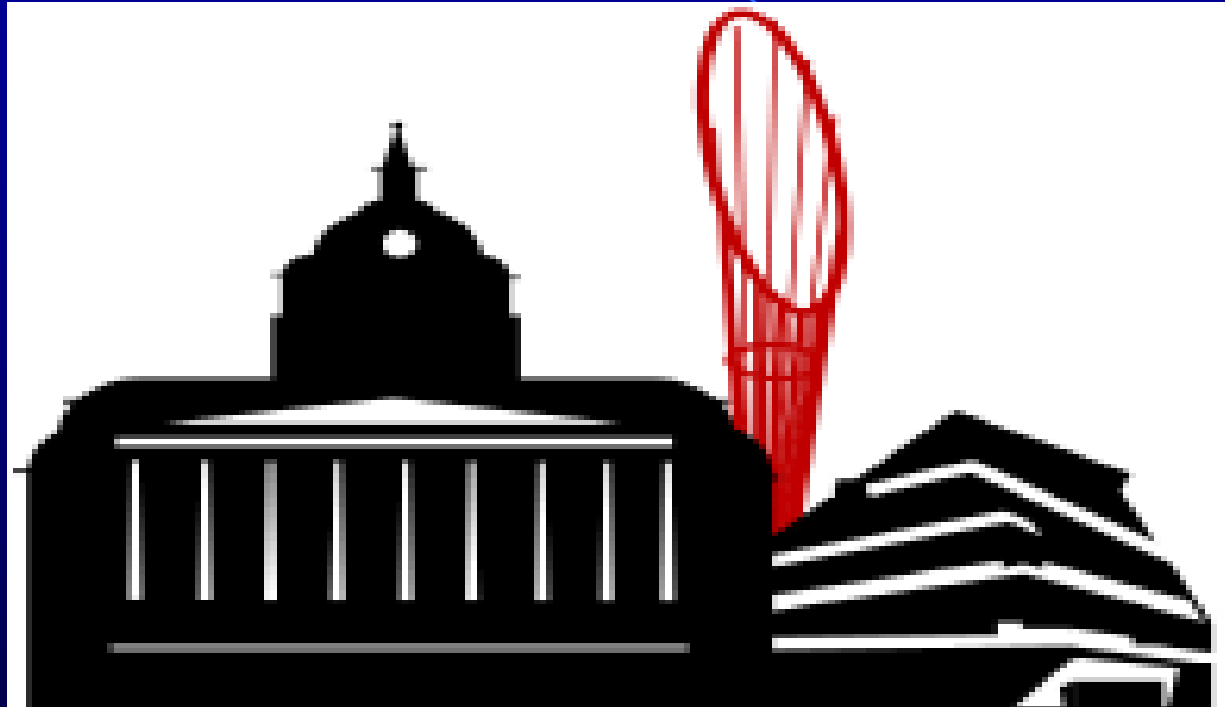
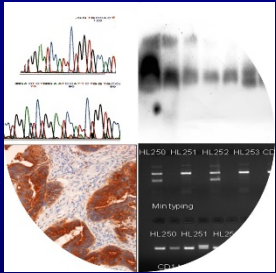


Practical Molecular Pathology of the lower GI tract



Transforming the Pathology Landscape

Mohammad Ilyas



www.nmpn.info/

Speaker Declarations

Name of Speaker: Mohammad Ilyas

This presenter has the following declarations of relationship with industry

- Personal payments/honoraria/fees: **None**
- Research grants: **None**
- Educational grants: **None**

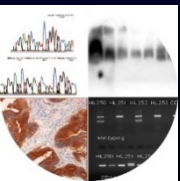
(sponsorship of **Molecular Diagnostics Training Course , Image Analysis Training Course, MSc projects**: Illumina, Roche, Merck, Thermofisher, Bristol Myers Squib, Sysmex, Biocartis, TissueGnostics, Source biosciences, Agilent)

- Travel grant or fellowship: **None**
- Equipment grant: **None**
- Sponsorship of fellow within department: **None**

[23rd November 2018]

Overview

- Ras testing
- Testing for Lynch Syndrome
 - Loss of Mismatch Repair (MMR) function and leads to microsatellite instability (MSI)
 - IHC versus PCR for loss of MMR function
 - An algorithm for Lynch Syndrome screening
 - Clinical implications of dMMR



Enough of the doom-mongering!



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- 100,000 Genomes Project ▾
- Taking Part ▾
- For Healthcare Professionals ▾
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- News & Events ▾

Home > News > Posts > Secretary of State for Health and Social Care announces ambition to sequence 5 million genomes within five years

Secretary of State for Health and Social Care announces ambition to sequence 5 million genomes within five years



Posted on October 2, 2018 at 5:00 pm

Secretary of State for Health and Social Care, the Rt Hon Matt Hancock MP, today set out an ambitious vision for genomic medicine in the NHS – with plans to sequence 5 million genomes over the next five years.

The announcement, made as part of the Secretary of State's speech to the Conservative Party Conference in Birmingham, recognises the critical importance of genomic medicine to the future of the NHS. Mr Hancock announced:

- Expansion of the 100,000 Genomes Project to see 1 million



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Ras testing



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Best practice

RAS testing of colorectal carcinoma—a guidance document from the Association of Clinical Pathologists Molecular Pathology and Diagnostics Group FREE

Newton ACS Wong¹, David Gonzalez², Manuel Salto-Tellez³, Rachel Butler⁴, Salvador J Diaz-Cano⁵, Mohammad Ilyas⁶, William Newman⁷, Emily Shaw⁸, Philippe Taniere⁹, Shaun V Walsh¹⁰

[Author affiliations +](#)

Abstract

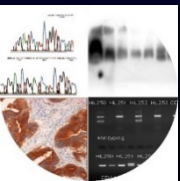
Analysis of colorectal carcinoma (CRC) tissue for *KRAS* codon 12 or 13 mutations to guide use of anti-epidermal growth factor receptor (EGFR) therapy is now considered mandatory in the UK. The scope of this practice has been recently extended because of data indicating that *NRAS* mutations and additional *KRAS* mutations also predict for poor response to anti-EGFR therapy. The following document provides guidance on RAS (i.e., *KRAS* and *NRAS*) testing of CRC tissue in the setting of personalised medicine within the UK and particularly within the NHS. This guidance covers issues related to case selection, preanalytical aspects, analysis and interpretation of such RAS testing.

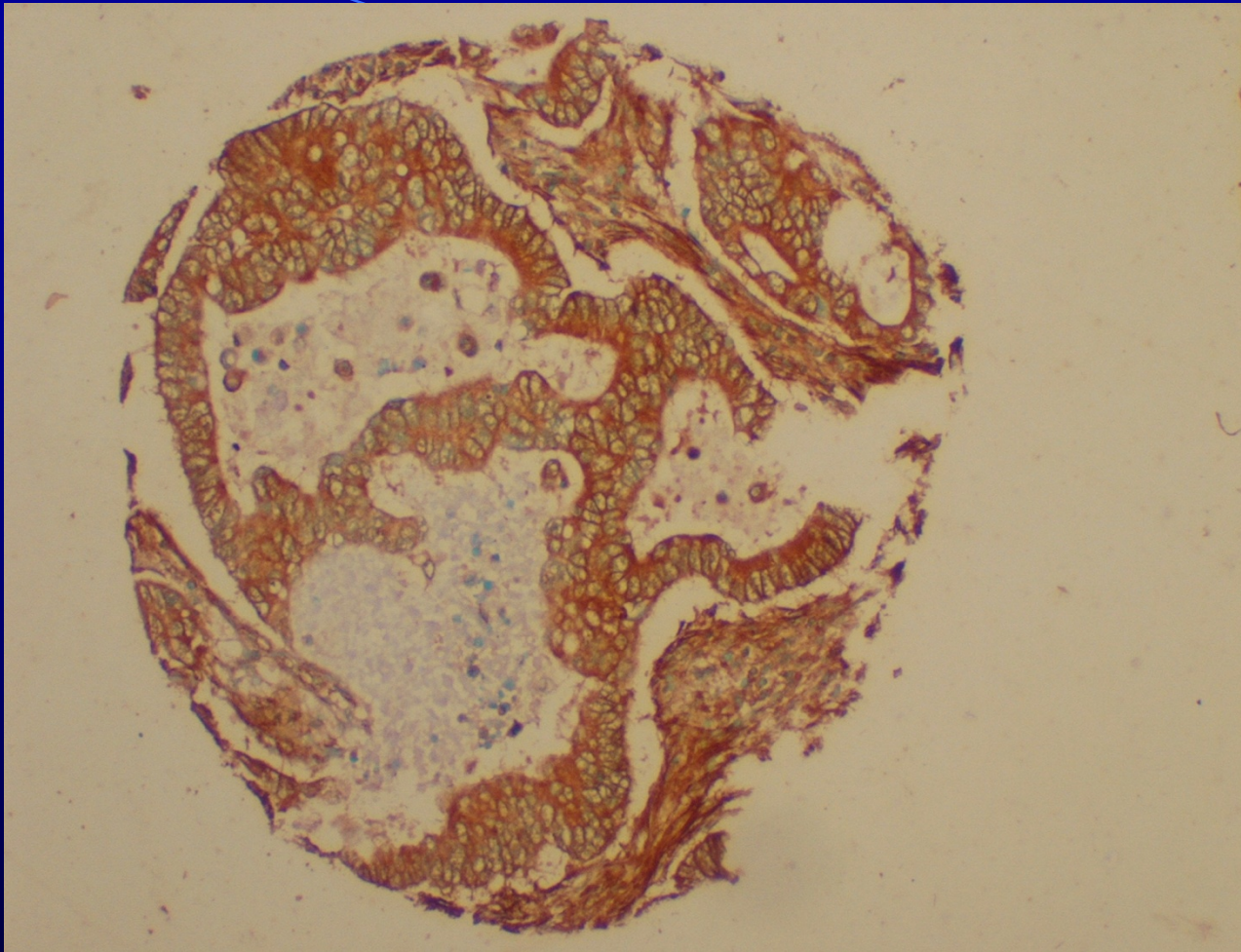


PDF

Ras testing: the role of the pathologist

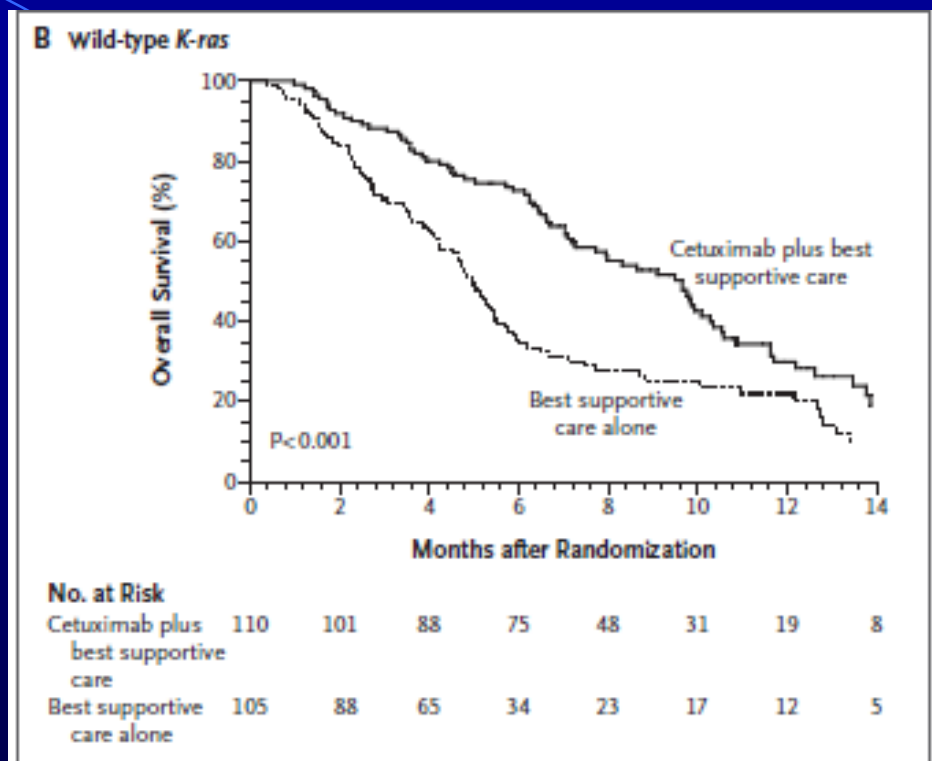
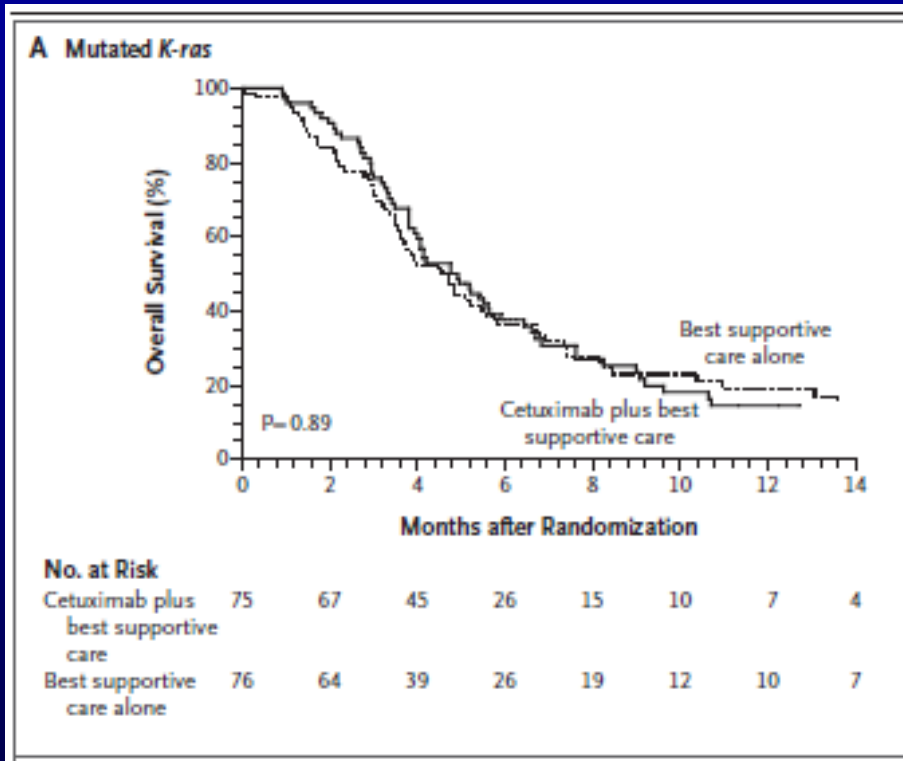
- Assess tumour burden in tissue sections
- (Evaluate the data)
- (Evaluate the results)
- Make intelligent comment on the results at the MDT



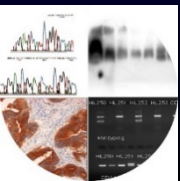


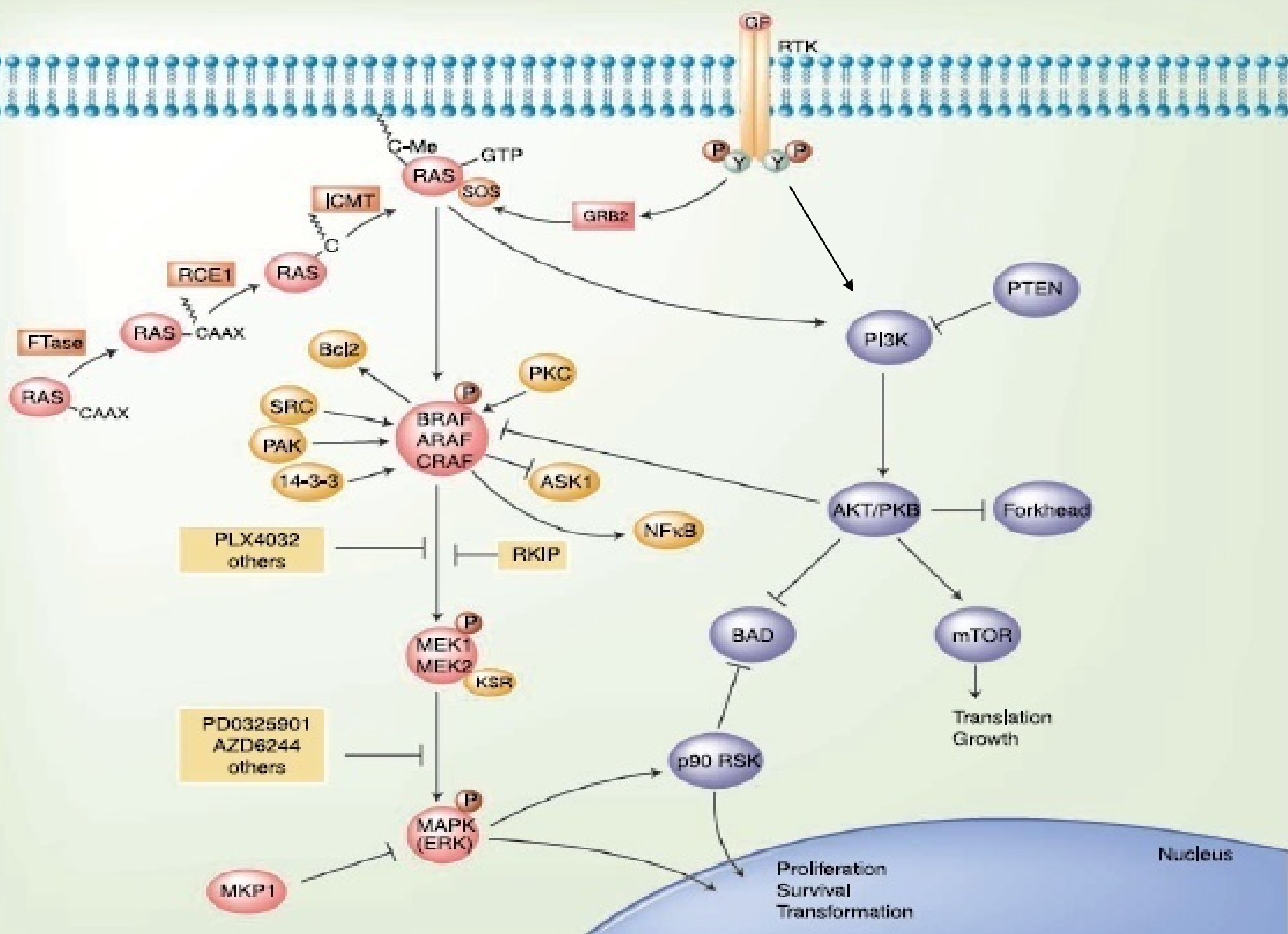
EGFR IHC

KRAS mutation in CRC



Patients whose tumours harbour a KRAS mutation will not respond to Cetuximab. Testing for KRAS mutation therefore stratifies patients into “treatment” and “non-treatment” groups

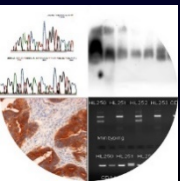




EGFR signals through RAS/BRAF pathway

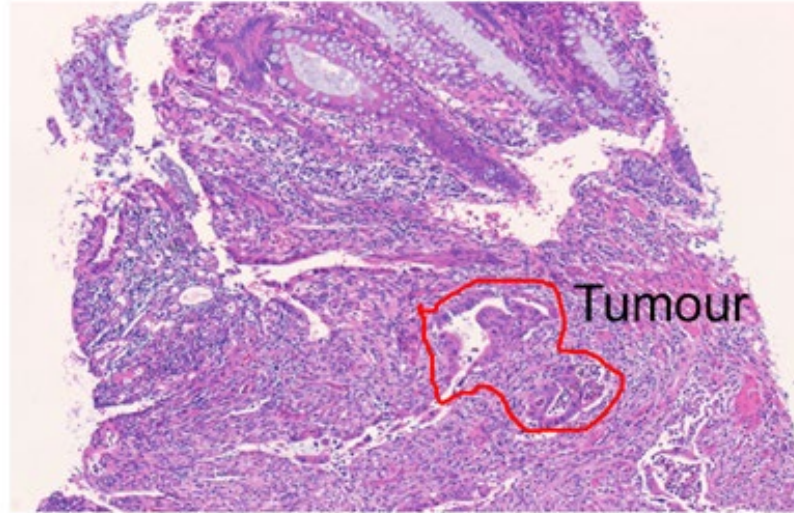
Ras testing

- Treatment with anti-EGFR biologics can improve survival in patients with CRC
- EGFR signals through the Ras/Raf signaling pathway
- Activation of this pathway through KRAS or BRAF mutation will negate the effect of the anti-EGFR treatment
- Ras testing is mandatory before administering anti-EGFR treatment



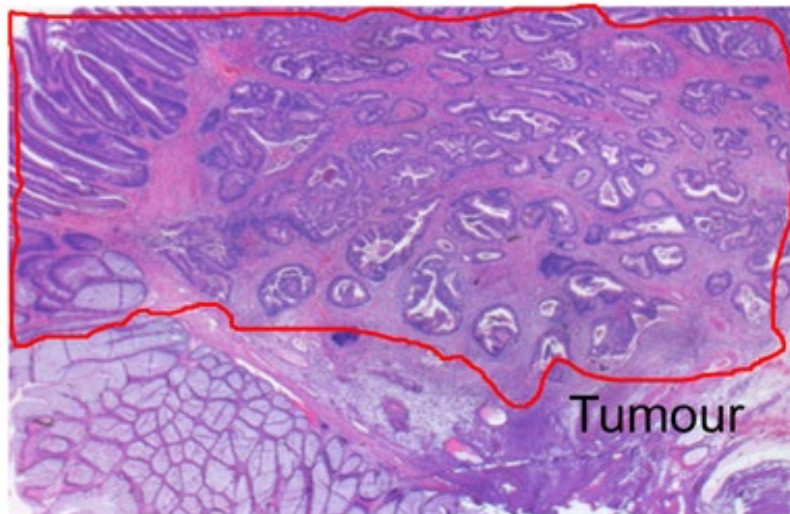
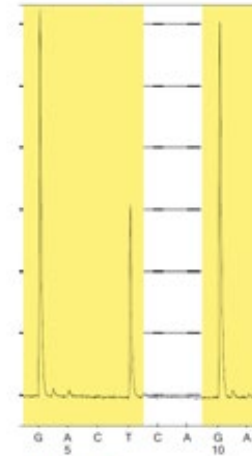
Ras testing: tumour burden

Figure 3



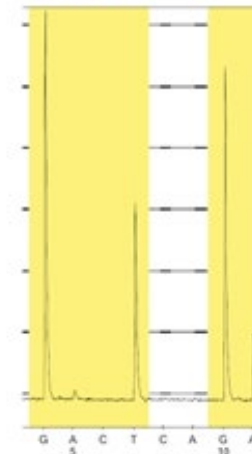
G:96.7%
A:3.2%
C:0.0%
T:0.1%

G:100.0%
A:0.0%



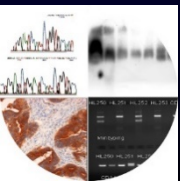
G:95.8%
A:4.1%
C:0.0%
T:0.1%

G:70.5%
A:29.5%



Ras testing: intelligent comments

- There was sufficient tumour present
- The limit of detection is 20% for Sanger Sequencing, 5% pyrosequencing and NGS
- There are co-incident KRAS and BRAF mutations – this is probably an artefact
- There is a discrepancy between tumour load and mutant allele frequency
- Although there is KRAS mutation, the site may mean it is still responsive
- Although it is wild-type, the profile suggests it will not respond



Testing for Lynch Syndrome

NICE National Institute for
Health and Care Excellence

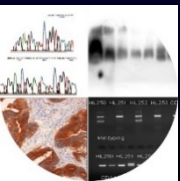


Molecular testing strategies for Lynch syndrome in people with colorectal cancer

Diagnostics guidance

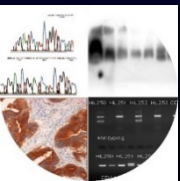
Published: TBC

[nice.org.uk/guidance/dg27](https://www.nice.org.uk/guidance/dg27)



Lynch Syndrome

- Also called Hereditary Non-Polyposis Colorectal Cancer (HNPCC)
- Rapid development of polyps into cancer rather than increased polyp numbers
- Penetrance variable
- Due to mutation of any one of several **mismatch repair genes**: *MSH2*, *MLH1*, *PMS2*, *MSH6*, (*EpCAM*)

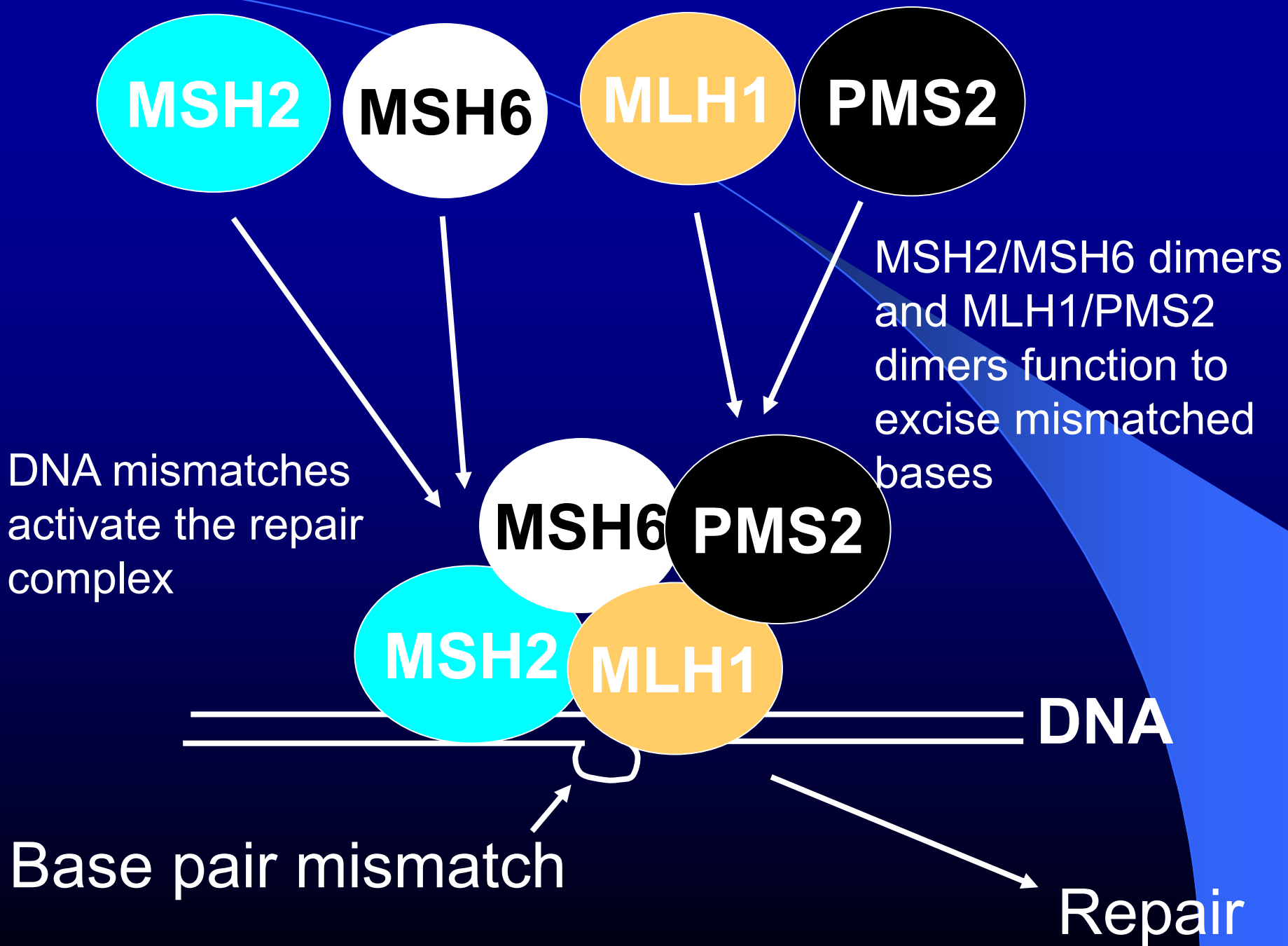




Mis-

Match

Repair





Loss of one of the proteins results in failure of the complex to repair the mismatch

Base pair mismatch

No repair

Monomorphic

C-A-C-A-C-A-C-A-C-A-C-A

G-T-G-T-G-T-G-T-G-T-G-T

6 repeats

C-A-C-A-C-A-C-A-C-A-C-A
G-T-G-T-G-T-G-T-G-T-G-T

C-A-C-A-C-A-C-A-C-A-C-A
G-T-G-T-G-T-G-T-G-T-G-T

7 repeats

C-A-C-A-C-A-C-A-C-A-C-A-CA
G-T-G-T-G-T-G-T-G-T-G-T-GT

6 repeats

C-A-C-A-C-A-C-A-C-A-C-A
G-T-G-T-G-T-G-T-G-T-G-T

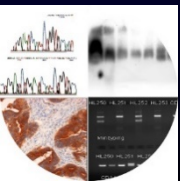
5 repeats

C-A-C-A-C-A-C-A-C-A
G-T-G-T-G-T-G-T-G-T

Polymorphic

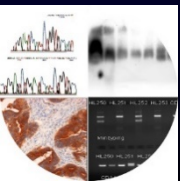
MMR function testing

- Loss of MMR proteins can result in loss of MMR function
- Loss of MMR function results in an *increased mutation rate*
- Microsatellites are highly prone to mutation
- Loss of MMR function can be tested either:
 - by IHC for loss of protein expression
 - by PCR for microsatellite instability



Immunostaining for MMR

- Antibodies can be fixation sensitive (thus biopsies are better than whole WTS)
- Stromal cells act as internal positive controls
- Score only nuclear staining
- Specific patterns are seen: don't forget the dimers!



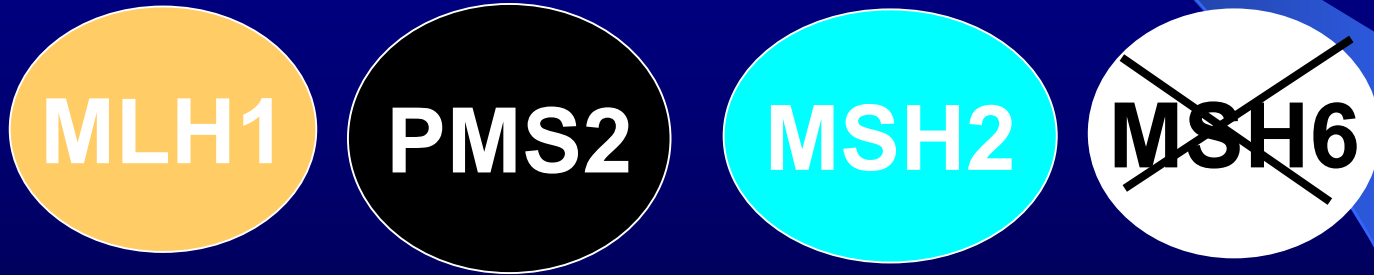
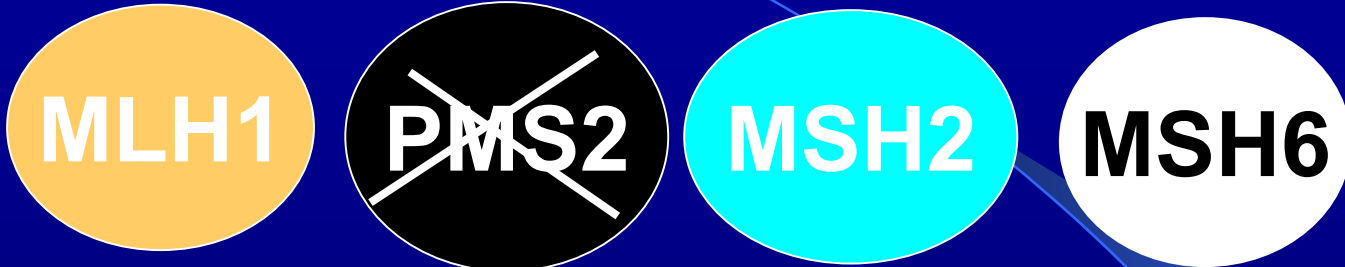
Immunostaining for MMR

MLH1 PMS2 MSH2 MSH6

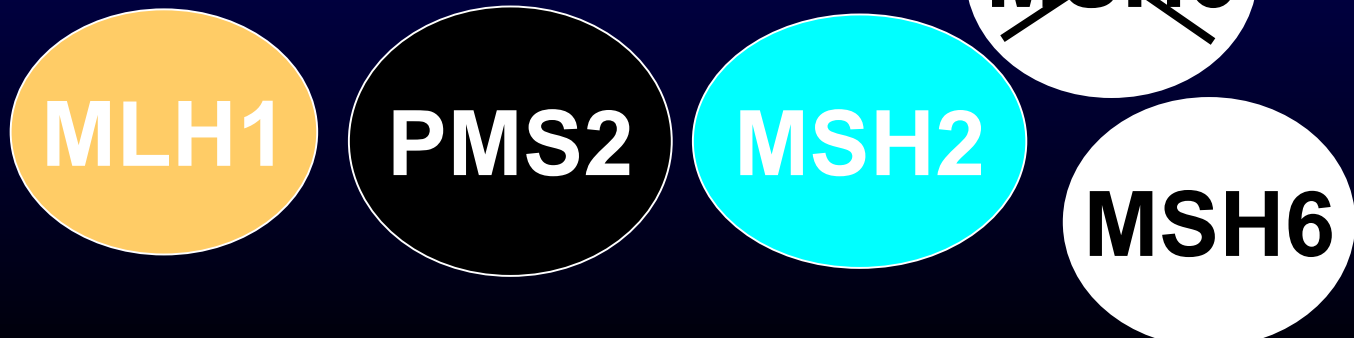
~~MLH1~~ ~~PMS2~~ MSH2 MSH6

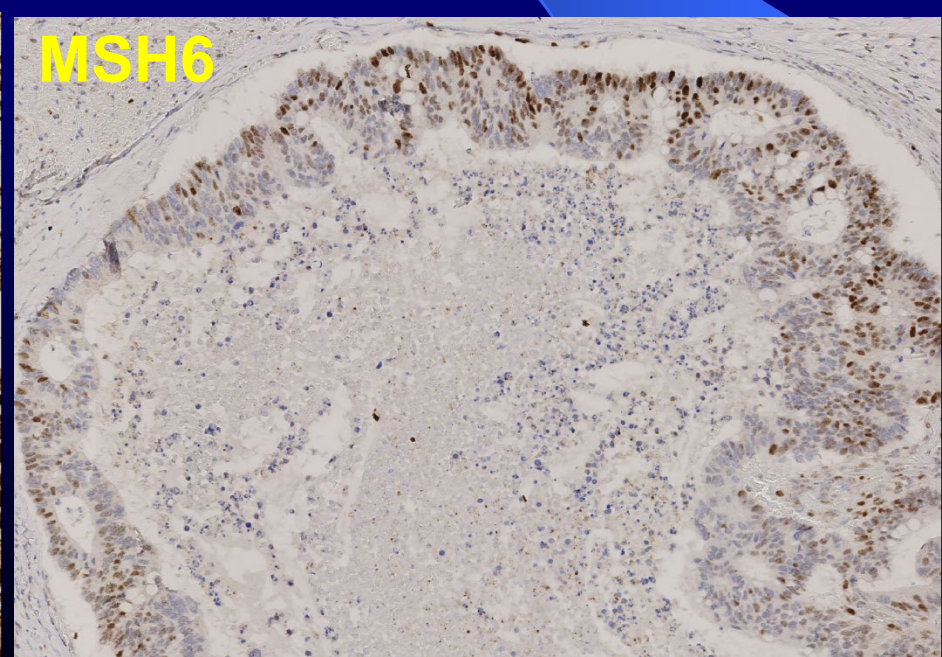
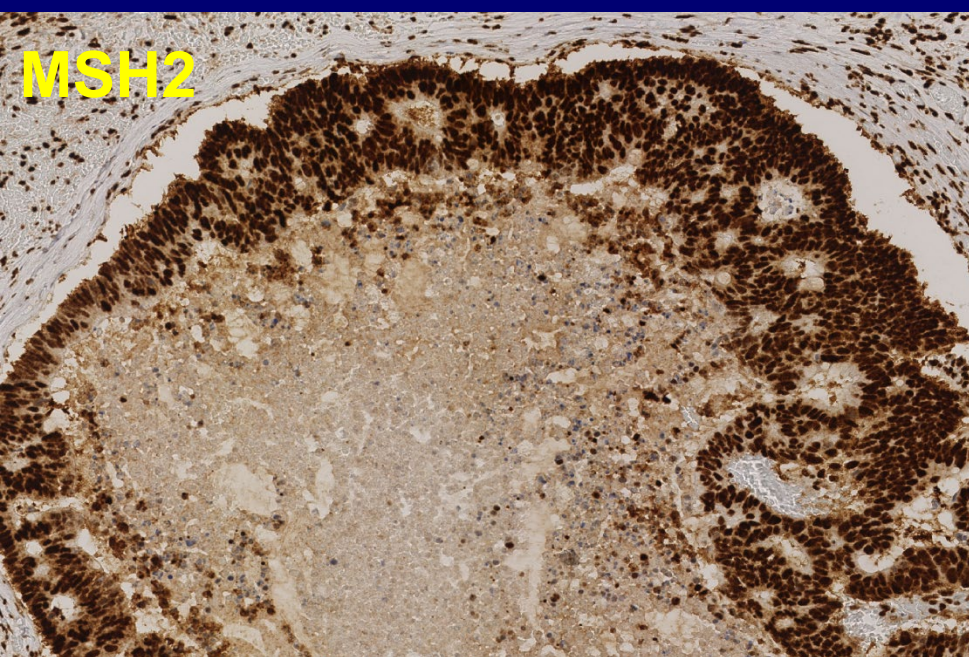
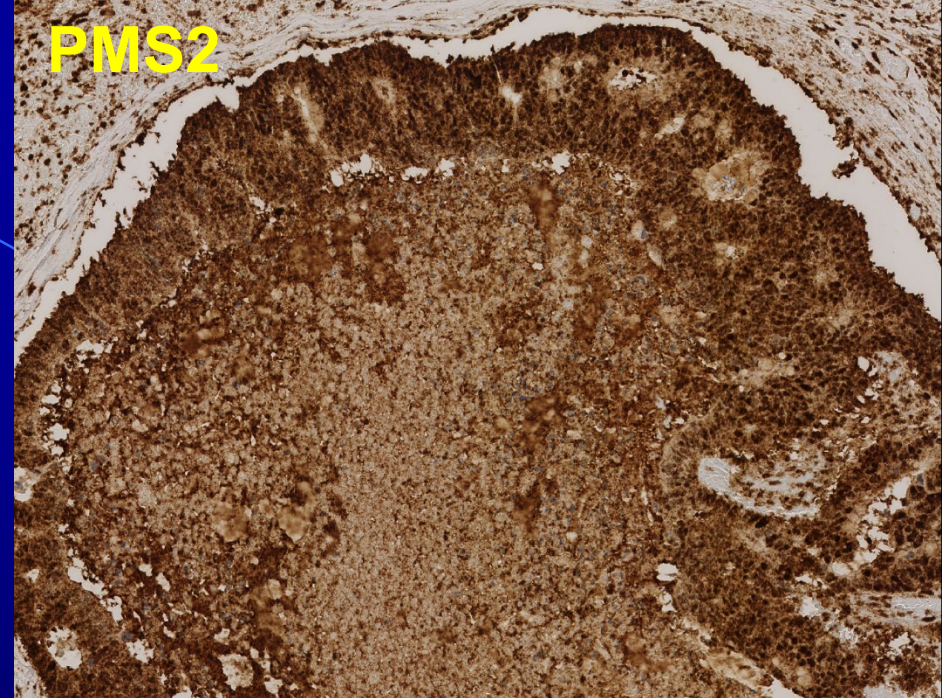
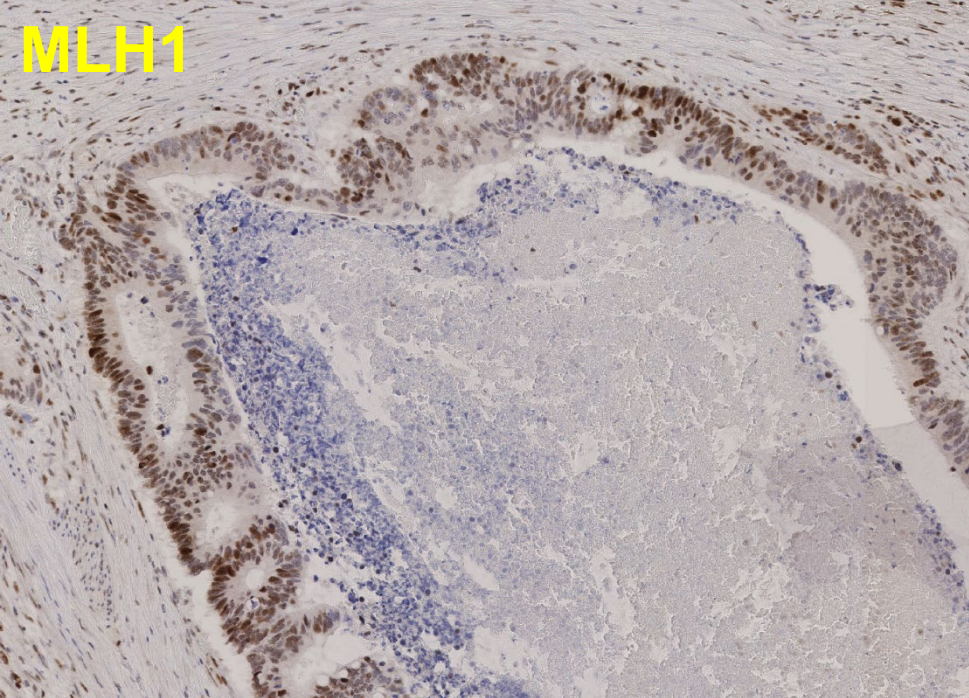
MLH1 PMS2 ~~MSH2~~ ~~MSH6~~

Immunostaining for MMR

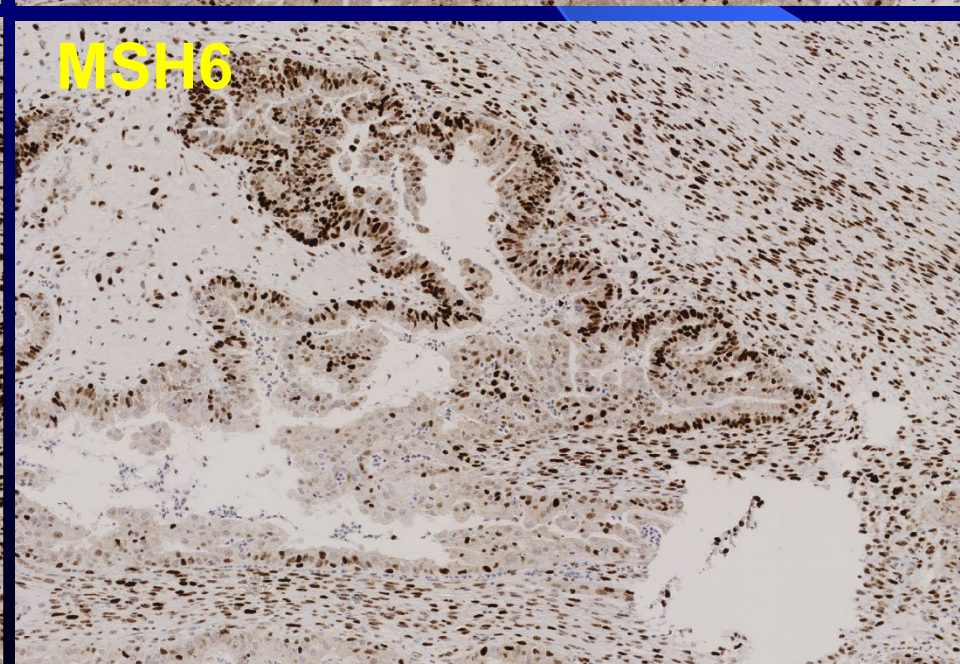
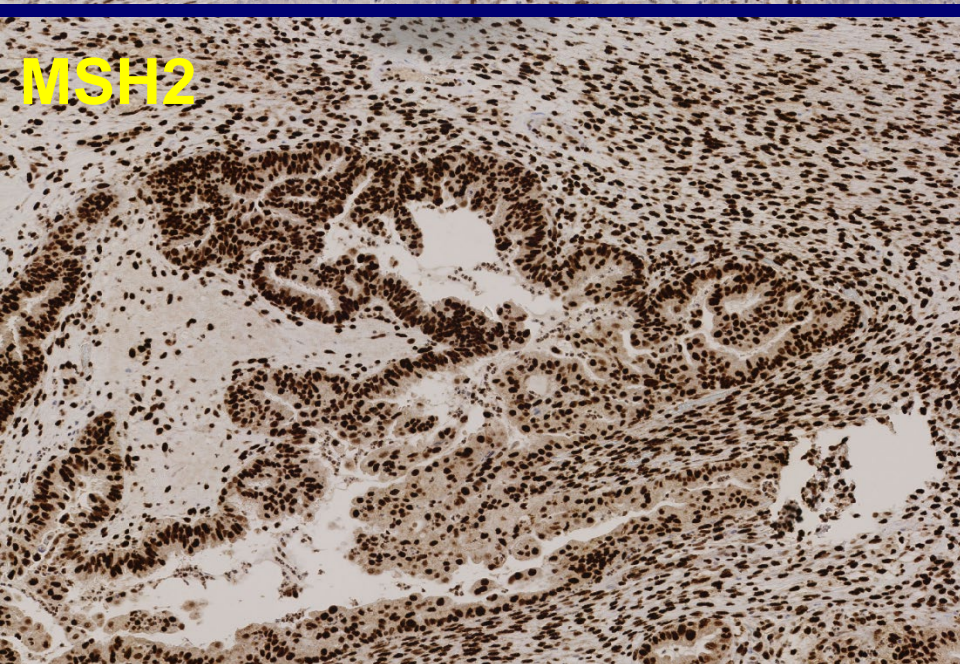
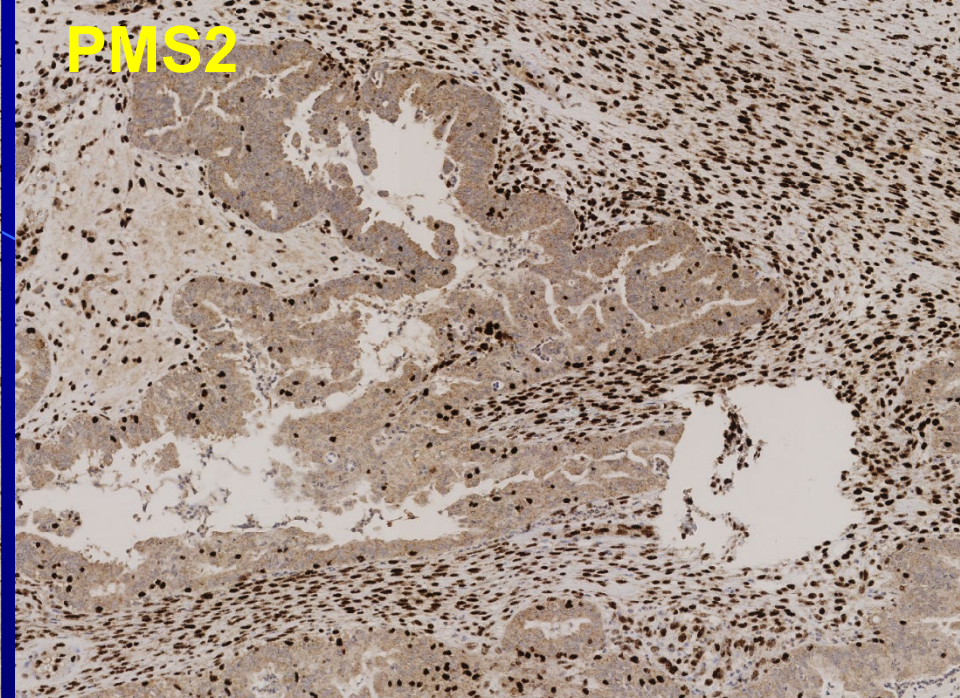
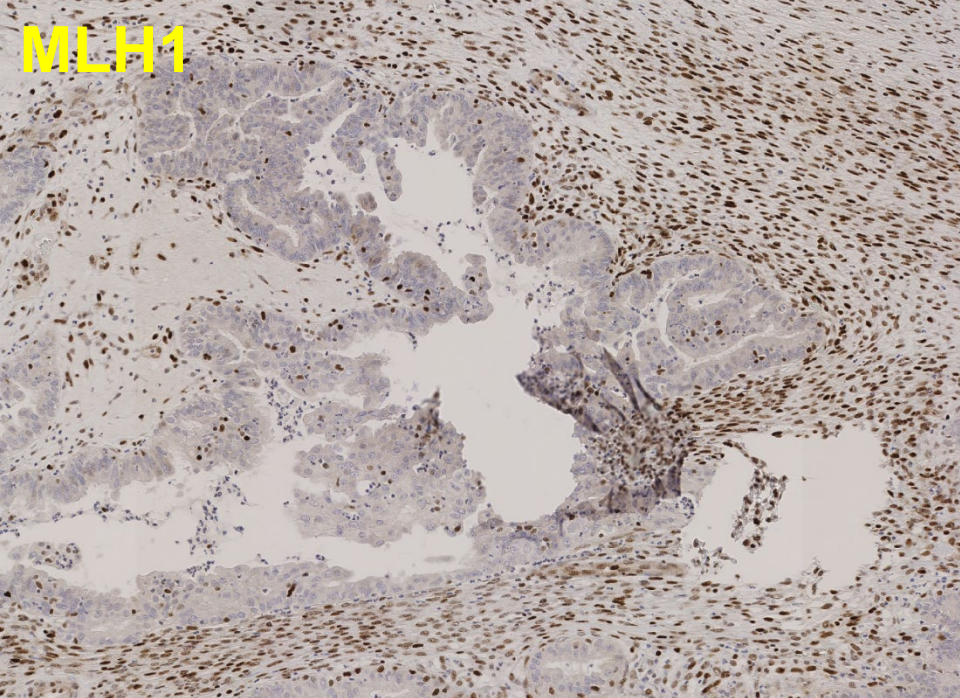


Radiation



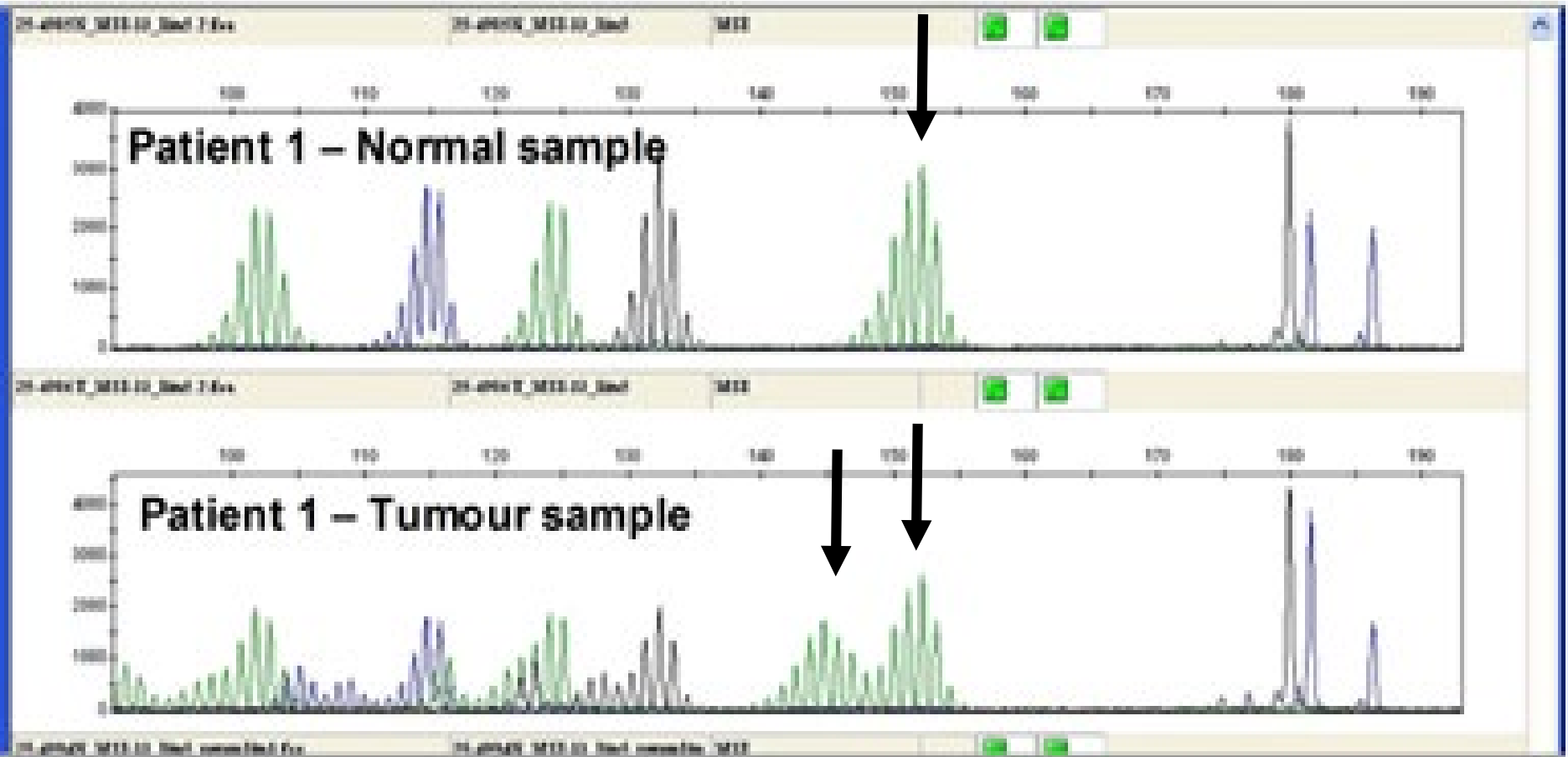


MMR proficient (pMMR)



MMR deficient (dMMR): MLH1/PMS2

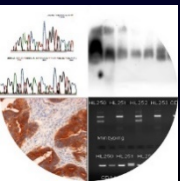
Figure 1



Microsatellite instability
Very good correlation with IHC

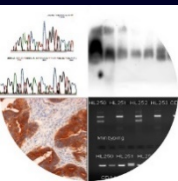
NICE guidance for CRC

- NICE guidance is that all CRC should be tested for Lynch Syndrome
- Health economics modelling shows there will be benefit to society
- However, 10-15% of sporadic CRCs will also have loss of MMR or MSI
- These need to be discriminated from Lynch Syndrome



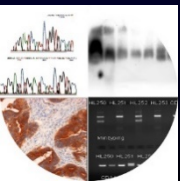
Separating syndromic and sporadic

- There are some molecular differences between Lynch Syndrome tumours and sporadic tumours with MSI:
 - MSH2 / PMS2 / MSH6 are rarely mutated in sporadic tumours
 - BRAF mutations are rare in LS but occur in 40 – 70% of sporadic CRCs
 - MLH1 promoter methylation almost never occurs in Lynch Syndrome

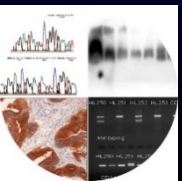
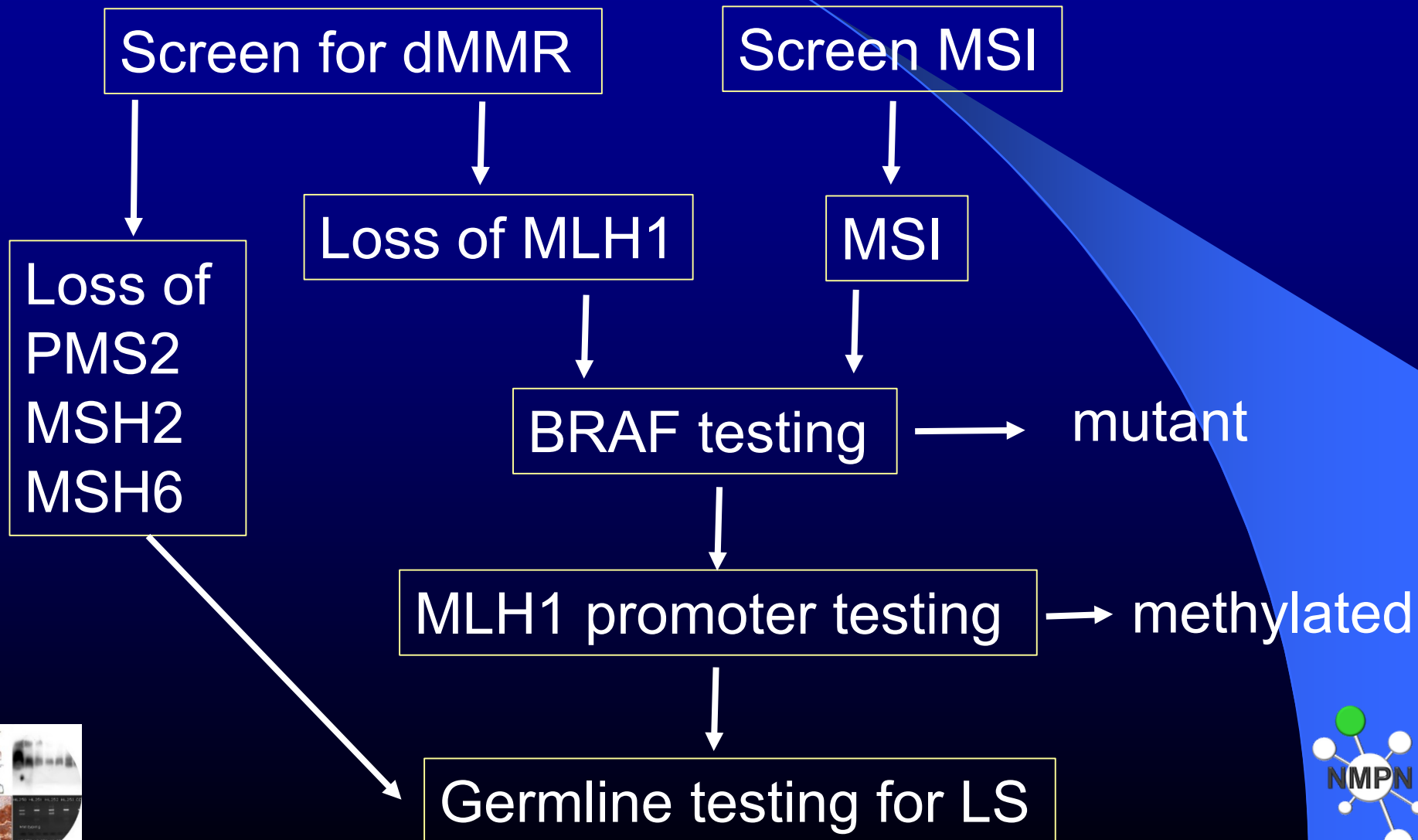


Separating syndromic and sporadic

- There are some molecular differences between Lynch Syndrome tumours and sporadic tumours with MSI:
 - *CTNNB1* mutation only occurs in LS
 - *RNF43* and *ZNRF3* mutations occur more frequently in sporadics (and possibly form part of the serrated pathway)

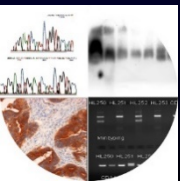


Screening for Lynch Syndrome



Clinical implications of dMMR

- Risk of Lynch Syndrome
- Good prognosis if there is no metastatic spread
- Poor prognosis if there is metastatic spread
- Resistance to 5FU and sensitivity to Irinotecan
- Sensitivity to Immunotherapy

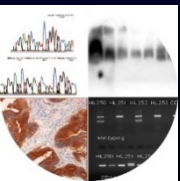


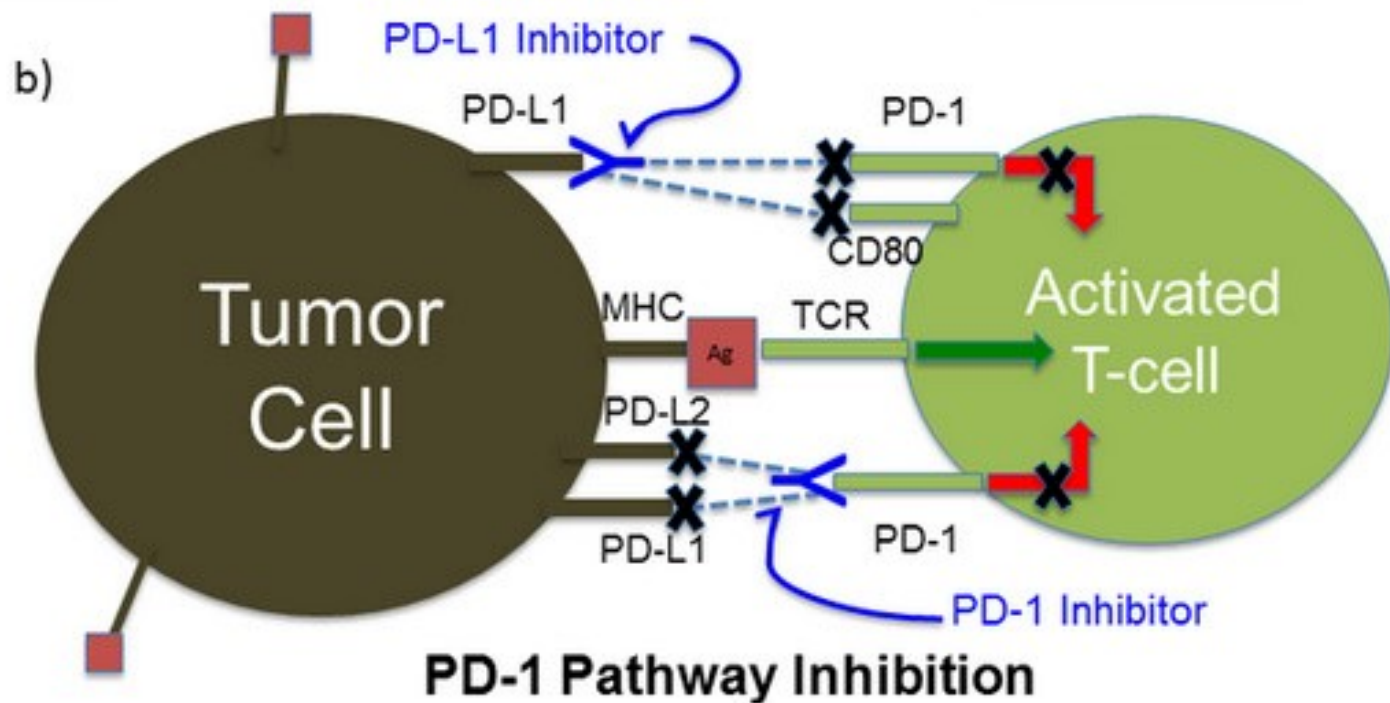
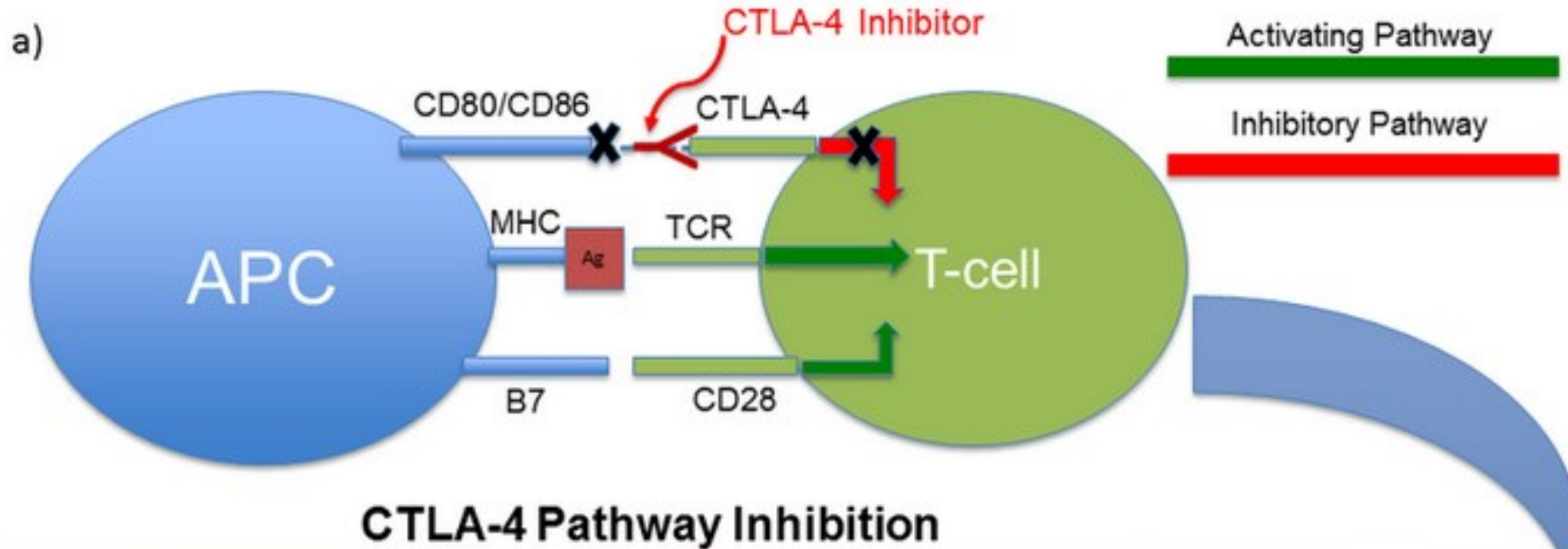


Immunotherapy
Immunotherapy
Immunotherapy

The rationale for immunotherapy

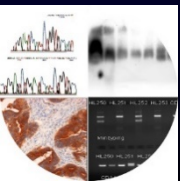
- Immunology is very complicated and nobody really understands it
- Immune response can be inhibited at several checkpoints to prevent auto-immunity
- There are two main targetable checkpoints:
 - Activation of T-cells by antigen presenting cells
 - T-cell mediated cytotoxicity

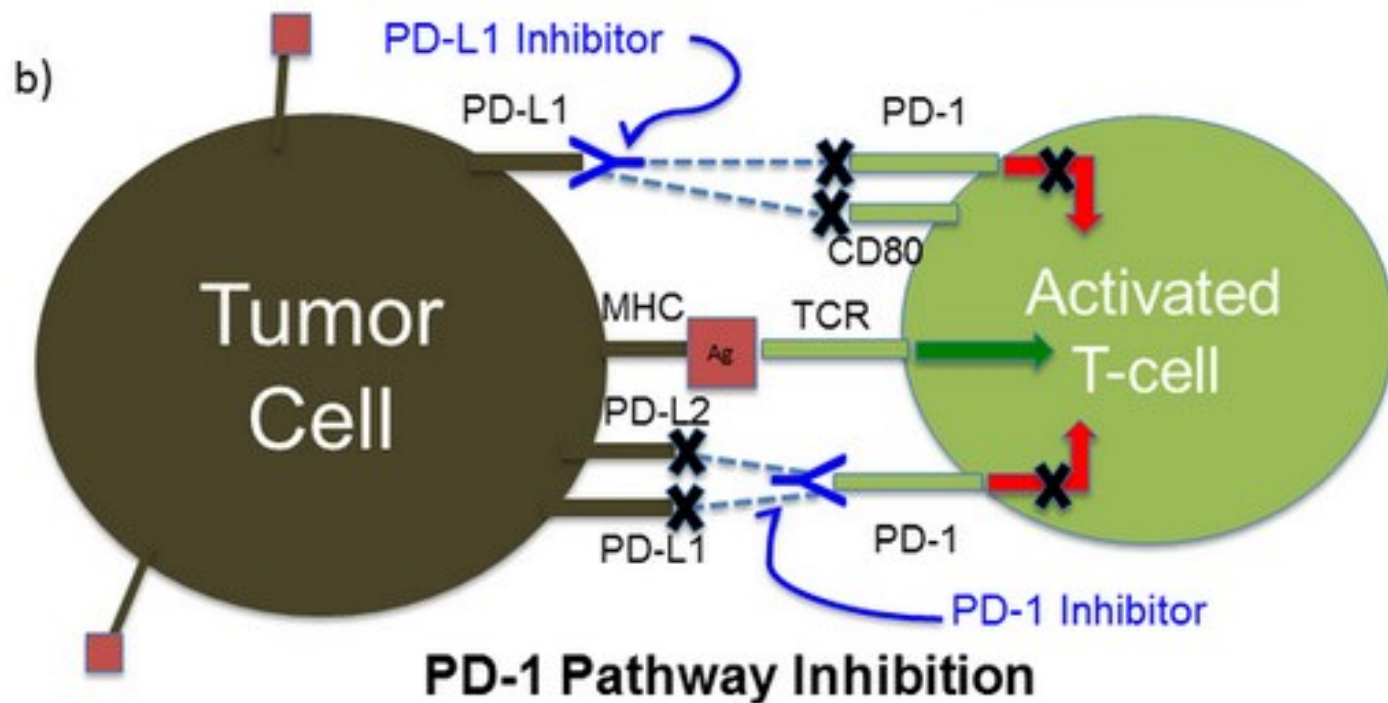
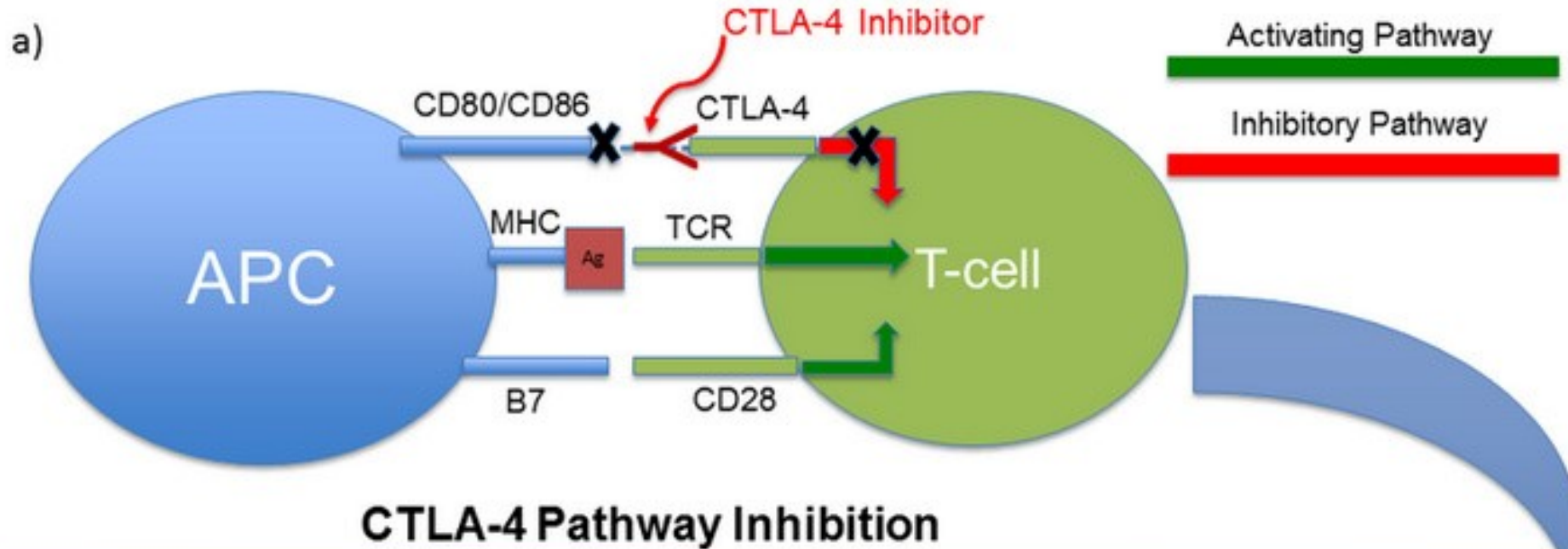




The rationale for immunotherapy

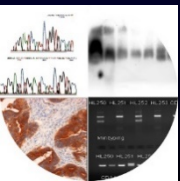
- T-cell activation and T-cell mediated cytotoxicity both require presentation of tumour antigens
- CD80/CTLA-4 interaction causes T-cell anergy
- PD-L1/PD1 interaction inhibits tumour cell killing
- The greater the antigenic diversity, the greater the likelihood of an immune response





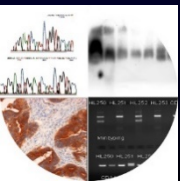
The rationale for immunotherapy

- Immunotherapy enhances the endogenous immune response
- Checkpoint inhibitors allow T-cell activation and T-cell mediated cytotoxicity
- The greater the number of antigens, the more likely there is to be an immune response
- A higher mutation rate will result in a greater number of *neo-antigens*



The rationale for immunotherapy

- Immunostaining for the checkpoint molecules is not easy (either in application or interpretation)
- An alternative method is to look at *Tumour Mutation Burden*
- This requires extensive sequencing to look for random mutations
- These are a reflection of the mutation rate and hence the antigenicity in a tumour



Monomorphic

C-A-C-A-C-A-C-A-C-A-C-A

G-T-G-T-G-T-G-T-G-T-G-T

6 repeats

C-A

C-A-C-A-C-A-C-A-C-A-C-A

G-T-G-T-G-T-G-T-G-T-G-T

C-A

C-A-C-A-C-A-C-A-C-A

G-T-G-T-G-T-G-T-G-T

7 repeats

C-A-C-A-C-A-C-A-C-A-C-A-CA

G-T-G-T-G-T-G-T-G-T-G-T-GT

6 repeats

C-A-C-A-C-A-C-A-C-A-C-A

G-T-G-T-G-T-G-T-G-T-G-T

5 repeats

C-A-C-A-C-A-C-A-C-A

G-T-G-T-G-T-G-T-G-T

Polymorphic

CANCER BIOMARKERS

Mismatch repair deficiency predicts response of solid tumors to PD-1 blockade

Dung T. Le,^{1,2,3} Jennifer N. Durham,^{1,2,3*} Kellie N. Smith,^{1,3*} Hao Wang,^{3*} Bjarne R. Bartlett,^{2,4*} Laveet K. Analkh,^{2,4} Steve Lu,^{2,4} Holly Kemberling,³ Cara Wilt,³ Brandon S. Luber,³ Fay Wong,^{2,4} Nilofer S. Azad,^{1,3} Agnieszka A. Ruckl,^{1,3} Dan Laheru,³ Ross Donehower,³ Atif Zaheer,⁵ George A. Fisher,⁶ Todd S. Crocenzi,⁷ James J. Lee,⁸ Tim F. Greten,⁹ Austin G. Duffy,⁹ Kristen K. Ciombor,¹⁰ Aleksandra D. Eyring,¹¹ Bao H. Lam,¹¹ Andrew Joe,¹¹ S. Peter Kang,¹¹ Matthias Holdhoff,³ Ludmila Danilova,^{1,3} Leslie Cope,^{1,3} Christian Meyer,³ Shibin Zhou,^{1,3,4} Richard M. Goldberg,¹² Deborah K. Armstrong,³ Katherine M. Bever,³ Amanda N. Fader,¹¹ Janis Tambe,^{1,3} Franck Housseau,^{1,3} David Spetzler,¹⁴ Nianqing Xiao,¹⁴ Drew M. Pardoll,^{1,3} Nickolas Papadopoulos,^{3,4} Kenneth W. Kinzler,^{3,4} James R. Eshleman,¹⁵ Bert Vogelstein,^{1,3,4} Robert A. Anders,^{1,3,15} Luis A. Diaz Jr.^{1,2,3,†}

The genomes of cancers deficient in mismatch repair contain exceptionally high numbers of somatic mutations. In a proof-of-concept study, we previously showed that colorectal cancers with mismatch repair deficiency were sensitive to immune checkpoint blockade with antibodies to programmed death receptor-1 (PD-1). We have now expanded this

The genomes of mismatch repair-deficient tumors all harbor hundreds to thousands of somatic mutations, regardless of their cell of origin. We therefore sought to investigate the effects of PD-1 blockade (by the anti-PD-1 antibody pembrolizumab) in mismatch repair-deficient tumors independent of the tissue of origin. In the current study, we prospectively evaluated the efficacy of PD-1 blockade in a range of different subtypes of mismatch repair-deficient cancers (ClinicalTrials.gov number NCT01875511).

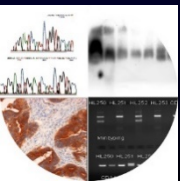
Eighty-six consecutive patients were enrolled between September 2013 and September 2016 (table S1). The data cutoff was 19 December 2016. All patients received at least one prior therapy and had evidence of progressive disease prior to enrollment. Twelve different cancer types were enrolled in the study (Fig. 1). All enrolled patients had evidence of mismatch repair deficiency as assessed by either polymerase chain reaction or immunohistochemistry. For most cases, germline sequencing of *MSH2*, *MSH6*, *PMS2*, and *MLH1* was performed to determine whether the mismatch repair deficiencies were associated with a germline change in one of these genes (i.e., whether the patients had Lynch syndrome) (table S2). Germline sequence changes diagnostic

Le et al., *Science* **357**, 409–413 (2017)

28 July 2017

The rationale for immunotherapy

- Tumours with MSI have a high TMB and enhanced IR to CIs
- Tumours with **microsatellite instability** have a high **tumour mutation burden** and enhanced **immune response to checkpoint inhibitors**
- Tumours which are not MSI may still respond if there is high TMB
- This will be tested using NGS panels



Overview

- Ras testing
- Testing for Lynch Syndrome
 - Loss of Mismatch Repair (MMR) function and leads to microsatellite instability (MSI)
 - IHC versus PCR for loss of MMR function
 - An algorithm for Lynch Syndrome screening
 - Clinical implications of dMMR

