Molecular Testing and Targeted Therapy

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Services
H. Lee Moffitt Cancer Center

July 10, 2014,

Protocol Support Committee Workshop





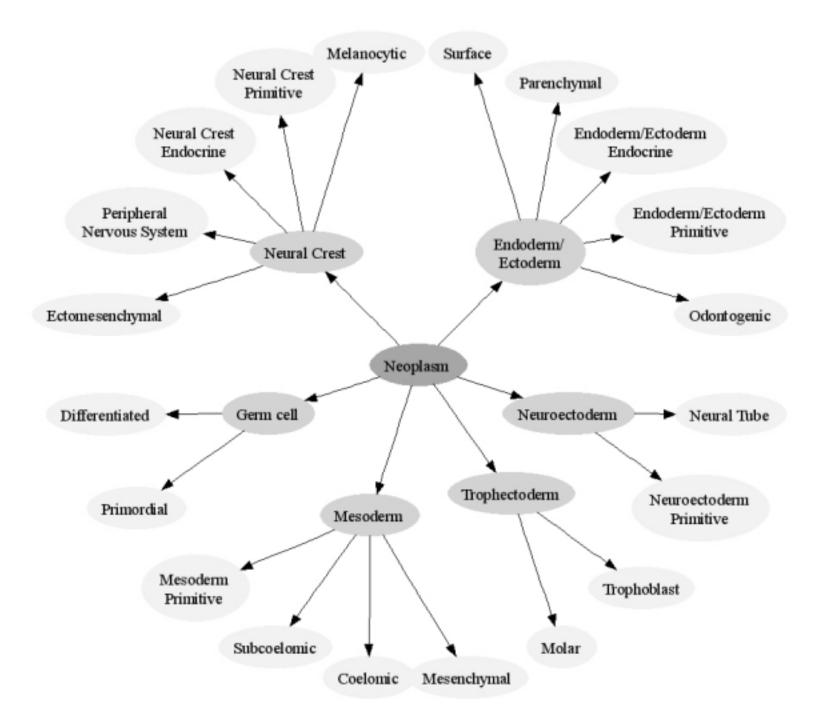
Molecular Testing

- Technologies
 - IHC
 - FISH
 - DNA / Next Generation technologies
 - Circulating Tumor Cells and CF DNA analysis
- Role in clinical trials
 - Molecular classification of cancer
 - Targeted therapies







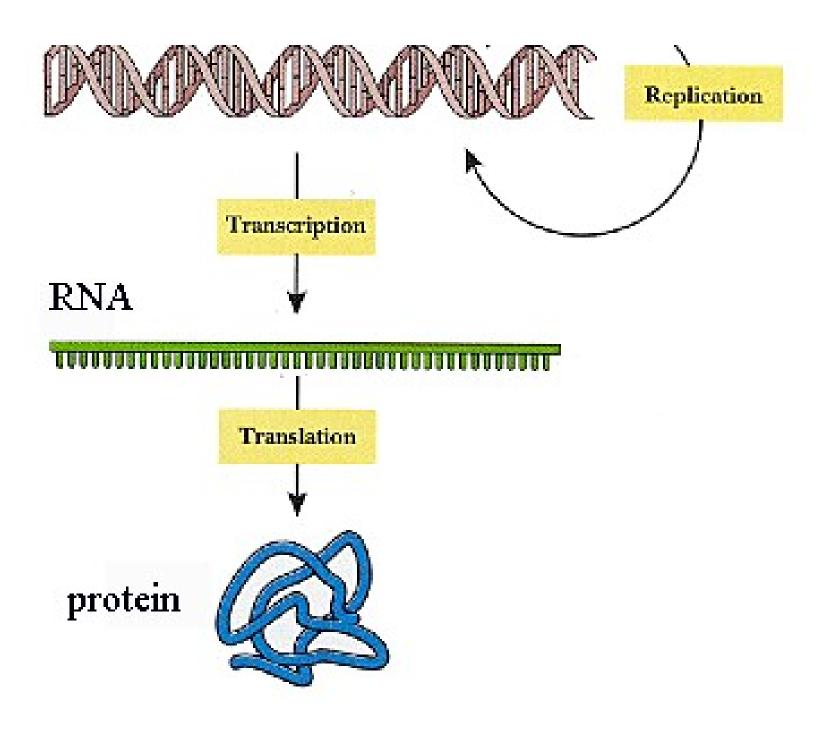


Microscopes

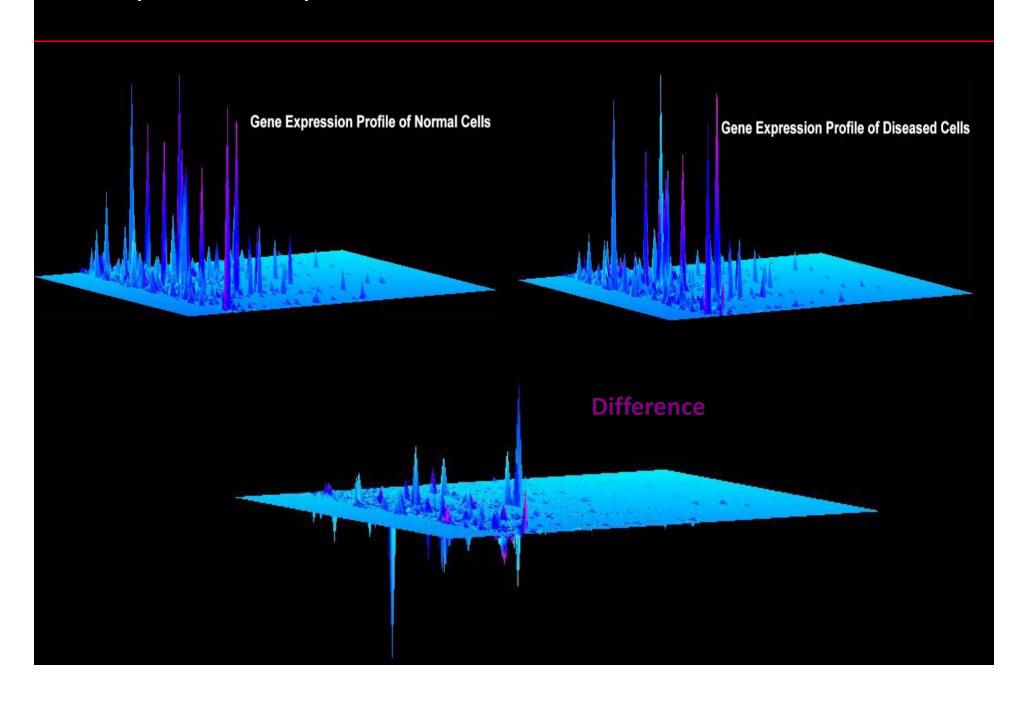


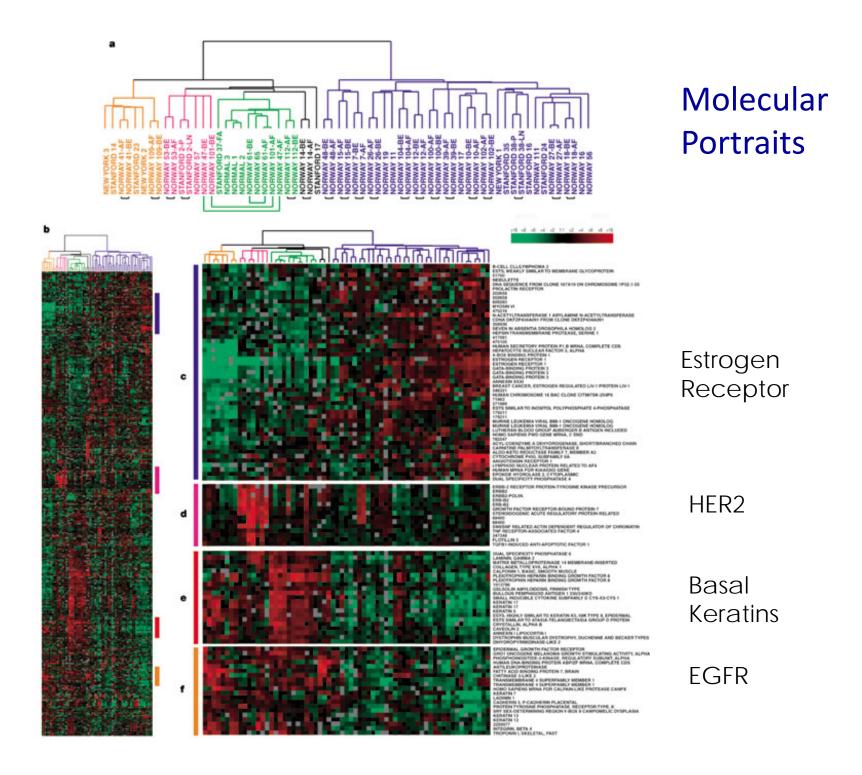
Antony van Leewenhoek (1632-1723).





Comparison of the Expression Profile of Entire Genomes





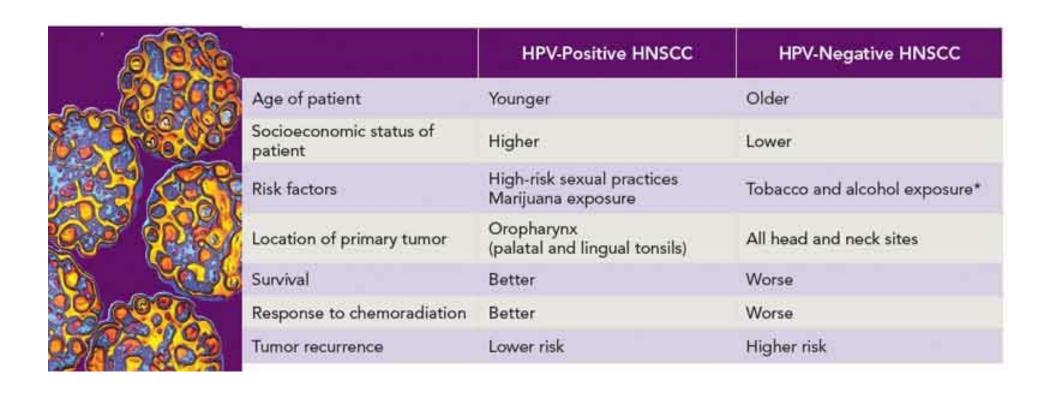


Table 1 Comparison of HPV-positive and HPV-negative head and neck cancers

	HPV-positive	HPV-negative
Incidence	Increasing	Decreasing
Age	Younger	Older
Gender	3:1 men	3:1 men
Risk factors	Sexual behavior	Tobacco, alcohol
Cofactors	Marijuana, immunosuppression	Diet, oral hygiene
Molecular genetics findings	P16 ↑	P16 ↓
	Rb ↓	Rb ↑
	P53 wild-type	P53 mutated
Anatomic site	Lingual and palatine tonsils	All sites
Pathologic findings		
Primary	Basaloid	Keratinized
Lymph node metastasis	Cystic	Solid
Survival	Better	Worse

High-Risk Human Papillomavirus Affects Prognosis in Patients With Surgically Treated Oropharyngeal Squamous Cell Carcinoma

Lisa Licitra, Federica Perrone, Paolo Bossi, Simona Suardi, Luigi Mariani, Raffaella Artusi, Maria Oggionni, Chiara Rossini, Giulio Cantù, Massimo Squadrelli, Pasquale Quattrone, Laura D. Locati, Cristiana Bergamini, Patrizia Olmi, Marco A. Pierotti, and Silvana Pilotti

J Clin Oncol 24:5630-5636. @ 2006 by American Society of Clinical Oncology

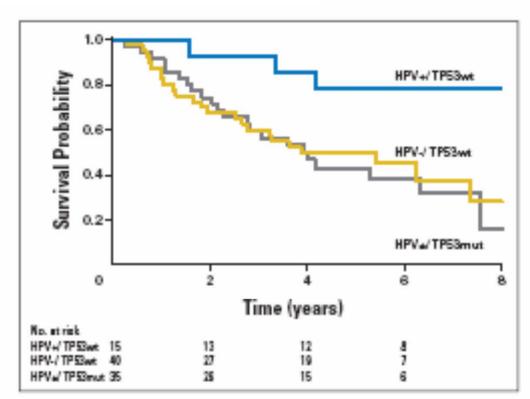


Fig 1. Overall survival according to human papillomavirus (HPVVTP53 status, mut, mutated; wt, wild type.

90 surgical pts 64% post op RT

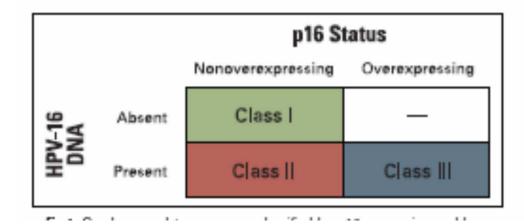
HPV 16 – 18 by PCR E2 and E6 TP53 gene sequence p16INK4a gene p16 immunohistochemistry

Molecular Classification Identifies a Subset of Human Papillomavirus-Associated Oropharyngeal Cancers With Favorable Prognosis

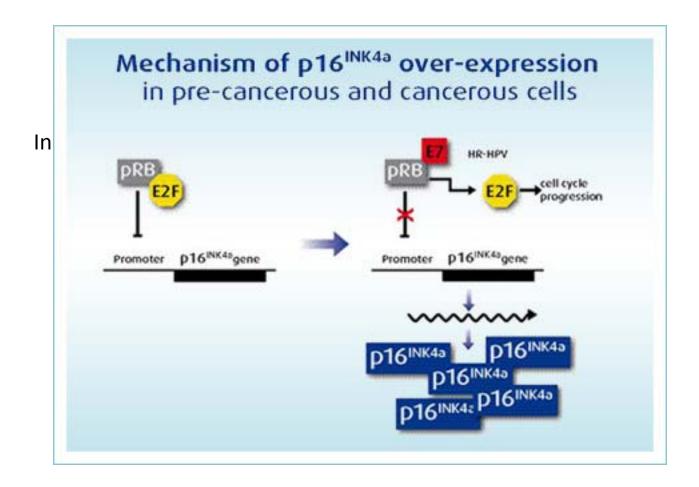
Paul M. Weinberger, Ziwei Yu, Bruce G. Haffty, Diane Kowalski, Malini Harigopal, Janet Brandsma, Clarence Sasaki, John Joe, Robert L. Camp, David L. Rimm, and Amanda Psyrri

Conclusion

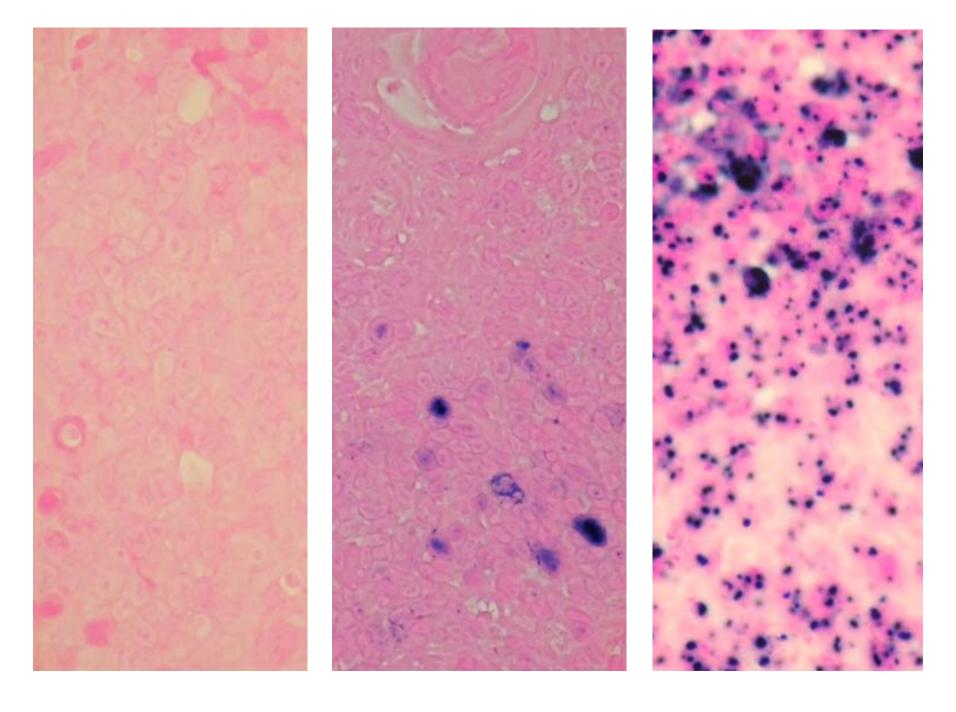
Using this system for classification, we define the molecular profile of HPV+ OSCC with favorable prognosis, namely HPV+/p16 high (class III). This study defines a novel classification scheme that may have value for patient stratification for clinical trials testing HPV-targeted therapies.



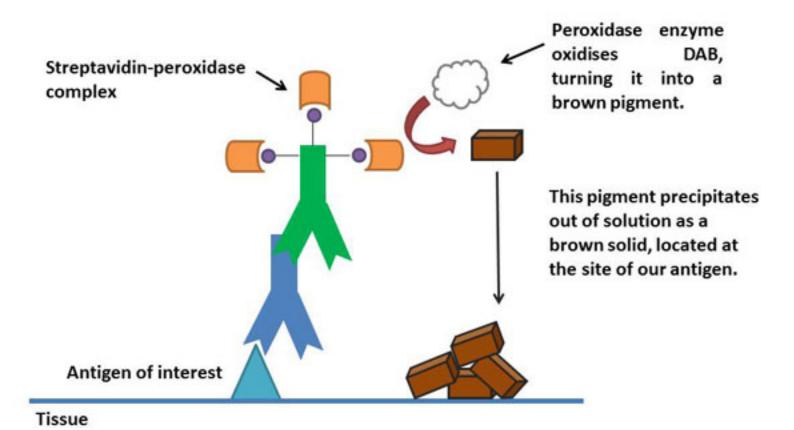
Antibody Target	Species	Туре	Dilution	Company	Identifier
RЬ	Mouse	Monodonal	1:50	NeoMarkers*	Clone 1F8
p63	Mouse	Monodonal	1:100	DAKOt	Clone DO7
p16	Mouse	Monodonal	1:25	DAKO	k5334



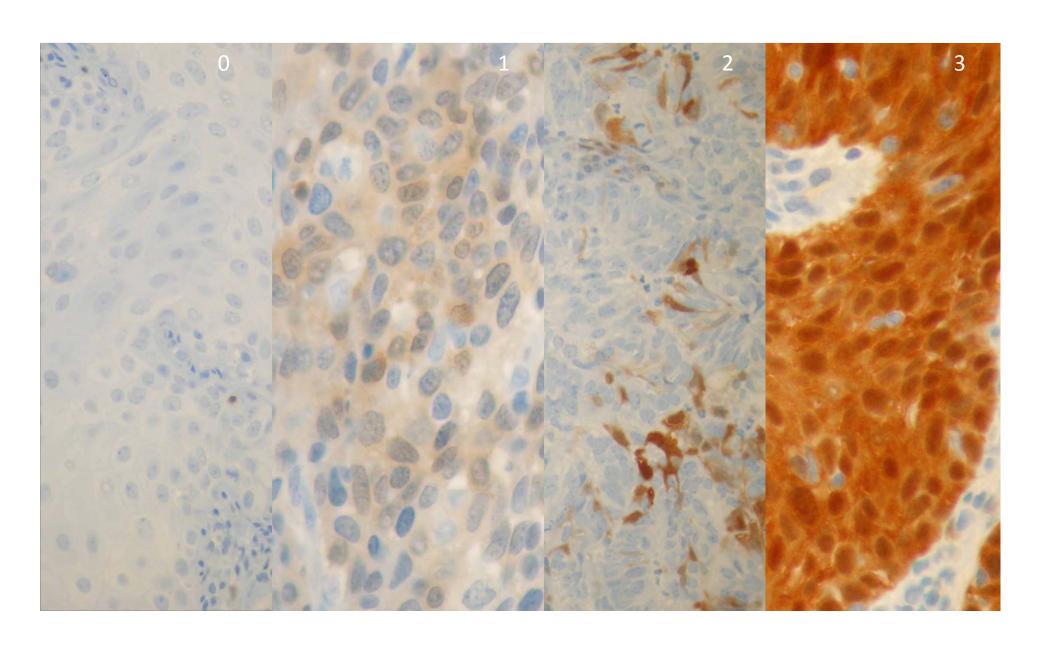
HPV in situ

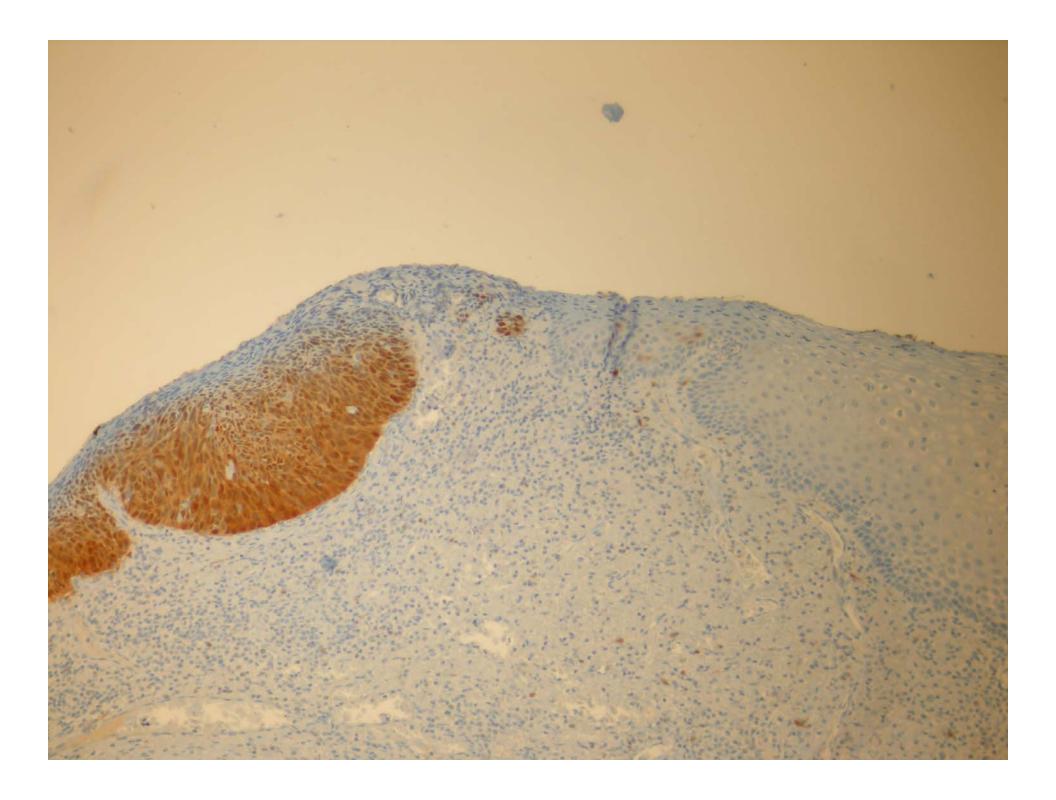


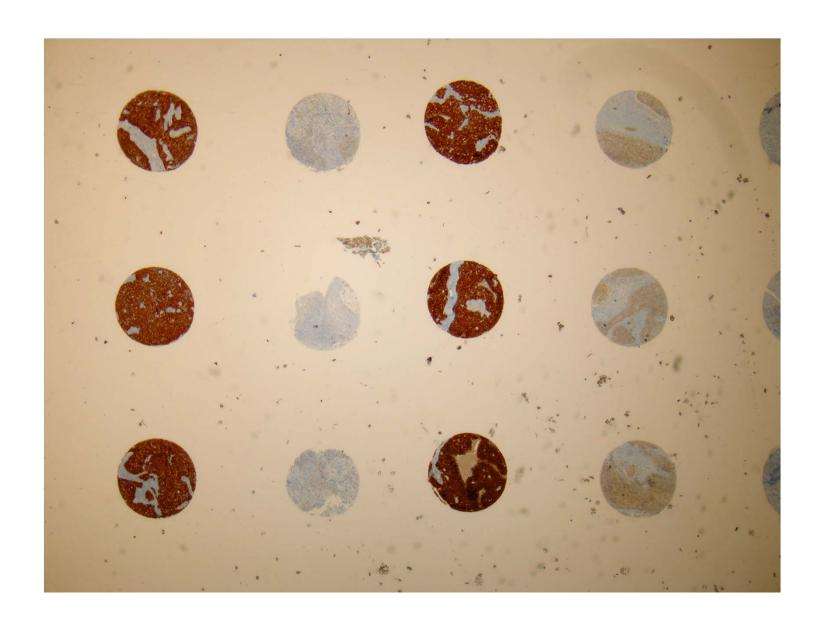
IMMUNOHISTOCHEMISTRY



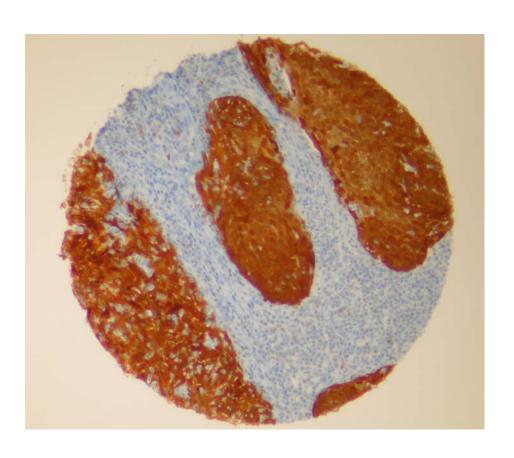
P16 IHC Invasive Cervical Carcinoma

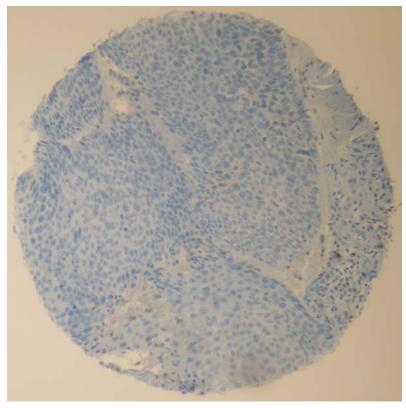


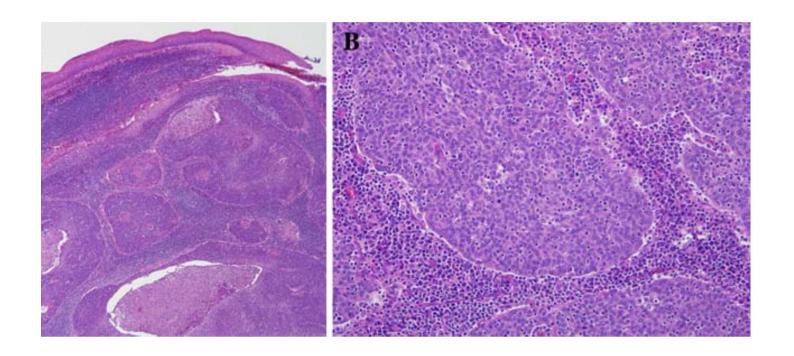




P16 Head and Neck







TBCC patient cohort

P16 status	P16 positive N=29	P16 negative N=26
Median Age	52	62
Male: Female	24 : 5	21:5
Primary Site		
Oral Cavity	0	1
Oropharynx	21	7
Hypopharynx	3	6
Larynx	1	12
Unknown	4	0
Stage II	1	2
III	1	9
IV	23	15
X	4	0
Smoking Status		
Never	11	2
Prior	7	9
Current	11	15
% CR	28 (97%)	20 (77%)

TBCC patient cohort

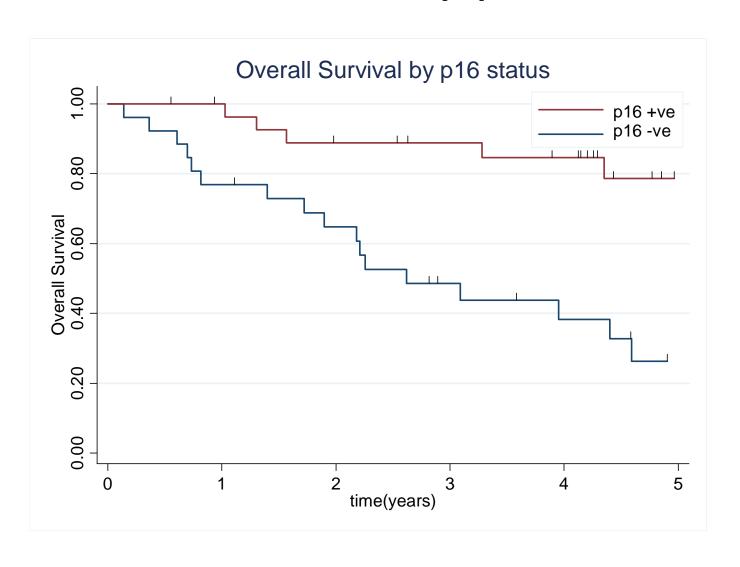
p16 status	P16+ve N=29 52 (± 8)		P16-ve N=26 62 (± 8)		p-value
Mean Age (±SD)					<0.0001
Stage IV at diagnosis	24	83%	15	58%	0.04
Never smokers	11	38%	2	8%	0.008
Oropharyngeal Primary	21	72%	7	27%	<0.0001

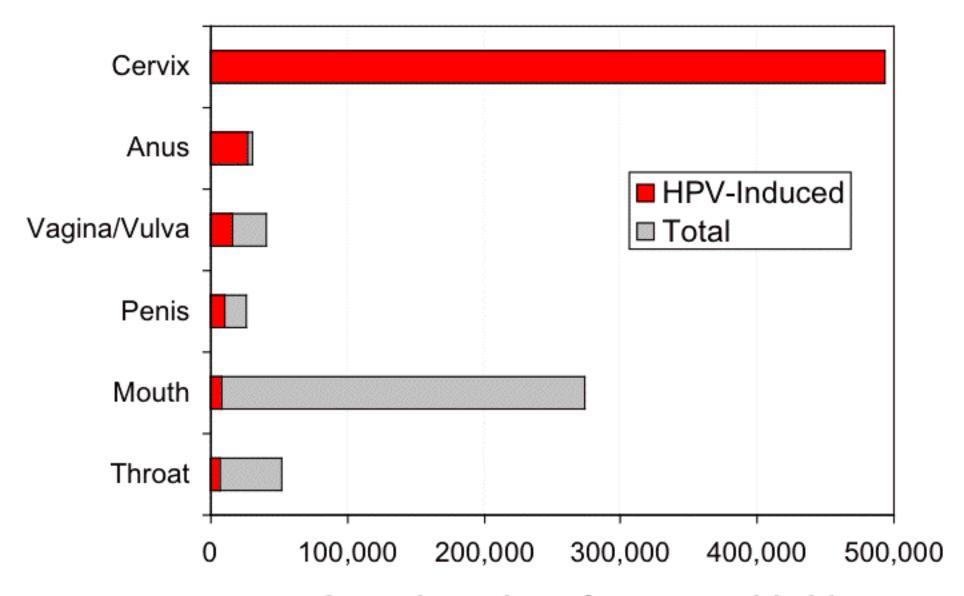
TBCC cohort: results

p16 status	P16+ve N=29	P16-ve N=26	p-value
Overall survival*	79%	26%	<0.0001
Disease-specific survival*	91%	34%	<0.0001
Locoregional recurrence	11%	60%	<0.0001

^{*5-}year survival rate; median follow-up 38 months (range 3 - 85months)

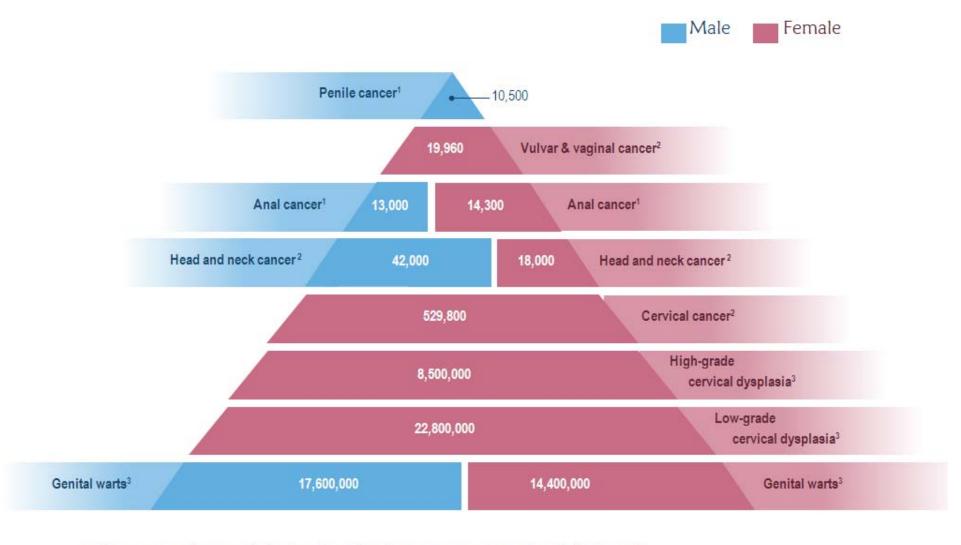
Overall Survival by p16 status





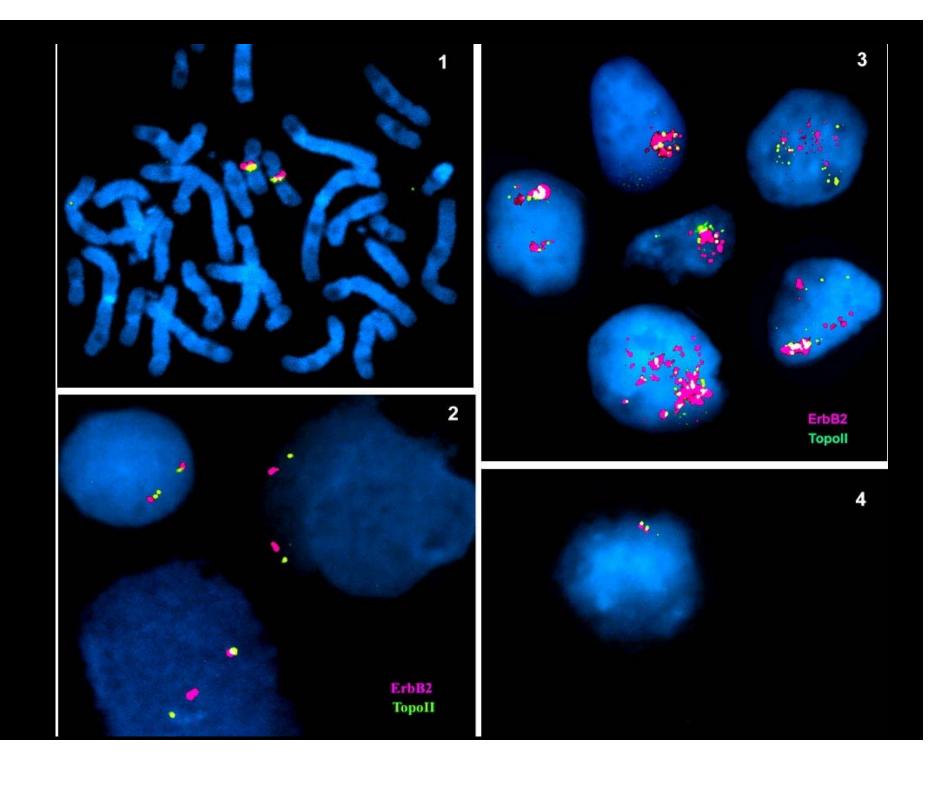
Annual number of cases worldwide

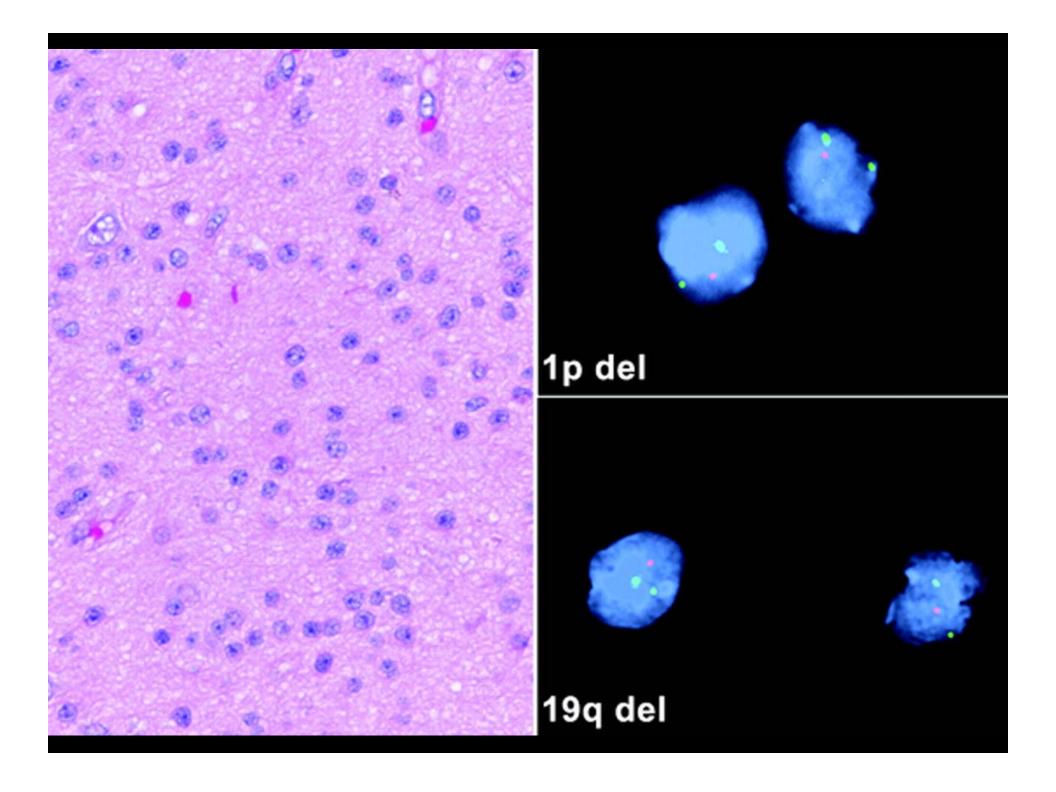
Estimated annual new HPV-related disease cases in males and females globally

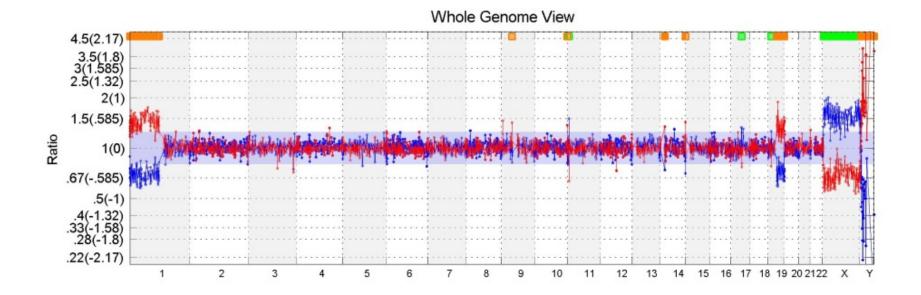


Glioma- Use of FISH for Prognosis

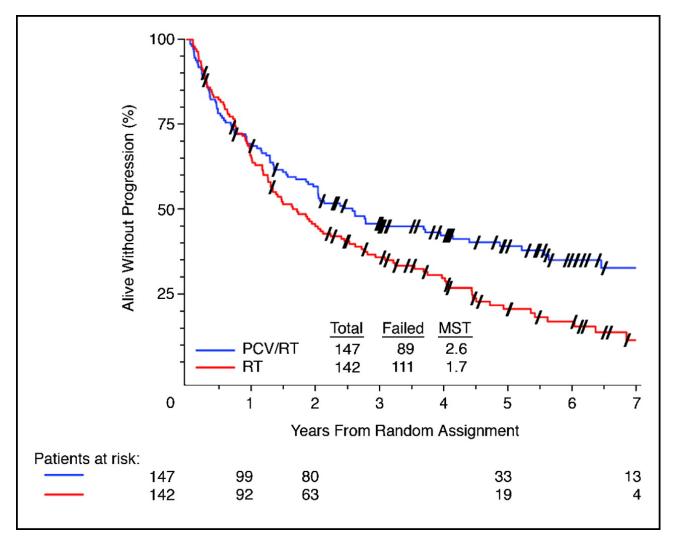
Insert diagram of FISH Procedure





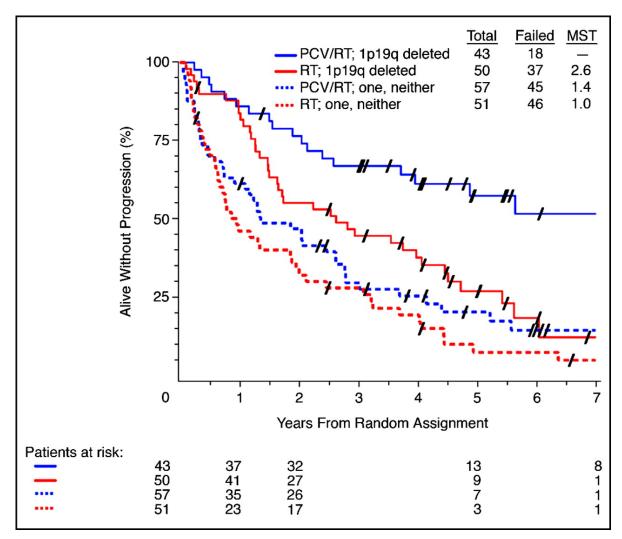


Kaplan-Meier estimates of progression-free survival by treatment group.



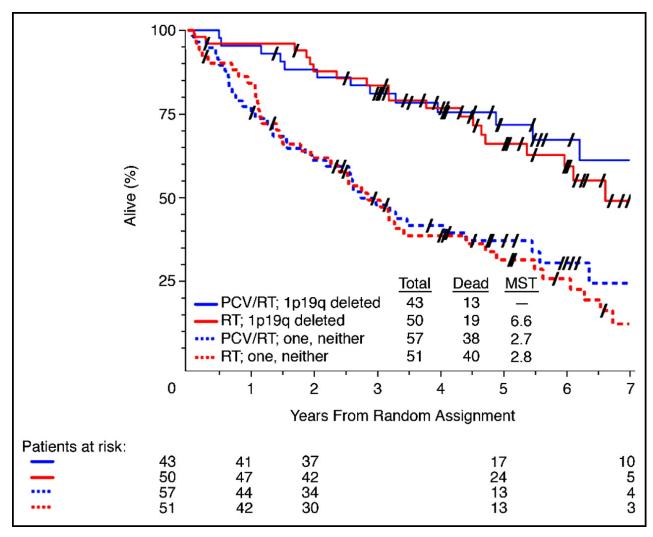
Cairncross G et al. JCO 2006;24:2707-2714

Kaplan-Meier estimates of progression-free survival by treatment and genotype.



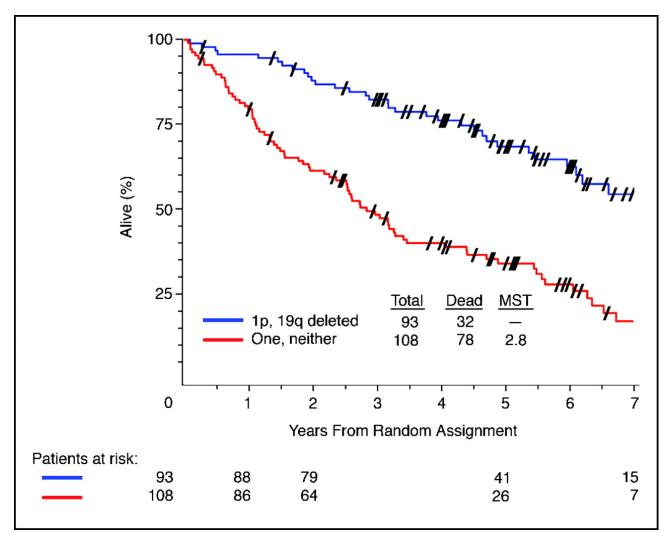
Cairncross G et al. JCO 2006;24:2707-2714

Kaplan-Meier estimates of overall survival by treatment and genotype.



Cairncross G et al. JCO 2006;24:2707-2714

Kaplan-Meier estimates of overall survival by 1p and 19q deletion.



Cairncross G et al. JCO 2006;24:2707-2714

Next Generation Sequencing





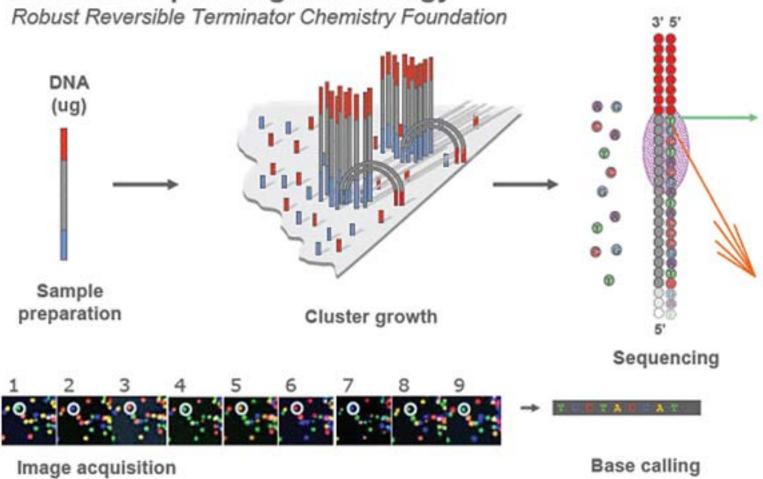


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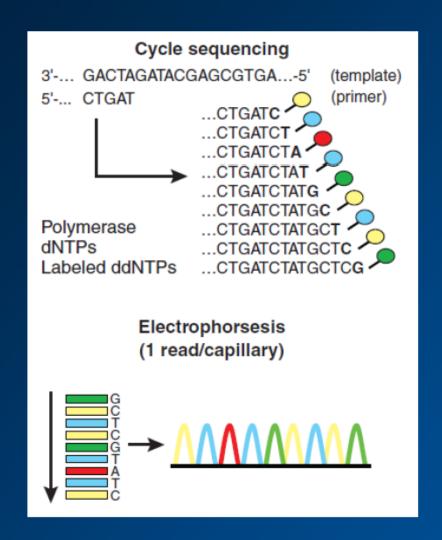
MiSEQ

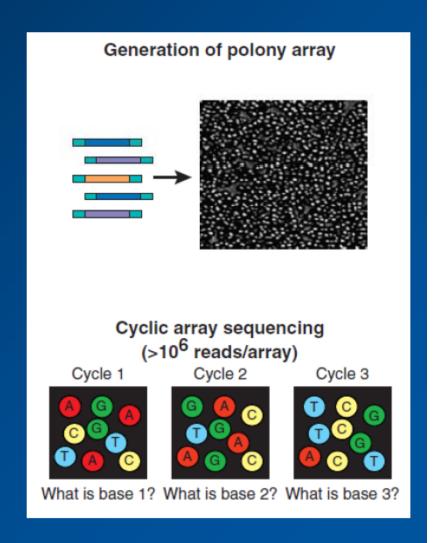


Illumina Sequencing Technology



Sanger vs Next Generation Sequencing





Illumina Genome Analyzer

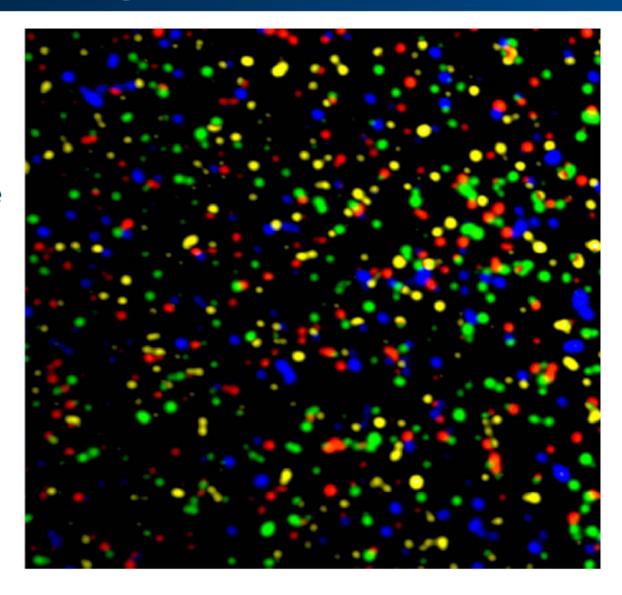
Compiled Image

A lacksquare

Т

C

G ^O



Flow Cell Clusters

Qualitative and Quantitative Information

GCCACCGCGGTGCACCGCCCGACCTCGTGGTGTCCGCCGGGTTTATGAAGATTCTTGGACCGCAGTTCCTTTCGCAGTTC-TTGGGCCGCG GCCACCGCGGTGCACCGCCCCGC GCCACCGCGGCGCACCGCCCCGACC GCCACCGCGTGCACCGCCCCGACCTCGTT GCCACCGCGTGCACCGCCCGACCTCGTTG GCCACCGCGTGCACCGCCCGACCTCGTTG GCCACCGCGTGCACCGCCCGACCTCGT--TGTC CCACCGCGGTGCACCGCCCGACCTCGTTGTCTCCG CCGCGGTGCACCGCCCGACCTCGTTGTCTCCGCCG CGCGGTGCACCGCCCGACCTCGTTGTCTCCGCCGG GGTGCACCGCCCGACCTCGTTGTCTCCGCCGGATT TGCACCGCCCGACCTCGTTGTCTCCGCCGGATTTA C-CCGCCCGACCTCGTTGTCTCCGCCGGATTTATGA C-CCGCCCGACCTCGTTGTCTCCGCCGGATTTATGA GACCTAGTTGTCTCCGCCGGATTTATGAAGATTCTT ACCTCGTTGTCTCCGCCGGATTTATGAAGATTCTTG CCTCGTTGTCTCCGCCGGATTTATGAAGATTCTTGG CGCGTTGTCTCCGCCGGATTTATGAAGATTCTTGGA CTCGTTGTCTCCGCCGGATTTATGAAGATTCTTGGA TCGTTGTCTCCGCCGGATTTATGAAGATTCTTGGAC CGTTGTCTCCGCCGGATTTATGAAGATTCTTGGACC CGTTGTCTCCGCCGGATTTATGAAGATTCTTGGACC GTTGTCTCCGCCGGATTTATGAAGATTCTTGGACCG GTTGTCTCCGCCGGATTTATGAAGATTCTTTGACCG TTGTCTCCGCCGGATTTATGAAGATTCTTGGACCGC TGTCTACGCC GGAT TATGAAGATTCTTGGACCGCA TCTCCGCCGGAT TTATGAAGATTCTTGGACCGCAGT CGCCGCC GGAT TATGAAGATTCTTGGACCGCAGTT CTCCGCCGGATTTATGAAGATTCTTGGACCGCAGTT CTCCGCCGGATTTATGAAGATTCTTGGACCGCAGTT CCGCCGGAT TTATGAAGATTCTTGGACCGCAGTTCC CGCC GGAT TTATGAAGATTCTTGGACCGCAGTTCCT

Ref Seq

Coverage or number of reads

Next Generation Sequencing: Steps in Workflow

Analytical Wet Bench Process: sample handling, library preparation, sequence generation



Bioinformatics process:
Alignment, variant calling, and variant annotation



Clinical Interpretation

The Cost of Genome Sequencing is Decreasing Rapidly and Driving Clinical Adoption of Genomic Analysis

Cost per Genome Data Generation, Sep 2001 - Oct 2011



Cost for genome sequence data generation today is <\$3,000

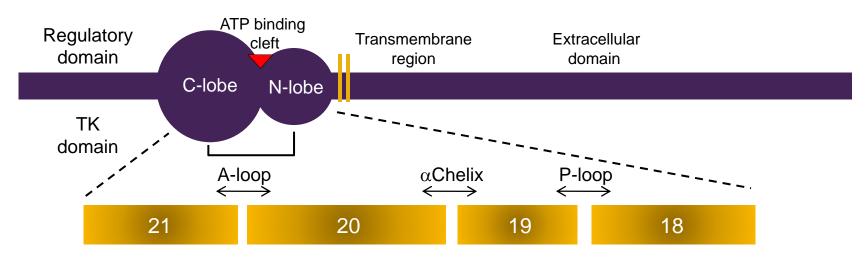
New Clinical Molecular Testing

EGFR as an Example

The significance of EGFR activating mutations

- The EGFR is a transmembrane receptor
- Somatic mutations in the kinase domain increase activity of the EGFR
 - EGFR mutations are 10-15% of cases in North America and Western Europe, but 30%-40% in East Asian
 - Mutations are associated with adenocarcinoma and bronchoalveolar histology
 - Mutations are also observed more frequently in women and non-smokers with NSCLC

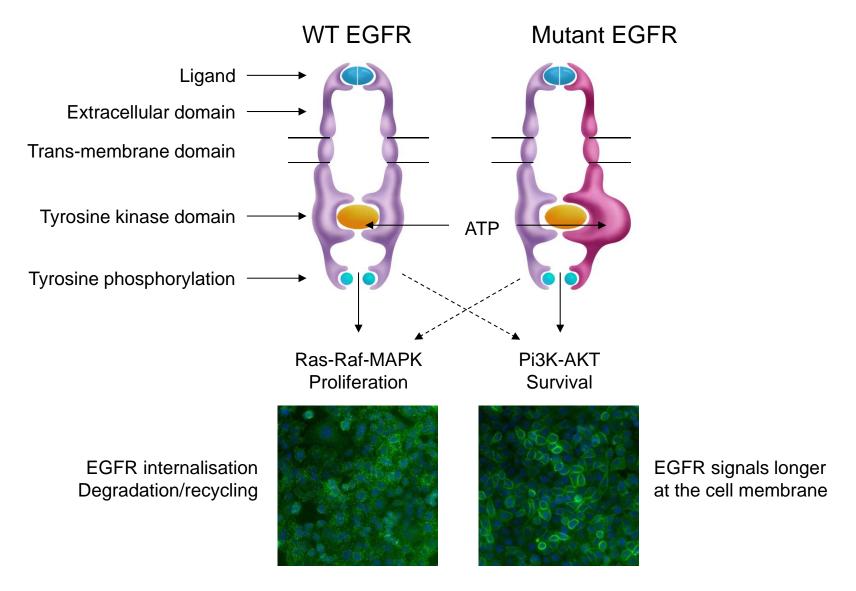
The distribution of activating mutations among EGFR mutation positive patients is similar in Asian and Non Asian studies



Distribution of mutation types (% of mutations)		
Literature review	Asian studies	Non-Asian studies
Most prevalent mutation types	Literature (n=1523)	Literature (n=583)
Exon 19 deletion	51%	58%
Exon 21 point mutation L858R	42%	32%
Exon 20	2%	6%
Exon 18 G719A/C	3%	2%
Exon 21 L861Q	1%	1%

Some patients had more than one mutation type

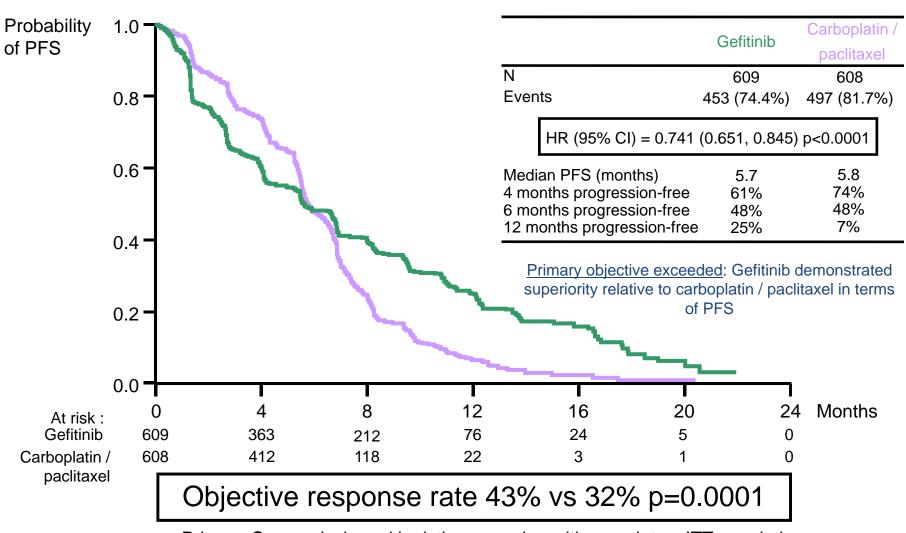
Mutation status causes conformational change and increased activation



The IPASS Trial

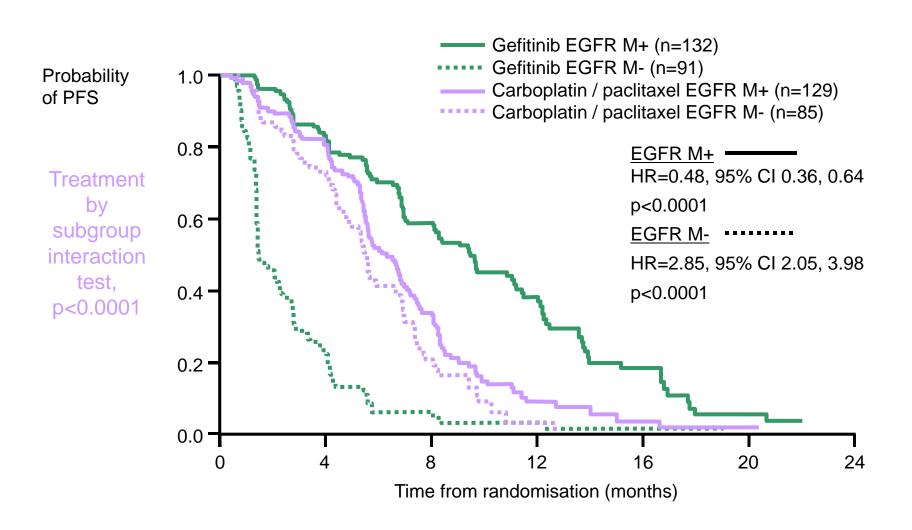
The Phase III IRESSA Pan-Asia Study (IPASS) compared the efficacy, safety and tolerability of IRESSA vs. carboplatin/paclitaxel in clinically selected chemonaïve patients in Asia with advanced non-small-cell lung cancer (NSCLC).

IPASS: Superior PFS and ORR with gefitinib vs doublet chemotherapy; PFS effect not constant over time

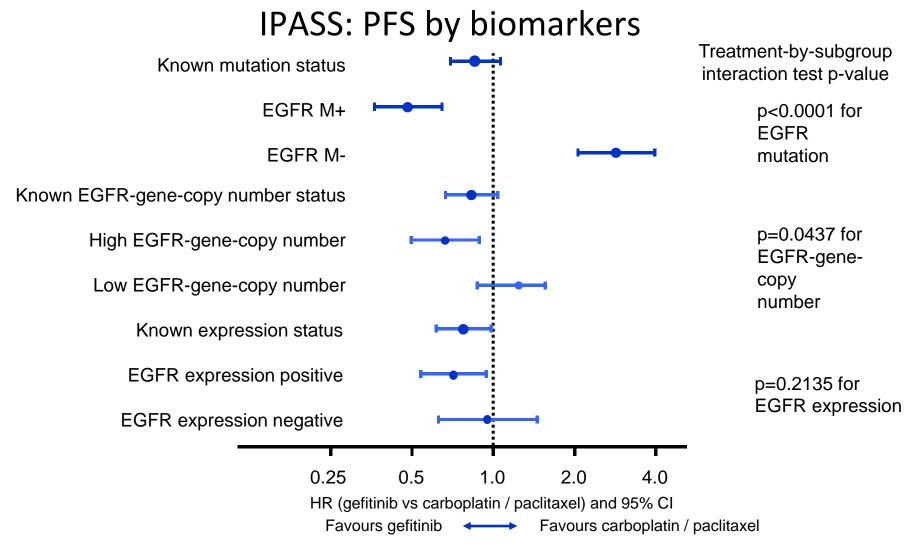


Primary Cox analysis and logistic regression with covariates; ITT population HR <1 implies a lower risk of progression on gefitinib

IPASS: EGFR mutation is a strong predictor for differential PFS benefit between gefitinib and doublet chemotherapy



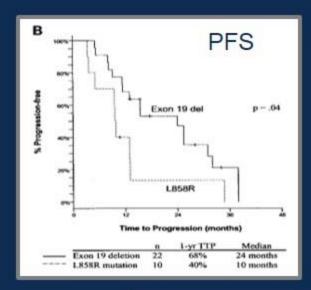
M+, mutation positive; M-, mutation negative

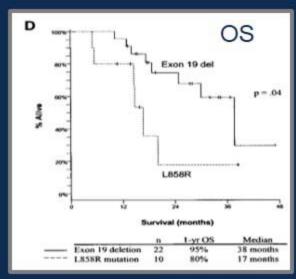


ITT population; Cox analysis with covariates; HR <1 implies a lower risk of progression on gefitinib

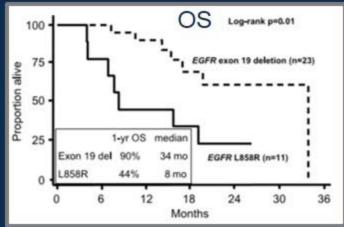
Differences in Efficacy of Gefitinib/ Erlotinib: Exon 19 Del vs. L858R

Jackman, Clin Cancer Res, 2006





Riely, Clin Cancer Res, 2006





Clinical factors that independently predict EGFR mutation status in Caucasian patients

Analysis in Caucasian patients (INTEREST, INVITE, ISEL, INTACTs and IDEALs combined [n=786])

- Smoking status p<0.0001
 - Odds of mutation <u>6.5</u> times higher in <u>never-smokers</u>
- **Histology** p<0.0001
 - Odds of mutation <u>4.4</u> times higher in <u>adeno</u>
 than non-adeno
- **Gender** p=0.0397
 - Odds of mutation <u>1.7</u> times higher in <u>females</u>
 than males

Other factors tested: Age (<65yrs, ≥ 65 yrs), WHO PS (0-1, \ge 2) Overall EGFR mutation positive rate 9.5%

Summary

- EGFR mutation status is the most robust predictive biomarker of clinical benefit in NSCLC
- EGFR mutation status is predictive irrespective of ethnicity
 - Incidence rates may differ, but response rates do not
- Clinical characteristics can not be used to determine EGFR mutation status but may be helpful in determining who to test

Types of Biomarkers

Prognosis

Who needs extra treatment?

Prediction

What Treatment?

Toxicity

Who should avoid Treatment?

Level of Evidence

Level 1

- prospective, high power, specifically addressing utility of marker in question
- meta analysis of several small studies

• Level 2

- Clinical Trial companion study in which marker is also evaluated
- Level 3
 - performed on assembly of cases taken for other reasons

Integral Markers in Trials

- Marker is used to make a CLINICAL DECISION
 - Assignment to a specific treatment
 - le Kinase mutation
 - -Witholding treatment
 - le Low risk prognostically

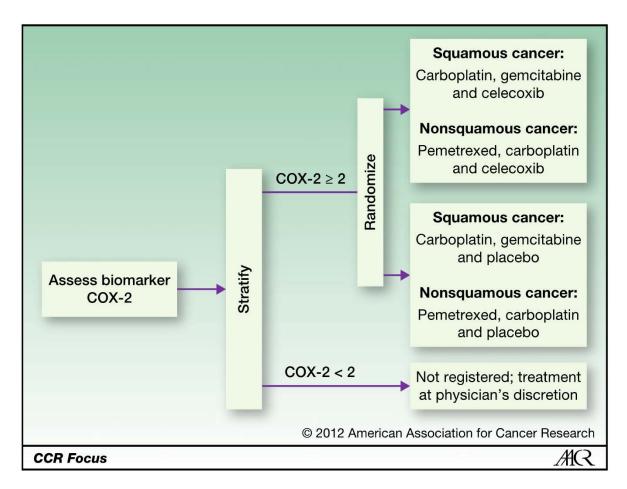
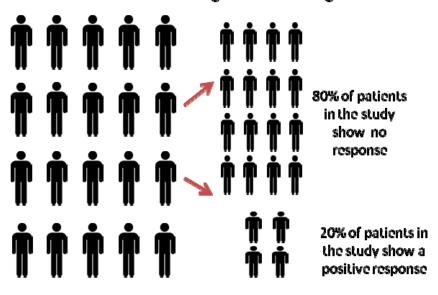


Figure 1. CALGB-30801. Randomized phase III trial for stage IIIB or IV NSCLC (adenocarcinoma, large cell, squamous, or mixture). The trial will allow evaluation of the cut point for the COX-2 assay.

Typical Drug Development Example

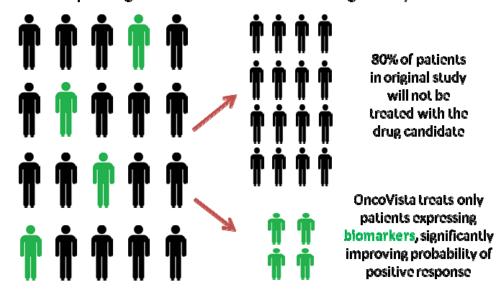
A pharmaceutical company performs trials on patients who have identical cancer diagnosis with a drug candidate



Efficacy below minimum threshold, drug is abandoned

Targeted Drug Development Example

OncoVistalicenses a drug candidate & identifies patients expressing biomarkers correlated with drug efficacy



Efficacy exceeds minimum threshold, OncoVista has a viable drug candidate

Personalized medicine-The Goal



FDA, CLIA, and Assays



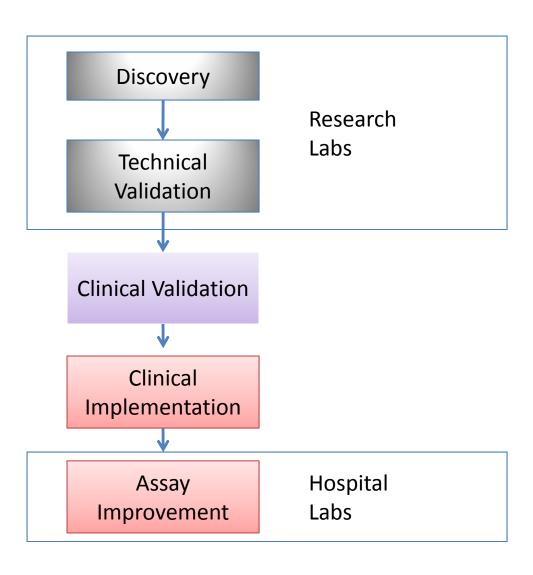
- FDA Approved
- FDA Cleared



LDTs (Laboratory Developed Assays)

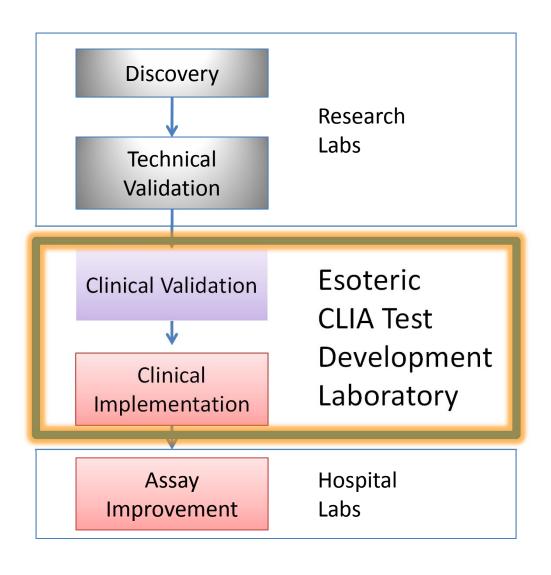


Development of a Clinical Assay



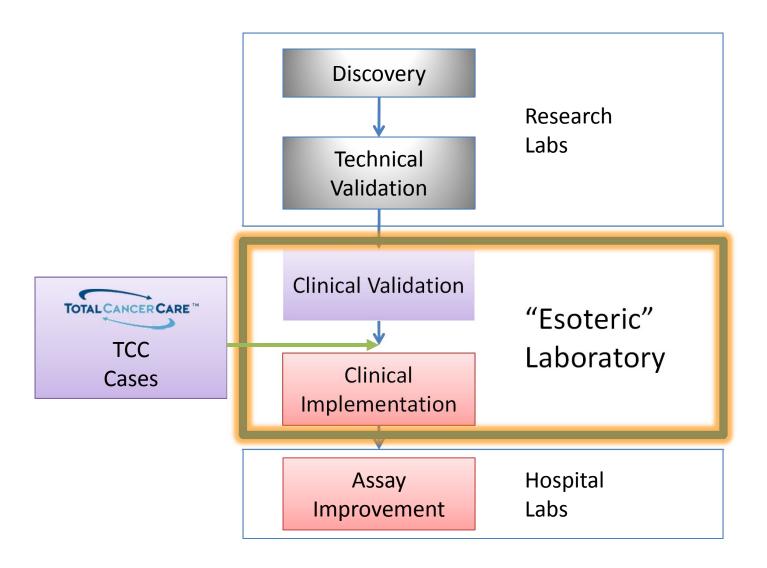


Product Cycle of Biomarker

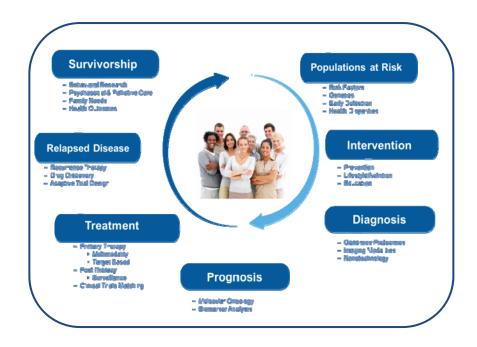




Product Cycle of Biomarker



Vision of Total Cancer Care



- Identify the needs of the patient & their families
- Develop an evidence-based approach to meet those needs
- Develop markers to predict need so they can be prevented

The TCC Protocol



The Total Cancer Care TM Protocol

- May we follow you throughout your lifetime?
- May we study your tumor using molecular technology?
- May we re-contact you?

The Total Cancer Care Protocol represents Moffitt's unique approach to Personalized Medicine, and is the foundation upon which M2Gen is built.

The TCC Consortium

M2Gen currently partners with several Consortium Sites (including Moffitt) to collect patient tissue and data



- Hartford Hospital, Hartford, CT
- St. Joseph's Candler Health System, Savannah, GA
- Greenville Hospital System, Greenville, SC
- Moffitt Cancer Center, Tampa, FL (Coordinating Site)
- Baptist Health South Florida, Miami, FL
- Martin Memorial Medical Center, Stuart, FL
- Morton Plant Mease Health Care, Clearwater, FL
- Sarasota Memorial Health Care, Sarasota, FL
- Watson Clinic Center for Research, Lakeland, FL
- Norton Healthcare, Louisville, KY
- Lehigh Valley Health Network, Allentown, PA
- Billings Clinic, Billings, MT

Total Cancer CareTM to Date

18 Consortium
Sites
(including MCC)

96,972 Consented Patients MCC (62%) Sites (38%)

34,923 Tumors Collected MCC (38%) Sites (62%) 16,226
Gene Expression
Profiles
(TCC Consented since inception)

As of May 29, 2013

Data Generated from Specimens		
CEL Files (Gene Expression Data)	16,226 files	
Targeted Exome Sequencing	4,016 samples	
Whole Exome Sequencing (Ovary, Lung, Colon)	535 samples	
Whole Genome Sequencing (Melanoma)	13 samples with normal pairs	
SNP/CNV (Lung, Breast, Colon)	559 samples	

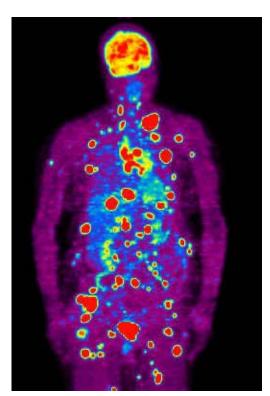
Nexus Biostore

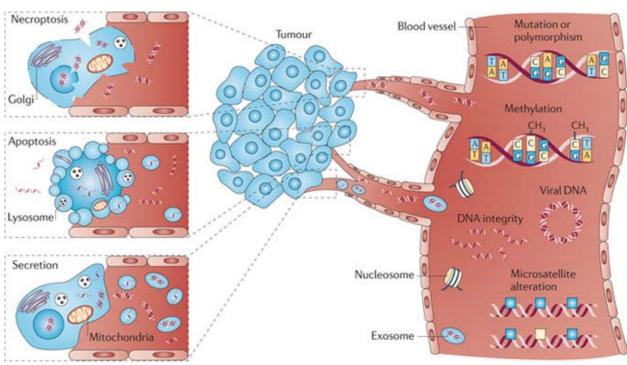


- Four unit capacity of 2.4 Million samples
- Stores samples in a -80°C environment
- Handles samples in a -20°C environment
- Retrieves samples using NEXUS proprietary
 'Cool Transition' technology
- Flexibility to accommodate a wide variety of samples, vessels and labware
- Automated 24/7 monitoring system in place
- Automated Inventory functionality provides real-time inventory tracking of stored biospecimens

CIRCULATING TUMOR CELLS

METASTASIS

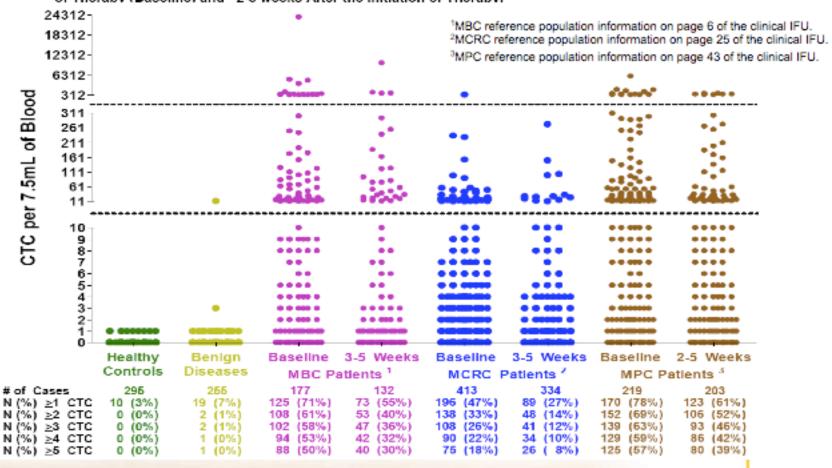




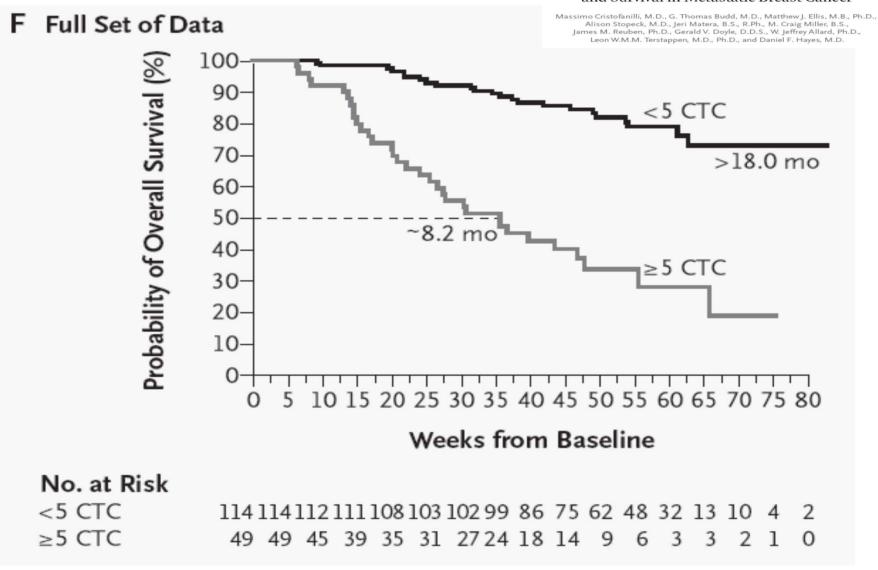
Nature Reviews | Cancer

Frequency of CTC

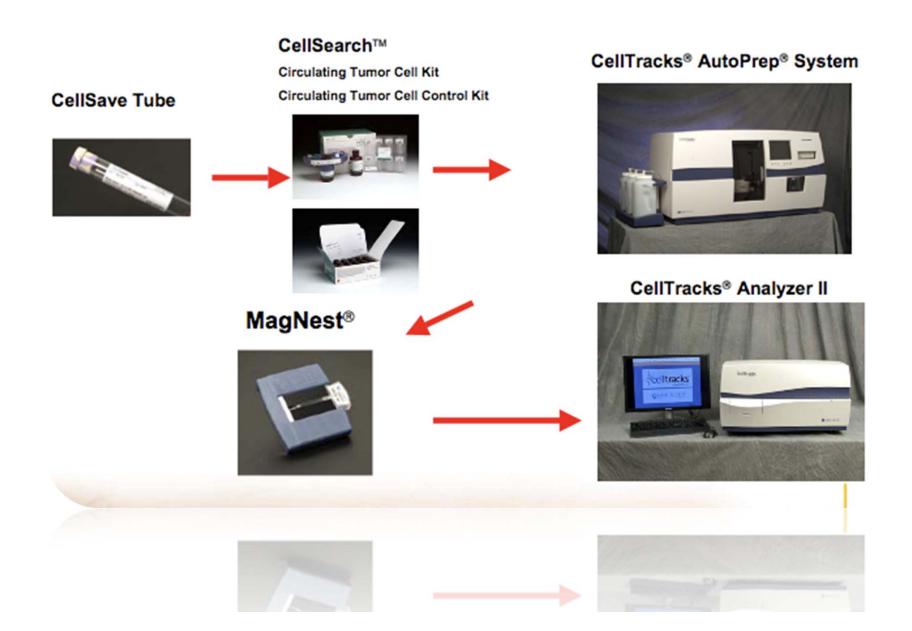
Figure 1. Frequency of CTC in Controls (Subjects without Cancer) and Patients with Metastatic Breast¹ (MBC), Metastatic Colorectal² (MCRC) or Metastatic Prostate Cancer³ (MPC) before Initiation of a new line of Therapy (Baseline) and ~2-5 weeks After the Initiation of Therapy.



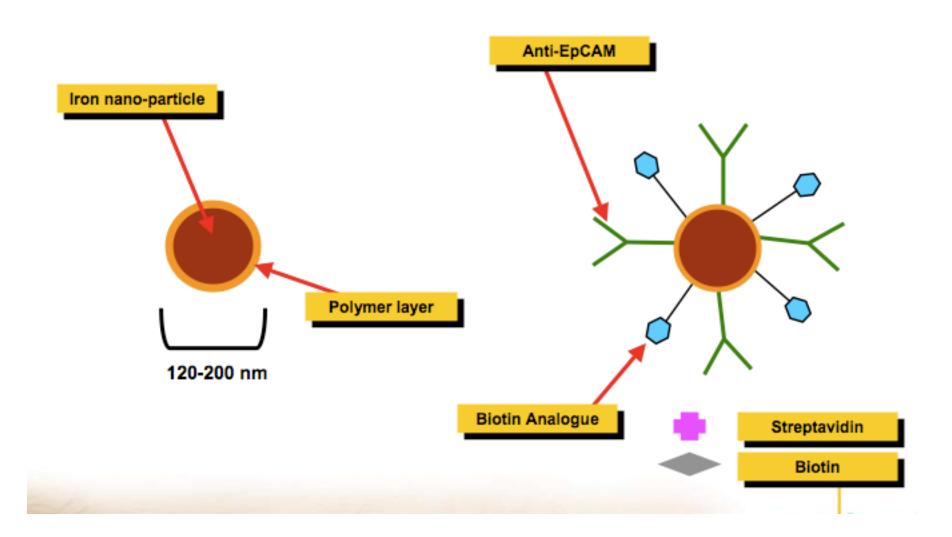
Circulating Tumor Cells, Disease Progression, and Survival in Metastatic Breast Cancer



CellSearch™ System

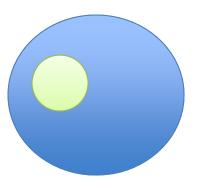


Anatomy of Ferrofluid



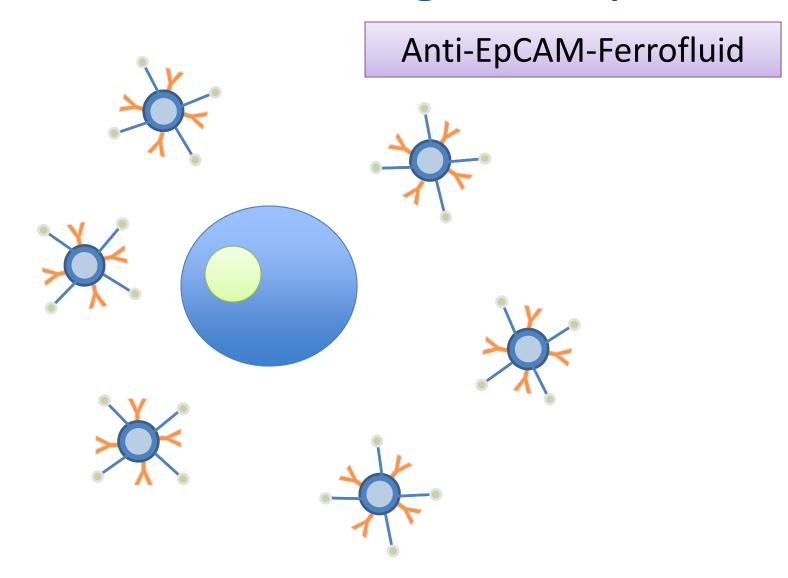
Automated Optimization of Ferrofluid Binding Activity

Circulating Tumor Cell





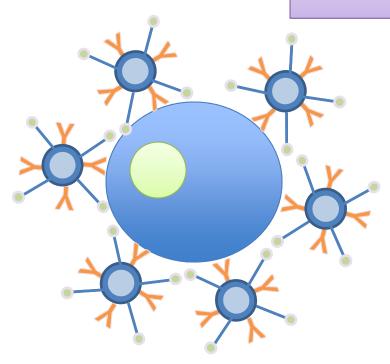
Automated Optimization of Ferrofluid Binding Activity





Automated Optimization of Ferrofluid Binding Activity

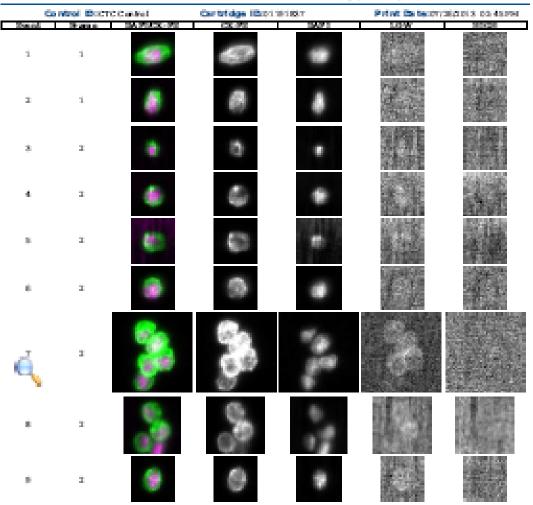
Anti-EpCAM-Ferrofluid binds to CTCs



Control HCT-116 cells

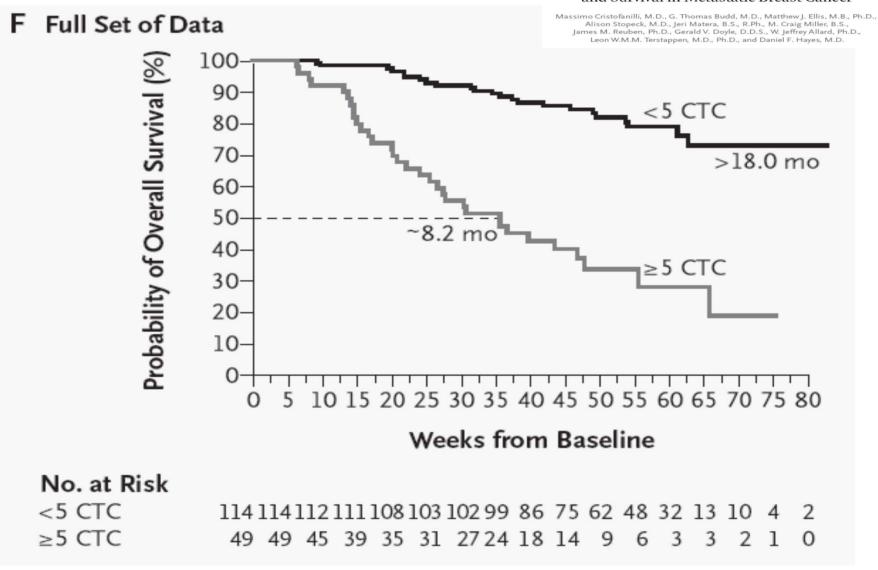


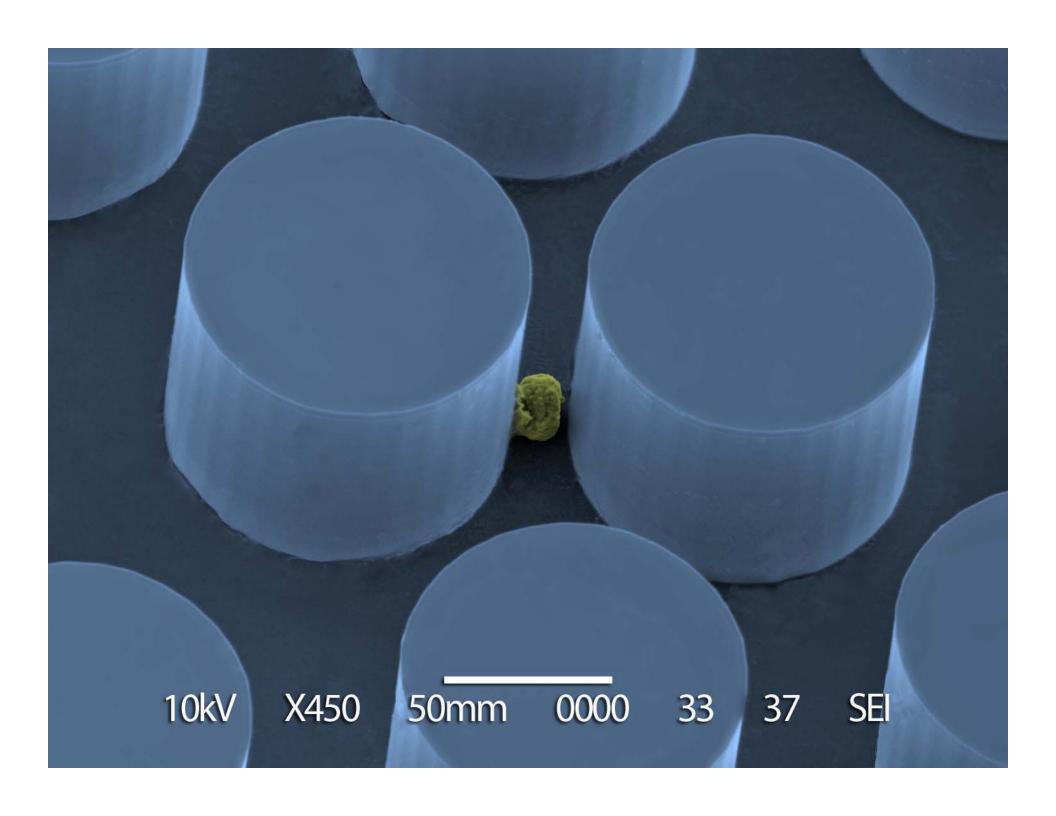
CONTROL REVIEW PRINT



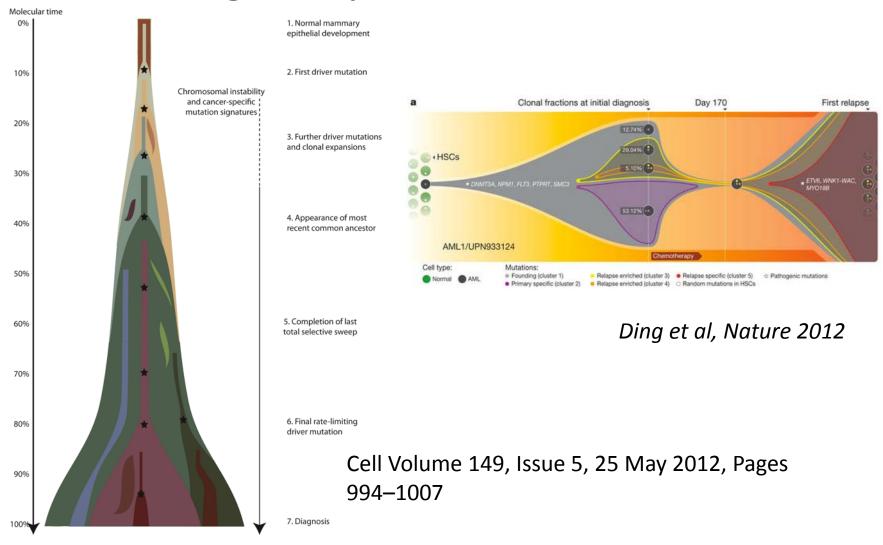
Cultured HCT-116 EpCaM+ cells were run on the Veridex/Janssen Celltracks CTC system and evaluated for CK and DAPI expression.

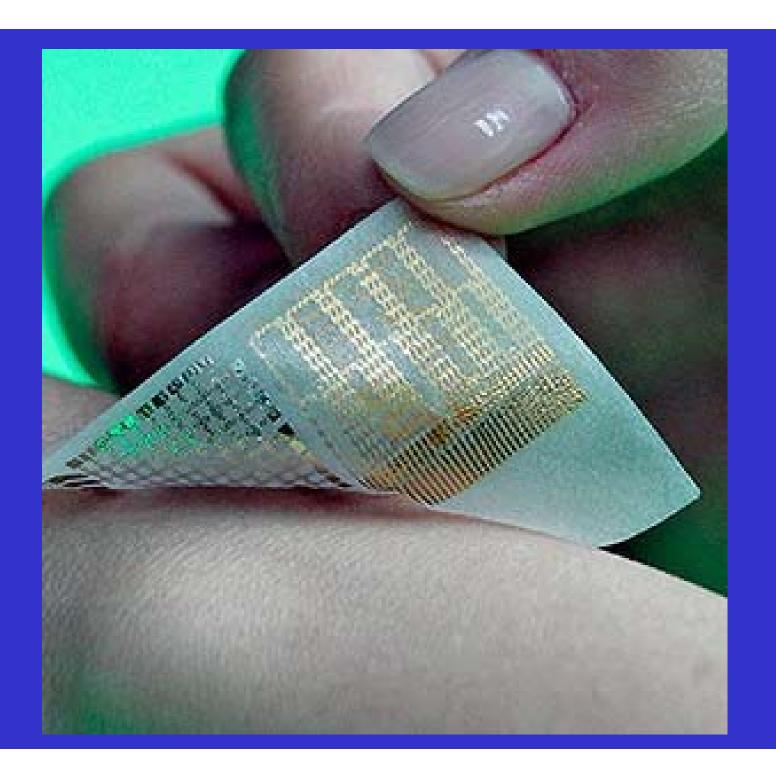
Circulating Tumor Cells, Disease Progression, and Survival in Metastatic Breast Cancer





Heterogeneity and tumor evolution



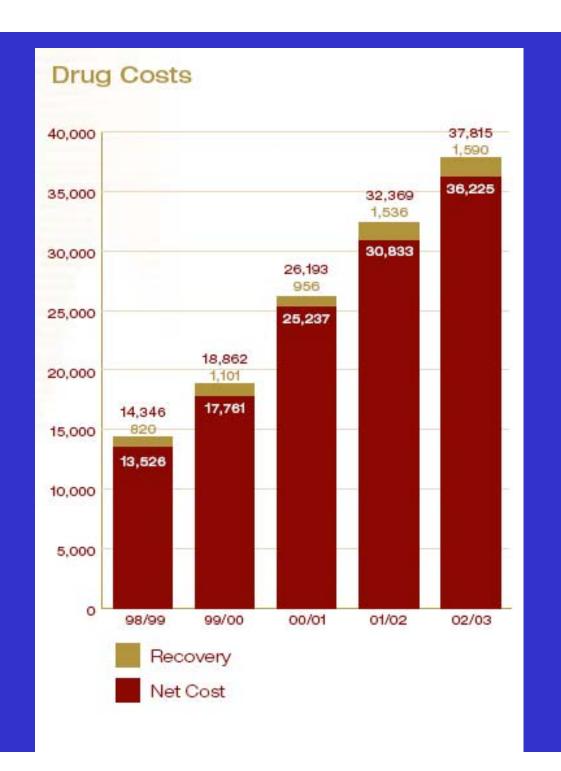


CTCs

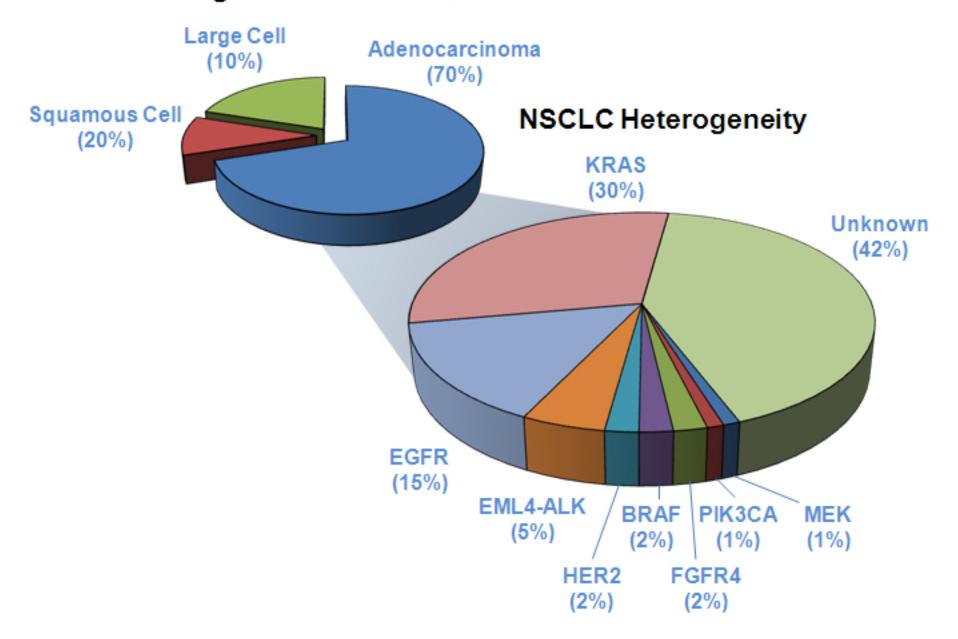
- FDA approved for Breast, Colon, Prostate
- Must be analyzed within 48 hrs
- Monitor response to therapy / early recurrence in metastatic setting
- Opportunity to use open channel- other antibody, FISH
- May be complementary to cell free serum circulating DNA studies

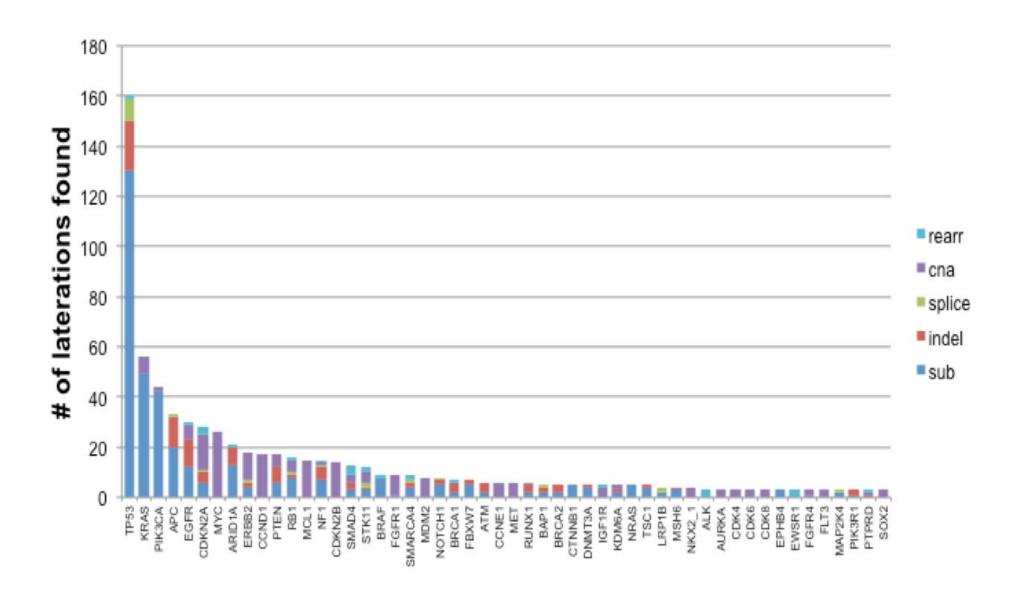
• Why do we need better biomarkers?





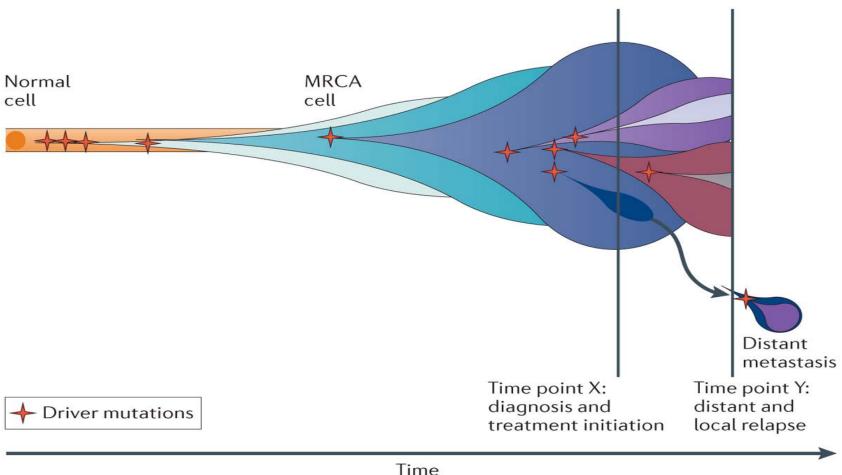
Lung Adenocarcinomas

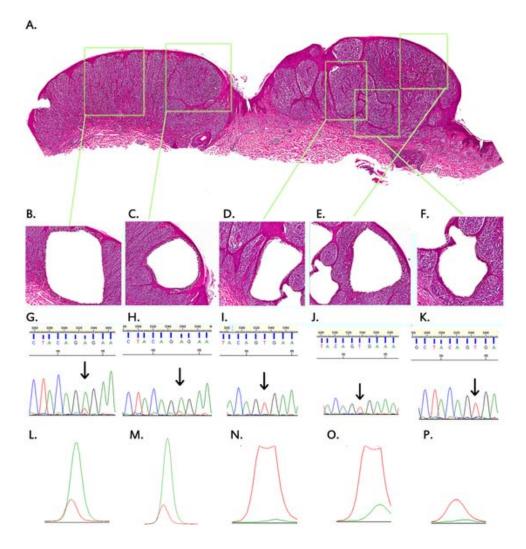






(M) Cancer Biology and Metastasis





Yancovitz M, Litterman A, Yoon J, Ng E, et al. (2012) Intra- and Inter-Tumor Heterogeneity of BRAFV600EMutations in Primary and Metastatic Melanoma. PLoS ONE 7(1): e29336. doi:10.1371/journal.pone.0029336

http://www.plosone.org/article/info:doi/10.1371/journal.pone.0029336



The Future

- Better trials based on molecular selection
- Adaptive designs
- Better monitoring

The right treatment for the right patient at the right time!