Molecular Testing for Clinical Practice

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Disclosures

- I have acted as Consultant to and/or given sponsored lectures for
- Astra Zeneca, Roche/Genetech, Eli Lilly, Pfizer, Novartis, Boehringer Ingelheim, Glaxo Smith Klein, Merck Serono, Abbott Diagnostics

The pivotal role of pathology in the management of lung cancer

Morgan R. Davidson^{1,2}, Adi F. Gazdar^{3,4}, Belinda E. Clarke^{1,5}

Revolution in Lung Cancer

New Challenges for the Surgical Pathologist

Philip T. Cagle, MD; Timothy C. Allen, MD, JD; Sanja Dacic, MD, PhD; Mary Beth Beasley, MD; Alain C. Borczuk, MD; Lucian R. Chirieac, MD; Rodolfo Laucirica, MD; Jae Y. Ro, MD, PhD; Keith M. Kerr, MD

Targ Oncol (2013) 8:1–2 DOI 10.1007/s11523-013-0265-x

EDITORIAL

Lung cancer: how to face the revolution?

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Histopathology 2012, 60, 531-546. DOI: 10.1111/j.1365-2559.2011.03854.x

REVIEW

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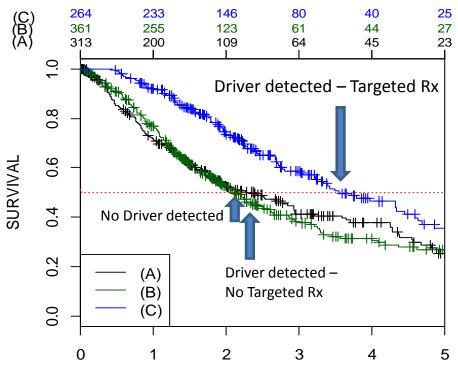
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REVIEW

Personalized medicine for lung cancer, new challenges for pathology

It is worthwhile finding an actionable genetic alteration in Lung cancer



YEARS

PRESIDENTIAL SYMPOSIUM INCLUDING TOP RATED ABSTRACTS TUESDAY, OCTOBER 29, 2013 - 08:15-09:45 WCLC, Sydney

PL03.07 TREATMENT WITH THERAPIES MATCHED TO ONCOGENIC DRIVERS IMPROVES SURVIVAL IN PATI-ENTS WITH LUNG CANCERS: RESULTS FROM THE LUNG CANCER MUTATION CONSORTIUM (LCMC)

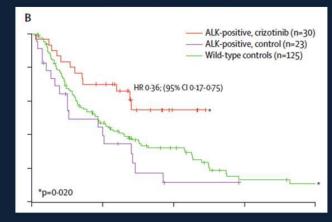
Mark G. Kris¹, Bruce Johnson², Lynne Berry³, David Kwiatkowski⁴, et al

Comparison of survival for patients with lung adenocarcinoma in Japan before and after gefitinib approval EGFR EGFR mut+patients All patients в Α MST (months) MST (months After approval 200 18.1 78 27.2 After approval Before approval 130 12.5 Before approval 58 13.6 Proportion Surviving Proportion Surviving HR = 0.66 (95% Cl. 0.52 to 0.84) HR = 0.48 (95% Cl. 0.32 to 0.71) 0.8 0.8 Log rank P < .001 Log rank P < .00" 0.6 0.6 0.4 0.4 0.2 0.2 0 0 Survival Time (years) Survival Time (years)

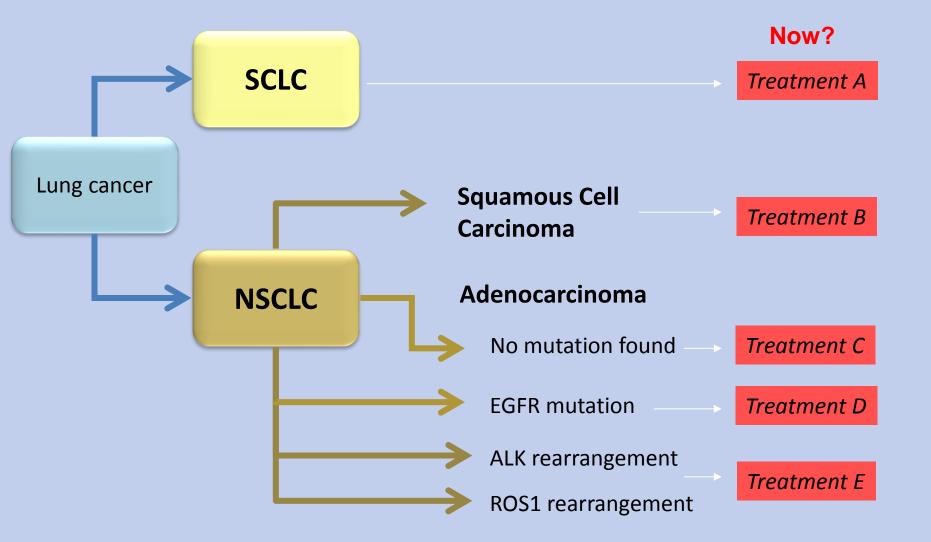
ALK

Takano, JCO 2008

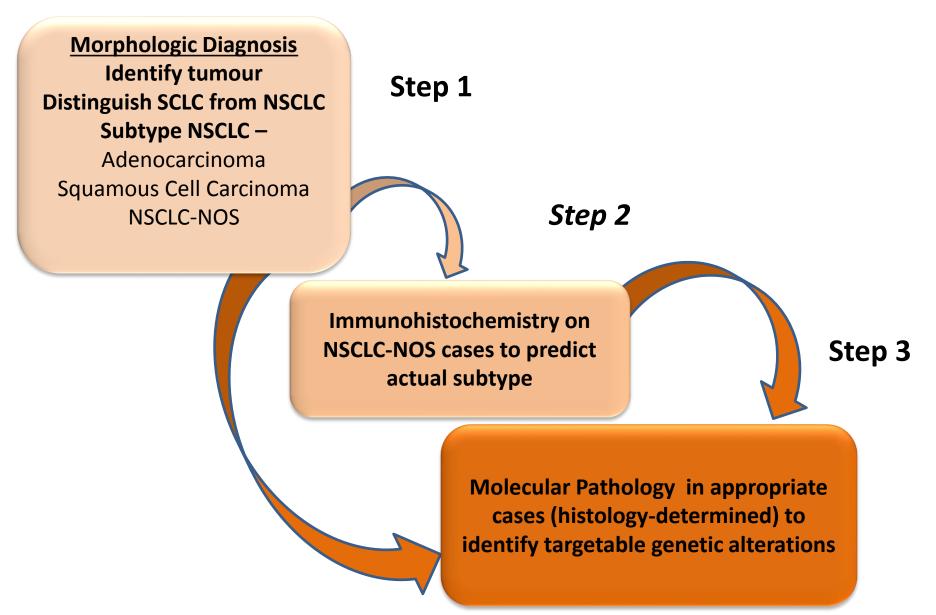
Comparison of survival for patients with lung adenocarcinoma in second line before and after crizotinib approval



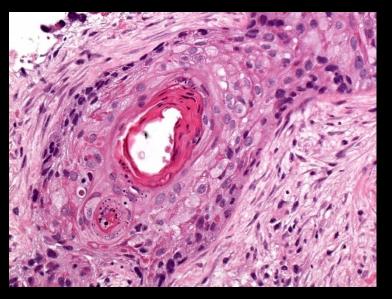
Tumour histology and genotype influences treatment in Lung Cancer



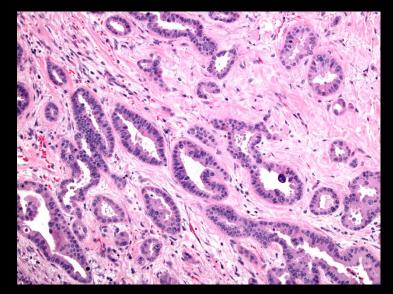
Lung Cancer Diagnosis



Squamous Cell Carcinoma

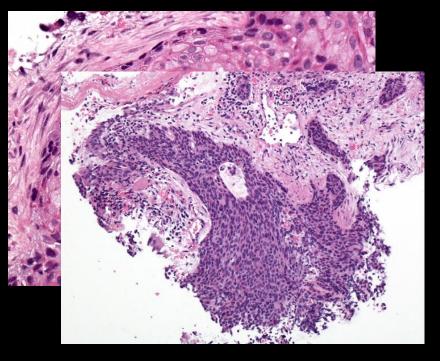


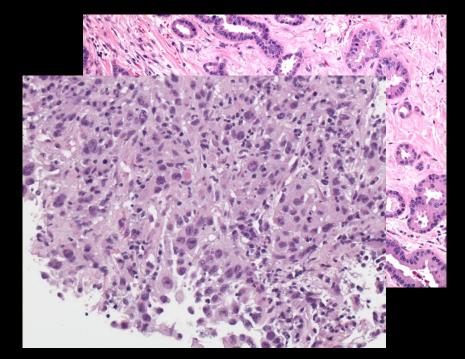
Adenocarcinoma



Histological Subtyping of NSCLC: Small sample – biopsy/cytology Adenocarcinoma

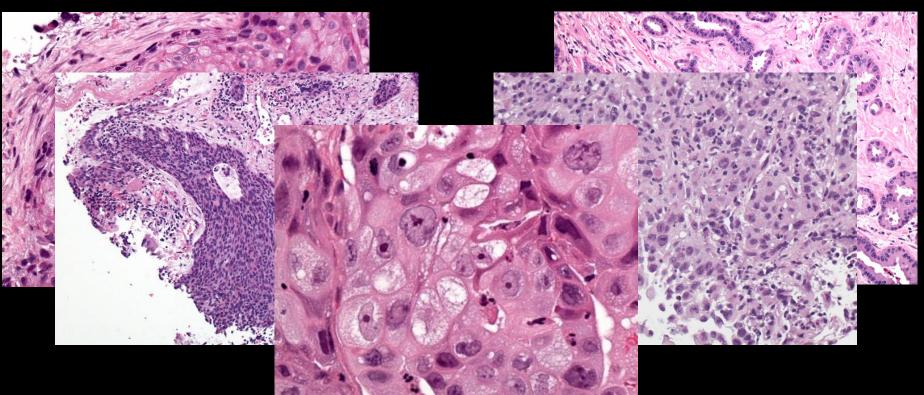
Squamous Cell Carcinoma





Squamous Cell Carcinoma

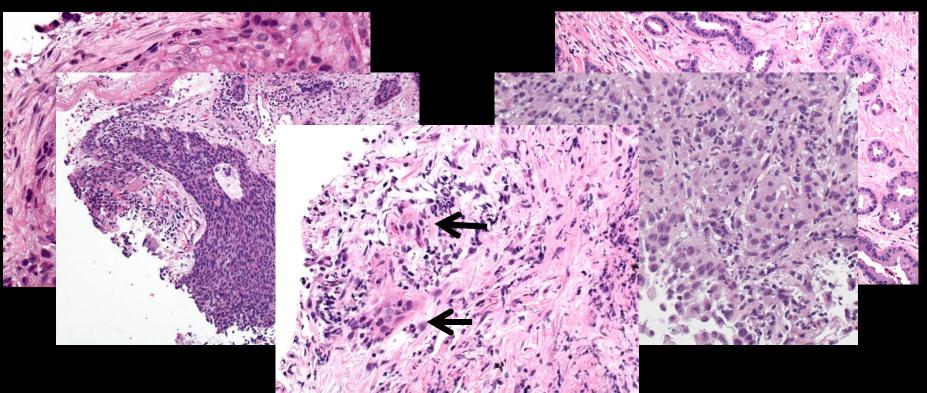
Adenocarcinoma



NSCLC-NOS

Squamous Cell Carcinoma

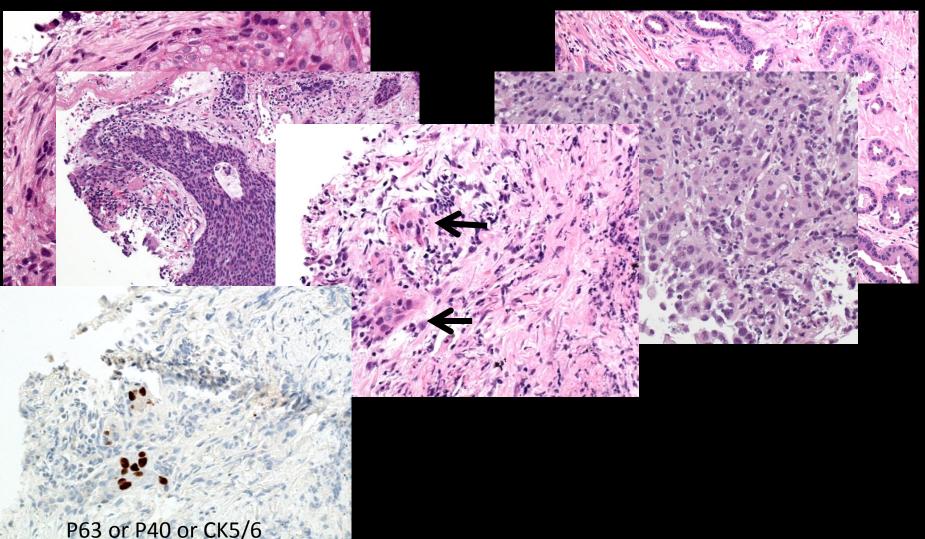
Adenocarcinoma



NSCLC-NOS

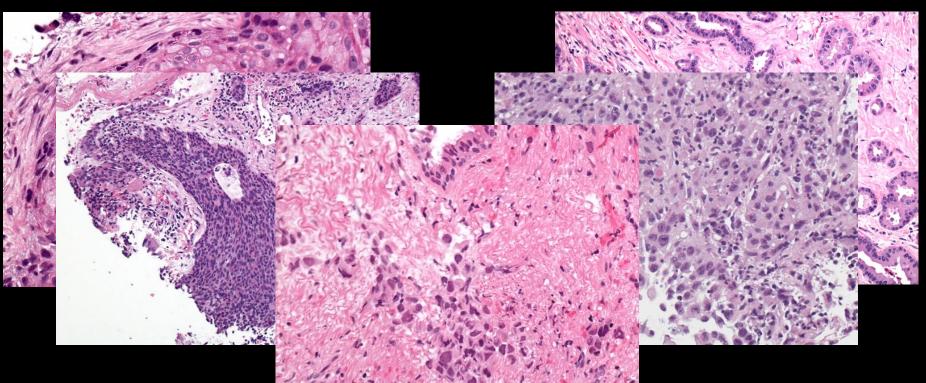
Squamous Cell Carcinoma

Adenocarcinoma



Squamous Cell Carcinoma

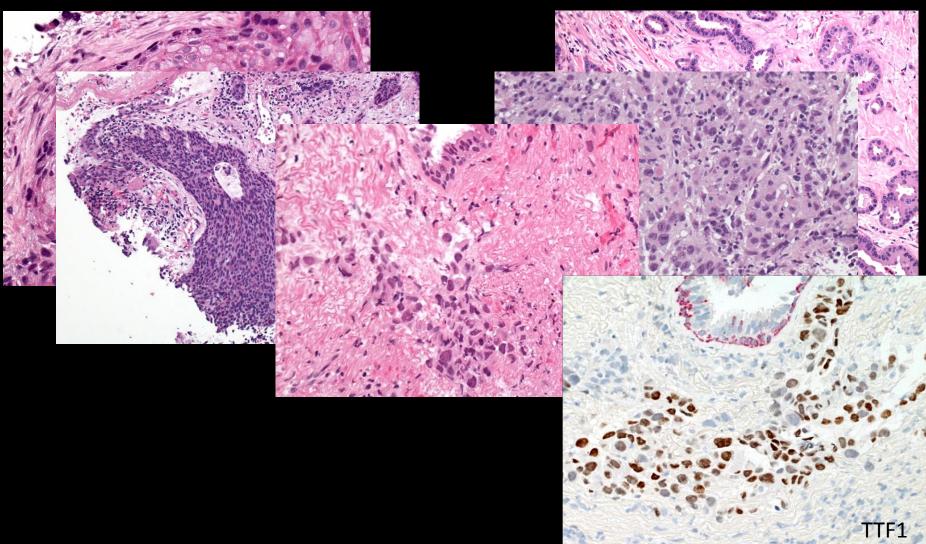
Adenocarcinoma



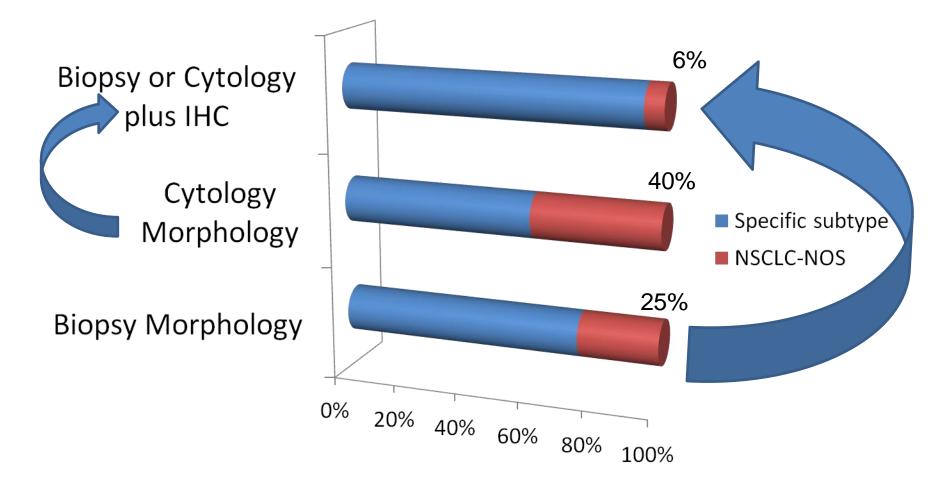
NSCLC-NOS

Squamous Cell Carcinoma

Adenocarcinoma



Subtyping NSCLC: How good?



Predictive IHC has 'levelled the playing field'
 Better diagnosis possible on poorer specimens

Morphological diagnosis in advanced NSCLC

- Squamous cell carcinoma
- NSCLC, probably squamous cell (IHC)

- Adenocarcinoma
- NSCLC, probably adenocarcinoma (IHC)

- NSCLC-NOS cannot be resolved (null IHC)
 Sarcomatoid features?
- Other specific type (carcinoid tumour, etc.)

Molecular Pathology in appropriate cases (histology-determined) to identify targetable genetic alterations

Prognostic Factors ?

Adjuvant therapy

Predictive Biomarkers?

Advanced disease

Biomarker

Target of drug

Drug target & biomarker are co-factors

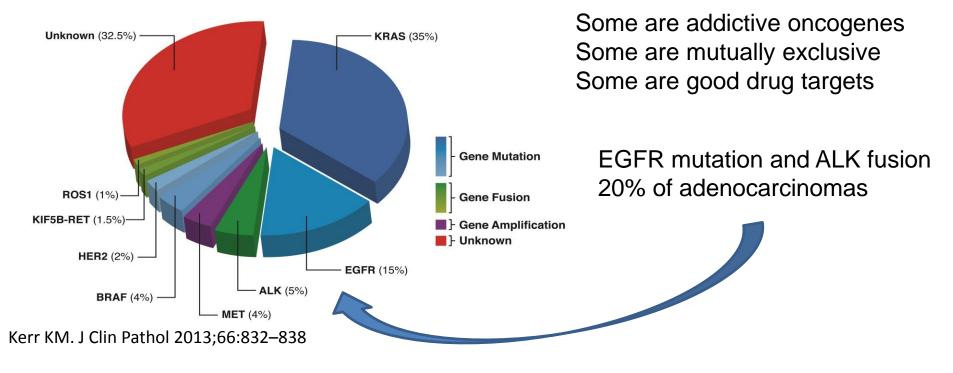
Factor countering drug effect

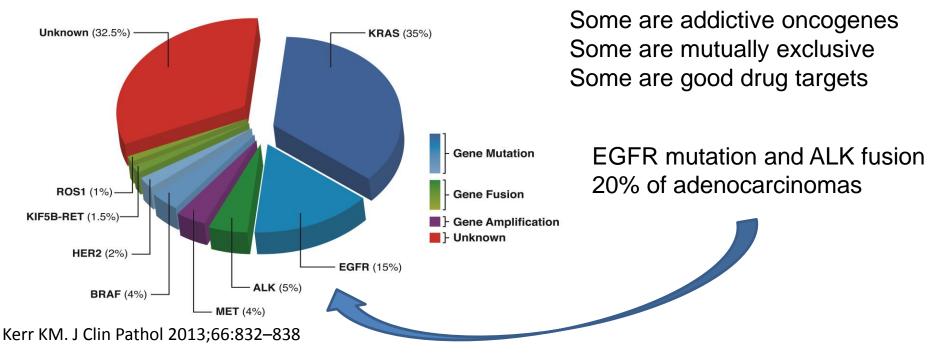
There are MANY **potential** biomarkers in lung cancer but.....

In clinical practice.....

- EGFR mutation testing
 - EGFR tyrosine kinase inhibitors
- ALK gene rearrangement testing

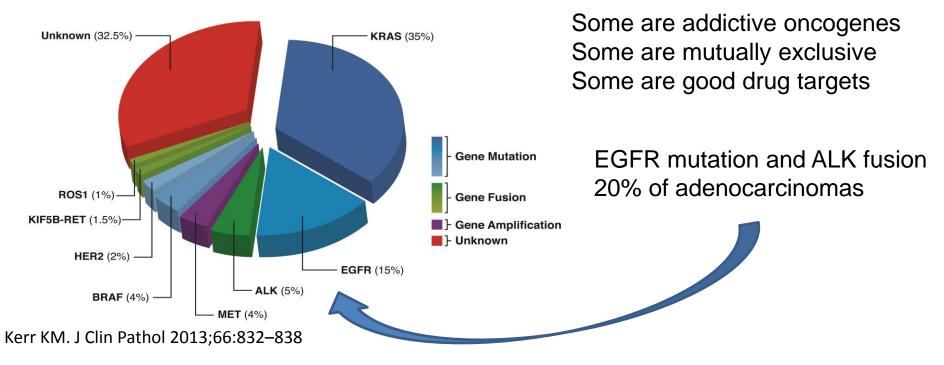
ALK tyrosine kinase inhibitors





So we should test

- Adenocarcinomas
- Probably adenocarcinomas
- 'cannot exclude adenocarcinoma'
- Partly adenocarcinoma

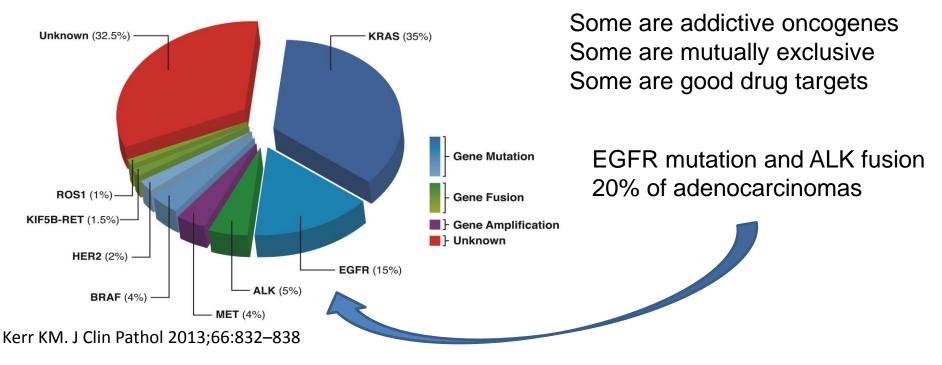


So we should test

- Adenocarcinomas
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And we should test

- Smokers
- Males
- Any ethnic group



So we should test

- Adenocarcinomas
- Probably adenocarcinomas
- 'cannot exclude adenocarcinoma'
- Partly adenocarcinoma

And we should test

- Smokers
- Males
- Any ethnic group
- Any tumour in a never smoker
 - Or long time ex-smoker.....

Who orders the test? Reflex versus Bespoke testing

Reflex – pathologist driven

- Fast
- Cases not missed, becomes 'routine'
- Ready for tumour board decision
- Potential for waste
 - Time
 - Tissue
 - Money

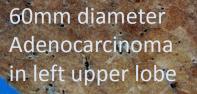
Bespoke – to order from oncologist

- Only when needed
- Preserves tissue
- Lab time not wasted?
- 'Cost' higher per test
- Slower turnaround
- Could be illogical; cases may be missed

What do we use for the test?

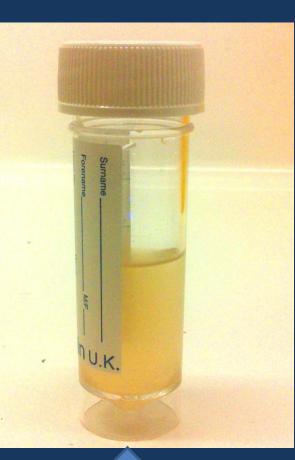
- Whatever is available we need tumour cells!!!
- Tissue or Cytology Cell block sections
 - Maximise tumour cells in material submitted for DNA extraction
 - Minimise non-tumour cells in material submitted for DNA extraction
 - For IHC or FISH less clear

Such rules are difficult to establish How much tumour tissue? At least 10% . . . or 50% tumour At least 100–200 tumour cells?



25mm





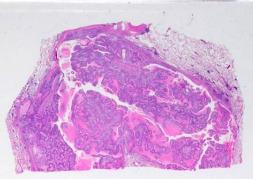
Most Lung Cancer **samples** are small biopsies or cytology-type samples

What do we use to test?

	Aberdeen Royal Infirmary, UK*	Aichi Cancer Centre, Nagoya,
		Japan
Sample type	Percentage of cases submitted	
Surgical Tumor Resection	19%	46%
Lung core biopsy	20%	21%
Bronchial biopsy	19%	11%
Pleural biopsy	7.3%	0.7%
Other biopsy types	22%	4.2%
Total Biopsy samples	87.3%	82.9%
Aspiration cytology	6.5%	9.3%
Pleural fluid cytology	5.0%	6.6%
Bronchial cytology	1.2%	1.2%
Total Cytology samples	12.7%	17.1%

2010 data: In Aberdeen Cytology type samples now ~50% of those tested

Abundant tumour tissue in a block taken from a resected tumour



Lung biopsy fragments 1mm or less

Although each section shows 5 fragments, only two remain in the block (left), after sections are cut for IHC and molecular testing

Cell pellet formed from EBUS procedure

The plastic cassettes used for processing tissue are also used to support the paraffin wax embedded block

Sections cut from the block, mounted on glass slide and stained with Haematoxylin and eosin (H&E)

а

b

С

Is there enough material for these studies?



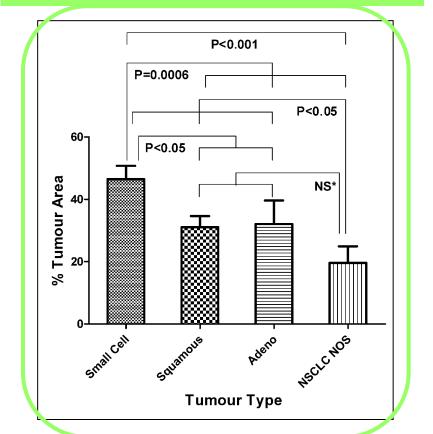
- Morphologic diagnosis
- Immunohistochemistry
- Molecular testing
- Conserve tissue
- Don't waste

Two biopsy fragments <1mm

Is there enough material for these studies?



% tumour in bronchial biopsy samples

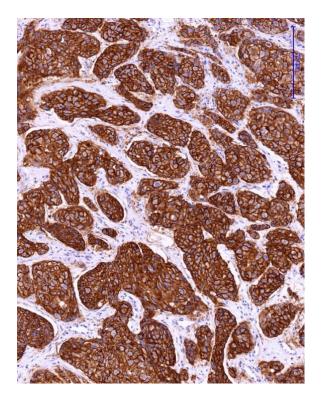


Two biopsy fragments <1mm

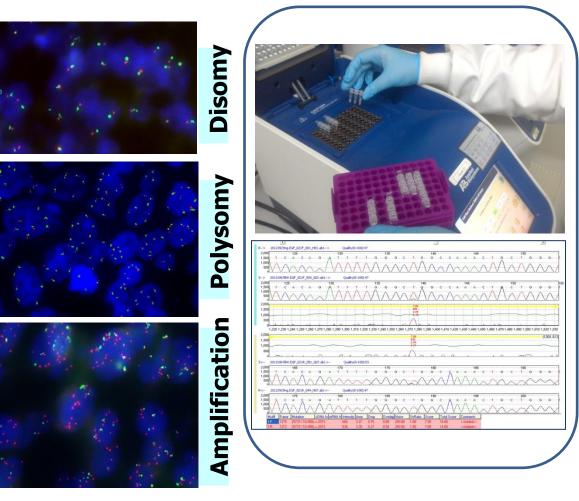
In 'malignant' bronchial biopsy samples 33-50% of fragments do not contain tumour

Coghlin CL et al, JTO 2010, 5:448-452

'Test for EFGR'.....



EGFR IHC? Or.....



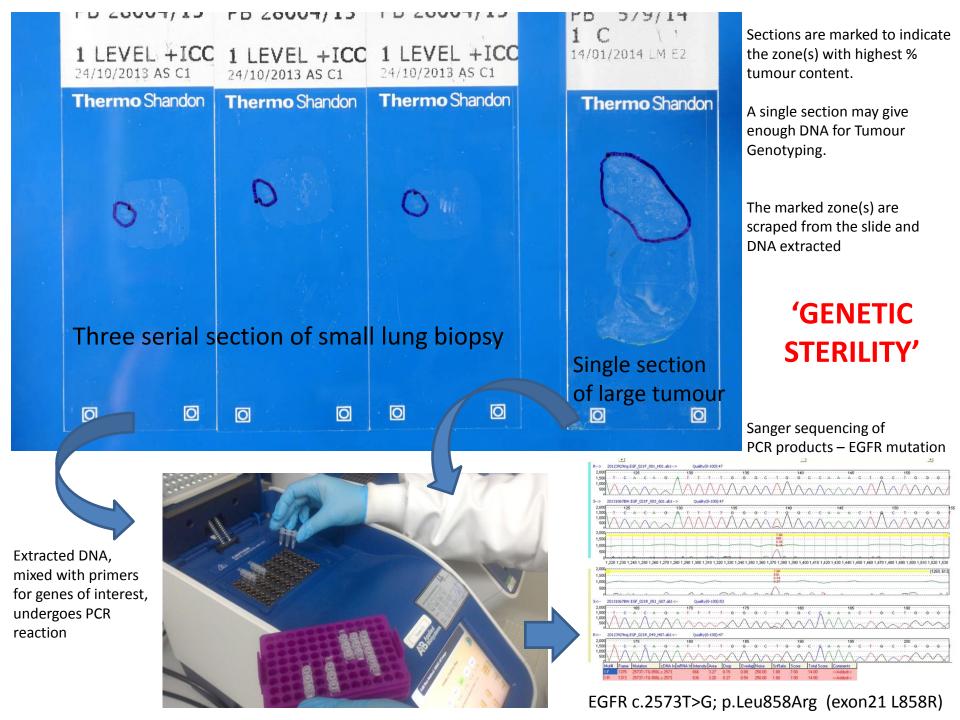
EGFR FISH test? Or.....

EGFR mutations?

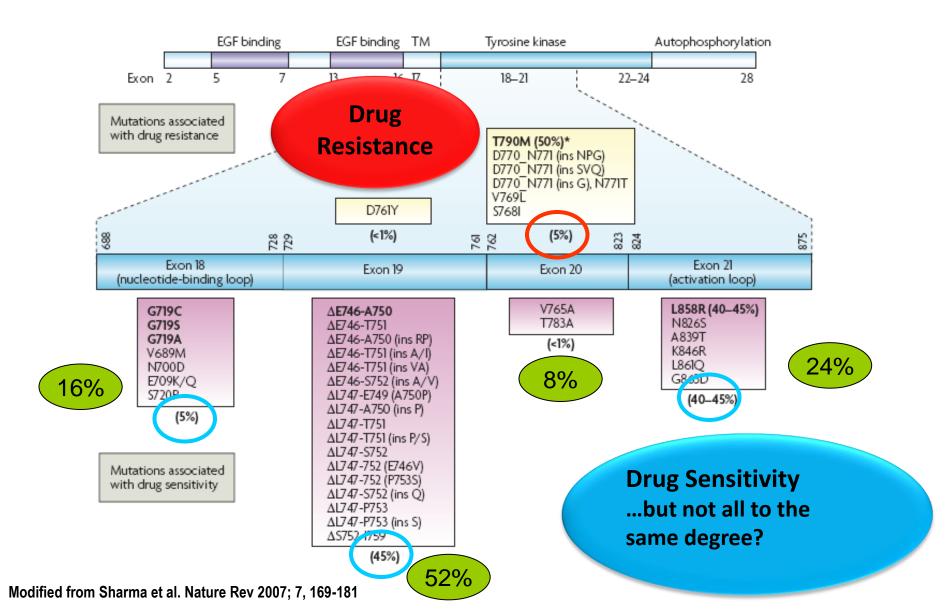
Pathological assessment for molecular testing

- There is tumour present
- It has been prepared in an appropriate way
 Fixation window 6-48hrs.....

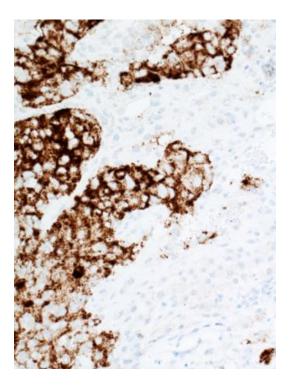
- There is enough tumour?
- The molecular lab knows what it is getting?
 - % tumour in extraction sample
 - Tumour cell number?



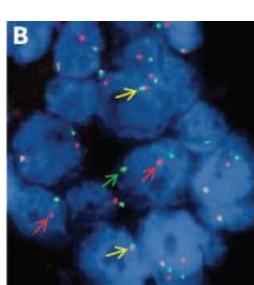
All EGFR mutations are not equal



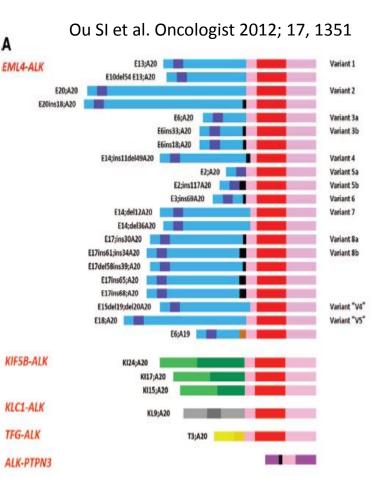
'Test for ALK'.....



The protein? or ...

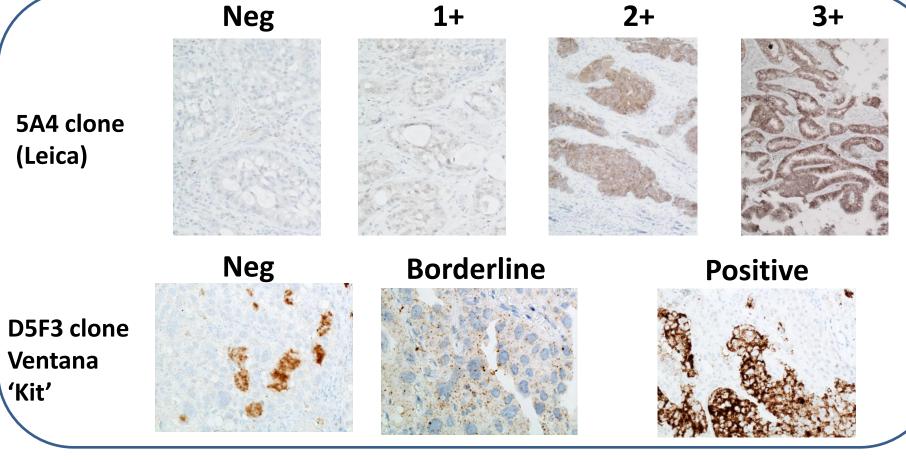


The break apart FISH test? Or...



Abnormal gene sequence by multiplex PCR

ALK Screening by immunohistochemistry (IHC)

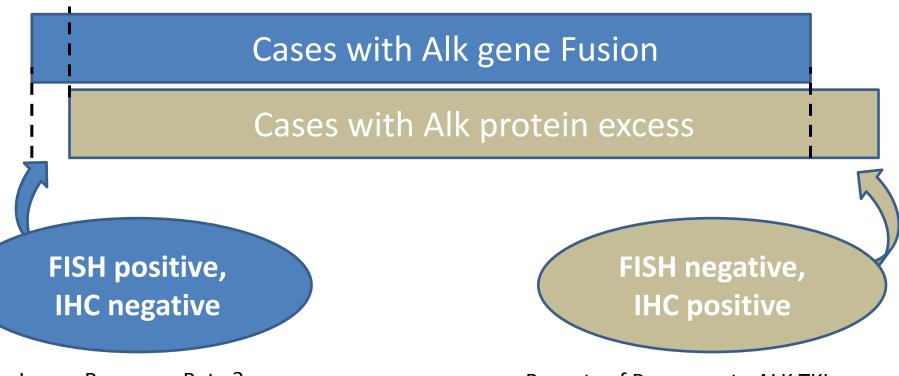


Almost 100% NEGATIVE

FISHTest?

Variable: Majority Negative Almost 100% POSITIVE

The protein does the job The protein is the target of the drug

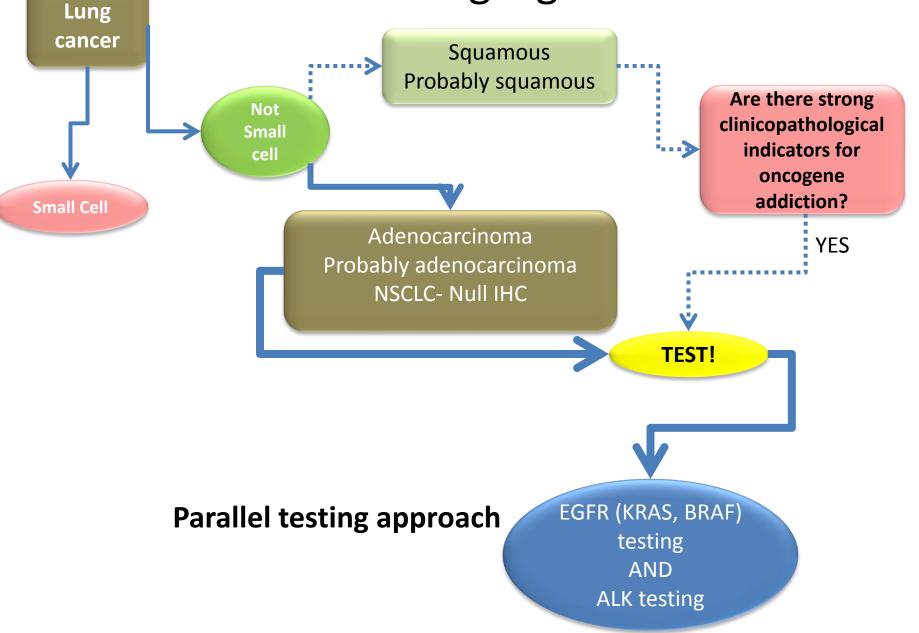


Lower Response Rate ?

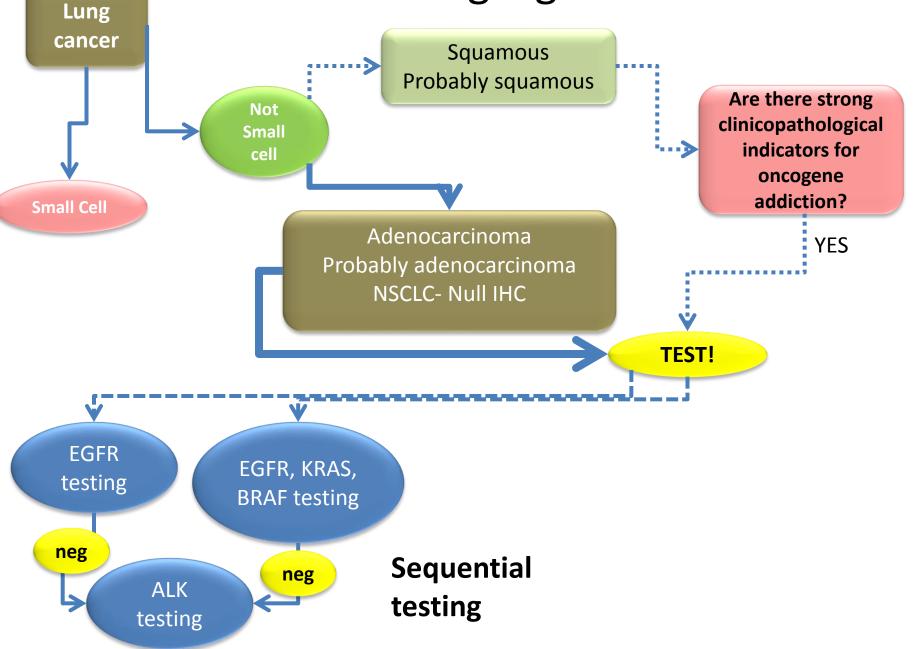
Reports of Response to ALK TKI

Role of Multiplex PCR in 'discrepant cases'?

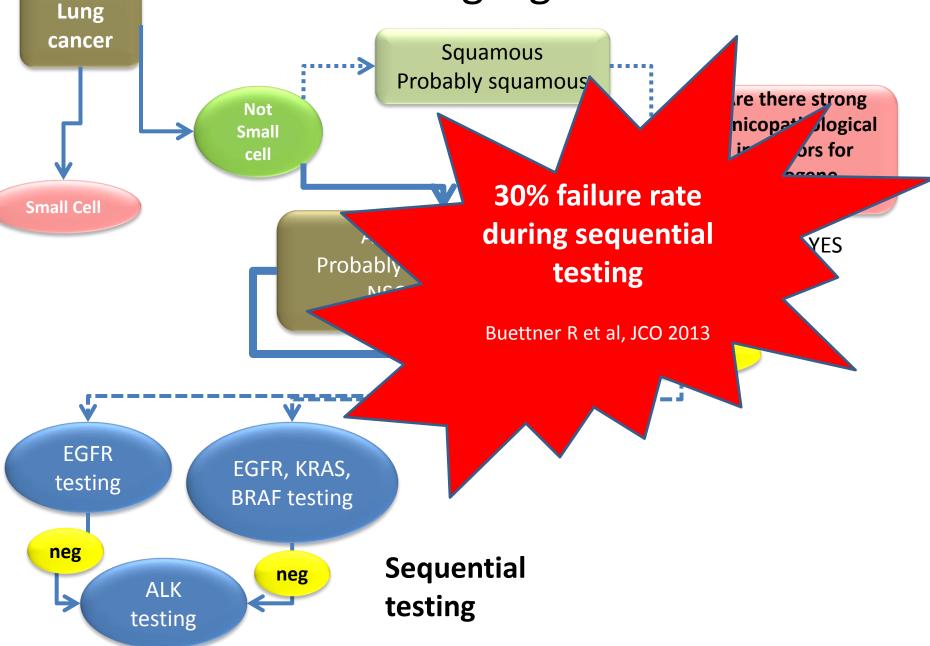
A testing algorithm.....



A testing algorithm.....



A testing algorithm.....



Do we always succeed?

- Diagnostic IHC rarely insufficient
 - Occasionally it just doesn't work!
- EGFR mutation

- ALK rearrangement

 IHC screening
 - Confirmation by FISH

Experience from Clinical Trials

Battle Trial Tam AL et al. J Thorac Oncol 2013;8:436

- 20g needle core biopsies
- 3 PCR sequencing targets
- Two FISH tests
- 6 IHC markers
- 83% adequate for full set

EURTAC Benlloch et al. J Clin Oncol 2012;30:s10596

- 70% Bronchial biopsy
- 15% blocks insufficient for EGFR.
- Additional 3% PCR failure
- Testing 'beyond EGFR' not possible in 47% as block exhausted

MSKCC Squamous Paik et al. J Clin Oncol 2012;30, s7505

- 72% Core biopsy 11% FNAC
- 17% Resections
- Sequenom, 1 FISH, 1 IHC test
- 87% complete full set
- 8% partial set

IPASS Yang JC et al Lung Cancer 2014; 83, 174-181

- Initially rejected samples (<100 cells)
- 99 histology cases **80% success**
- 116 cytology cases **19% success**
- Positives clinically responded

EBUS samples: How do they go?

- 434 malignant samples
 - 70% specific cell type, 30% NSCLC-NOS
 - Navani N et al, AJRCCM 2012

Ref	% EBUS INSUFF for EGFR mutation test	Comment
GarciaOlivia et al 2010	28%	12% for core biopsy
Schuurbiers et al JTO 2010	23%	
Esterbrook et al, Lung Cancer 2013	12%	Cell block based
Navani et al, AJRCCM 2012	10%	
Rekhtman et al, JTO 2011	2%	

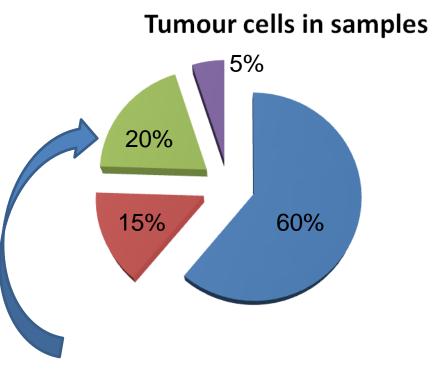
Molecular Pathology, Aberdeen Royal Infirmary

>50%

31-50%

10-30%

<10%



Cytology samples over-represented in this group

- EGFR, KRAS, BRAF
- For EGFR alone
 - 1.63% total fail rate
 - 3.3% partial fail
- In 'POOR' cases
 - 6.5% total fail rate
 - 6.5% partial fail
- Huge range with 'outside' cases (up to 35%)

Alk testing 'success'??

- In Aberdeen
 - About 4% of cases insufficient for ALK IHC
 - About 10% cases insufficient for ALK FISH
 - 50-60 assessable cells
 - 4 high power fields to assess
- Up to 20% of samples may be 'insufficient' for ALK FISH testing
 - Lantuejoul S et al in IASLC ALK Atlas

Strategy to Preserve Tissue

- It is still necessary to make the best diagnosis possible!
- The NSCLC-NOS issue
 - Use the minimum amount of extra material
 - Antibody cocktails double staining?
- Do not chase 'phantom' metastatic disease
- Process all 'fluids' if possible
- Reflex section cutting?

EGFR mutation testing: what do the results mean?

Is the result 'real'?

- False negatives
 - ➢ Real risk
 - Poor samples
 - Pre-analyticals
 - Sample preparation
 - Insensitive analysis

- False positives * Te
 - More dangerous?
 - Poor testing methodology
 - Artefacts
 - Contamination

- Test failures
 - Not enough DNA
 - PCR failure
 - Test failure
 - Partial results

> Heterogeneity

Mutation

- KRAS
- BRAF
- MEK
- ERK
- NRAS
- PI3K
- AKT
- STK11
- P53
- DDR2
- FGFR2&3

Mutation Gene rearrangements – fusion genes

- **ROS1** fusion
 - **RET** fusion
 - NTRK1 fusion
 - CD74-NRG1 fusion
 - FGFR3-TAC3 fusion

Gene copy number

- MET
- HER2
- **PI3KCA**
- FGFR1

NRAS PI3K •

•

•

•

KRAS

BRAF

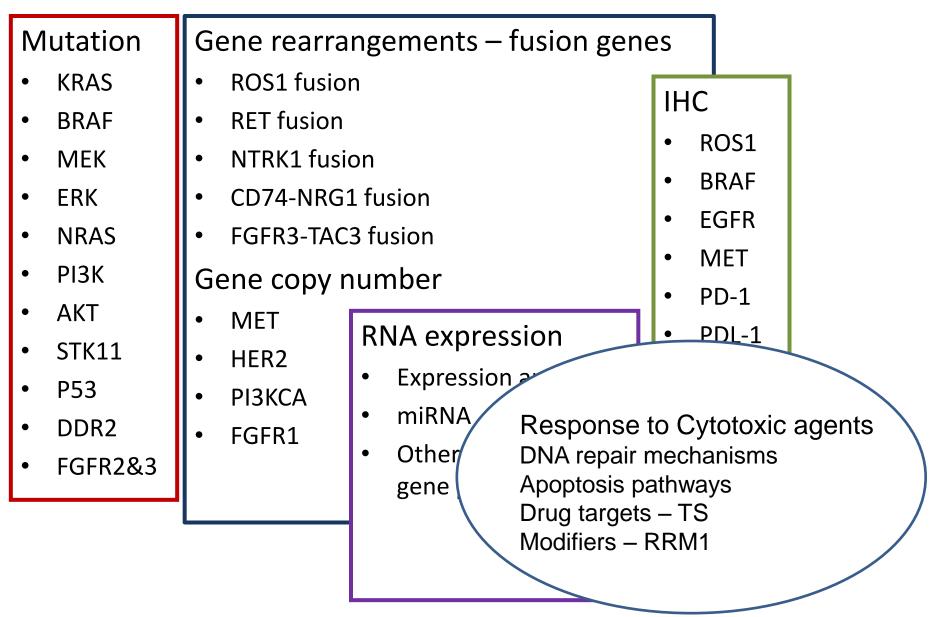
MEK

ERK

- AKT •
- STK11
- P53
- DDR2
- FGFR2&3

Mutation	Gene rearrangements – fusion genes			
• KRAS	ROS1 fusion			
• BRAF	RET fusion			
• MEK	NTRK1 fusion			
• ERK	CD74-NRG1 fusion			
• NRAS	FGFR3-TAC3 fusion			
• PI3K	Gene copy number			
• AKT	• MET DNA evenesion			
• STK11	• HER2	A expression		
• P53	• PI3KCA •	Expression arrays		
• DDR2	• FGFR1 •	miRNA		
• FGFR2&3	•	Other individual gene products		

Mutation KRAS 	Gene rearrange • ROS1 fusion	ments – fusion gen	es	
 BRAF MEK ERK NRAS PI3K AKT 	 RET fusion NTRK1 fusion CD74-NRG1 fusion FGFR3-TAC3 fusion Gene copy num 	on L fusion 3 fusion	• B • E • N	OS1 RAF GFR 1ET D-1
 STK11 P53 DDR2 FGFR2&3 	 HER2 PI3KCA FGFR1 O 	A expression Expression arrays miRNA Other individual gene products	• P	DL-1

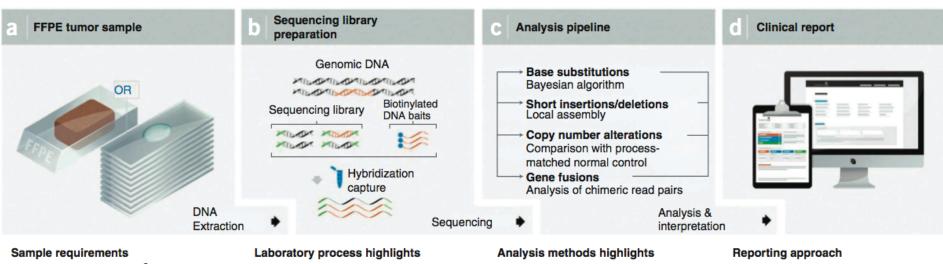


NGS for molecular testing

- Quoted amounts of DNA required rather variable
 - Technology dependant
 - Size of panel
- Mutation > Fusion gene > gene copy number
- Fragmentation of DNA
- Bioinformatic analysis
- 80% samples complete panel of mutations
- 95% samples EGFR, KRAS, BRAF, HER2 mutations
- 'minimum 2000 cells' 5 x 10um thick sections

Myerson M et al. Nat Rev Gen 2010

Much still to define



- Surface area: ≥25 mm²
- Sample volume: ≥1 mm³
- Nucleated cellularity: ≥80% or ≥30,000 cells
- Tumor content: ≥20%

Fraction of patients with tissue insufficient for analysis: 10–15%

- Requires ≥50 ng of dsDNA (quantified by PicoGreen)
- Fragmentation by sonication (Covaris) and 'with-bead' library construction
- Hybridization capture with biotinylated DNA oligonucleotides
- 49 × 49 paired-end sequencing on the Illumina HiSeq platform to >500× average unique coverage, with >100× at >99% of exons

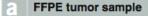
- Sensitivity to variants present at any mutant allele frequency
- Detection of long (1–40 bp) indel variants using de Bruijn graph-based local assembly
- CGH-like analysis of readdepth for CNAs assessment

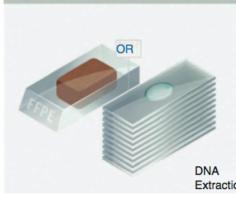
Interpretation without a matched normal

- Germline variants from 1000 Genomes Project (dbSNP135) removed
- Known driver alterations (COSMIC v62) highlighted as biologically significant

A concise summary of the biomedical literature and current clinical trials is provided for each highlighted alteration

- False-negative calls were predominantly low (<10%) mutant allele frequencies substitutions, indels or low-magnitude copy number alterations.
- **Comprehensive genomic profiling was successful for 95% of clinical cases** Frampton G, *et al.* Nature Biotechnology 2013; Epub ahead of print.





Sample requirements

- Surface area: ≥25 mm²
- Sample volume: ≥1 mm³
- Nucleated cellularity: ≥80% or ≥30,000 cells
- Tumor content: ≥20%

Fraction of patients with tissue insufficient for analysis: 10–15%

More than 25mmsq = 5 x 5mm area

1mm cube of tumour

Cellularity >80% or > 30,000 cells

Tumour content > 20% - 1500 tumour cells

10 -15% insufficient for analysis

- False-negative calls were predominantly low (<10%) mutant allele frequencies substitutions, indels or low-magnitude copy number alterations.
- **Comprehensive genomic profiling was successful for 95% of clinical cases** Frampton G, *et al.* Nature Biotechnology 2013; Epub ahead of print.

Consensus for EGFR Mutation Testing in Non-small Cell Lung Cancer

Results from a European Workshop

Pirker R et al. JTO 2010

TABLE 1. Biopsy Techniques					
	21-g Needle Aspiration	19-g Needle Aspiration	Transbronchial Biopsy	CT-Guided Needle Biopsy	
Total no. of cells per biopsy/ aspiration	≥100	≥150	≥300	≥500	
No. of biopsies	4	4	4-5	2–3	
	400 -600 cells		~1500	cells	



PLEASE Mr Pulmonologist or Interventional Radiologist

H: NI H: NI

Success in Biomarker testing?



- Be aware! Anticipate testing......
- Maximize tissue collection do no harm
- Process tissue appropriately
- ANY SAMPLE TYPE is *potentially* adequate for biomarker testing
- Take steps to 'improve' the test sample
- Quality-assured molecular testing
- Plan your testing strategy
 - This is a MULTIDISCIPLINARY effort
- Everyone on the team UNDERSTANDS WHY testing is important
- Communication, communication, communication.....

Molecular Testing Guideline for Selection of Lung Cancer Patients for EGFR and ALK Tyrosine Kinase Inhibitors

Guideline from the College of American Pathologists, International Association for the Study of Lung Cancer, and Association for Molecular Pathology

Quality control by pathologist :

Number of cells?

- Fixation : 6-12 hrs 10% neutral-buffered formalin
- Estimate the **cellular tumour content and tumour purity** Ideally :

high proportion (>30-50%) of malignants cells relative to nonneoplastic cells

+

minimal proportion (<20%) of substances that may inhibit amplification (e.g. necrosis, mucin)

Lindeman et al. J Thorac Oncol 2013;8:823-59.