Cytogenetics

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National Institutes of Health

NIH NATIONAL CANCER INSTITUTE
Center for Cancer Research

6/20/2025

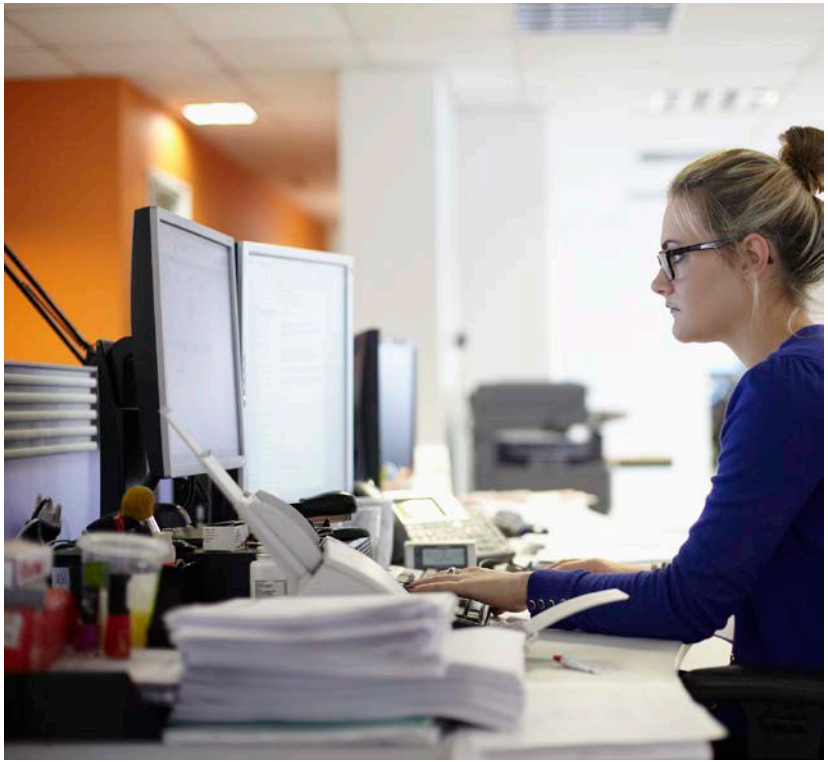
Disclosure to Participants

- To participate in the CEU course, participants must have:
  - Already enrolled to the Quality Assurance Webinar June 20, 2025 - Cytogenetics course in ExpertusOne.
  - Joined the webinar via their individual login. If you are attending as a group in a conference room, only the person that logged into the ExpertusOne system can obtain CEUs for participation.
- To receive 1.0 CEU contact hour the participant must:
  - **Attend the entire educational activity and then complete and submit the post activity-evaluation form via the Survey Monkey link that will be provided via WebEx chat message at the conclusion of the webinar.**
  - CEU certificates for webinar participation will be batch-issued, approximately one week after the webinar, to all attendees who have completed the post-activity evaluation.
  - Note: For site staff who were unable to attend the entire webinar: 1 hour CEU will also be offered via review of the webinar recording and completion of the post-course evaluation within a forthcoming CTSU CLASS SWOG: Cytogenetics course, which will be posted ~2-3 weeks after the webinar. When available in CLASS, the link to the post-meeting enduring course will be accessible from: SWOG Quality Assurance Live Webinar Series and the CTSU CLASS catalog.
- There is no relevant financial relationships with ineligible companies for those with the ability to control content of this activity exist.
- This nursing continuing professional development activity was approved by the Georgia Nurses Association, an accredited approver by the American Nurses Credentialing Center's Commission on Accreditation.
- Georgia Nurses Association Approval Code: 203266399.
- The expiration date of this activity is June 12, 2027.

Objectives

Participants will be able to:

- List one benefit evidence-based use of cytogenetic testing.
- Identify specific sections of a cytogenetic report
- Identify abnormalities in genomic findings.



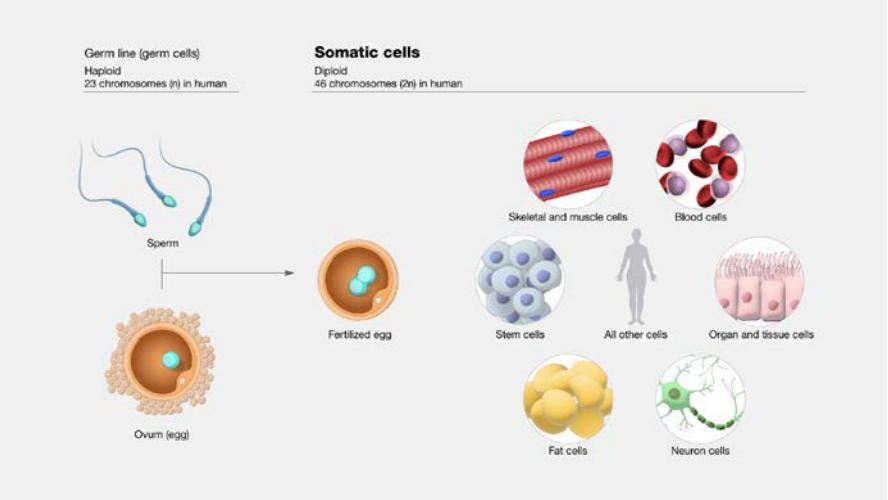
Poll Question 1

Have you had any formal training in genomics?

1. Yes
2. No
3. Not sure

Genomic Key Concepts

- Genetics versus genomics
  - Having to do with genes which are sequences of DNA that contain information for making specific RNA molecules or proteins that perform important functions in a cell
  - Genomics is the complete set of DNA (including all of its genes) in a person or other organism



- Somatic versus germline genetic variants
  - Somatic variants occur after conception and cannot be passed on to children
  - Germline variants are inherited at the time of conception

https://www.genome.gov/genetics-glossary/Somatic-Cells
https://www.cancer.gov/publications/dictionaries/cancer-terms/def/genetic
https://www.cancer.gov/publications/dictionaries/cancer-terms/expand/G

Deoxyribonucleic Acid (DNA)

- DNA is made up of four nucleotides:
- Adenine (A), Thymine (T), Guanine (G), Cytosine (C).
- Nucleotides attach to each other (A with T, and G with C) to form chemical bonds called base pairs, which connect the two DNA strands.
- Genes are made up of sequences of nucleotides at specific locations on chromosomes in the nucleus of cells.
- The DNA sequence provides the code for making specific proteins that lead to the expression of a particular physical characteristic or traits, i.e. eye color, or specific cell functions.

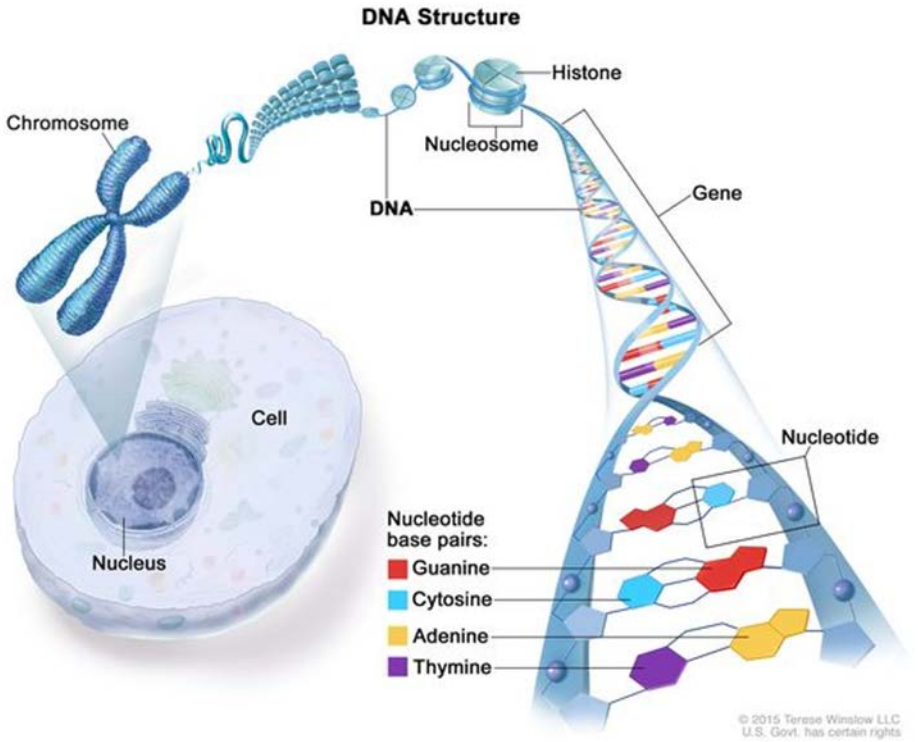
Proteins

- Proteins are large, complex molecules that play many important roles in the body.
- Proteins are essential to the work done by cells
- Required for the structure, function and regulation of the body's tissues and organs.
- A protein is made up of one or more long, folded chains of amino acids
- Amino acid sequences are determined by the DNA sequence of the protein-encoding gene.

https://www.genome.gov/genetics-glossary/Protein

Chromosomes

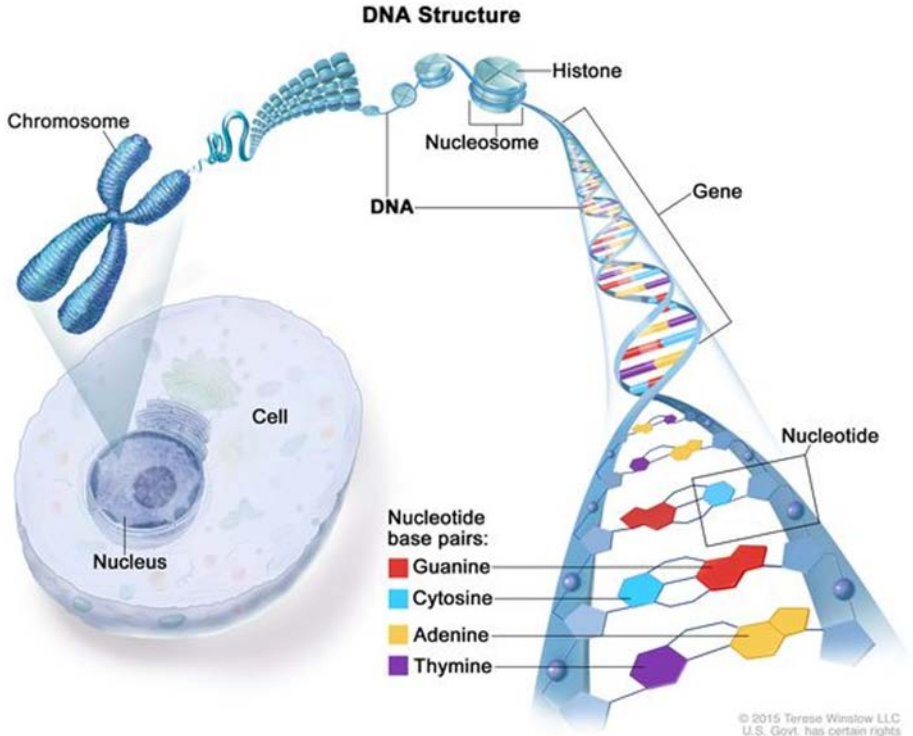
- Located inside the nucleus of a cell
  - A chromosome is made up of proteins and DNA organized into genes
  - Each cell normally contains 23 pairs of chromosomes
    - One chromosome from each parent
  - Telomeres are the ends of chromosomes
    - Shorten with age



https://www.genome.gov/about-genomics/fact-sheets/Chromosome-Abnormalities-Fact-Sheet
https://www.genome.gov/genetics-glossary/histone
https://www.cancer.gov/publications/dictionaries/genetics-dictionary/def/telomere

Chromosomes, cont

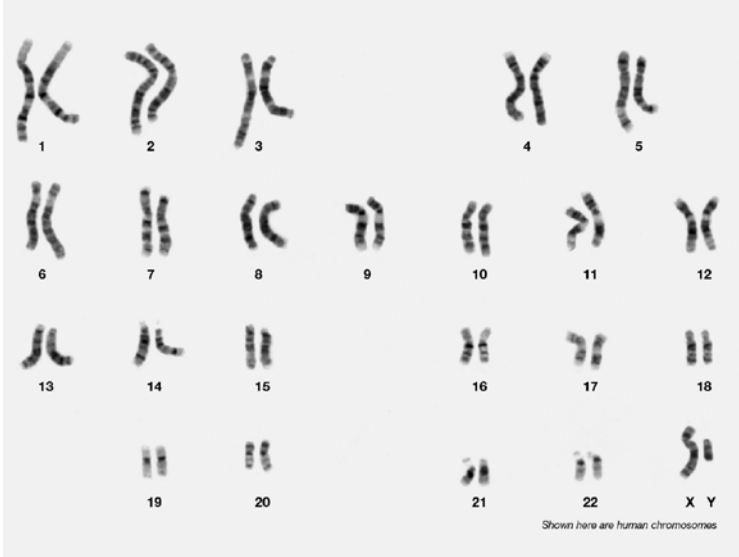
- Separated by a pinched region, the centromere. The shorter arm is called the "p" arm. The longer arm is called the "q" arm
- Chromosome contain a long molecule of DNA, which must fit into the cell nucleus
  - DNA wraps around histone proteins, giving the chromosome a more compact shape
  - Histones also play a role in regulation of gene expression

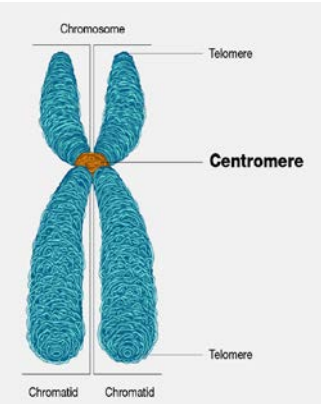


https://www.genome.gov/about-genomics/fact-sheets/Chromosome-Abnormalities-Fact-Sheet
https://www.genome.gov/genetics-glossary/histone

Cytogenetics

- The study of chromosomes and their inheritance
  - Can be germline or somatic
- Staining techniques can be used to assess the number and structure of a person's chromosomes as part of diagnostic testing.
- The number and/or structure of chromosomes
  - Known to be altered in certain genetic diseases including cancer
  - Autosomes Chr 1-22, Sex Chr XX or XY, short arm p, long arm q, centromere-thin part that joins the arms, telomere-end of chromosome

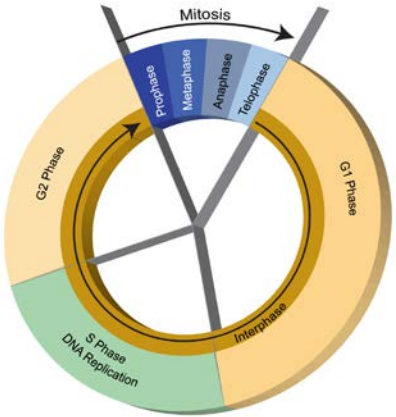


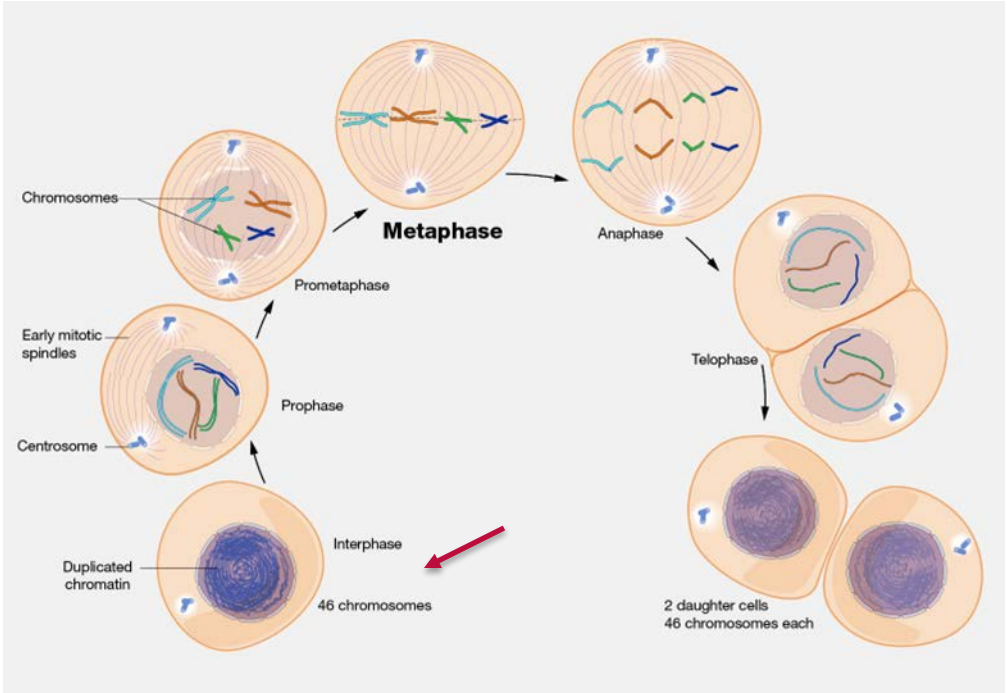


https://www.genome.gov/genetics-glossary/Cytogenetics;
https://www.genome.gov/genetics-glossary/Centromere
https://www.genome.gov/genetics-glossary/Telomere

Interphase

- A cell spends most of its time in **Interphase**
  - Grows
  - Replicates
  - Prepares for cell division

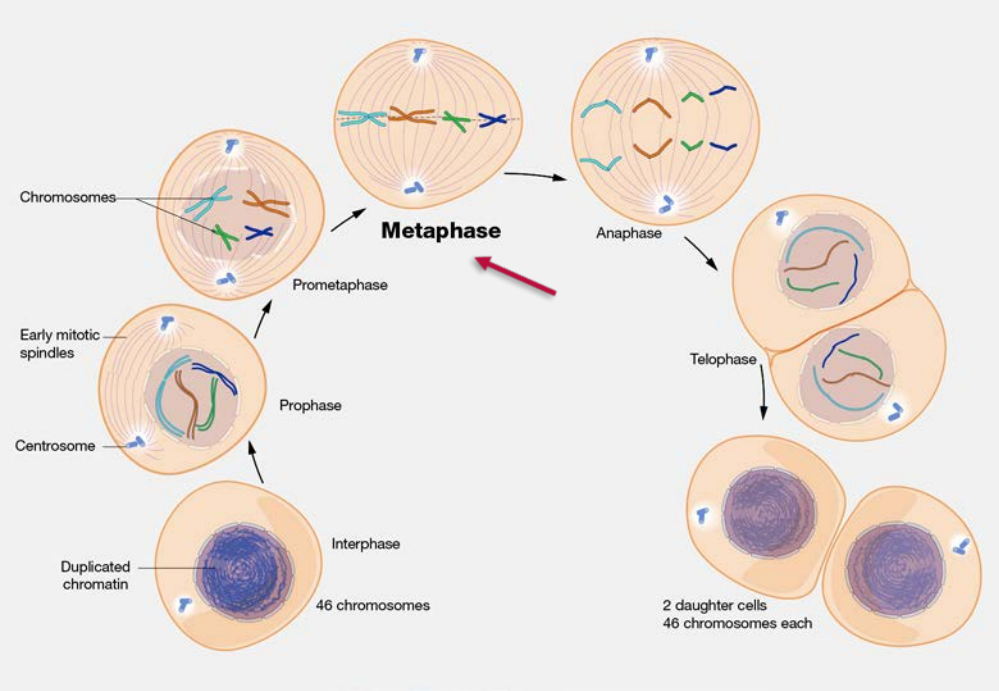




https://www.genome.gov/search?terms=interphase

Metaphase

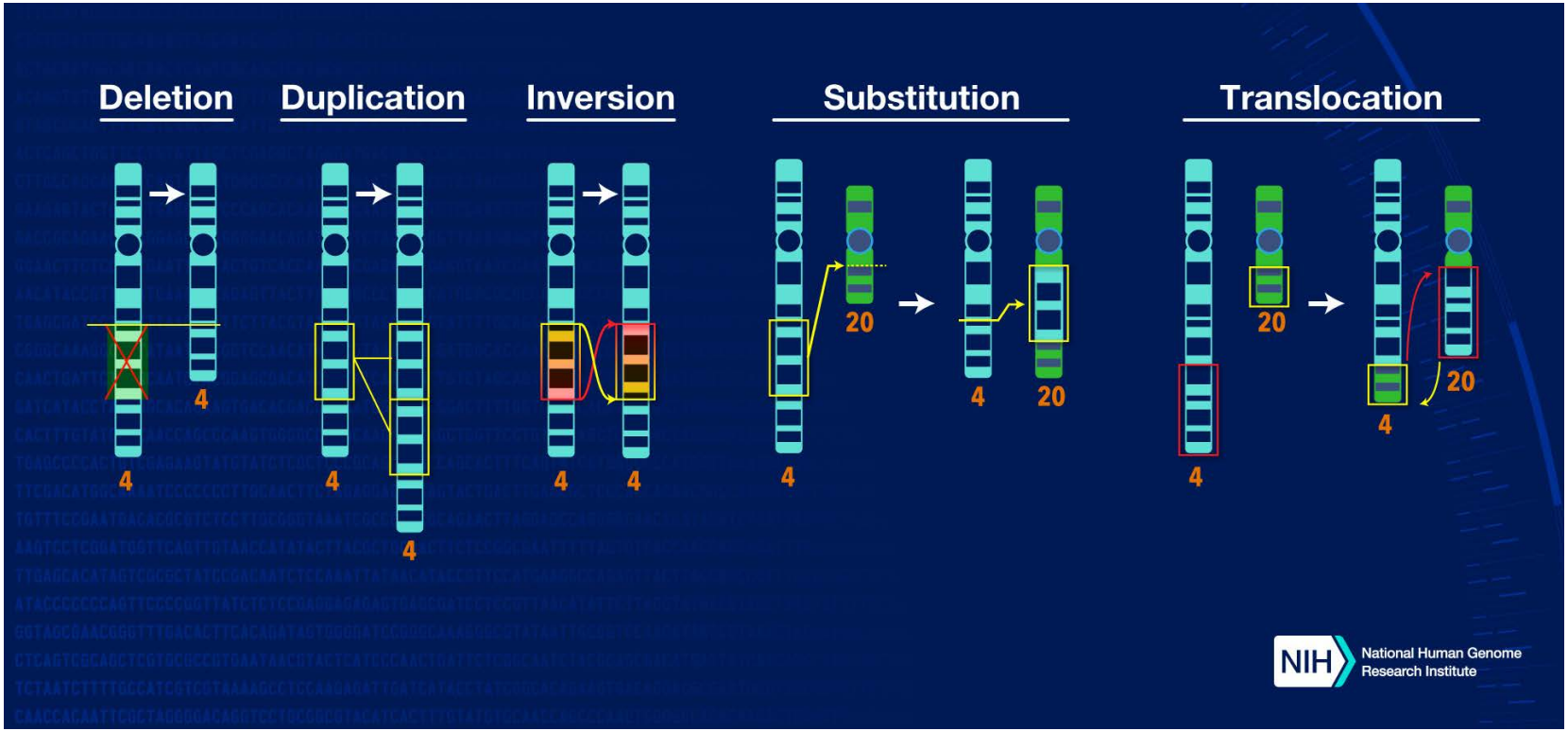
- Metaphase is a stage during the process of cell division (mitosis or meiosis).
  - The nucleus dissolves and the cell's chromosomes condense and move together, aligning in the center of the dividing cell.
  - Chromosomes are distinguishable when viewed through a microscope.
  - Metaphase chromosomes are used in karyotyping.



Mitosis-cellular process that replicates chromosomes and produces two identical nuclei in preparation for cell division.
Meiosis-type of cell division in which each daughter cell receives half the amount of DNA as the parent cell. Meiosis occurs during formation of egg and sperm cells in mammals.

https://www.cancer.gov/publications/dictionaries/cancer-terms/def/meiosis; https://www.genome.gov/genetics-glossary/Mitosis
https://www.genome.gov/genetics-glossary/Metaphase

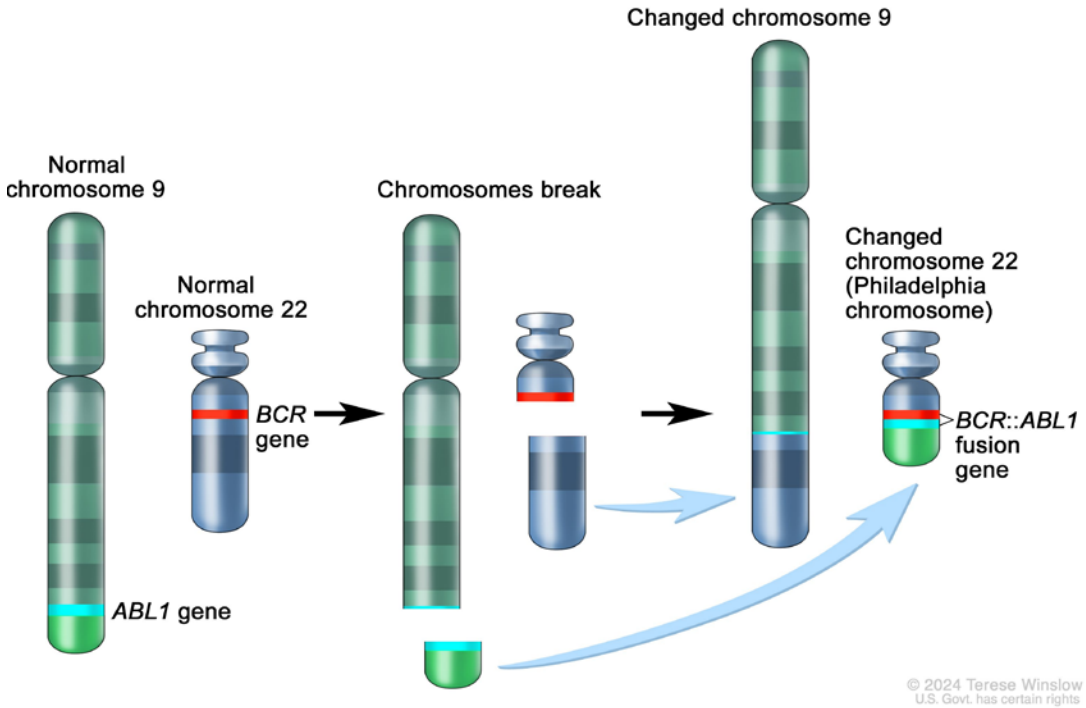
Chromosome Abnormalities



https://www.genome.gov/about-genomics/fact-sheets/Chromosome-Abnormalities-Fact-Sheet

Example: Philadelphia Chromosome

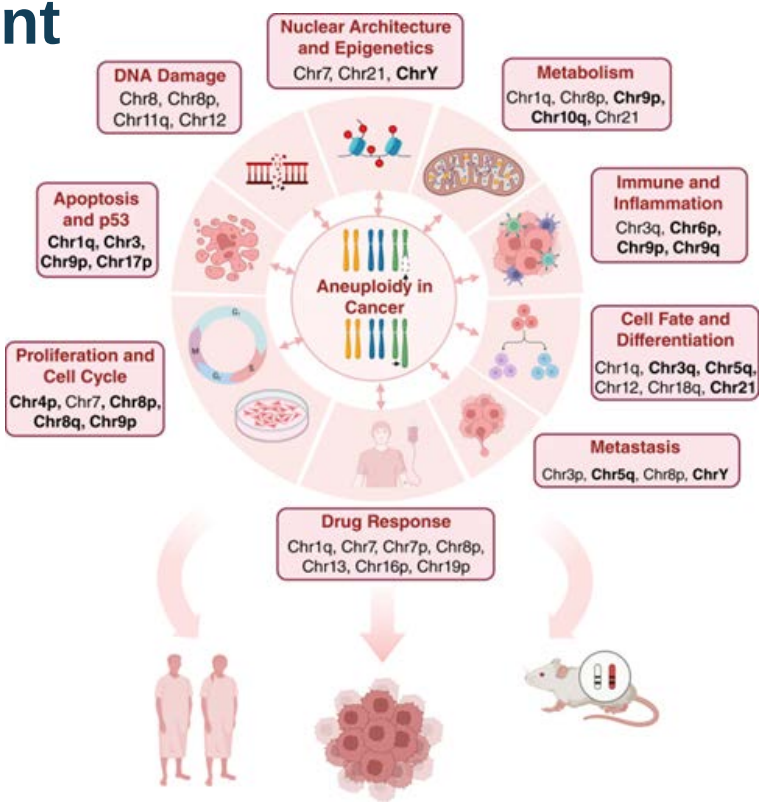
- Translocation results in an abnormal fusion gene *BCR::ABL1*
- The protein made by *BCR*::*ABL1* fusion gene results in growth of immature white blood cells
- Associated with chronic myelogenous leukemia and some acute lymphocytic leukemia or acute myelogenous leukemia
- Discovered in 1960



https://www.cancer.gov/publications/dictionaries/cancer-terms/def/philadelphia-chromosome

Chromosome Abnormalities, cont

- Aneuploidy
  - The occurrence of one or more extra or missing chromosomes in a cell or organism due to loss or duplication
    - i.e. Trisomy-presence of three copies of a specific chromosome in some or all of the body's cells instead of the usual two copies
  - The most prevalent genomic change in cancer



Zhakula-Kostadinova, N., Alison M. Taylor, A.M. (2024). Patterns of Aneuploidy and Signaling Consequences in Cancer. Cancer Res. 84, 2575-2587.

Shih, J. et al. (2023). Cancer aneuploidies are shaped primarily by effects on tumour fitness. Nature, 619, 793–800.

https://www.cancer.gov/publications/dictionaries/genetics-dictionary/def/aneuploidy

https://www.genome.gov/genetics-glossary/Aneuploidy

https://www.cancer.gov/publications/dictionaries/cancer-terms/def/trisomy

Mosaicism

- Mosaicism refers to the presence of cells in a person that have a different genome from the body's other cells.
  - Could be due to a specific genomic variant, for example, or the addition or loss of a chromosome.
  - A genetic change that occurs after fertilization of an egg, during very early embryo development, or it could occur later in development.
  - Mosaicism can affect any type of cell and does not always cause disease.

https://www.genome.gov/genetics-glossary/Mosaicism

Poll Question 2

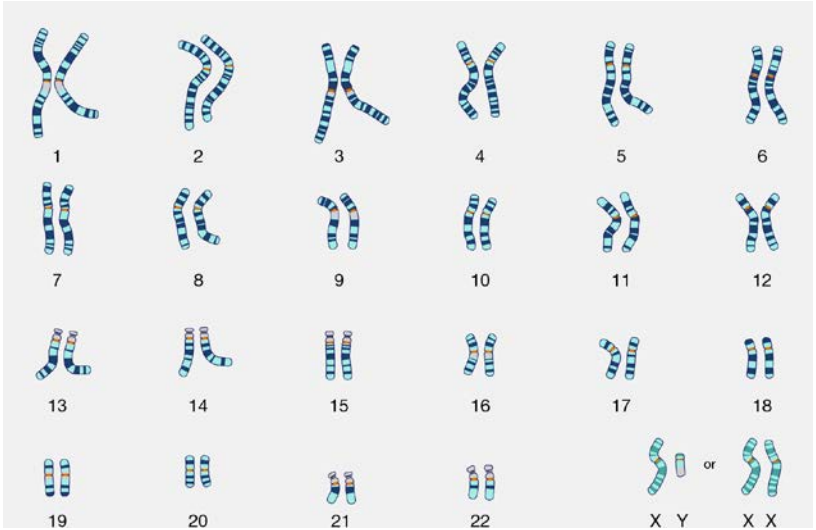
What is the most common chromosomal abnormality in cancer?

1. Translocation
2. Deletion
3. Duplication
4. Aneuploidy
5. Inversion
6. Substitution

Techniques Used in Cytogenetics

Karyotyping

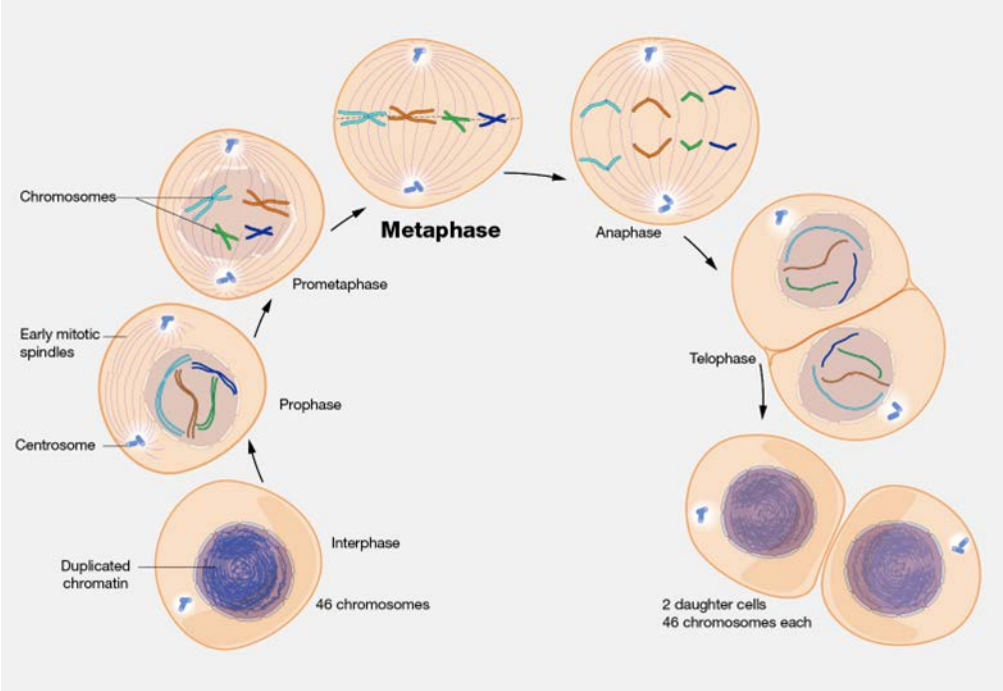
- Genetic test that analyzes the size, shape, and number of chromosomes in a sample of cells taken from blood, amniotic fluid, bone marrow, or other tissue.
- A laboratory-produced image of a person's chromosomes isolated from an individual cell and arranged in numerical order.
- A karyotype may be used to look for abnormalities in chromosome number or structure.



https://www.genome.gov/genetics-glossary/Karyotype
https://www.cancer.gov/publications/dictionaries/cancer-terms/def/karyotyping

Standards for Karyotyping

- Evaluate 20 metaphase cells looking for numeric and structural changes
  - A chromosome gain is considered clonal if observed in ≥2 metaphase cells.
    - Clonal means that the finding is from a single progenitor cell and they share the same genetic makeup
  - A single chromosome loss is considered clonal if it is observed in ≥3 metaphase cells.



Balciuiene, J., et al. (2024). Cancer cytogenetics in a genomics world: Wedding the old with the new. Blood Reviews. 66.

Karyotype Results

ME ratio: Decreased.

Hematopoiesis: Panhypoplasia.

Megakaryocytes: Present.

Megakaryocyte morphology: Normal.

Lymphoid infiltrate: None.

Bone trabeculae: Normal.

CLOT SECTION: N/A, not available at the time of slide review.

ANCILLARY TESTS:

Flow cytometry: Performed.

Cytogenetics: Pending.

FISH: N/A

Molecular: Buffy coat stored.

SPECIMEN SUBMITTED
A: BONE MARROW, ASPIRATE LPIC
B: BONE MARROW, BIOPSY LPIC
C: BONE MARROW, CLOT LPIC

ADDITIONAL PROCEDURE(S)
CYTOGENETICS
Date Ordered: 4/1/2021 Date Reported: 4/14/2021

Procedure Results and Interpretation
See Below
(NOTE)

Clinical diagnosis: T-lymphoblastic leukemia
Specimen Type: Bone marrow

Number of cells counted: 20
Number of cells analyzed: 20
Number of cells karyotyped: 20
Banding resolution: 400
Banding method: G-banding

DIAGNOSIS: 46,XY[20]

INTERPRETATION: Normal, male karyotype

COMMENT: Ten metaphase cells were analyzed from the overnight culture
and 10 metaphase cells were analyzed from the 72 hour unstimulated culture. Twenty cells analyzed showed a 46,XY karyotype, or had random chromosomal loss, attributed to culture artifact. One cell showed a gain of the Y chromosome, which is also likely due to culture
artifact. There was no significant numerical chromosome abnormality and no structural change detected within the limits of resolution.

The analyses in March 2021, February 2021, and September 2019 also showed normal karyotypes, while the analysis in February 2020 showed a
gain of the Y chromosome in 2 cells, likely due to culture artifact.

Clinical and pathologic correlation is recommended.

Poll Question 3

What is the metaphase?

1. Metaphase chromosomes are used in karyotyping.

2. The nucleus dissolves and the cell's chromosomes condense and move together, aligning in the center of the dividing cell.

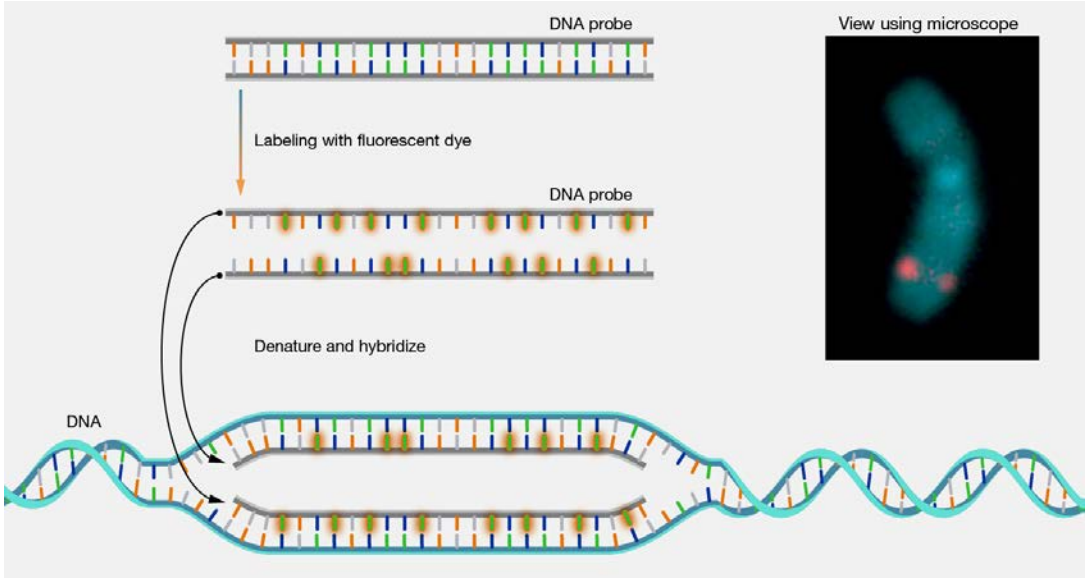
3. Chromosomes are distinguishable when viewed through a microscope.

4. All of the above

5. None of the above

Fluorescence In Situ Hybridization (FISH)

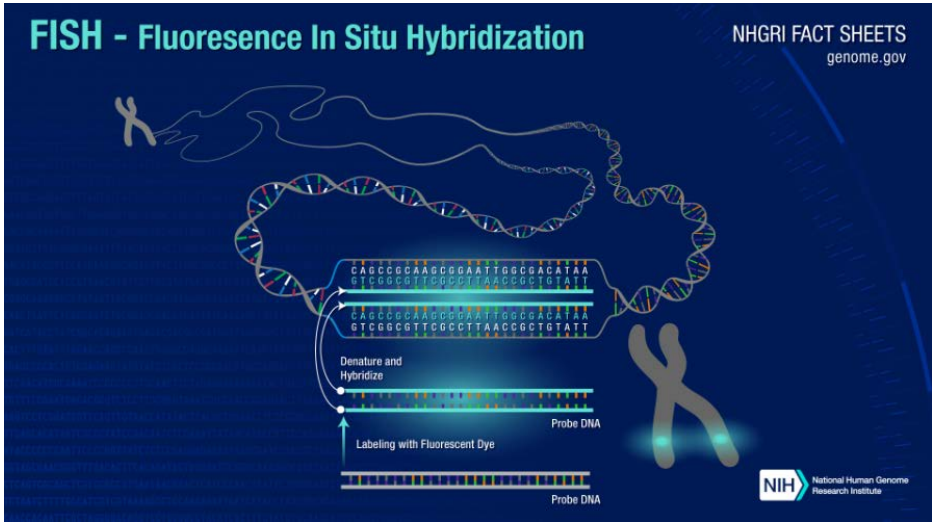
- Technique that identifies specific chromosomes or chromosomal regions by hybridization (attachment) of fluorescently-labeled DNA probes to denatured chromosomal DNA.
  - Denature means the DNA unwinds and is single stranded
- Examination through a microscope under fluorescent lighting detects the presence or absence of the colored hybridized signal.
  - The presence or absence of the chromosome material.



https://www.genome.gov/genetics-glossary/Fluorescence-In-Situ-Hybridization-FISH
https://www.cancer.gov/publications/dictionaries/genetics-dictionary/def/fluorescence-in-situ-hybridization

Value of FISH

- Targeted, specific as to location
- Identifies small deletions or insertions not detectable by other methods
- Provides a way to visualize and map the genetic material in an individual's cells, including specific genes or portions of genes
- Can be performed on non-dividing cells such as fixed samples
- Useful for cancers with low proliferative index or poor chromosome morphology, i.e. Multiple Myeloma



https://www.genome.gov/about-genomics/fact-sheets/Fluorescence-In-Situ-Hybridization
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Nucleic Acid In Situ Hybridization (nuc ish)

- Test was performed on nuclei using in situ hybridization on fixed tissues.
  i.e. nuc ish (D12Z3,MDM2)X2[100],(TP53X1,D17Z1X2)[44/100]
  - D12Z3 refers to a DNA sequence located on chromosome 12 in the region of the centromere
    - Helps identify and quantify chromosome 12 where MDM2 gene is located
    - Can detect amplification of MDM2 which regulates TP53
    - This result shows that there are 2 copies of MDM2
  - TP53X1 indicates that there is only one copy of TP53
  - D17Z1X2 is a DNA probe on chromosome 17 in the region of the centromere
    - Used as a control to count the number of chromosome 17 copies
    - "X2" indicates two copies of the chromosome 17 centromere
    - 44/100 indicates this was detected in 44/100 cells

Fish and nuc ish Results

Enhanced Report for FISH Testing

Accession #:	**123-456-78899**
Patient:	**Jane Doe**
DOB:	**01/01/1900**
Sex:	**Female**
Ordering Provider:	
Completion Date:	**09/10/2009 14:19:23**

Specimen Received:

Specimen Type:	Bone marrow
Reason for Referral:	COG AML Panel
Test Performed:	FISH, Interphase

FISH Results:

ABNORMAL FISH RESULT
nuc ish 8q22(RUNX1T1x3),21q22(RUNX1x3)(RUNX1T1 con
RUNX1x1)[182/200]

NORMAL FISH RESULT
nuc ish 5q31(EGR1x2)
7cen(D7Z1x2),7q31(D7S486x2)
11q23(MLLx2)
16q22(CBFBx2)

Diagnostic Impression:

Fluorescence in situ hybridization (FISH) analysis with the EGR1, D7S486, RUNX1/RUNX1T1 (also known as AML1/ETO), MLL, and CBFB probes (Abbott Molecular) showed evidence of a fusion of RUNX1 and RUNX1T1 in 182/200 cells scored (91%). The signal pattern
was suggestive of a 3-way translocation such as t(8;21;var). The pending chromosome study will likely identify the additional chromosome involved in this translocation. A t(8;21;var) is observed in approximately 3% of cases with a RUNX1/RUNX1T1 fusion.

FISH analysis with the remaining probes (EGR1, D7S486, MLL and CBFB) showed no evidence of abnormalities involving these loci in 200 cells scored for each probe.

Reporting | Report Date: 10/7/2009

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ARUP is an enterprise of the University of Utah and its Department of Pathology.

Patient:	**Jane Doe**
DOB:	**01/01/1900**
Accession #:	**123-456-78899**
Sample Type:	**Bone Marrow**

Recommendation:

For increased sensitivity in follow-up studies, monitor for the abnormal clone by FISH analysis with RUNX1/RUNX1T1 in addition to standard chromosome studies.

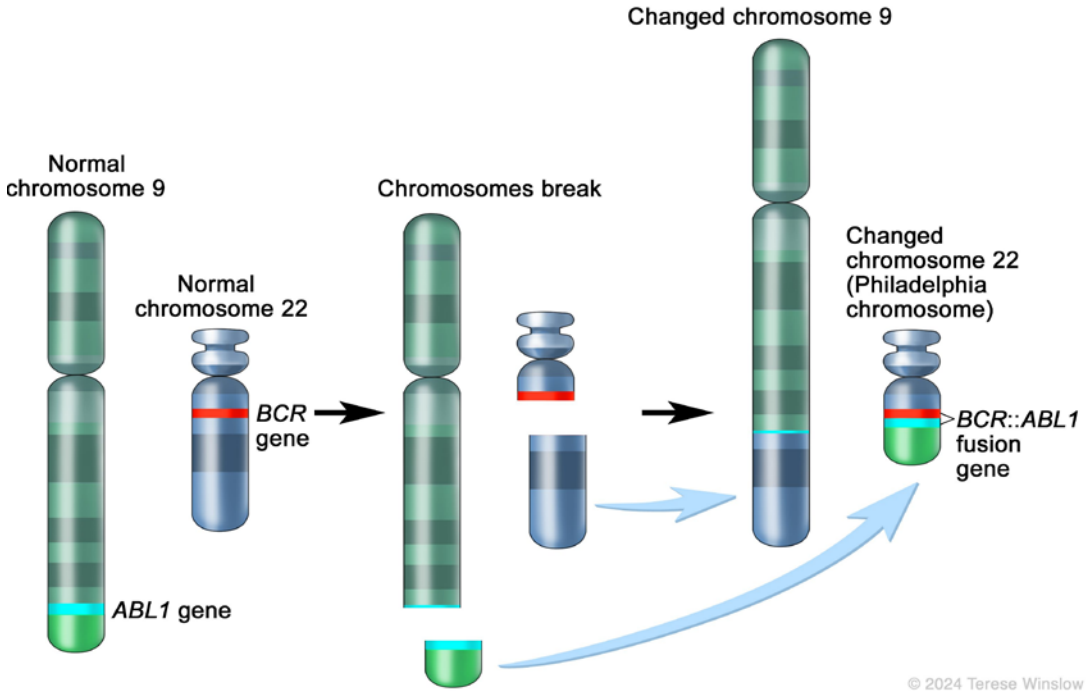
This study was performed by the University of Utah Cytogenetics Program at ARUP Laboratories.

This result has been reviewed and approved by
Sarah South, Ph.D., FACMG
Electronic Signature

Fusion Gene

- A gene made by joining parts of two different genes.
- Fusion genes, and the fusion proteins that come from them can be made naturally in the body when part of the DNA from one chromosome moves to another chromosome.
- Fusion proteins produced by this change may lead to the development of some types of cancer.
- Gene fusions can occur in 2 or more genes.
- Fusion genes and proteins may also be found in several other types of cancer, including soft tissue sarcoma, cancers of the prostate, breast, lung, bladder, colon, and rectum, and CNS tumors.

Philadelphia Chromosome



Poll Question 4

What is the advantage of using FISH?

1. Can be performed on tissue blocks

2. Is useful for identifying small genetic changes such as insertions or deletions of base pairs

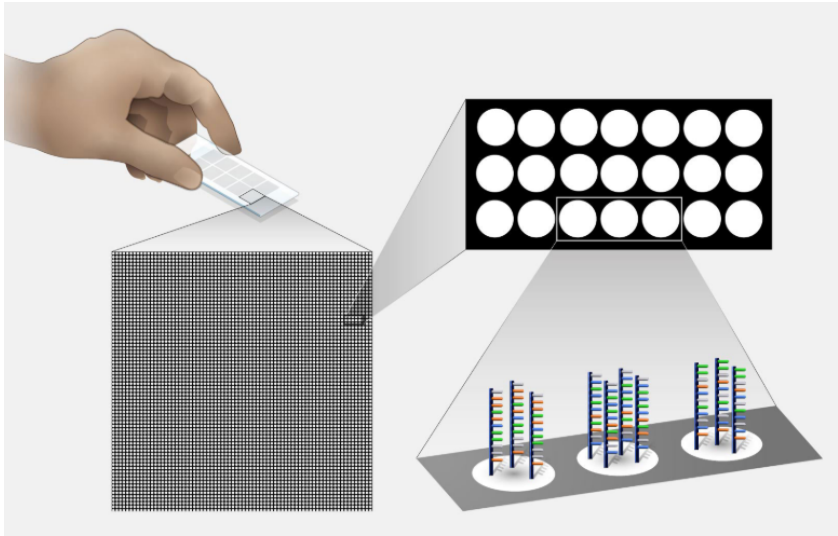
3. Targeted and highly specific

4. All of the above

5. None of the above

Microarray

- Fish in some instances is being replaced by microarrays
  - Binds thousands to millions of known nucleic acid fragments to a solid surface, “chip.”
  - Chip is then bathed with DNA or RNA isolated from a study sample (such as cells or tissue).
  - Complementary base pairing between the sample and the chip-immobilized fragments produces light through fluorescence that can be detected using a specialized machine.
    - Can be used for gene expression, specific DNA sequences, can detect single nucleotide polymorphisms and copy number changes



https://www.genome.gov/genetics-glossary/Microarray-Technology
Balciuiene, J., et al. (2024). Cancer cytogenetics in a genomics world: Wedding the old with the new. Blood Reviews. 66.

Newer Techniques

- Optical Genome Mapping
  - Uses large strands of DNA to detect genome wide changes
    - Copy number changes, structural changes, deletions, duplications, balanced translocations, unbalanced translocations, and rearrangements
- Next generation sequencing
  - Sequence millions of DNA molecules
- Amplicon-based next generation sequencing
  - Greater depth which facilitates detection of lower frequency variants and tumor heterogeneity
    - Tumor heterogeneity: the difference between cancer cells within a single tumor, or the differences between a primary (original) tumor and a secondary tumor.

Balciuiene, J., et al. (2024). Cancer cytogenetics in a genomics world: Wedding the old with the new. Blood Reviews. 66.
https://www.cancer.gov/publications/dictionaries/cancer-terms/def/tumor-heterogeneity

Sequencing

Myeloid Molecular Panel (Final result)

Source
Bone Marrow

Interpretive Summary
POSITIVE for previously reported pathogenic variant **TP53 M237I** and newly reported pathogenic variant **SF3B1 G742D** (which was present in the previous sample but not reported since it did not meet quality metrics).

The NCCN Guidelines (v.3.2022) state that TP53 mutation is associated with unfavorable prognosis, low response rates to chemoimmunotherapy and the risk of developing Richter transformation in CLL patients, whereas SF3B1 mutations in CLL are reportedly enriched in fludarabine-refractory CLL samples.

Classification 1: Strong Clinical Significance
Additional Details for Mutations

Gene	Protein Change	DNA Change	VAF%	Depth	Transcript
TP53	p.M237I	c.711G>A	19 %	15888	NM_000546.5
SF3B1	p.G742D	c.2225G>A	21 %	603	NM_012433.3

- Is this somatic or germline?
- Variant Allele Frequency
  - Frequency in which the variant is detected in the sample
    - High VAF (i.e. 50%) can indicate the variant is coming from the germline

INTERPRETATION OF GENOMIC ASSAYS - FAQs

What do all these different symbols and numbers mean?
The variety of terms helps people with different training and experience to identify the same variant. Variants may be identified by alteration to protein (*e.g. BRAF* p.V600E), nucleotide (*e.g. BRCA1* c.5266dupC), or non-standard nomenclature (*e.g. TERT* C228T promoter mutations or *EML4/ALK* fusion transcripts). The genomic location and transcript IDs are often included as universal references for additional clarity. *See below for examples.*

I am not familiar with the variant identified in the report. Where can I go for additional information?
In addition to any information issued in an interpretation (see below for a generic example) there are many online resources that may be useful, including MyCancerGenome.org, PubMed, GoogleScholar, FDA.gov, and ClinicalTrials.gov. Advanced users may find databases such as COSMIC or cBioPortal useful. *For additional assistance, please contact the laboratory or the molecular professional who issued the report.*

Will the assay detect the ABC mutation in gene *XYZ*?
Check the assay description - Is gene *XYZ* included on the panel? Is the region including the ABC mutation included on the panel? Does the assay detect this type of mutation (*e.g.,* large indels or structural variants)? *For additional assistance, please contact the laboratory or the molecular professional who issued the report.*

The report says there are no mutations in gene *XYZ*. Could the assay have missed anything?
Any given assay has limits on its capabilities. There is always a lower limit of detection; moreover, genomic assays do not necessarily identify every type of variant with equivalent sensitivity. An assay may perform well in identifying single-nucleotide variants (SNVs), less well in identifying insertions and deletions (indels), and may not be able to identify larger indels at all. *Negative results must always be interpreted with caution.*

What is the significance of the Variant Allele Frequency (VAF)?
The VAF is the frequency at which the variant is detected in a specimen. It is often used as a proxy for disease burden (*e.g.,* a VAF of 50% may suggest a germline variant, whereas a VAF of 15% may suggest a neoplastic disease burden of 30%). However, the VAF is affected by many factors including the variance of the assay (often as high as +/-15%), sampling, assay design, and cytogenetic changes at the allele including amplification or loss of heterozygosity (LOH). *The VAF should always be interpreted with caution. For additional assistance, please contact the laboratory or the molecular professional who issued the report.*

Standard nomenclature | Helps resolve confusing terminology | Not always included; see assay methodology for performance

Gene Name	Nucleotide Variant	Protein Variant	Genomic Location	Transcript ID	Quantitation
JAK2	c.1849G>T	p.V617F	chr9:5073770	NM_001322196.1	VAF 22%
EGFR	c.2240_2257delTAAGAGAAGCAACATCTC	p.L747_P753delinsS	chr7:5524270	NM_005228	VAF 89%
BRCA1	c.5266dupC	p.Q1756Pfs*74	chr17:41209080	NM_007294.3	Heterozygous
EML4/ALK	N/A	N/A	chr2:42523824; chr2:29446685	NM_019063.4; NM_004304.4	N/A
ERBB2 (Her2)	Copy number gain	N/A	chr17:37,856,200-37,885,000	NM_004448.3	Gain of 6-fold

Legacy and standard nomenclature may or may not be included together | Requires knowing the reference genome used by the assay (see assay methodology)

Example Interpretation: *XYZ* p.ABC: A single base substitution was detected in the *XYZ* gene, resulting in a missense variant. *XYZ* functions as a [tumor suppressor/oncogene/other], regulating downstream cellular processes including ###. This variant occurs in the ### domain, altering the ability of the protein to ####, resulting in ####. The p.ABC variant confers a [better/worse] prognosis, and is a target for the US-FDA approved therapy, #######.

Methodology of the assay (the fine print) should include: Reference genome used (*e.g.* hg19); target gene list; regions of genes covered (*e.g.* entire coding region vs. hotspots); minimum mean depth of coverage; performance characteristics of the assay (lower limits of detection, maximum size of detectable indels, variance, etc.); contact information for the laboratory.

AMP EDUCATION GUIDELINES
Prepared by the Association for Molecular Pathology Training and Education Committee
For more educational resources, see: *www.amp.org/education/education-overview/*

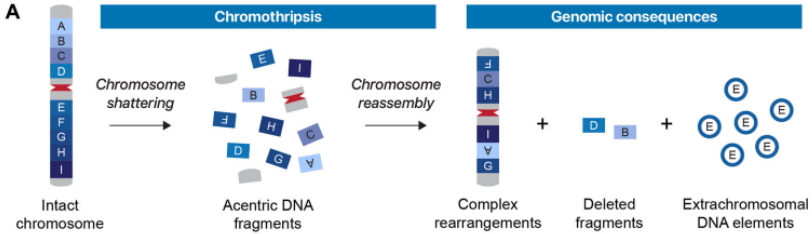
"Molecular in My Pocket" reference cards are educational resources created by the Association of Molecular Pathology (AMP) for laboratory and other health care professionals.
The content does not constitute medical or legal advice, and is not intended for use in the diagnosis or treatment of individual conditions. See www.amp.org for the full "Limitations of Liability" statement.

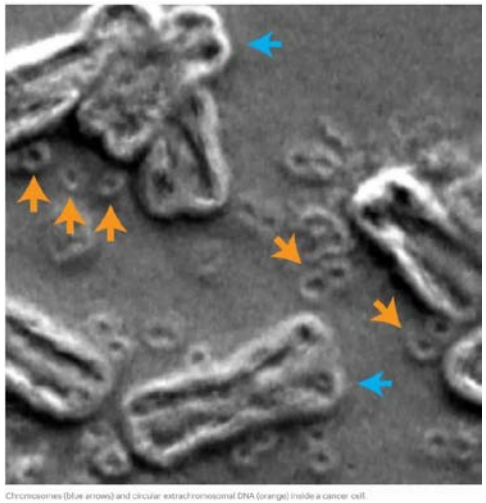
Revised 2/18

https://www.amp.org/AMP/assets/File/education/resources/NGS_Interpretation_FINAL_2_28_18.pdf?pass=9

Chromosome Instability and Cancer

- Chromothripsis
  - Widespread DNA damage
  - Formation of complex chromosomal rearrangements as a result of shattering
    - The shattered chromosome then undergoes faulty DNA repair
- Extra-chromosomal DNA (ecDNA)
  - Mechanism for amplification
- Driver of rapid genome evolution
- Epigenetic reprogramming
- Driver of tumor promoting inflammation
- Driver of cancer metastasis
- Tumor immune evasion and therapeutic resistance





Mazzagatti, A. et al. (2024). Boveri and beyond: Chromothripsis and genomic instability from mitotic errors. Mol Cell. 84, 55–69.
Chen et al. (2025). Chromosomal instability as a driver of cancer progression. Nature Reviews Genetics, 26, 31-46.

SWOG Cytogenetics Report and CRF

Collect date

Sample

Number and gender

Fish results

Metaphase quality indicator (400-550)

Karyotype listed first (subclones)

metaphases, nml and abn

Location of translocation

chr copies

Staining method used to see the chr bands

CYTOGENETICS HEM/ONC BLOOD CHROMOSOME ANALYSIS (W/FISH): 21KD-121C0003

Order: 293744169

Collected: 5/1/2021 13:15 Status: Final result Visible to patient: No (inaccessible in MyChart)

Component	
Cytogenetics Hem/Onc Blood Chromosome W/FISH	Abnormal
Chromosome Results	Abnormal

Impressions and Recommendations

KARYOTYPE:
46,XX,t(5;9)(q31;p22)[4]/47,idem,+6[10]/46,XX[7]

Fourteen of twenty-two metaphase cells examined were abnormal, with an apparently balanced translocation between the chromosome 5 long arm and the chromosome 9 short arm; many of these cells were also trisomy 6. Seven cells were normal female, and one cell, not counted above, had a non-specific change.

FISH with probes for PDGFRB (5q33) and 9p21 were used to assess disruption and/or develop a mechanism to follow the t(5;9) in interphase. Both probes were normal, with two signals in all cells.
One available metaphase cells, one PDGFRB signal (intact) was on the der(9) and the 9p signals were retained on the chromosome 9 homologues, ie the normal 9 and the der(9)/ These probes are not disrupted, deleted or duplicated by this translocation, and these probes will NOT be useful to follow this clone.

Thank you very much for your referral. If you have any questions regarding this report or future cytogenetic testing issues, please feel free to contact us.

Reason for Referral: t-all

The clinical interpretation was made by the clinical geneticist.

Number of Cells Karyotpyed	6
Number of Cells Analyzed:	22
Number of Cells Counted:	N/A
Banding Level:	450
Banding Method:	GTW

SWOG
S1905 CYTOGENETICS LAB REPORT FORM

Patient Identifier | Study Identifier S 1 9 0 5 | Registration Step 1

Patient Initials _____ (L, F M)

Page: Cytogenetics Lab Report

CYTOGENETICS ANALYSIS

Date specimen collected ☐☐/☐☐/☐☐☐☐

Number of metaphases

Bone marrow

- Unstimulated short-term culture (24-72 hours) ☐☐
- Direct preparation (metaphases) ☐☐
- Stimulated culture (metaphases) ☐☐
  - Mitogen type _____
  - Other culture method ☐☐
  - Culture method and duration _____

Peripheral blood

- Unstimulated short-term culture (24-72 hours) ☐☐
- Stimulated culture ☐☐
  - Mitogen type _____
  - Other culture method ☐☐
  - Culture method and duration _____

Total number of metaphases ☐☐☐

Total number of abnormal metaphases ☐☐☐

Are results based on at least 400-band level for banded analysis? ☐ Yes ☐ No ☐ Unknown

Karyotype description _____

Were FISH studies performed? ☐ Yes ☐ No ☐ Unknown

If Yes, FISH ISCN description _____

continued on next page

(Not imported) Page 2 of 5 500729: Version 1.0

Clinical Utility of Cytogenetics

- Cytogenetics is used to identify chromosomal abnormalities that are specific to certain cancer type or stage
  - Informs diagnosis
  - Disease classification
  - Disease prognosis
  - Monitoring of disease
  - Increasingly fast (i.e. <3 day turnaround)
- Cost effective
- Elucidating chromosome copy number changes and structural abnormalities informs the underlying genomic disease mechanisms which may inform therapeutic decision-making and the development of novel therapeutic targets

Balciuniene, J. et al. (2024). Cancer cytogenetics in a genomics world: Wedding the old with the new. Blood Reviews, 66.

Questions/Discussion

Calzonek@mail.nih.gov
240-760-6178

Prior QA Webinars Accessible for Review

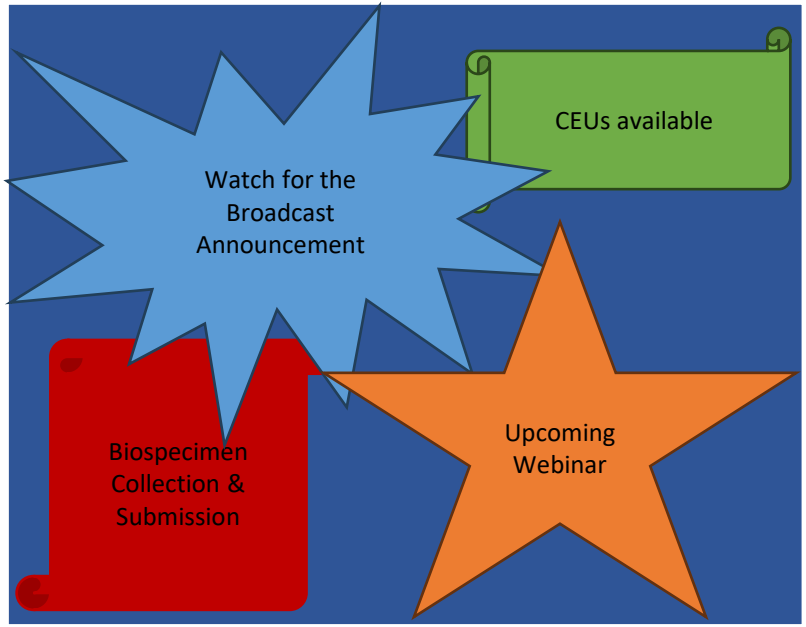
Previous Webinars and Upcoming Webinar Information is posted at:
SWOG Quality Assurance Live Webinar Series | SWOG

CEU Courses posted in CLASS:

- **Serious Adverse Event Reporting & Updates**
  (1 contact hour)
- **Workload Prioritization in Clinical Trials**
  (1.5 contact hours)
- **Disease Assessment in Solid Tumors**
  (1 contact hour)
- **Best Practices for Informed Consent**
  (1 contact hour)
- **Research Protocol Deviations vs Deficiencies**
  (1 contact hour)

Non-CEU Courses posted in CLASS:

- **Adverse Event Reporting**
- **SWOG Audits: Preparing for Success and Audit Process**
- **How to Develop a CAPA Plan**



This activity will be submitted to the Georgia Nurses Association for approval to award contact hours. Georgia Nurses Association is accredited as an approver of nursing continuing professional development by the American Nurses Credentialing Center's Commission on Accreditation.

Upcoming QA Live Webinar

Biospecimen Collection and Submission

~Presented by:
Nationwide Children's Hospital / SWOG Biospecimen Bank:
Lisa Beaverson, Biorepository Protocol Coordinator and
Hannah Brown, Biorepository Protocol Coordinator

Friday, October 17th, 2025
12:00 PM Eastern Time

Registration information will be distributed via:

- SWOG Broadcast Emails,
- CTSU Broadcast Emails, and at
- SWOG's Fall Group Meeting in Chicago.