SWOG Spring Meeting 2025

Oishi Symposium

Welcome Back to San Francisco!

In honor of and with gratefulness for

Noboru Oishi MD

(1928 – 2020)

and

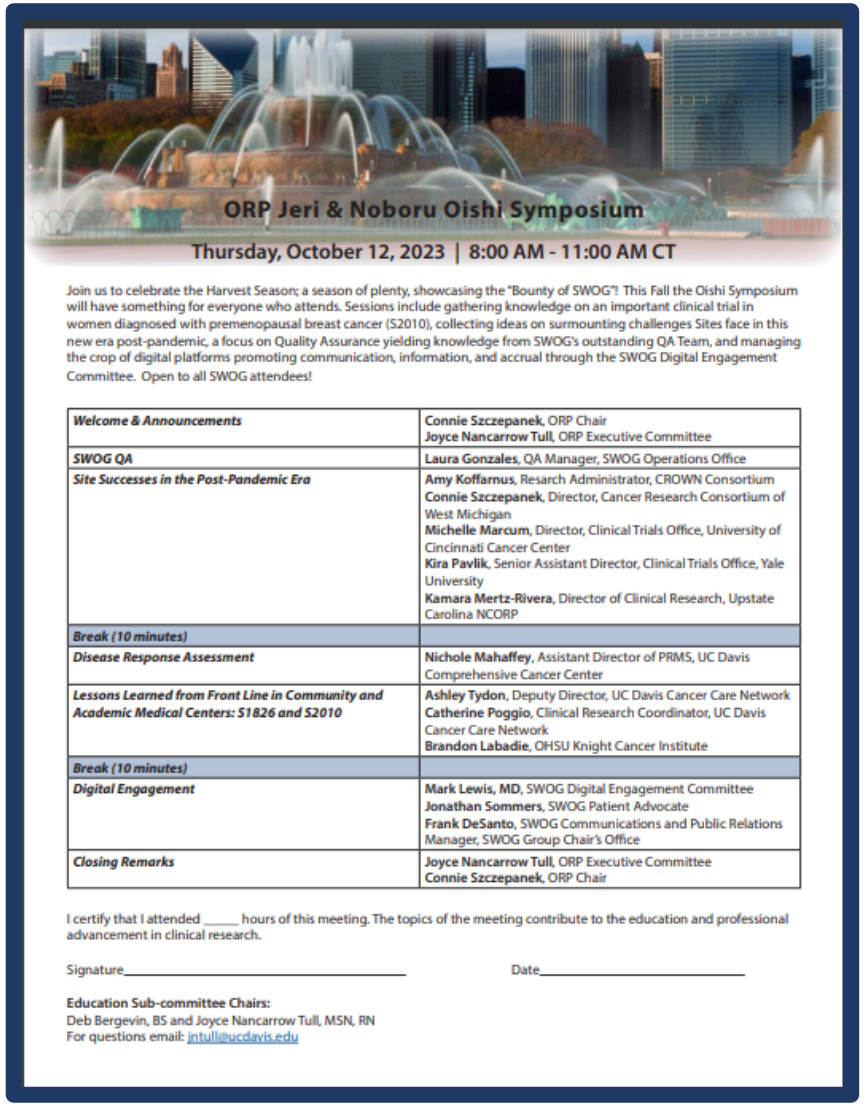
Jeri Oishi, RN

Although there are no formal CE credits for this meeting,

PLEASE KEEP YOUR COPY

of the agenda to reflect your attendance

(For use with certification)



ORP Jeri & Noboru Oishi Symposium

Thursday, October 12, 2023 | 8:00 AM - 11:00 AM CT

Join us to celebrate the Harvest Season; a season of plenty, showcasing the "Bounty of SWOG"! This Fall the Oishi Symposium will have something for everyone who attends. Sessions include gathering knowledge on an important clinical trial in women diagnosed with premenopausal breast cancer (S2010), collecting ideas on surmounting challenges Sites face in this new era post-pandemic, a focus on Quality Assurance yielding knowledge from SWOG's outstanding QA Team, and managing the crop of digital platforms promoting communication, information, and accrual through the SWOG Digital Engagement Committee. Open to all SWOG attendees!

Welcome & Announcements	**Connie Szczepanek**, ORP Chair **Joyce Nancarrow Tull**, ORP Executive Committee
SWOG QA	**Laura Gonzales**, QA Manager, SWOG Operations Office
Site Successes in the Post-Pandemic Era	**Amy Koffarnus**, Resarch Administrator, CROWN Consortium **Connie Szczepanek**, Director, Cancer Research Consortium of West Michigan **Michelle Marcum**, Director, Clinical Trials Office, University of Cincinnati Cancer Center **Kira Pavlik**, Senior Assistant Director, Clinical Trials Office, Yale University **Kamara Mertz-Rivera**, Director of Clinical Research, Upstate Carolina NCORP
Break (10 minutes)	
Disease Response Assessment	**Nichole Mahaffey**, Assistant Director of PRMS, UC Davis Comprehensive Cancer Center
Lessons Learned from Front Line in Community and Academic Medical Centers: S1826 and S2010	**Ashley Tydon**, Deputy Director, UC Davis Cancer Care Network **Catherine Poggio**, Clinical Research Coordinator, UC Davis Cancer Care Network **Brandon Labadie**, OHSU Knight Cancer Institute
Break (10 minutes)	
Digital Engagement	**Mark Lewis, MD**, SWOG Digital Engagement Committee **Jonathan Sommers**, SWOG Patient Advocate **Frank DeSanto**, SWOG Communications and Public Relations Manager, SWOG Group Chair's Office
Closing Remarks	**Joyce Nancarrow Tull**, ORP Executive Committee **Connie Szczepanek**, ORP Chair

I certify that I attended _____ hours of this meeting. The topics of the meeting contribute to the education and professional advancement in clinical research.

Signature_____ Date_____

Education Sub-committee Chairs:
Deb Bergevin, BS and Joyce Nancarrow Tull, MSN, RN
For questions email: jntull@ucdavis.edu

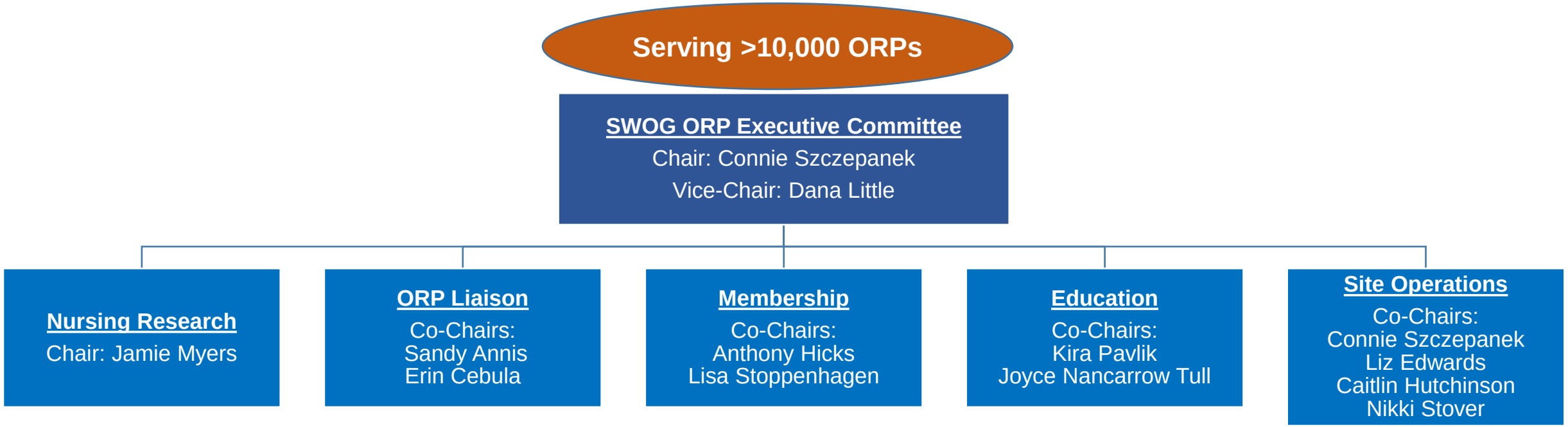
YOU are The ORP Committee!

"SWOG holds a fundamental conviction that the **O**ncology **R**esearch **P**rofessionals (ORP) play a crucial role in the successful development, implementation, and analysis of any SWOG clinical trial."

ORP Executive Committee Members

Sandy Annis	Caitlin Hutchinson
Deb Bergevin	Dana Little
Annette Betley	Jamie Myers
Erin Cebula	Joyce Nancarrow Tull
Liz Edwards	Lisa Stoppenhagen
Anthony Hicks	Connie Szczepanek
Nikki Stover	Kira Pavlik

The SWOG Oncology Research Professionals (ORP) Committee & Sub-Committees



SWOG Cancer Research Network's Mission

- To significantly improve lives through cancer clinical trials and translational research.

ORP Committee Mission

- To support SWOG activities through promotion of integrity and excellence in clinical research through education, guidance, & collaborative contributions.

For quick reference…

See the SWOG Website:

Member Resources / Oncology Research Professionals

https://www.swog.org/member-resources/

Quick Links to:

- Contact info of Committee Leaders
- Lead ORP (Head CRA) Training Modules
- APP Workshop

To get more deeply involved…

…See the SWOG Website:

Member Resources / Membership / Committee Membership

https://www.swog.org/member-resources/membership/committee-membership

Key Involvement Opportunities

- Disease Specific Liaisons
- Liaisons at Large
- Education Team

Opportunity for Advanced Practice Providers to Learn or Refresh on Clinical Trial Essentials

Advanced Practice Provider (APP) Clinical Trial Workshop

Web-based training focused on essentials for APPs (NP, PA, PharmD, PhD) to provide safe care to patients on clinical trials and enhance their involvement in NCI-sponsored research.

Workshop content includes:

- Overview of NCI clinical trial networks
- How to become a non-physician investigator (NPIVR)
- Types of protocols
- CTCAE grading, RECIST criteria

3 hours of CME upon completion

Use this link for more information and to view the workshop:

https://www.swog.org/clinical-trials/clinical-research-resources/current-training-opportunities

Hope at 30 – Share Our Story

Share our messaging toolkit: thehopefoundation.org/30-next-generation

THE HOPE FOUNDATION

30 YEARS

A GENERATION OF IMPACT

The Hope Foundation was founded 30 years ago – a full generation.

To honor and further Hope's impact, we're raising $300,000 to fund the next generation, and **we need your help.**

Scan to view the full toolkit

Printed Toolkit material available at Hope's table near SWOG meeting registration. Come visit us!

Agenda

- We will do our best to be faithful to the schedule as we've compressed into 2 ½ hours.
- Please feel free to use facilities whenever you wish as we've eliminated breaks.
- Speakers from this morning's program will be available at Open Forum
- We encourage you to attend Open Forum following a ½ hour break beginning at 11:00 am.

Topic	Time
Opening & Announcements	8:00 – 8:10 am
CTSU	8:10 – 8:40 am
Cytogenetics	8:40 – 9:10 am
Deciphering Chromosomes: Cracking the Code	9:10 – 9:40 am
Quality Assurance in Cytogenetics – Lessons Learned	9:40 – 10:10 am
Fan Favorite: Cytogenetics Lightening Round	10:10 – 10:30 am

Reminder: PLEASE KEEP YOUR AGENDA AS IT IS YOUR PROOF OF CE

Oishi Symposium

welcomes

Rachel Albershardt
CTSU

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Linking practice to progress

CTSU Updates

Rachel Albershardt, CTSU Product Owner

Agenda

- CTSU Website
- Delegation of Tasks Log (DTL) Enhancements
- Data Quality Portal (DQP) Tips, Reminders & Frequently Asked Questions (FAQ)
- Electronic Medical Record (EMR) Templates
- CTSU Patient Transfer Process
- OPEN Modernization

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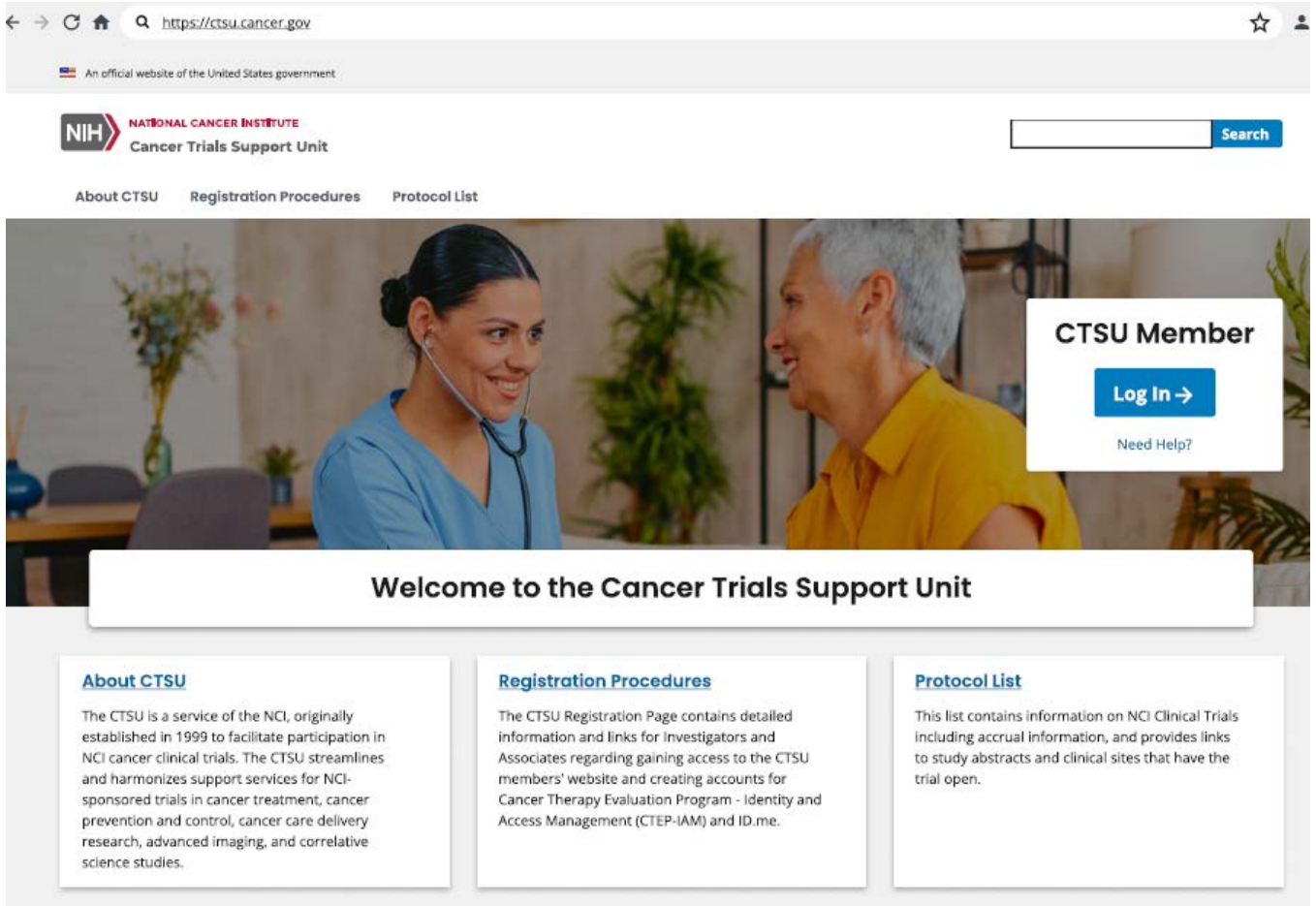
Linking practice to progress

CTSU Website

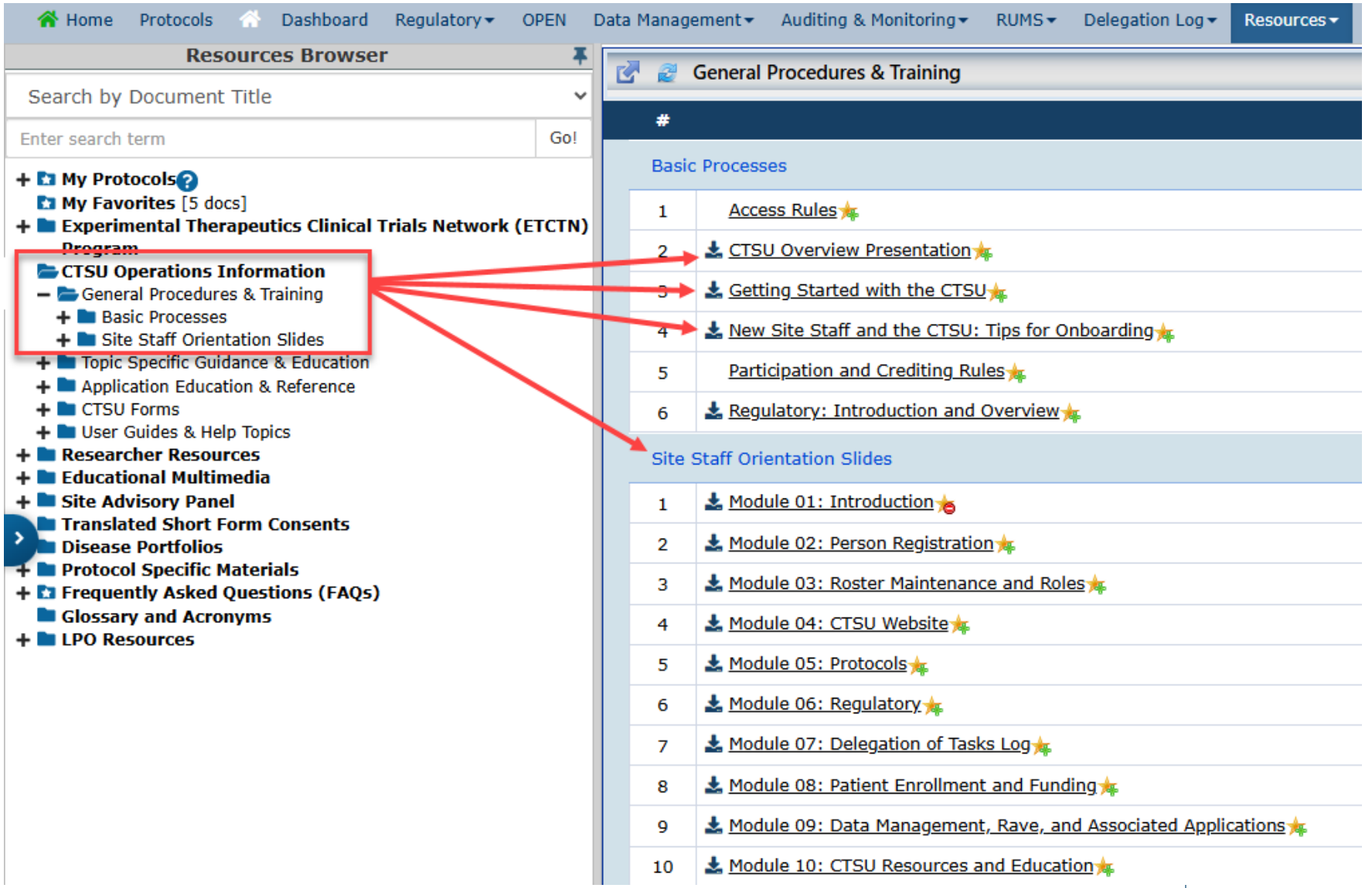
New CTSU Public Website

- Moving to a .gov domain
- Refreshed look, same content
- Log in to the CTSU Member website



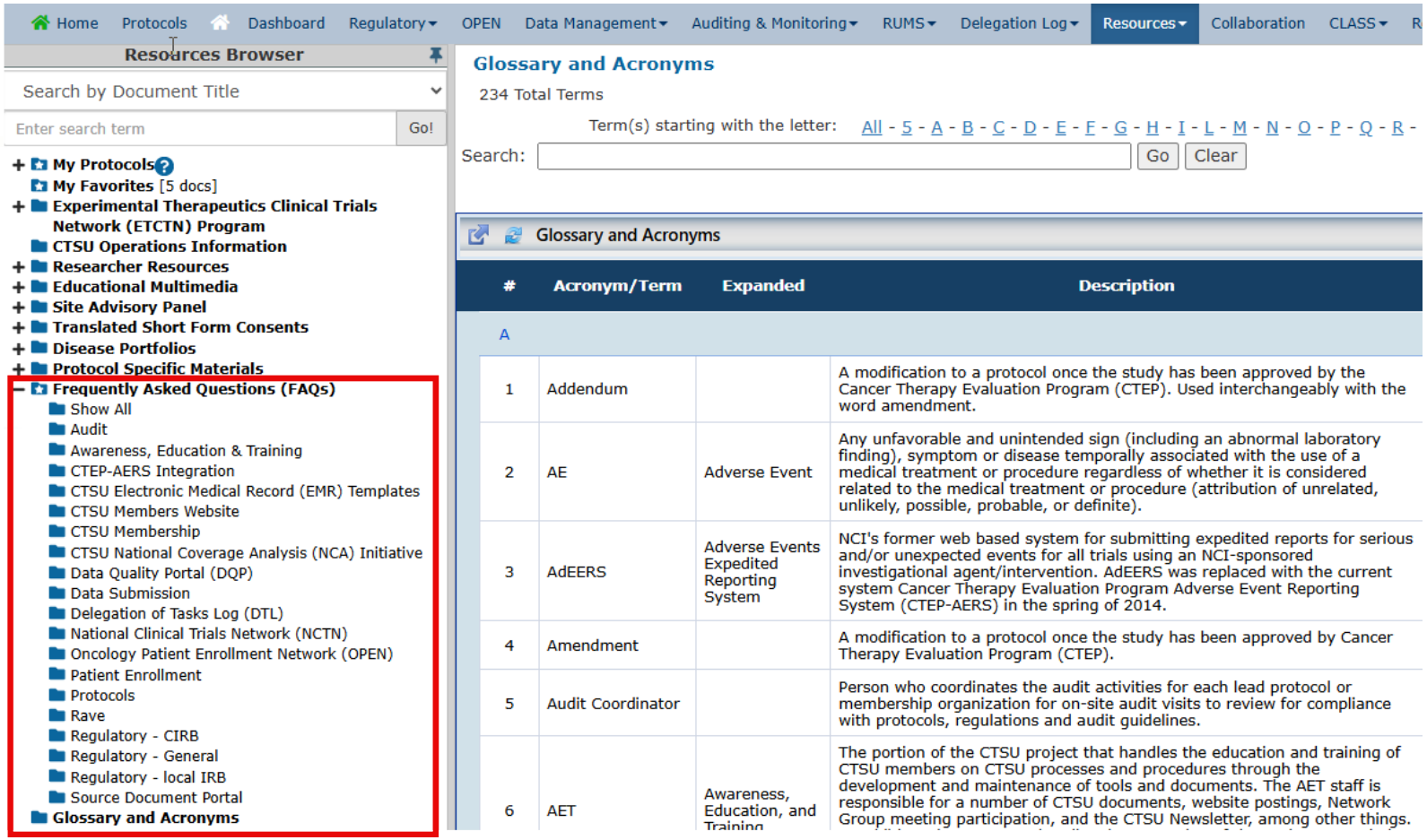
Orienting New Staff

- General Procedures & Training area
- Public website can be used until credentials are obtained



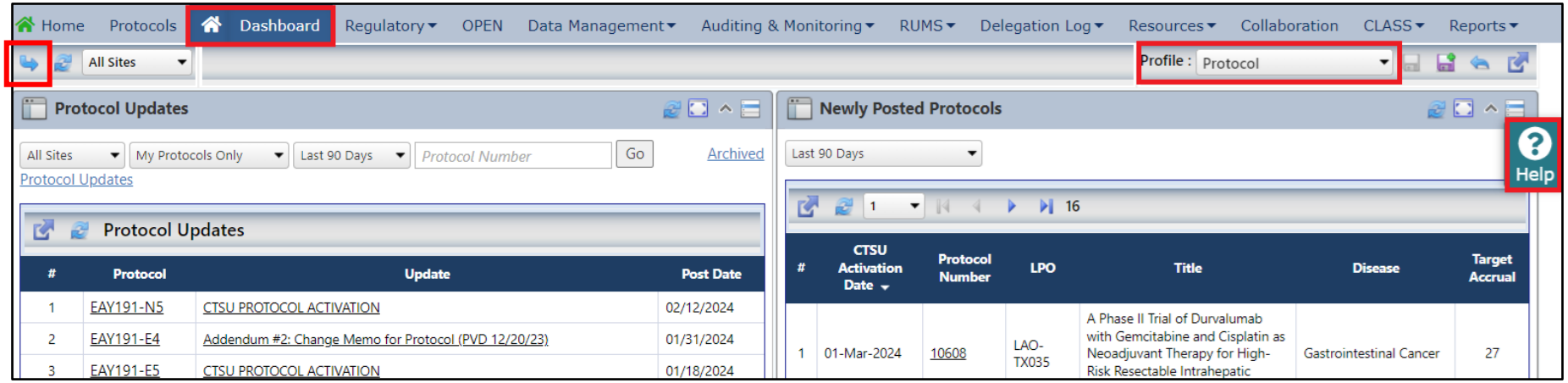
Resources

- >200 FAQs covering 19 subjects
- >200 acronyms defined
- Help Topics on all CTSU webpages



The Dashboard

- Presents data based on user roster and role
- Ability to customize your profile
- Help Topics contains link to Dashboard tour

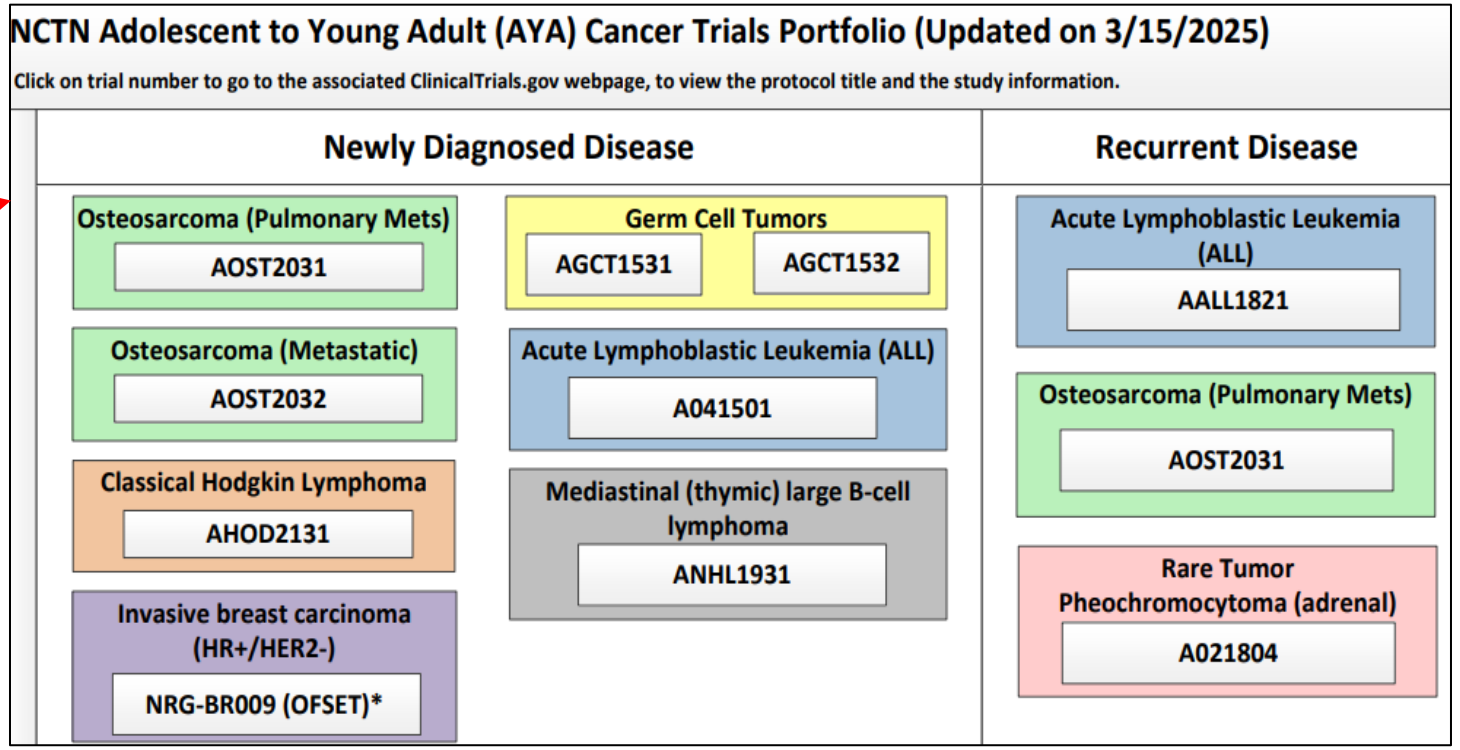


Disease Portfolios

- Disease Portfolios are developed and maintained by NCI
- Found in Resources on CTSU website; hosted on CTEP website
- Updated monthly

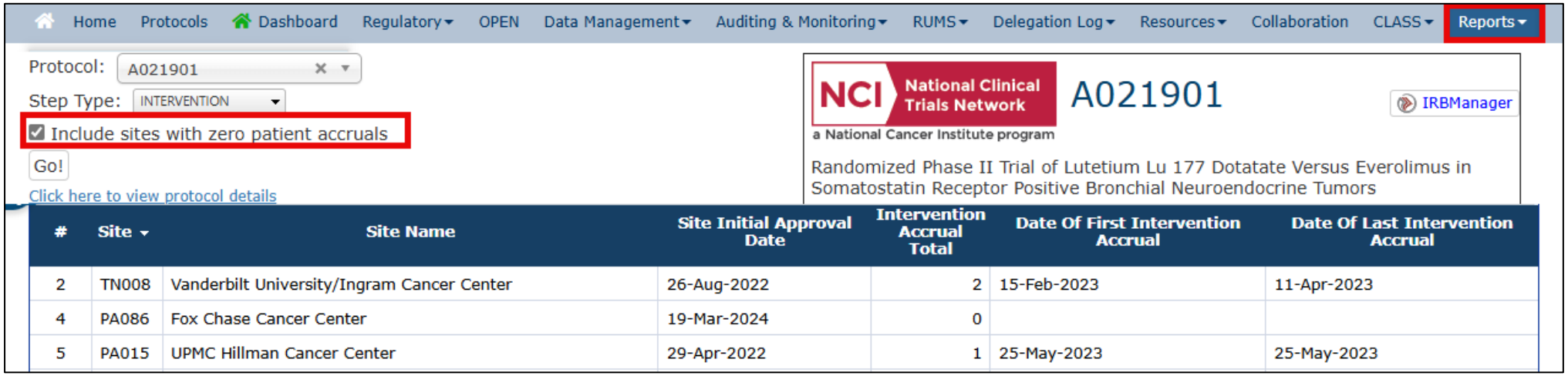
NCTN

Title	Post Date
Adolescent and Young Adult (AYA) Cancer Trials Portfolio	20-Mar-2025
Brain Cancer Trials Portfolio	20-Mar-2025
Breast Cancer Trials Portfolio	20-Mar-2025
Endocrine/Neuroendocrine Cancer Trials Portfolio	20-Mar-2025
Gastrointestinal Cancer Trials Portfolio	20-Mar-2025
Genitourinary Cancer Trials Portfolio	20-Mar-2025
Gynecologic Cancer Trials Portfolio	20-Mar-2025
Head and Neck Cancer Trials Portfolio	20-Mar-2025
Leukemia Trials Portfolio	20-Mar-2025



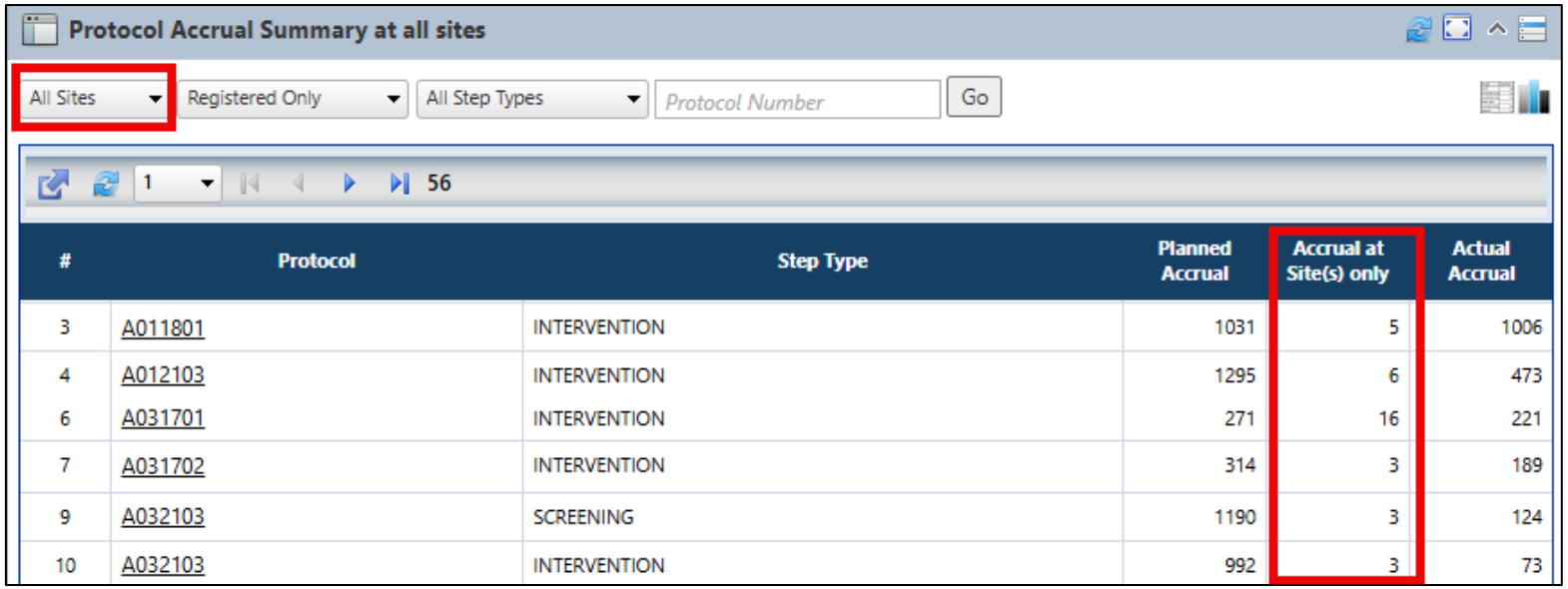
Protocol Resources

- Pie chart on protocol-specific homepage
  - Links to Reports
- Protocol tree accrual report
- Public accrual reports

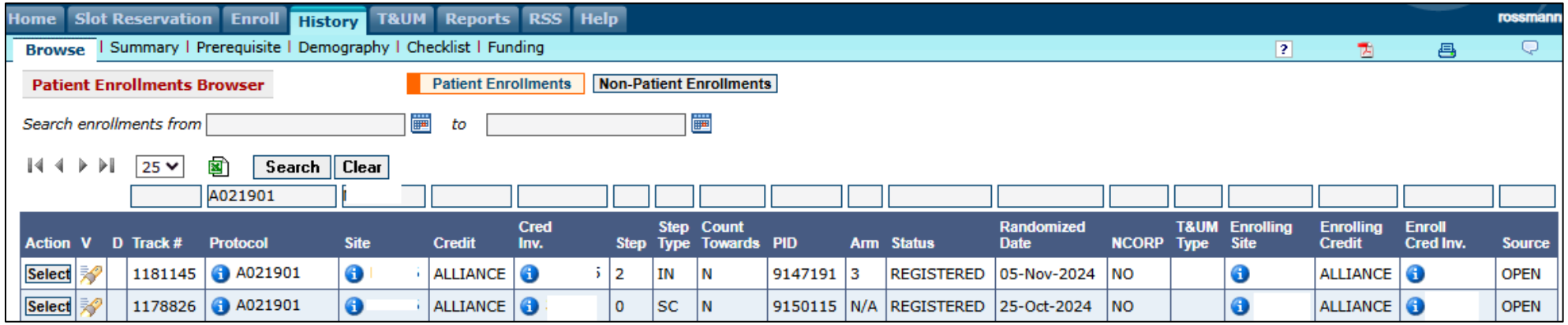


Protocol Resources: Accrual at your Sites

- Dashboard > Protocol Accrual Summary
  - Filter by site
- In OPEN > History

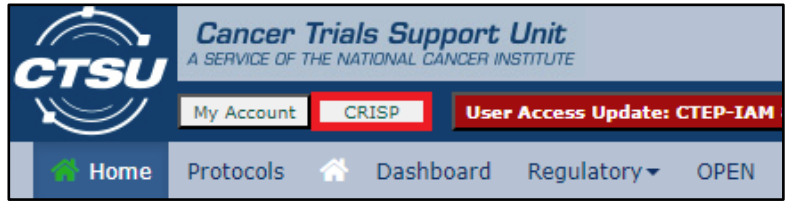


#	Protocol	Step Type	Planned Accrual	Accrual at Site(s) only	Actual Accrual
3	A011801	INTERVENTION	1031	5	1006
4	A012103	INTERVENTION	1295	6	473
6	A031701	INTERVENTION	271	16	221
7	A031702	INTERVENTION	314	3	189
9	A032103	SCREENING	1190	3	124
10	A032103	INTERVENTION	992	3	73

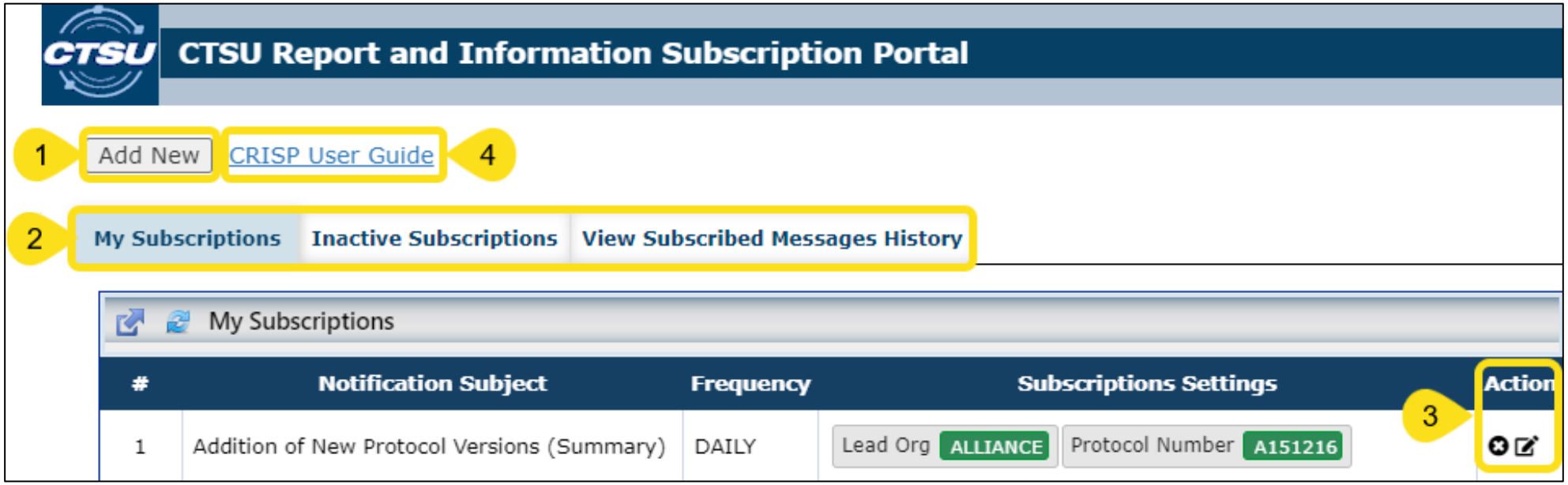


Action	V	D	Track #	Protocol	Site	Credit	Cred Inv.	Step	Step Type	Count Towards	PID	Arm	Status	Randomized Date	NCORP	T&UM Type	Enrolling Site	Enrolling Credit	Enroll Cred Inv.	Source
Select			1181145	A021901		ALLIANCE		2	IN	N	9147191	3	REGISTERED	05-Nov-2024	NO			ALLIANCE		OPEN
Select			1178826	A021901		ALLIANCE		0	SC	N	9150115	N/A	REGISTERED	25-Oct-2024	NO			ALLIANCE		OPEN

Protocol Resources: CTSU Report and Information Subscription Portal (CRISP)



- Available actions:
  1. Add new notifications
  2. View subscription history
  3. Edit current subscription settings
  4. View User Guide



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Linking practice to progress

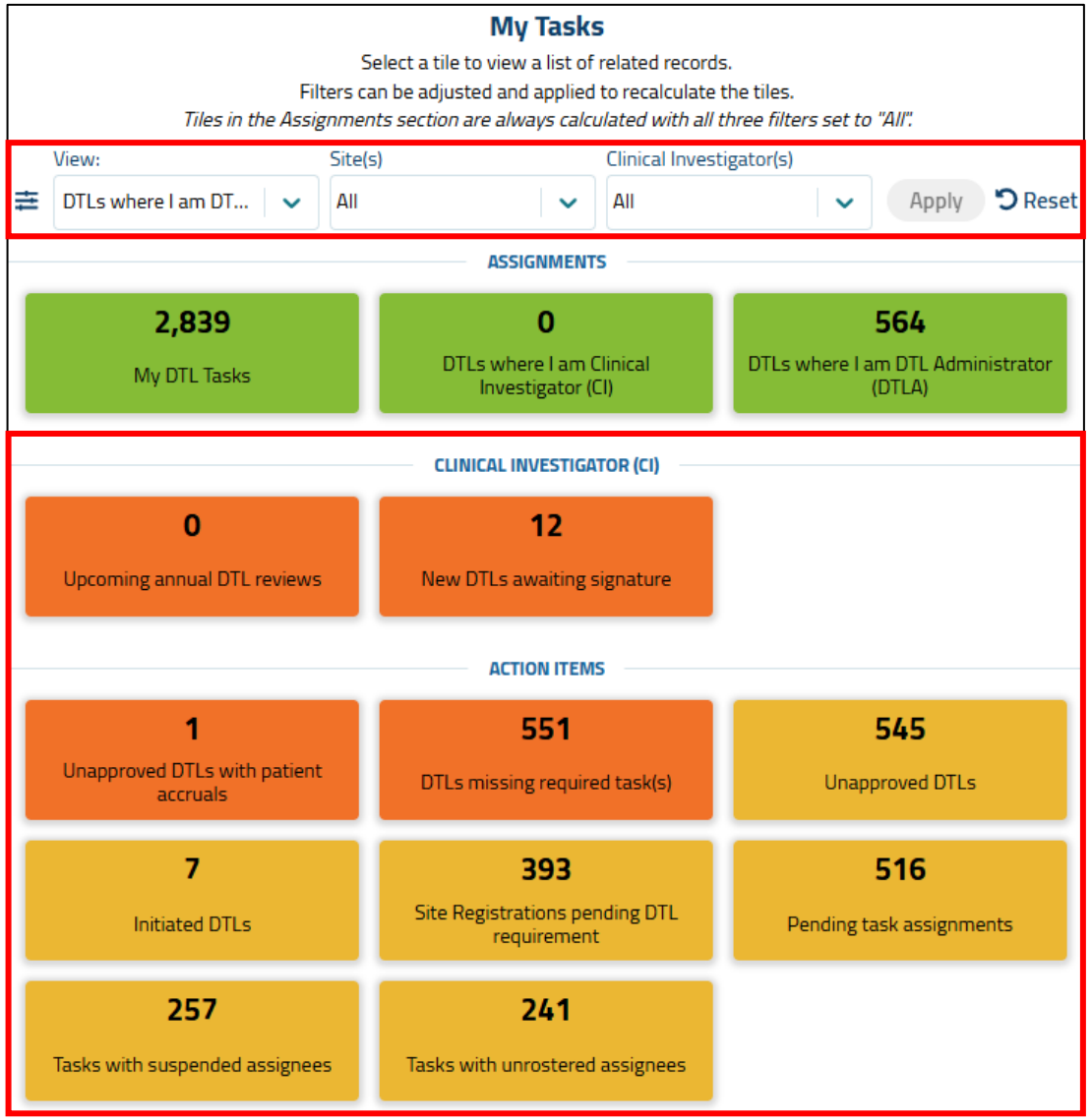
Delegation of Tasks Log (DTL) Enhancements

New Dashboard Filters

New Site(s) and Clinical Investigator(s) filters

These metrics do not change

Changes to the filters affect the metrics in these two sections



Site User Manual Retirement and Re-Initiation of Site DTLs

Manual Retirement

NEW

- User has permission to edit the site DTL (i.e., is DTLA or CI)
- **No** patients are enrolled to the study at the site
- Site DTL is Approved, Unapproved, Initiated*, or Awaiting CI Approval*
- Protocol is any status *except* FDAAA Complete

*If signed at least once in the past

Manual Reinitiation

NEW

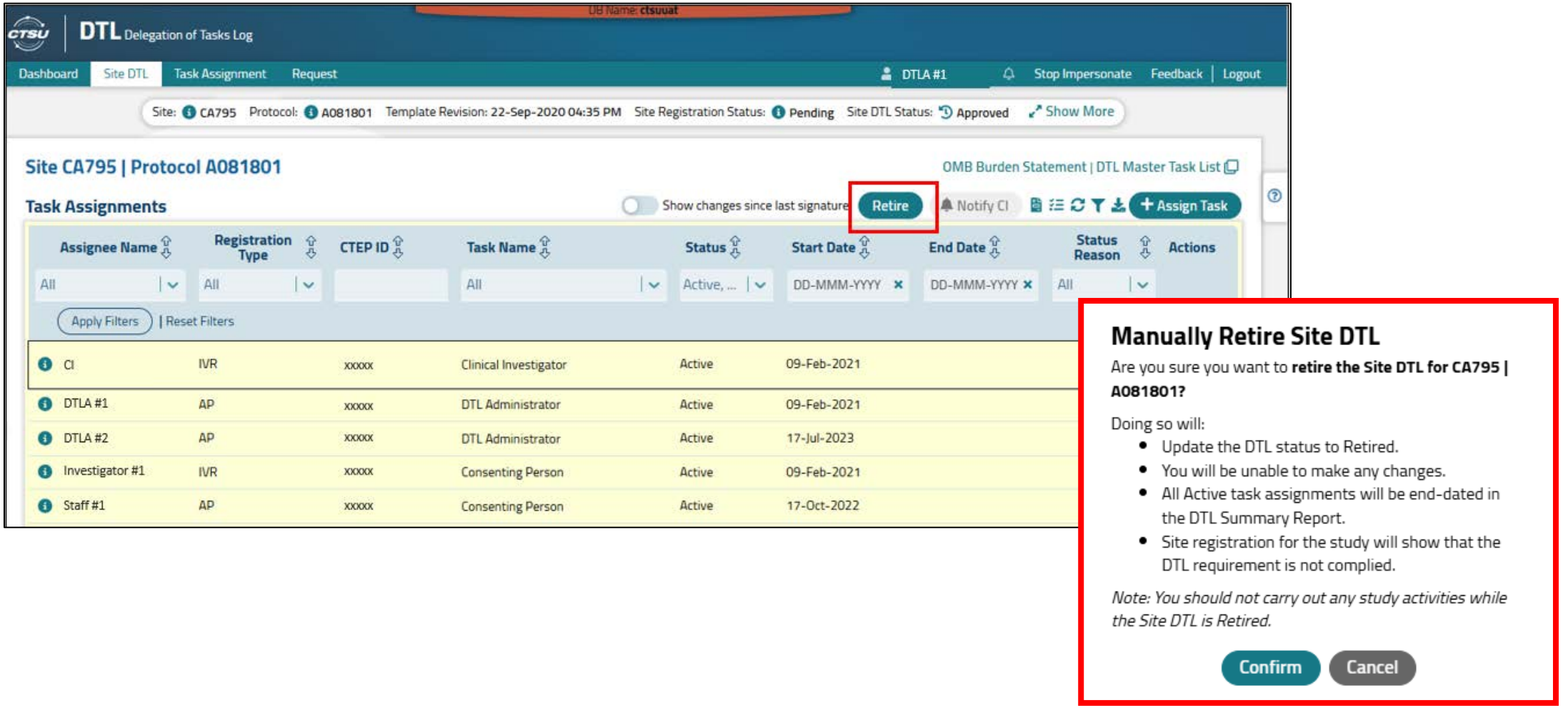
- Template version of retired DTL is current active version
- DTL was manually retired or DTL was automatically retired when study/site registration was Withdrawn
- Site registration status for the study is Pending or Closed (if Withdrawn, must be updated to Pending or Closed first)

Site DTL Browser Screen ☒ Delete

If site DTL is manually retired, Delete icon will not be visible if/when the DTL is moved back to an Initiated status

- **Users cannot delete a DTL that was ever signed**

Retire DTL



Manually Retire Site DTL

Are you sure you want to **retire the Site DTL for CA795 | A081801?**

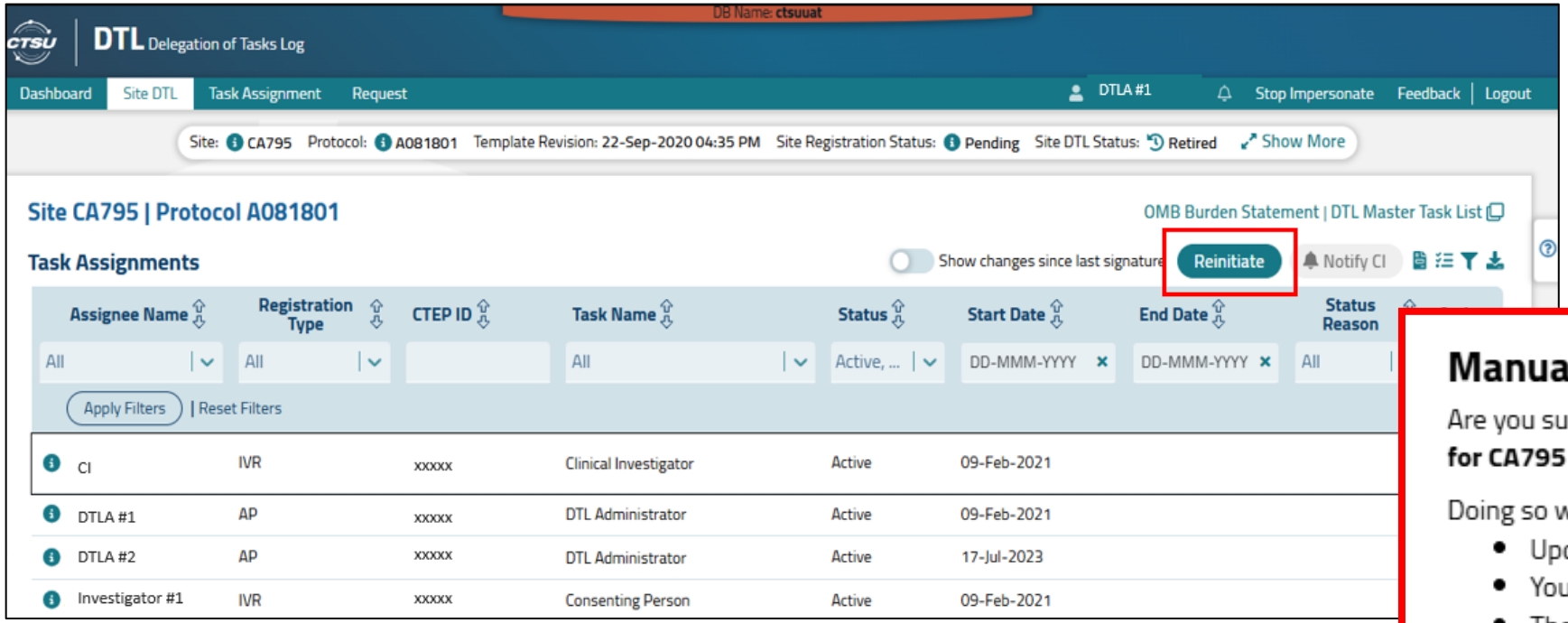
Doing so will:

- Update the DTL status to Retired.
- You will be unable to make any changes.
- All Active task assignments will be end-dated in the DTL Summary Report.
- Site registration for the study will show that the DTL requirement is not complied.

Note: You should not carry out any study activities while the Site DTL is Retired.

Confirm Cancel

Reinitiate Retired DTL



Manually Reinitiate Site DTL

Are you sure you want to **reinitiate the retired Site DTL for CA795 | A081801?**

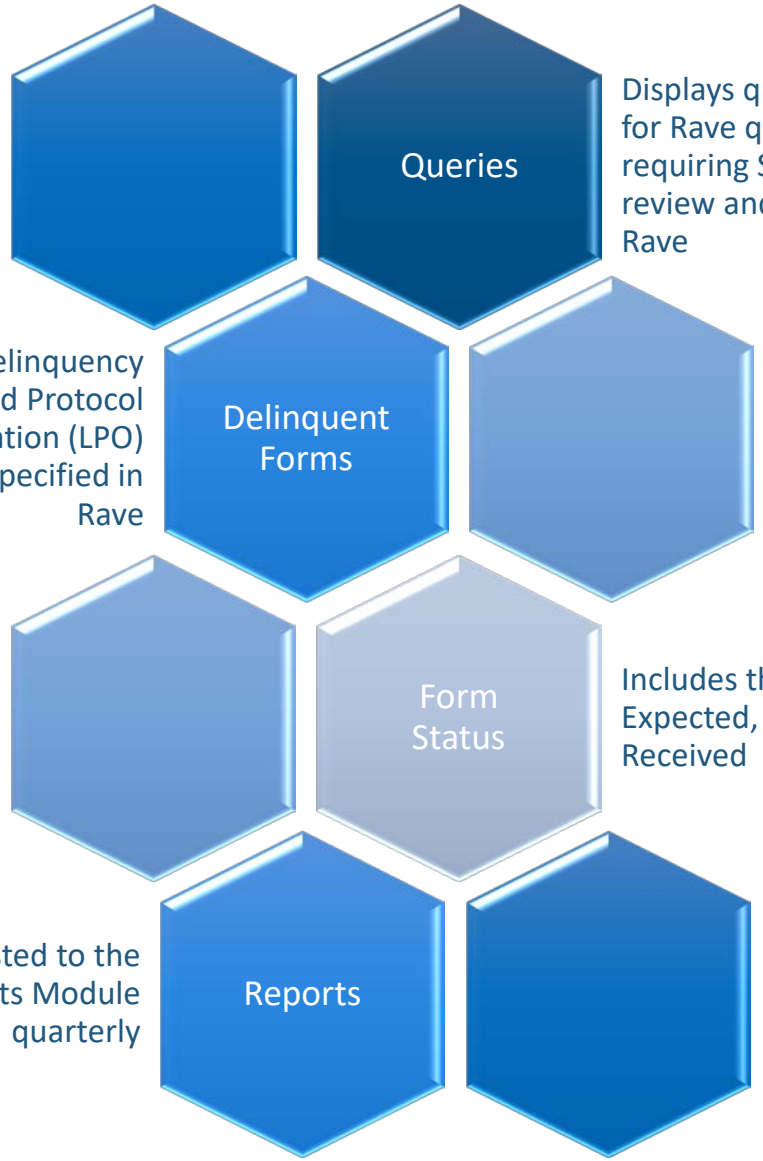
Doing so will:

- Update the DTL status to Initiated.
- You will be able to make changes.
- The reinitiated version must be signed/approved by the Clinical Investigator before the site can resume any study activities.

Confirm Cancel

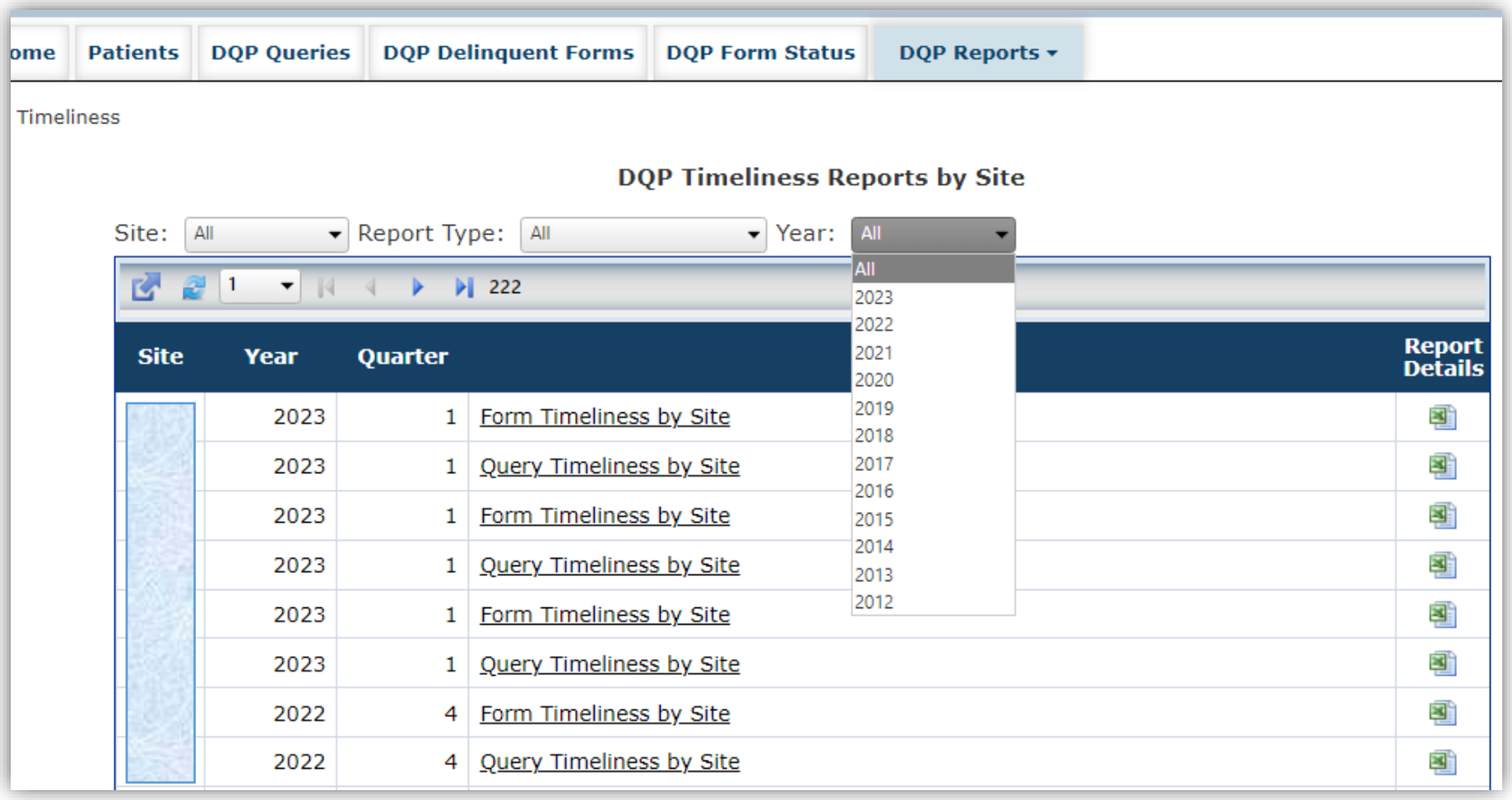
Data Quality Portal (DQP) Tips, Reminders & FAQs

Data Quality Portal (DQP) Modules



DQP Timeliness Reports Module

EXAMPLE



Data Quality Portal

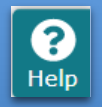
Exporting Reports

- DQP Reports can be exported via the More Commands icon  or the Excel icon  .

FAQs

- Available via the CTSU Website > Resources > Frequently Asked Questions (FAQs) > Data Quality Portal (DQP).

Help Topics

- The DQP Help Topics aid in using the DQP and are accessible via the Help Topics icon 

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Linking practice to progress

Electronic Medical Record (EMR) Templates

Electronic Medical Record (EMR) Templates

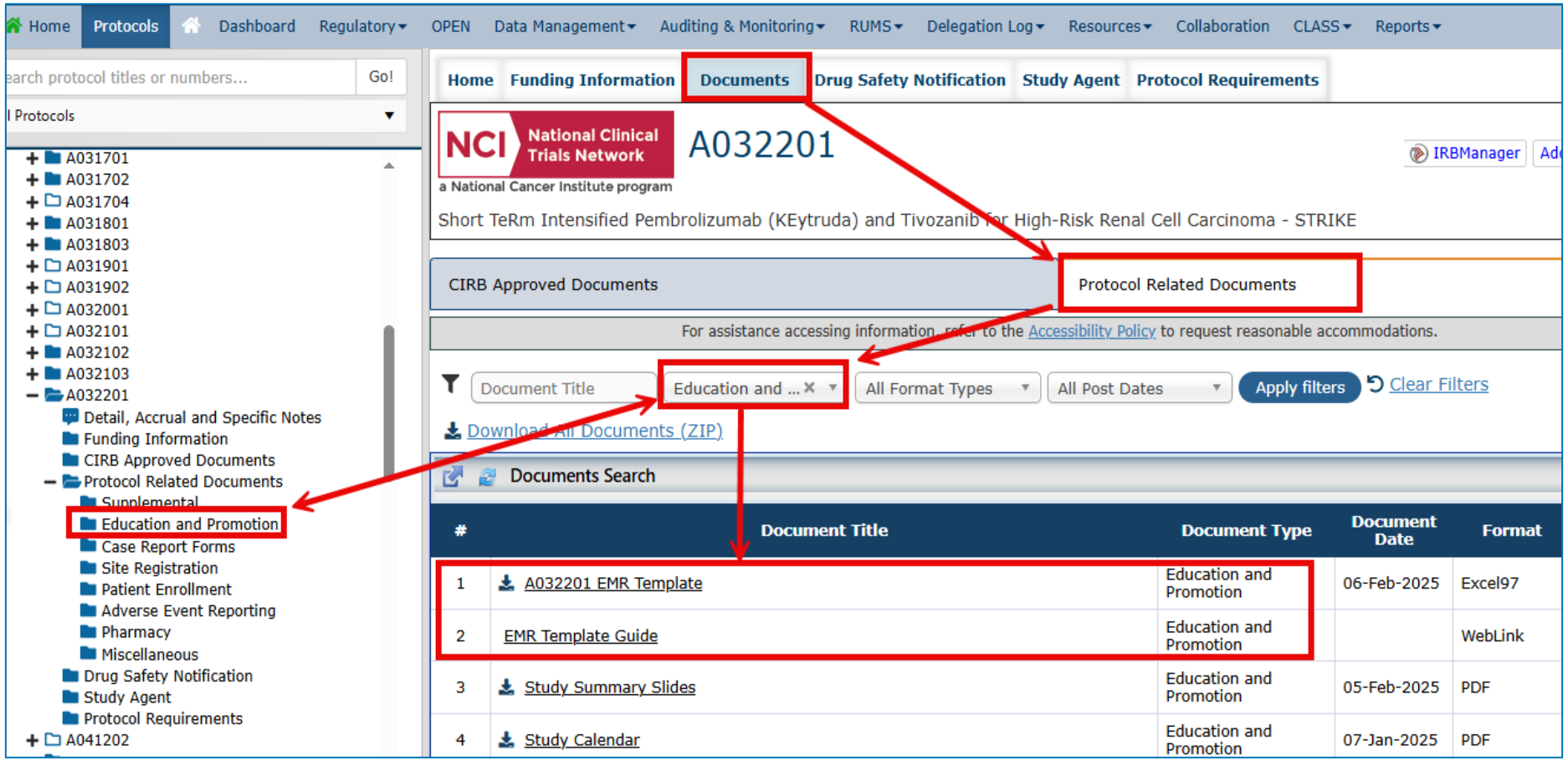
- **For new NCTN protocols**
  - Investigational agent
  - Standard of care drugs when dosages are included in protocol
- **Not a substitute for protocol!**
  - Excludes study elements not in EMR builds
- **Posted at study activation**
  - Updated at amendment
  - Major amendments require review by LPO

Protocol Name and Number:	EAY191-N4: A Randomized Trial of Selumetinib and Olaparib or Selumetinib Alone in Patients with Recurrent or Persistent RAS Pathway Mutant Ovarian and Endometrial Cancers: A ComboMATCH Treatment Trial
Protocol Version Date:	2/2/2023
Study Chair/LPO:	Shannon N. Westin, MD, MPH/NRG
Principal Investigator:	(Entered by individual site)
Protocol Coordinator:	(Entered by individual site)
Indication (Diagnosis):	Ovarian cancer, Endometrial cancer
Study supplied drug(s):	Selumetinib (PMB) and olaparib (PMB)
Other drug(s):	N/A
Other study intervention (e.g. radiation, surgery, transplant):	N/A
Location of Use (e.g. inpatient, outpatient, both, or not specified in protocol):	Outpatient
Type of protocol (e.g. Treatment or Supportive):	Treatment
Number of Cycles:	N/A (Repeat cycles every 28 days until disease progression or unacceptable side effects prohibit further therapy)
Cycle length:	28 days
Dosing Weight/BSA (e.g. actual, ideal, adjusted, not specified, N/A):	Flat dose regimen of selumetinib and olaparib
Weight (%)/BSA criteria for dose recalculations:	Flat dose regimen of selumetinib and olaparib
Treatment Arms:	Cohort 1 and Cohort 2 / Treatment Regimen 1: selumetinib and olaparib; Cohort 1 and Cohort 2 / Treatment Regimen 2: selumetinib only

TREATMENT PERIOD	Cohort 1 and Cohort 2 / Treatment Regimen 1: Selumetinib and Olaparib	Cohort 1 and Cohort 2 / Treatment Regimen 2: Selumetinib Only	COMMENTS
CYCLE 1: Research Labs/Specimens PK only (e.g. funded by study)	N/A	N/A	
CYCLE 1: Labs (e.g. hematological)	CBC with differential (includes basophils, eosinophils, hematocrit, hemoglobin, lymphocytes, mean corpuscular hemoglobin, mean corpuscular hemoglobin concentration, mean corpuscular volume, monocytes, neutrophils, platelet count, red blood cell count, and total white cell count)	CBC with differential (includes basophils, eosinophils, hematocrit, hemoglobin, lymphocytes, mean corpuscular hemoglobin, mean corpuscular hemoglobin concentration, mean corpuscular volume, monocytes, neutrophils, platelet count, red blood cell count, and total white cell count)	≤ 3 days of D1. Note: baseline laboratory assessments conducted within 3 days of therapy start do not need to repeated on C1 day 1 of treatment unless otherwise noted. See protocol Section 4.1.
CYCLE 1: Labs (e.g. serum chemistries)	Serum chemistry labs (sodium, potassium, chloride, bicarbonate, BUN, creatinine, glucose, albumin, calcium, AST (SGOT), ALT (SGPT), alkaline phosphatase, total bilirubin, total	Serum chemistry labs (sodium, potassium, chloride, bicarbonate, BUN, creatinine, glucose, albumin, calcium, AST (SGOT), ALT (SGPT), alkaline phosphatase, total bilirubin, total	≤ 3 days of D1. Note: baseline laboratory assessments conducted within 3 days of therapy start do not need to repeated on C1 day 1 of treatment unless otherwise noted. See protocol Section 4.1.
CYCLE 1: Labs Other (e.g. TSH, PT/INR, amylase)	LDH, magnesium	LDH, magnesium	≤ 3 days of D1. Note: baseline laboratory assessments conducted within 3 days of therapy start do not need to repeated on C1 day 1 of treatment unless otherwise noted. See protocol Section 4.1.
CYCLE 1:	Serum beta HCG (pregnancy test)	Serum beta HCG (pregnancy test)	Within 72 hours prior to 1st dose of therapy and as clinically

Electronic Medical Record (EMR) Templates

The EMR Template and EMR Template Guide are in Protocol Related Documents > Education and Promotion.



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Linking practice to progress

CTSU Patient Transfer Process

Types of Transfers and Updates

Patient Transfers

- Transfer to a different institution
- May also involve a change to credential information

Credential Updates

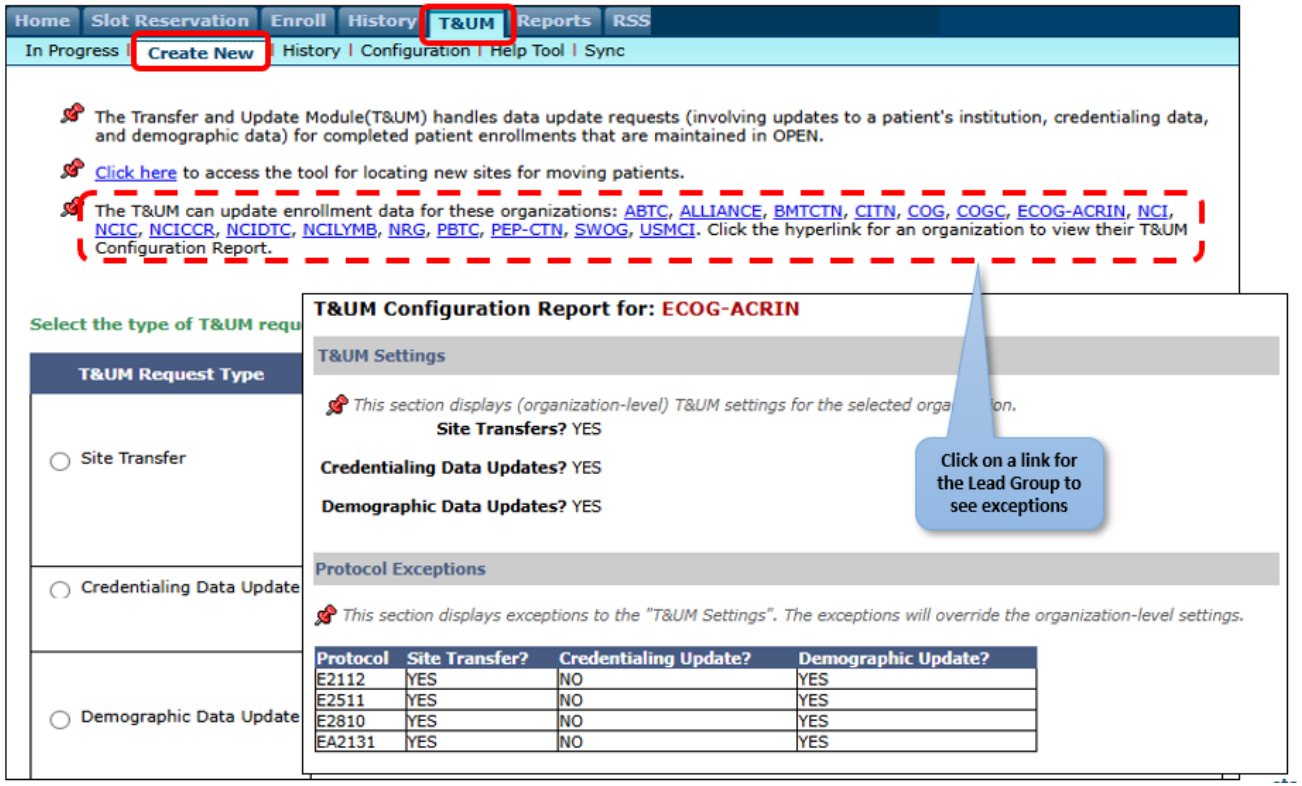
- Types:
  - Persons associated with the enrollment
  - Network Group Credit
  - Radiation Therapy/Imaging (RT/I) Provider
- Credit updates only allowed at subsequent steps when site is no longer a member of original credited group

Demography Updates

- Correcting or changing the demography data to reflect data **at time of enrollment**
- Ensure all data is correct at initial step before proceeding to enrollment on subsequent steps

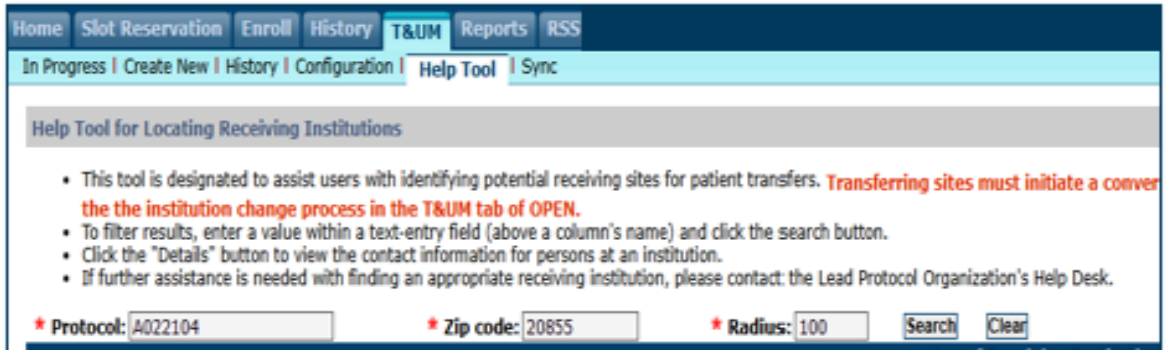
Transfer and Update Module (T&UM)

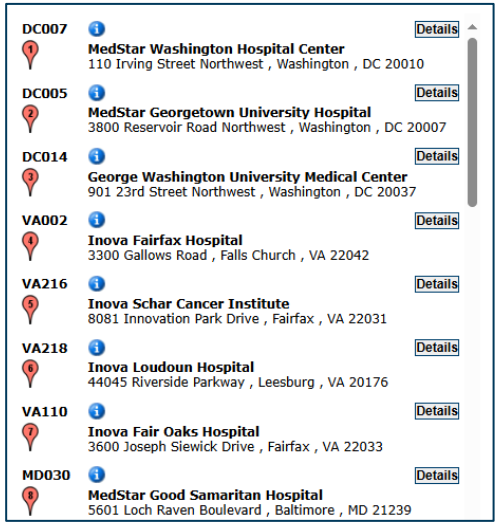
- Available for select network group protocols
- Each network group configures their T&UM settings individually
- Can be used for protocols in *all statuses*
- Cannot be used if site registration is expired



Patient Transfers in Transfer and Update Module (T&UM)

- Patient transfers in T&UMs are initiated by the current site
  - Help Tool identifies potential receiving sites for patient transfers
  - Current site should initiate conversation with the potential receiving site





- The receiving site receives notification email
  - Must accept or reject the patient transfer
  - Some transfers also require LPO approval
- Guidance:
  - The T&UM History section
  - OPEN T&UM Quick Reference Site User Guide

CTSU Patient Transfer Form

When to use?

- Legacy enrollments completed by CTSU registrars
- Transferring site/staff with Withdrawn or Follow-up roster status
- Site Transfers not supported by T&UM for network group protocols (group-level or protocol-level exceptions)
- Bulk transfers

Where to access?

- CTSU website in the Resources Folder under CTSU Forms
- Upload completed form to Regulatory Submission Portal on the CTSU website. (*Select Enrollment/Transfers*)

What happens next?

- The CTSU Transfer Coordinator will process the patient transfer in OPEN on behalf of the site
- Email confirmations sent upon completion

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OPEN Modernization

Phased Plan

Phase 1

Focused on administrative screens that Lead Protocol Organizations (LPOs) can access for form setup

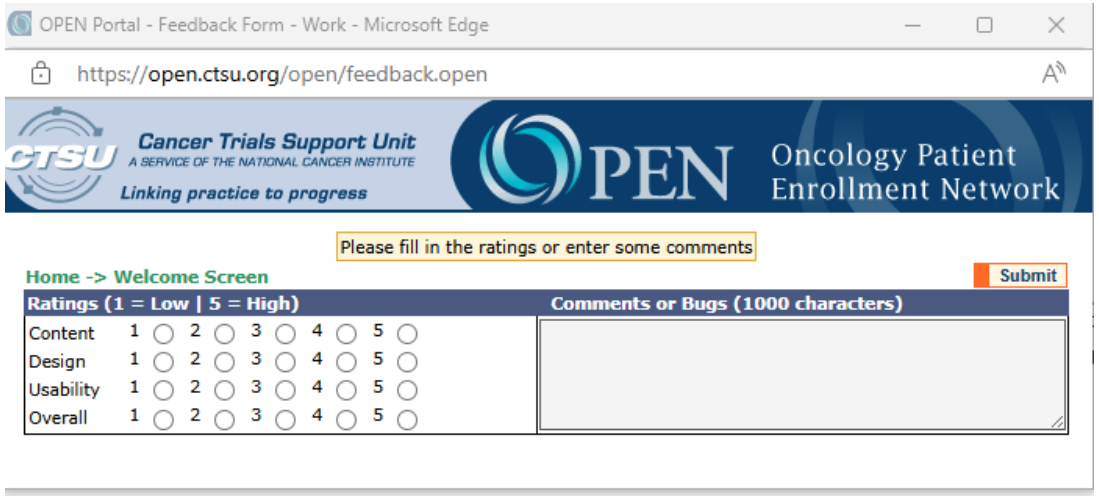
Phase 2

Updates to site-facing screens related to enrollment:

- Enrollment screens
- Practice mode screens
- History screen
- Slot reservation
- Funding screen

Feedback Opportunities

- OPEN feedback icon
- Group meetings: Open Forum
- Future Opportunities:
  - OPEN Modernization Survey
  - Site Advisory Panel



Questions?

CTSU Help Desk

1-888-823-5923

CTSUContact@Westat.com

Oishi Symposium

welcomes

Min Fang, MD, PhD, FACMG
Cytogenetics

Fred Hutch Cancer Center

Triaging Clinical Trial Patients with Cytogenetics and Genomic Testing

Min Fang, MD, PhD, FACMG

Professor, Translational Research & Therapeutics Division,

Fred Hutchinson Cancer Center

Professor, Department of Laboratory Medicine and Pathology,

University of Washington Medical Center

Senior Director of Clinical Cancer Genomics, Fred Hutch Cancer Center

SWOG Spring Meeting, Oishi Symposium, San Francisco, CA

May 2nd, 2025

UW Medicine

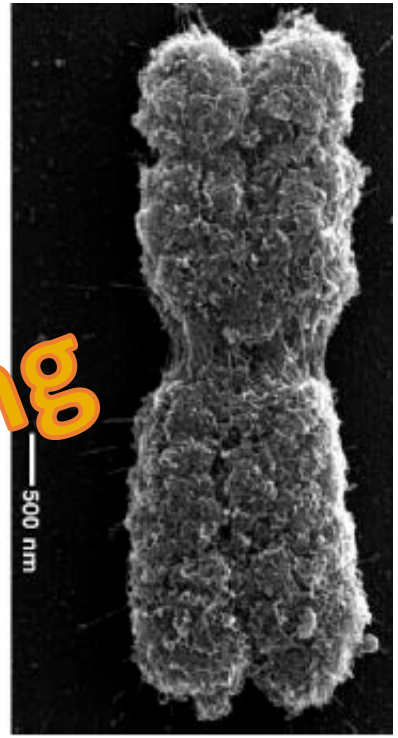
1 Appraise the current technical modalities for clinical cytogenetics and genomic testing

2 Appreciate how various genomic testing tools are used to triage patients in clinical trials (AML, CLL, PCN)

3 Understand the prognostic impact of the most common cytogenetic abnormalities and tools for risk stratification in clinical trials

Cytogenetics Karyotyping – the “good old” whole genome analysis tool

69 Amazing years



46 human chromosomes discovered in 1956

Celebrating our past – Amazing 69 years

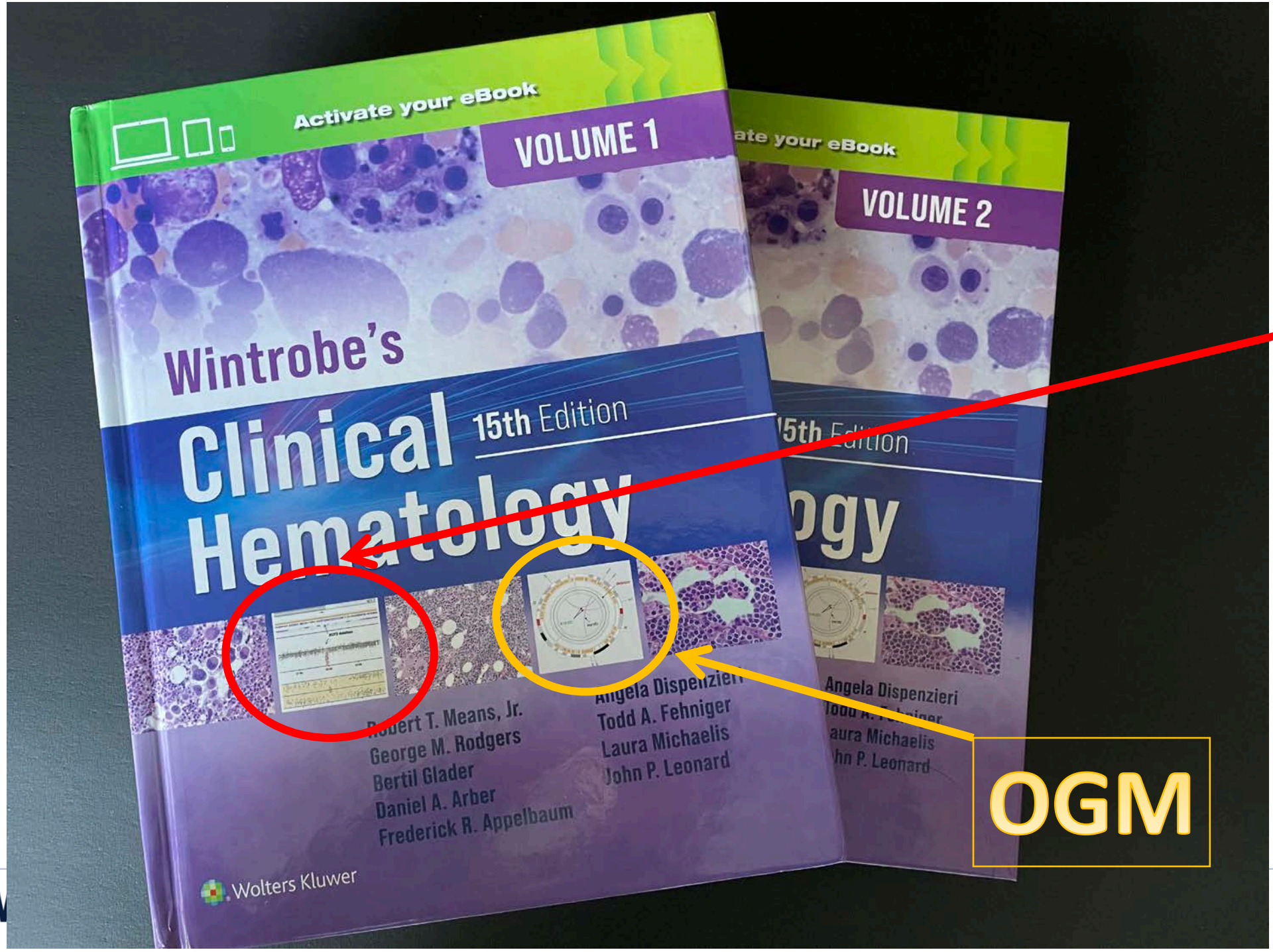
- **1969**, *Gall and Pardue* first described *in situ* Hybridization
- **1981**, *Harper and Saunders* mapped human genes; *Langer et al* introduced fluorescently tagged probe – beginning of clinical FISH
- **1988**, *Pinkel et al* described chromosome painting probes
- **1992**, Kallioniemi et al introduced comparative genome hybridization (CGH) using metaphase chromosomes as the interrogator
- **2004-2006**, BAC CGH arrays were the first arrays used clinically for the detection of copy number changes
- **2009-current**, oligo arrays and SNP arrays more widely used clinically

In loving memory of Athena (Tena) M. Cherry, PhD,
former Director of Cytogenetics, Stanford University School of Medicine

Source: Wintrobe's Clinical Hematology, 14th and 15th editions

Timeline of molecular technologies

- **1977** Sanger sequencing
- **1983** PCR
- **2008** NGS for fetal aneuploidy screening
- ***2012*** Fred Hutch launched chromosome genomic array testing (CGAT) clinically
- ***2014*** NGS used for cancer at UWMC clinically
- ***2020*** Fred Hutch CCGL Launched RNA-based NGS for fusion detection clinically



2024

CGAT

OGM

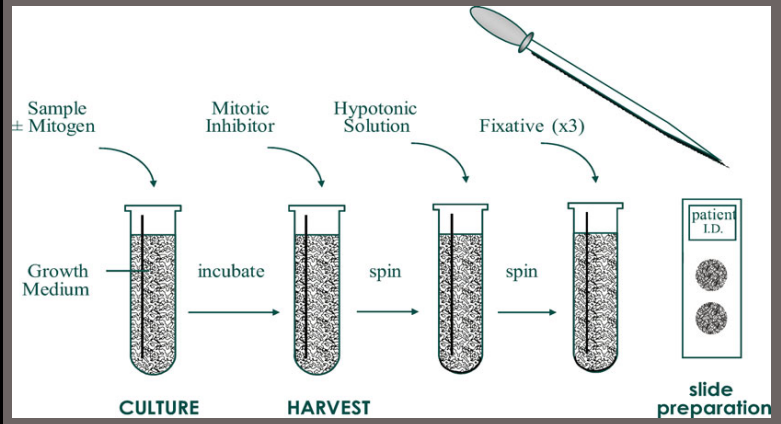
Common acronyms

- ***GTW –*** Giemsa with Wright stained karyotyping, 1970
- ***PCR –*** polymerase chain reaction, 1983
- ***FISH –*** fluorescent in situ hybridization, 1986
- ***CGAT/CMA –*** chromosome genomic array testing/ chromosome microarray (1992 CGH), 2010 for clinical use
- ***NGS –*** next generation sequencing, 2005/2013-15
  - ***Sanger sequencing***, 1977
- ***WES –*** whole exome sequencing, 2012
- ***WGS –*** whole genome sequencing, 2012/2020
- ***OGM*** – optical genomic mapping, 2019-2020

Karyotype Analysis

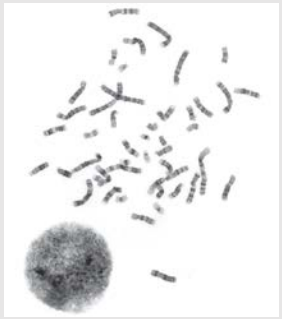
Reveal

Culture, Harvest



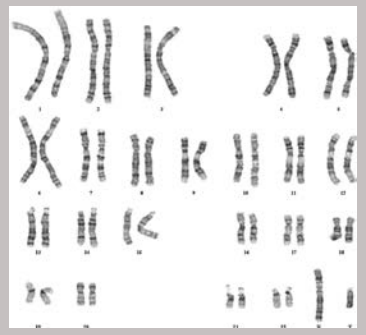
Detect/Image

Analysis tech (Scanner)



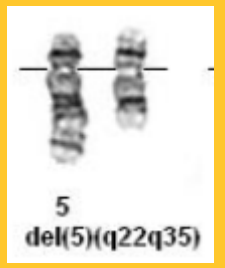
Interpret 1

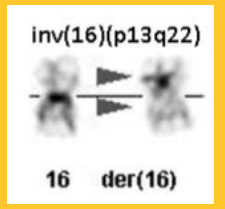
Karyogram

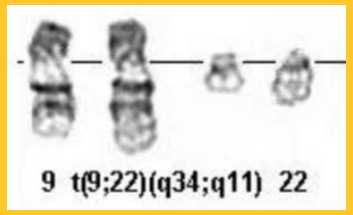


Interpret 2

Call abnormality

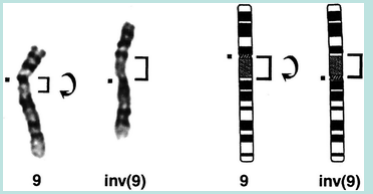




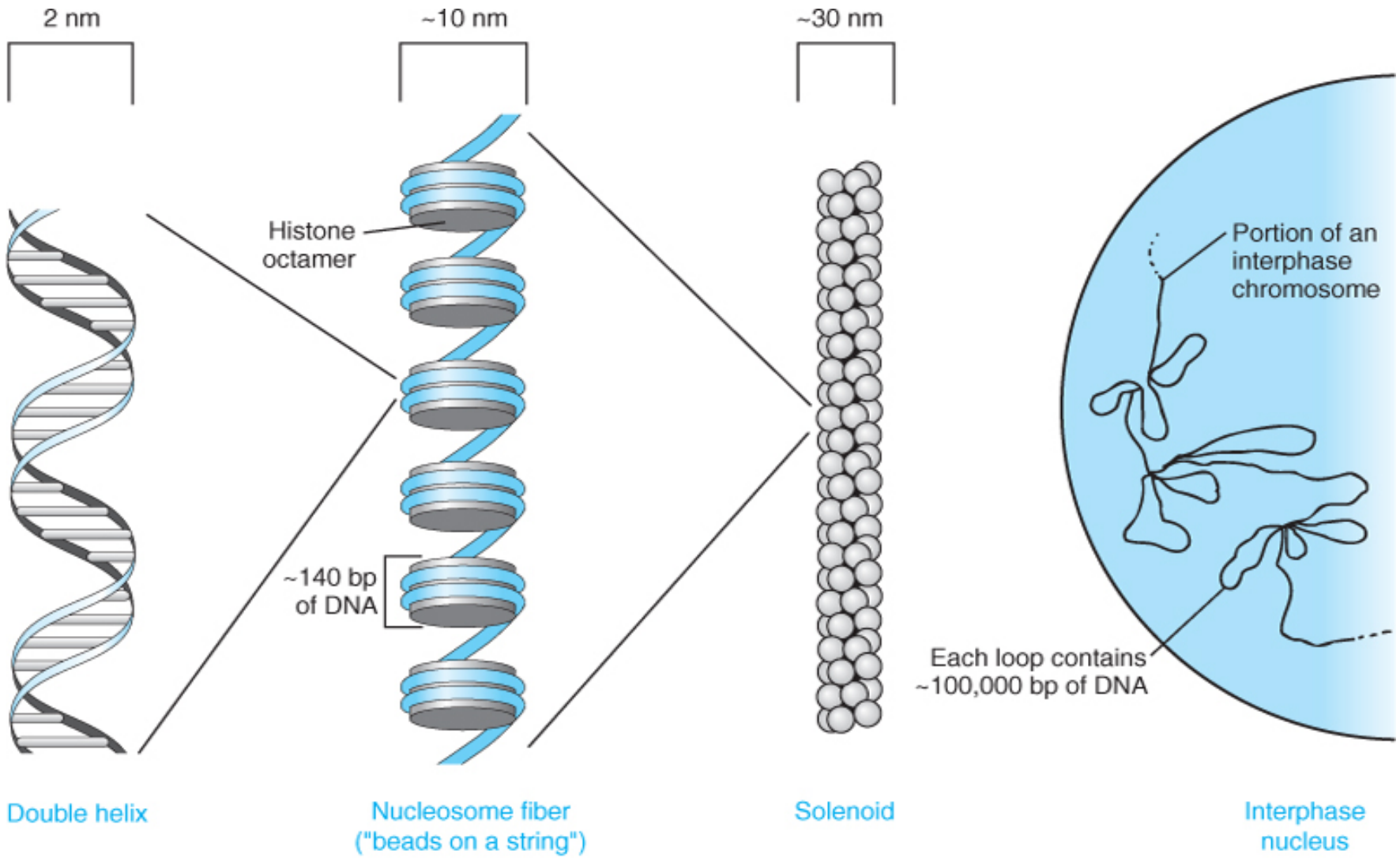


Interpret 3

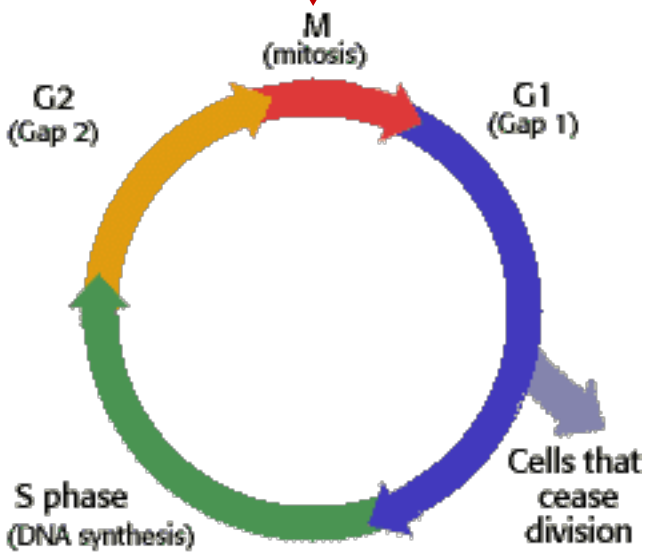
Benign? Clonal?



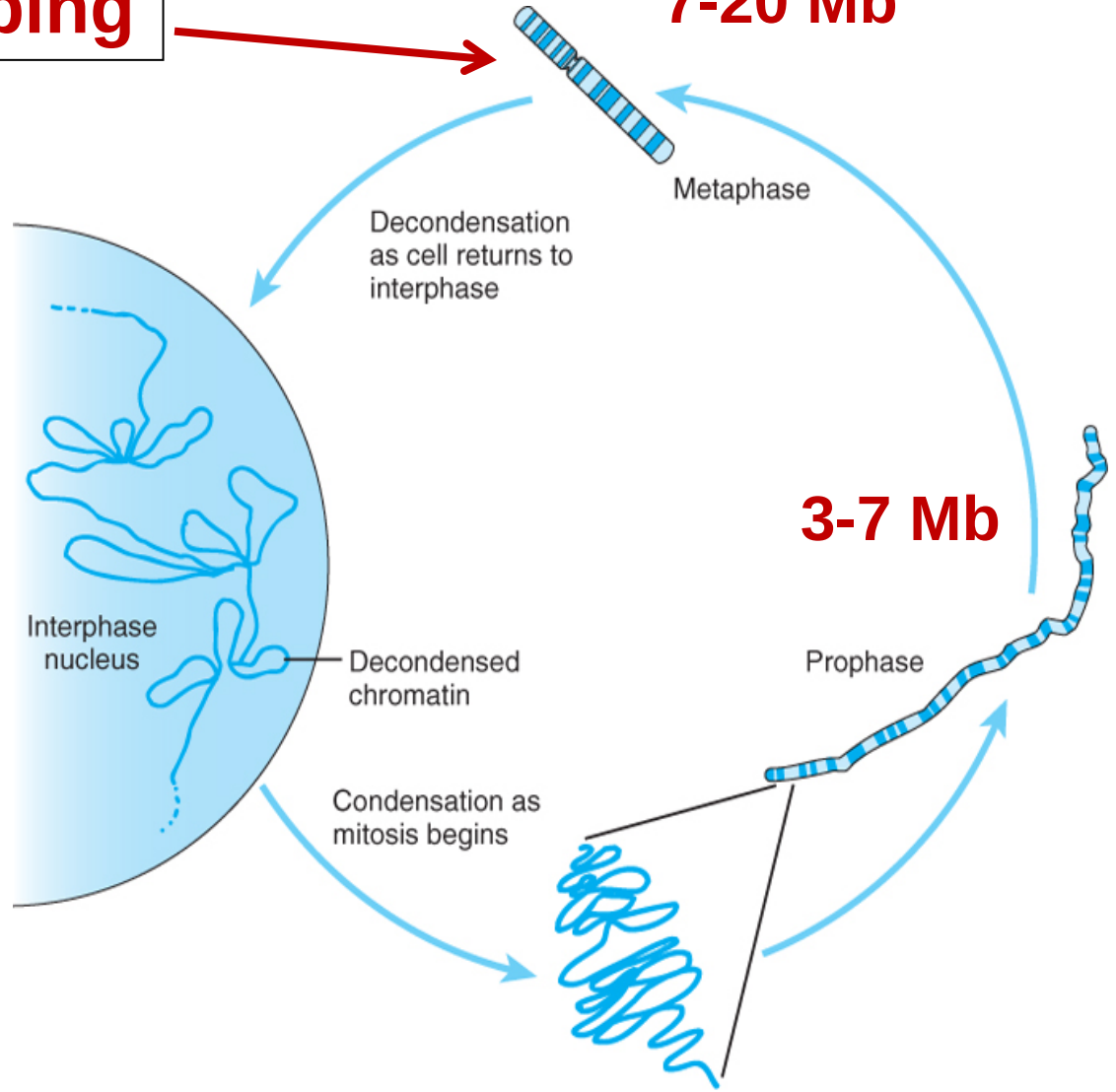
https://atlasgeneticsoncology.org/



Tested by karyotyping



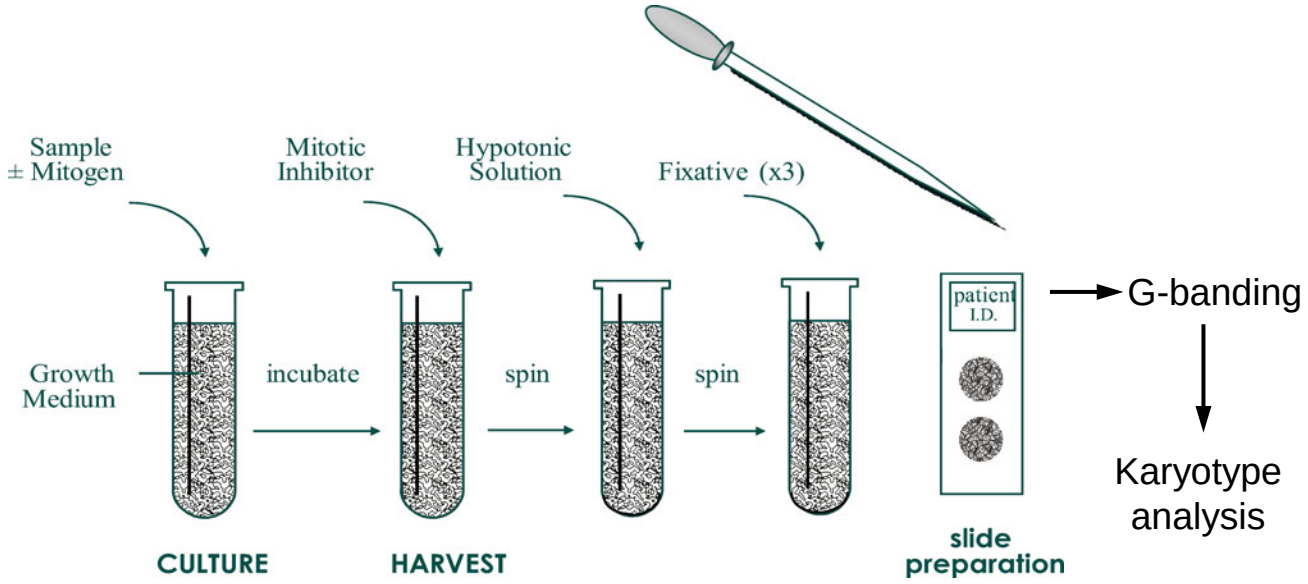
7-20 Mb



3-7 Mb

Karyotype Analysis

Aka Conventional Cytogenetics



Requires

- Fresh viable and sterile specimen
- Tissue culture (Limiting factor for analytical sensitivity and turnaround time)

PRO's

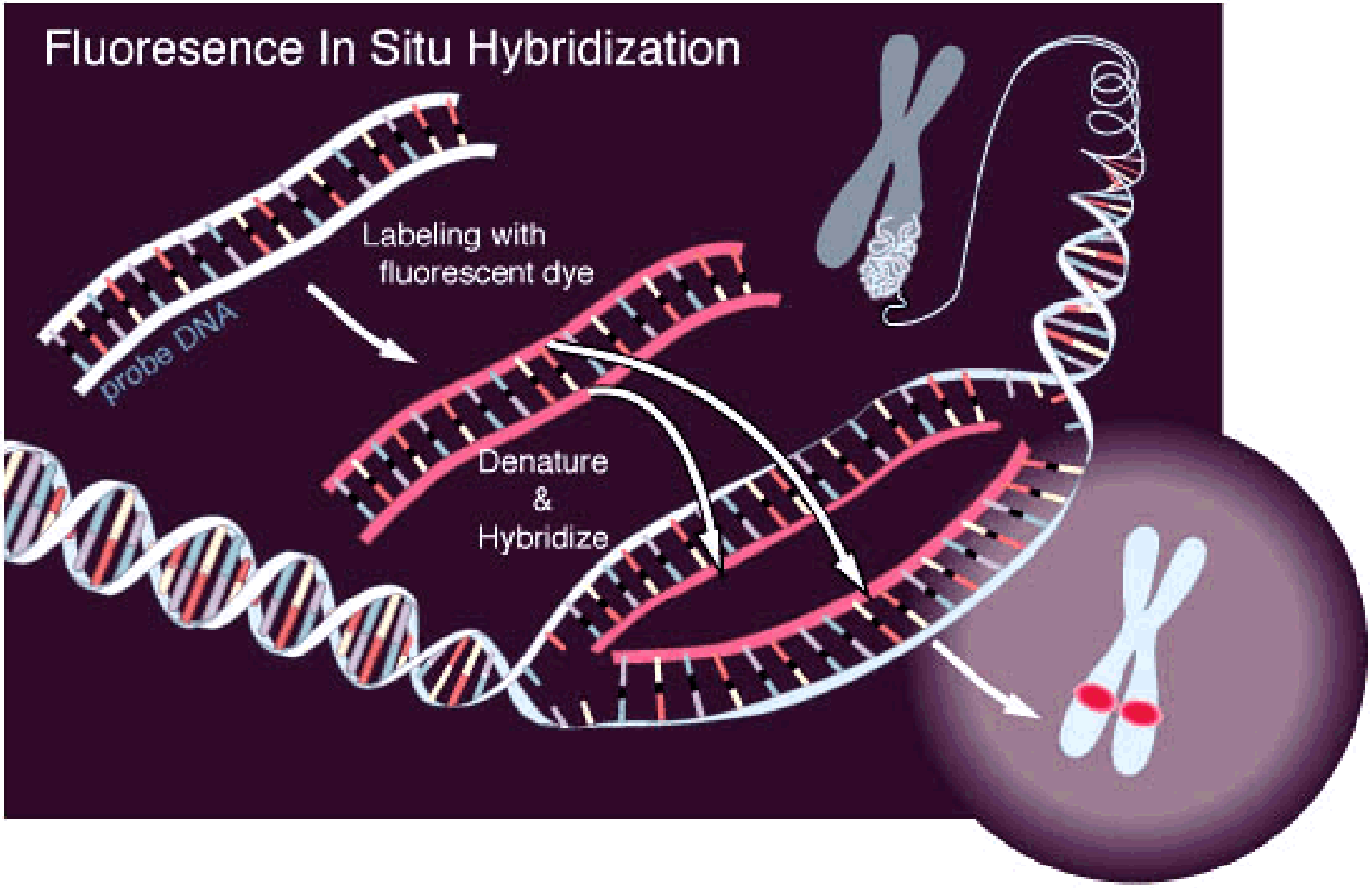
- Whole genome
- Single cell based
- Demonstrate clonal evolution unambiguously

CON

- Primarily manual and labor intensive

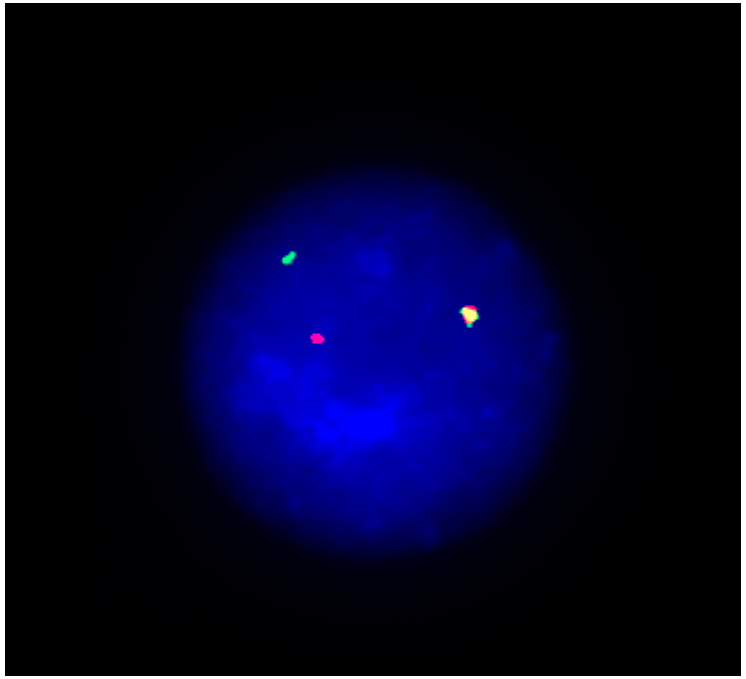
Information from metaphase cells only

FISH

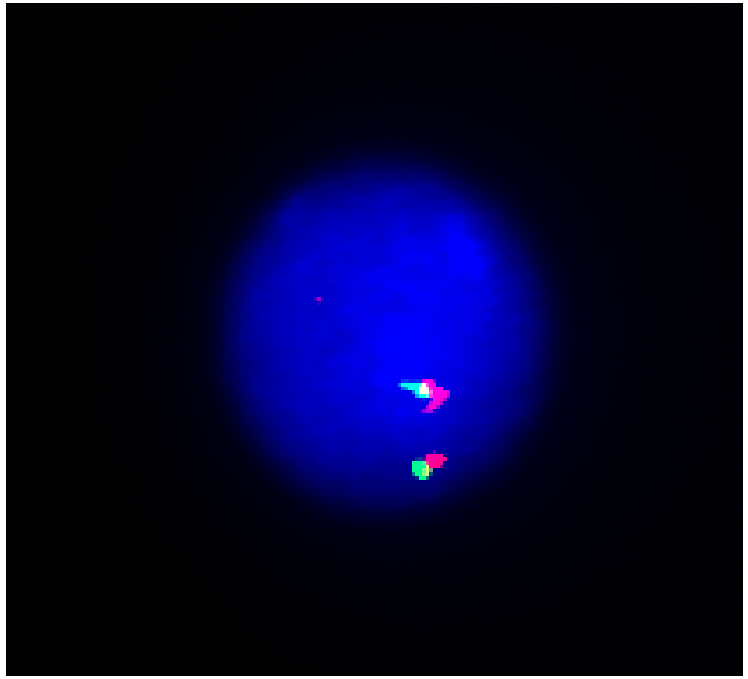


Partially overcome the low-resolution barrier of karyotyping, and the need for dividing cells.

Typical FISH signal pattern using break-apart probes to detect gene rearrangement



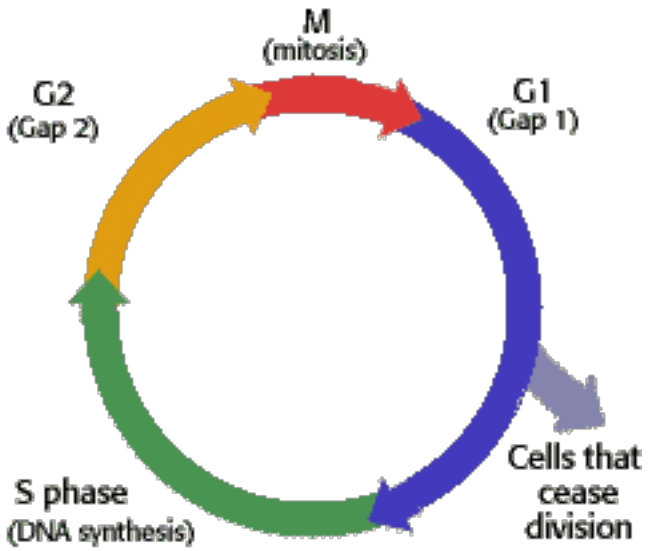
KMT2A rearranged nucleus

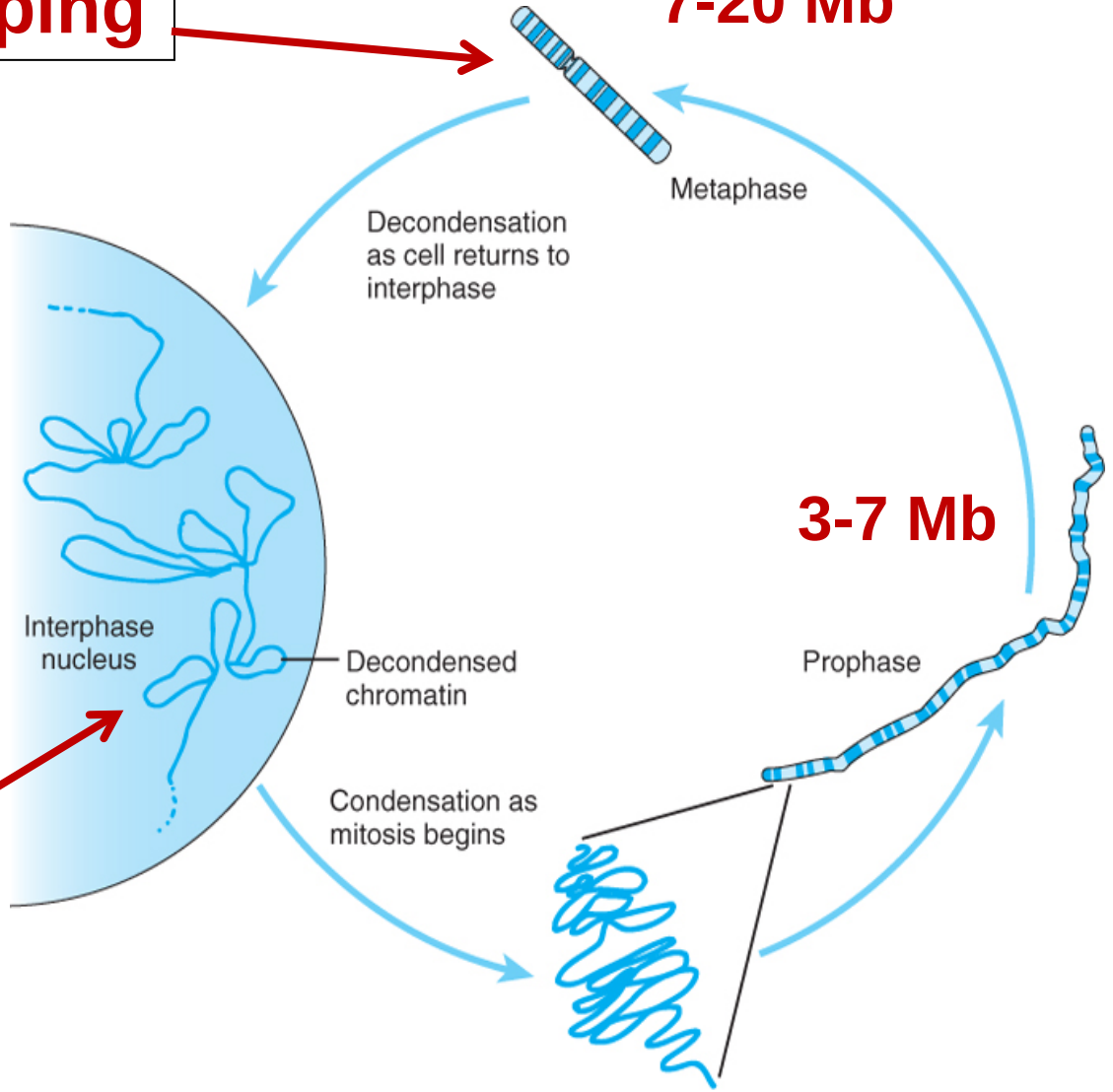


Normal nucleus

Tested by karyotyping

7-20 Mb



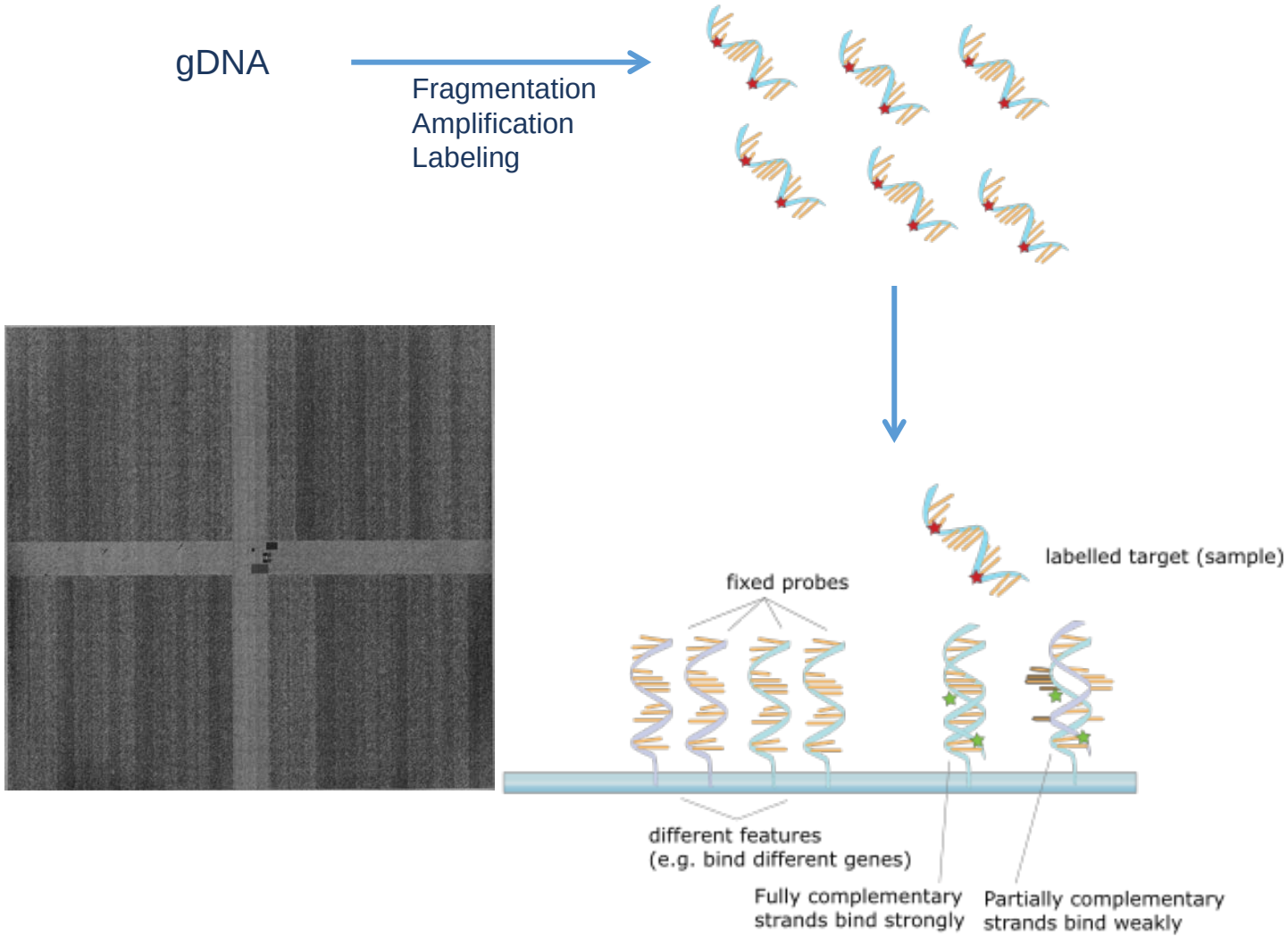


3-7 Mb

Tested by FISH

100-500 kb

Chromosome Genomic Array Testing (aka CMA)



Fresh, frozen, and archived specimens

- No need for tissue culture

Can

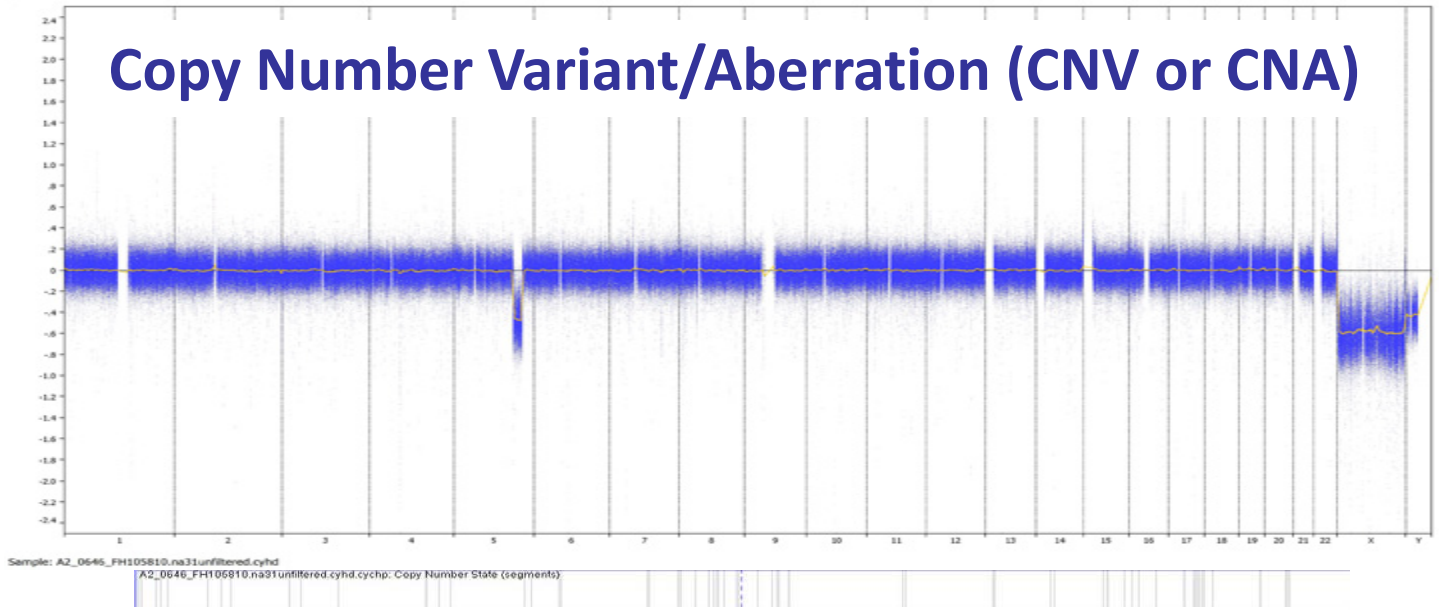
- Whole genome or targeted
- Detect submicroscopic genomic lesions
- Detect loss of heterozygosity (LOH)
- Infer clonal evolution

Cannot

- Detect low-level aberrations (MRD <10%)
- Distinguish between cells
- Detect balanced translocations

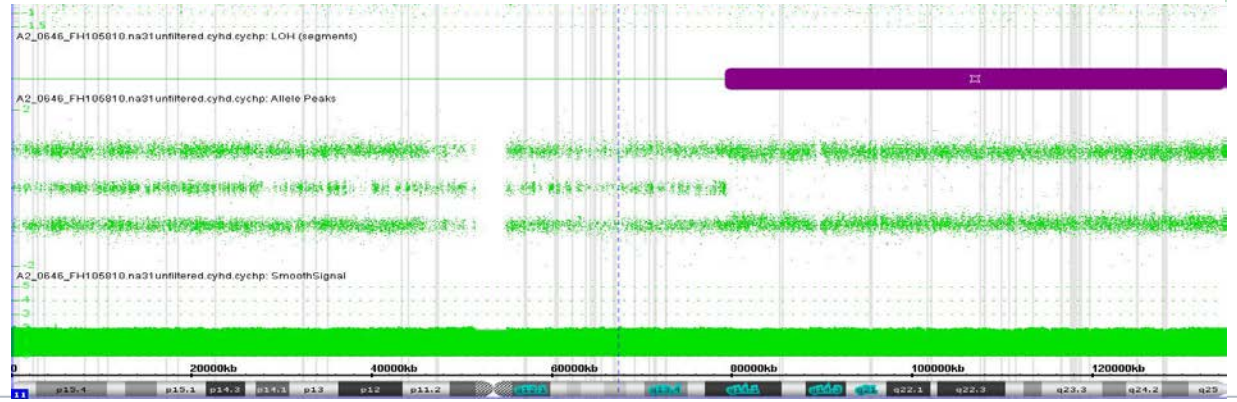
Chromosome Genomic Array Testing (CGAT)

Copy Number Variant/Aberration (CNV or CNA)



5q deletion
in a male

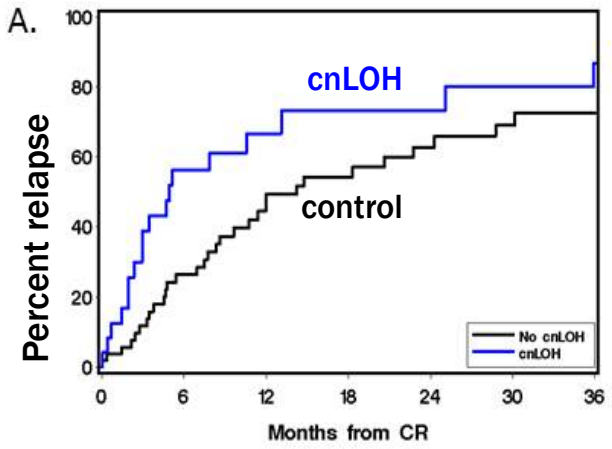
Copy neutral loss of heterozygosity (cnLOH)



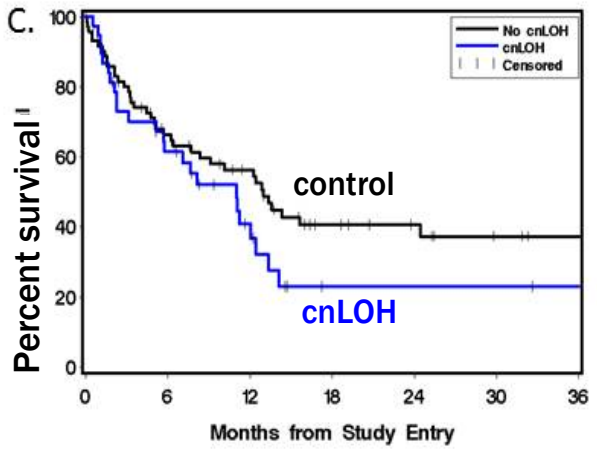
11q cnLOH

Experience from Fred Hutch

HR 1.87



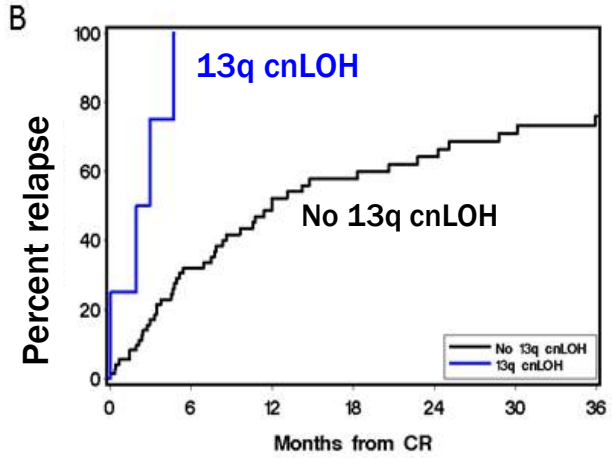
P=0.04



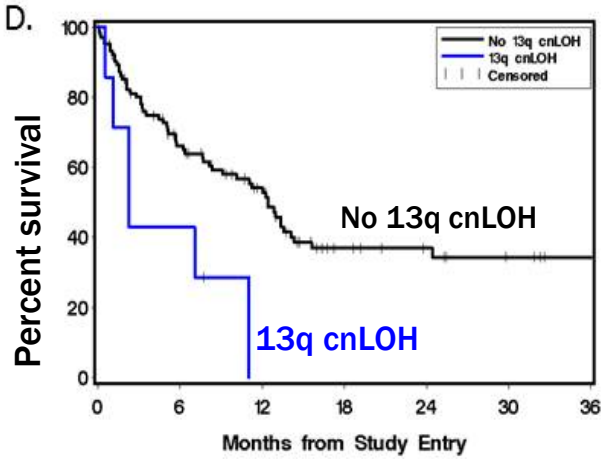
HR 1.82

P=0.03

HR 6.64



P=0.006



HR 3.45

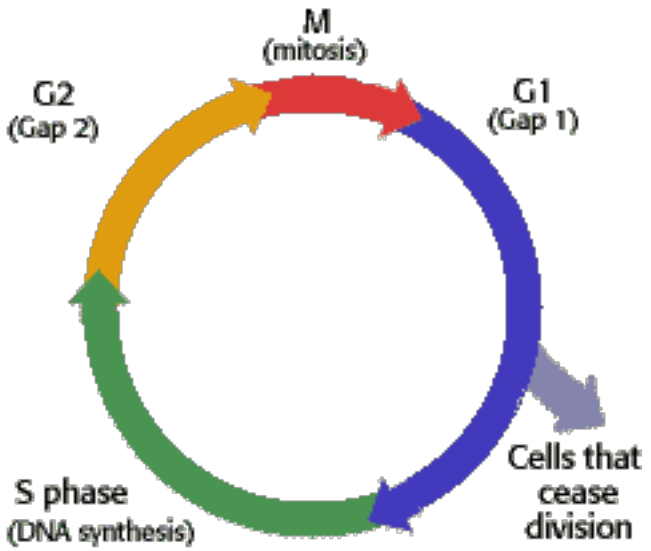
P=0.02

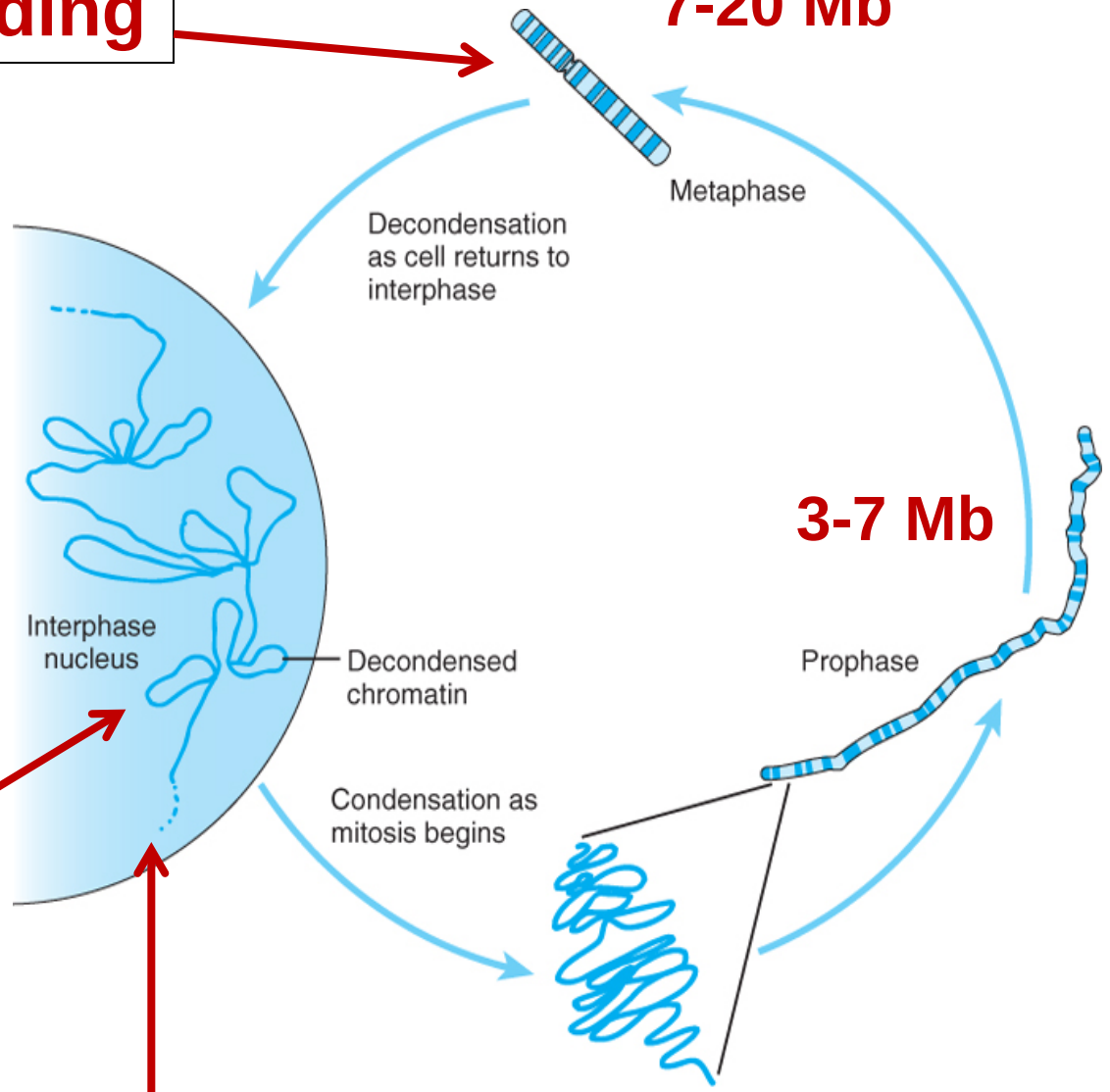
Gronseth et al. Prognostic significance of acquired copy-neutral loss of heterozygosity in acute myeloid leukemia. 2015 Cancer

Relapse **Survival**

Tested by G-banding

7-20 Mb





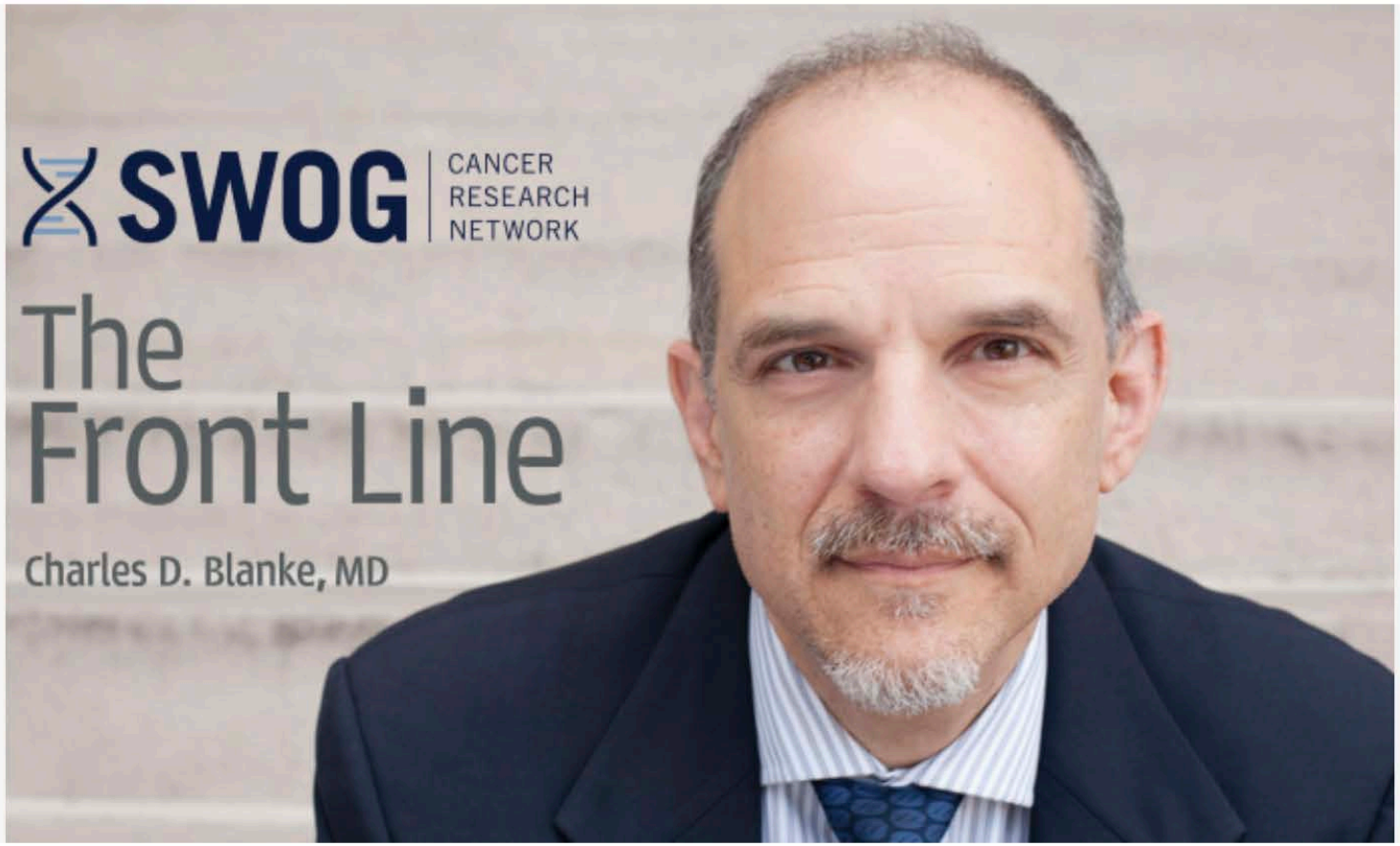
3-7 Mb

Tested by FISH

100-500 kb

Tested by CGAT

30-100 kb



MyeloMATCH Set to Make Its Make Its Mark

September 11, 2020

Group Chair

Share

Next year, we expect to launch a new master protocol – MyeloMATCH, an umbrella trial that will test treatments for acute myeloid leukemia (AML) and myelodysplastic syndromes (MDS).

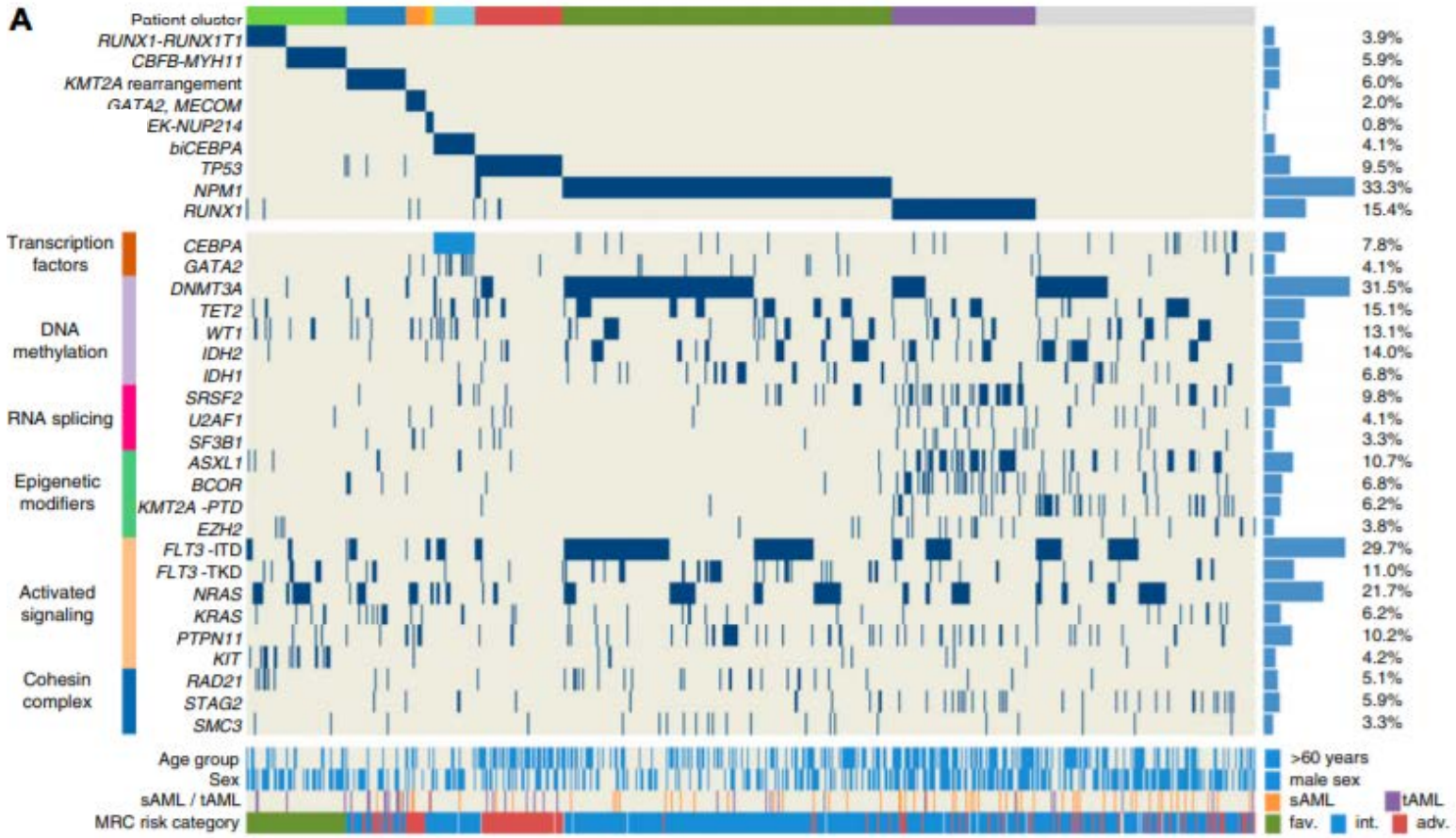
Acute myeloid leukemia (AML) outcome

Seer data

Background: The Mutational Heterogeneity of AML

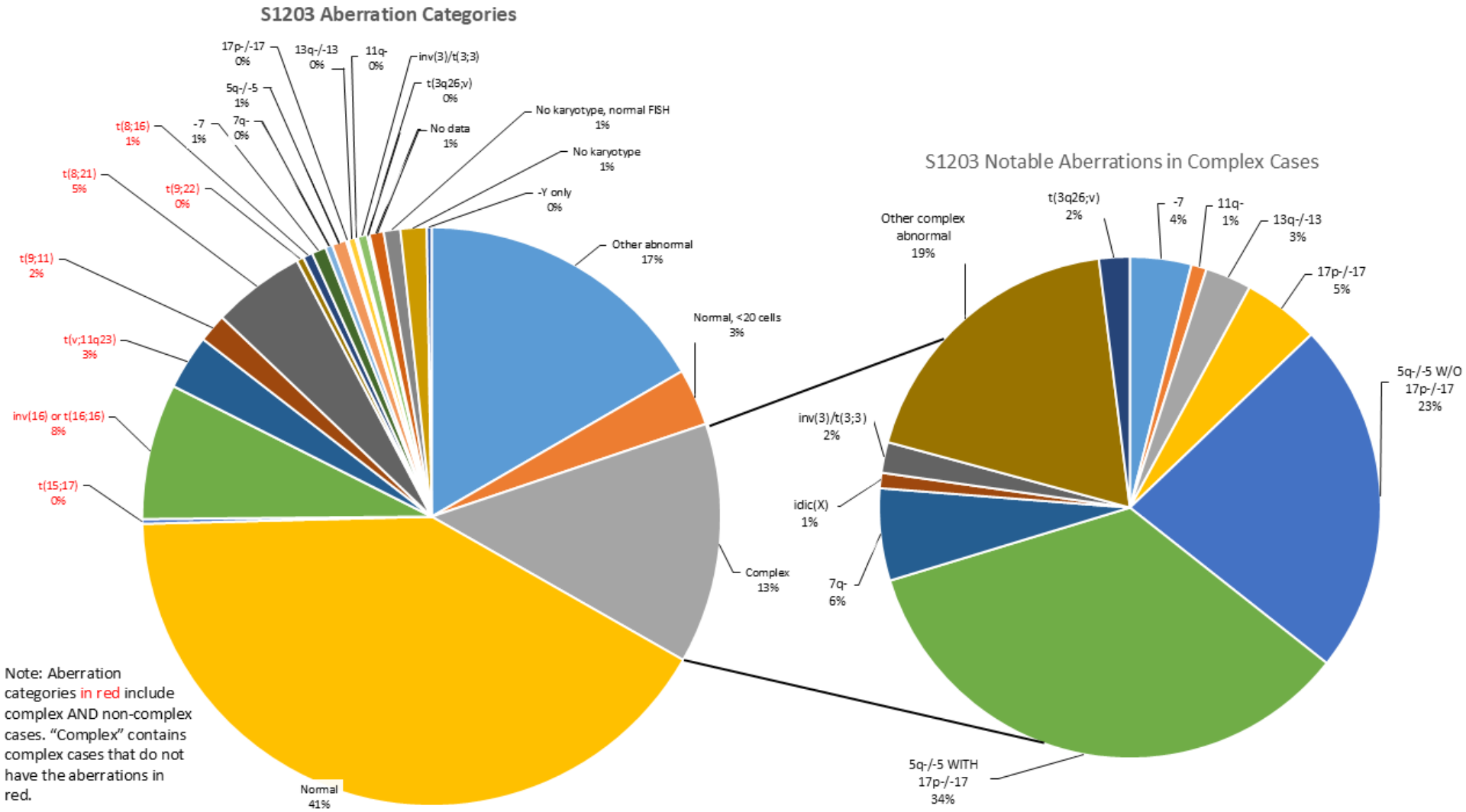
Patient Clusters

- CBF leukemias (n=65): *RUNX1-RUNX1T1; CBFB-MYH11*
- *KMT2A*-rearranged (n=39)
- *GATA2, MECOM* (n=13)
- *DEK-NUP214* (n=5)
- *CEBPA* double mutated (n=27)
- *TP53* mutated (n=59)
- *NPM1* mutated (n=217)
- *RUNX1* mutated (n=94)
- others (n=145)



Metzeler KH, et al. *Blood.* 2016; 128: 686-696.

The Cytogenetic Heterogeneity of AML (S1203)



Unpublished data, K. Lee, Fang lab

myeloMATCH

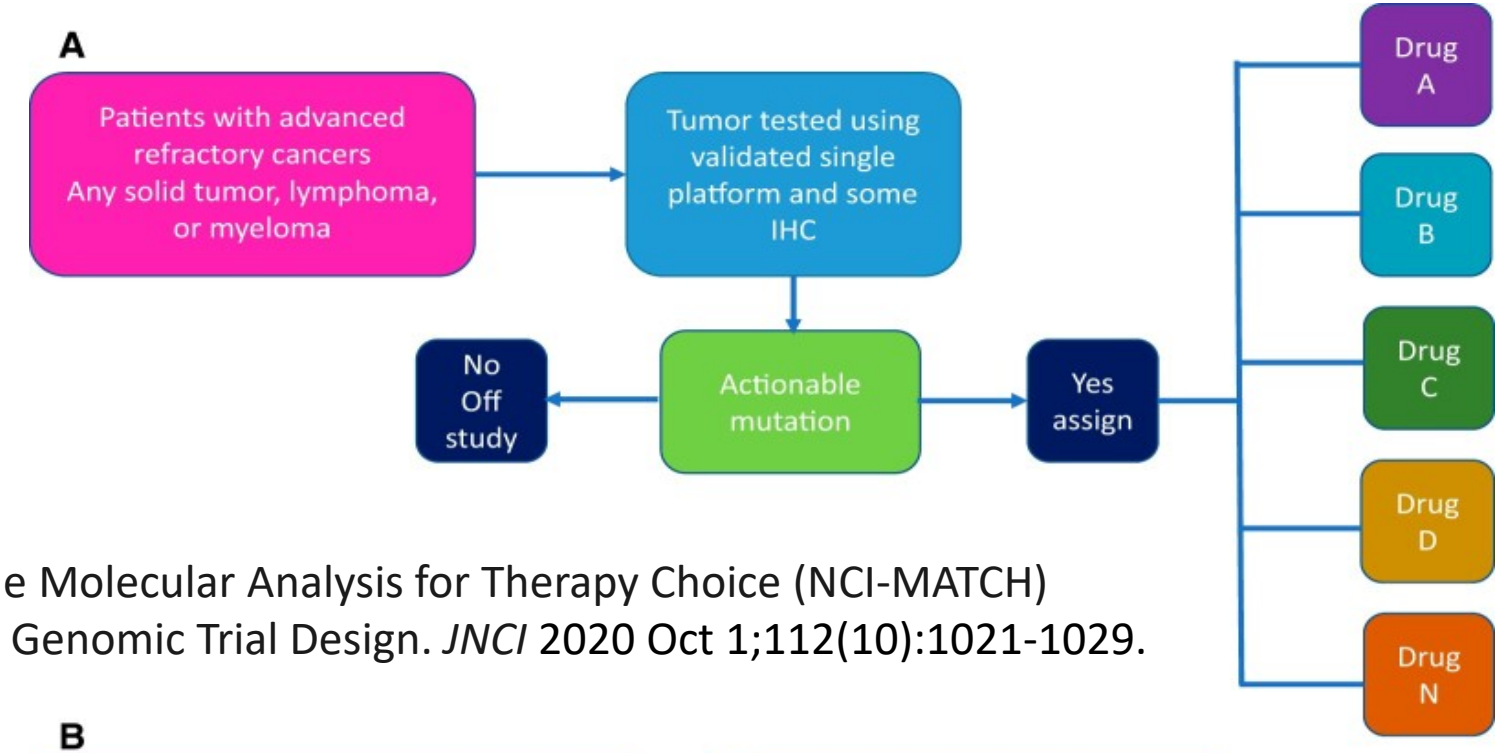
Myeloid Malignancies Molecular Analysis for Therapy Choice

NCI National Clinical Trials Network

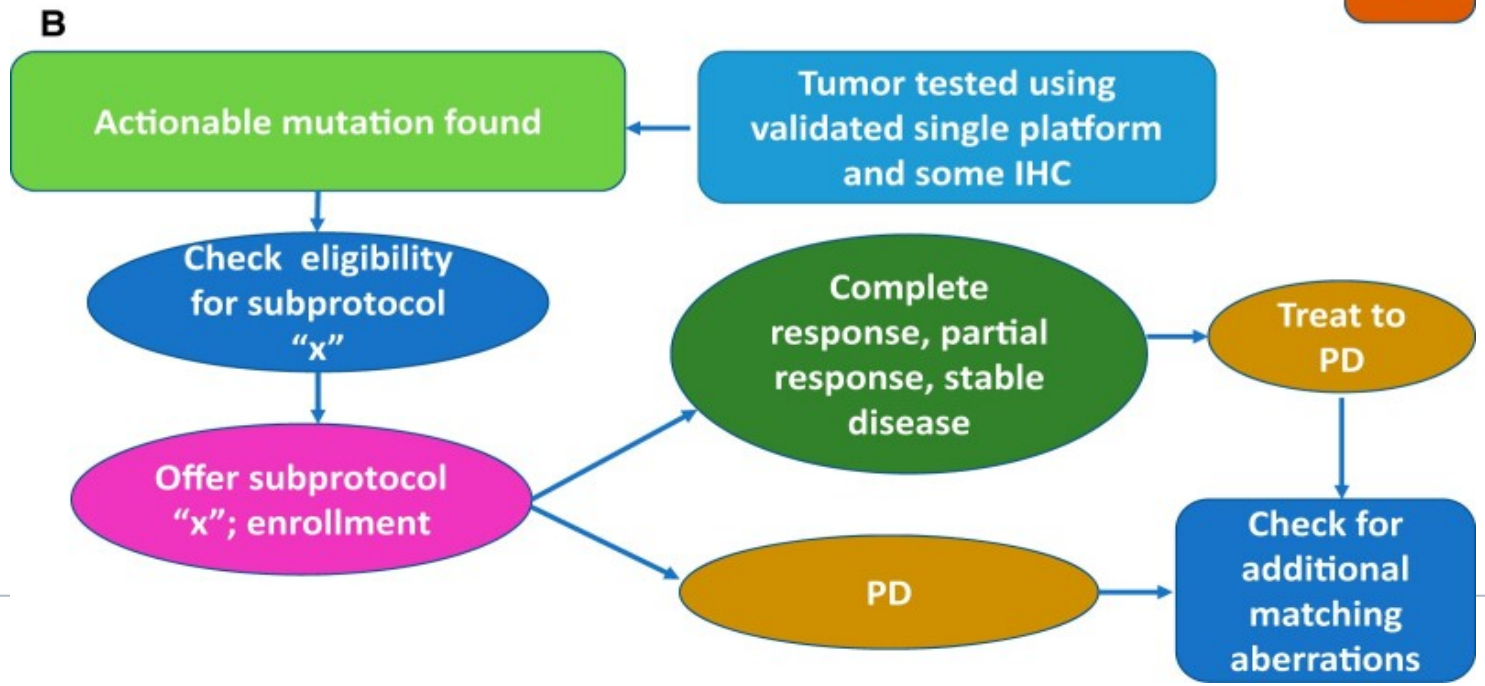
National Cancer Institute

U.S. DEPARTMENT OF HEALTH AND HUMAN SERVICES

National Institutes of Health



Flaherty et al. The Molecular Analysis for Therapy Choice (NCI-MATCH) Trial: Lessons for Genomic Trial Design. *JNCI* 2020 Oct 1;112(10):1021-1029.



NCI Myeloid Malignancies **M**olecular **A**nalysis for **T**herapy **Ch**oice **"myeloMATCH"**

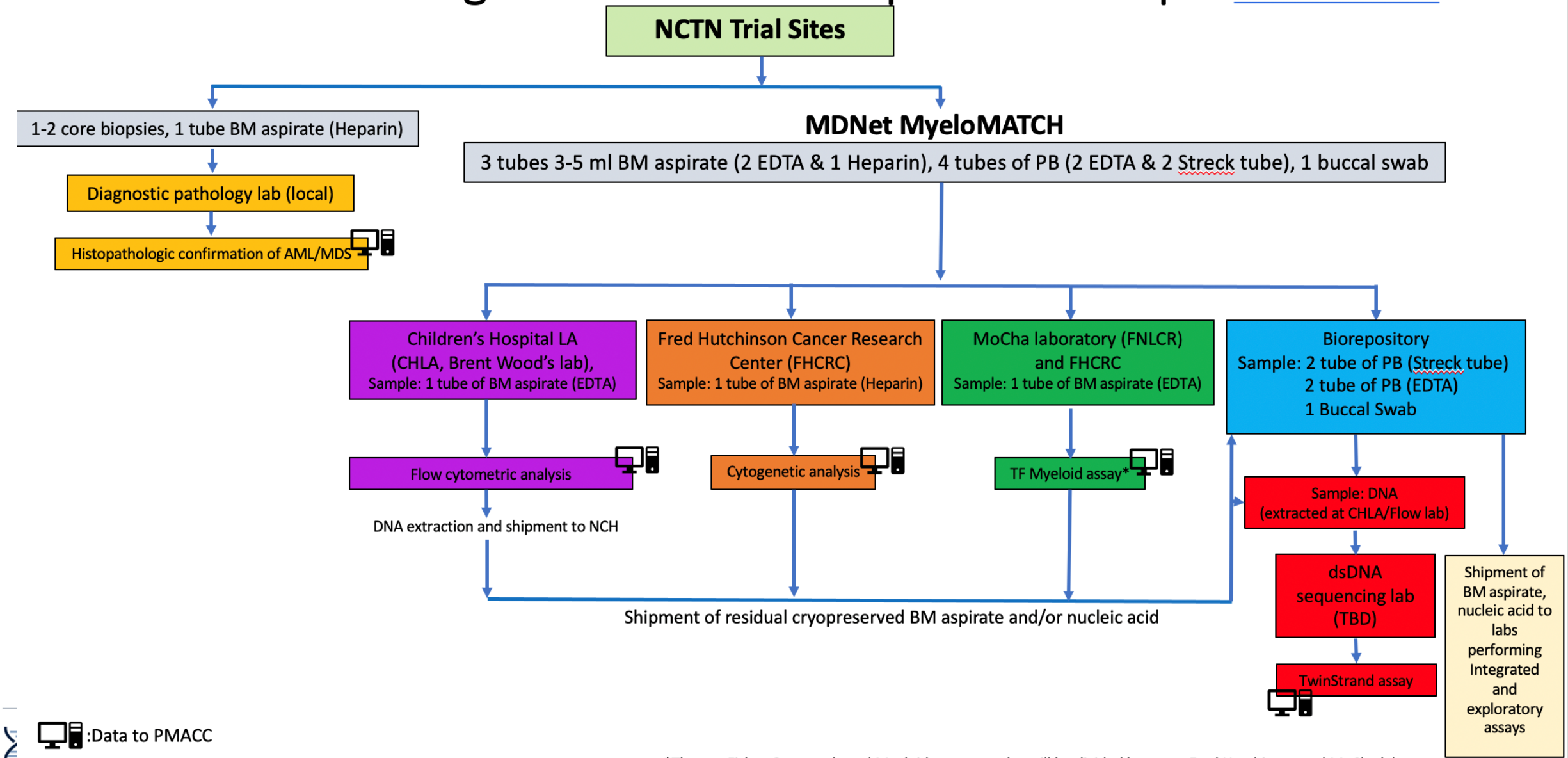
1. **Genetics driven** protocol assignment (cyto, mutations)
2. Predominately **phase 2** trials
3. Predominately **MRD driven** endpoints (**flow cytometry**)

Molecular Diagnostics Laboratory Network (MDNet) Integral Assays Under NCI's FDA-IDE

72 Hours for Initial Patient Assignment and 10 Days for Subsequent Assignment

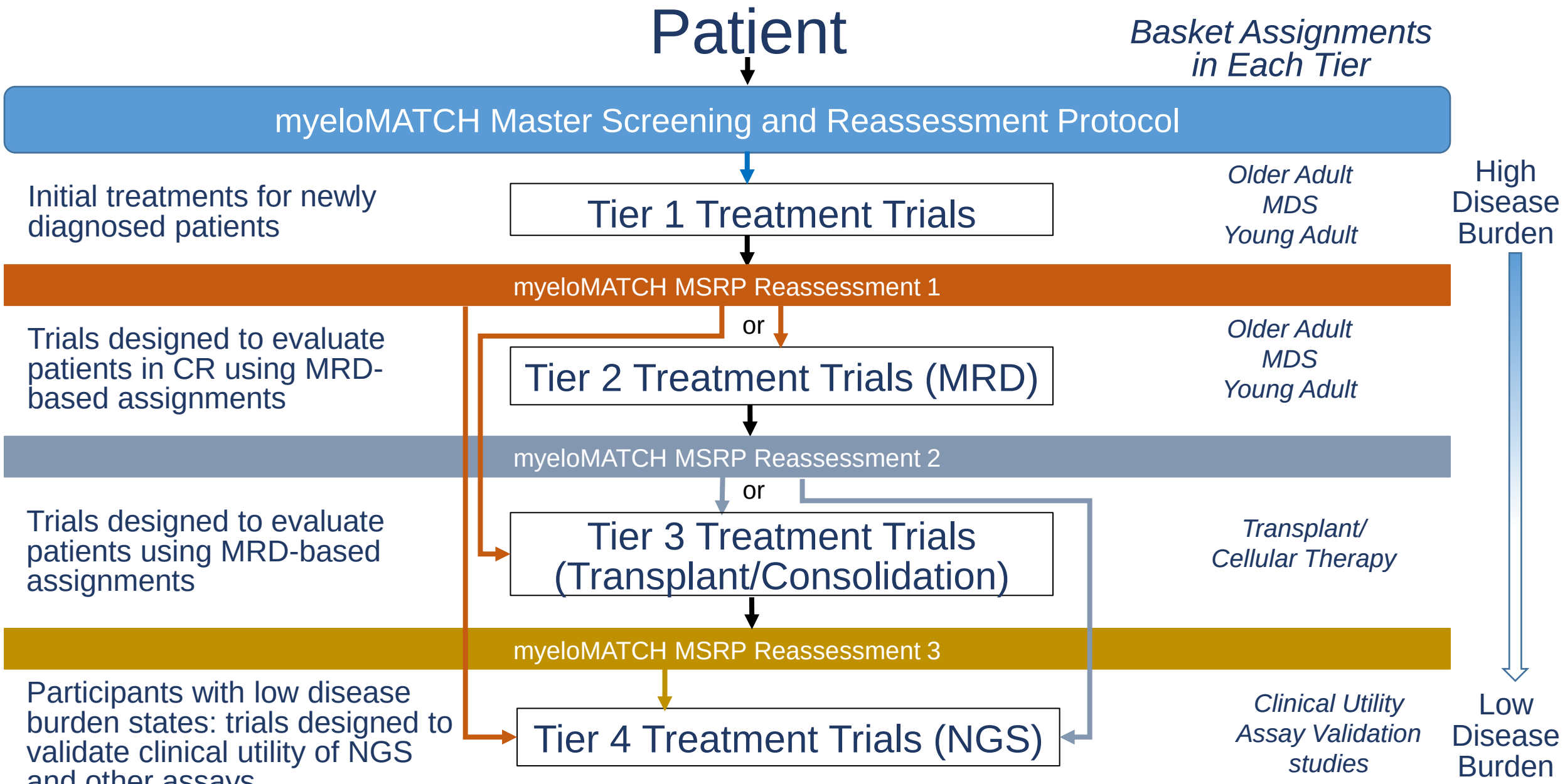
- Cytogenetics and FISH
- NCI Myeloid Assay version 2
- Error-corrected Sequencing (Duplex Sequencing)
- Flow Cytometric Analysis

MyeloMATCH:
Master screening and reassessment protocol sample work flow



:Data to PMACC

*Thermo Fisher Genexus-based Myeloid assay samples will be divided between Fred Hutchinson and MoCha labs

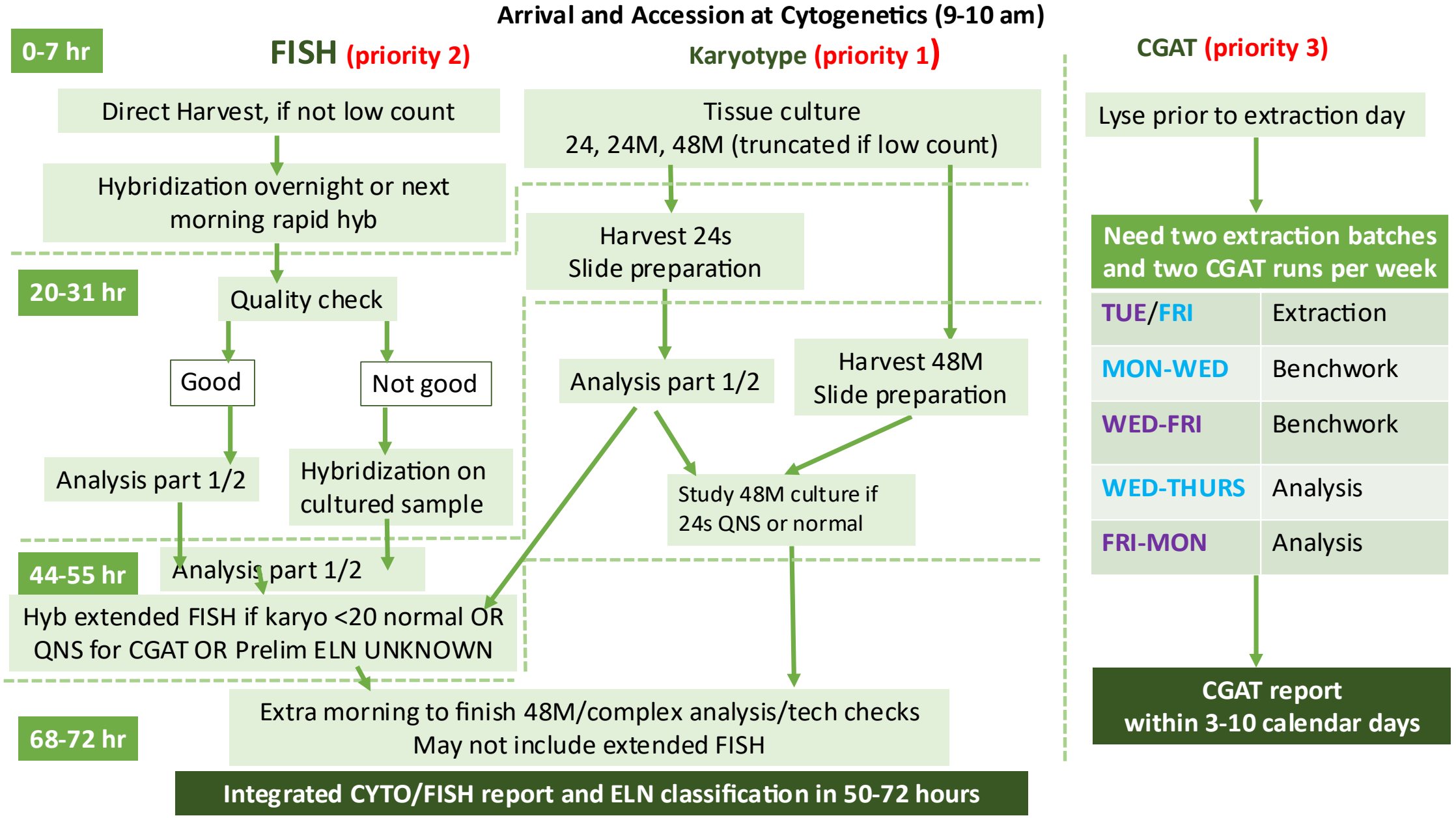

Patient
Basket Assignments in Each Tier
myeloMATCH Master Screening and Reassessment Protocol
Initial treatments for newly diagnosed patients
Tier 1 Treatment Trials
Older Adult
MDS
Young Adult
High Disease Burden
myeloMATCH MSRP Reassessment 1
Trials designed to evaluate patients in CR using MRD-based assignments
or
Tier 2 Treatment Trials (MRD)
Older Adult
MDS
Young Adult
myeloMATCH MSRP Reassessment 2
Trials designed to evaluate patients using MRD-based assignments
or
Tier 3 Treatment Trials (Transplant/Consolidation)
Transplant/ Cellular Therapy
myeloMATCH MSRP Reassessment 3
Participants with low disease burden states: trials designed to validate clinical utility of NGS and other assays
Tier 4 Treatment Trials (NGS)
Clinical Utility Assay Validation studies
Low Disease Burden

MyeloMATCH Cytogenetics Testing (FDA-IDE)

- *Karyotype* – on all samples
- *Standard FISH panel + CGAT* – on majority of samples with sufficient material
- *Expanded FISH panel* – on suboptimal samples with insufficient material
- Standard FISH panel: 8-probe set for balanced rearrangements
- Extended FISH panel: 15-probe set with the addition of 5/7/8/20 and ETV6, RUNX1, NUP98

Standard FISH panel (8-probe set)

EVI1 (3q26)	t(6;9)	t(8;21)	t(9;22)	KMT2A (MLL)	t(15;17)	inv(16)/ t(16;16)	TP53	NUP98	ETV6	RUNX1
2.16%	0%	0%	0%	0.11%	0%	0%		2.40%	0.40%	0.20%


Arrival and Accession at Cytogenetics (9-10 am)
0-7 hr
FISH (priority 2)
Karyotype (priority 1)
CGAT (priority 3)
Direct Harvest, if not low count
Hybridization overnight or next morning rapid hyb
Tissue culture
24, 24M, 48M (truncated if low count)
Harvest 24s
Slide preparation
20-31 hr
Quality check
Good
Not good
Analysis part 1/2
Hybridization on cultured sample
Analysis part 1/2
Harvest 48M
Slide preparation
Study 48M culture if
24s QNS or normal
44-55 hr
Analysis part 1/2
Hyb extended FISH if karyo <20 normal OR
QNS for CGAT OR Prelim ELN UNKNOWN
68-72 hr
Extra morning to finish 48M/complex analysis/tech checks
May not include extended FISH
Integrated CYTO/FISH report and ELN classification in 50-72 hours
Lyse prior to extraction day
Need two extraction batches and two CGAT runs per week
TUE/FRI
Extraction
MON-WED
Benchwork
WED-FRI
Benchwork
WED-THURS
Analysis
FRI-MON
Analysis
CGAT report
within 3-10 calendar days

2017 ELN

Döhner H, Estey EH, Amadori S, et al. Diagnosis and management of acute myeloid leukemia in adults: recommendations from an international expert panel, on behalf of the European LeukemiaNet. Blood 115:453-74, 2017.

Table 5. 2017 ELN risk stratification by genetics

Risk category*	Genetic abnormality
Favorable	t(8;21)(q22;q22.1); *RUNX1-RUNX1T1*
	inv(16)(p13.1q22) or t(16;16)(p13.1;q22); *CBFB-MYH11*
	Mutated *NPM1* without *FLT3*-ITD or with *FLT3*-ITD^{low}†
	Biallelic mutated *CEBPA*
Intermediate	Mutated *NPM1* and *FLT3*-ITD^{high}†
	Wild-type *NPM1* without *FLT3*-ITD or with *FLT3*-ITD^{low}† (without adverse-risk genetic lesions)
	t(9;11)(p21.3;q23.3); *MLLT3-KMT2A*‡
	Cytogenetic abnormalities not classified as favorable or adverse
Adverse	t(6;9)(p23;q34.1); *DEK-NUP214*
	t(v;11q23.3); *KMT2A* rearranged
	t(9;22)(q34.1;q11.2); *BCR-ABL1*
	inv(3)(q21.3q26.2) or t(3;3)(q21.3;q26.2); *GATA2,MECOM(EVI1)*
	−5 or del(5q); −7; −17/abn(17p)
	Complex karyotype,§ monosomal karyotype‖
	Wild-type *NPM1* and *FLT3*-ITD^{high}†
	Mutated *RUNX1*¶
	Mutated *ASXL1*¶
	Mutated *TP53*#

Table 5. 2017 ELN risk stratification by genetics

Risk category*	Genetic abnormality
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	inv(16)(p13.1q22) or t(16;16)(p13.1;q22); *CBFB-MYH11*
	Mutated *NPM1* without *FLT3*-ITD or with *FLT3*-ITD^{low}†
	Biallelic mutated *CEBPA*
Intermediate	Mutated *NPM1* and *FLT3*-ITD^{high}†
	Wild-type *NPM1* without *FLT3*-ITD or with *FLT3*-ITD^{low}† (without adverse-risk genetic lesions)
	t(9;11)(p21.3;q23.3); *MLLT3-KMT2A*‡
	Cytogenetic abnormalities not classified as favorable or adverse
Adverse	t(6;9)(p23;q34.1); *DEK-NUP214*
	t(v;11q23.3); *KMT2A* rearranged
	t(9;22)(q34.1;q11.2); *BCR-ABL1*
	inv(3)(q21.3q26.2) or t(3;3)(q21.3;q26.2); *GATA2,MECOM(EVI1)*
	−5 or del(5q); −7; −17/abn(17p)
	Complex karyotype,§ monosomal karyotype‖
	Wild-type *NPM1* and *FLT3*-ITD^{high}†
	Mutated *RUNX1*¶
	Mutated *ASXL1*¶
	Mutated *TP53*#

Table 6. 2022 ELN risk classification by genetics at initial diagnosis*

Risk category†	Genetic abnormality
Favorable	• t(8;21)(q22;q22.1)/*RUNX1*::*RUNX1T1*†,‡ • inv(16)(p13.1q22) or t(16;16)(p13.1;q22)/*CBFB*::*MYH11*†,‡ • Mutated *NPM1*†,§ without *FLT3*-ITD • bZIP in-frame mutated *CEBPA*‖
Intermediate	• Mutated *NPM1*†,§ with *FLT3*-ITD • Wild-type *NPM1* with *FLT3*-ITD (without adverse-risk genetic lesions) • t(9;11)(p21.3;q23.3)/*MLLT3*::*KMT2A*†,¶ • Cytogenetic and/or molecular abnormalities not classified as favorable or adverse
Adverse	• t(6;9)(p23.3;q34.1)/*DEK*::*NUP214* • t(v;11q23.3)/*KMT2A*-rearranged# • t(9;22)(q34.1;q11.2)/*BCR*::*ABL1* • t(8;16)(p11.2;p13.3)/*KAT6A*::*CREBBP* • inv(3)(q21.3q26.2) or t(3;3)(q21.3;q26.2)/*GATA2*, *MECOM(EVI1)* • t(3q26.2;v)/*MECOM(EVI1)*-rearranged • −5 or del(5q); −7; −17/abn(17p) • Complex karyotype,** monosomal karyotype†† • Mutated *ASXL1*, *BCOR*, *EZH2*, *RUNX1*, *SF3B1*, *SRSF2*, *STAG2*, *U2AF1*, and/or *ZRSR2*‡‡ • Mutated *TP53*[a]

Culture condition needs differ for workup of different diseases

- DSP30/IL2 Improved Detection of Clonal Abnormalities in Chronic B-cell Disorders by karyotype analysis

  CLL detection rate (Fred Hutch data)
  - **60%** abnormal rate with DSP30/IL-2 culture vs 20% with unstimulated cultures
  - **23%** abnormal rate for MRD with flow abnormal 0.01-5%
  - **77%** abnormal rate for diagnostic samples with flow >5%

- Multiple myeloma detection needs longer culturing time (72hr)

Most common abnormalities in chronic lymphocytic leukemia (CLL)

- Trisomy 12 (+12) intermediate risk
- Deletion 11q (*ATM*)
  unfavorable
- Deletion 17p
  poor prognosis
- Deletion 13q as a sole abnormality
  - favorable prognosis

Chun et al. 2018 Cancer Genetics

Most common abnormalities in multiple myeloma

- *IGH* rearrangements
  - t(11;14) - intermediate or favorable; also predictive marker for venetoclax
  - t(4;14), t(14;16), t(14;20) – poor prognosis
  - t(6;14) - favorable prognosis
- Monosomy 13 (-13)

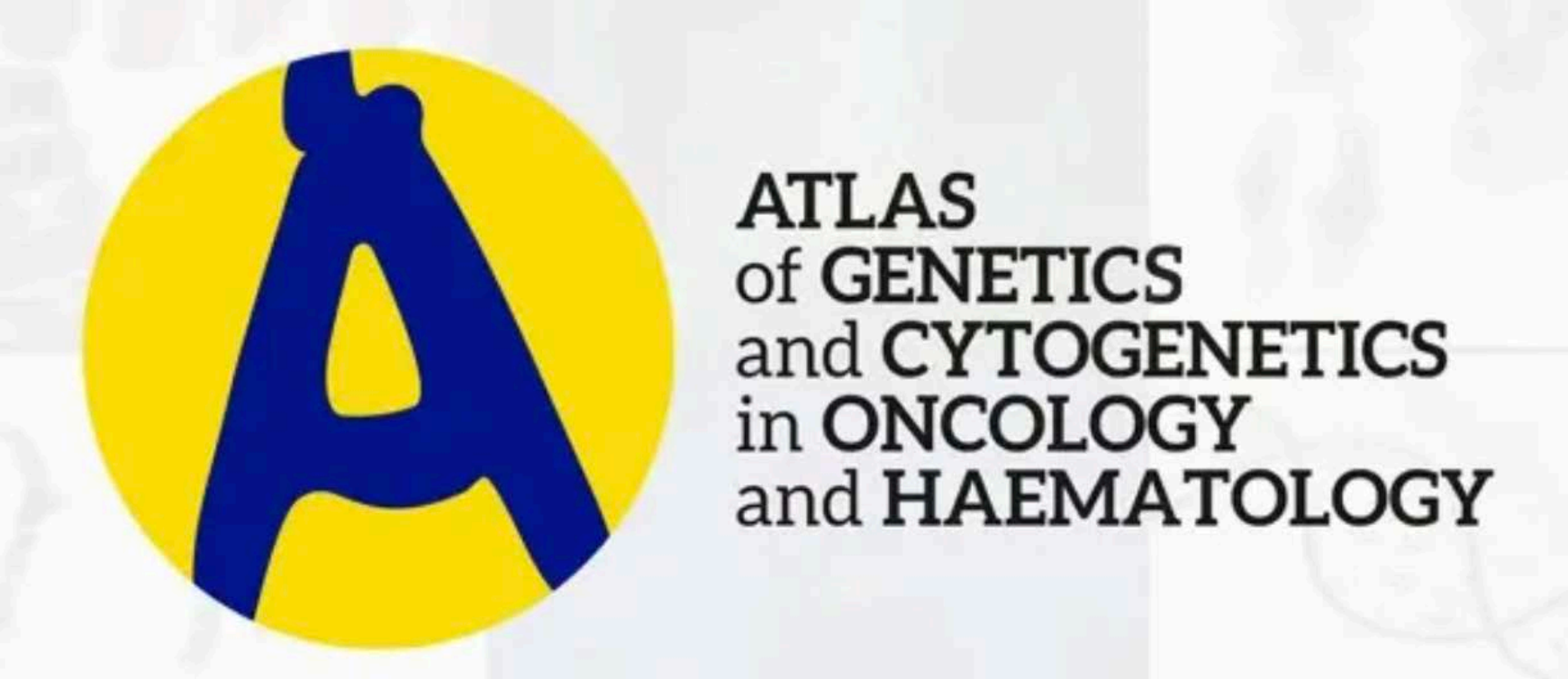
  Poor prognosis if seen by karyotype analysis
- Deletion 17p

  poor prognosis
- Deletion 1p or gain/amplification of 1q
  - Poor prognosis

Pugh et al. 2018 Cancer Genetics

Useful reference website

https://atlasgeneticsoncology.org/



1 Paradigm shifting

2 Process changing

3 Policy setting

Acknowledgement

The fabulous Fred Hutch-UW CCG team

And numerous awesome colleagues at the FHCC, SWOG, and NCI

Fred Hutch Cancer Center

UW Medicine

Thank you

Oishi Symposium

welcomes

Rose Ermete, RN, BSN, OCN, CRN-BC, CCRP

Deciphering Chromosomes: Cracking the Code

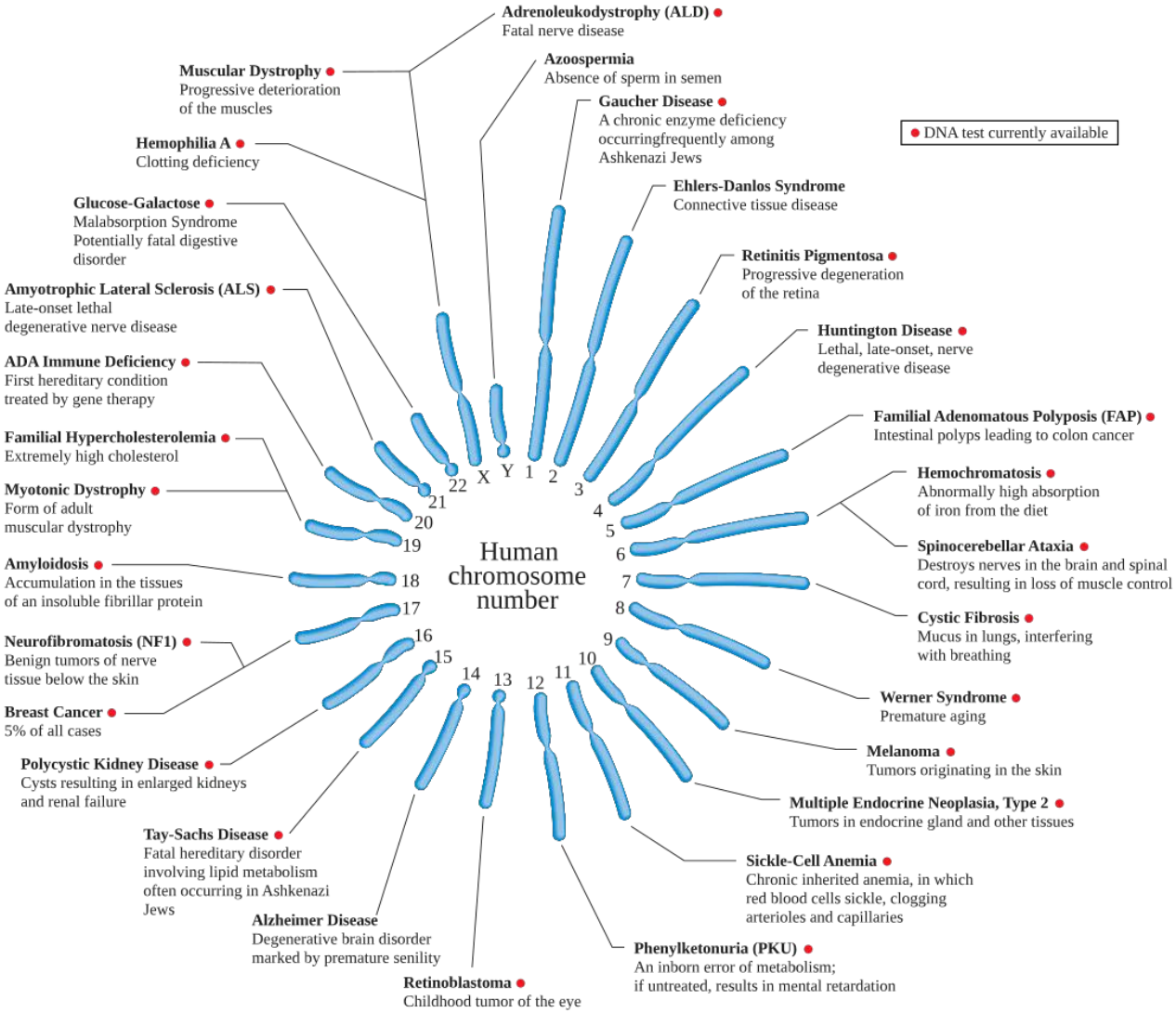
Deciphering Chromosomes Cracking the code

Rose Ermete, BSN, RN, OCN, CRN-BC, CCRP

Senior Quality Assurance Nurse Auditor

The importance of correctly reporting results.

- Diagnosis & prognosis
- Target specific factors that drive the cancer
- Statistical analysis



https://www.researchgate.net/figure/The-human-chromosome-set-indicating-examples-of-locations-for-pathogenic-gene-variants_fig3_352131611

Interpreting the code

- Standardization
- Nomenclature / ISCN description

ISCN Nomenclature

Symbols

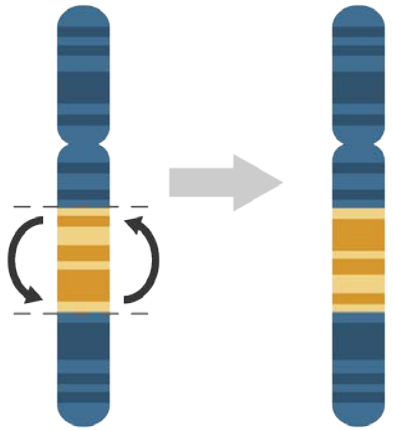
[ ]	# of cells in a line, or metaphases
:	Chromosomal break
::	Chromosomal break and reunion or fusion
,	Separates chromosome #& abnormalities
-	Loss
X	Multiple copies or number of copies
( )	Surround altered chromosomes or genes
+	Additional chromosome
;	Separates altered chromosome or break
>	Substitution

Aberrations

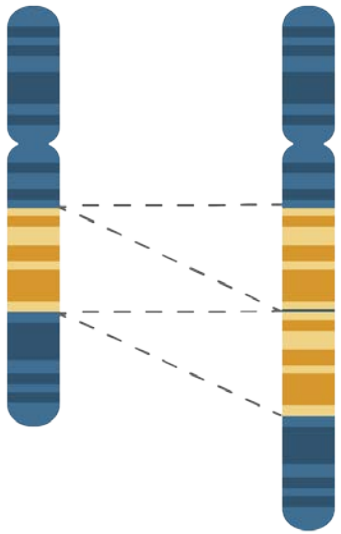
add	Additional material attached to chromosome
del	Deletion or loss of chromosome material
dup	Part of a chromosome is repeated
der	Rearrangement involve ≥ 2 chromosomes or by multiple aberrations.
dic	1 chromosome replaces 2 normal ones.
ins	Addition of material in a chromosome
inv	Part of chromosome inverted
rec	Recombinant, due to meiotic crossing over
t	Exchanged material between 2 chromosomes

Examples

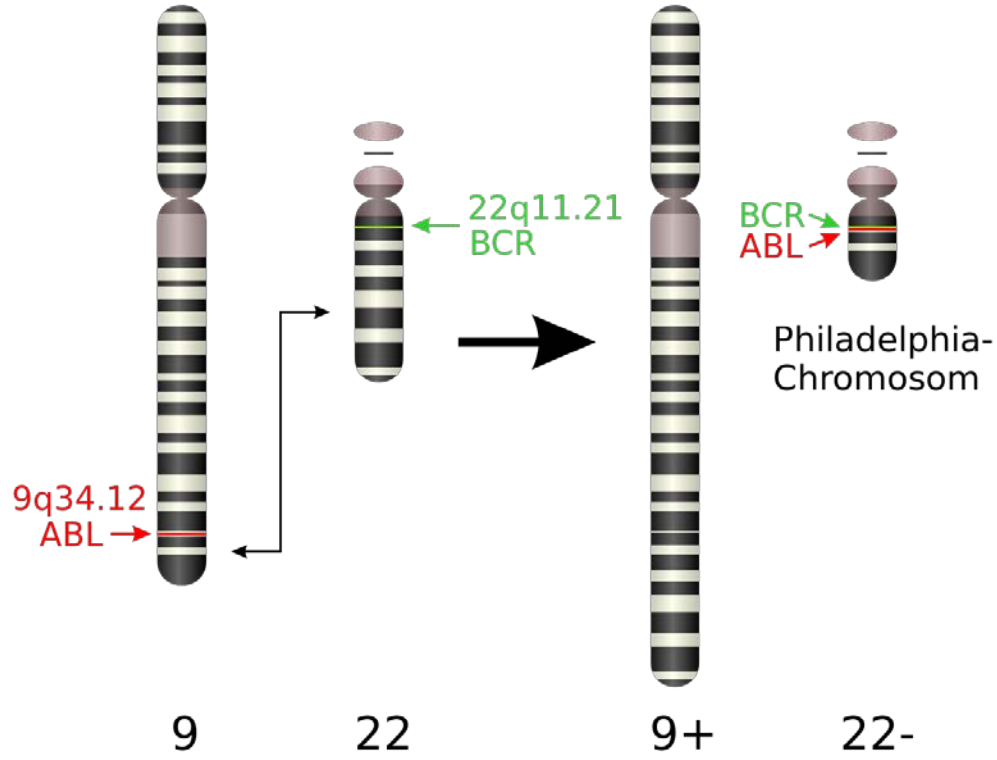
Inversion



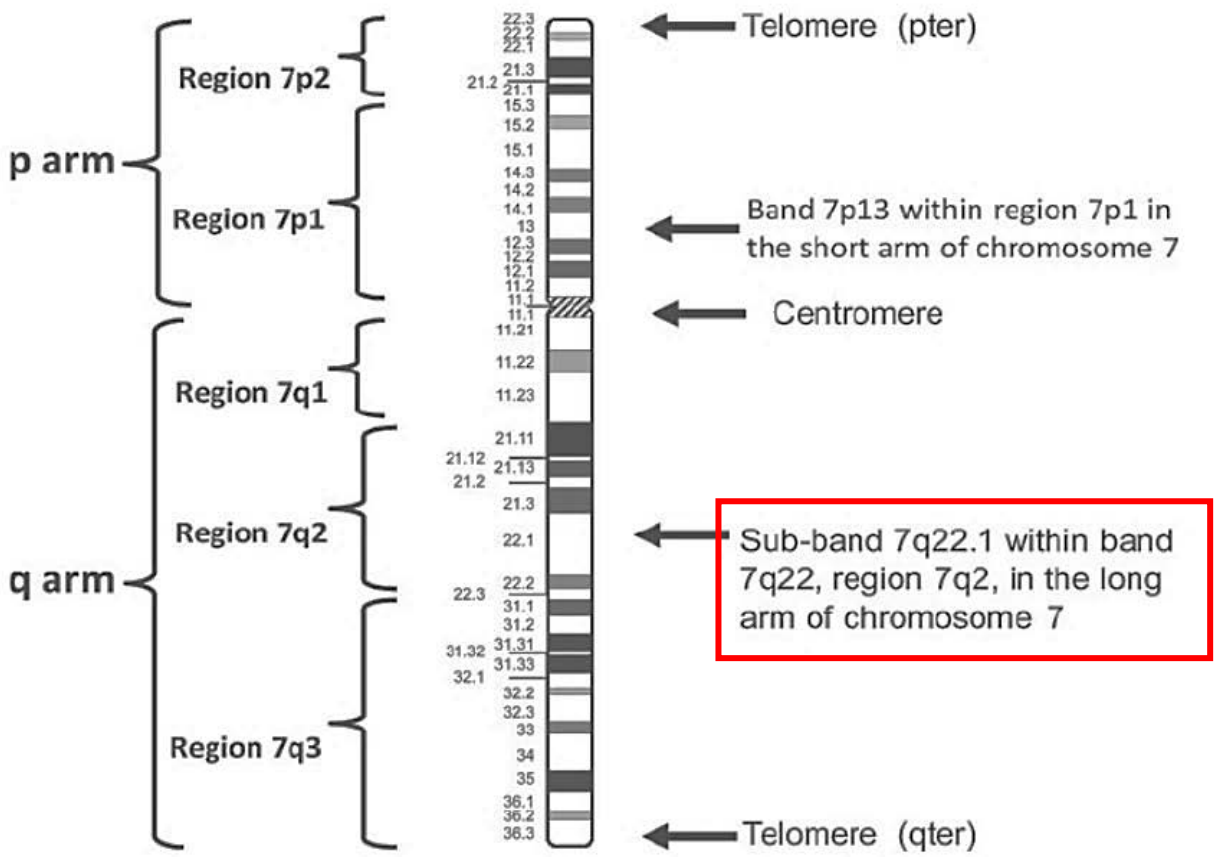
Duplication



Translocation



Anatomy of a Chromosome



Location of Genes

Gene	Location	Description
TP53	17p13.1	Regulation of cell division, acts as a tumor suppressor
IgVH	14q32.33	Involved in the production of antibodies by B cells.
Trisomy 12	+12	Extra copy of Chromosome 12; cellular adhesion and migration
ATM	11q22-q23	DNA repair and cell cycle control
CCND1	11q13	Regulates cell cycle t(11;14) is a more favorable prognosis
BCR::ABL	t(9;22)	Philadelphia chromosome
MYC	8q24.21	Cell cycle progression, apoptosis & cell transformation

S1925 CLL/SLL

Was cytogenetic analysis performed?	◯ Yes ◯ No
If yes, what was the date the specimen was collected?	☐☐ ☐☐☐ ☐☐☐☐
If yes, what was the type of specimen?	◯ Bone Marrow ◯ Peripheral Blood
If yes, what was the method?	◯ Karyotype From Stimulated Culture ◯ Karyotype From Unstimulated Culture
If yes, what was the number of total metaphases analyzed?	☐☐☐
If yes, what was the number of total abnormal cells?	☐☐☐
If yes, what was the karyotype ISCN description? *(Example 46, XY; 46, XX; etc)*	_____

"Peripheral blood lymphocytes were cultured and stimulated with PHA to induce mitosis"

"Unstimulated 24 – 48 hour culture of cells from peripheral blood"

S1925

Was cytogenetic analysis performed?	◯ Yes ◯ No
If yes, what was the date the specimen was collected?	☐☐ ☐☐☐ ☐☐☐☐
If yes, what was the type of specimen?	◯ Bone Marrow ◯ Peripheral Blood
If yes, what was the method?	◯ Karyotype From Stimulated Culture ◯ Karyotype From Unstimulated Culture
If yes, what was the number of total metaphases analyzed?	☐☐☐
If yes, what was the number of total abnormal cells?	☐☐☐
If yes, what was the karyotype ISCN description? *(Example 46, XY; 46, XX; etc)*	_____

Cells counted:	20
Band Level:	400
Cells Analyzed:	20
Cells karyotyped:	3

S1925

Was cytogenetic analysis performed?	◯ Yes ◯ No
If yes, what was the date the specimen was collected?	☐☐ ☐☐☐ ☐☐☐☐
If yes, what was the type of specimen?	◯ Bone Marrow ◯ Peripheral Blood
If yes, what was the method?	◯ Karyotype From Stimulated Culture ◯ Karyotype From Unstimulated Culture
If yes, what was the number of total metaphases analyzed?	☐☐☐
If yes, what was the number of total abnormal cells?	☐☐☐
If yes, what was the karyotype ISCN description? *(Example 46, XY; 46, XX; etc)*	_____

48, XY, +3, +5, del(5)(q13q14), t(8;14)(q24;32) [2]

S1925

nuc ish (D12Z3,MDM2)x3 [56/100], (TP53 x1,D17Z1x2)[44/100]

If yes, what was the FISH ISCN description? *(Example nuc ish 3q27(BCL6x2)[200]; etc)*	_____
If yes, was a del(17p) abnormality identified?	○ Yes ○ No
If yes, what was the total number of interphases/metaphase cells analyzed?	☐☐☐
If yes, of the total cells scored, what was the number of abnormal cells?	☐☐☐
If yes, was a del(13q) abnormality identified?	○ Yes ○ No
If yes, what was the total number of interphases/metaphase cells analyzed?	☐☐☐
If yes, of the total cells scored, what was the number of abnormal cells?	☐☐☐
If yes, was a trisomy 12 abnormality identified?	○ Yes ○ No
If yes, what was the total number of interphases/metaphase cells analyzed?	☐☐☐
If yes, of the total cells scored, what was the number of abnormal cells?	☐☐☐
If yes, was a del(11q) abnormality identified?	○ Yes ○ No
If yes, what was the total number of interphases/metaphase cells analyzed?	☐☐☐
If yes, of the total cells scored, what was the number of abnormal cells?	☐☐☐

S1925

nuc ish (D12Z3,MDM2)x3 [56/100], (TP53x1,D17Z1x2)[44/100]

If yes, what was the FISH ISCN description? *(Example nuc ish 3q27(BCL6x2)[200]; etc)*	_____
If yes, was a del(17p) abnormality identified?	○ Yes ○ No
If yes, what was the total number of interphases/metaphase cells analyzed?	☐☐☐
If yes, of the total cells scored, what was the number of abnormal cells?	☐☐☐
If yes, was a del(13q) abnormality identified?	○ Yes ○ No
If yes, what was the total number of interphases/metaphase cells analyzed?	☐☐☐
If yes, of the total cells scored, what was the number of abnormal cells?	☐☐☐
If yes, was a trisomy 12 abnormality identified?	○ Yes ○ No
If yes, what was the total number of interphases/metaphase cells analyzed?	☐☐☐
If yes, of the total cells scored, what was the number of abnormal cells?	☐☐☐
If yes, was a del(11q) abnormality identified?	○ Yes ○ No
If yes, what was the total number of interphases/metaphase cells analyzed?	☐☐☐
If yes, of the total cells scored, what was the number of abnormal cells?	☐☐☐

S1925

nuc ish (D12Z3,MDM2)x3 [56/100], (TP53 x1, D17Z1x2)[44/100]

If yes, what was the FISH ISCN description? *(Example nuc ish 3q27(BCL6x2)[200]; etc)*	_____
If yes, was a del(17p) abnormality identified?	◯ Yes ◯ No
If yes, what was the total number of interphases/metaphase cells analyzed?	☐☐☐
If yes, of the total cells scored, what was the number of abnormal cells?	☐☐☐
If yes, was a del(13q) abnormality identified?	◯ Yes ◯ No
If yes, what was the total number of interphases/metaphase cells analyzed?	☐☐☐
If yes, of the total cells scored, what was the number of abnormal cells?	☐☐☐
If yes, was a trisomy 12 abnormality identified?	◯ Yes ◯ No
If yes, what was the total number of interphases/metaphase cells analyzed?	☐☐☐
If yes, of the total cells scored, what was the number of abnormal cells?	☐☐☐
If yes, was a del(11q) abnormality identified?	◯ Yes ◯ No
If yes, what was the total number of interphases/metaphase cells analyzed?	☐☐☐
If yes, of the total cells scored, what was the number of abnormal cells?	☐☐☐

S1925

nuc ish (D12Z3,MDM2)x3 [56/100], (TP53 x1,D17Z1x2)[44/100]

If yes, what was the FISH ISCN description? *(Example nuc ish 3q27(BCL6x2)[200]; etc)*	_____
If yes, was a del(17p) abnormality identified?	○ Yes ○ No
If yes, what was the total number of interphases/metaphase cells analyzed?	☐☐☐
If yes, of the total cells scored, what was the number of abnormal cells?	☐☐☐
If yes, was a del(13q) abnormality identified?	○ Yes ○ No
If yes, what was the total number of interphases/metaphase cells analyzed?	☐☐☐
If yes, of the total cells scored, what was the number of abnormal cells?	☐☐☐
If yes, was a trisomy 12 abnormality identified?	○ Yes ○ No
If yes, what was the total number of interphases/metaphase cells analyzed?	☐☐☐
If yes, of the total cells scored, what was the number of abnormal cells?	☐☐☐
If yes, was a del(11q) abnormality identified?	○ Yes ○ No
If yes, what was the total number of interphases/metaphase cells analyzed?	☐☐☐
If yes, of the total cells scored, what was the number of abnormal cells?	☐☐☐

Was TP53 mutational analysis testing performed? ◯ Yes ◯ No

If yes, what was the date the specimen was collected? ☐☐ ☐☐☐ ☐☐☐☐

If yes, what was the type of specimen? ◯ Bone Marrow ◯ Peripheral Blood

If yes, what was the result? ◯ Mutated ◯ Not Mutated

If mutated, what is the estimated level of the mutated clone(s)?
(Another term for this is variant allele frequency (VAF). Take this number from the genetic sequencing report for TP53 mutation, NOT the CLL FISH panel. The estimated level of TP53 mutated clone (or VAF) is different from % of del(17p) on the FISH report.)

☐☐☐.☐ %

If yes, which mutation was identified?
(Report in the format of this example:
TP53 (NM_000546.6) exon 5 p.Leu194Arg (c.581T>G)
- TP53=name of gene
- NM=TP53 normal status that the gene has been compared to—typically 000546.0, 000546.5 or 000546.6
- Exon=sometimes this is not listed on the report, ok to leave out
- p.=protein that is affected. In this example Leucine is changed to Arginine at the 194 locus. Sometimes the amino acid will be listed as a one letter abbreviation. If this is the case in this example would be listed as p.L194R.
- c.=DNA change and location that is noted.)

TP53(NM_000546.5) p.M2371 (c.711G>A)

Additional Details for Mutations

Gene	Protein Change	DNA Change	VAF%	Depth	Transcript
TP53	p.M237I	c.711G>A	19 %	15888	NM_000546.5

S1925

Was IgVH mutational analysis testing performed?	◯ Yes ◯ No
If yes, what was the date the specimen was collected?	☐☐ ☐☐☐ ☐☐☐☐
If yes, what was the type of specimen?	◯ Bone Marrow ◯ Peripheral Blood
If yes, what was the result?	◯ Mutated ◯ Not Mutated
Was Chromosome Genomic Array Testing (CGAT) or Chromosome Microarray performed?	◯ Yes ◯ No
If yes, what was the date the specimen was collected?	☐☐ ☐☐☐ ☐☐☐☐
If yes, what was the type of specimen?	◯ Bone Marrow ◯ Peripheral Blood
If yes, what was the result?	◯ Normal ◯ Abnormal
If abnormal, what was the result per ISCN2016? *(Example arr(1-22,X)x2; etc)*	_____
If abnormal, what was the estimated level of the abnormal clone(s)?	☐☐☐.☐ %

IGHV Mutation Analysis by Sequencing Non Mutated

S1925

Was IgVH mutational analysis testing performed?	◯ Yes ◯ No
If yes, what was the date the specimen was collected?	☐☐ ☐☐☐ ☐☐☐☐
If yes, what was the type of specimen?	◯ Bone Marrow ◯ Peripheral Blood
If yes, what was the result?	◯ Mutated ◯ Not Mutated
Was Chromosome Genomic Array Testing (CGAT) or Chromosome Microarray performed?	◯ Yes ◯ No
If yes, what was the date the specimen was collected?	☐☐ ☐☐☐ ☐☐☐☐
If yes, what was the type of specimen?	◯ Bone Marrow ◯ Peripheral Blood
If yes, what was the result?	◯ Normal ◯ Abnormal
If abnormal, what was the result per ISCN2016? *(Example arr(1-22,X)x2; etc)*	_____
If abnormal, what was the estimated level of the abnormal clone(s)?	☐10·0 %

arr[GRCh37]
8p23.2p11.22(3011099_38871615)x1[0.1],11q14.2q22.1(85754392_98901956)x3[0.1]

S1905 T-cell ALL

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

Instructions: **Registering Institution:** Please send this form along with the cytogenetics specimen to the cytogenetics lab of choice. When the results are received from the lab, submit the data from this form online and upload any available cytogenetics and FISH reports via MediData Rave (see Section 14.3).

Cytogenetics Lab: Please complete this form and submit along with the cytogenetics and FISH reports to the registering institution at the contact listed below.

Registering Institution Contact Name: _____

Email: _____

This form is completed at pretreatment and any time a bone marrow (or blood) exam including cytogenetics and/or FISH is performed. Date is in **DD MON YYYY** format. Explain any blank fields or blank dates in the **Comments** section.

S1905

Bone marrow	
Unstimulated short-term culture (24-72 hours)	1 0
Direct preparation (metaphases)	
Stimulated culture (metaphases)	
Mitogen type	
Other culture method	1 0
Culture method and duration	Overnight culture

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

S1905

Total number of metaphases	20
Total number of abnormal metaphases	19
Are results based on at least 400-band level for banded analysis?	☐ Yes ☒ No ☐ Unknown
Karyotype description	

Stemline: 47,XX,del(6)(q21q25),del(17)(p13.1),+19[4]
Sideline 1: 47,sl,del(4)(q21q31.3)[10]
Sideline 2: 47,sdl1,del(3)(p23p13)[5]

Banding Resolution	375 – 400
Metaphase Cells Counted	20
Analyzed	20
Karyogramed	8

S1905

Were FISH studies performed?	☒ Yes ☐ No ☐ Unknown
If Yes, FISH ISCN description	Nuc ish(D6z1,MYB)X3[21/200]

Abnormal FISH Results

nuc ish(D6Z1,MYB)x3[21/200]

FISH results: **POSITIVE for 3 signals for the D6Z1locus (pericentromeric region of chromosome 6) and the MYB locus (6q23) in 10.5% of cells**

Probe set: D6Z1 locus (pericentromeric region) and MYB locus (6q23) - In 21 of the 200 cells scored (10.5%), 3 signals were present for both probes. In the remaining cells a normal (or apparently random) probe signal pattern was noted.

Within Normal Limits

FISH Results

nuc ish(alpha sat4,alpha sat10,D17Z1)x2[500]

FISH results: **Negative for gain or loss of the pericentromeric regions of chromosomes 4, 10, or 17**

Probe set: Pericentromeric region of chromosome 4, 10, and 17 (alpha satellite DNA probes [for 17 this is locus D17Z1]) - A total of 500 interphase nuclei were scored. The probe signal values were not significantly different from negative controls.

S1905

If FISH studies were performed, enter all probes and abnormal signal patterns:			
Probe 1: D6Z1locus6q23			
Total number of interphase nuclei	2	0	0
Total number of abnormal interphases		2	1
Total number of metaphases			
Total number of abnormal metaphases			

nuc ish(D6Z1,MYB)x3[21/200]

FISH results: **POSITIVE for 3 signals for the D6Z1locus (pericentromeric region of chromosome 6) and the MYB locus (6q23) in 10.5% of cells**

Probe set: D6Z1 locus (pericentromeric region) and MYB locus (6q23) - In 21 of the 200 cells scored (10.5%), 3 signals were present for both probes. In the remaining cells a normal (or apparently random) probe signal pattern was noted

S1905

Abnormalities *(select all that apply)*	
del(1)(p32p32)	☐
t(1;14)(p32;q11)	☐
t(1;14)(p32;q11)	☐
Small insertion	☐
t(10;14)(q24;q11)	☐
t(7;10)(q34;q24)	☐
t(10;14)(q24;q11)	☐
t(5;14)(q35;q11)	☐
t(5;14)(q35;q32)	☐
inv(7)(p15;q34)	☐
t(10;11)(p13;q14)	☐
del(9)(q34;q34)	☐
inv(14)(q11;q13)	☐
T(14;20)(q11;p11)	☐

nuc ish(D6Z1,MYB)x3[21/200]

Probe set: D6Z1 locus (pericentromeric region) and MYB locus (6q23)

t(11;14)(p15;q11)	☐
t(11;14)(p13;q11)	☐
del(5)(q14;q14)	☐
t(7;19)(q34;p13)	☐
t(11;14)(p11;q32)	☐
dup(6) (q23;q23)	?
t(6;7)(q23;q34)	☐
Number of unrelated cytogenetic abnormalities	☐☐☐
Monosomy	☐ Yes ☐ No

45,XX,-13

nuc ish(D13Z1)X1

S2209 Multiple Myeloma

Was fluorescence in situ hybridization (FISH) performed and reviewed?	Yes
If yes, what was the date the specimen was collected?	06/07/2024
If yes, what was the type of specimen?	Bone Marrow
If yes, what plasma cell enrichment method was used?	CD-138 Enriched
If yes, was a del(17p) abnormality identified?	
If yes, was a t(14;16) abnormality identified?	
If yes, was a t(14;20) abnormality identified?	
If yes, was a 1q+ abnormality identified?	
If yes, was a t(4;14) abnormality identified?	

- ◯ CD-138 Enriched
- ◯ cIG-FISH
- ◯ None
- ◯ Unknown

Specimen Type: CD138+ cells enriched from bone marrow aspirate

S2209 Multiple Myeloma

Was fluorescence in situ hybridization (FISH) performed and reviewed?	Yes
If yes, what was the date the specimen was collected?	06/07/2024
If yes, what was the type of specimen?	Bone Marrow
If yes, what plasma cell enrichment method was used?	CD-138 Enriched
If yes, was a del(17p) abnormality identified?	
If yes, was a t(14;16) abnormality identified?	
If yes, was a t(14;20) abnormality identified?	
If yes, was a 1q+ abnormality identified?	
If yes, was a t(4;14) abnormality identified?	

del(17p) = TP53 loss
t(14,16) = MAF
t(14;20) = MAFB
t(4;14) = MMSET /MFGFR3
1q+ = MCL1 & CKS1B

1q+

amp(1q)
1(q21)X3
der(1;5)(q10;q10),
der(1;16)(q10;p10)

Faiman & Tariman; 2021, Wiedmeir-Nutor & Bergsagel; 2022, https://omim.org/entry/254500

S2114: Follicular B-cell Lymphoma

- ◯ Diffuse large B-Cell lymphoma (DLBCL) NOS
- ◯ DLBCL, Germinal-center B-cell type
- ◯ DLBCL, Activated B-cell type
- ◯ T-cell histiocyte-rich large B-cell lymphoma
- ◯ Primary cutaneous DLBCL, leg type
- ◯ Intravascular large B-cell lymphoma
- ◯ EBV^{+} DLBCL, NOS
- ◯ DLBCL associated with chronic inflammation
- ◯ HHV8^{+} DLBCL, NOS
- ◯ High-grade B-cell lymphoma with MYC and BCL2 and/or BCL6 rearrangements
- ◯ High-grade B-cell lymphoma, NOS
- ◯ Follicular lymphoma grade 3b
- ◯ Primary mediastinal (thymic) B-cell lymphoma

ISCN description:

- **MYC rearrangement**: t(8;14)(q24;q32)
- **BCL2 rearrangement**: t(14;18)(q32;q21)
- **BCL6 rearrangement**: t(3;14)(q27;q32)

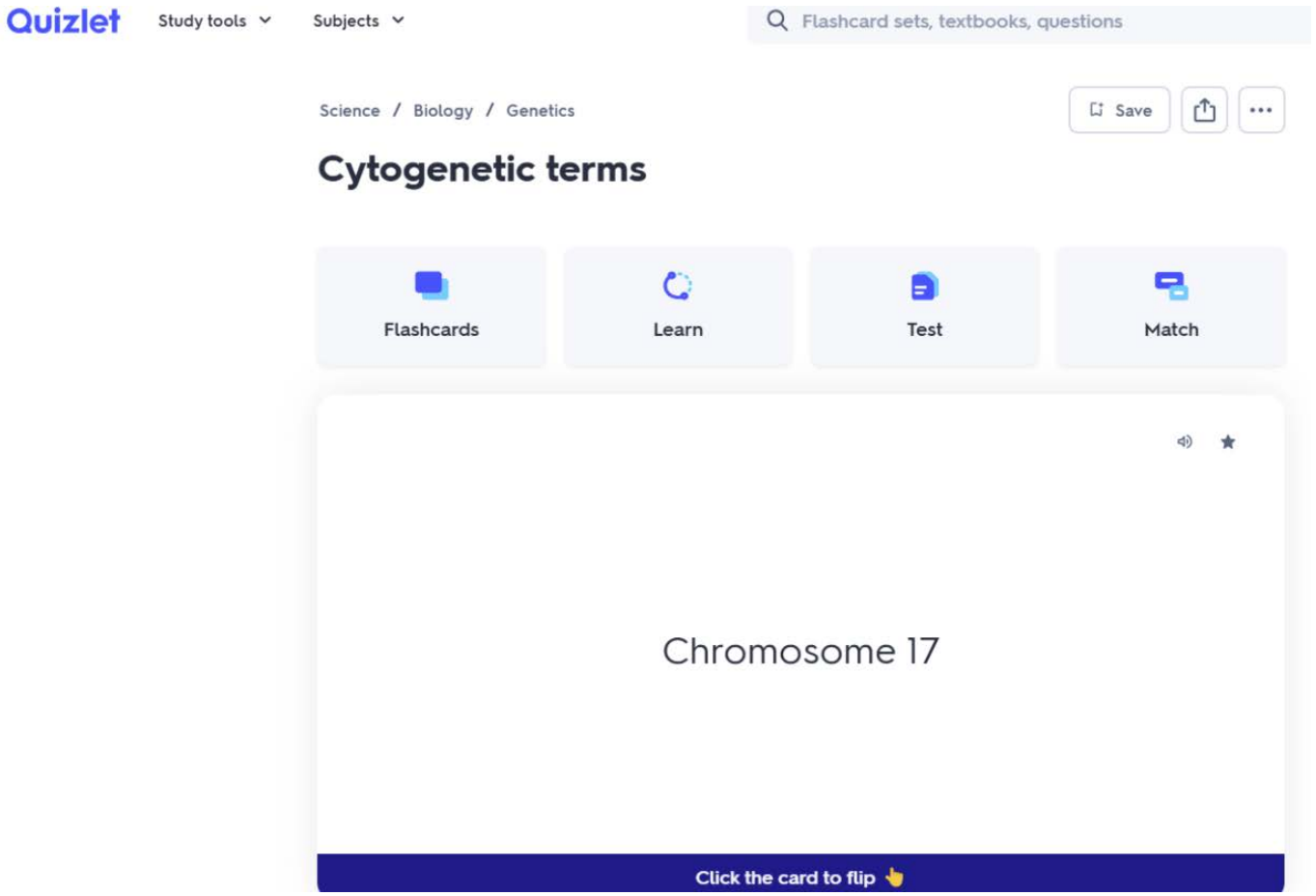
A case with both MYC and BCL2 rearrangements might be described as:

- **46,XX,t(8;14)(q24;q32),t(14;18)(q32;q21)**

And a case with MYC and BCL6 rearrangements might be described as:

- **46,XX,t(8;14)(q24;q32),t(3;14)(q27;q32)**

Quizlet



https://quizlet.com/1025310447/cytogenetic-terms-flash-cards/?i=6htuet&x=1jqt

Resources

- Genetic Testing Methods
  - https://www.jax.org/education-and-learning/clinical-and-continuing-education/ccep-non-cancer-resources/genetic-testing-methods
- Genetic and Precision Oncology Learning Library (ONS)
  - https://www.ons.org/genomics-and-precision-oncology-learning-library
- Gene Cards: https://www.genecards.org/
- NIH US National Library of Medicine – MedlinePlus
  - https://medlineplus.gov/genetics/
- Cancer Genomics Overview
  - https://www.cancer.gov/publications/pdq/information-summaries/genetics/overview-hp-pdq
- National Human Genome Research Institute
  - https://www.genome.gov/dna-day/15-ways/cancer-genomics
- Learn Genetics
  - https://learn.genetics.utah.edu/content/basics/
- Precision Medicine Advisors
  - https://precision-medicine-academy.thinkific.com/
- Friend, P. & Mahon, S. (2023). How did the variant get its name? Understanding Gene and variant nomenclature. CJON, 27(3): 251 – 254. DOI:10.1188/23.CJON.251-254

Oishi Symposium

welcomes

Laura Gonzales, RN, BSN
Quality Assurance Updates

Oishi Symposium
SWOG QA Audit Updates: Continuing to Embrace the New Normal

Friday, May 2, 2025

Speaker

Laura Gonzales, BSN, MA, RN, OCN
SWOG Quality Assurance Manager

SWOG QA Audits: By the Numbers

2023 Audits

- 34 treatment audits performed
  - 18 audits onsite
  - 16 audits remote

2024 Audits

- 52 treatment audits performed
  - 41 audits onsite
  - 11 audits remote

QA Audit Team prefers onsite treatment audits, but we understand the post-pandemic process changes at sites.

SWOG QA Audits: By the Numbers

2023 Audits

182 registration audits performed

2024 Audits

190 registration audits performed

Post-pandemic, Registration Study audits are conducted remotely unless in conjunction with a treatment audit or at the site's request.

SWOG QA Audits: Continuing to Embrace the New Normal

We have seen stabilization and improvement in the post-pandemic environment

SWOG QA continues to provide education and support to site staff

SWOG QA Audits: Continuing to Embrace the New Normal

- From 8/1/23 to 7/31/24, QA conducted 46 audits with 8 audits unacceptable for patient case and two audits unacceptable for regulatory.

- From 8/1/24 to 1/1/25, QA conducted 30 audits with only one audit unacceptable for patient case.

SWOG QA Audits: Audit Findings

Common Major Deficiencies:

Patient Case:
Eligibility:
Tests/scans conducted out of window

Adverse Events:
Late reporting of SAEs

Data Quality:
Specimens not collected/submitted
Delinquent data submission

SWOG QA Audits: Recommendations

Eligibility – Tests/Scans Conducted out of Window

- Refer to Section 5 of the protocol for eligibility criteria
- Use an Eligibility Checklist and have two people review prior to patient registration

SWOG QA Audits: Recommendations

Adverse Events - Late Reporting of SAEs

- Document date of discovery for all SAEs in RAVE
- Any questions about reporting SAEs, contact ADR@swog.org

SWOG QA Audits: Recommendations

Data Quality - Specimens Not Collected/Submitted

- Refer to Section 15 of protocol
- Confirm patient consented to specimen submission
- Refer to Specimen Requirements Summary in Specimen Tracking System on CRA Workbench
- If unable to collect specimen, document in the research record and in Specimen Tracking System

SWOG QA Audits: Recommendations

Data Quality – Delinquent Data Submission

- Refer to Section 14 of protocol for data submission requirements
- Any questions regarding data submission in RAVE, contact the data coordinators at the SWOG Statistics and Data Management Center (SDMC) via the email listed on the Protocol Contact Information page of the protocol

Questions?

QAmail@swog.org

Educational presentation hosted by the SWOG Quality Assurance Department

SWOG CANCER RESEARCH NETWORK

LIVE WEBINAR SERIES

CYTOGENETICS
Webinar Agenda:
Overview presentation followed by
Question & Answer + interactive discussion forum

Presented by:

- ***Kathleen Calzone, PhD, RN, AGN-BC, FAAN***

Upcoming 1 hour Webinar:
Friday, June 20, 2025
12:00pm – 1:00 pm Eastern Time

SWOG Spring Meeting 2025
Oishi Symposium & Open Forum
Evaluation Information

- This year the combined evaluation for Oishi and Open Forum are available via QR code and email link.
- Participants attending remotely will receive a link to the survey within one week of the meeting.
- In person attendees can scan the QR code to the right.

Oishi Symposium

welcomes

Christine Magner

“Cytogenetics Lightening Round”

Oishi Symposium
Poll Everywhere
Cytogenetics “Lightening Round”

Friday, May 2, 2025

8:00 am – 10:30 am

San Francisco, CA

SWOG CANCER RESEARCH NETWORK

NCI National Clinical Trials Network
a National Cancer Institute program

NCI Community Oncology Research Program
A program of the National Cancer Institute of the National Institutes of Health

In 1981, the number one song on the charts was “Bette Davis Eyes” by Kim Carnes. This was also when human genes were first mapped and fluorescently tagged probe was introduced. Thus was the beginning of...

A. Clinical Salmon
B. Clinical FISH
C. Clinical Phishing
D. Clinical Trout

Fred Hutch launched CGAT clinically in 2012. What does CGAT stand for?

A. Cats, Goats, Amphibians and Tortoises
B. Clinically Gotta Attain Testosterone
C. Chromosome Genomic Array Testing
D. Christine & Grayson Are Terrific!

SWOG's master protocol MyeloMATCH, is an umbrella trial that test treatments for AML and MDS, primarily using the magic of cytogenetics. What inspired the MyeloMATCH name?

A. Milo and Otis find love on MATCH.com
B. My Elmo doll from childhood just matched on e-bay for big bucks
C. Myeloma Makes A Terrible Costume Honestly
D. Myeloid Malignancies Molecular Analysis for Therapy Choice

Dr. Fang discussed the three Ps of her team's goal. Name them!

A. Paradigm shifting
B. Process changing
C. Policy setting
D. All of the above

Rose discussed the importance of correctly reporting results and interpreting the code. She showed a picture of Radio Orphan Annie's SS decoding ring, which, we all know Ralphie Parker feverishly used while he worked on decoding a secret message which wound up being a 'crummy commercial' urging kids to drink their ovaltine. Who was Ralphie's brother?

A. Roger

B. Richie

C. Ronnie

D. Randy

If you were “interpreting the [genomic] code” which system would you use?

A. Internal SytoCellular Name (ISCN)
B. International System for Cellular Nomenclature (ISCN)
C. Interpretation Synonyms for Cellular Nucleotides (ISCN)
D. International System for Human Cytogenomic Nomenclature (ISCN)

Several SWOG studies are using the power of genetic testing, including S1905, S1925, S2209 and S2114. When filling out forms, if you're unsure of what a field is wanting, what's the best course of action?

A. Reach out to Rose
B. Take your best shot and hope you don't get a query from the system or the Data Coordinator
C. Leave it blank and state in the Comments section at the bottom of the form that you weren't sure what to enter
D. Call or e-mail the Data Coordinator

About what percent of the 30 audits conducted by SWOG QA from 8/1/24 to 1/1/25 resulted in unacceptable for patient case?

A. <1%

B. 2%

C. 3%

D. 5%

Seriously though, of the following common abnormalities in chronic lymphocytic leukemia (CLL) which has a favorable prognosis?

A. Deletion 13q as the sole abnormality
B. Trisomy 12 (+12)
C. Deletion 11q (ATM)
D. Deletion 17 p

Specimens here, specimens there. Specimen collection on SWOG studies has really evolved. It's important to confirm what your patient has and hasn't consented to, what is required vs what is optional, when specimens need to be collected/shipped. Wouldn't it be great if there was one place that had this info? There is! It's the SWOG Specimen Tracking System on the CRA Workbench, where you can do the following:

A. Review/edit Pt consent answers

B. See all specimens for a study – Specimen Requirements Summary

C. Notify that Specimen Cannot be Submitted

D. All of the above

Can retired Site DTLs be reinitiated?

A. Yes, but they should check their benefits
B. Why would I want to do that?
C. I would like to retire
D. No, they should stay in retirement

Can Registration Study Audits be conducted remotely?

A. No, audits are on site always
B. Yes, unless in conjunction with a treatment audit or at the site's request

The symbols below are used for what purpose?

Symbols

[ ]	# of cells in a line, or metaphases
:	Chromosomal break
::	Chromosomal break and reunion or fusion
,	Separates chromosome #& abnormalities
-	Loss
X	Multiple copies or number of copies
( )	Surround altered chromosomes or genes
+	Additional chromosome
;	Separates altered chromosome or break
>	Substitution

Aberrations

add	Additional material attached to chromosome
del	Deletion or loss of chromosome material
dup	Part of a chromosome is repeated
der	Rearrangement involve ≥ 2 chromosomes or by multiple aberrations.
dic	1 chromosome replaces 2 normal ones.
ins	Addition of material in a chromosome
inv	Part of chromosome inverted
rec	Recombinant, due to meiotic crossing over
t	Exchanged material between 2 chromosomes

A. Why are you using Wingdings for this presentation?
B. That's R2D2's language
C. ISCN Nomenclature
D. Basic Excel functions

What is a “p-arm?”

A. An arm shaped like a “P”
B. A region of a chromosome
C. I prefer the “p-leg”
D. The arm after the “o-arm”

How have SWOG Audits been in the post-pandemic era?

A. Insane! People make the silliest mistakes!
B. Stable with improvement
C. Excellent, with a 20% decrease in major findings (Dr. B is so pleased!)
D. Educational: a 13% increase in Lesser findings indicating the need for more education.

SWOG QA finds which of the following major deficiencies more often:

A. Eligibility, Source Documents, Underreporting AEs
B. Delinquent Data submission, Overreporting AEs, Late Continuing Reviews
C. Tests/scans out of window, Late Reporting of SAEs, Delinquent data submission
D. Late amendments, Late SAEs, Late Continuing Reviews

SWOG QA is sponsoring a Live Webinar in June on what topic?

A. The life and times of Dr. Chuck Blanke
B. QA in the post-pandemic era
C. “The Tortuous Journey from Scientific Idea to Full Protocol in the NCI”
D. Cytogenetics

Bonus Question:
What was “Radio Orphan Annie”?

A. A Radio Show about Annabelle Lee
B. An adaptation of a comic strip from “the funny pages”
C. A Radio Show that aired from 1942-1945
D. A radio spokesperson trying to sell decoder rings

Oishi Symposium

Thank you for attending!

And see you in Chicago, IL
September 18-20, 2025