

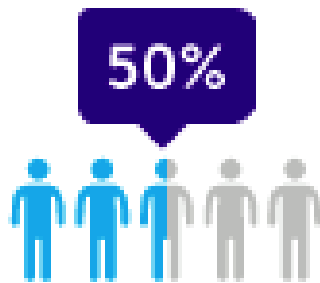


Cancer Validation in the 100,000 genomes project

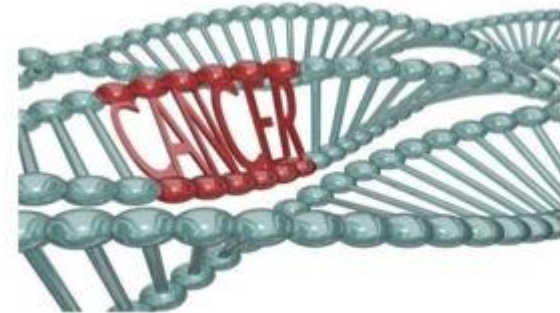
Dr Shirley Henderson
ACGS spring meeting
06/07/16

Cancer is a lesion of the Genome

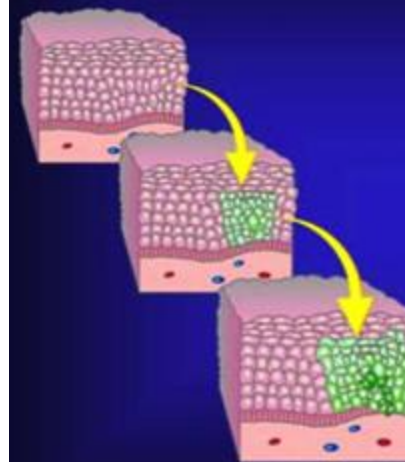
Lifetime risk



1 in 2 people born after 1960 in the UK will be diagnosed with some form of cancer during their lifetime



Cancer-Associated Mutations



- Oncogenes
- Tumor suppressor genes
- DNA repair genes
- Carcinogen
 - activating genes
 - deactivating genes
- Cell cycle genes
- Cell cycle checkpoint genes
- Cell death genes
- Cell signaling genes
- Cellular differentiation genes
- Cellular senescence genes
- Metastasis/invasion genes

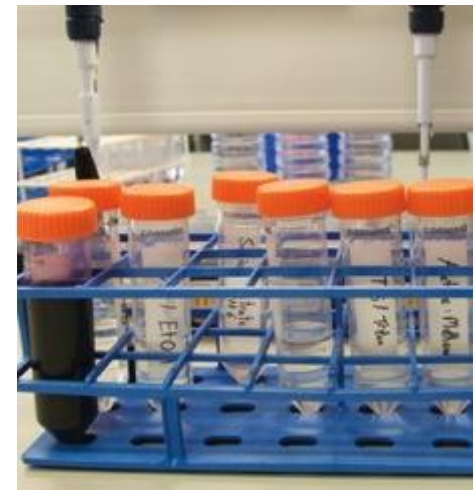
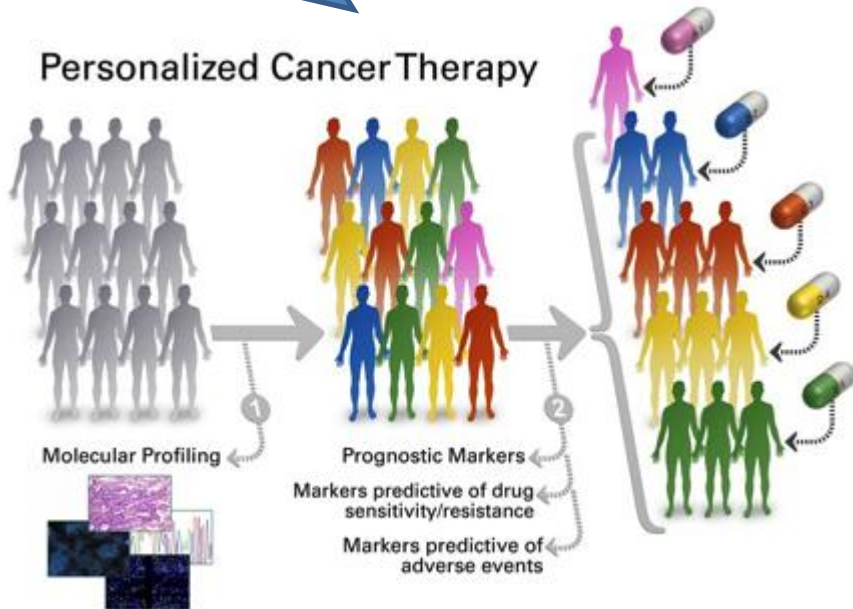


Diagnosis



Prognosis

Cancer Molecular Lesions



Disease Monitoring

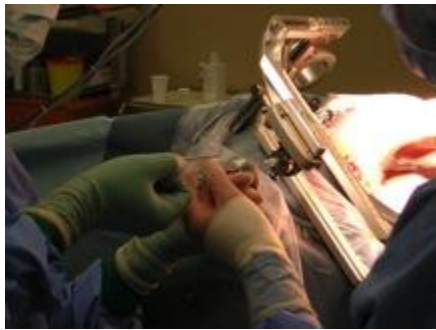
Why is Cancer Challenging?

- **Sample pathway issues**

- Hard to get the DNA –why leukaemia has led the way!
- Complex sample pathway, well established and difficult to change
- Often not much tissue available for DNA extraction after other diagnostic tests have been done
- Sample quality is poor due to tissue processing required for other tests – i.e. formalin. Not DNA friendly

- **Sample issues**

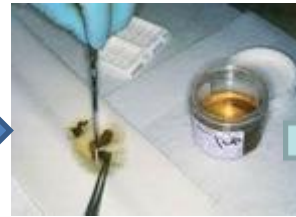
- Samples will be contaminated with normal tissue
- Difficulties in assessing neoplastic content – training required
- Tumours are heterogeneous – different mutations spatially and in frequency.
- Mutation Frequencies can vary from 0-100%



Surgical
Biopsy/resection



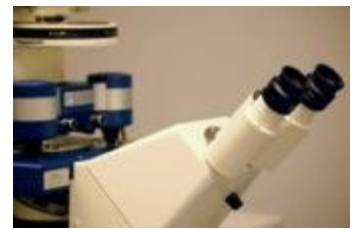
Cut up



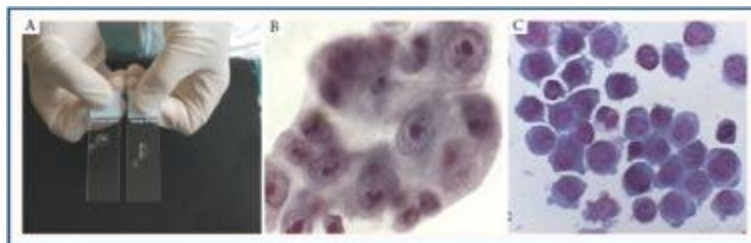
Formalin
fixation



Processing & Paraffin
embedding



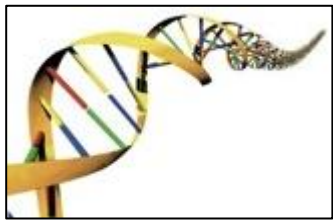
Microscopic examination to
identify neoplastic areas



Macro dissection of neoplastic areas
from mounted sections

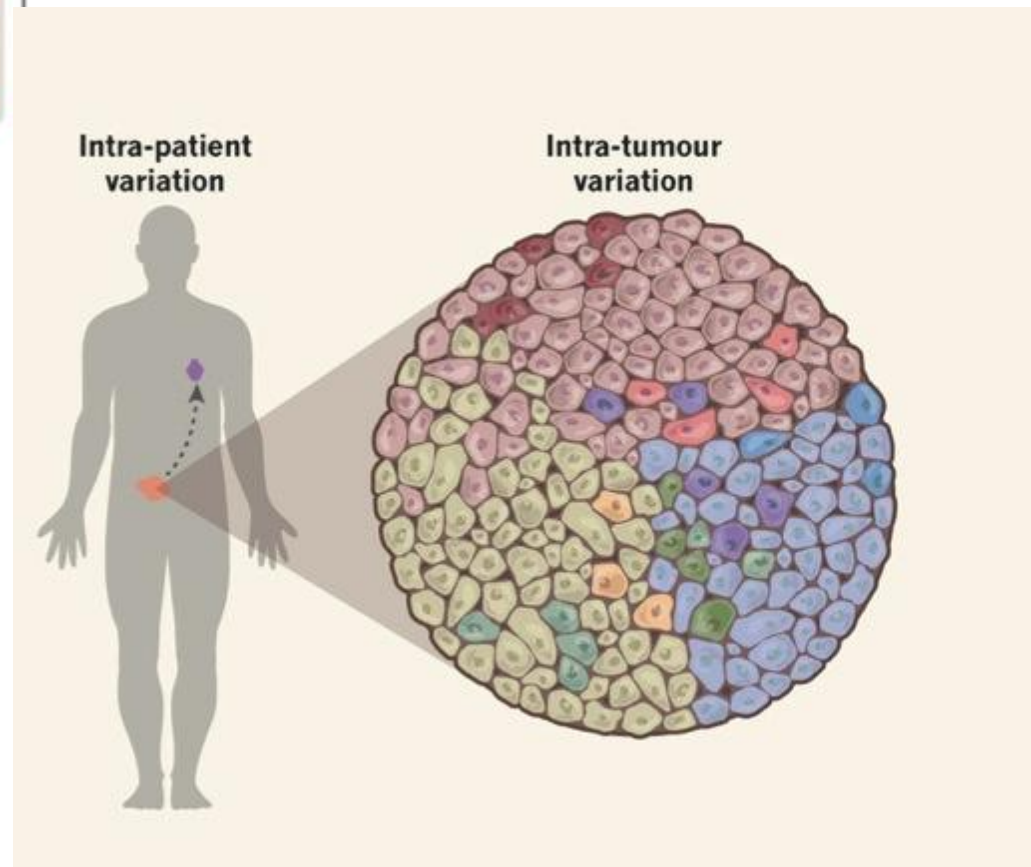
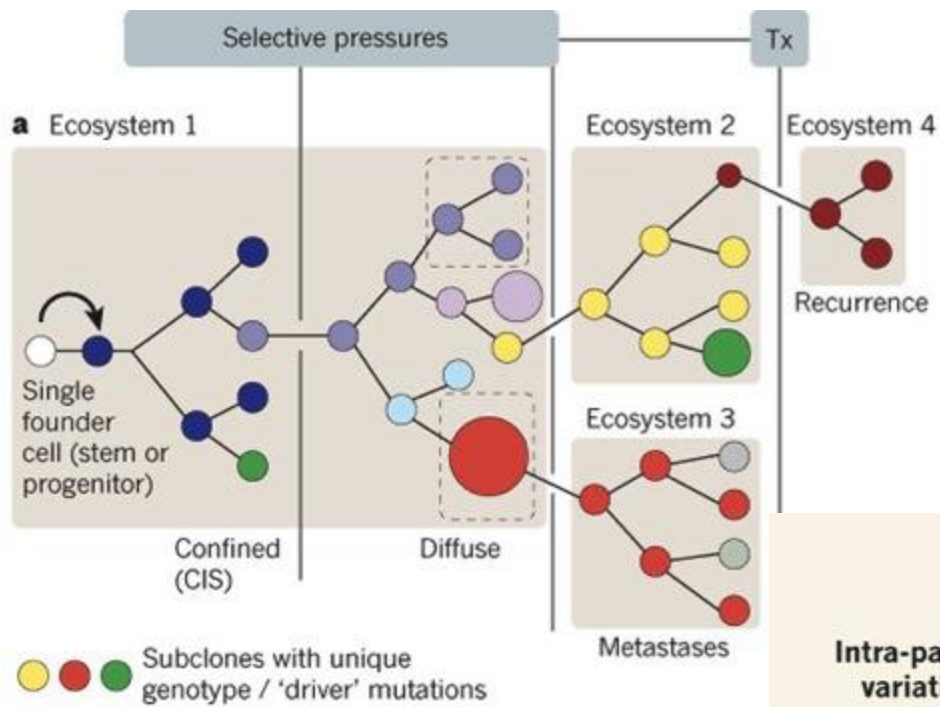


DNA extraction

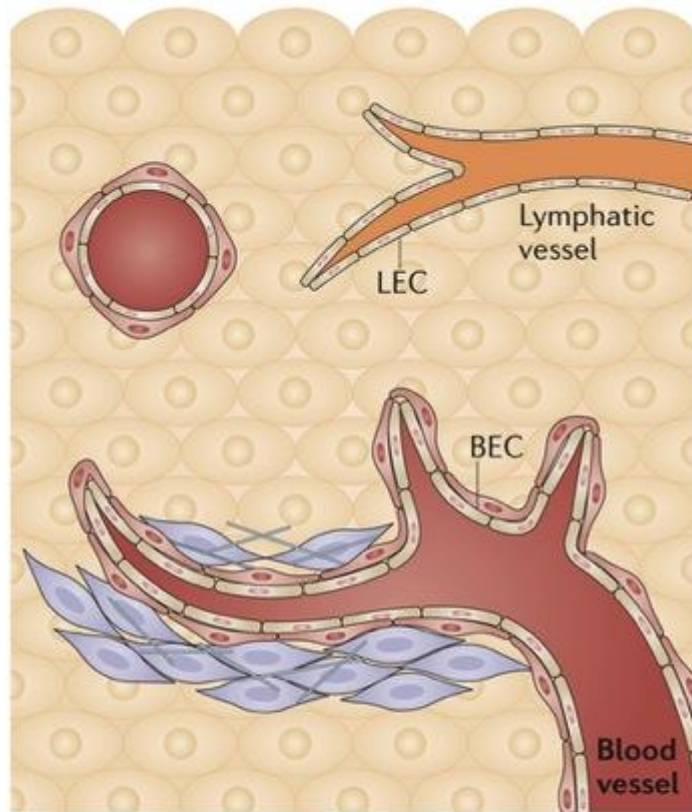


DNA diagnostic test

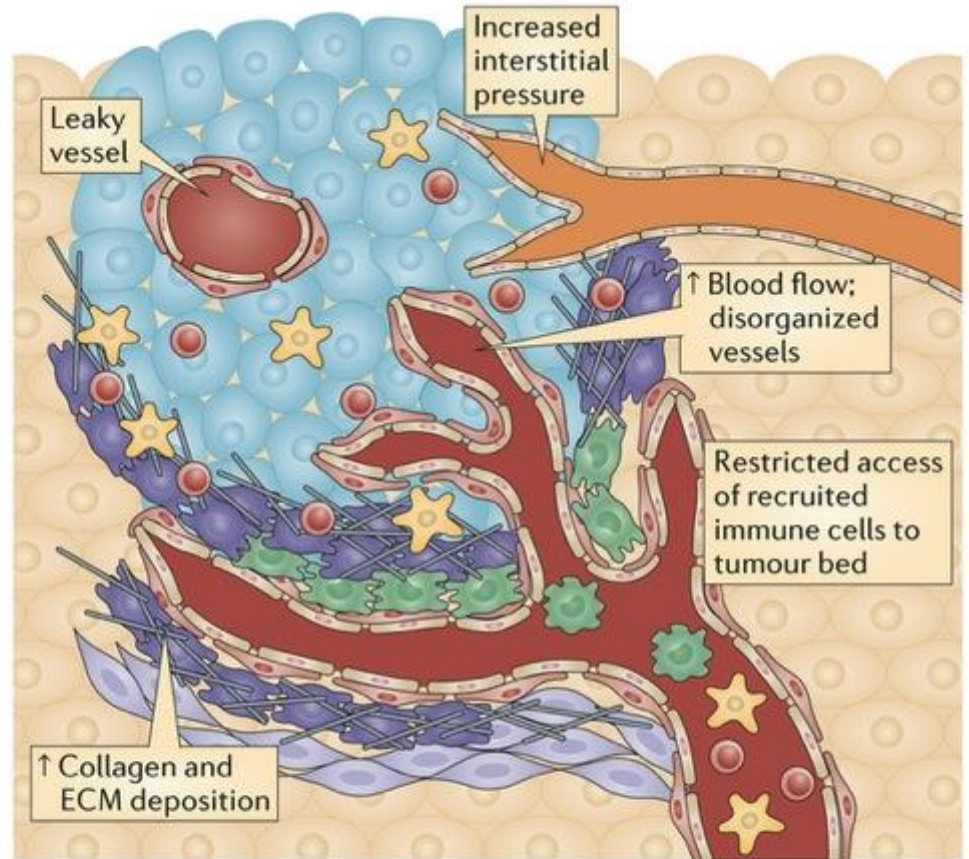
Current clinical pathway for
DNA diagnostics from
biopsy/resection material



a Healthy tissue



b Tumour microenvironment



Evolution of Existing Molecular Pathology Services (or lessons learn 't the hard way.....)

- Careful tumour assessment is required to ensure tumour present - work closely with pathologists
- Macro-dissection to improve neoplastic content
- Use robust methods that will work on low level and poor quality fragmented DNA obtained from FFPE samples
- Select sensitive methods that will detect variants at low frequency (due to tumour heterogeneity or normal tissue contamination) e.g Pyrosequencing & Real Time
- Use of NGS panels increasing – Good sensitivity due to high coverage, often targeted and amplicon based as they work well on low level/poor quality DNA
- Test must be cost effective – Cancer is common and diagnostic tests are not centrally commissioned – it is often unclear who should pay for the test
- Turnaround times must be short.

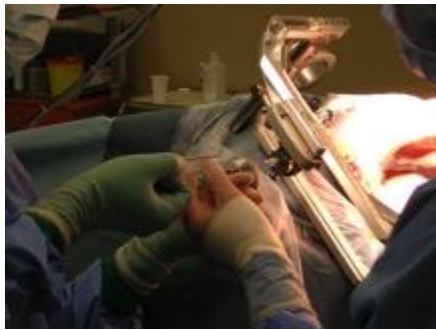
Cancer 100,000 genomes Project

WGS:- Potential to detect all Cancer mutations (CNS, indels, SV, CNVS) – exome and intron

CRUK & BRC WGS Pilots :-WGS quality from FFPE tissue is highly variable between centres and often of poor.

GEL experimental phase 1:-

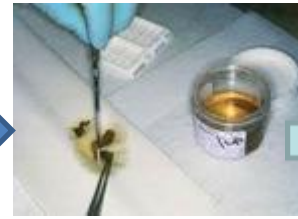
- Tissue handling variables (fixative, length of time in formalin, block size) have a critical effect on the quality of the DNA extracted from FFPE and the downstream WGS
- Optimal tissue handling can certainly improve the quality of WGS from FFPE but currently not to the quality seen from fresh frozen samples.



Surgical
Biopsy/resection



Cut up



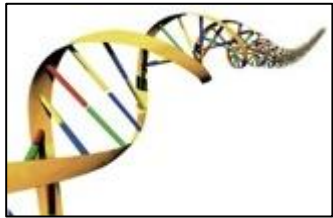
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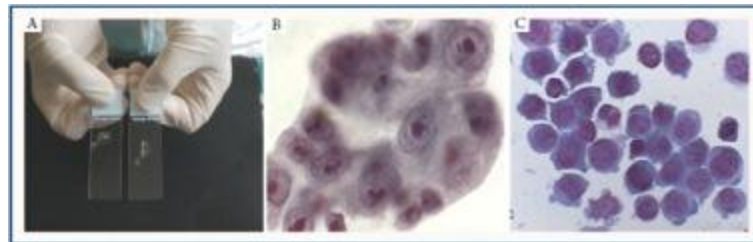
Microscopic examination to
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DNA diagnostic test



DNA extraction



Macro dissection of neoplastic areas
from mounted sections

Current clinical pathway for
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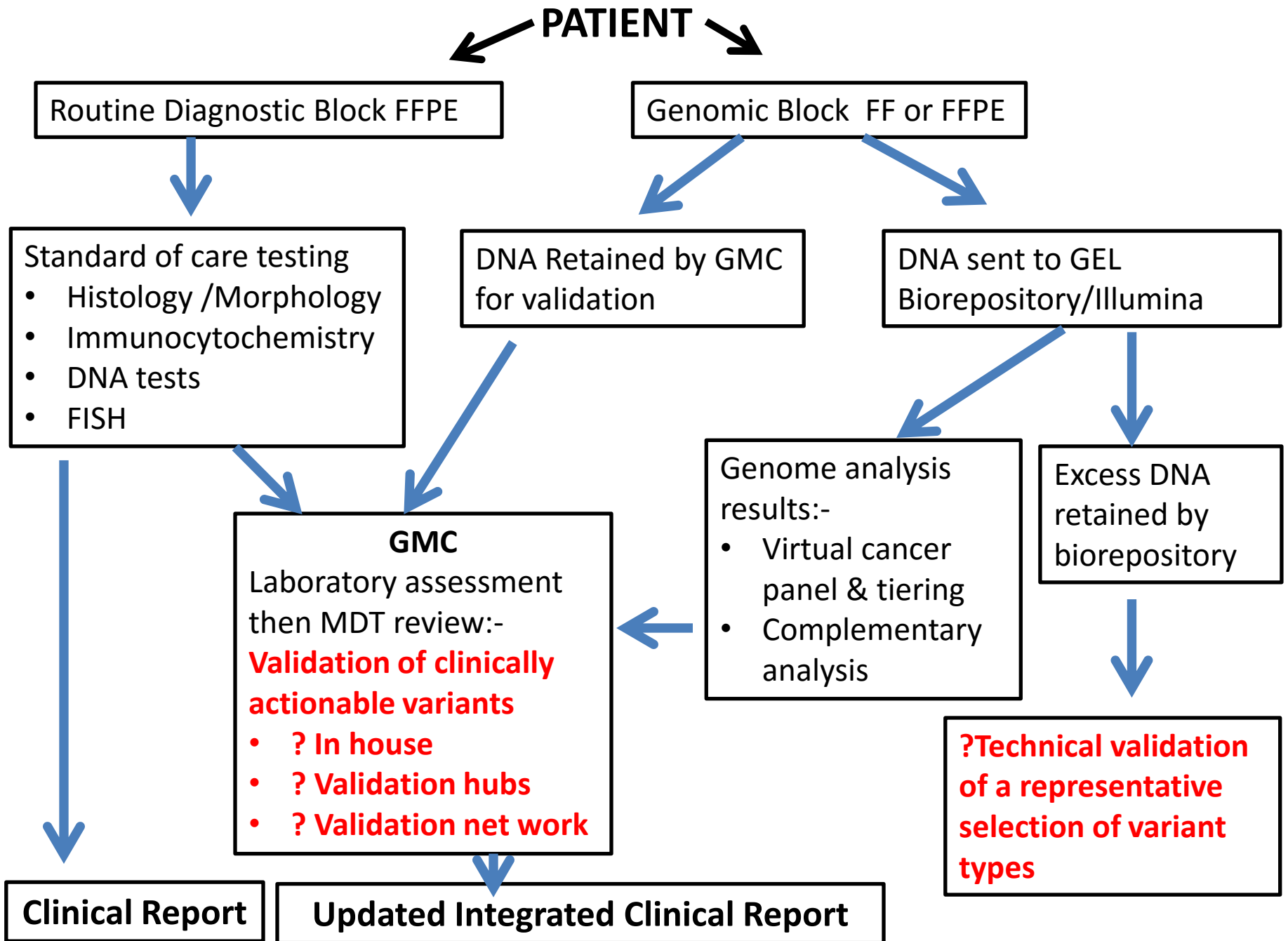
Fresh Frozen

Validation

- GEL WGS pathway not accredited
- Fresh frozen preferred but there will always be occasions when this is not possible. FFPE will be the only option for some patients/tumours
- Confirmatory test used will need to have been validated for FF and FFPE (UKAS requirement)

GMCs will need to validate any results that are going to be clinically acted upon:-

- Drugable
 - Diagnostic
 - Prognostic
-
- Absence of a mutation may be just as clinically actionable as the presence of a mutation. Therefore likely to be necessary to validate negative results on some occasions.
 - Potentially actionable variants will be flagged on the GEL WGS result but the decision as to whether a variant should be acted upon will depend entirely on the Clinical context.



PATIENT

Routine Diagnostic Block FFPE

Genomic Block FF or FFPE

Standard of care testing

- Histology /Morphology
- Immunocytochemistry
- DNA tests
- FISH

DNA Retained by GMC for validation

DNA sent to GEL Biorepository/Illumina

GMC

Laboratory assessment then MDT review:-

Validation of clinically actionable variants

- ? In house
- ? Validation hubs
- ? Validation network

Genome analysis results:-

- Virtual cancer panel & tiering
- Complementary analysis

Excess DNA retained by biorepository

? Technical validation of a representative selection of variant types

Clinical Report

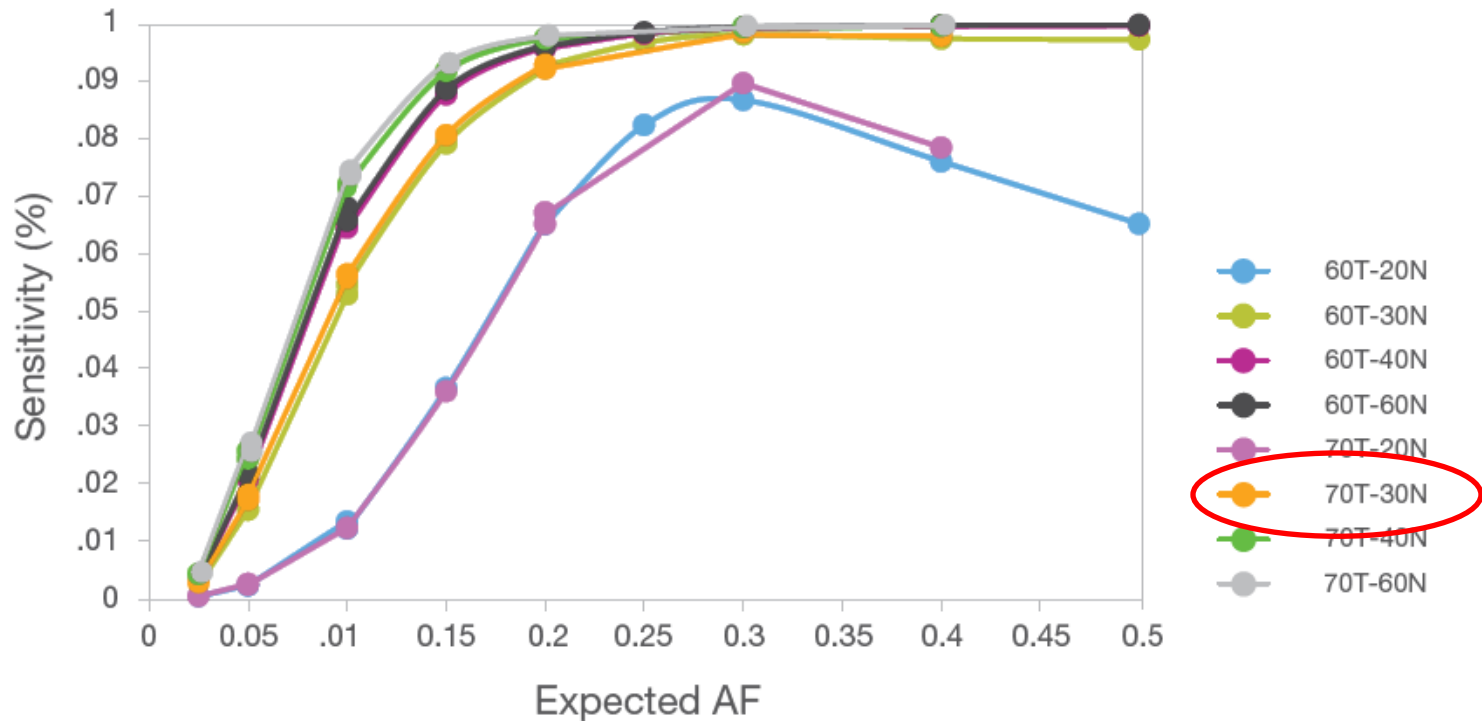
Updated Integrated Clinical Report

How will GMCs validate clinically actionable results?

- Standard of care testing will have already been done
 - wide variation throughout the UK in what people do – some do individual tests others gene panels.
- In-house
 - Generally too time consuming/expensive to set up a whole new assay – Sanger often too insensitive. If panels are already up and running as part of standard of care, the additional genes on them may be useful for validation in some cases.
- Validation Network or Hubs
 - Labs who can test for the various mutations.
- How will the validation tests be funded (in-house or sending away)?

Impact of read depth on somatic variant detection

(Somatic Variant discovery in Cancer - Illumina Application Note:- Cancer genomics)



- **70T-30N**

- alleles with VF of >30% detected with sensitivity of 99%
- Alleles with VF of 20% detected with sensitivity of 90%
- alleles with VF of 15% detected with sensitivity of 80%
- alleles with VF of 10% detected with sensitivity of 55%
- alleles with VF of 5% detected with sensitivity of 18%

Issue of WGS sensitivity and negative results

- Negative results can be just as important as positive results
- The Sensitivity of WGS is not as good as most of the methods currently used in molecular pathology.
- This means standard of care testing will likely flag up some lower level mutations missed by WGS
- How will we ensure Clinicians appreciate the significance of differences in sensitivity between WGS and routine standard of care tests?

Cancer Validation Questions

- **How will the validation networks/hubs be organised?**
- **How will we validate the different mutation types?**
 - SNPs, indels, CNVs, SVs
- **Sensitivity of Cancer validation tests**
 - How sensitive do the tests we use to validate negative results have to be?
 - Should we all be using methods of similar sensitivity for validation?
 - How will we ensure clinical teams understand the differences in sensitivity between WGS and routine services?
- **How can we ensure there is enough DNA for validation?**
 - How much DNA is likely to be left over at the GMC?
 - Is there potential for using the routine diagnostic DNA sample?
- **How can we fund the validation test?**

Acknowledgements

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