



*Better health through
laboratory medicine.*

PEARLS OF LABORATORY MEDICINE

Pearl Title **Molecular Testing of Solid Tumors**

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Introduction

- Molecular testing of solid tumors
 - Complementary to other tests
 - Diagnostic
 - Prognostic and Predictive
 - Therapeutic Targets





Specimen Type

- Formalin fixed paraffin embedded (FFPE): Most common
 - DNA degraded over time to fragments less than 500 base pair in length
 - In vitro mutations (fixation and processing artefacts)
 - Fixation time < 48-72 hours
- Cytology specimens
- Fresh/ snap frozen





Fixatives to Avoid

- Acids in decalcifying solutions damage nucleic acids
- Heavy metals mercuric chloride inhibit enzymes used in amplification



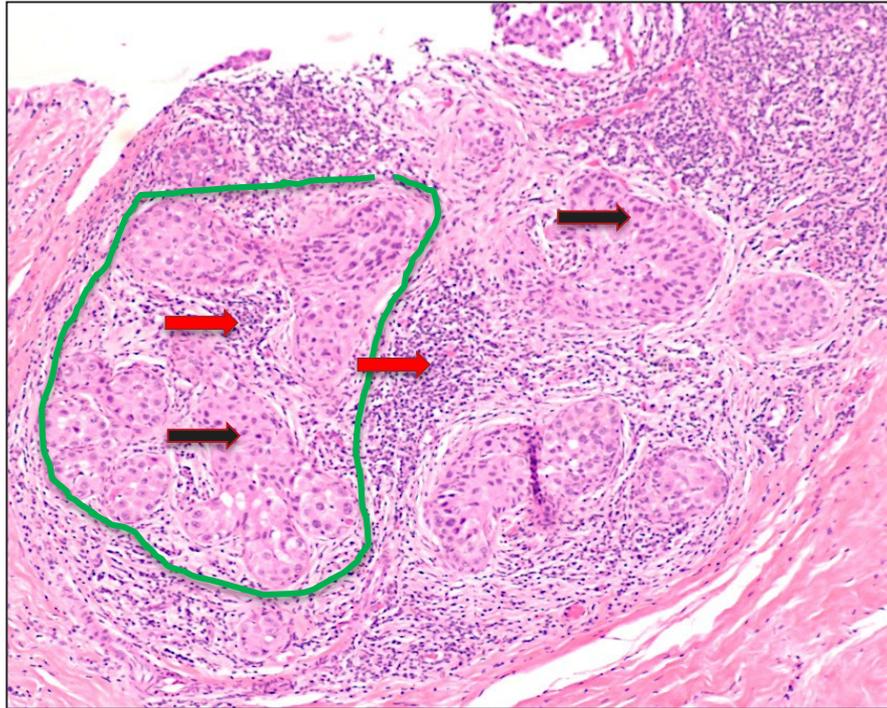


Specimen Selection

- Mark an area enriched for neoplastic cells
 - Cellularity: Preferable to have minimum 30-40% enrichment for neoplastic cells
 - Macro and micro dissection
 - Select best block with highest tumor concentration
 - Inflammatory cells: dilute out the neoplastic cells, careful evaluation
 - Avoid crushed, cauterized cells, necrotic areas

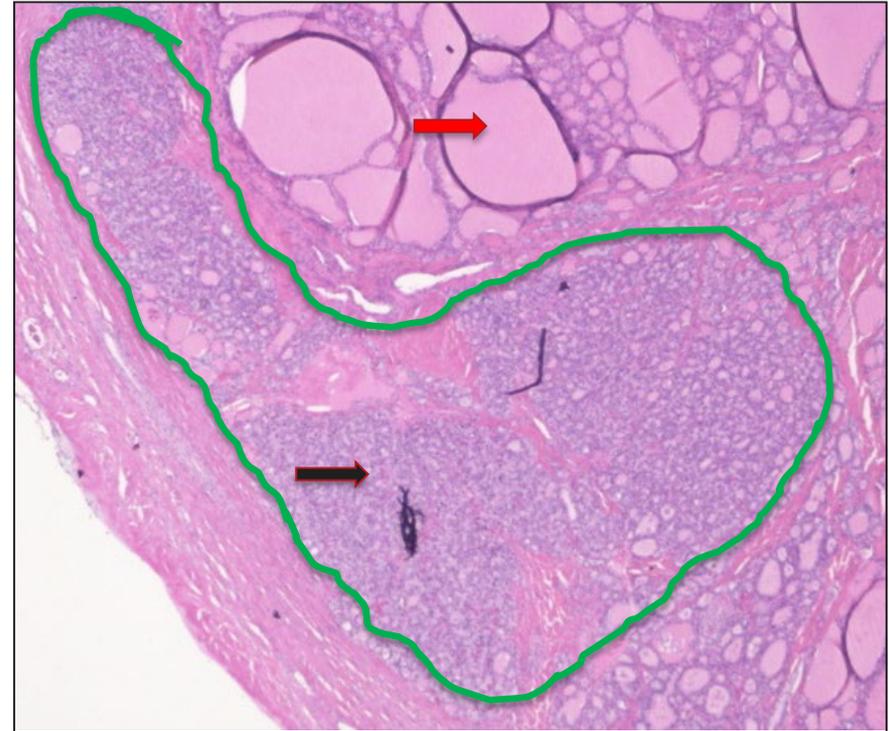


Specimen Selection: Tumor Enrichment



→ Tumor

→ Inflammatory cells

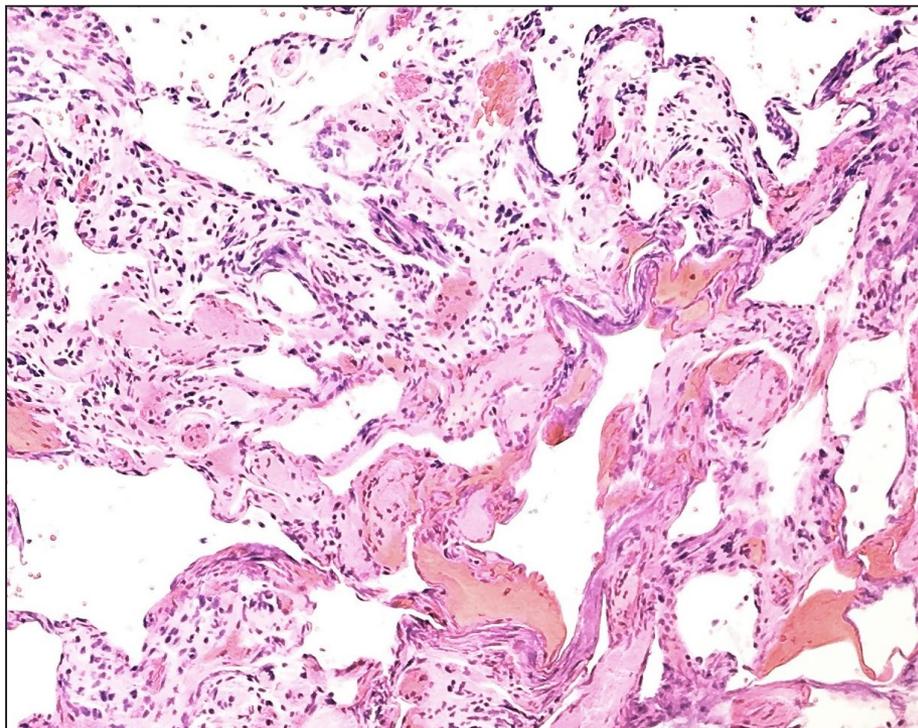
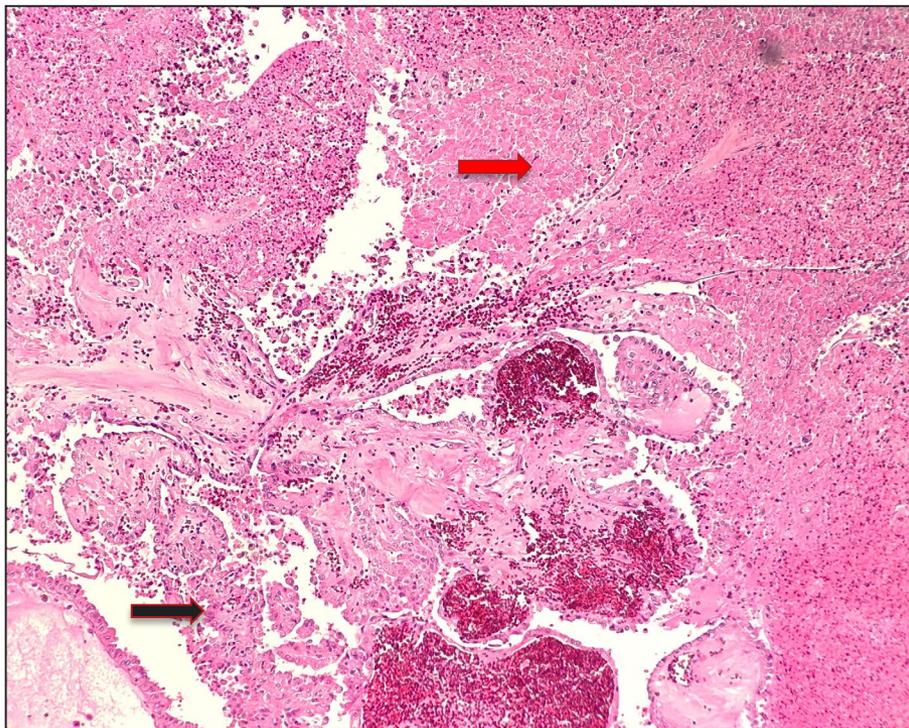


→ Tumor

→ Normal



Specimen Selection: Necrosis and Artefacts



→ Tumor

→ Necrotic Tissue

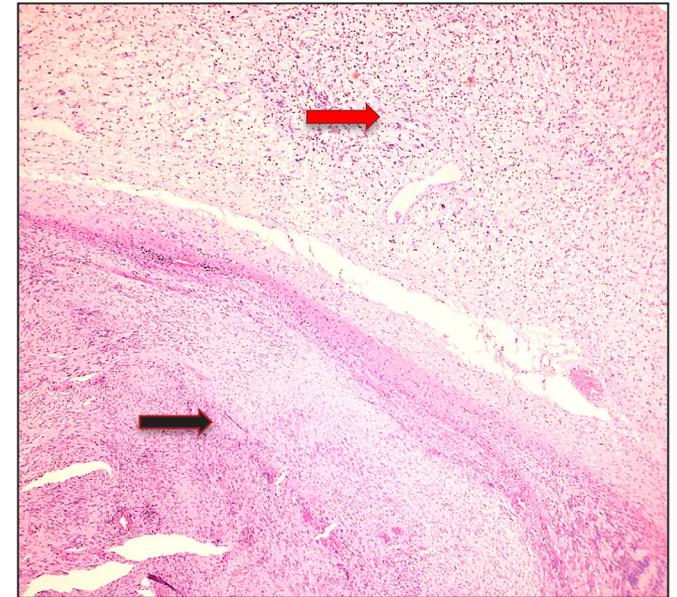
Cauterized Tissue





Specimen Selection: Tumor Heterogeneity

- Tumor heterogeneity
 - Variation in morphology and grade:
 - Selection of higher grade
 - May require testing on different morphologic patterns



→ Tumor with areas of 2 distinctive morphologic patterns



Specimen Selection: Other Considerations

- Choice of tissue: primary/ metastatic
- Tumor and normal tissue
 - Comparative analysis
 - Germline alterations
- Having selected a specimen, the choice of assay is guided by the clinically expected underlying molecular alteration





Clinically Significant Alterations in Solid tumors

- Single base change
- Insertions, deletions
- Duplications, inversions, translocations
- Copy number changes
- Methylation
- Oncogenic viruses





Testing Methodologies to Detect Clinically Significant Alterations

- FISH
- Sanger sequencing
- Single gene tests
- Next generation sequencing
- Methylation testing





Fluorescence in Situ Hybridization (FISH)

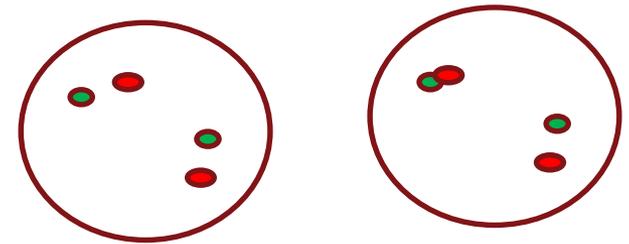
- Fluorescently tagged DNA or RNA probes are used to identify region of interest
 - Gene amplification
 - Gene deletion
 - Structural rearrangements
- Can be done on tissue sections
- Allows for correlation with morphology
- Rapid
- Limited number of probes
- Example:
 - ERBB2 amplification in breast carcinoma
 - ALK rearrangement in Non small cell lung carcinoma



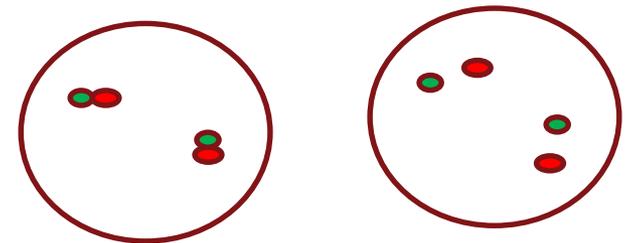


FISH: Fusion Gene Detection

- Dual color FISH probes
 - 2 probes with different wavelengths hybridize to 2 different regions generating 2 different colors
- When fused, they generate a 3rd color



Fusion probes

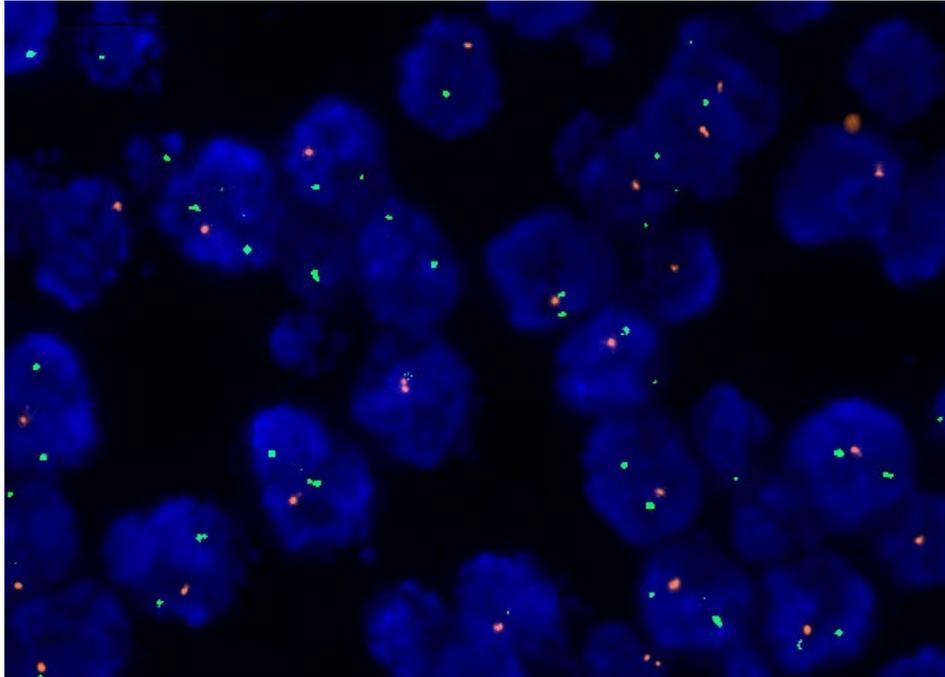


Break apart probes

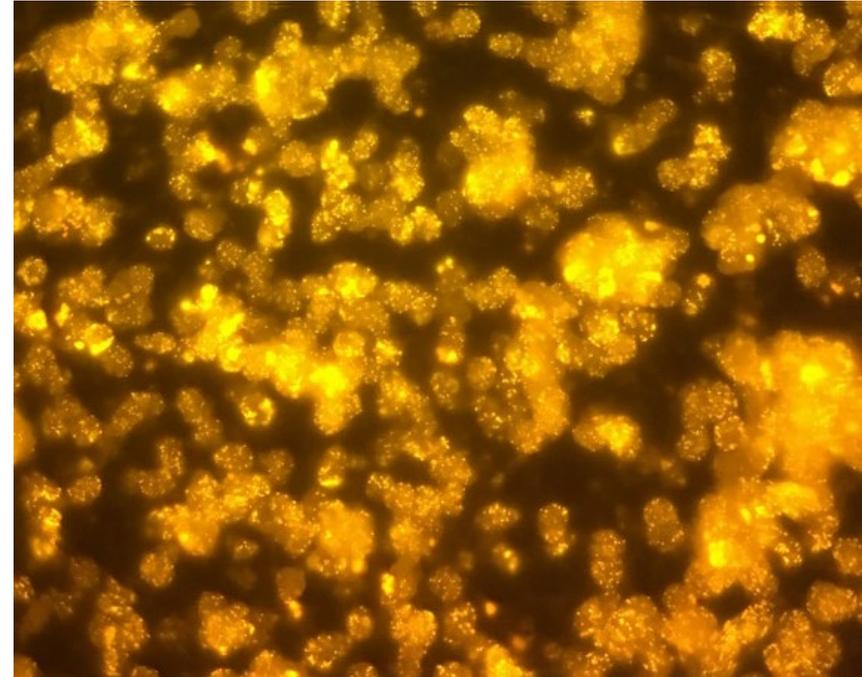




FISH: Deletion and Amplification



1p deletion in gliomas. Seen here is 1 orange test probe directed to 1p and 2 reference green probes



EGFR amplification in a glioma visualized by multiple orange signals in each cell





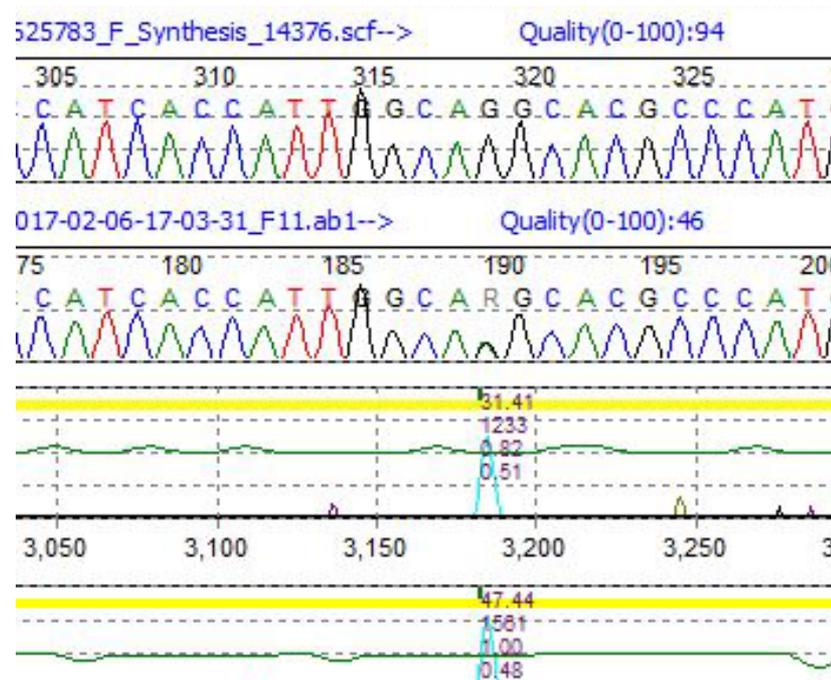
Chromogenic in situ hybridization (CISH)

- Colorimetric probes
- Do not fade with time
- No fluorescent microscope



Sanger Sequencing

- Variant detection
 - Single nucleotide variants (SNVs)
 - Small and medium size insertions/deletions
- Analytic sensitivity ~20%
- Considered the gold standard
- Requires 10ng DNA
- Example: EGFR, BRAF, c-KIT





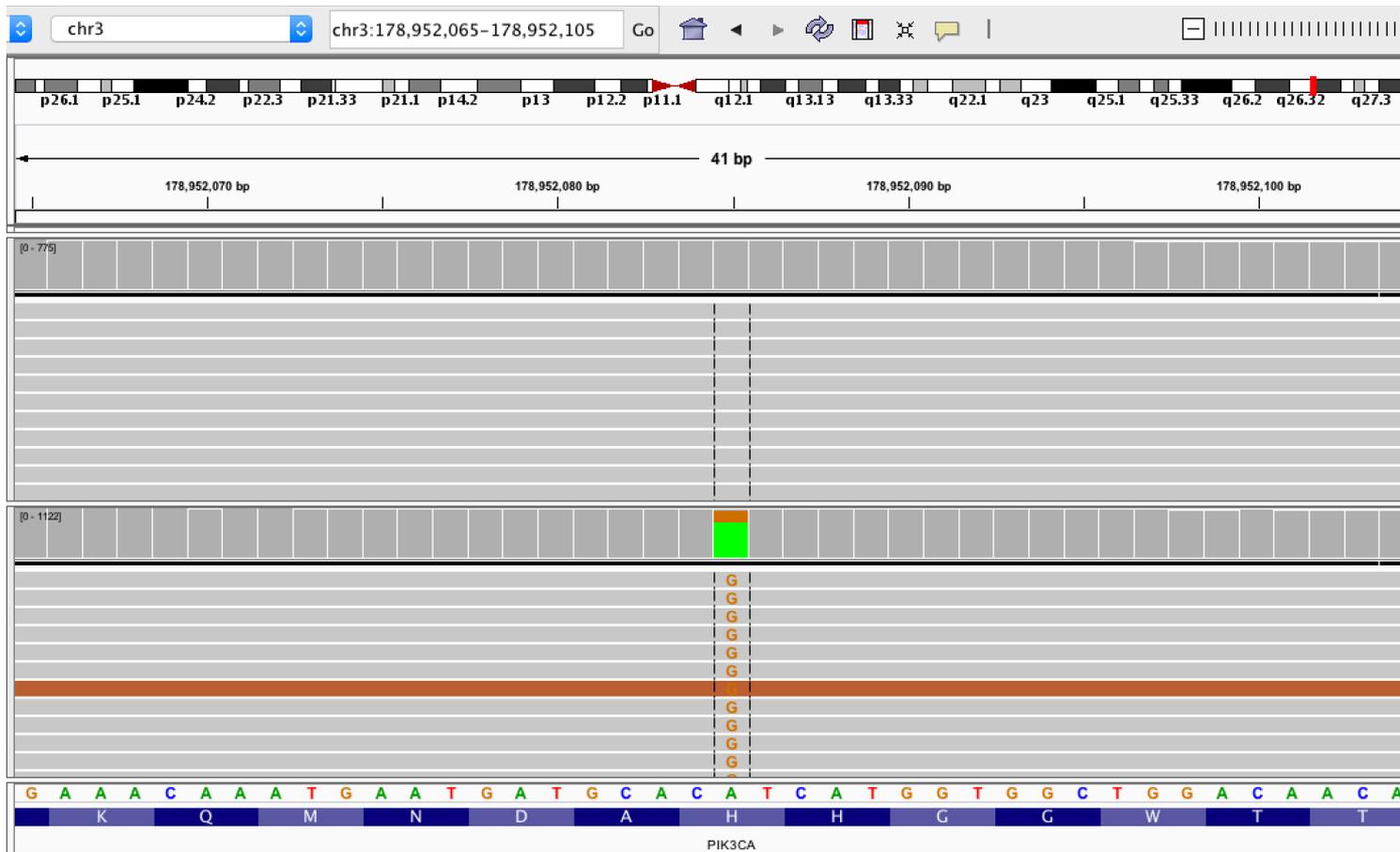
Next Generation Sequencing

- Cost effective way to detect many genetic alterations
 - Single base change
 - Insertions, deletions, duplications, inversions, translocations
 - Copy number changes
- Analytical sensitivity 5% allele frequency
- Requires 100 ng of DNA
- Shorter read lengths compared to Sanger





Single Base Changes/ Small- Medium Indels



Normal

Tumor

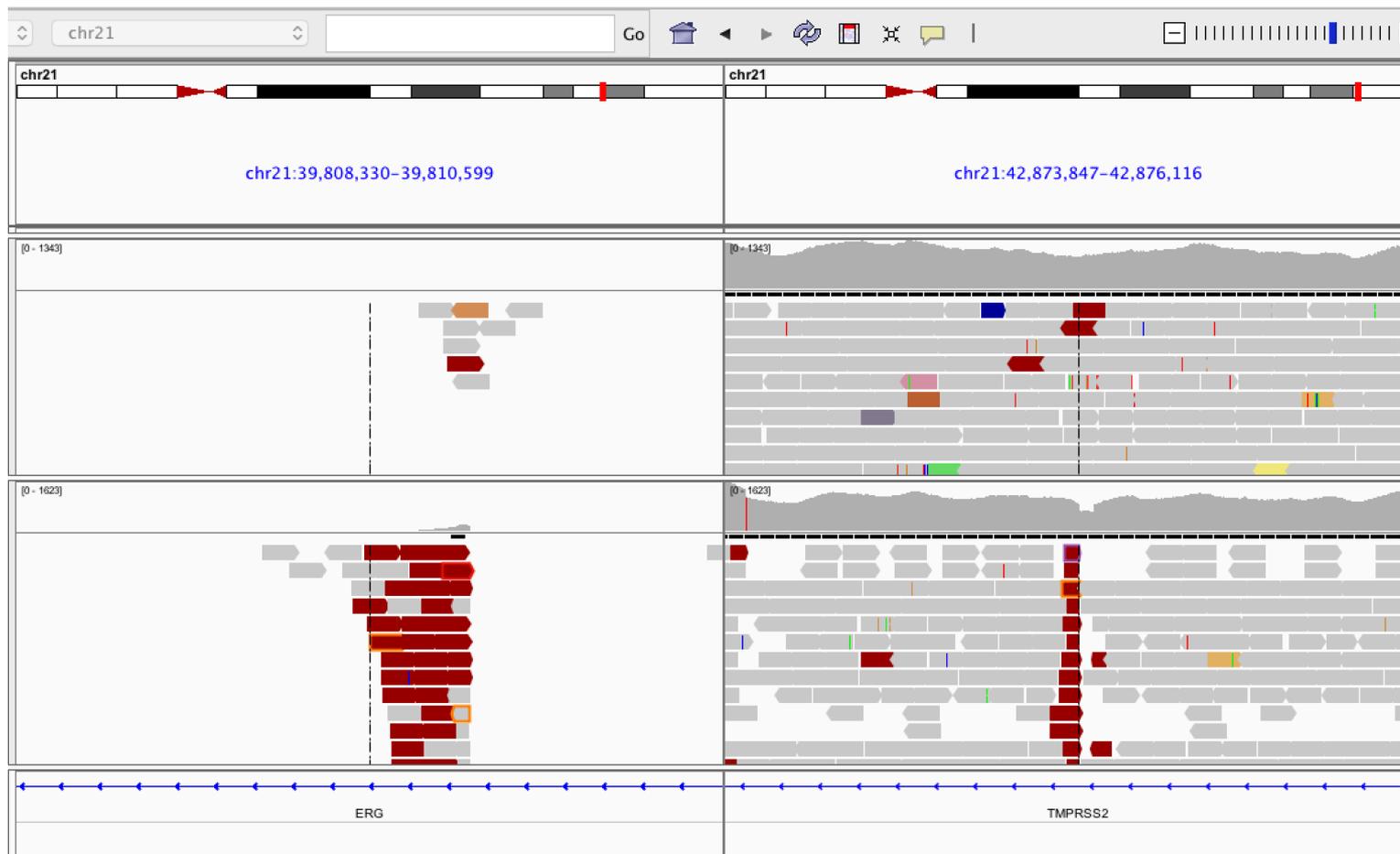




Structural Variants

Normal

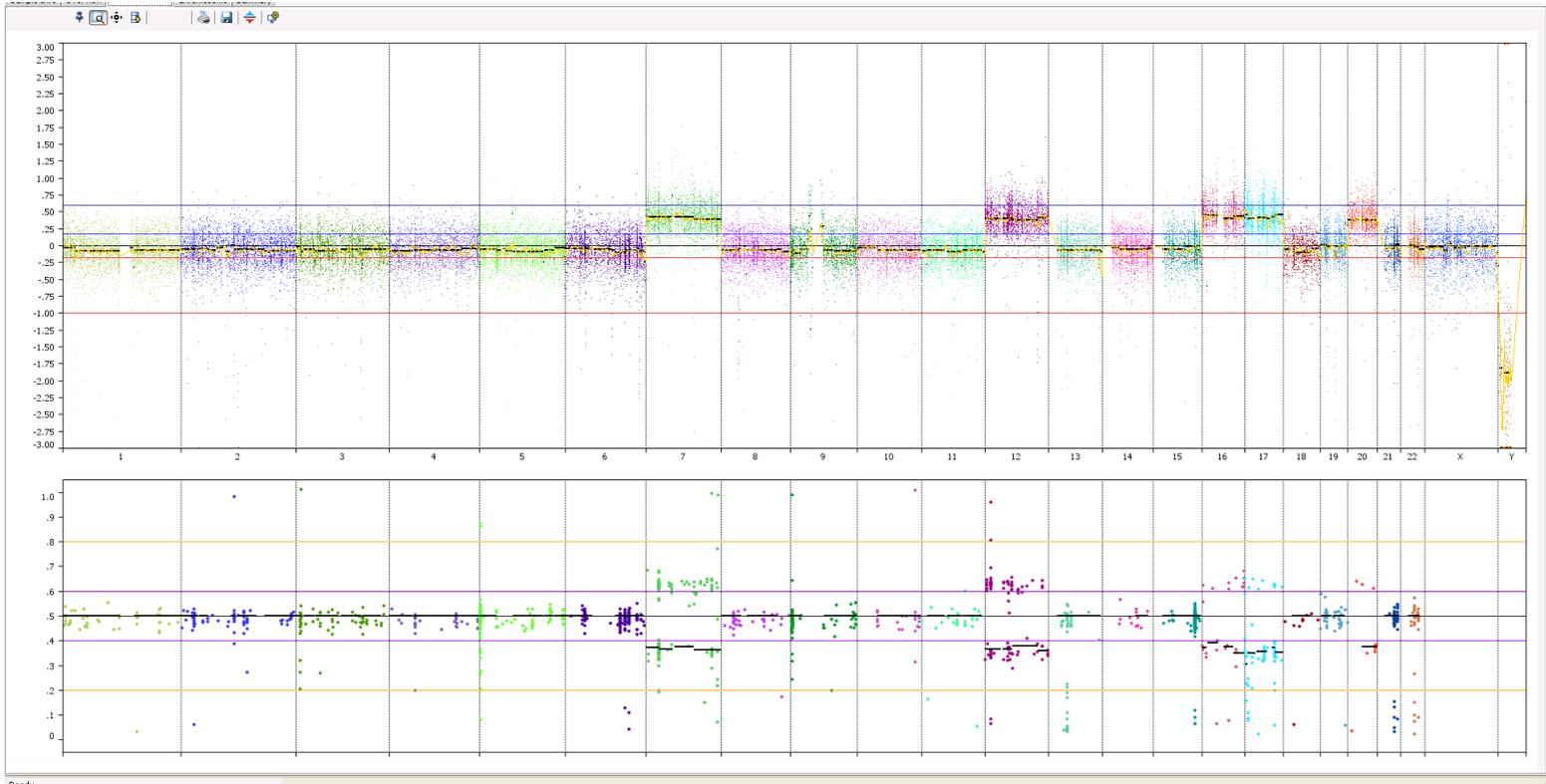
Tumor





Copy Number Changes

Log 2 ratio



B Allele frequency





DNA Methylation

- CpG dinucleotides present in 5' promoter regions of genes
- Prone to spontaneous methylation of Cytosine that results in silencing of the gene
- Methylation of tumor suppressor genes is a frequent mechanism of inactivation in cancers





DNA Methylation

- Treatment with sodium metabisulfite converts unmethylated cytosine to uracil, leaving methylated cytosine intact
- Cytosine and uracil can then be distinguished by different methods
 - Sequencing
 - Methylation specific PCR
 - Restriction endonuclease digestion with methylation-sensitive enzymes
- MLH1 hypermethylation
- MGMT methylation





Summary

- Major advancements in molecular testing of solid tumors
- Correct sample selection and assessment is crucial to solid tumor testing
- Assay selection based on specific molecular alteration in consideration



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Disclosures/Potential Conflicts of Interest

Upon Pearl submission, the presenter completed the Clinical Chemistry disclosure form. Disclosures and/or potential conflicts of interest:

- **Employment or Leadership:** No disclosures
- **Consultant or Advisory Role:** No disclosures
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