus Cell Membrane Composite

**CK-PE
pos**

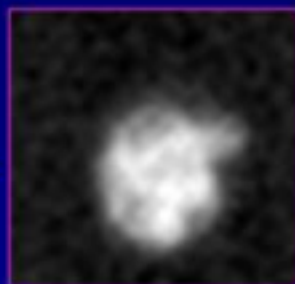
**DAPI
pos**

**CD45-APC
neg**

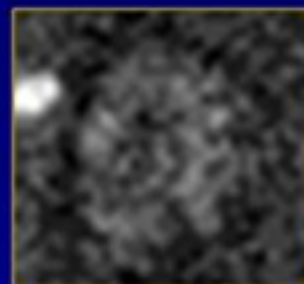
Tumor Cell



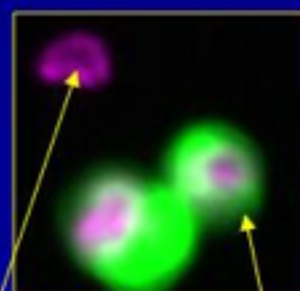
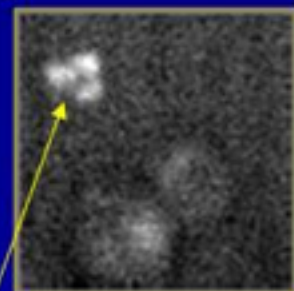
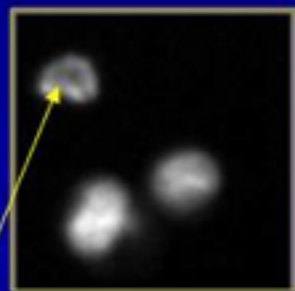
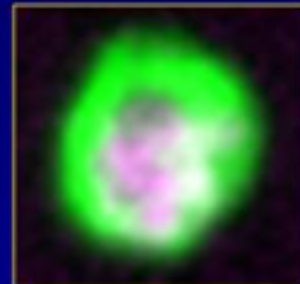
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-



=



**Leukocyte
nucleus**

**CD45⁺
Membrane**

**Leukocyte
Tumor Cell**

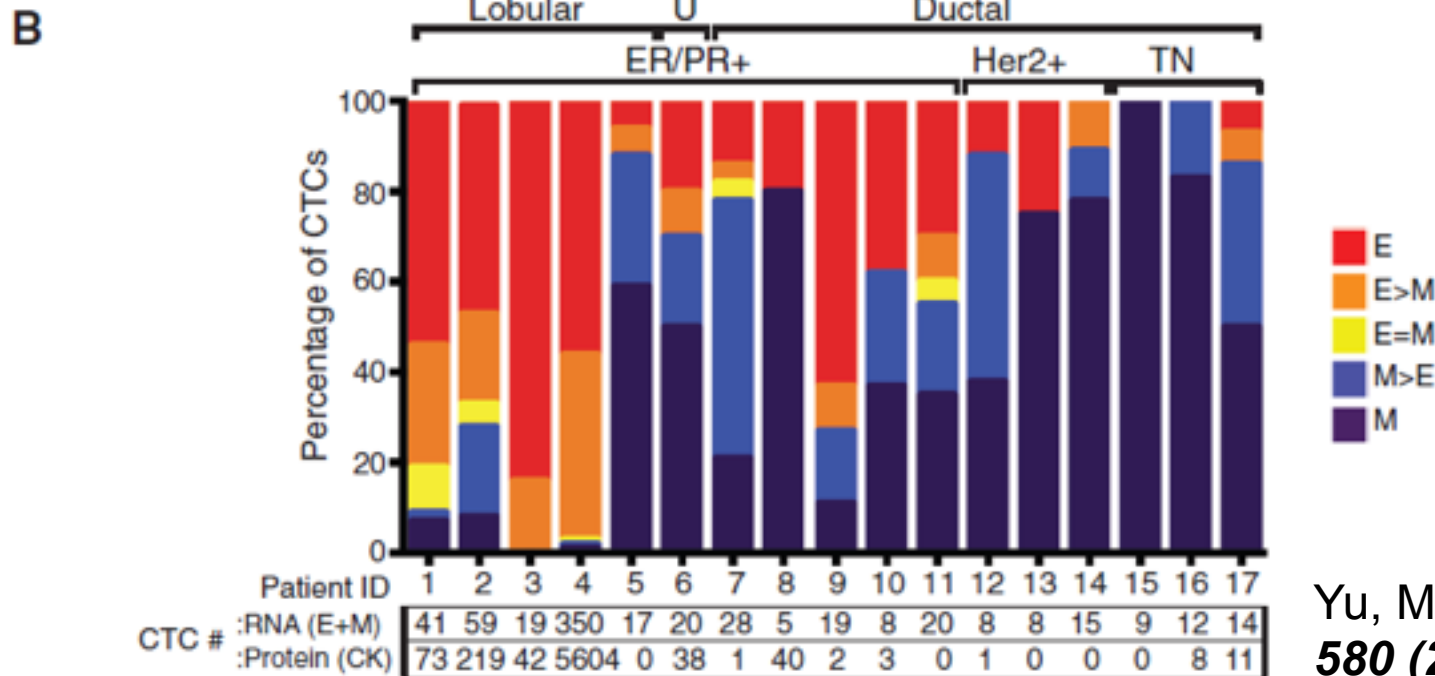
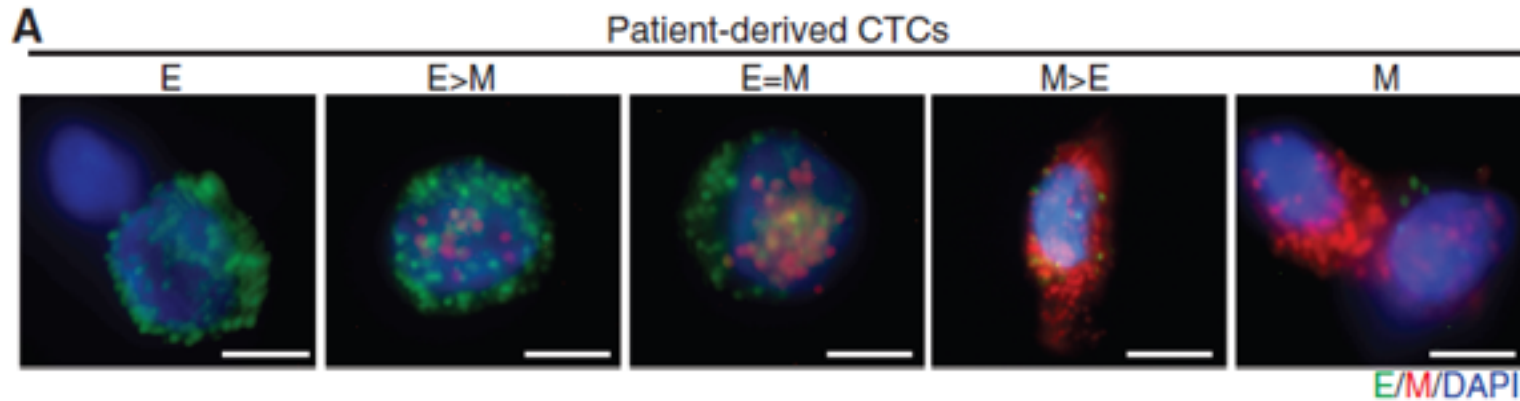
EpCAM-based assays for epithelial tumor cell detection in cerebrospinal fluid

Table 2 Overview CELLSEARCH® and flow cytometry studies in CSF with reported sensitivity and specificity versus cytology

Study	Assay	N	Patient population	Sensitivity (95% CI)	Specificity (95% CI)	Sensitivity (95% CI) cytology	Specificity (95% CI) cytology
Tu et al. [4]	C	18	MRI confirmed LM/lung cancer	77.8 (52.4–93.6)	100 (47.8–100)	44.4 (21.5–69.2)	Not reported
Lee et al. [5]	C	38	Confirmed LM/suspected LM/breast cancer	80.95 (58.1–94.4)	84.62 (54.5–97.6)	66.67 (43.04–85.35)	Used as gold standard 100%
Nayak et al. [6]	C	51	Clinical suspicion of LM/solid tumors (mainly NSCLC and breast cancer)	100 (78.1–100)	97.2 (85.4–99.9)	66.7 (38.3–88.1)	Used as gold standard
Jiang et al. [7]	C	21	NSCLC patients with suspected LM	95.2 (NA)	100 (NA)	57.1 (NA)	Not reported
Acosta et al. [26]	FC	6 ^a	Clinical suspicion of LM previous diagnosed carcinoma	100% (NA)	100% (NA)	Not reported	Not reported
Milojkovic Kerklaan et al. [8]	FC	29	Clinical suspicion of LM but a negative or inconclusive MRI, previously diagnosed carcinoma	100 (75–100)	100 (79–100)	61.5 (32–86)	100 (79–100)
Subirá et al. ^b [10]	FC	144	Confirmed LM or clinically suspected LM	79.8 (NA)	84 (NA)	50 (NA)	100 (NA)
Subirá et al. ^b [9]	FC	78	Clinically suspected LM and previous diagnosis of epithelial-cell neoplasia	75.5 (63.5–87.6)	96.1 (88.8–100)	65.3 (52.0–78.6)	100 (100–100)

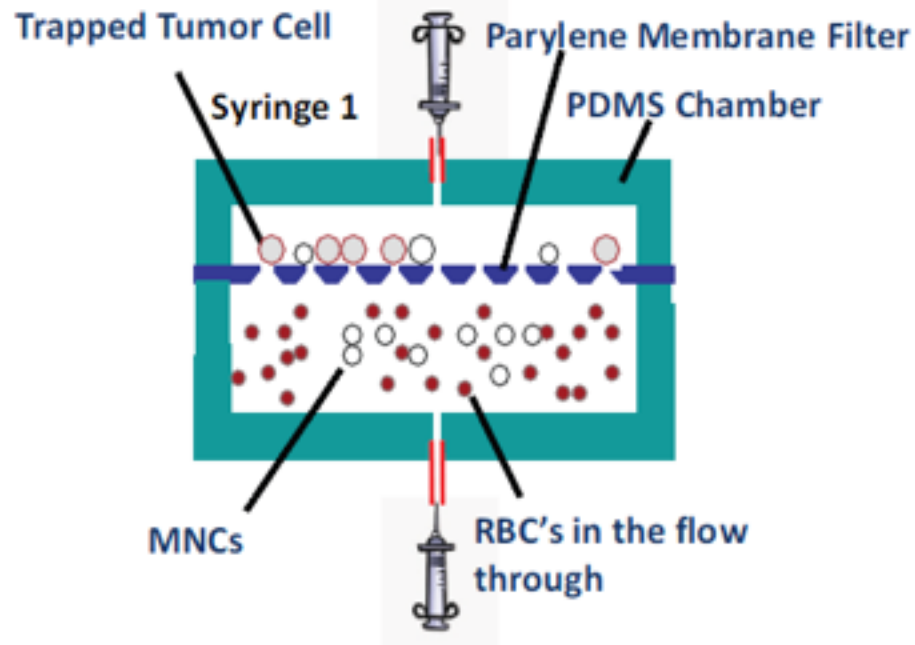
C CELLSEARCH®, FC flow cytometry, 95% CI 95% confidence interval, MRI magnetic resonance imaging, LM leptomeningeal metastases, NA not available

Circulating Breast Tumor Cells Exhibit Dynamic Changes in Epithelial and Mesenchymal Composition

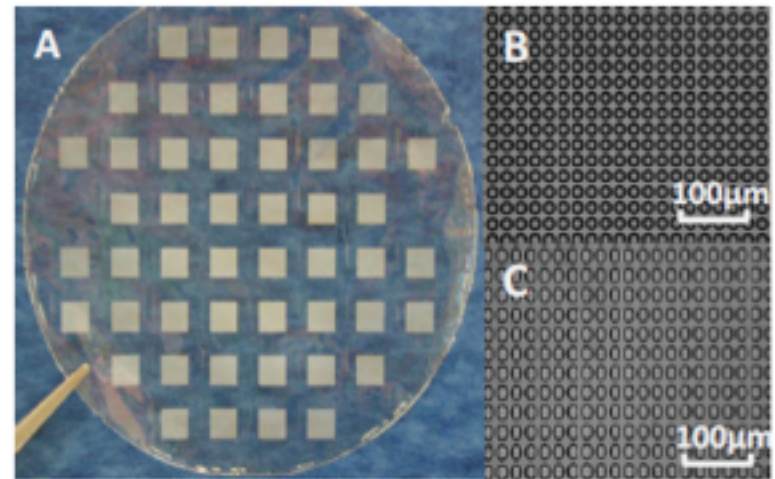


Yu, M. et al *Science* **339**, 580 (2013);

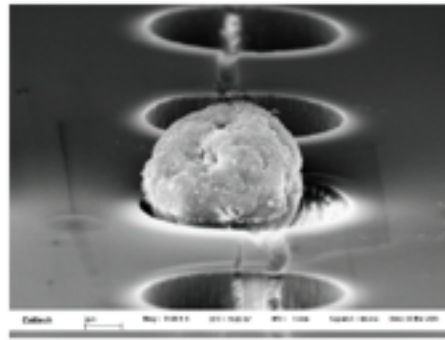
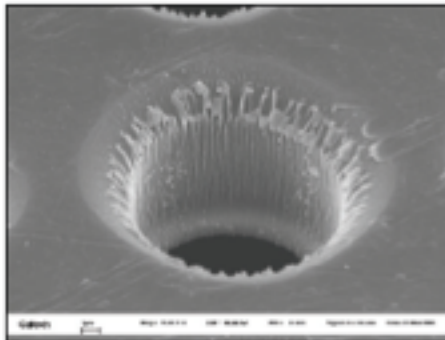
Microfluidics Based Cell Separation



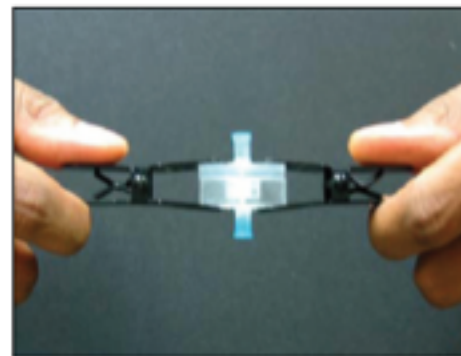
Parylene Filter Membrane



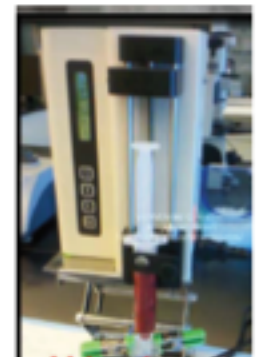
SEM of Cell Captured on filter

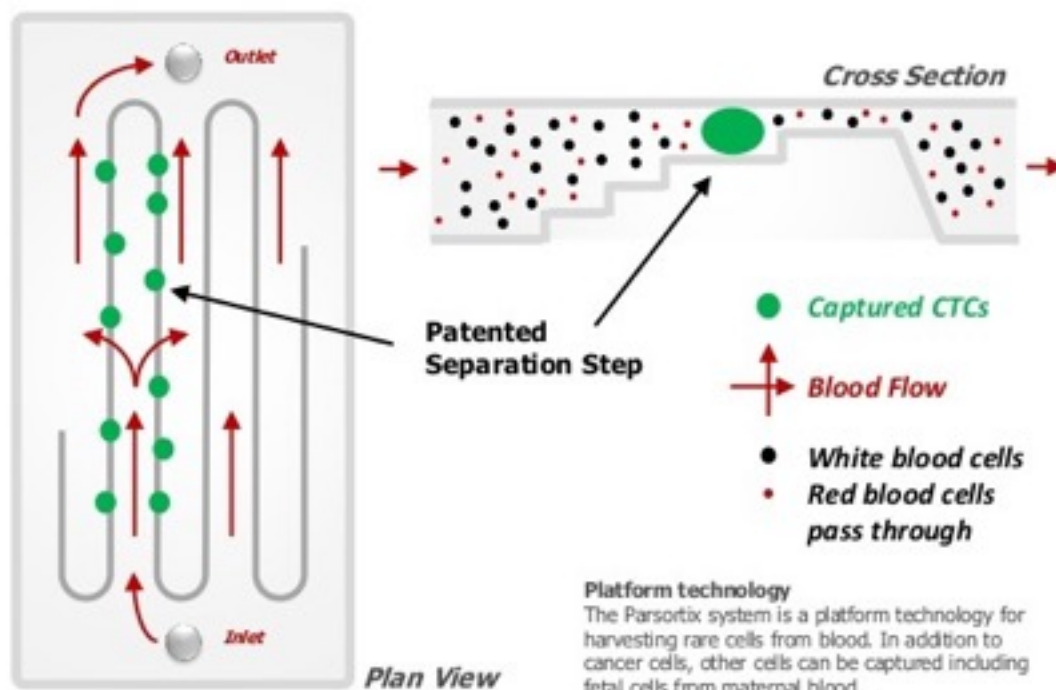


Assembled Filter Device



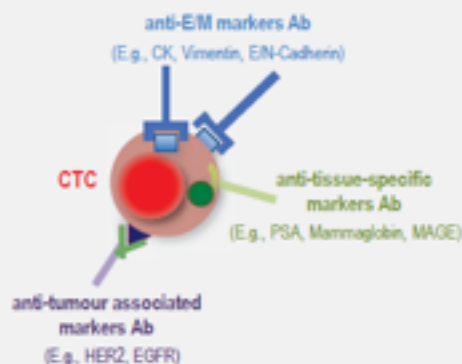
Automated Flow Device





APPROACHES FOR CTC DETECTION

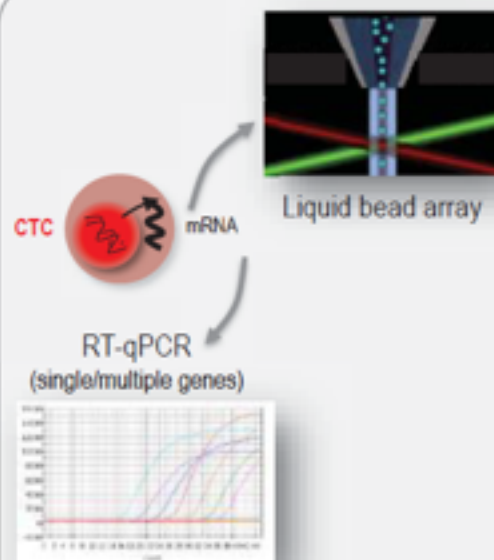
Immunocytological technologies



Technologies

- Immunocytochemistry
- CellSearch® system
- Flow Cytometry
- DEParrray®

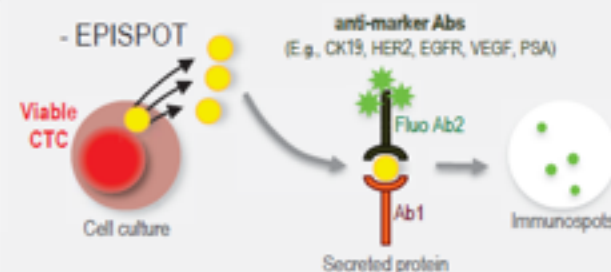
Molecular technologies



RNA-based Technologies

Functional assays

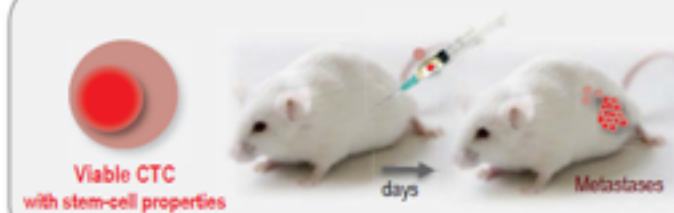
In vitro Cell Culture



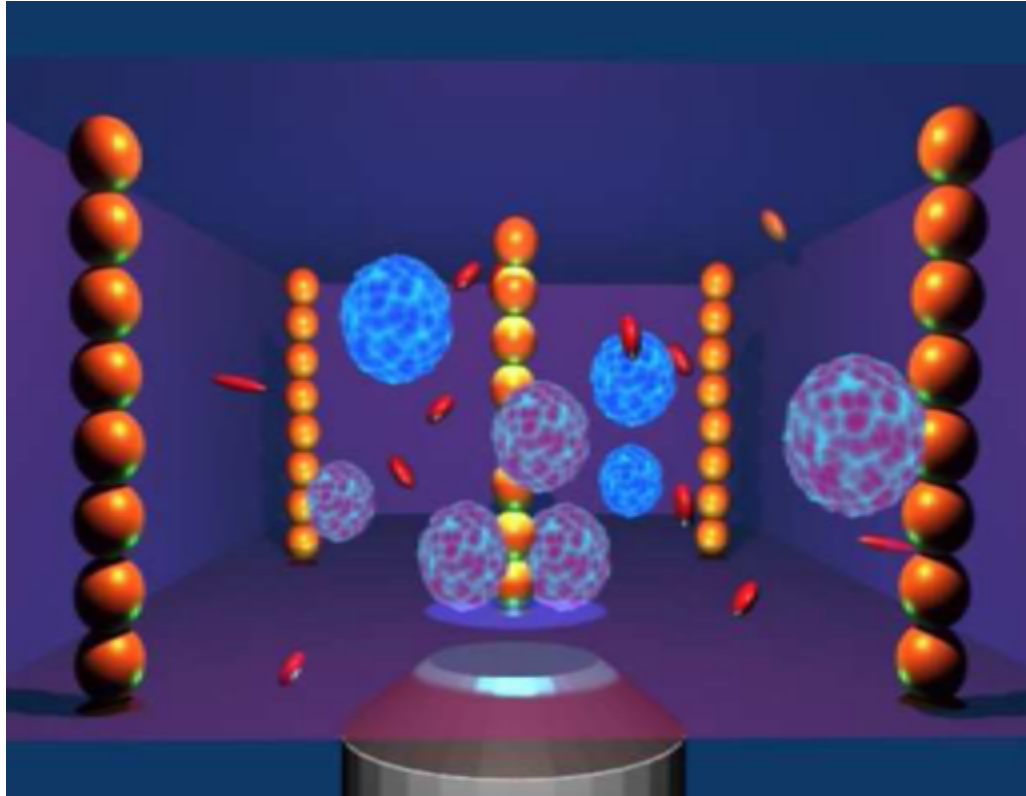
- Invasion assay



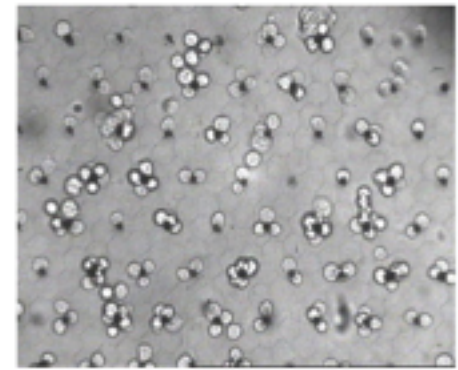
Xenotransplantation models (CDx)



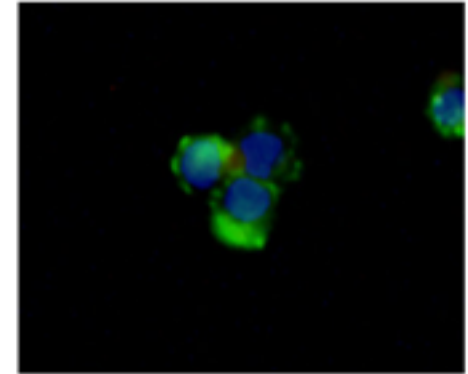
MICROFLUIDIC EPHESIA



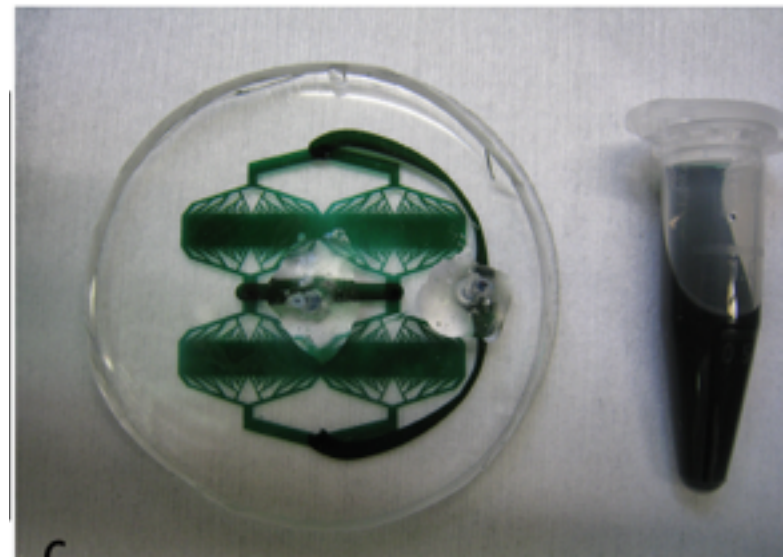
(b)



(c)



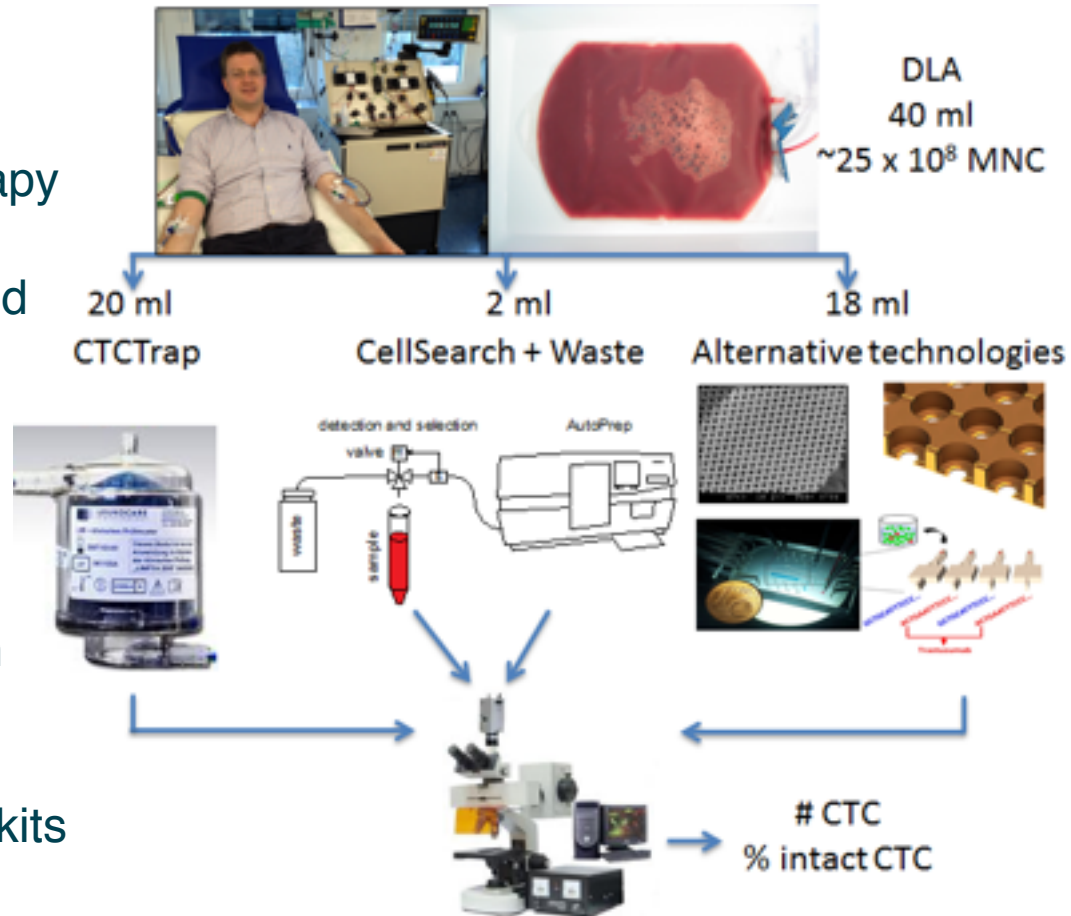
Saliba AE, L Saias, JL Viovy PNAS 2010
Laboratoire Physicochimie Curie, CNRS UMR 168
Autebert J Methods 2012

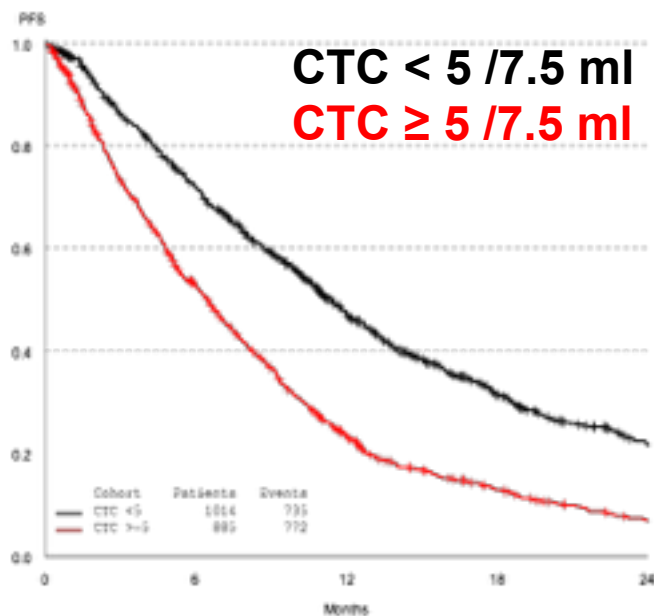


DLA as a Method for Expansion of Analysed Blood Volume

Diagnostic Leukapheresis (DLA):

- Safe, FDA approved procedure established in context of immunotherapy for prostate cancer
- Equivalent of 2.8 L of peripheral blood used for MNC enrichment, even 2-4x total blood volumes safe in solid tumor patients
- Well tolerated by patients
- Ethical approval at UDUS
- Enables liquid biopsy in patients with too few CTCs for analysis
- Costs reduced compared to use of a corresponding number of CellSearch kits



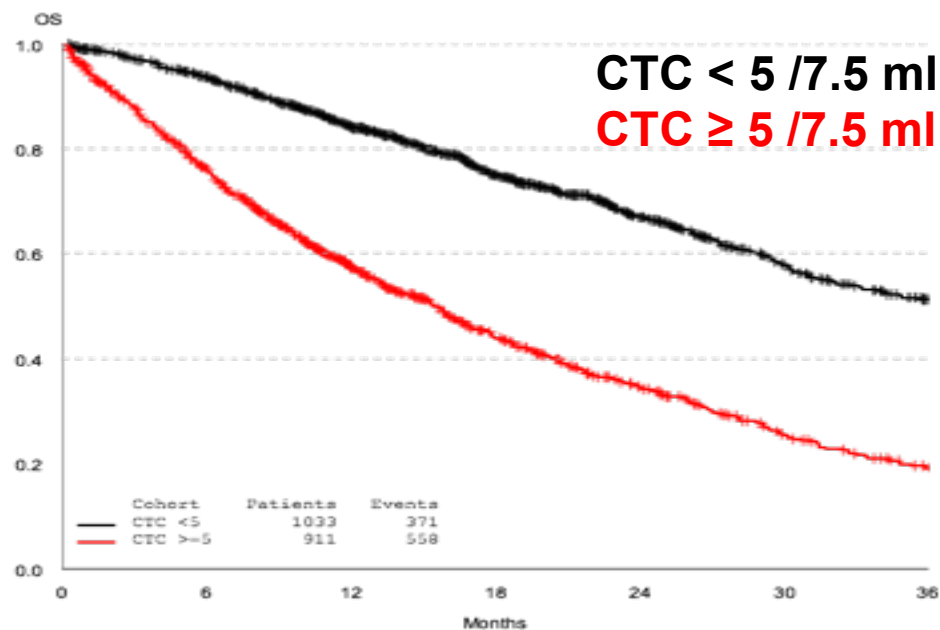


Progression-Free Survival

N= 1,899 patients

HR = 1.92

p<0.0001



Overall Survival

N= 1,944 patients

HR = 2.77

p<0.0001

Essai LANDSCAPE - Bachelot et al, *Lancet Oncol* 2012

Lapatinib plus capecitabine in patients with previously untreated brain metastases from HER2-positive metastatic breast cancer (LANDSCAPE): a single-group phase 2 study



Thomas Bachelot, Gilles Romieu, Mario Campone, Véronique Diéras, Claire Cropet, Florence Dalenc, Marta Jimenez, Emilie Le Rhun, Jean-Yves Pierga, Anthony Gonçalves, Marianne Leheurteur, Julien Domont, Maya Gutierrez, Hervé Curé, Jean-Marc Ferrero, Catherine Labbe-Devilliers

Key Inclusion Criteria

- HER2+ MBC
- Newly diagnosed brain metastases, at least 1 cm in diameter (T1 gado. MRI)
- Not candidate for brain surgery or SRS
- Any previous treatment except WBR, lapatinib or capecitabine
- ECOG PS status 0-2

Treatment:

L: 1,250 mg/d, PO, continuous **C:** 2,000 mg/m²/d, PO, d1–14 q3weeks

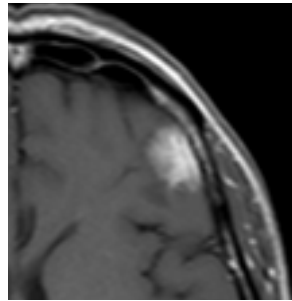
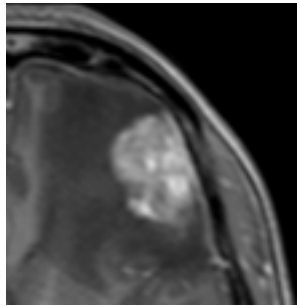


**Primary endpoint:
CNS volumetric response**

CNS Volumetric change	n = 44	%
CNS objective response	29	65% (95% CI: 50.1-79.5)
≥ 80% Reduction	9	20%
50- <80% Reduction	20	45%
20- <50% Reduction	6	14%
> 0- <20% Reduction	2	5%
Progression*	7	16%

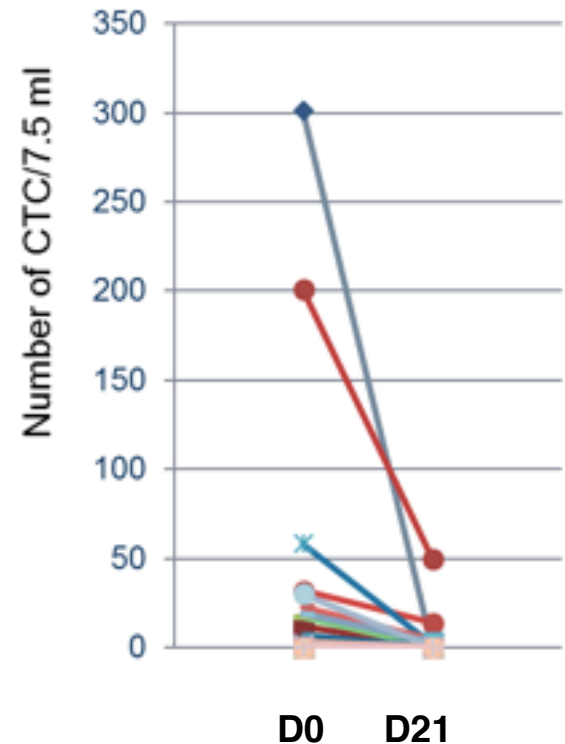
***2 patients had extra-CNS disease progression**

LANDSCAPE: a Unicancer phase II study with lapatinib and capecitabine in patients with brain metastases from HER2-positive metastatic breast cancer before whole brain radiotherapy



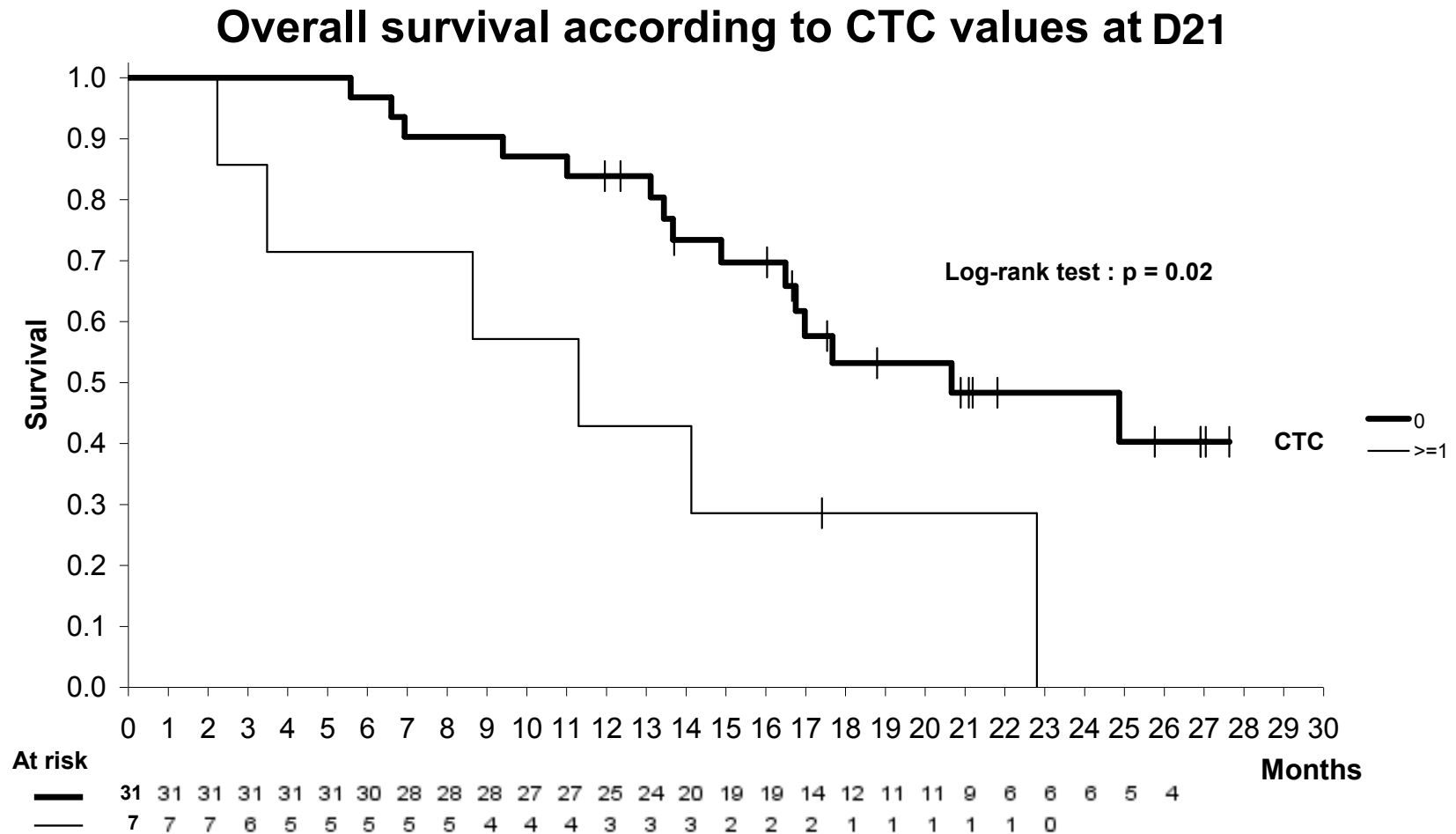
CTC/7.5ml at baseline and changes under treatment

Correlation with CNS-OR, (n=40)



Date of sampling	CTC Status	CNS-OR (%)	<i>p</i>
Baseline (n=41)	0 at baseline	(81)	NS
	≥ 1 at baseline	(57.9)	
Day 21 (n=38)	0 at day 21	(80.6)	0.03
	≥ 1 at day 21	(33.3)	

LANDSCAPE OS according to CTC at D21



Evaluation of Genomic Applications in Practice and Prevention (EGAPP) Working Group

(www.egappreviews.org/workingrp.htm)

- **Analytical performance**

how accurately and reliably the test detects the analyte(s) of interest;

- **Clinical validity**

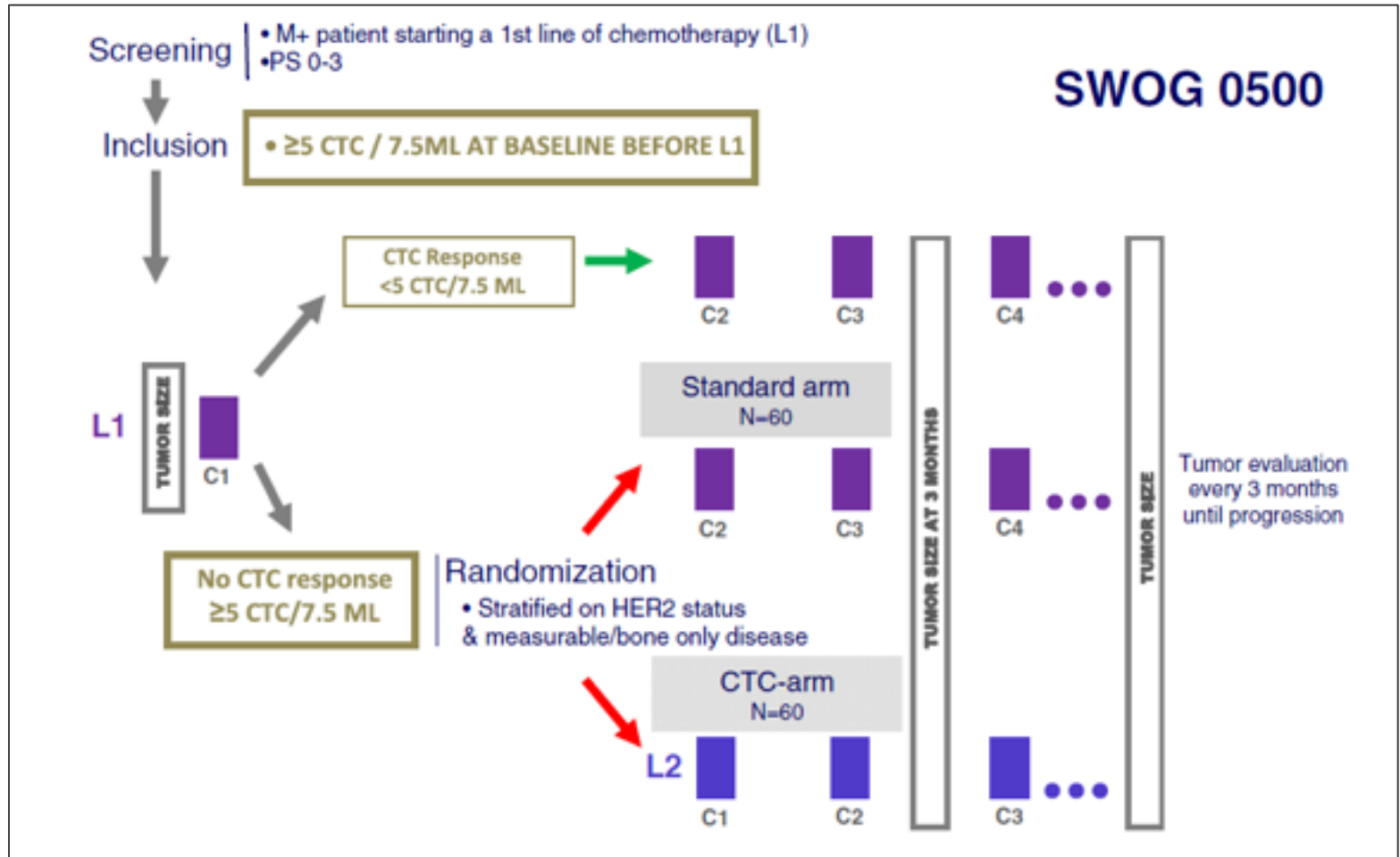
how well the test relates to the clinical outcome of interest
(such as survival or response to therapy);

- **Clinical utility**

Whether the results of the test provide information that contributes to and improves current optimal management of the patient's disease

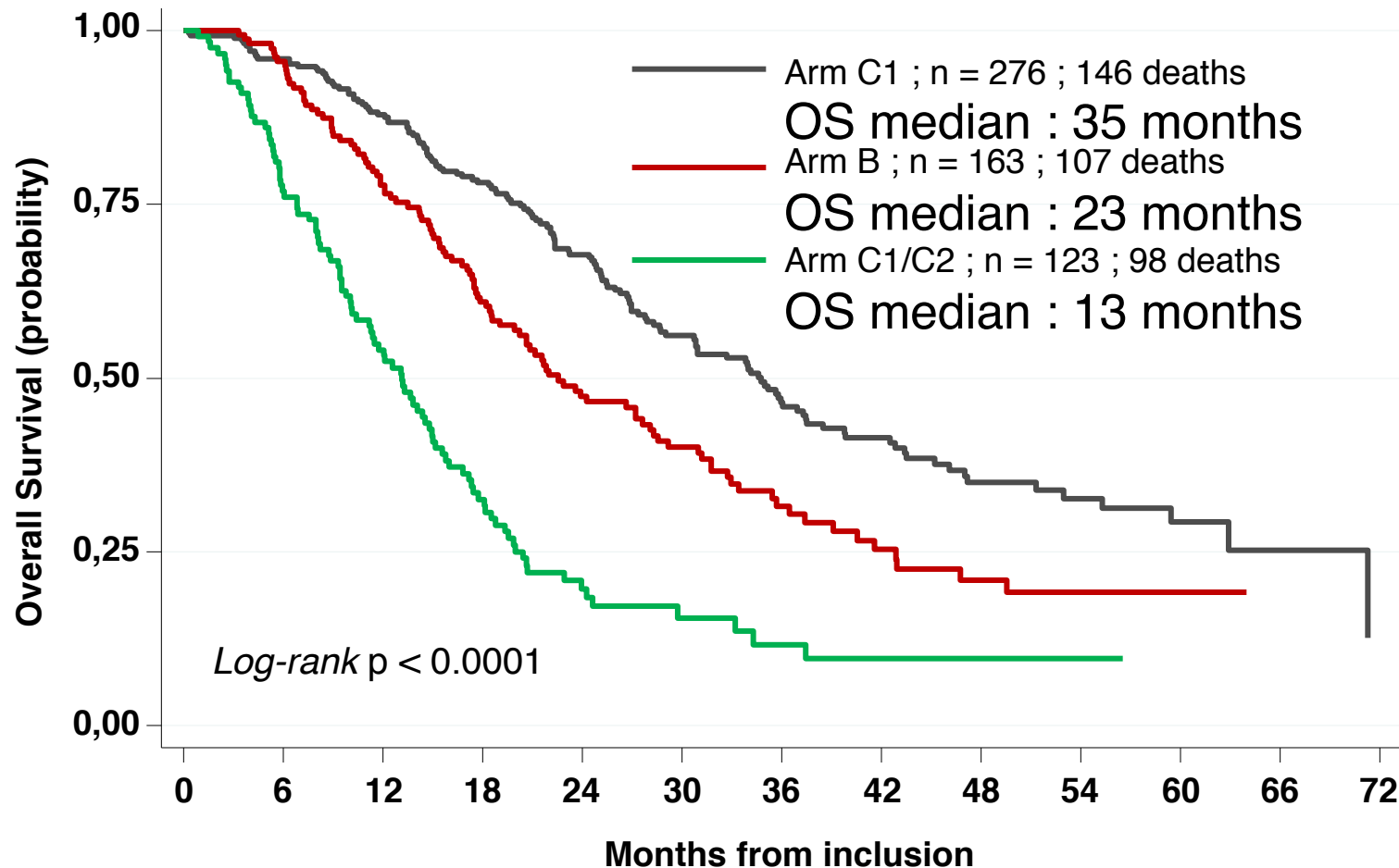


The SWOG 0500 trial



SWOG S0500 Study

Overall survival/arm



The SWOG 0500 trial

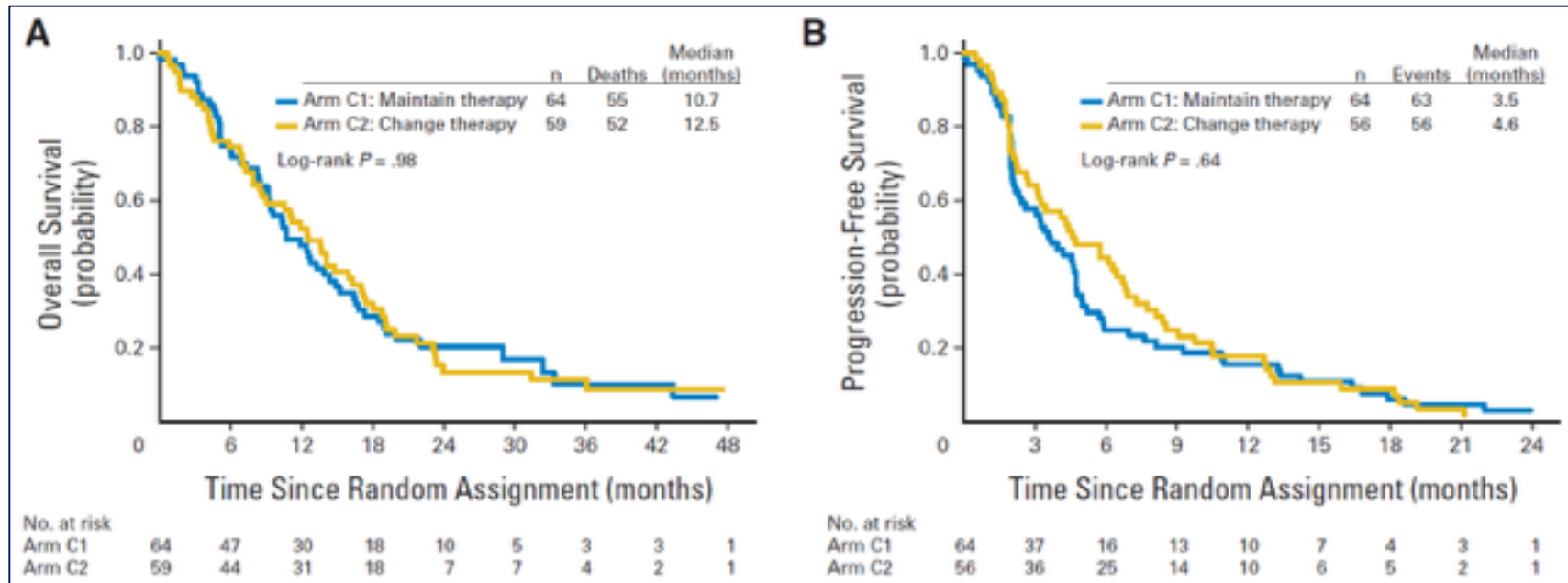
VOLUME 32 • NUMBER 31 • NOVEMBER 1 2014

JOURNAL OF CLINICAL ONCOLOGY

ORIGINAL REPORT

Circulating Tumor Cells and Response to Chemotherapy in Metastatic Breast Cancer: SWOG S0500

Jeffrey B. Smerage, William E. Barlow, Gabriel N. Hortobagyi, Eric P. Winer, Brian Leyland-Jones,
 Gordan Sikilovic, Sheela Tejwani, Anne F. Schott, Mark A. O'Rourke, Danika L. Lew, Gerald V. Doyle,
 Julie R. Gualow, Robert B. Livingston, and Daniel F. Hayes



Use of Biomarkers to Guide Decisions on Systemic Therapy for Women With Metastatic Breast Cancer: American Society of Clinical Oncology Clinical Practice Guideline

Catherine Van Poznak and Daniel F. Hayes,
University of Michigan Comprehensive
Cancer Center, Ann Arbor, MI; Mark R.
Somerfield, American Society of Clinical
Oncology

Catherine Van Poznak, Mark R. Somerfield, Robert C. Bast, Massimo Cristofanilli, Matthew P. Goetz, Ana M. Gonzalez-Angulo, David G. Hicks, Elizabeth G. Hill, Minetta C. Liu, Wanda Lucas, Ingrid A. Mayer, Robert G. Mennel, William F. Symmans, Daniel F. Hayes, and Lyndsay N. Harris

- Data are insufficient to recommend use of CEA, CA 15-3, and CA 27-29 alone for monitoring response to treatment.
- The recommendation for use is based on clinical experience and Panel informal consensus in the absence of studies designed to evaluate the clinical utility of the markers.
- A number of studies have evaluated the role of CTCs in metastatic disease and have clearly shown that CTCs are associated with poor prognosis in this setting.
- However, none of the reviewed studies assessed predictive value using clinical utility guidelines, with one exception.

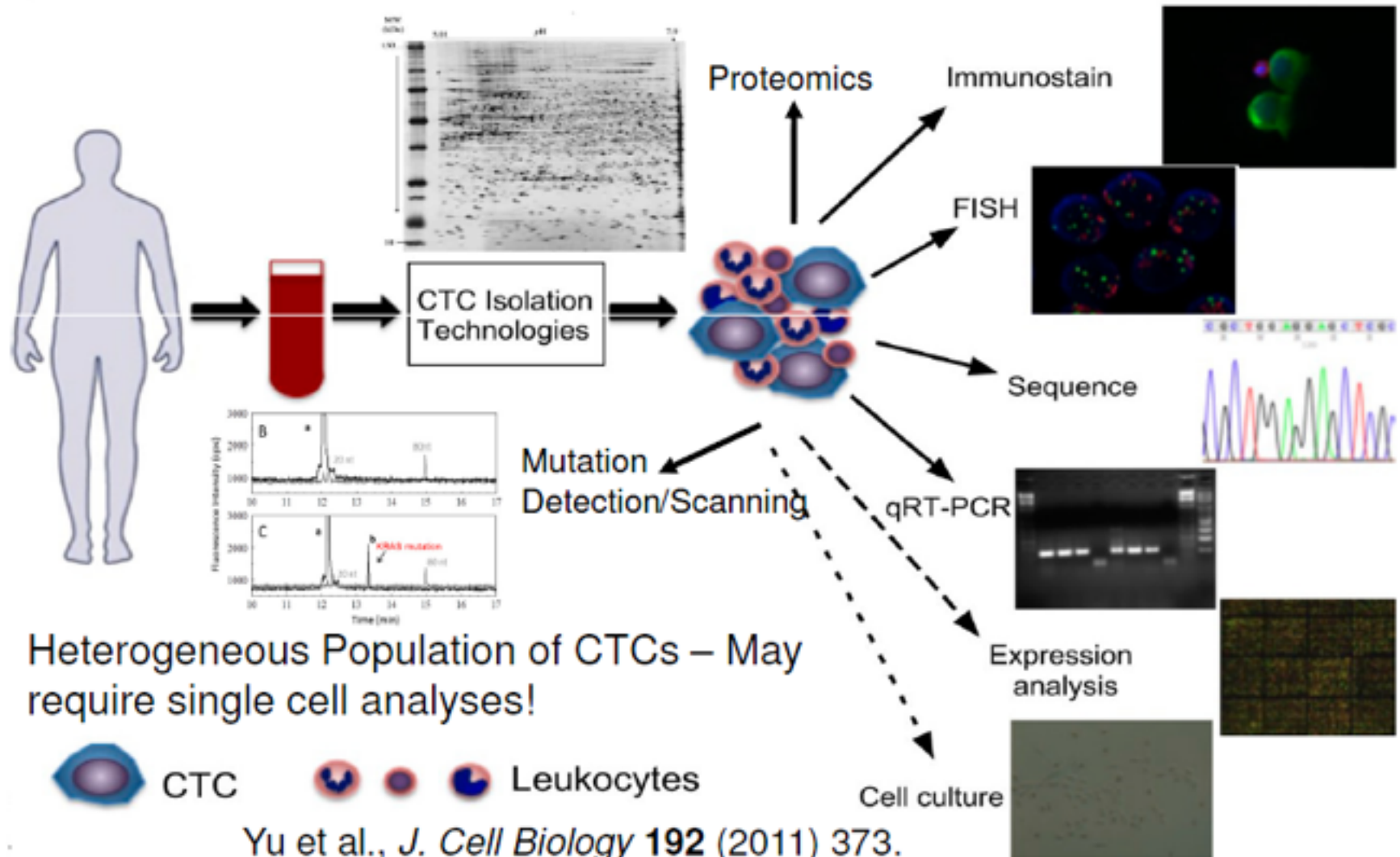
Dealing with Mass-Limited Samples – Don't Just Count, Analyze

Patient Blood

CTC Isolation

CTCs

Applications



Detection of therapeutic target molecules on CTC

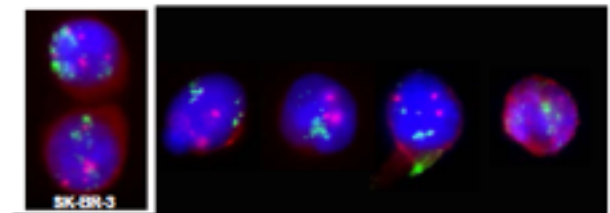
Example: HER2 in breast cancer

CTC without HER2 gene amplification

Potential benefit from anti-HER2 therapy (e.g., trastuzumab) also in patients with „HER2-negative“ tumors (Paik *et al.*, NEJM 2008)

CTC with HER2 gene amplification

						2+
						3+
B	Composite	CK	DAPI	CD45	HER2	
MCF-7						0
BT20						1+
T47D						1+
MDA-MB-453						2+
SK-BR-3						3+
BT474						3+

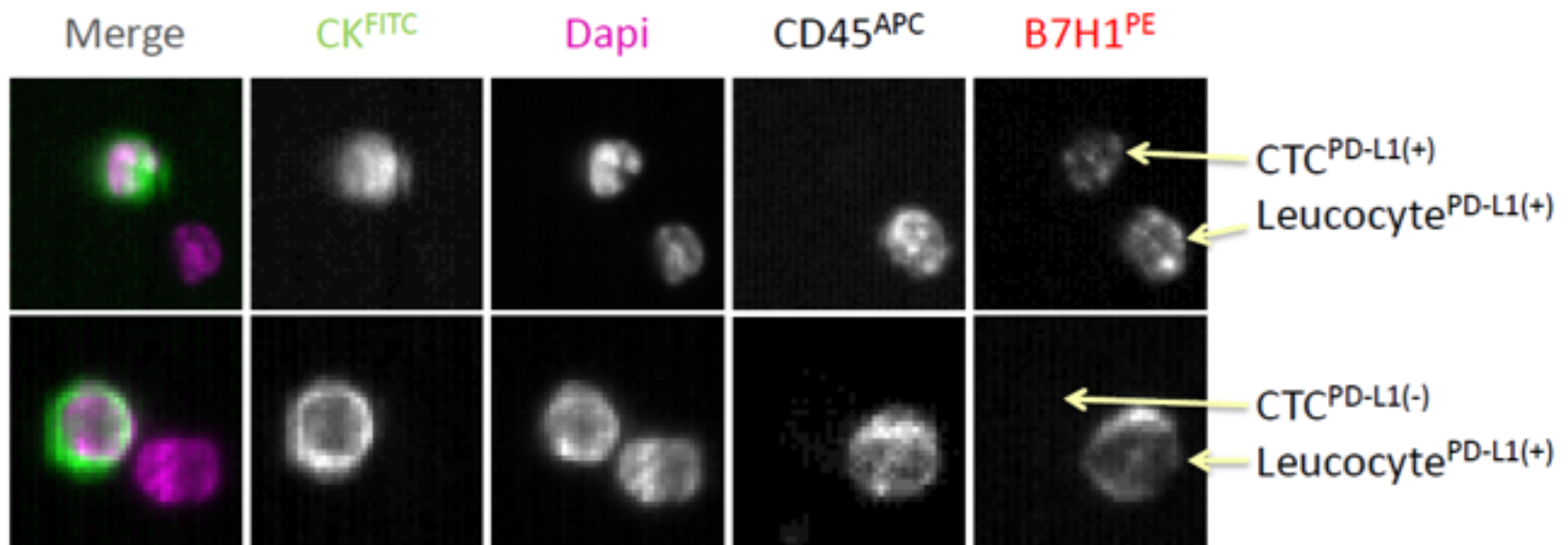


- HER2-pos. CTC in pats w HER2-neg. primary tumors
- HER2-neg. & HER2-pos. CTC after trastuzumab

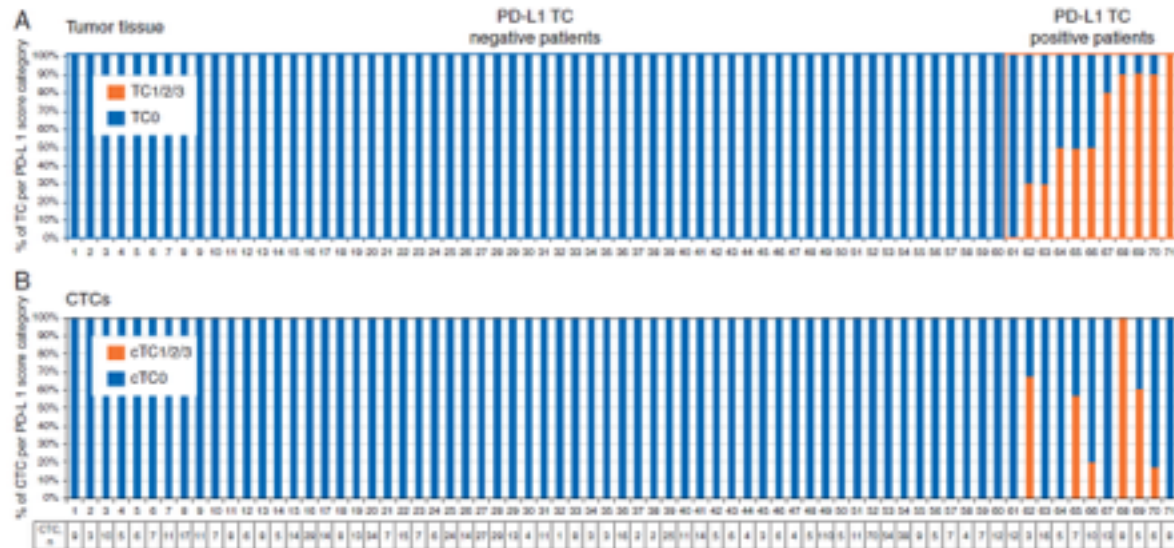
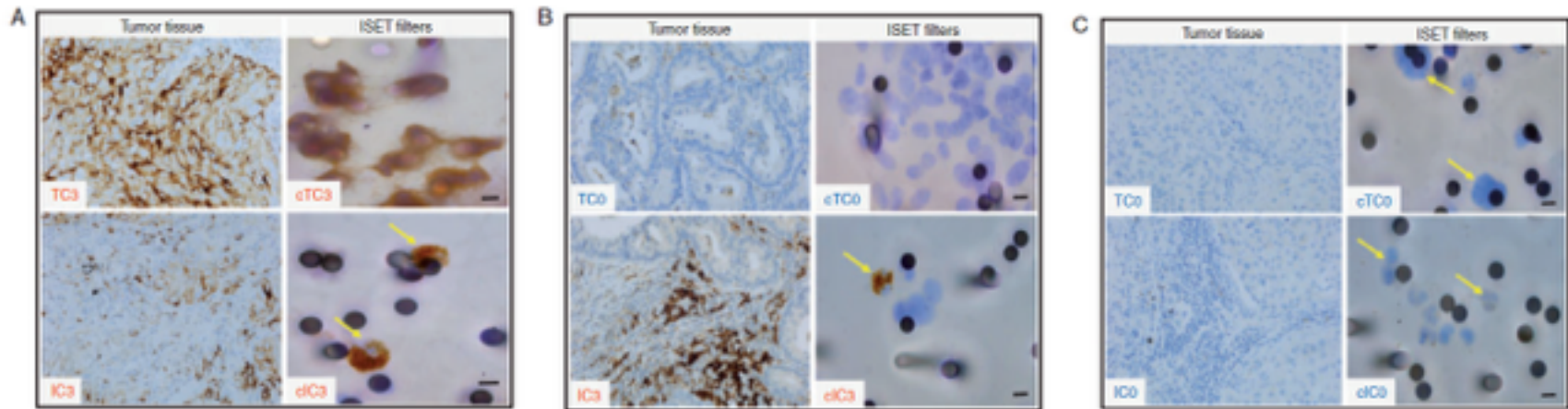
Frequent expression of PD-L1 on circulating breast cancer cells.

Sixteen patients with circulating tumor cells (CTCs) using the CellSearch® system: PD-L1(+) CTCs in 11 patients (68.8%).

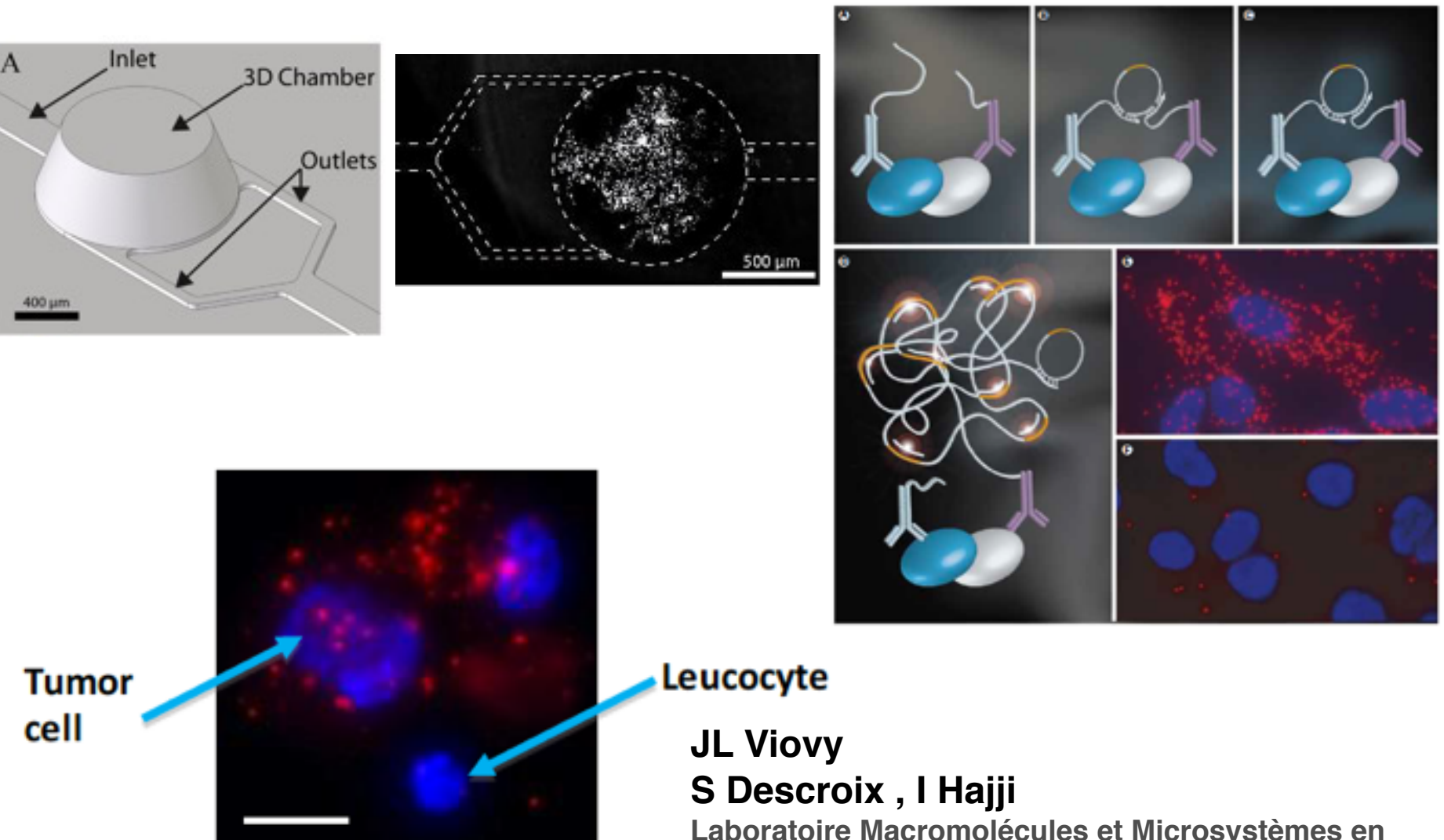
The fraction of PD-L1(+) CTCs varied from 0.2 to 100% in individual patients.



Concordant PD-L1 staining in tumor tissue and corresponding ISET filters from selected NSCLC patients.



Proximity-Ligation Assay (PLA) HER2-HER3

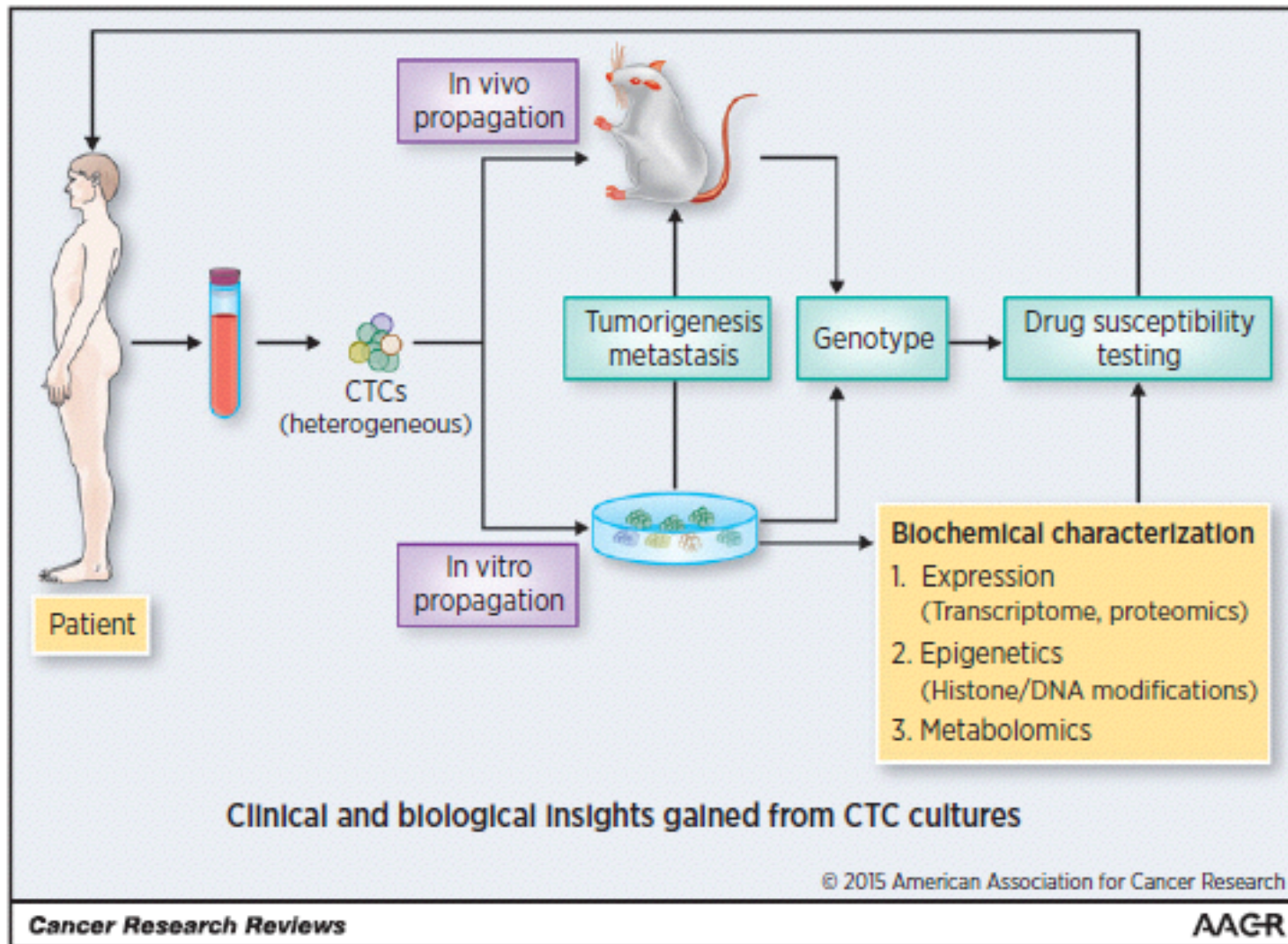


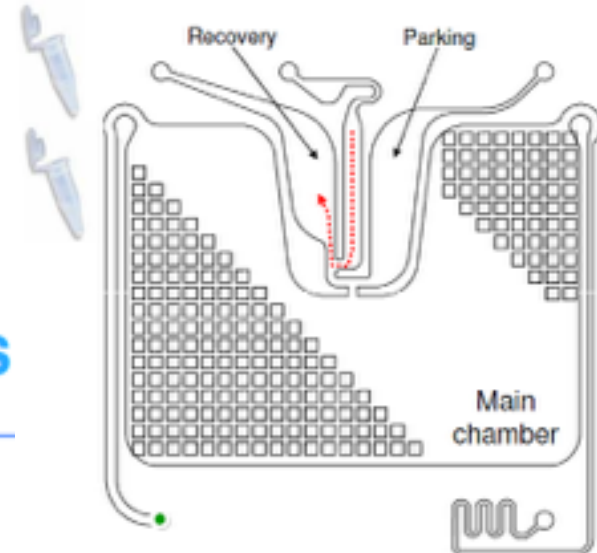
JL Viovy

S Descroix , I Hajji

Laboratoire Macromolécules et Microsystèmes en
Biologie et Médecine Institut Pierre-Gilles de Gennes

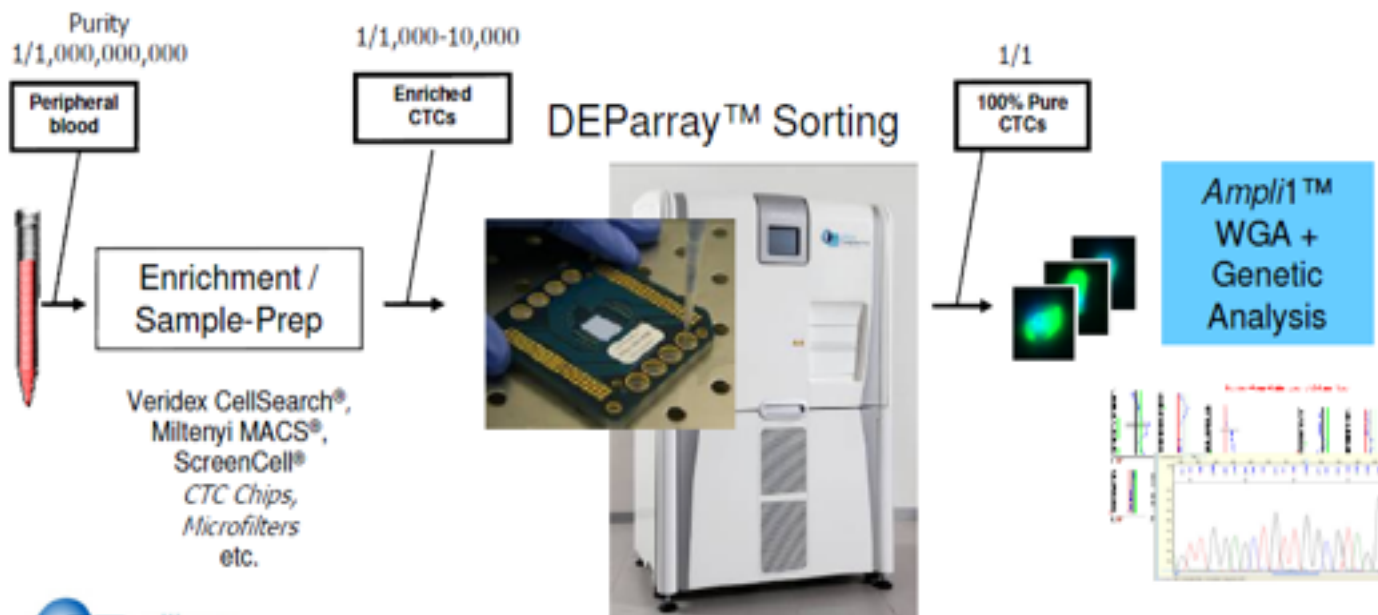
Ex Vivo Culture of CTCs: An Emerging Resource to Guide Cancer Therapy





DEPArray™ Delivers 100%-Pure CTCs

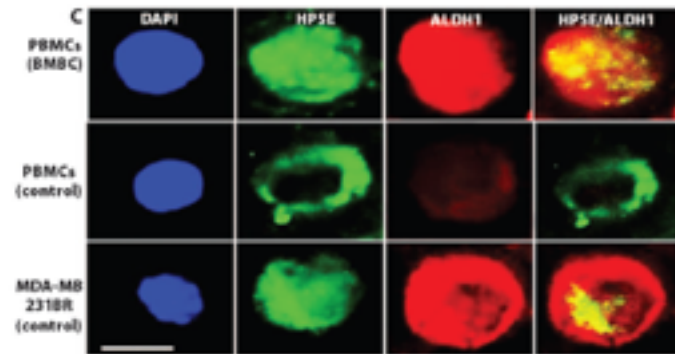
We bridge the gap between enrichment and single-cell analysis



The Identification and Characterization of Breast Cancer CTCs Competent for Brain Metastasis

- CTCs isolated from peripheral blood mononuclear cells of patients with breast cancer and also develop CTC lines from three of these patients

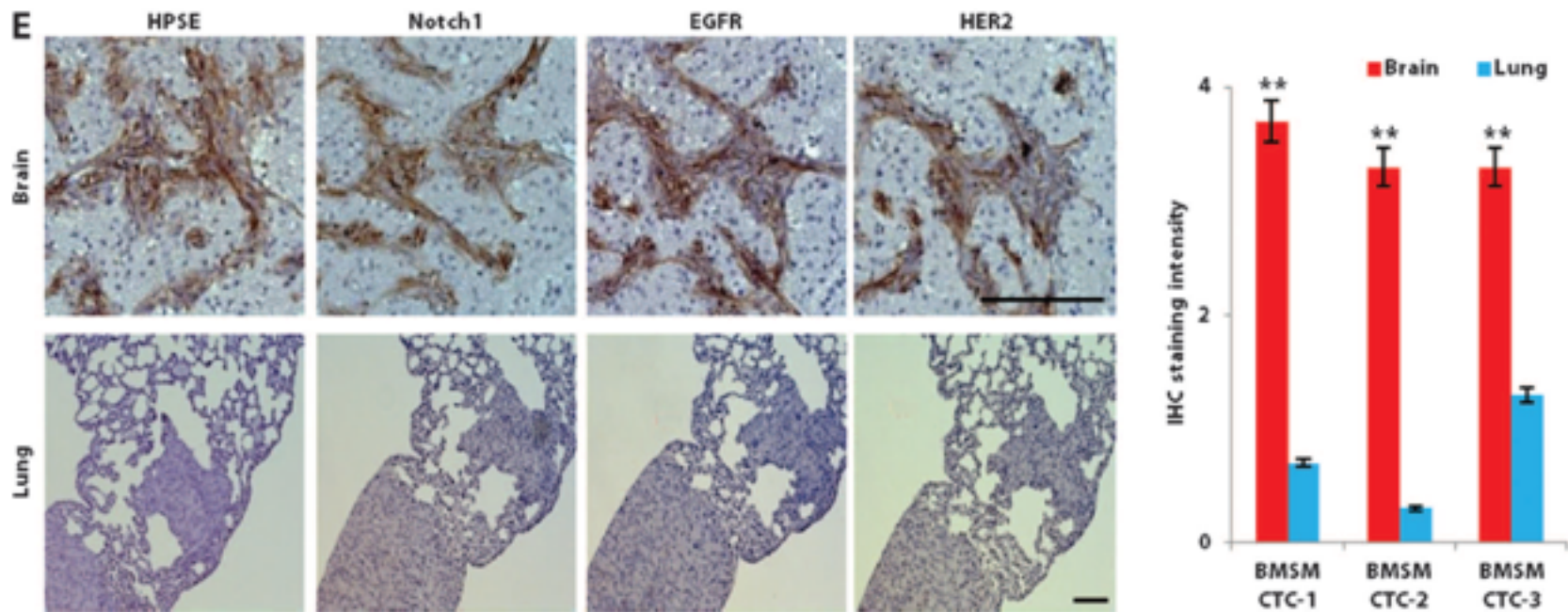
- “brain metastasis selected markers (BMSMs)” HER2+/EGFR+/HPSE+/Notch1+



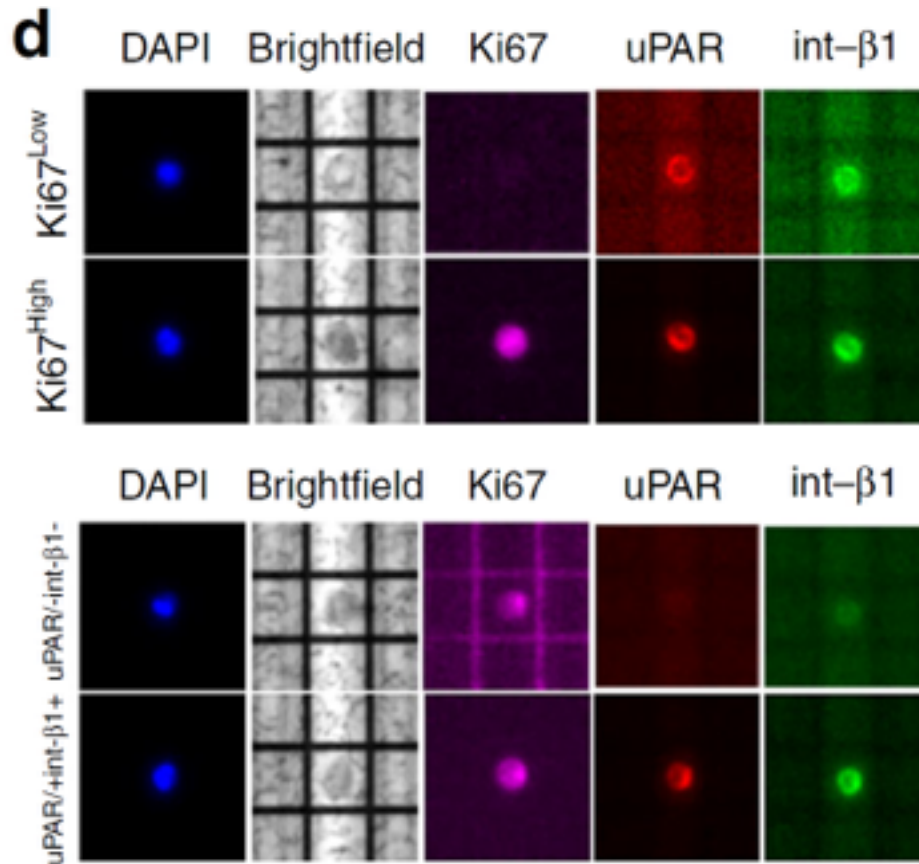
Cells injected	Pathology	Tumor incidence in lung (%)	<i>P</i> for lung	Tumor incidence in brain (%)	<i>P</i> for brain
CTC-1	Spindle perivascular Epithelioid micrometastases	80	—	20	—
CTC-2	Spindle perivascular	60	—	0	—
CTC-3	Spindle perivascular	60	—	0	—
BMSM CTC-1	Spindle perivascular Epithelioid micrometastases	100	<0.01 (compared to CTC-1)	80	<0.001 (compared to CTC-1)
BMSM CTC-2	Spindle perivascular Epithelioid micrometastases	80	<0.01 (compared to CTC-2)	60	<0.001 (compared to CTC-2)
BMSM CTC-3	Spindle perivascular	80	<0.01 (compared to CTC-3)	60	<0.001 (compared to CTC-3)
PBMcs	No tumor	0	—	0	—

The Identification and Characterization of Breast Cancer CTCs Competent for Brain Metastasis

- murine brain and lung sections from animals injected with BMSM CTC-1 and analyzed for BMSM signature protein expression by immunohistochemistry

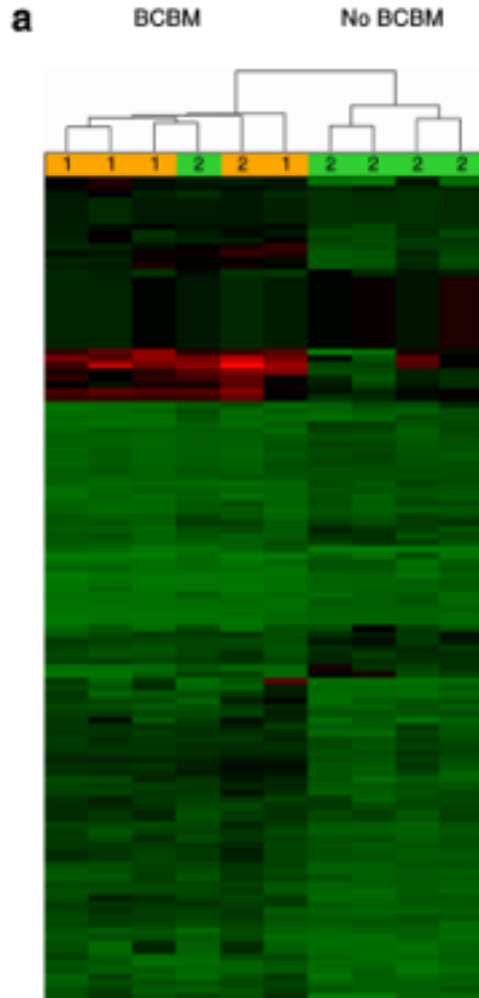


Molecular characterization of breast cancer CTCs associated with brain metastasis



- Demonstration of Ki67, uPAR, and int- β 1 staining of single CTCs by DEPArrayTM.

Molecular characterization of breast cancer CTCs associated with brain metastasis

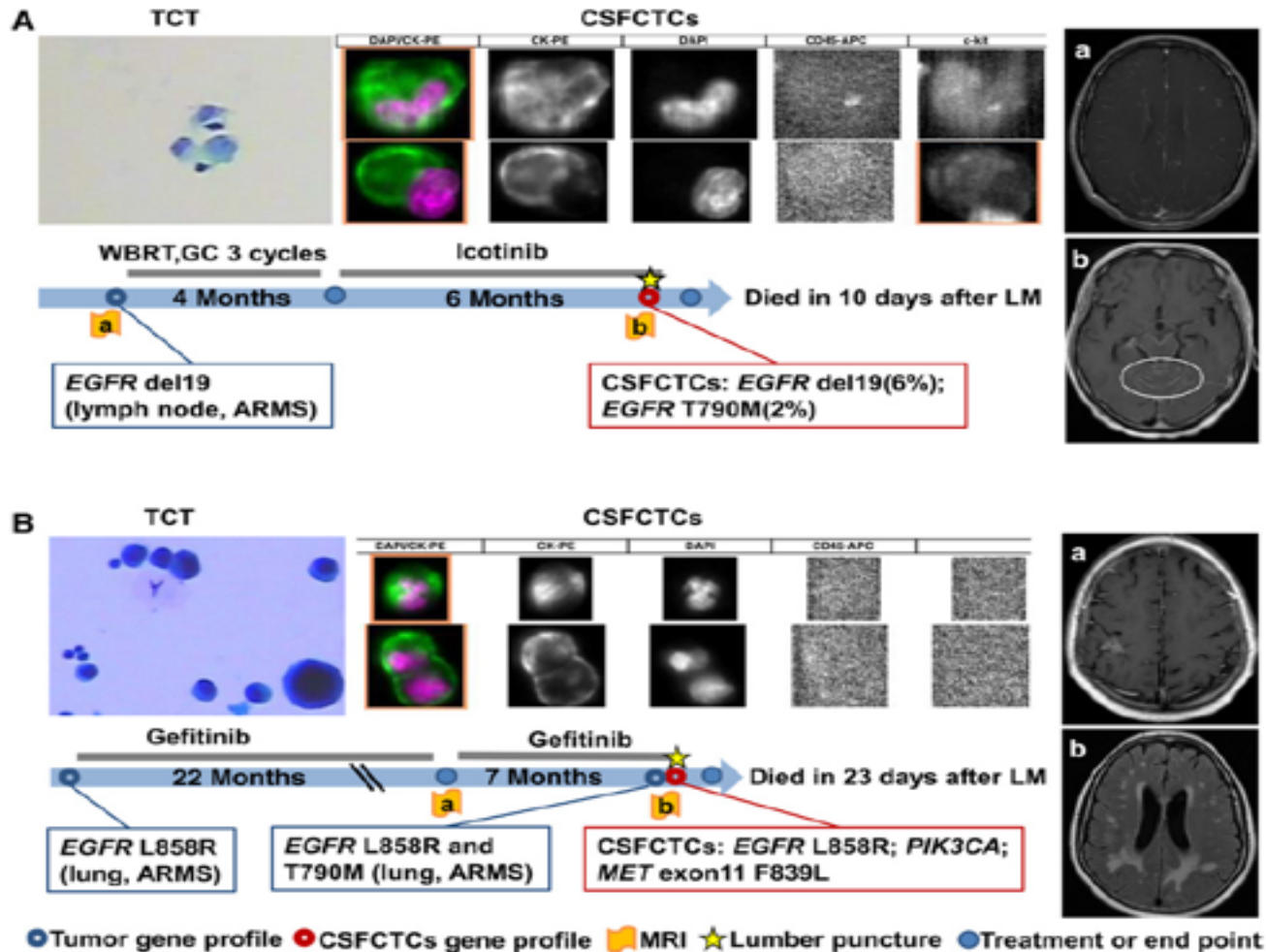


- Deriving from a comprehensive analysis of CTC transcriptomes, a unique “circulating tumor cell gene signature” that is distinct from primary breast cancer tissues.
- This signature included enrichment of several genes associated with activation of Notch signalling, or with novel immune-evasion pathways.
- The validity of transcriptomic data was confirmed by the immunocytochemical detection of Notch 1 in 72% of CTCs from patients with confirmed BCBM, versus only 16% in CTCs from patients without BCBM.

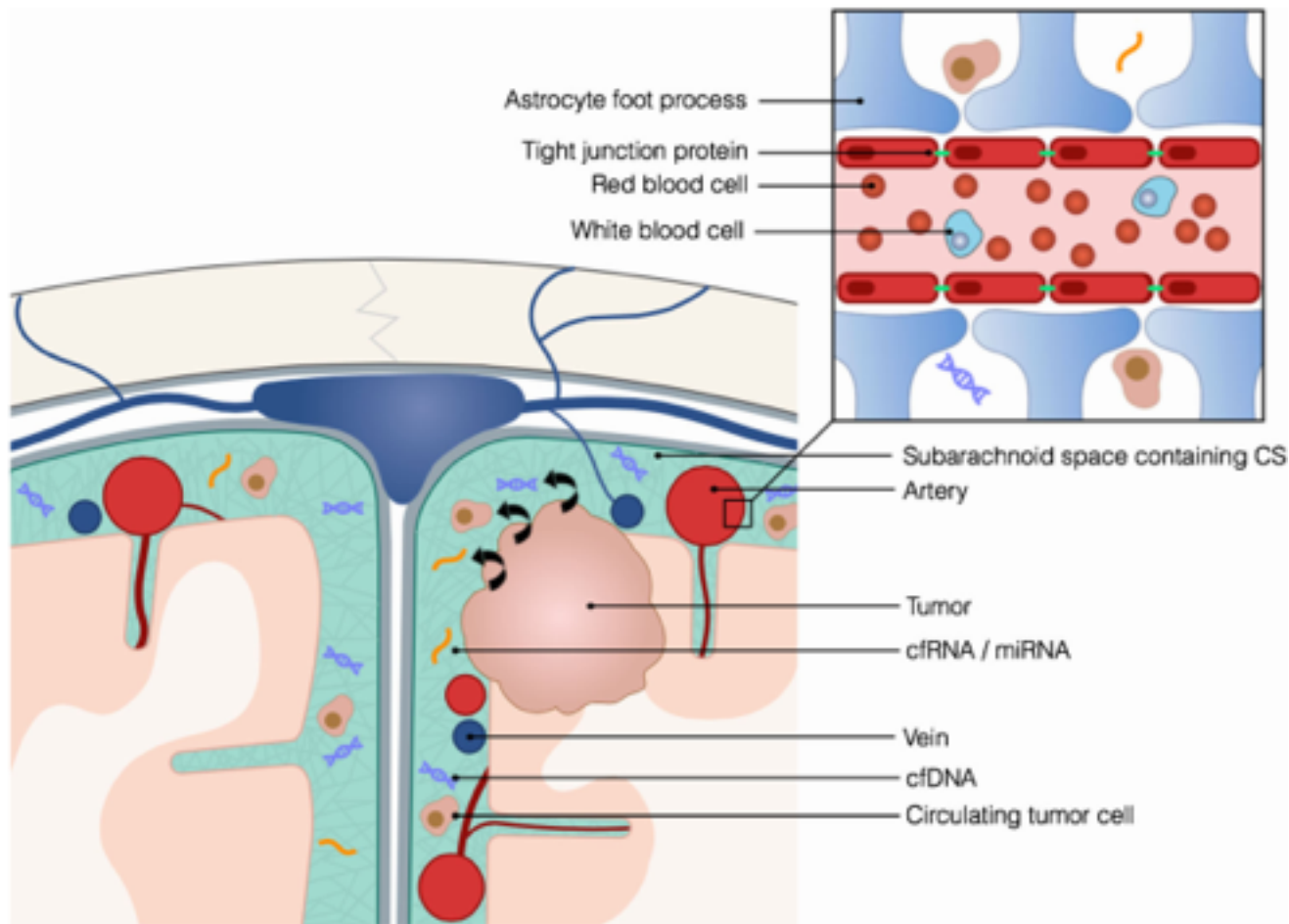
Detection of Driver and Resistance Mutations in Leptomeningeal Metastases of NSCLC by Next-Generation Sequencing of Cerebrospinal Fluid Circulating Tumor Cells

No.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
Definitive LM	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
CSFCTCs (cells/7.5 mL)	1310	2214	752	260	1283	72	2716	0	156	2300	1336	1009	252	4496	151	27	797	2060	929	14888	764
TCT	+	-	+	+	+	-	+	-	-	+	-	+	+	-	-	-	+	+	-	+	+
MRI	-	+	-	+	-	-	-	+	+	-	+	-	-	+	-	+	+	-	+	-	+
Combined MRI and TCT	+	+	+	+	+	-	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+
CTCs (cells/7.5 mL)	2	2	0	0	2	0	4	0	0	0	0	2	0	0	UA	UA	UA	UA	UA	UA	UA

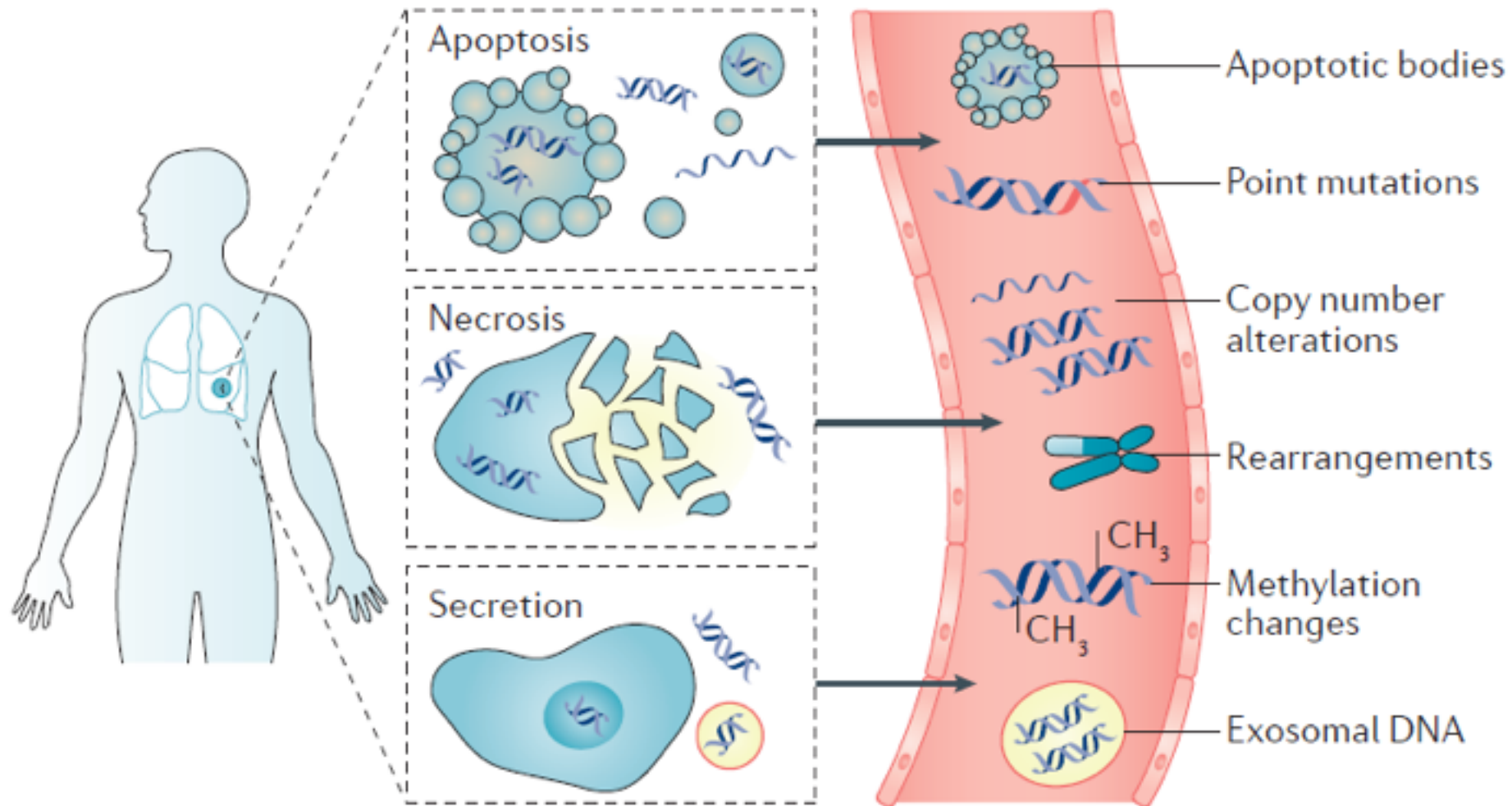
Detection of Driver and Resistance Mutations in Leptomeningeal Metastases of NSCLC by Next-Generation Sequencing of Cerebrospinal Fluid Circulating Tumor Cells



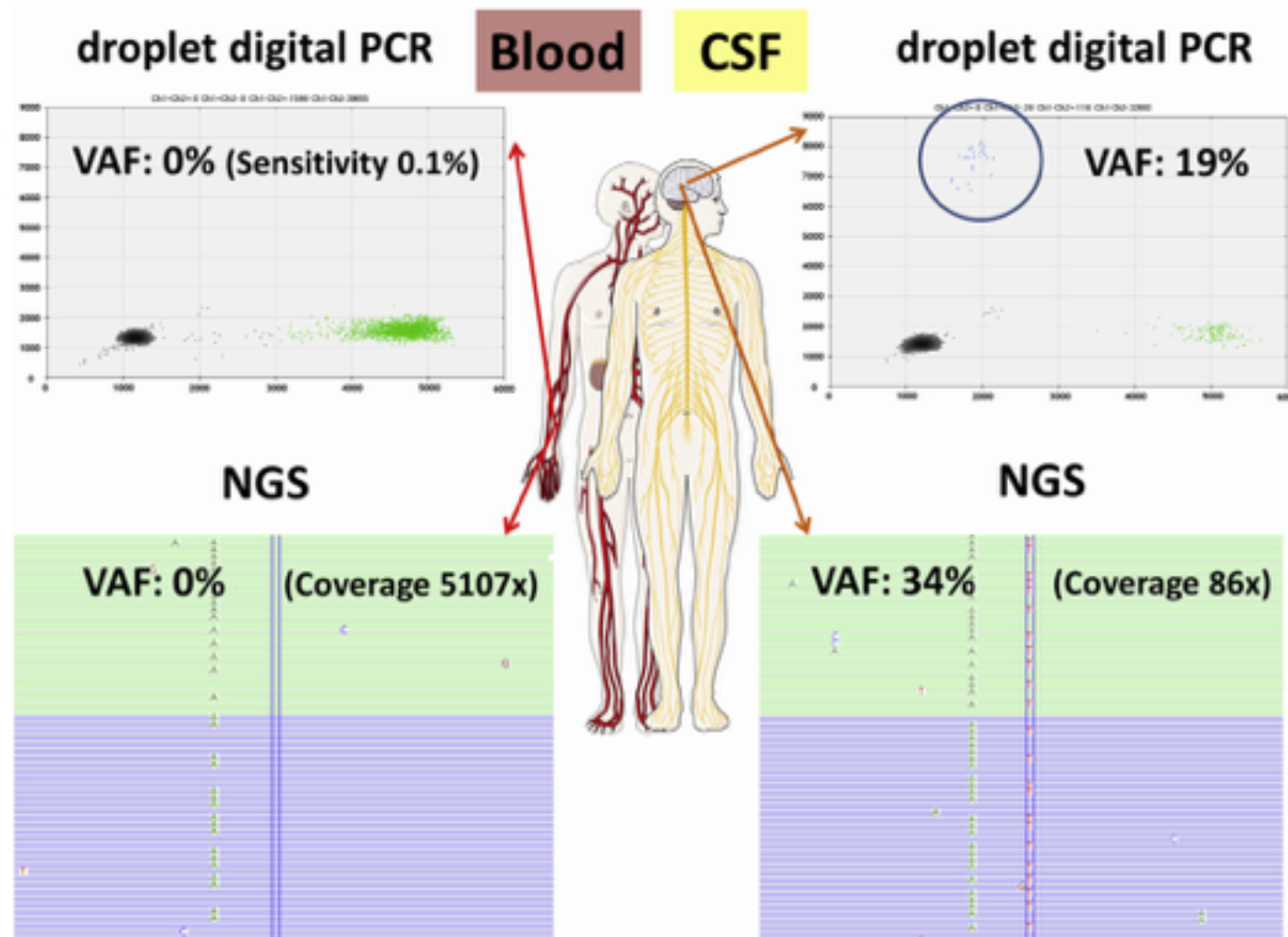
CSF may be a more optimal source of tumor-derived circulating nucleic acids than blood which may have poorer signal-to-noise ratios due to the presence of the BBB and native blood cells



Circulating tumor DNA ctDNA

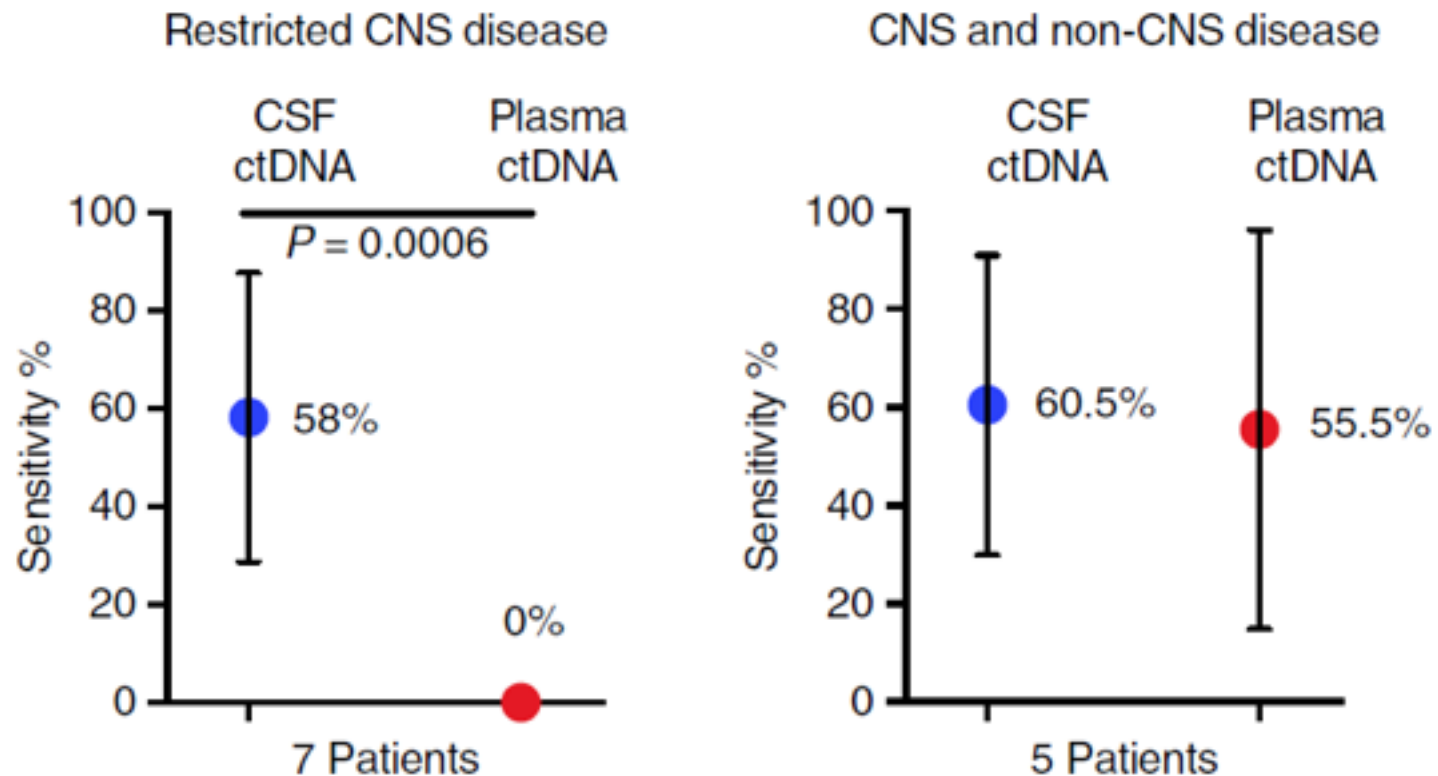


T790M EGFR Mutation Detection in Cerebrospinal Fluid and Response to Osimertinib in a Lung Cancer Patient with Meningeal Carcinomatosis

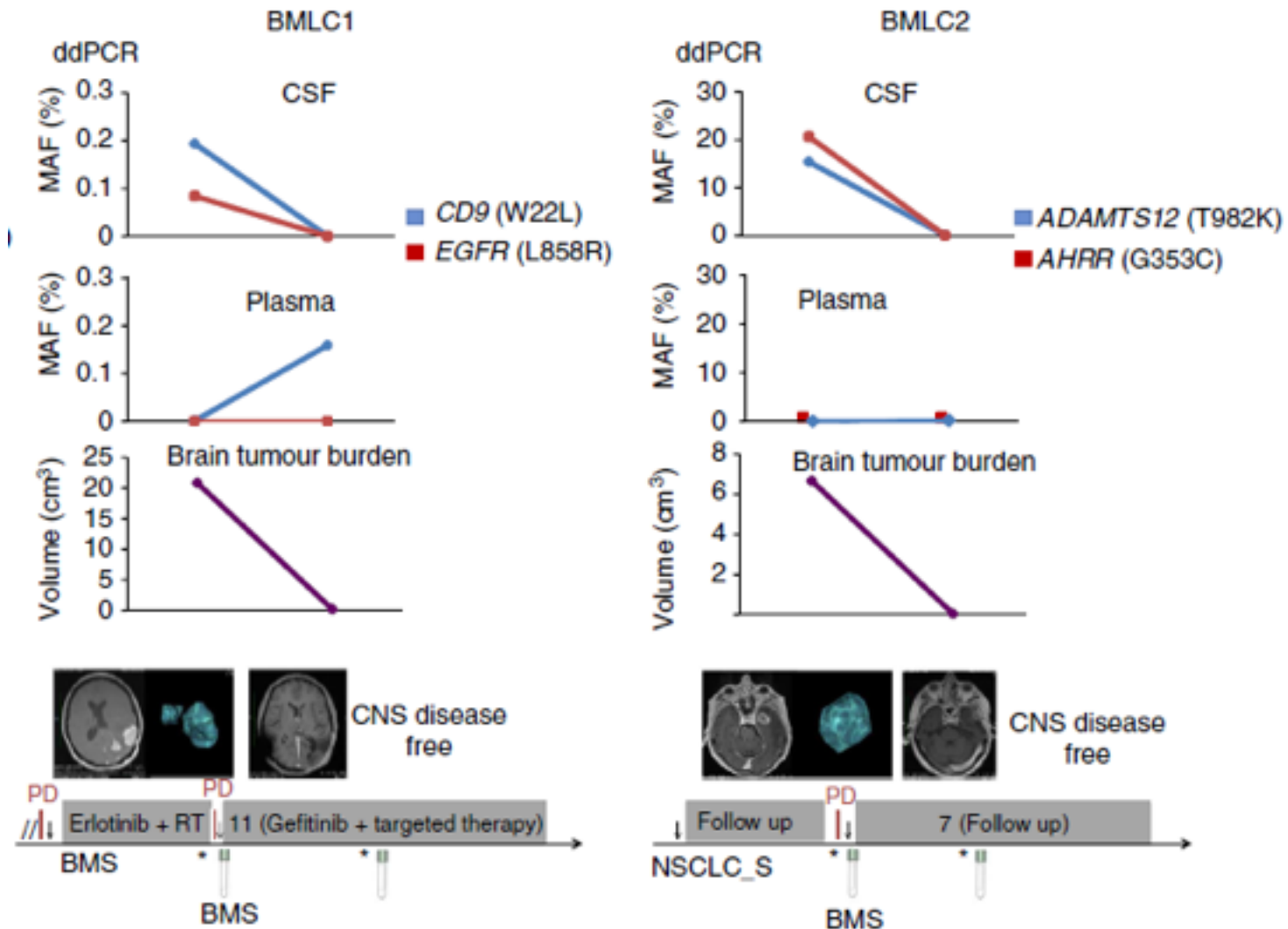


Cerebrospinal fluid-derived circulating tumour DNA better represents the genomic alterations of brain tumours than plasma

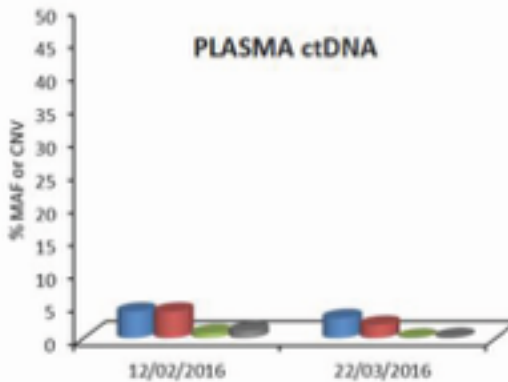
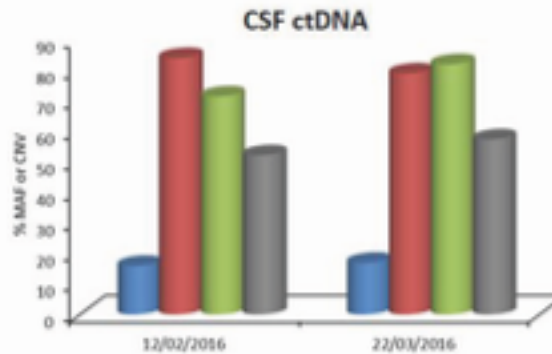
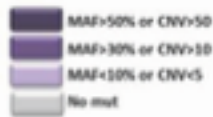
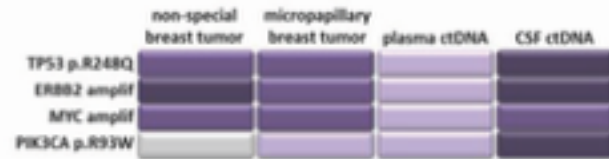
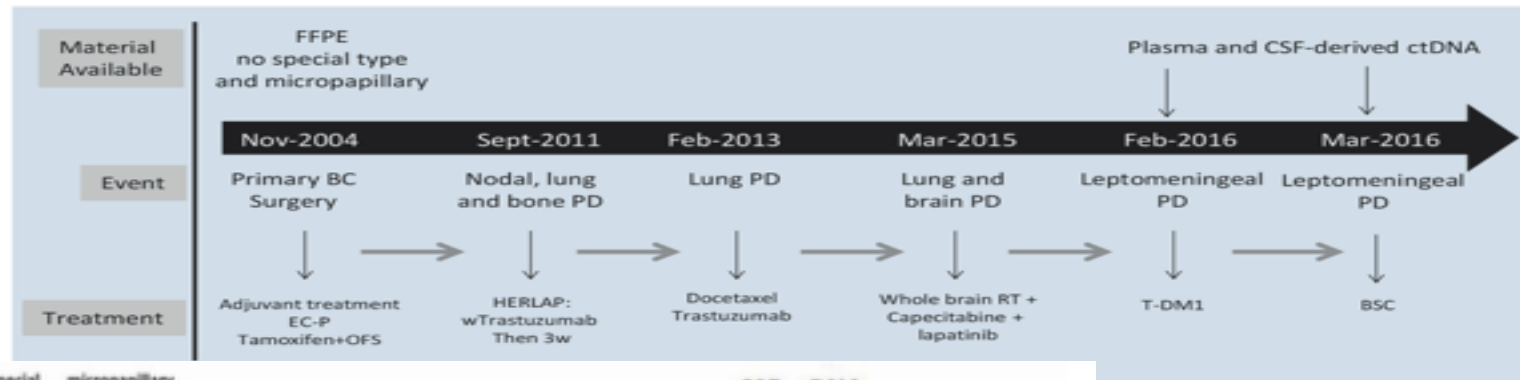
12 patients



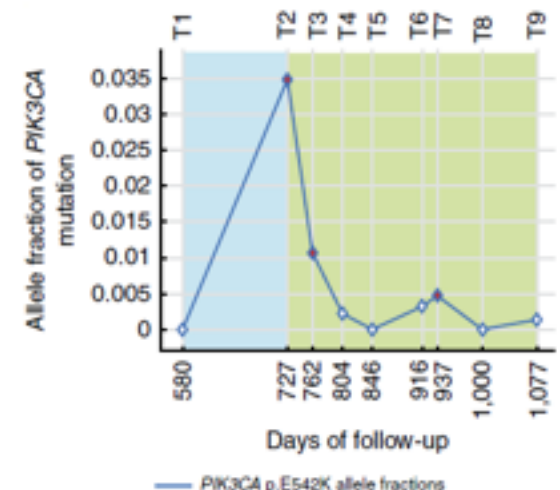
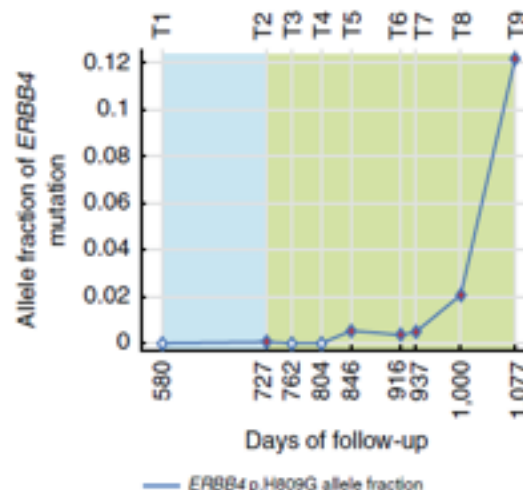
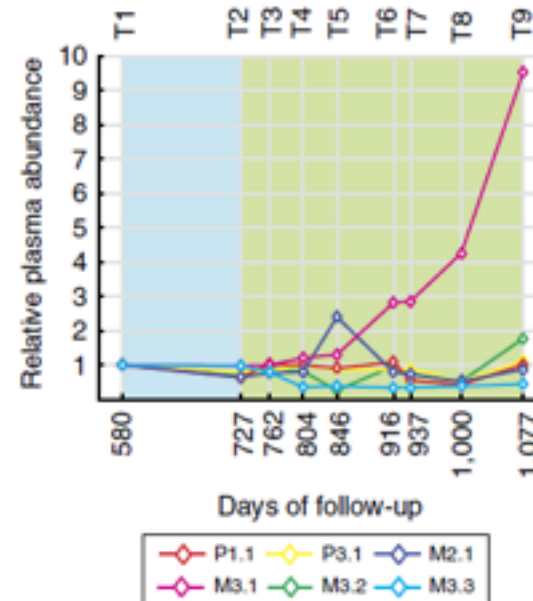
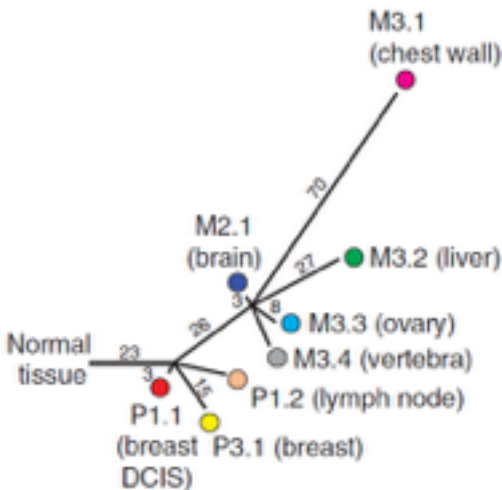
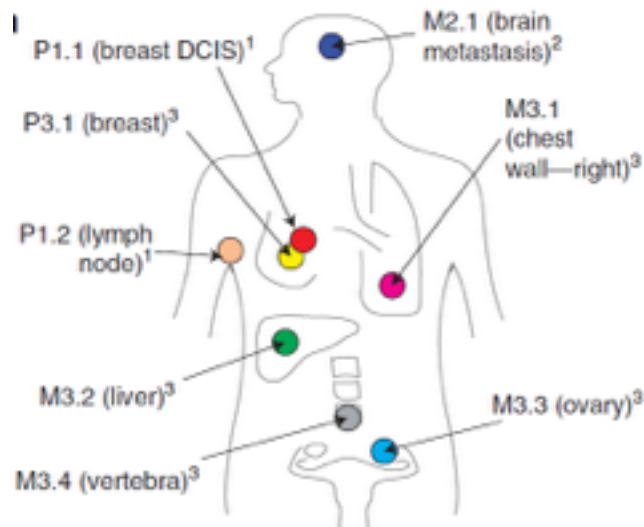
Cerebrospinal fluid-derived circulating tumour DNA better represents the genomic alterations of brain tumours than plasma



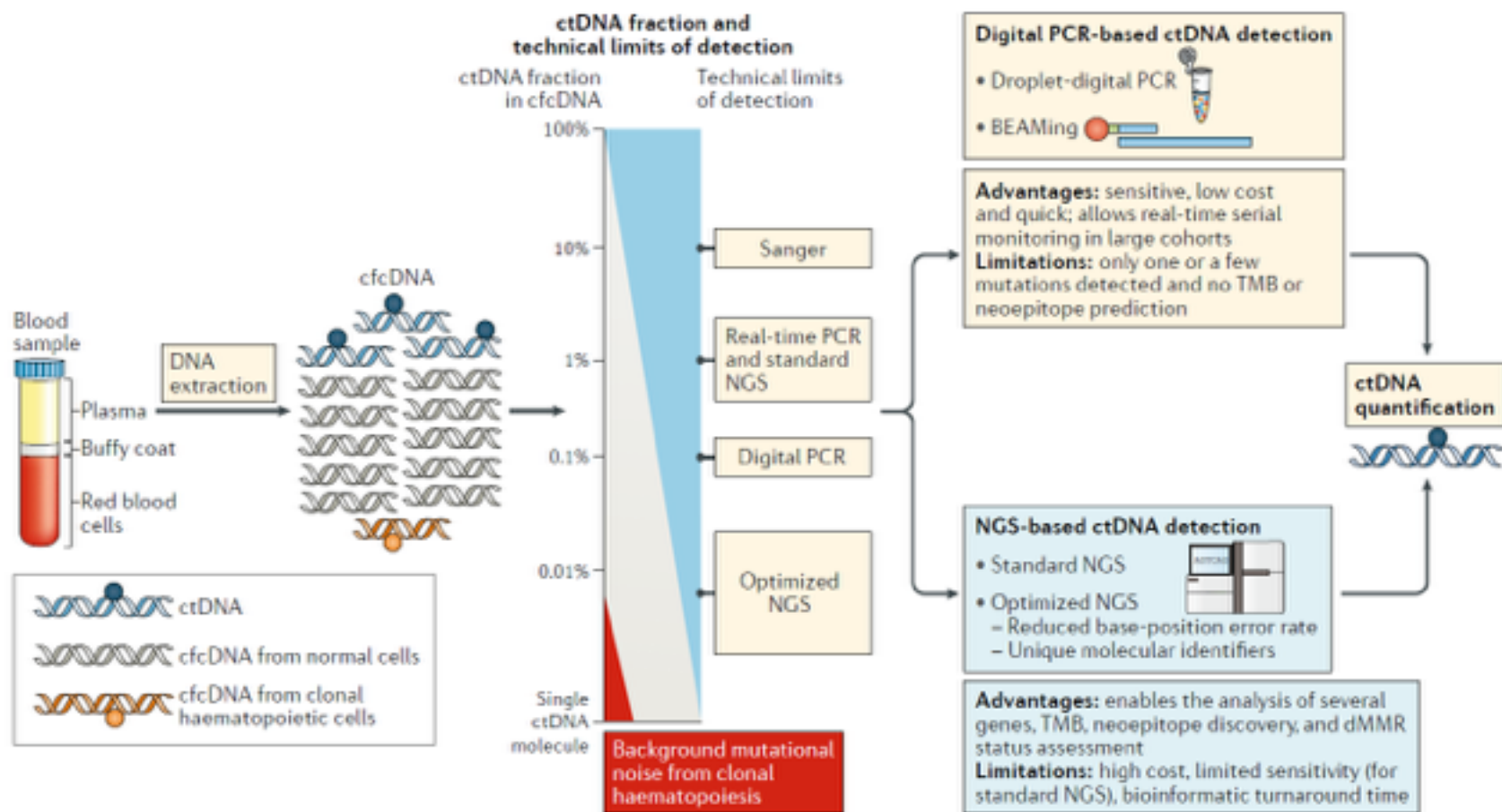
Genotyping tumour DNA in cerebrospinal fluid and plasma of a HER2-positive breast cancer patient with brain metastases



Multifocal clonal evolution characterized using circulating tumour DNA in a case of metastatic breast cancer (Murtaza et al, Nature Comm Nov 2015)



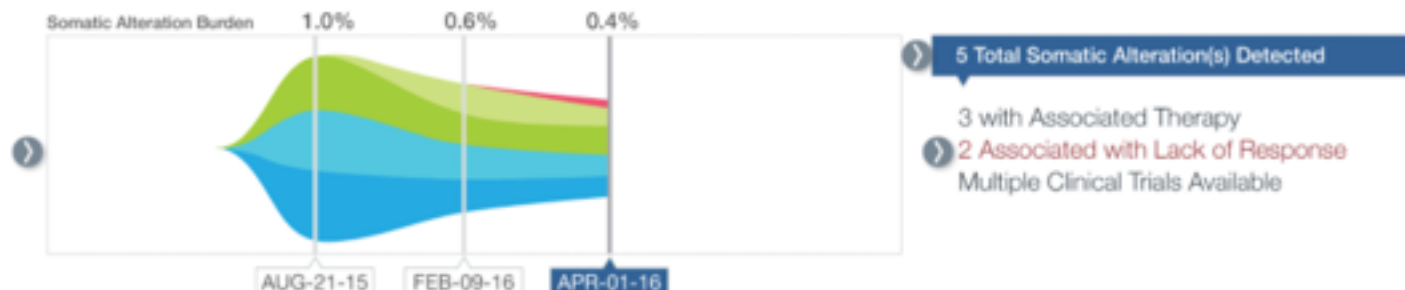
Analysis of ctDNA



Tumor Response Map

Guardant360 Tumor Response Map

The Guardant360 Tumor Response Map illustrates the mutant allele percentage (% cDNA) of observed somatic variants at each sample submission time point. The "Somatic Alteration Burden" value below refers to the maximum % cDNA detected at each time point. Amplifications are not plotted, and only the first and last four test dates are plotted. Please see the Physician Portal (<https://portal.guardanthealth.com>) for the Tumor Response Map with all test dates.



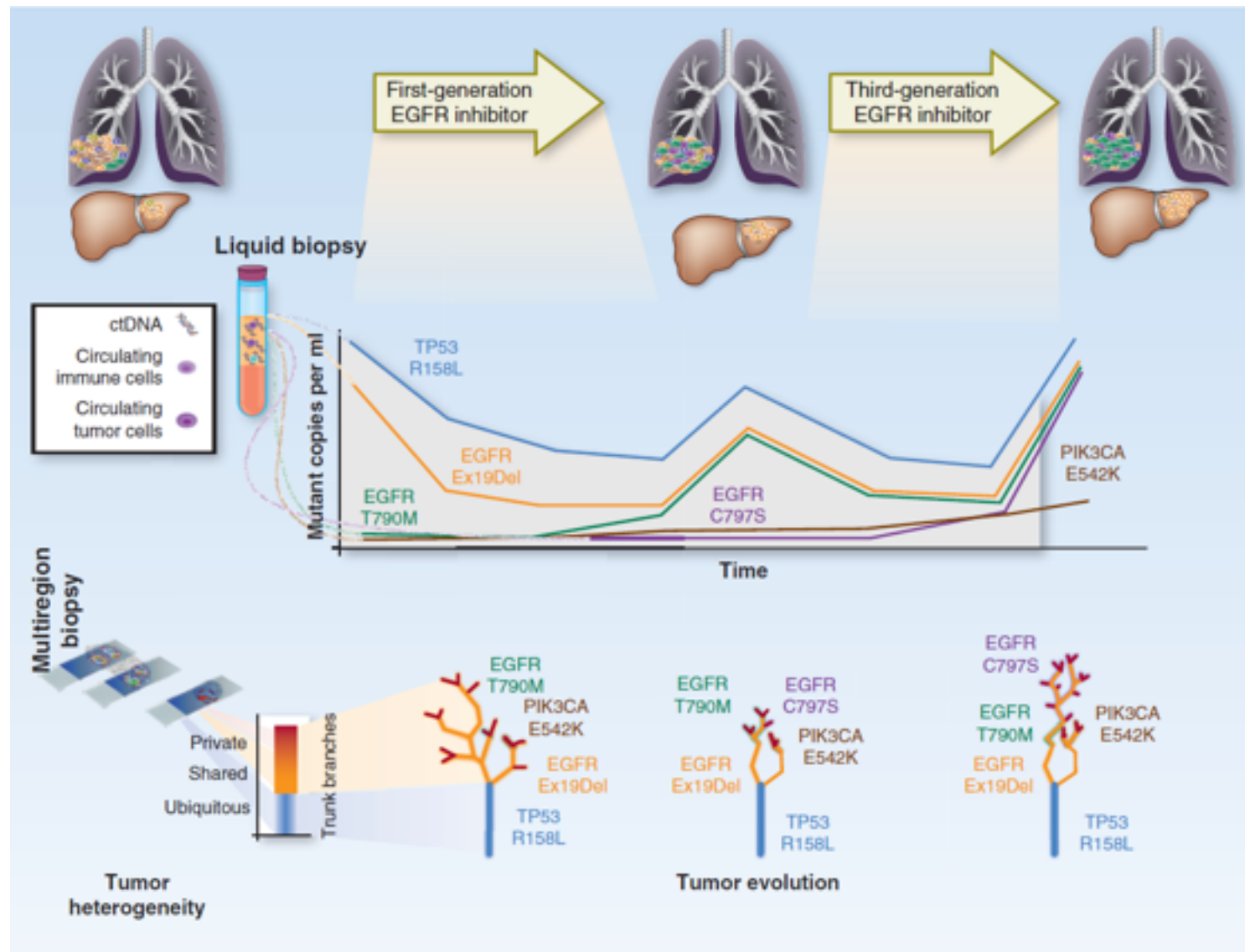
Alteration and Therapy List

Summary of Somatic Alterations & Associated Treatment Options

The percentage of altered cell-free DNA (% cDNA) circulating in blood is related to the unique tumor biology of each patient. Factors that may affect the % cDNA of detected somatic alterations include tumor growth, turn-over, size, heterogeneity, vascularization, disease progression, and treatment.

Alteration	Mutation Trend	% cDNA or Amplification	FDA Approved in Indication <small>see page 3</small>	Available for Use in Other Indications <small>see page 3</small>	Clinical Drug Trials <small>see page 70</small>
EGFR	L858R	0.3	Atatinib Erlotinib Gefitinib	None	Trials Available
	T790M	0.25	Osimeritinib Lack of Response: Erlotinib Gefitinib	Atatinib	Trials Available
	C797S	0.1	Erlotinib Lack of Response: Osimeritinib	None	Trials Available
TP53	Y220C	0.3	None	None	Trials Available Nearby
Additional Alterations					
EGFR	L392M	0.4	The functional consequences and clinical significance of this gene variant are not established. Similar to other alterations in circulating cDNA, the amount (% cDNA) of this variant may reflect disease progression or response to treatment; clinical correlation is advised.		

Diagnostic approaches to measure the impact of cancer therapies on clonal evolution.



Circulating Tumor DNA Analysis in Patients With Cancer: American Society of Clinical Oncology and College of American Pathologists Joint Review

Jason D. Merker, Geoffrey R. Oxnard, Carolyn Compton, Maximilian Diehn, Patricia Hurley, Alexander J. Lazar, Neal Lindeman, Christina M. Lockwood, Alex J. Rai, Richard L. Schilsky, Apostolia M. Tsimberidou, Patricia Vasalos, Brooke L. Billman, Thomas K. Oliver, Suanna S. Bruinooge, Daniel F. Hayes, and Nicholas C. Turner

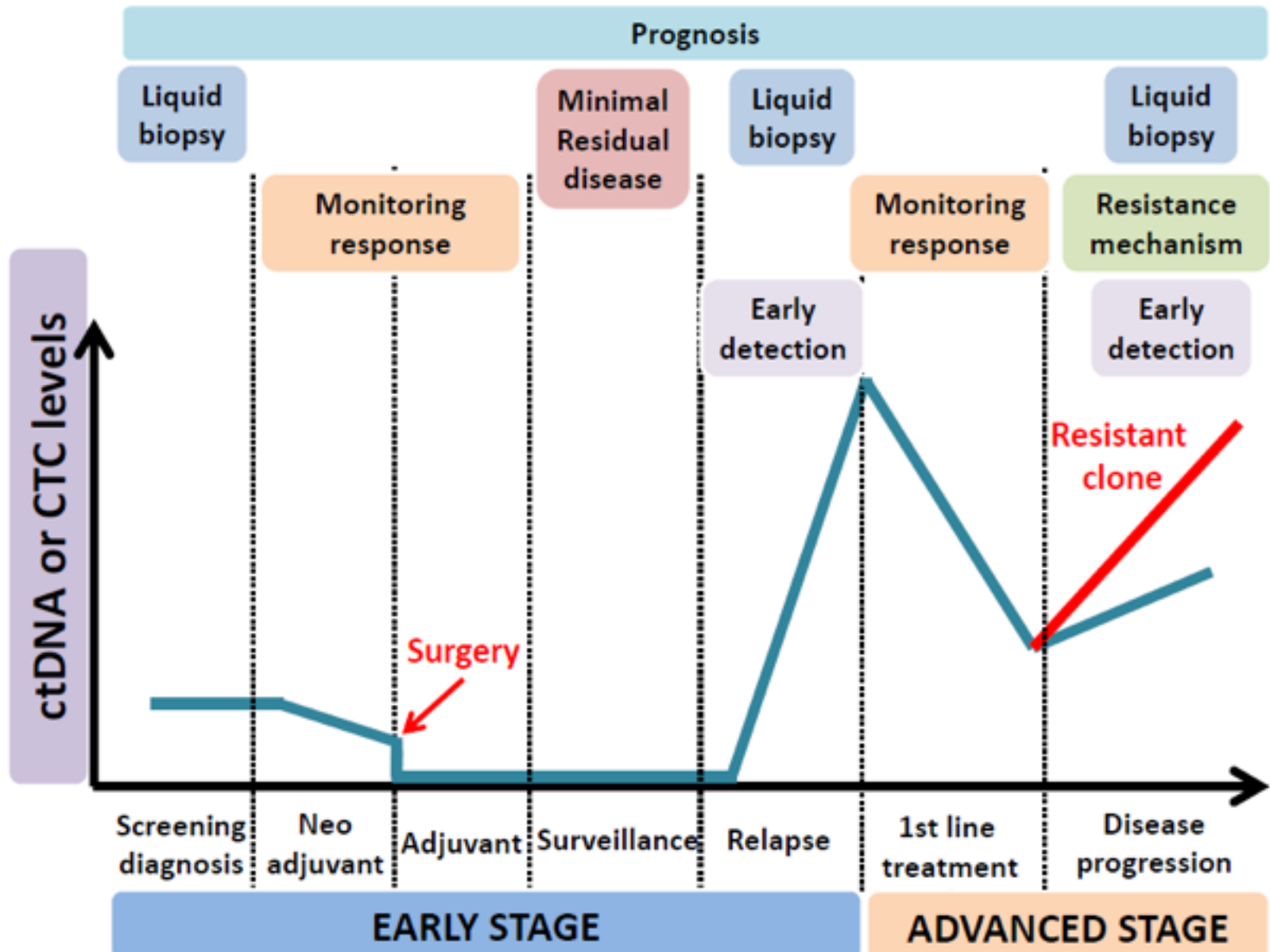
Some ctDNA assays have demonstrated clinical validity and utility with certain types of advanced cancer; however, there is insufficient evidence of clinical validity and utility for the majority of ctDNA assays in advanced cancer.

Evidence shows discordance between the results of ctDNA assays and genotyping tumor specimens and supports tumor tissue genotyping to confirm undetected results from ctDNA tests.

There is no evidence of clinical utility and little evidence of clinical validity of ctDNA assays in early-stage cancer, treatment monitoring, or residual disease detection.

There is no evidence of clinical validity and clinical utility to suggest that ctDNA assays are useful for cancer screening, outside of a clinical trial.

To recapitulate...



The team

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 Emmanuelle Jeannot
 Caroline Hego-Garnier
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NGS Platform: Sylvain Baulande

Genomics facility: David Gentien

PathEx: Anne Vincent-Salomon

CANCER-ID Partners



EFPIA



Clinical sites



Academic institutions



Prof. Klaus Pantel

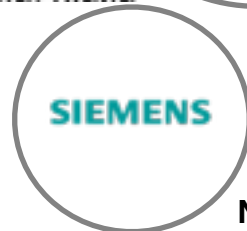
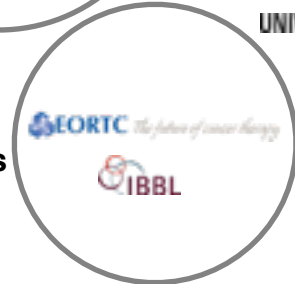


Prof. Leon Terstappen



SMEs

Non-profit organizations



Non-EFPIA/
non-SME

32 partners:

- 6 EFPIA companies (lead Bayer, co-lead Menarini)
- 17 academic/clinical sites
- 6 SMEs
- 2 non-profit organizations
- 1 non-SME/non-EFPIA

